

Greater Brockman:

Subterranean Fauna Survey

Biologic Environmental Survey

Report to Rio Tinto Iron Ore

March 2022

GREATER BROCKMAN

SUBTERRANEAN FAUNA SURVEY

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GLOSSARY

AWT	Above Water Table
BC Act	*Western Australian Biodiversity Conservation Act 2016*
BGCK	Boolgeeda Creek reference area
BoM	Bureau of Meteorology
BS1	Brockman Syncline 1 section
BS2	Brockman Syncline 2 section
BS3	Brockman Syncline 3 section
BS4	Brockman Syncline 4 section (includes Vivash and BGCK)
BWT	Below Water Table
BrIF	Brockman Iron Formation
cf.	In taxonomy, cf. refers to a species that closely matches the species following the designation, but differs morphologically in some minor ways
COI	Cytochrome Oxidase subunit 1, a gene used as a DNA barcode to identify species
DBCA	Department Biodiversity, Conservation and Attractions
EPA	Western Australian Environmental Protection Authority
EP Act	*Environmental Protection Act 1986*
EPBC Act	*Environment Protection and Biodiversity Conservation Act 1999*
HSTD	Homestead
mbgl	Metres below ground level
MMIF	Marra Mamba Iron Formation
nr	In taxonomy, nr refers to a potentially undescribed species nearest to the species following the designation
OTU	Operational taxonomic unit – species-equivalent taxonomic unit based on COI or 12S cluster similarity
PEC	Priority Ecological Communities
SGCCK	Silvergrass and Caves Creek area
SGW	Silvergrass West
SRE	Short-range Endemism
TEC	Threatened Ecological Communities
VIV	Vivash reference area
WAM	Western Australian Museum

EXECUTIVE SUMMARY

Rio Tinto Iron Ore Pty Ltd (Rio Tinto) owns and operates the Brockman 2/ Greater Nammuldi (B2NAM) Sustaining Project and the Brockman Syncline 4 (BS4) Sustaining Tonnes Project, collectively termed the Greater Brockman Project, located approximately 60 kilometres (km) north-west of the town of Tom Price in Western Australia's Pilbara region. An Order of Magnitude Study (OoM Study) has commenced to evaluate the potential development of several iron ore deposits and associated infrastructure within the Greater Brockman locality.

Biologic Environmental Survey Pty Ltd (Biologic) was commissioned to undertake a two-phase Level 2 subterranean fauna (stygofauna and troglofauna) survey within the Proposed Development Envelope for the Greater Brockman Project (the Study Area). The Level 2 survey was followed by a three-phase targeted survey. Due to the large size of the Study Area (covering approximately 64,100 hectares), the sampling effort was split across four sections, namely Brockman Syncline 1 (BS1), Brockman Syncline 2 (BS2), Brockman Syncline 3 (BS3), and Brockman Syncline 4 (BS4). The survey was designed and conducted in accordance with relevant EPA guidelines for subterranean fauna assessment, aiming to provide a comprehensive assessment of subterranean species and habitats occurring within the Study Area and surrounding reference areas. This report also aims to provide discussion on species distributions throughout the Study Area and the wider local/ regional area, and conservation significance to inform future Environmental Impact Assessment.

Comprehensive searches of relevant fauna databases (WA Museum records and Department of Biodiversity, Conservation and Attractions' Pilbara Stygofauna Survey data), and records from previous survey data revealed 45 troglofauna and 44 stygofauna occurring within a 45 km wide search area surrounding the Study Area, of which 23 troglofauna and 23 stygofauna were recorded inside the Study Area.

The current survey sampled 683 sites throughout the Study Area, resulting in a total of 1,468 subterranean fauna samples. The sampling methods comprised troglofauna litter trapping (401 samples), troglofauna scraping (701 samples), stygofauna net hauling (338 samples) and Karaman sampling (28 samples). The survey timing was concurrent between BS2 and BS3 sections (phase 1 dry season Oct 2018 – Dec 2018, and phase 2 wet season Apr 2019 – June 2019), while sampling at BS1 and BS4 was offset from this by approximately 6 months (Phase 1 wet season Apr 2019 – June 2019, and phase 2 dry season late June 2016 – Aug 2019). The targeted survey sampled selected sites within BS1, BS3 and BS4 sections and was undertaken in October 2020 (dry season), February 2021 (wet season), and August 2021 (dry season).

A total of 3,373 subterranean fauna specimens were collected, comprising 799 troglofauna and 2,574 stygofauna specimens. Using morphological and genetic (DNA barcoding) methods, 124 troglofauna species/ Operational Taxonomic Units (OTUs) were identified comprising spiders, palpigrades, pseudoscorpions, schizomids, scorpions, isopods, centipedes, pauropods, millipedes, symphylans, diplurans, cockroaches, beetles, polyxenids, hemipteran bugs, and silverfish. A total of 56 stygofauna species/ OTUs were identified, comprising oligochaete worms, water mites, ostracods, cyclopoid copepods, syncarids (bathynellaceans), calanoids, amphipods, and isopods. In combination with previous records, a total of 164 troglofauna species/ OTUs and 76 stygofauna species/ OTUs are known to occur within or immediately near the Study Area.

Assessment of the extent, thickness, and connectivity of subterranean habitats above and below water table (AWT/BWT) was undertaken based on available geological and hydrogeological information, and three-dimensional habitat models were developed from drill logging and diamond core data throughout key areas of the Study Area. The habitat modelling revealed a multitude of generally well connected AWT/BWT habitats throughout the Study Area, with thickness varying due to local geological, hydrogeological, and structural factors. Local habitat factors were taken into consideration in the assessment of wider potential distributions of the species/OTUs detected.

The high overall diversity of stygofauna and troglofauna species collected reflected the size and complexity of subterranean habitats present. Species turnover throughout the Study Area was evident within many of the fauna groups, likely due to geographical distance and habitat heterogeneity, although many taxa were also locally widespread throughout connected and apparently disconnected habitats.

Species accumulation modelling showed that the overall troglofauna species accumulation curve reached a plateau after approximately 1000 samples, suggesting that the survey captured a significant proportion of troglofauna species richness at Greater Brockman on a regional scale. Nevertheless, when broken down into the four sampling areas, none of the troglofauna curves and few of the stygofauna curves appear to be asymptotic. This is not unusual for subterranean fauna surveys, and the survey adequacy statistics for each sampling area compared favourably to previous similar surveys in the local area and in the region, providing confidence in the combined survey results to date.

As is commonly found throughout the region, the combined troglofauna results revealed few regionally or locally widespread species/OTUs, and higher proportions of taxa detected from single sites or from small spatial areas (95 OTUs), specifically:

- Arachnida (25 OTUs)
- Isopoda (7 OTUs)
- Myriapoda (29 OTUs)
- Diplura (15 OTUs)
- Insecta (19 OTUs)

Conversely, approximately half of the 76 stygofauna species/ OTUs collected within the Study Area were found to be regionally or locally widespread, while 38 stygofauna species/ OTUs were detected only from single sites, or localised spatial areas:

- Oligochaeta (7 OTUs)
- Acari (2 OTUs)
- Ostracoda (3 OTUs)
- Isopoda (1 OTU)
- Copepoda (4 OTUs)
- Bathynellacea (13 OTUs)
- Amphipoda (8 OTUs)

Although some of the above subterranean species/ OTUs may represent highly restricted troglobitic/ stygobitic taxa, the assessment of potential distributions and significance for future environmental impact assessment (EIA) placed these results within the context of available regional comparisons, the current state of taxonomic and ecological knowledge, regional precedent from published literature and other similar assessments, and local habitat extent/ connectivity.

1. INTRODUCTION

1.1 Background

Rio Tinto Iron Ore Pty Ltd (Rio Tinto) owns and operates the Brockman 2 / Greater Nammuldi (B2NAM) Sustaining Project and the Brockman Syncline 4 (BS4) Sustaining Tonnes Project, collectively termed the Brockman Syncline Proposal (BSP). The Greater Brockman Project is located within the Hamersley subregion, approximately 60 kilometres (km) north-west of the town of Tom Price in the Pilbara region of Western Australia (Figure 1.1).

A study has commenced to evaluate the potential development of several iron ore deposits within the Greater Brockman locality, including associated infrastructure. This project requires environmental approvals prior to further development.

Rio Tinto has commissioned Biologic Environmental Survey Pty Ltd (Biologic) to undertake a two-phase Level 2 subterranean fauna (stygofauna and troglofauna) survey within the BSP. The survey focused on four key areas within the Proposed Development Envelope (approximately 64,100 hectares), hereafter collectively referred to as the Study Area (Figure 1.2). The survey was designed and conducted in accordance with relevant EPA guidelines for subterranean fauna assessments (EPA, 2016a, 2016b, 2016c).

This report provides:

- a desktop review of all previous subterranean fauna records from surveys in the vicinity of the Study Area and existing subterranean fauna databases at the local/ sub-regional scale;
- results of a two-phase Level 2 stygofauna and troglofauna survey throughout the Study Area and wider local area, including morphological and molecular identifications of fauna collected;
- results of a three-phase targeted survey throughout the Study Area (primarily targeting stygofauna), including morphological and molecular identifications of fauna collected;
- an assessment of the suitability and extent of subterranean habitats within the Study Area and their potential wider connectivity throughout and beyond the Study Area, based on available geological and hydrogeological information and three-dimensional (3D) habitat modelling;
- assessment of the local occurrence and potentially wider distribution of all stygofauna and troglofauna species collected relative to key subterranean habitats, and
- a discussion of the conservation status of all subterranean species detected with reference to regional taxonomic comparisons and the most up-to-date ecological information.

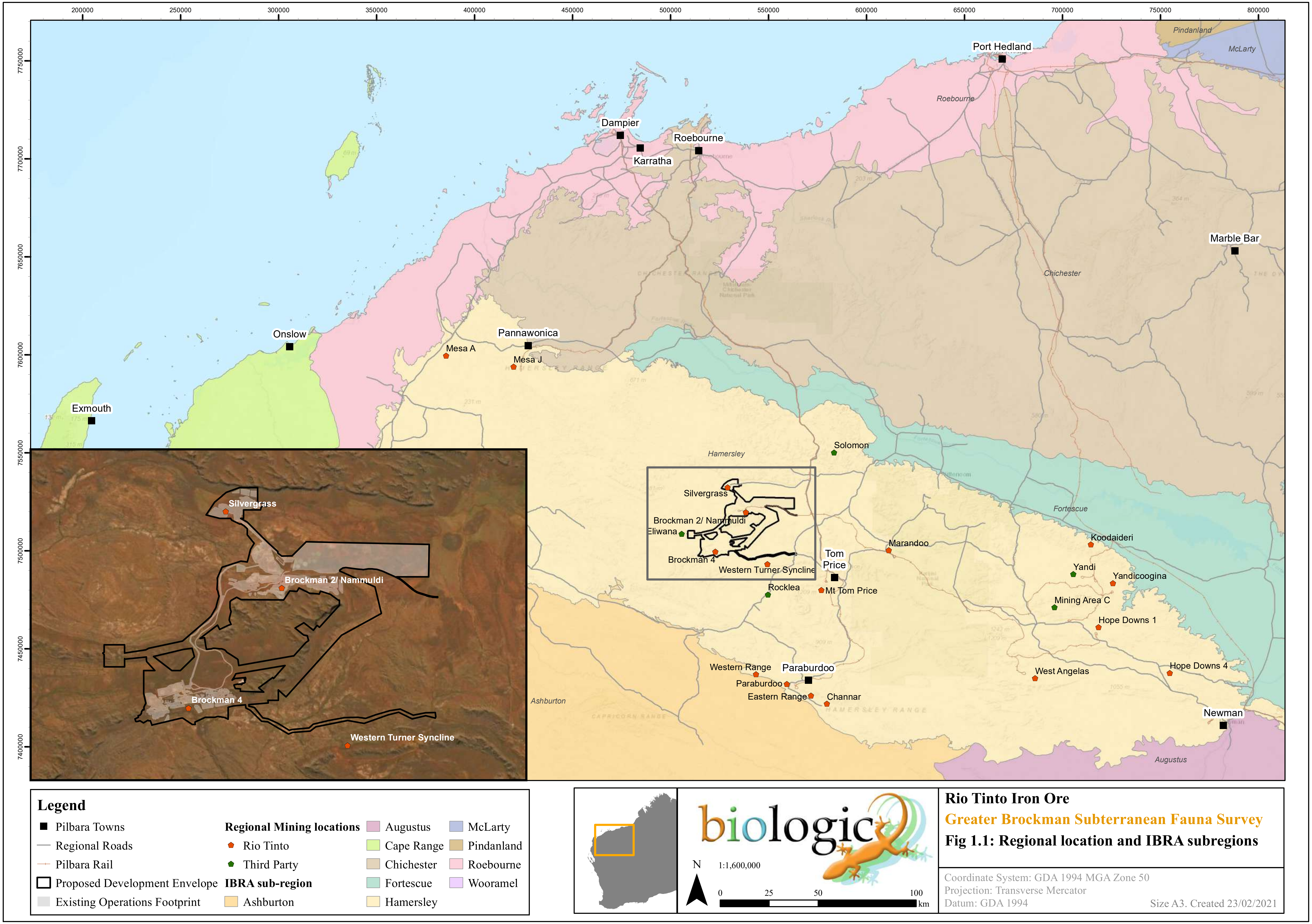

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Fig 1.1: Regional location and IBRA subregions

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

Size A3. Created 23/02/2021

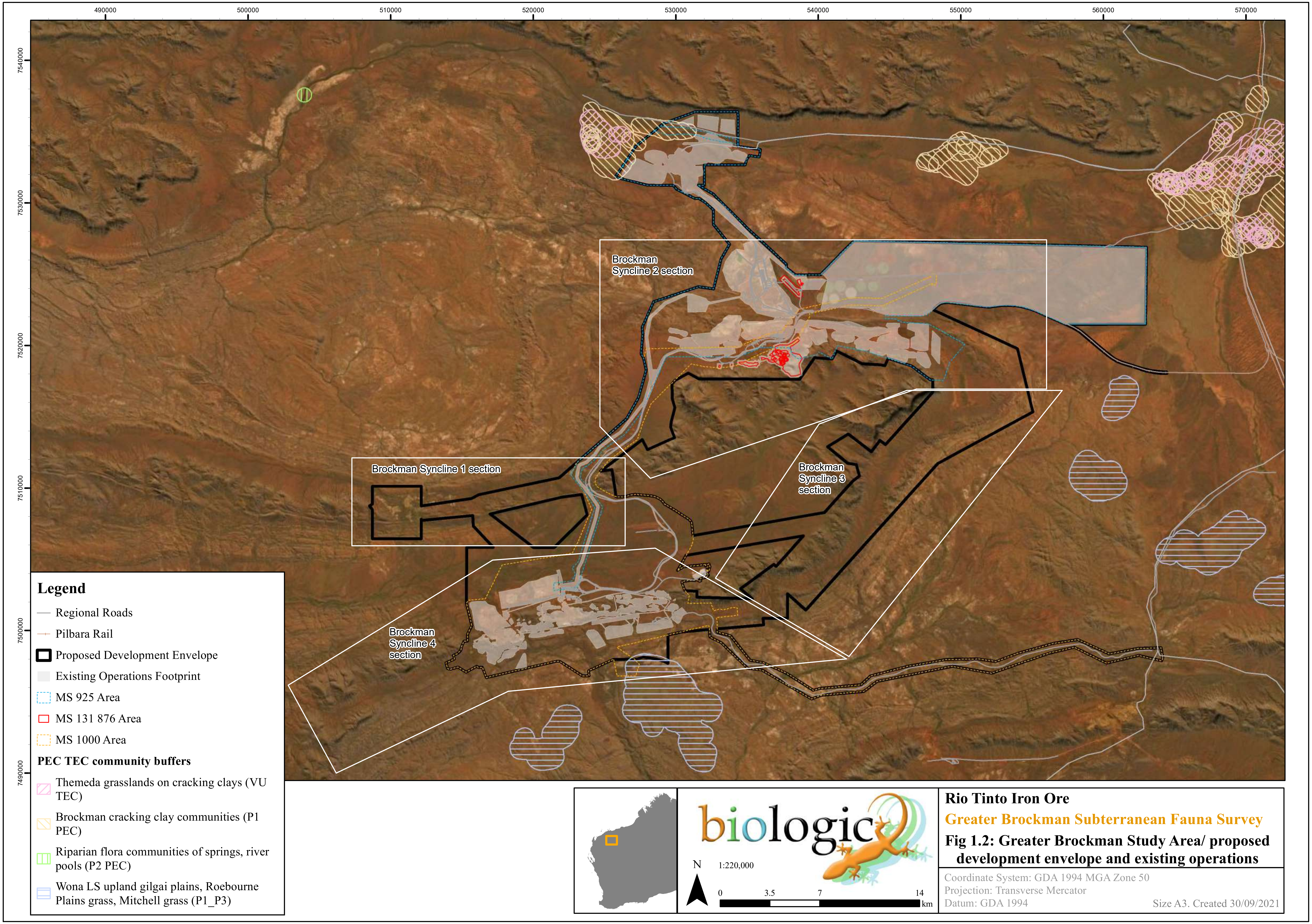

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Fig 1.2: Greater Brockman Study Area/ proposed development envelope and existing operations

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994
Size A3. Created 30/09/2021

1.2 Project Summary

The BSP is a proposed revision and overarching modernisation to three existing operations, namely:

- Brockman Syncline 2 (BS2) – authorised under Ministerial Statement (MS) 131 and MS 867.
- Brockman Syncline 4 (BS4) – authorised under MS 1000.
- Nammuldi-Silvergrass – authorised under MS 925.

The Proposal includes:

- The development of new above water table (AWT) and below water table (BWT) mining areas and associated infrastructure, including:
    - Extension of existing pits at BS4 to support BWT mining.
    - Development of new AWT and BWT pits at BS4.
    - Development of new AWT and BWT pits at Brockman Syncline 3 (BS3).
    - Development of new AWT and BWT pits at Brockman Syncline 1 (BS1)
    - Development of new AWT and BWT pits at BS2.
- Activities required to facilitate development of new mine pits.

No additional mining activities are planned at Silvergrass East (SGE) beyond those already approved under MS 925. SGE will however form part of the consolidated BSP revised MS.

1.3 Study Area

The Survey evaluated stygofauna and troglofauna in relation to several potential mineral deposits BWT and AWT within four key areas of the Study Area (the survey areas are shown in Figure 1.2):

- Brockman Syncline 1 section (BS1);
- Brockman Syncline 2 section (BS2);
- Brockman Syncline 3 section (BS3); and
- Brockman Syncline 4 section (BS4 - includes Vivash and Boolgeeda Creek reference sites).

1.4 Legislation and Guidance

Western Australia’s subterranean fauna is considered globally significant due to an unprecedented richness of species and high levels of short-range endemism (EPA, 2016c). The EPA’s environmental objective for subterranean fauna is to “protect subterranean fauna so that biological diversity and ecological integrity are maintained” (EPA, 2016a, p2). In this context, the EPA defines ecological integrity as “the composition, structure, function and processes of ecosystems, and the natural range of variation of these elements” (EPA, 2016a, p2).

Protection for conservation significant subterranean fauna species and/ or Threatened or Priority Ecological Communities (TECs and PECs) is provided under State and Federal legislation, comprising:

- *Environmental Protection Act 1986* (*EP Act 1986*) (WA);
- *Biodiversity Conservation Act 2016* (*BC Act 2016*) (WA); and
- *Environment Protection and Biodiversity Conservation Act 1999* (*EPBC Act 1999*) (Commonwealth).

Most subterranean fauna species and assemblages are not listed under these Acts, due to incomplete taxonomic or ecological knowledge. Consideration of range-restricted subterranean fauna is therefore also important, including species that only occur within restricted habitats, as these have a higher potential of being Short-Range Endemic (SRE) species (Eberhard *et al.*, 2009; Harvey, 2002).

This assessment has been undertaken in consideration of the following EPA guidance statements:

- EPA (2016a) Environmental Factor Guideline Subterranean Fauna; and
- EPA (2021) Technical Guidance - Subterranean Fauna Surveys for Environmental Impact Assessment.

1.4.1 Priority and Threatened Ecological Communities

Three Priority Ecological Communities (PECs) and one Threatened Ecological Community (TEC) occur within or in the vicinity of the Study Area (Figure 1.2, Table 1.1). None of these TECs/PECs are relevant to subterranean fauna and are therefore not further considered herein.

Table 1.1: Priority and Threatened Ecological Communities within and near the Study Area

Name	Description
PECs	
Brockman Iron cracking clay communities of the Hamersley Range	Rare tussock grassland dominated by *Astrebla lappacea* (not every site has presence of *Astrebla*) in the Hamersley Range, on the Brockman land system. Tussock grassland on cracking clays - derived in valley floors, depositional floors.
Riparian flora and plant communities of springs and river pools with high water permanence of the Pilbara region	The community includes flora with restricted distributions or populations that are highly disjunct or are major range extensions from northern and eastern Australia. These include: *Imperata cylindrica*, *Cladium procerum*, *Schoenus falcatus* and *Fimbristylis sieberiana*. In the Pilbara these taxa are almost exclusively restricted to the riparian zones of permanent wetlands with high soil moisture maintained by groundwater flows. Occurrences are disjunct with sites typically associated with groundwater discharge in gorge and valley wetlands that are often coupled with significant shading.
Wona Land System Basalt upland gilgai plains supporting Roebourne Plains grass and Mitchell grass tussock grasslands, minor hard spinifex grasslands or annual grasslands / herbfields	Potential Priority 1 or 3 PEC (no spatial data has been defined by the Department of Biodiversity, Conservation and Attractions (DBCA). The dataset was obtained from the Department of Agriculture.

Name	Description
TECs	
Themeda grasslands on cracking clays (Hamersley Station, Pilbara)	Grassland plains which are dominated by the perennial *Themeda* (Kangaroo Grass) and many annual herbs and grasses. It is currently classified as Vulnerable.

1.5 Subterranean Fauna

Subterranean fauna are animals that live underground. In Western Australia, subterranean fauna are mainly invertebrates such as crustaceans, insects, arachnids, myriapods, worms, and snails, but a small number of vertebrate taxa such as fish and reptiles have also been found (EPA, 2013; Humphreys, 1999). Subterranean fauna are grouped into two major ecological categories:

- stygofauna - aquatic animals that inhabit groundwater in caves, aquifers, and water-saturated interstitial voids; and
- troglofauna - air-breathing animals that inhabit air-filled caves and smaller voids above the water table.

Nevertheless, there are some taxa which cross-over between these categories and are known to occur in groundwater as well as air-filled subterranean habitats (*e.g.* enchytraeid worms), and yet other species that occur within subterranean habitats for only part of their lifecycles (stygoxenes/ stygophiles, and trogloxenes/ troglophiles respectively).

Following EPA (EPA, 2016c) guidelines, obligate subterranean fauna (known respectively as stygobites and troglobites) are defined as species that live their entire lives underground and are completely dependent upon, or restricted to, subterranean habitats. Such species are considered to have a high likelihood of being limited to very narrow ranges (*i.e.* short-range endemic (SRE) species). SRE species, as described by (Harvey, 2002), are species whose natural ranges are limited to <10,000 km^2 (or <100 km × 100 km), whereas Eberhard *et al.* (2009) regarded even this criterion as potentially too vast for range-restricted subterranean fauna, offering an alternative threshold of <1,000 km^2 for subterranean SRE species.

Troglobites and stygobites often display evolutionary adaptations to underground life; these include features such as reduced pigment, reduced or vestigial wings, reduced cuticle thickness, elongation of sensory appendages, and reduced eyes or eyelessness. Additional adaptations to underground life can include changes to physiology, lifecycle, metabolism, feeding and behaviour (Christiansen, 2005; Gibert & Deharveng, 2002).

As the darkness of hypogean environments precludes photosynthesis, subterranean ecosystems are generally dependent upon allochthonous inputs of nutrients and oxygen from the surface (except in cases where chemo-autotrophic bacteria are present) (Blatnik *et al.*, 2020; Hahn, 2009). Energy and nutrients are generally transported into subterranean ecosystems by the infiltration of water, particularly via the roots of groundwater dependent vegetation (Howarth, 1983; Humphreys, 2006; Malard & Hervant, 1999; Poulson & Lavoie, 2000). Thus, the porosity (or otherwise) of the overlying geologies, the distance from the surface, and the presence/absence of caves or fissures that can provide a conduit for water and nutrients are important physical features that influence the suitability of underground habitats for subterranean fauna (Hahn & Fuchs, 2009; Strayer, 1994). Groundwater physicochemistry (including salinity, pH, dissolved oxygen and redox potential) is also an important determinant of habitat suitability for stygofauna (Eberhard *et al.*, 2009; Hahn, 2009; Humphreys, 2008; Saccò *et al.*, 2020a; Watts & Humphreys, 2004).

2. ENVIRONMENT

2.1 Biogeography

The Study Area is located within the Pilbara bioregion (Figure 1.1), as defined by the Interim Biogeographic Regionalisation of Australia (IBRA; Thackway & Cresswell, 1995). The Pilbara bioregion is characterised by vast coastal plains and inland mountain ranges with cliffs and deep gorges (Thackway & Cresswell, 1995). Vegetation is predominantly mulga low woodlands or snappy gum over bunch and hummock grasses (Bastin, 2008). Within the Pilbara bioregion, the Study Area is located within the Hamersley (PIL 3) subregion. The Hamersley subregion is characterised by mountainous areas of Proterozoic sedimentary ranges (ironstone ranges) and plateaux dissected by gullies and gorges (Kendrick, 2001). Mulga low woodland over bunch grasses on fine-textured soils dominates in valley floors, while on the skeletal soils of the ranges snappy gum (*Eucalyptus leucophloia*) over *Triodia brizoides* predominates (Kendrick, 2001). Drainage is typically into either the Fortescue River to the north, the Ashburton River to the south, or the Robe River to the west (Kendrick, 2001).

2.2 Climate

The Pilbara bioregion has a semi-desert to tropical climate, with rainfall occurring sporadically throughout the year, although mostly during summer (Thackway & Cresswell, 1995). Summer rainfall is usually the result of tropical storms in the north or tropical cyclones that impact upon the coast and move inland (Leighton, 2004). The winter rainfall is generally lighter and is the result of cold fronts moving north easterly across the state (Leighton, 2004). The average annual rainfall ranges from 200-350 mm, although there are significant fluctuations between years (BoM, 2021), with some locations receiving up to 1,200 mm in some years (McKenzie *et al.*, 2009).

Long-term climatic data is not available for the Study Area itself; however, long term climatic data is available from the Bureau of Meteorology (BoM) weather station at Paraburdoo Airport (Station 007185), located approximately 80 km south of the Study Area (BoM, 2021). The Paraburdoo Airport weather station is expected to provide the most accurate long-term average (LTA) dataset for climatic conditions experienced within the Study Area (Figure 2.1).

The sub-regional area experiences a wide range of temperatures throughout the year, with an average temperature range between 18.3 °C and 33.6 °C. However, extreme temperatures may vary significantly from the monthly averages. The maximum recorded diurnal temperature between 1996 and 2021 was 47.8 °C, while the minimum recorded overnight temperature was 1.3 °C (BoM, 2021). Rainfall is also highly variable throughout the year due to the influence of tropical storms and cyclones. Average annual rainfall is 314.4 mm, with most rainfall received between December and April (Figure 2.1).

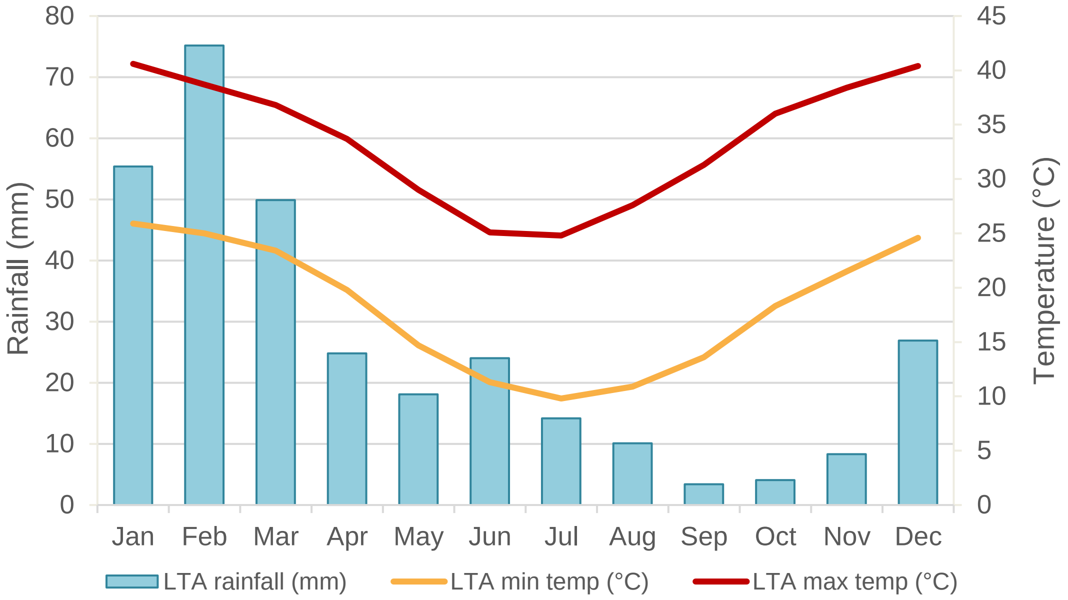

Figure 2.1: Long-term monthly average rainfall and temperature at Paraburdoo Airport (BoM 2019)

2.3 Topography and Landforms

The dominant topographical feature within the Study Area is the Brockman Syncline which strikes from east to west. The Brockman Ranges are formed from the steep outer rim of the Brockman Syncline, while the centre of the syncline hosts a heavily eroded broad valley associated with Boolgeeda Creek (Figure 2.2). The Brockman Ranges are incised in many places by a series of steep gullies and gorges (Figure 2.2). The highest elevations in these mountainous areas reach over 1,127 m (Mount Brockman), and downslope to foot slope gradients are very steep.

The Brockman Syncline hosts all four survey areas. Brockman Syncline 1 and Brockman Syncline 2 occur along the northern lower flanks of the Brockman Ranges, whereas the Brockman Syncline 3 and Brockman Syncline 4 (including Vivash and Bolgeeda Creek) areas occur along the southern lower flanks of the ranges, encircling the Brockman Syncline (Figure 2.2). A large central alluvial plain is located immediately north of the Brockman Syncline. The landscape then rises to a series of low, heavily eroded undulating hills and breakaways (associated with outcrops of the Marra Mamba Iron Formation), before descending onto a relatively flat alluvial valley hosting Caves Creek (Figure 2.2). This pattern is mirrored in the south descending from the Brockman Ranges, although the initial alluvial valley and the subsequent low hills are narrower formations than their northern counterparts (Figure 2.2).

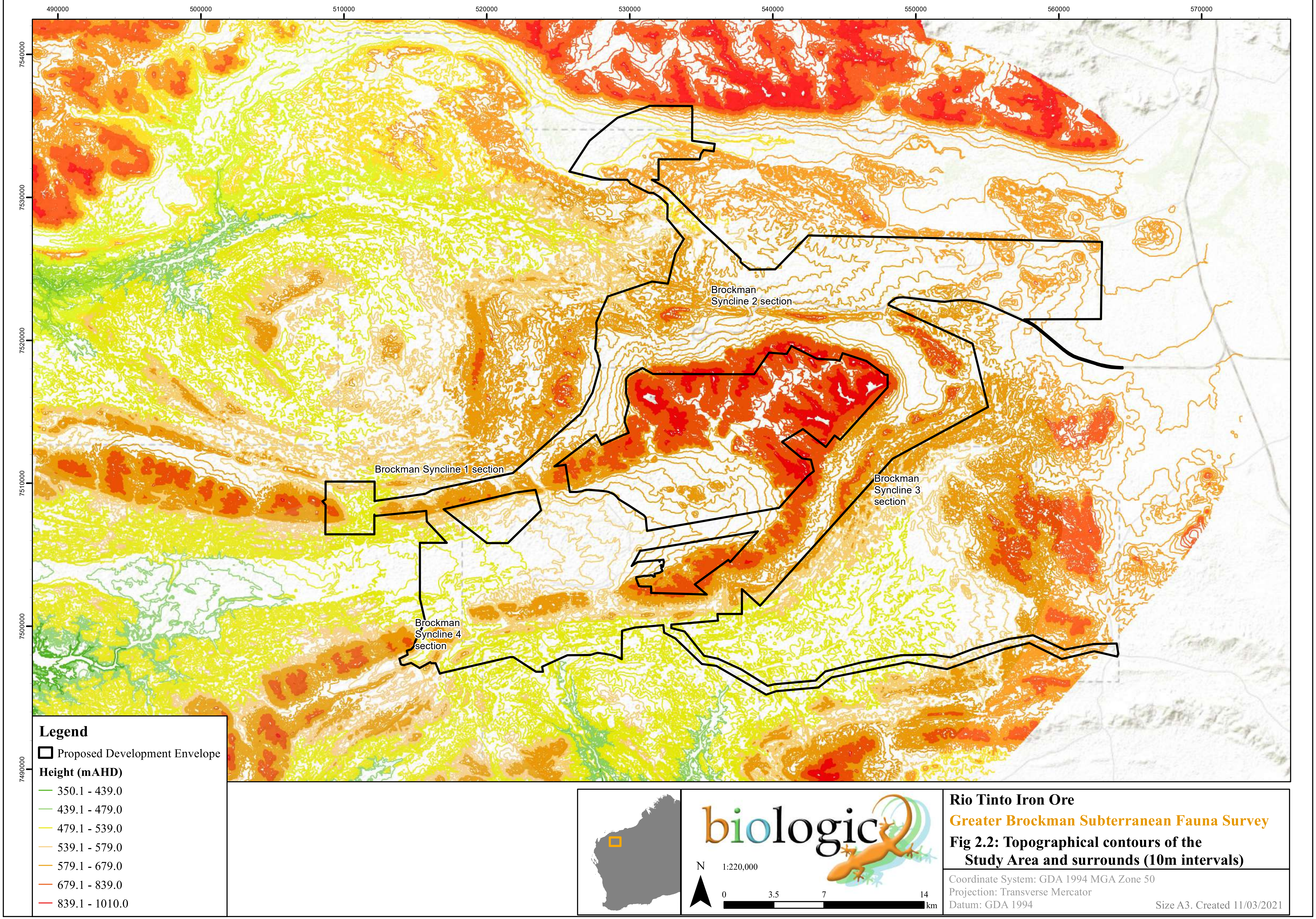

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Fig 2.2: Topographical contours of the Study Area and surrounds (10m intervals)

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

Size A3. Created 11/03/2021

2.4 Surface drainage and indicative catchments

The Study Area occurs within four sub-catchments that comprise part of the upper reaches of the Ashburton River catchment. The upper Duck Creek sub-catchment occupying the central part of the Jeerinah Anticline, and the Caves Creek sub-catchment in the north of the Study Area; merge to the west of the Study Area to form Duck Creek (Rio Tinto, 2010) (Figure 2.3). The Boolgeeda Creek sub-catchment drains the centre of the Brockman Syncline, flowing south-westward in the vicinity of the Study Area before turning north-westward to merge with Duck Creek, which ultimately drains into the Ashburton River at the western edge of the Hamersley Ranges (~120 km west of the Study Area).

In the south-east of the Study Area, the Beasley River sub-catchment drains south-westwards into the Hardey River (Figure 2.3), which flows in a north-west direction and subsequently joins the Ashburton River south of Duck Creek. Bordering the Study Area to the north, east, and south of the Jeerinah Anticline are other sub-catchments draining into the Robe River, Caliwinga Creek/ Weelumurra Creek (Lower Fortescue catchment), and upper Hardey River (Ashburton catchment) (Figure 2.3).

The Duck Creek catchment represents the largest regional catchment within the Study Area and covers an area of approximately 3,110 km^2 (Strategen, 2012). Duck Creek has a well-defined channel and features several permanent pools and numerous waterholes (Rio Tinto, 2011). Caves Creek and Boolgeeda Creek are both major tributaries of the Duck Creek system (Figure 2.3).

The Caves Creek catchment spans approximately 1,500 km^2 (Strategen, 2012) and is bounded by a steep range of Brockman Iron Formation (BrIF) to the north, and a low-lying ridge of Marra Mamba Iron Formation (MMIF) to the south (Figures 2.2 & 2.3). The low-flow drainage channel in Caves Creek is poorly defined with minor braiding, but features several permanent and semi-permanent water holes and pools, including Palm Springs (Rio Tinto, 2010). Significant rainfall events can generate high velocity runoff within Caves Creek, owing to the steep topography to the north and south (Rio Tinto, 2010).

The Boolgeeda Creek catchment covers an area of approximately 1,650 km^2, although its extent within the Study Area is mainly characterised by a broad, braided, meandering watercourse dominated by multiple active and inactive channels (Rio Tinto, 2014b). The Boolgeeda Creek system is typically much drier than Duck Creek or Caves Creek, and features only transient pools following rainfall events rather than permanent or semi-permanent groundwater-fed pools (Rio Tinto, 2014b).

The Beasley River flows in a south-westerly direction parallel to the southern flank of the Brockman Range before discharging into the Hardey River (Figure 2.3). The Beasley River system is also largely ephemeral and features only semi-permanent and transient pools following decent rainfall events.

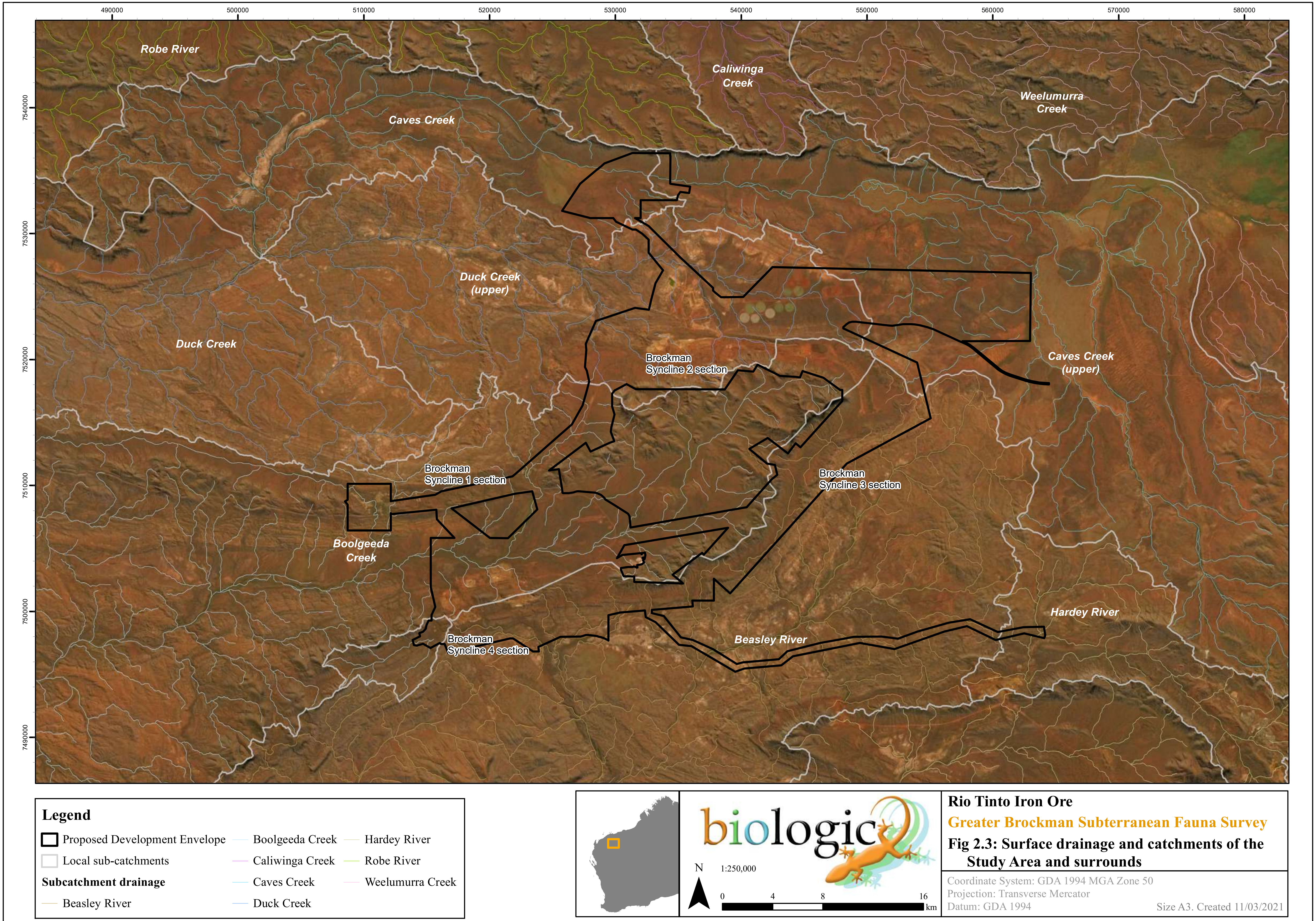

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Fig 2.3: Surface drainage and catchments of the Study Area and surrounds

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994
Size A3. Created 11/03/2021

2.5 Geology

The surface geology of the Greater Brockman Study Area is shown in Figure 2.4, based on GSWA mapping at 1:250,000. Table 2.1 shows a generalised stratigraphy of the major Brockman Syncline geological units occurring within the Study Area, with notes relating to subterranean fauna habitat suitability, based on regional knowledge.

The east-west striking Brockman Syncline, formed largely in Brockman Iron Formation (BIF), dominates the local stratigraphy of the Greater Brockman area and hosts the survey areas (Figure 2.4). Hematite-goethite-martite enriched zones occur on the flanks of the Brockman Syncline as pisolitic duricrust or hardcap due to secondary weathering processes (Figure 2.4). The lower slopes of the Brockman Syncline are covered in superficial, unconsolidated deposits of colluvium/ alluvium (detrital layers). A band of Marra Mamba Iron Formation outcropping (BIF, chert, mudstone/siltstone) surrounds the Brockman ranges (Figure 2.4). These extensive geological units encircling the Brockman Syncline (Brockman and Marra Mamba Iron Formations, alluvial and colluvial detritals) are known to support subterranean fauna in the region (Table 2.1, depending upon the degree of cavities, weathering, and enrichment). Geological mapping suggests that these prospective subterranean fauna habitats form potentially connected networks of suitable habitat along the Brockman Syncline, though some compartmentalisation may exist due to north-west striking dykes which are numerous in the area (Figure 2.4).

Deep deposits of alluvium, colluvium, Robe Pisolite (also known as Channel Iron Deposits, CID) and carbonate-rich calcrete and dolomite deposits can be found along the alluvial valleys (Figure 2.4). All these geological units are known to support subterranean fauna and typically extend outside of the Study Area (Figure 2.4). The Wittenoom Formation occurs at greater depths below the colluvium and comprises the highly porous Paraburdoo Member which is known to support subterranean fauna in the region, and the less porous West Angela Member. Below the Wittenoom Formation lies the highly porous Mt Newman Member of the Marra Mamba Iron Formation which is also known to support subterranean fauna in the region (Figure 2.4).

A large central alluvial plain occurs to the north of the Brockman Syncline. This wide central valley is formed in Jeerinah and Bunjinah Formation volcanic sequences which have been extensively overlain by quaternary sediments in the central and eastern parts (Figure 2.4).

Table 2.1: Stratigraphy of Greater Brockman and generalised suitability for subterranean fauna

Unit			Description	Generalised suitability for subterranean fauna AWT/ BWT
Detrital layers (alluvium/ colluvium)			Cainozoic and Quaternary age superficial deposits (scree, gravel, sand, silt, clay) occur over extensive areas at Greater Brockman, mainly associated with lower flanks of ranges, valleys, and drainage lines. Calcrete, silcrete, and CID can be common along drainage lines and buried within valley sediments.	Known to support subterranean fauna (especially stygofauna in unconsolidated alluvium associated with drainage lines) throughout the region. Suitability varies depending upon degree of weathering, consolidation, particle size, depth of groundwater, and presence of secondary deposits such as calcrete/ CID/ unconsolidated sediments.
Channel Iron Deposits (CID)			Secondarily weathered deposits of Robe Pisolite unaltered hematite-goethite pisoliths occur mainly along drainage lines at Greater Brockman, such as Boolgeeda Creek, Beasley River and Caves Creek. Thickness is highly variable and dependent on associated beds and exposure/ erosion.	Known to support subterranean fauna (stygofauna and troglofauna) throughout the region.
Wyloo Group and Shingle Creek Group			The upper layers (Wyloo Group) comprise of sandstone, mudstone, conglomerate, banded iron formation and chert. The lower layers (Shingle Creek Group) comprise fine to coarse grained sandstone, metasandstone and metabasalt.	May have some potential to support subterranean fauna, dependent on availability of vugs, cavities, fractures, or void spaces in dolomite and calcrete.
Dolerite Dykes			The structural geology of much of Greater Brockman is dominated by faulting, many of which have been intruded by dolerites. Most dykes strike from north-west to south-east.	Potential barrier to subterranean fauna species dispersal.
Turee Creek				
Kungarra Formation			Small outcrops occur along Boolgeeda Creek. Consists of ~1600 m of predominantly fine-grained sandstone, siltstone and mudstone.	Unknown/ uncertain.
Hamersley Group				
Boolgeeda Formation			Consists of deep to shallow iron-rich sedimentary successions (BIF). Minor amounts of chert, Jaspilite, siltstone and shale are also present. Within the Study Area, it occurs along Boolgeeda Creek.	Unknown/ uncertain.
Woongarra Formation			Outcrop features of Woongarra Rhyolite and dacite volcanics (lavas, pyroclastic rocks and BIF) occur along Boolgeeda Creek.	Unknown/ uncertain.
Weeli Wolli Formation (HJ)			Comprises a sequence of BIF units (commonly jaspilitic), separated by shale and siltstone bands. Commonly interlayered by metadoleritic sills. Within the Study Area, it mainly occurs along Boolgeeda Creek.	May have some potential to support subterranean fauna, dependent on the degree of cavities/ weathering/ enrichment and proportions of shale to BIF/dolomite.
Brockman Iron Formation (HB)	Yandicoogina Shale Member (BY)		Consists of interbedded chert and shale bands which have been intruded by a number of dolerite sills. It is 40 to 60 m thick and is commonly mineralised.	May have some potential to support subterranean fauna, dependent on the degree of cavities/ weathering/ enrichment and proportions of shale to BIF/chert.
	Joffre Member (BJ)	Unit 6 (J6)	Thickest member of the Brockman Iron Formation (up to 250 m thick when unmineralized). Consists of BIF and shale bands; however, the shale	Known to support subterranean fauna throughout the region. Suitability varies depending upon the degree of cavities/
		Unit 5 (J5)		

Unit			Description	Generalised suitability for subterranean fauna AWT/ BWT
		Unit 4 (J4)	bands are generally discontinuous. The Joffre Member has an informal subdivision into six strands (J1 to J6), with the 'odd' strands (J1, J3 and J5) being relatively shale rich and the 'even' strands (J2, J4 and J6) being relatively shale poor.	weathering/ enrichment and the proportions of shale to BIF/ chert. Shale bands are expected to be relatively impermeable (except where faulted) and may act as barrier to dispersal. Dolerite sills occurring throughout the J3 band may form a potential barrier for subterranean species.
		Unit 3 (J3)		
		Unit 2 (J2)		
		Unit 1 (J1)		
	Whaleback Shale Member (BW)	WS2	Approximately 50 m thick. Comprises interbedded chert and shale bands, and some very minor BIF bands. Subdivided from the base into Whaleback Shale 1 (WS1) and Whaleback Shale 2 (WS2). WS1 consists of two thick shale bands and a lower thin chert rich BIF and a thick (2-3 m) BIF band. WS2 consists of interbedded shale and chert bands.	May have some potential to support subterranean fauna, dependent on the degree of cavities/ weathering/ enrichment and proportions of shale to BIF/chert.
		WS1		
	Dales Gorge Member (BD)		Approximately 142 m thick. Comprises 16 interbedded BIF and shale bands which have been labelled B0 to B16 and S0 to S16 respectively.	Known to support subterranean fauna assemblages throughout the region. Suitability varies depending upon the degree of cavities/ weathering/ enrichment and the proportions of shale to BIF/ chert.
Mount McRae Shale Formation (HR)			50 to 60 m thick shale sequence comprising two main strands, the lower shale rich (pyrite rich black shale when fresh) zone and the upper Colonial Chert Member (referred to as the Foot Wall Zone). Occurs throughout Greater Brockman, mainly in association with lower flanks of ranges and valleys	Unlikely to support subterranean fauna. Considered a potential barrier to species dispersal.
Mount Silvia Formation (HS)			Comprises three BIF bands, separated by chert shale sequences. Thickness varies from 30 to 45 m. Occurs throughout Greater Brockman, mainly in association with lower flanks of ranges and valleys.	May have some potential to support subterranean fauna, dependent on the degree of cavities/ weathering/ enrichment. Shale bands are expected to be relatively impermeable (except where faulted) and may act as barrier to dispersal.
Wittenoom Formation (HD)	Bee Gorge Member (HGc)		Ranges in thickness from 100 to 227 m and consists of an upper shale and dolomite sequence, also containing subordinate thickness of carbonate, chert, volcaniclastics and BIF.	May have some potential to support subterranean fauna, dependent on the degree of cavities/ weathering/ enrichment and proportions of shale to BIF/dolomite.
	Paraburdoo Member (HP)		Comprises a majority of dolomite with minor chert and argillite partings. The thickness ranges from 260 and 420 m.	Known to support subterranean fauna assemblages throughout the region. Suitability varies depending upon the degree of cavities/ weathering/ enrichment and the proportions of shale to BIF/ dolomite.
	West Angela Member (DA)		The member ranges in thickness from 30 to 50 m and consists of a basal shale and BIF section, interbedded with dolomite and dolomitic argillite.	May have some potential to support subterranean fauna, dependent on the degree of cavities/ weathering/ enrichment.

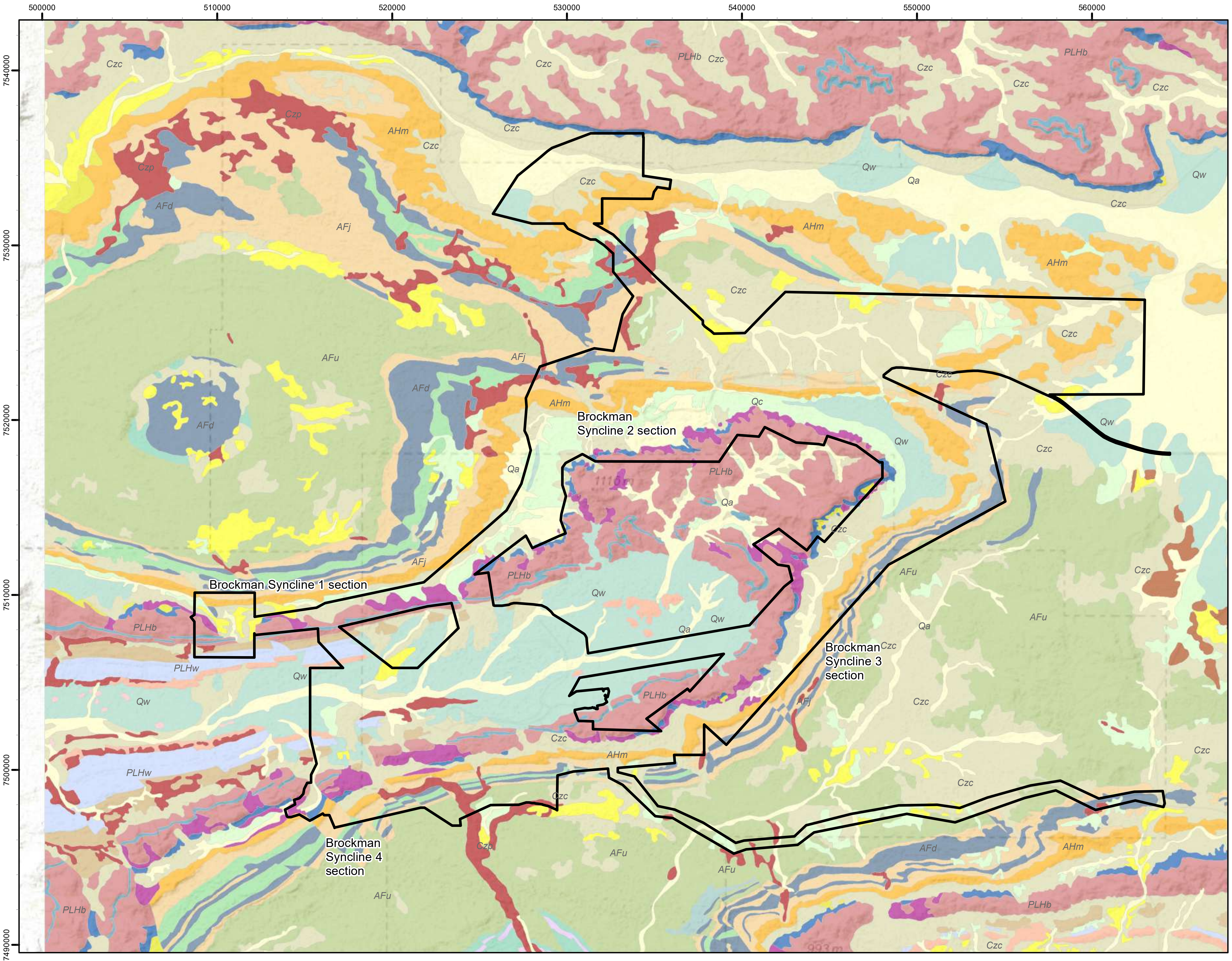
Unit		Description	Generalised suitability for subterranean fauna AWT/ BWT
Marra Mamba Iron Formation (HM)	Mount Newman Member (MN)	Banded iron interbedded with carbonate and shale, between 45 and 60 m thick containing eight identified shale bands.	Known to support subterranean fauna assemblages throughout the region. Habitat suitability is typically high but depends on the degree of cavities/ weathering/ enrichment and the proportions of shale to BIF/ carbonate.
	McLeod Member (MM)	Banded iron, chert and carbonate along with interbedded shales, 25 to 45 m. The upper most beds contain the most shale units, closely spaced together.	May have some potential to support subterranean fauna, dependent on the degree of cavities/ weathering/ enrichment and proportions of shale to BIF/carbonate.
	Nammuldi Member (MU)	Cherty, banded iron formation interbedded with thin shales. The un-mineralised Nammuldi Member is between 75 and 100 m thick	May have some potential to support subterranean fauna, dependent on the degree of cavities/ weathering/ enrichment.
Fortescue Group			
Jeerinah Formation (FJ)		Consists of thin basalts flows interbedded with shale, chert, BIF, mudstone, quartzite and thinly bedded dolomite. A thin cover of calcrete and/or soil covers much of the Jeerinah Formation within the area.	May have some potential to support subterranean fauna, dependent on the degree of cavities/ weathering/ enrichment. Calcrete and dolomite overlying the Jeerinah Formation are regarded as high suitability.
Bunjinah Formation, Pyradie Formation, Boongal Formation		Consist of thick (800–1000 m) metabasaltic flows and breccia. Occur throughout large areas within Greater Brockman, mainly associated with the plains to the north and south of the Brockman Ranges.	Unknown/ uncertain.
Hardey Formation		Sedimentary deposits of pelite, metasandstone and conglomerate. At Greater Brockman, it is only found near Beasley and Hardey River to the south of the Brockman Ranges.	Unknown/ uncertain.

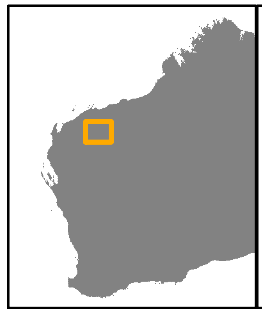
Legend

□ Proposed Development Envelope

Surface Geology (GWSA 1:250k)

- ■ AFd> Metadolerite sills, intrusive
- ■ AFj> Jeerinah Frm. pelite, shale, chert, BIF, Dolerite sills
- ■ AFjl> Metabasalt, pyroxene basalt, basaltic flows, breccia
- ■ AFl> Metapyroxenite sills, Fortescue intrusive
- ■ AFp> Pyradie Frm. metabasaltic flows
- ■ AFpk> Metakomatiite flow
- ■ AFu> Bunjinah Frm, metabasaltic flows
- ■ AFub> Metabasalt, pyroxene basalt, basaltic flows, breccia
- ■ AHd> Wittenoom Frm. dolomite, chert, shale, BIF
- ■ AHm> Marra Mamba Iron Frm. Chert, BIF, pelite
- ■ AHs> Mt McRae Shale and Mt Sylvia Frm.
- ■ Czc> Colluvium (Cz) - partly cons. gravel, rock valley fill
- ■ Czk> Calcrete, drainage associated
- ■ Czl> Laterite - pisolitic ferruginous duricrust
- ■ Czp> Robe Pisolite, drainage associated
- ■ Czr> Hematite-geothite deposits on BIF
- ■ PLHb> Brockman Iron Frm. BIF, chert, shale
- ■ PLHj> Weeli Wolli Frm. BIF, shale, dolerite sills
- ■ PLHo> Boolgeeda Frm. BIF, chert
- ■ PLHt> Metadolerite sills, intrusive
- ■ PLHw> Woongarra Frm. rhyolite and dacite volcanics
- ■ PLTUk> Kungarra Frm. pelite and metasandstone
- ■ Qa> Alluvium (Qt) - partly cons. silt, sand, gravel along drainage
- ■ Qc> Colluvium (Qt) - uncons. sand, gravel, rock valley fill
- ■ Qw> Alluvium-Colluvium (Qt), sandy-clayey soil on sheetwash





Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Fig 2.4: Surface geology of the Study Area and surrounds (GWSA 1:250,000)

N 1:220,000

0 3.5 7 14 km

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

Size A3. Created 04/03/2021

2.6 Hydrogeology

Figure 2.5 shows the hydrogeology (including hydraulic barriers) within the Study Area and surrounds, and the hydraulic conductivity of some of the geologies is shown in Table 2.2. Areas containing geologies that are generally characterised by higher permeabilities are depicted in turquoise (Figure 2.5). These geologies, which comprise tertiary detritals, Brockman Iron Formation, Wittenoom Formation (Paraburdoo Member), and Marra Mamba Iron Formation (Mount Newman Member), are likely to host aquifers throughout much of their extent. However, the occurrence of such aquifers is indicative only. The high-permeability geologies are mainly found along the northern and southern slopes of Mount Brockman, and along Caves Creek to the north of the Study Area (Figure 2.5).

Table 2.2: Modelled hydraulic conductivity for a subset of geological units

Geological unit	Hydraulic conductivity (k)*
Tertiary detritals	2-3
Wittenoom Formation: Paraburdoo and Bee Gorge Members	6
Wittenoom Formation: West Angela Member	1.5
Marra Mamba Iron Formation: Mount Newman Member (mineralised)	5
Alluvium	5
Unmineralised BIF	0.001

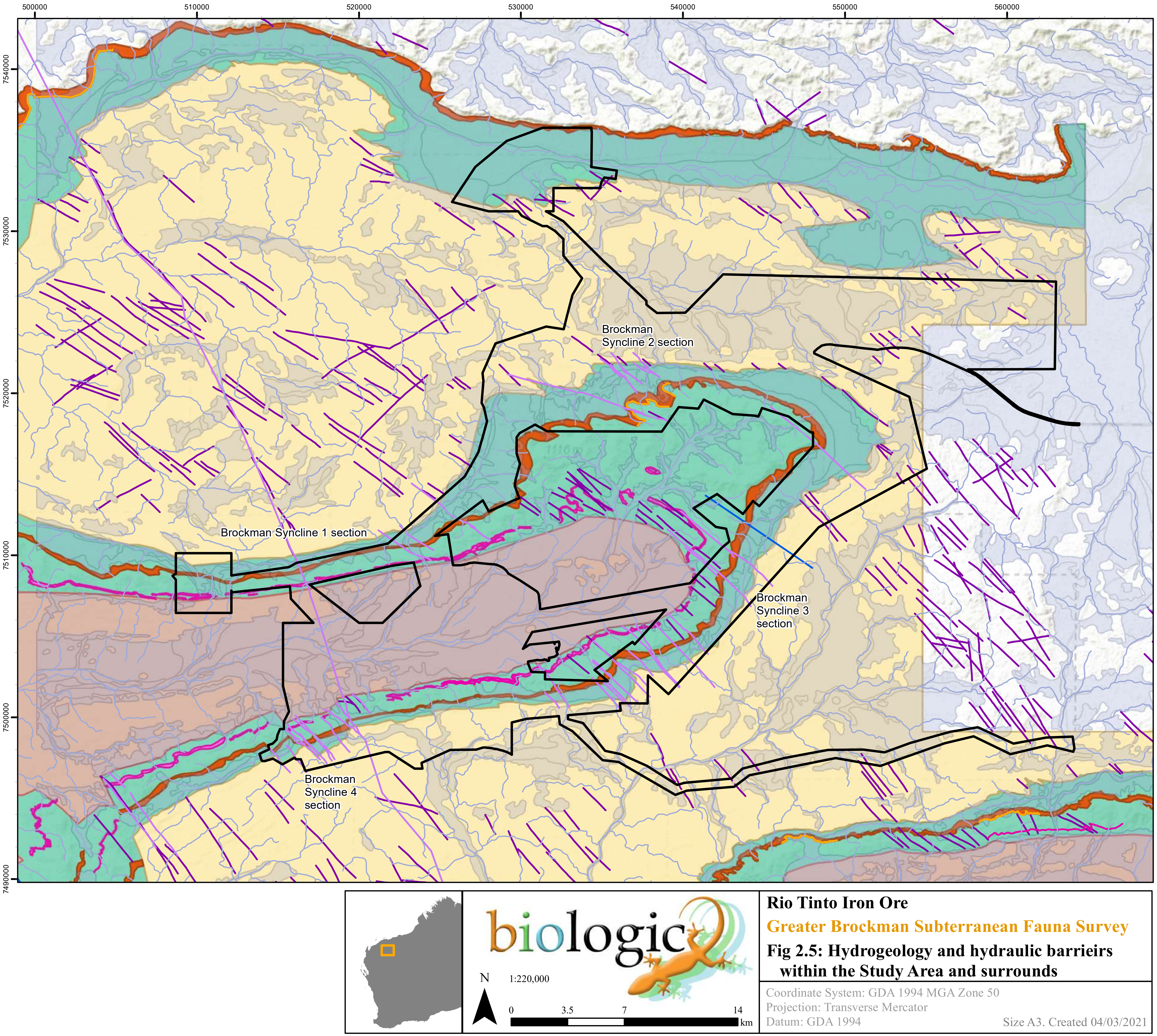
*values obtained from URS (2010a, 2010b).

Geologies within the Study Area that are considered to have lower permeabilities (acting as potential aquitards) comprise Dolerite sills, MacLeod member / Nammuldi Member / Fortescue Group, Mt McRae Shale / Mt Sylvia formations, and Turee Creek Group / Boolgeeda Iron Formation / Wongarra Rhyolite / Weeli Wolli formation (Figure 2.5). These basement rocks are less likely to host regional aquifers based on their physical characteristics. However, localised aquifers/aquitards may still occur where geologies are sufficiently fractured and/or faulted.

Surficial formations of alluvium, colluvium, calcrete and Robe Pisolite (CID) are depicted in light blue (Figure 2.5). These geologies have the potential to host superficial aquifers which may connect the deeper regional aquifers periodically.

Confirmed and potential (with reasonable amount of confidence) hydraulic barriers to groundwater flow are shown for regional context (Figure 2.5).

Groundwater tables are shallowest at Caves Creek to the north of the Study Area, where the groundwater level is approximately 5 m below ground level (mgbl). At Brockman 2 / Greater Nammuldi, pre-mining groundwater levels were approximately 40 mbgl and at BS4, pre-mining groundwater levels were approximately 32 mbgl (Strategen, 2012).



Legend

▭ Proposed Development Envelope

— Surface drainage

Regional Aquifers: higher permeability

🟩 Tertiary Detritals/ Brockman Frm/ Wittenoom Frm/ Marra Mamba Frm Aquifers

▨ Potential superficial aquifers (alluvium, colluvium, Calcrete, Robe Pisolite)

Regional Aquitards: lower permeability

▨ Dolerite Sill

🟨 Macleod Member/ Nammuldi Member/ Fortescue Group

🟧 Mt McRae Shale/ Mt Sylvia Frm

▨ Turee Creek Group/ Boolgeeda Iron Frm/ Wongarra Rhyolite/ Weeli Wolli Frm

Hydraulic barriers (Indicative)

— Dyke

— Groundwater Divide

— McRae Shales

— Sill

— GSWA 250k Dykes

biologic

Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Fig 2.5: Hydrogeology and hydraulic barrieirs within the Study Area and surrounds

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994
Size A3. Created 04/03/2021

3. METHODS

3.1 Database search and review of previous reports

Four databases were searched for subterranean fauna records in August 2019 (Table 3.1):

- Western Australian Museum (WAM) Arachnida/ Myriapoda database;
- WAM Crustacea database;
- DBCA's Pilbara Stygofauna Survey species list (Halse *et al.*, 2014); and
- Biologic's internal database of publicly available records.

All records were filtered based on collection methods and known stygofauna/ troglofauna taxonomic groups where information on subterranean status was not present in the data.

Table 3.1: Databases searched for subterranean fauna records

Database	Parameters
WAM Arachnida/ Myriapoda	45 km radius around 22°25`11"S and 117°09`48"E
WAM Crustacea	45 km radius around 22°25`11"S and 117°09`48"E
DBCA's Pilbara Stygofauna Survey	45 km radius around 22°25`11"S and 117°09`48"E
Biologic's internal database	45 km radius around 22°25`11"S and 117°09`48"E

Reports from subterranean fauna surveys within and surrounding the Greater Brockman Study Area were reviewed for local and regional context. Reports from relevant surveys are listed below:

- Nammuldi Stygofauna Assessment Programme (Biota, 2003);
- Brockman Syncline 4 Project - Baseline Stygofauna Assessment (Biota, 2005);
- Brockman Syncline 4 Boolgeeda Creek Stygofauna Survey (Biota, 2007);
- Beasley River Subterranean Fauna Survey 2009 (Biota, 2009);
- Nammuldi – Silvergrass Subterranean Fauna Assessment (Biota, 2010);
- Nammuldi – Silvergrass Troglobitic Fauna Assessment (Biota, 2011);
- Silvergrass and Caves Creek Subterranean Fauna Assessment (Biologic, 2020) (unpublished data);
- West Turner Syncline Stage 2 B1 and Section 17 Deposits Subterranean Fauna Survey (Biota, 2012);
- Rio Tinto Regional Troglobitic Fauna Study (Biota, 2013);
- Western Turner Syncline Section 10 Below Water Table and Satellite Ore Bodies Subterranean Fauna Survey (Biota, 2014);
- Brockman Syncline 4 Marra Mambas Subterranean Fauna Assessment (Biota, 2016e);
- BS4 Marra Mambas Troglobitic Fauna Addendum Report (Biota, 2016b);
- Western Turner Syncline S10 Hub Subterranean Fauna Assessment Addendum Report (Biota, 2016c); and
- Western Turner Syncline Section 10 Hub Subterranean Fauna Assessment (Biota, 2016d).

The extensive ranges of Banded Iron Formation (BIF) and Channel Iron Deposits (CID) to the north of Greater Brockman have also been intensively surveyed for subterranean fauna, including at Fortescue Metals' Solomon Project (Bennelongia, 2010, 2013; Subterranean Ecology, 2010, 2011) and Central Pilbara Prospects (*e.g.* Serenity and Sheila Valley), and at Flinders Mines' Blacksmith and Anvil Prospects (Bennelongia, 2011). Other areas to the south and east have been sampled, such as Rio Tinto Iron Ore's West Turner Syncline and Marandoo Projects (Biota, 2008a, 2008b) and the Robe Valley Mesas to the west and north (Biota, 2006). Project reports from these areas were not considered to be relevant to the current assessment and were not reviewed herein. The chances of any significant subterranean fauna species occurring in any of these areas as well as the current Study Area is exceptionally low, as any species which does occur over these kinds of distances would also occur across different geological formations and therefore would most likely be regionally widespread, or a non-obligate subterranean species.

3.2 Survey timing and weather conditions

The Level 2 subterranean fauna survey was originally a two-phase survey, undertaken in accordance with guidelines for subterranean fauna assessments (EPA, 2016a, 2016b, 2016c). The Level 2 baseline survey was followed by a three-phase targeted subterranean fauna survey (Table 3.2). The results of the targeted sampling are included in the results of this report. Included in the discussion of this report are also all consolidated results of previous species records for the BSP (see Appendix H and I for list containing all species known from the BSP to date).

The survey was conducted under a DBCA Regulation 17 license 08-002769-1 and Regulation 27 licence BA27000038 (Appendix A). Due to the large size of the Study Area (64,100 ha), sampling was undertaken by two teams as shown in Table 3.2.

Table 3.2: Survey timing

Phase	Trip	Team	Sections sampled	Season	Survey timing	Sampling tasks
1	1	1	BS2/ BS3	Dry	3 – 14 Oct 2018	Trap deployment, scrape/ haul sampling
		2	BS1/ BS4	Wet	10 – 18 April 2019	
	2	1	BS2/ BS3	Dry	29 Nov – 7 Dec 2018	Trap retrieval, scrape/ haul sampling
		2	BS1/ BS4	Wet	5 – 11 June 2019	
2	3	1	BS2/ BS3	Wet	9 – 18 April 2019	Trap deployment, scrape/ haul sampling
		2	BS1/ BS4	Dry	18 – 27 June 2019	
	4	1	BS2/ BS3	Wet	6 – 14 June 2019	Trap retrieval, scrape/ haul sampling
		2	BS1/ BS4	Dry	12 – 22 August 2019	
3 (targeted)	5	1	BS3	Dry	15 – 21 October 2020	Scrape/ haul sampling
		2	BS1			
4 (targeted)	6	1	BS3	Wet	20 – 25 February 2021	Scrape/ haul sampling
		2	BS1/ BS4			
5 (targeted)	7	1	BS3	Dry	19-25 August 2021	Scrape/ haul sampling
		2	BS1/ BS4			

Note: BS2/ BS3 = Brockman Syncline 2/ Brockman Syncline 3, and BS1/ BS4 = Brockman Syncline 1/ Brockman Syncline 4 (includes Vivash and Boolgeeda Creek reference areas).

At BS2/ BS3, the first phase of sampling was undertaken during the dry season months October – December 2018, with the second phase being undertaken in April – June 2019 (representing a wet season survey) (Table 3.2). At BS1/ BS4, the first phase of sampling was being undertaken during the wet season months April – June 2019, with the second phase being undertaken in the dry season months June – August 2019 (Table 3.2). Targeted sampling of selected sites at BS3 and BS1/ BS4 was undertaken in October 2020 (dry season), February 2021 (wet season) and August 2021 (dry season).

Observed weather conditions prior to and during all surveys are shown in Figure 3.1, alongside long-term climatic data for Paraburdoo Airport. Paraburdoo Airport received no rainfall in the three months prior to Phase 1 survey deployment at BS2/ BS3 (3 – 14 Oct 2018) (Figure 3.1). This is slightly below the long-term average rainfall for the same time period (27.7 mm). Similarly, during the period Phase 1 traps were deployed in this area, Paraburdoo Airport received slightly below average rainfall (11.6 mm; 26.5 mm below the long-term average) (BoM, 2019). Daily maximum and minimum temperatures between October and December 2018 were consistent with the long-term average temperatures for the same period (Figure 3.1). Overall, the conditions during Phase 1 at BS2/ BS3 are considered typical for a dry season survey, and the slightly below average rainfall received during this time is not expected to have significantly reduced the abundance of subterranean fauna.

The 2018/2019 wet season was considerably hotter and drier than the long-term average conditions, with mean maximum temperatures ranging from 35.1 °C to 43.7 °C (on average 2.28°C hotter than the long-term average), and total observed rainfall reaching only 113 mm, or 44% of the long-term average (258 mm) (BoM, 2019). In the three months prior to the wet season surveys (Phase 2: BS2/ BS3; Phase 1: BS1/ BS4), only 89.2 mm of rainfall (91 mm below the long-term average) were recorded at Paraburdoo Airport, and rainfall during trap deployment at these areas was below average (52 mm, or 78% below the long-term average) (Figure 3.1). These conditions have the potential to influence the results of the wet season surveys at Greater Brockman, with infiltration to groundwater likely to be minimal and groundwater levels likely to be at very low levels, potentially influencing troglofauna and stygofauna distributions and niche occupancy (Saccò *et al.*, 2020a).

Similarly, the conditions during the dry season survey at BS1/ BS4 (June – August 2019) were drier than the long-term average (Figure 3.1). Only 7.6 mm of rain were received in those months (84% below the long-term average for the same time period (BoM, 2019)), potentially influencing the distribution patterns of troglofauna and stygofauna (Saccò *et al.*, 2020a)

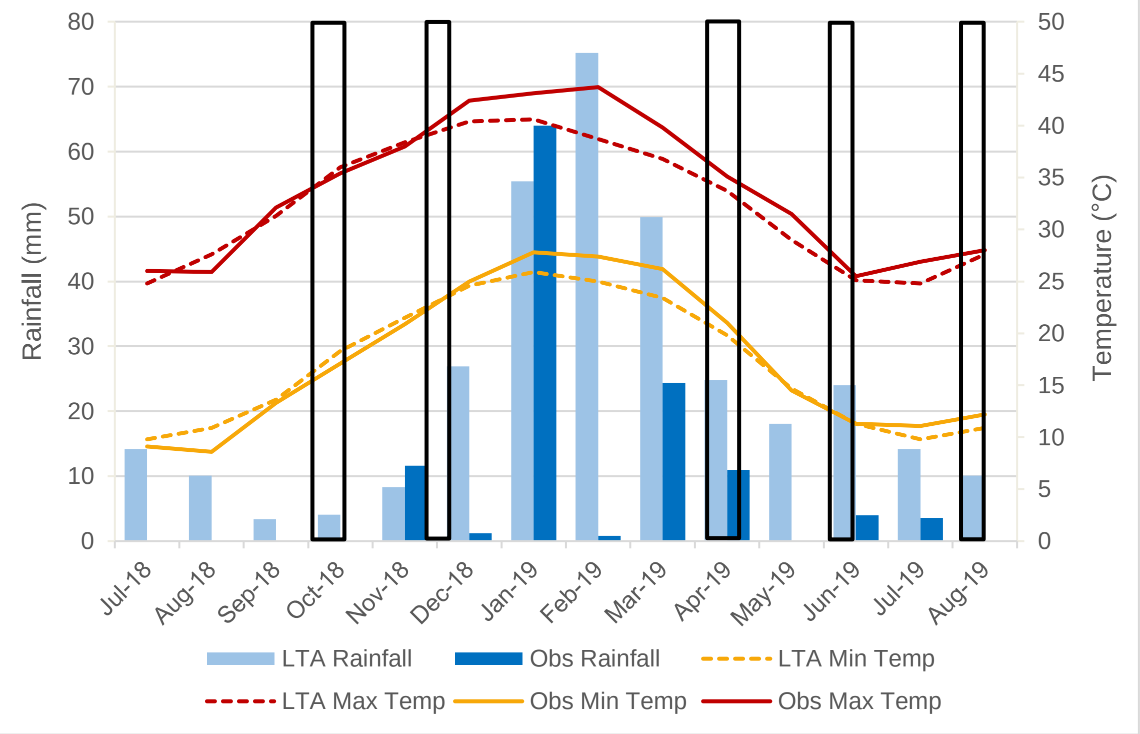


Figure 3.1: Long term average (LTA) and current (2018–2019) climatic data at Paraburdoo Airport (Station 007185), data from BoM 2019*)

*Note: Data includes total monthly rainfall (mm) and average monthly maximum and minimum temperatures (°C). Approximate survey timing is indicated by the black boxes.

3.3 Site selection and survey effort

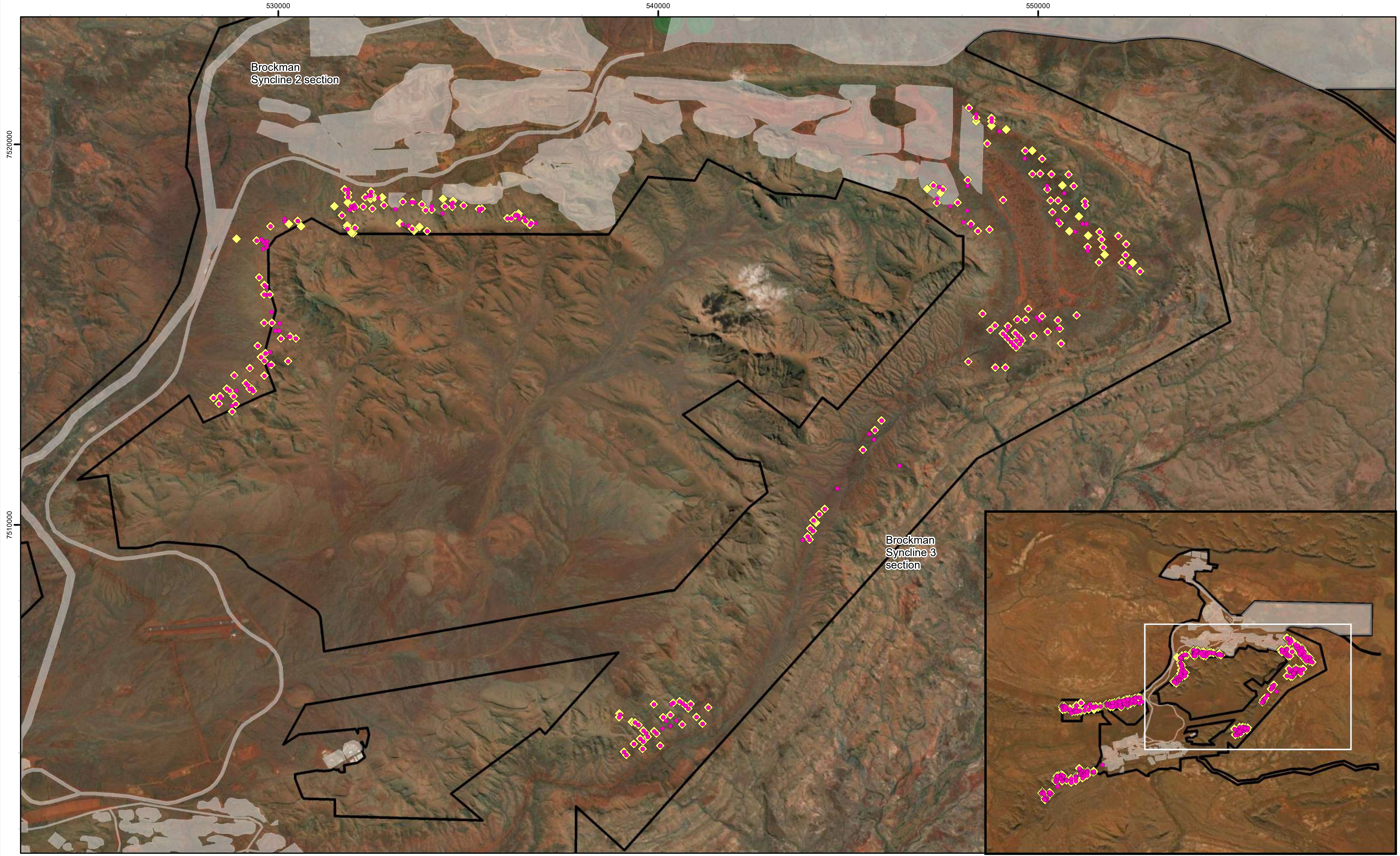
Within the Study Area, site selection for subterranean fauna sampling was limited to accessible, vertical bores (*i.e.* cased, production or monitoring bores) and drill holes (uncased holes). The ratios of troglofauna trapping to scraping and net hauling within and near each deposit were dependent upon drill hole construction (uncased required for troglofauna), angle (90° required for scraping and net hauling), time since drilling (ideally >6 months required for stygofauna, following EPA 2016*b*), and whether the holes intercepted groundwater (required for stygofauna).

A total of 683 bores and holes were sampled throughout the Study Area using three major sampling methods (often including multiple methods at the same hole): 376 holes were sampled by troglofauna trapping, 498 holes were sampled by scraping, and 267 bores and holes were sampled by stygofauna net-hauling. Karaman sampling (described in Section 3.4.4) for stygofauna was performed at 26 sites.

A total of 1,468 subterranean fauna samples were collected during the survey. This comprised 1,102 troglofauna samples collected by trapping (401 samples) and scraping (701 samples), and 366 stygofauna samples collected by net hauling (338 samples) and Karaman sampling (28 samples). Table 3.3 provides details of the number of samples collected within and nearby each sampling section with respect to the methods employed, and Figures 3.2 – 3.5 show the location of holes visited and sampled throughout the Study Area. Details of bores and drill holes visited during the survey are provided in Appendix B.

Table 3.3: Number of samples collected for each sampling section and phase

	BS1	**BS2**	**BS3**	**BS4**	**Total**
PHASE 1					
Traps retrieved	38	77	21	44	**180**
Scrapes	26	94	52	42	**214**
Net hauls	11	15	24	10	**60**
Karaman samples	0	0	0	6	**6**
PHASE 2					
Traps retrieved	60	57	64	40	**221**
Scrapes	138	91	87	102	**418**
Net hauls	47	20	42	26	**135**
Karaman samples	0	0	0	2	**2**
PHASE 3 (targeted)					
Scrapes	6	0	17	0	**23**
Net hauls	9	0	28	0	**37**
PHASE 4 (targeted)					
Scrapes	1	0	45	0	**46**
Net hauls	7	0	47	6	**60**
Karaman samples	1	0	13	6	**20**
PHASE 5 (targeted)					
Net hauls	29	5	11	1	**46**
Troglofauna total	269	319	286	228	**1102**
Stygofauna total	75	35	154	56	**366**
Grand total, all samples	**373**	**359**	**451**	**285**	**1468**



Legend

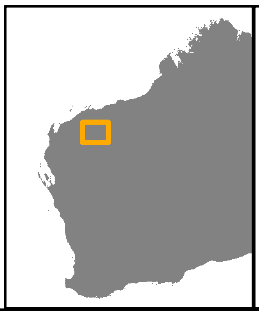
▭ Proposed Development Envelope

▨ Existing Operations Footprint

Troglofauna sampling

◆ Troglofauna trapping

● Troglofauna scraping



biologic

N

1:90,000

0 1.25 2.5 5 km

Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Fig 3.2: Sites sampled for troglofauna during the current survey (BS2 and BS3 sections)

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

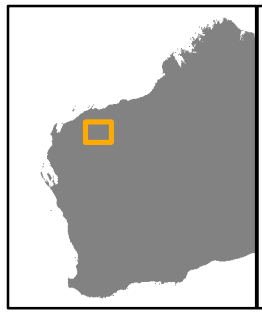
Size A3. Created 11/03/2021

Legend

- Proposed Development Envelope
- Existing Operations Footprint

Troglofauna sampling

- ◆ Troglofauna trapping
- ● Troglofauna scraping



biologic

N

1:90,000

0 1.25 2.5 5 km

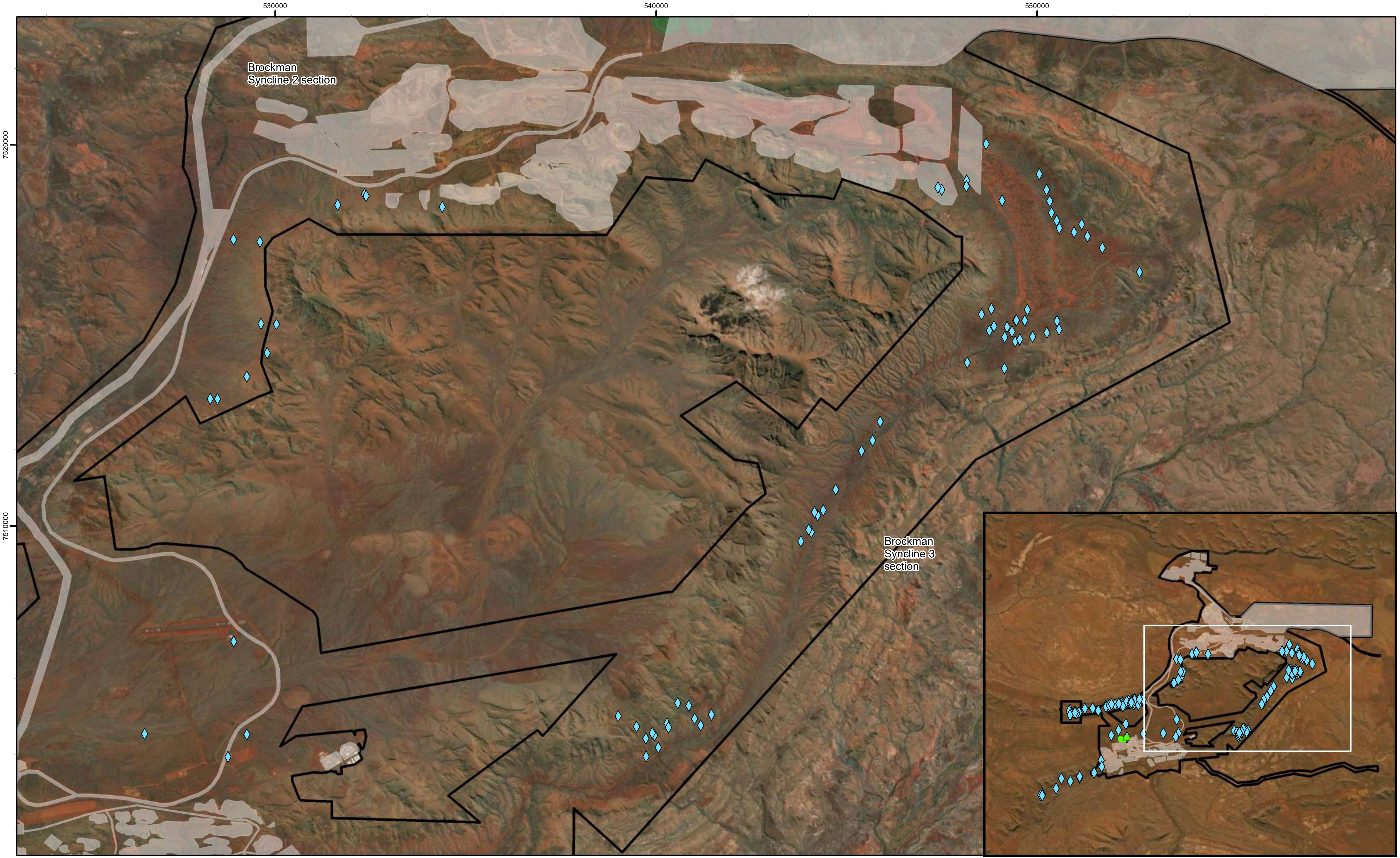
Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Fig 3.3: Sites sampled for troglofauna during the current survey (BS1 and BS4 sections)

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

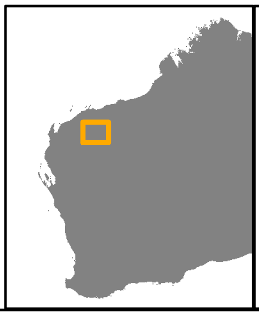
Size A3. Created 11/03/2021



Legend

□ Proposed Development Envelope **Stygofauna sampling**

▨ Existing Operations Footprint ◆ Net hauling



N

1:90,000

0 1.25 2.5 5 km

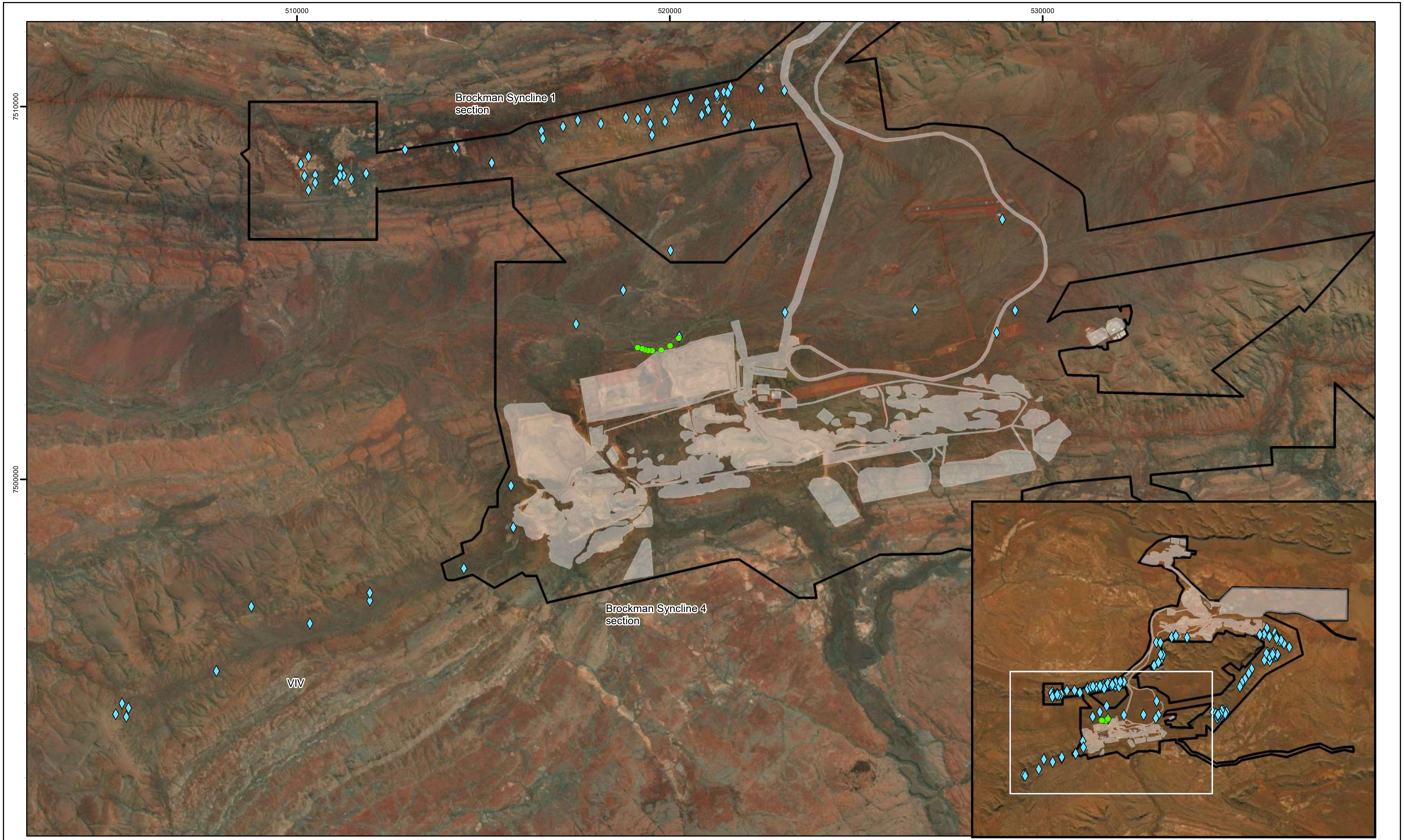
Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Fig 3.4: Sites sampled for stygofauna during the current survey (BS2 and BS3 sections)

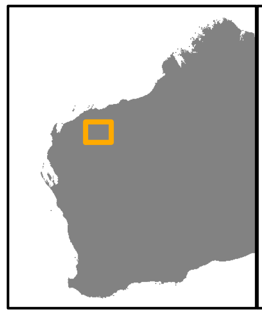
Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

Size A3. Created 11/03/2021



Legend

▭ Proposed Development Envelope	**Stygofauna sampling**
▭ Existing Operations Footprint	◇ Net hauling
	● Karaman



biologic

N

1:90,000

0 1.25 2.5 5 km

Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Fig 3.5: Sites sampled for stygofauna during the current survey (BS1 and BS4 sections)

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

Size A3. Created 11/03/2021

3.4 Sampling methods

The sampling methods used were consistent with EPA's "Technical Guidance: subterranean fauna survey" (EPA, 2016c) and "Technical Guidance: sampling methods for subterranean fauna" (EPA, 2016b), and the Stygofauna Sampling Protocol developed for the Pilbara Biodiversity Study Subterranean Fauna Survey (Eberhard *et al.*, 2005; Eberhard *et al.*, 2009). The field work was undertaken by Dean Main, Fabian Rudin, Shae Callan, Morgan Lythe, Syngeon Rodman, Tom de Silva, Arnold Slabber, Jessica Delaney, Aidan Williams, and Kim Nguyen. Laboratory sorting was undertaken by Dean Main, Shae Callan, Dr Nihara Gunawardene, Syngeon Rodman, Dr Fabian Rudin, Mary van Wees, Juliana Pille Arnold, Morgan Lythe, Dr Tabitha Rudin and Stephanie Floeckner.

3.4.1 Troglofauna trapping

Trapping utilises custom made cylindrical PVC traps (approximately 50 mm × 300 mm) baited with decaying leaf litter (dead spinifex / acacia sourced from the Pilbara region), which were sterilised with boiling water. Traps are lowered *via* a nylon cord to a suitable depth and left in operation six to eight weeks, before being collected and transported back to the laboratory in Perth.

3.4.2 Troglofauna scraping

Scraping was undertaken at vertical, uncased drill holes using a reinforced 150 µm weighted stygofauna net, with a specialised scraping attachment used above the net to maximise gentle contact with the walls of the hole. The net was lowered and raised through the full length of the hole at least three (3) times for holes where no water was present, with each haul being emptied into a sample bucket as per net-hauling. Where the water table was intercepted, a combined net-haul / scrape sample was taken using the scraping attachment, comprising six (6) hauls throughout the full length of the hole from top to bottom, including both the air filled and below water subterranean habitats. The contents of the sample were elutriated, processed, and stored in 100 % ethanol as per net-hauling. This technique can frequently result in stygofauna by-catch where scraping nets are lowered below the water table to collect any invertebrates that may have fallen past the net.

3.4.3 Stygofauna net-hauling

Stygofauna were sampled by standard net-hauling methods, using a plankton net of a diameter to suit each bore or drill hole (in most cases 30–80 mm). Each haul sample comprised a total of six hauls from the bottom of the hole to the top, with three hauls using a 150 µm mesh and three hauls using a 50 µm mesh. The base of the net was fitted with a lead weight and a sample receptacle with a base mesh of 50 µm. To stir up sediments, the net was raised and lowered at the bottom of the hole prior to retrieval and hauled at an even pace through the water column to maximise filtration of the water.

The sample from each haul was emptied into a bucket, which was elutriated after the final haul to remove coarse sediments and filtered back through the 50 μm net/ sample receptacle to remove as much water as possible. The sample was transferred to a 50–120 mL preservation vial (depending upon the quantity of sediment) and preserved in 100% ethanol. The ethanol and the samples were kept chilled on ice to facilitate cool-temperature DNA fixation.

3.4.4 Karaman-Chappuis sampling

Stygofauna occupying shallow groundwater habitats beneath gravel stream beds (hyporheos) were sampled by the Karaman-Chappuis (Karaman) method at sites where permanent pools or springs indicated the presence of near-surface groundwater. This technique involves excavation of a hole in the stream bed nearby a pool or flowing stream, approximately 50–100 cm diameter, and 30–50 cm depth below groundwater level. Care must be taken to choose substrates with mainly larger gravels and sand, rather than silt or clay. Water is bailed out of the hole using a bucket and sieved through a 150 μm stygofauna net as described above. As buckets of water are removed, care must be taken to avoid the same water flowing back into the hole – inflow of new hyporheic groundwater can usually be seen as clearer water entering from the upstream side of the hole. This process can be continued for any length of time depending on how quickly groundwater inflow continues to fill the hole, usually with the aim of sampling approximately 20–50 L in total.

Karaman sampling can be a very useful method of achieving samples where no or few bores/ drill holes exist (as long as there is near-surface groundwater) and can also be helpful to assess the potential for stygofauna species or communities to be more widely dispersed throughout the hyporheic zone of local drainage networks. These samples also tend to collect an abundance of surface fauna, which can be difficult to distinguish from stygofauna taxa where characters of eyelessness and pale cuticle are inherent throughout the group (*e.g.* worms, some crustaceans, some mites).

3.4.5 Water physicochemistry

Prior to stygofauna sampling, a groundwater sample was collected using a 1 m plastic cylindrical bailer, for the purposes of physicochemical measurements. The bailer was lowered down the hole until reaching groundwater and a water sample was collected at a depth of 2 m below the surface. As such the results were not indicative of water parameters throughout the entire bore (or aquifer) but rather provide a general indication of near surface conditions. Conditions sampled during pumping were measured using a sample collected from the pump outflow, which would have artificially increased the dissolved oxygen readings. Groundwater physicochemical data (including EC, pH, TDS, Redox ORP, and dissolved oxygen) was measured using a multi-parameter water meter. Constrictions in piezometer bores, blockages from root material, or excessive depths to groundwater inhibited the collection of physicochemical readings at some sites.

3.4.6 Sorting and taxonomy

Sorting and parataxonomy were undertaken in-house using dissecting microscopes. The personnel involved (D. Main, S. Callan, N. Gunawardene, S. Rodman, F. Rudin, M. van Wees, J. Pille Arnold, M. Lythe, T. Rudin, and S. Floeckner) were all suitably trained and experienced in sorting and parataxonomy of subterranean fauna.

Parataxonomy of the specimens utilised published literature and taxonomic keys, where available. Each morphospecies from each sample was assigned a separate labelled vial and labelled with a specimen tracking code. Taxonomic groups were examined in as much detail as possible using in-house expertise, before sending a reference collection to specialist taxonomists for detailed taxonomic advice. Species comparisons and alignments were performed using regional specimens collected beyond the Study Area throughout the wider sub-regional area. Giulia Perina, Jane McRae, and Stuart Halse provided specialist taxonomic identifications and regional alignments.

3.4.7 DNA analysis

Molecular genetic analysis (DNA barcoding using the mitochondrial gene COI) was conducted by Biologic on certain subterranean taxa to validate morphological identifications and provide a basis for species-level identifications and regional comparisons where taxonomic resolution was limited. Refer to Appendix C and D for further details regarding the methods of DNA extraction, choice of primers, sequencing, and analysis.

3.5 Conservation status and SRE classification

A few subterranean species and assemblages from the Pilbara region are listed under relevant legislation as threatened species, or as Threatened or Priority Ecological Communities in certain locations.

The likelihood of taxa representing SRE species (*i.e.* distribution <10,000 km^2 following Harvey 2002, or <1,000 km^2 following Eberhard *et al.* 2009) was assessed based on the known local species distribution, and regional comparisons where data was available, following advice from the WAM and other relevant taxonomic specialists. The assessment of SRE status was highly dependent on:

1. the degree of taxonomic certainty at the genus and species levels;
2. the current state of taxonomic and ecological knowledge for each taxon (including whether a regional genetic context has been investigated);
3. the scale and intensity of the local and regional sampling effort; and
4. whether or not relevant taxonomic specialists were available to provide advice.

The SRE status categories used in this report follow the WAM's categorisation for SRE invertebrates. This system is based upon the 10,000 km^2 range criterion proposed by Harvey (2002), and uses three broad categories to deal with varying levels of taxonomic certainty that may apply to any given taxon (Table 3.4). Because most subterranean fauna are poorly known taxonomically, and the general limitations to sampling subterranean fauna, the majority of morphospecies invariably fall within one (or several) of the five Potential SRE sub-categories.

Table 3.4: SRE categorisation used by WAM taxonomists

	Taxonomic Certainty	**Taxonomic Uncertainty**
Distribution <10 000km^2	Confirmed SRE • A known distribution of <10,000km^2 • The taxonomy is well known • The group is well represented in collections and/ or *via* comprehensive sampling	Potential SRE • Patchy sampling has resulted in incomplete knowledge of geographic distribution. • Incomplete taxonomic knowledge. • The group is not well represented in collections. • Category applies where there are significant knowledge gaps. **SRE Sub-categories may apply:** A) Data Deficient B) Habitat Indicators C) Morphology Indicators D) Molecular Evidence E) Research & Expertise
Distribution >10 000km^2	Widespread (not an SRE) • A known distribution of >10,000km^2 • The taxonomy is well known • The group is well represented in collections and/ or *via* comprehensive sampling	

The degree of stygomorphy or troglomorphy (observable physical adaptations to subterranean habitats such as eyelessness, depigmentation, elongation of sensory appendages and thinning of the cuticle) assessed to determine each morphospecies' 'subterranean status', *i.e.* whether a taxon was more or less likely to be an obligate subterranean species (stygobite/ troglobite). It is acknowledged that the current EPA guideline for subterranean fauna does not account for non-obligate subterranean fauna, stating, *"…subterranean fauna are defined as fauna which live their entire lives (obligate) below the surface of the earth.... Fauna that use a subterranean environment for only part of the day or season (e.g. soil-dwelling or burrowing species, cave-dwelling bats and birds) are not considered as subterranean fauna for this EAG*" (EPA, 2013).

Nevertheless, there may be fauna with restricted distributions <10,000 km^2 following Harvey (2002), or <1,000 km^2 following Eberhard *et al.* (2009) that are of interest because of their SRE status, regardless of whether they can be definitively regarded as 'obligate' subterranean fauna. For this reason, this report presents an assessment of both the subterranean status and the SRE status of each taxon collected, to the best available knowledge.

3.6 Habitat assessment and modelling

An assessment of the prospective suitability, extent, thickness, and connectivity of subterranean habitats above and below water table has been undertaken across the Study Area.

The subterranean habitat assessment integrated three layers of assessment/ modelling:

1. Categorisation of the 2D surface geology for habitat suitability (throughout the Development Envelope and the wider local area surrounding it);
2. 3D habitat modelling from drill hole information (AWT throughout the Development Envelope, and BWT at Silvergrass/ Caves Creek zone); and
3. 3D hydrostratigraphic modelling (BWT at Brockman Syncline zone).

The 3D habitat modelling, which was performed in the program Leapfrog® Geo v4.3.1, used drill hole information to model suitable subterranean fauna habitats based on lithology/ stratigraphic units and the physical structure of the rock. The intent of the 3D modelling was to define the most suitable areas of habitat for subterranean fauna within and surrounding the current and proposed areas of impact, and throughout an ‘area of high confidence’ in the geological/ hydrogeological information available. This ‘area of high confidence’, or habitat modelling boundary, was determined to be an area within a 300m radial buffer around each drill hole, from the surface to the maximum depth of drilling. To ensure conservative estimation of the extent, thickness, and connectivity of subterranean habitats, any modelled habitat less than 1m thick was excluded.

Where 3D habitat modelling was not possible due to the sparsity or lack of drill holes, interpretation of the wider potential extent of subterranean fauna habitat was undertaken by 2D characterisation of surface geological information (GSWA 1:250,000 series). While this categorisation of geology was not as detailed or fine scale as the 3D habitat modelling, it represents a reasonable approximation of the information available for areas beyond the ‘high confidence’ modelling boundary.

BWT habitats at the Brockman Syncline were modelled using 3D hydrostratigraphic modelling, as bores and drill holes intercepting groundwater in parts of this zone were too sparse to use a 300m confidence boundary, and did not accurately represent the extent of BWT habitats revealed by sampling. Instead, 3D hydrostratigraphic modelling was derived from the regional hydrogeological models, covering a spatial area relevant to the modelling of proposed groundwater impacts, and extending throughout the major aquifer bearing formations within the Brockman Syncline. In order to ensure conservative estimation of the extent, thickness, and connectivity of BWT habitats relevant to stygofauna, the hydrostratigraphic modelling was clipped at a maximum of 100m depth from the topographic surface. In addition to the exclusion of any BWT habitat modelled <1m thick, this 100m maximum depth threshold was used to ensure that the focus of the BWT modelling was on the most likely habitable zone for stygofauna throughout the Syncline.

Full details of the subterranean habitat assessment and modelling methodology are presented and discussed in Biologic (2022).

3.7 Sampling adequacy

Sampling adequacy was assessed using species accumulation curves and species richness estimation models in the program EstimateS v 9.1.0 (Colwell, 2013). Abundance data from the current survey was transformed into an appropriate matrix format for input into EstimateS using

Microsoft Excel®, with each sample representing a unique combination of site/ visit/ method (*i.e.* traps and scrapes collected from the same hole were not combined). To adjust for differences in taxonomic resolution and the effects of sub-sampling for DNA analysis, the stygofauna and troglofauna species data were filtered using a parsimonious approach to exclude higher-level identifications that could potentially represent other recorded species (*i.e.* indeterminate taxa).

Data from previous Rio Tinto surveys in the area and in similar geological settings were also analysed using species accumulation curves to provide a comparison with the results from the three Greater Brockman sub-regions. Survey data used for this purpose comprised:

- Nammuldi–Silvergrass Troglofauna and Stygofauna Survey (Biota, 2010, 2011),
- Brockman Syncline 4 Marra Mambas Subterranean Fauna Assessment (Biota, 2016a), and
- Greater Paraburdoo Subterranean Fauna Survey (Biologic, 2019).

Data from these surveys were selected based on being publicly available, covering the same or similar geographical areas, employing similar methods (trapping, scraping, and net hauling), and representing a reasonable sampling effort for stygofauna or troglofauna (exceeding the EPA minimum requirements). However, it was acknowledged that there were some considerable differences between these previous surveys and the current survey that may have limited the suitability of the data sets for comparison, particularly regarding:

1. Methodology - the ratios of trapping to scraping sites,
2. Identification methods - the use of genetic analyses to confirm species identifications, and
3. Survey scale - the multitude of potentially different habitat units sampled throughout Greater Brockman in contrast to the other survey areas.

These issues are discussed in more detail in section 7.

Data from the previous surveys were treated the same as Greater Brockman data in the analysis and in terms of analysis settings, except that the parsimonious approach to filtering the species data was not required, and the stygofauna data from Nammuldi–Silvergrass (Biota, 2010) was listed by site, not by sample; therefore the Greater Brockman stygofauna data was also transformed to site based records for the species accumulation curves.

Species accumulation curves were plotted in Microsoft Excel® using EstimateS output data from S(est) and Coleman Rarefaction curves; separately for stygofauna and troglofauna and for each data set (Silvergrass West/ Homestead, Brockman 2–Nammuldi, Brockman 1/ Vivash, Greater Paraburdoo, Nammuldi – Silvergrass, and Brockman Syncline 4).

The analyses were run with the following settings in EstimateS:

- Abundance data by sample (troglofauna) or by site (stygofauna);
- 1,000 randomizations;
- No extrapolation;

- Estimate at every sample/site;
- Classic formulas for Chao 1 & 2;
- Upper abundance limit for rare species = 2; and
- Randomizing individuals without replacement.

Species richness estimation was predicted from each dataset using coverage-based models ACE, Chao 1, Jackknife 1 (Jack 1), and Bootstrap (all mean values), while the Michaelis-Mentin (MMMeans 1 run) estimator was used to indicate a stopping point (Colwell, 2013). The final value of S(est) (*i.e.* the observed species richness) was compared to each of the predicted species richness values from these models using a proportional bar chart in Microsoft Excel®, and values representing the observed species richness as a percentage of the predicted species richness under each model.

3.8 Constraints and limitations

Much remains uncertain regarding subterranean fauna taxonomy and ecology, and taxonomic frameworks are still in development, which provides challenges for the interpretation of results and species distributions, particularly when combining new and old records from historical sampling. Many subterranean species (particularly troglofauna) are rare and difficult to detect throughout their range or habitat extent. Subterranean fauna inhabit cryptic, concealed habitats that are mainly sampled only via bores and drill holes that create an artificial disturbance. As a result, surveys typically reveal only part of the total diversity and abundance of animals present in underground habitats, and even large sampling efforts feature low detection rates, low measures of completeness, and high numbers of infrequently detected species. The results and conclusions of the survey are nevertheless based upon the best available information under these constraints, although in some cases, residual uncertainty is unavoidable.

Specific limitations relating to the current and previous survey data are listed below.

- Spatial/ geographical spread of sampling – sampling was limited to the locations of available drill holes and bores (and areas near waterbodies for Karaman sampling), which varied across and between different AWT/BWT habitat units. Best efforts were made to refine the sampling plan between surveys to enhance spatial coverage relative to potential impact areas, likely habitat units, and knowledge gaps, but not all areas contained available and suitable bores/ holes.
- Depth of drilling – the depth of drilling in some areas limited the number of drill holes intercepting groundwater habitats (i.e. suitable for stygofauna sampling), as well as the number and type of construction of water bores. Best efforts were made to enhance stygofauna sampling by repeated bore/ hole sampling where groundwater was intercepted, and the addition of Karaman sampling in targeted areas.
- Groundwater physicochemical measurements from bailer sampling - some bores/ holes were too deep (>60 m) to sample successfully by bailers. Due care was taken to exclude

obviously erroneous results, but bailer sampling can sometimes alter physicochemical measurements (e.g. dissolved oxygen, temperature). The conditions sampled by bailer sampling in bores may not reflect the conditions within the wider aquifer and were thus interpreted cautiously.

- Rainfall conditions prior to sampling – Rainfall conditions prior to subterranean fauna sampling can influence the abundance, distribution patterns and niche occupancy of subterranean fauna, with some taxa showing greater distributions and higher abundance following rainfall events, whilst other taxa show the opposite pattern (Saccò *et al.*, 2020b). The 2018/2019 wet season and the 2019 dry season were considerably drier than the long-term average conditions which may have affected some of the distribution patterns of the subterranean fauna occurring at Greater Brockman. However, as sampling was conducted over four phases in most areas, it is expected that natural fluctuations in distribution patterns of subterranean fauna at Greater Brockman have been adequately captured in the results of this survey.
- Taxonomy and genetics – specimen identifications were assessed by a combination of morphology and genetic analyses wherever possible. Best practices were followed in the field and lab to enhance genetic success rates; however, some sequencing failure is unavoidable. Appendices C and D contain full details and specific constraints/ limitations in relation to the genetic analyses undertaken for the survey.
- Sub-sampling for genetic (and external morphological) analysis – the high specimen load collected throughout the large spatial area of the survey necessitated a degree of sub-sampling for more detailed genetic analysis and morphological taxonomy. Detailed in-house parataxonomic work was undertaken to provide a preliminary assessment of the diversity and spatial locations of taxa present throughout the Study Area as a whole, at achievable parataxonomic levels which varied between groups. Individuals were then targeted for genetic analysis or more detailed morphological work within each taxonomic group, based on the spatial spread of the group throughout the landscape (both within and across different habitat units), with a degree of redundancy to allow for sequence failures/ poor specimen quality. The results of the first round of genetic work and detailed morphological analysis were fed back into the assessment, and a second round of work was undertaken to fill remaining knowledge gaps in the spatial understanding of species distributions and species turnover within and between sampling areas/ habitat units.
- The resulting spatial coverage of morphological and genetic information across all taxonomic units provided a degree of confidence in the assessment of distributions, within the constraints of sampling success. Excluding sequence failures and poor-quality specimens, at the end of this process, very few gaps remained in the spatial coverage of species/ OTUs confirmed by genetic and morphological information, for most of the taxonomic groups. Additional OTUs may still occur due to sampling artefacts, or because of genetic sub-sampling or sequence failure; nevertheless, this approach provided

confidence in the assessment of distributions patterns and species turnover throughout the Study Area for the known species/ OTUs.

- Incorporation of previous results - many taxa/ morphospecies recorded from previous surveys could not be compared to OTUs from the current survey due to the specimens or DNA being unavailable, and/ or due to updated taxonomic frameworks between the previous and current surveys; therefore synonyms and data artefacts could remain in the combined (historical and current) species lists.
- Putative OTUs based on morphology and spatial patterns - certain indeterminate taxa that were unique (*i.e.* not represented by any other groups detected from the Study Area), but unable to be sequenced or locally/ regionally compared were treated as distinct OTUs (*e.g.* Ptinella? \`sp. BS1\`). In a few other cases, a conservative approach was used for unique indeterminate morphospecies from groups prone to short-range endemism that were collected from sampling areas distinct and disconnected from the other members of their group (*e.g. Atopobathynella* sp. indet. from BGCK became *Atopobathynella* \`sp. BGCK\`). Where the assessment was uncertain (due to limited information or the inability to directly compare specimens/ sequences) whether an indeterminate taxon collected from different spatial areas and disconnected habitats was unique or the same, a conservative approach was taken to treat the specimens as unique (*e.g.* Pezidae sp. indet. from BGCK and BS3 became Pezidae \`sp. BGCK\` and Pezidae \`sp. BS3\`).
- Statistical analysis of survey adequacy – where diverse subterranean fauna assemblages are detected, species accumulation curves typically fail to reach an asymptote, even after much greater sampling effort than is required under EPA guidelines. Surveys can result in insufficient replication, datasets that violate modelling assumptions, high proportions of rare/ infrequent species, and results affected by sampling artefacts (Halse & Pearson, 2014). Although the practicalities of sampling for EIA can create a trade-off between repeated sampling of the same holes (for better species accumulation) or increasing geographical coverage between phases/ sampling events, the latter is always preferred due to the increased chances of detecting wider species distributions.
- Habitat modelling - The habitat modelling is a conservative estimate within the limitations of the geological drill logging data used to develop it, and the diamond core information used for validation. High and Medium (certain) habitats were mapped and modelled throughout a 300 m confidence boundary surrounding the drill holes. Structural features such as dykes/ sills, faults, and shears were likely underrepresented at a fine scale in the modelling (due to the large scale of the areas modelled), except where they were a fundamental part of the regional stratigraphy. The information from drill logging was denser in some areas than others, possibly enhancing variability in the modelled extent and thickness of habitat. The BWT habitat for stygofauna may appear artificially patchy in some areas due to lower numbers of holes intercepting the water table.

- Habitat suitability factors - The assessment of high and medium (certain) habitat thickness was limited to geology and geomorphology factors as indicated by the strand/ tag combinations. Other potentially important factors (such as depth from surface, structural barriers, geochemical or hydrogeochemical factors, and groundwater physicochemical characteristics) that may influence the likelihood of subterranean fauna occurring could not be included in the model. Diamond drill holes were very sparsely undertaken throughout the landscape, therefore the amount of core photos that were available for visual confirmation of physical characteristics was limited. Nevertheless, the few cores that were available confirmed High to Medium (certain) suitability habitats were found from the top of the geological profile to depths varying between 60 mbgl and approximately 90 mbgl across all sampling areas.

4. DESKTOP ASSESSMENT

4.1 Database searches

Excluding defunct OTUs/synonyms and indeterminate taxa, the WAM, DBCA's Pilbara Stygofauna Survey and previous survey records (Biologic internal database & Biota 2005-2016) indicated 45 troglofauna (including potential troglofauna) taxa belonging to 15 higher level taxonomic groups, and 44 stygofauna (including potential stygofauna) taxa from ten higher level taxonomic groups occur within 45 km of the Study Area (Table 4.1). An overview of the locations of these subterranean fauna records is provided Figure 4.1, with area specific-details provided in Maps 1 – 6 (Appendix E). Twenty-three troglofauna taxa and twenty-three stygofauna taxa from the database searches were recorded within the Study Area (highlighted in green font in Table 4.1).

Based on current knowledge, none of the described troglofauna or stygofauna species appear on any threatened species lists. Particularly in relation to the stygofauna taxa, many of the records comprise widespread species known to occur beyond the Study Area. However, owing to the indeterminate identifications of many of the taxa recorded, several records cannot be assessed for wider local/ regional distributions. All database search records are listed in Appendix F.

Table 4.1: Troglofauna and stygofauna taxa recorded in the databases and previous surveys within 45 km of the Study Area (search parameters as per Table 3.1). Taxa from within the Study Area are highlighted in green font.

Taxonomy	Likely subterranean status	SRE status where known	Source
Platyhelminthes			
Platyhelminthes sp. indet.	Potential Stygofauna	Uncertain	Biota (2010)
Nematoda			
Nematoda sp. 18	Potential Stygofauna	Uncertain	DBCA
Nematoda sp. indet. *	Potential Stygofauna	Uncertain	Biota (2010)
Polychaeta			
Namanereis sp. indet.	Potential Stygofauna	Uncertain	DBCA
Oligochaeta			
Phreodrilus peniculus	Stygoxene	Widespread	DBCA
Phreodrilid `sp. dissimilar ventral chaetae`	Stygofauna	Widespread	DBCA
Phreodrilidae `sp. similar ventral chaetae`	Stygofauna	Widespread	Biota (2010)
Enchytraeidae sp. indet.	Potential Stygofauna	Uncertain	Biota (2010)
Ostracoda			
Areacandona `sp. BOS1020`	Stygobite	Potential SRE	Biologic
Areacandona arteria	Stygofauna	Widespread	Biota (2010)
Areacandona bluffi	Stygofauna	Widespread	Biota (2010)
Areacandona nammuldi	Stygobite	Confirmed SRE	WAM & DBCA
Areacandona novitas (syn. *Neocandona novitas*)	Stygobite	Confirmed SRE	Biota (2010)

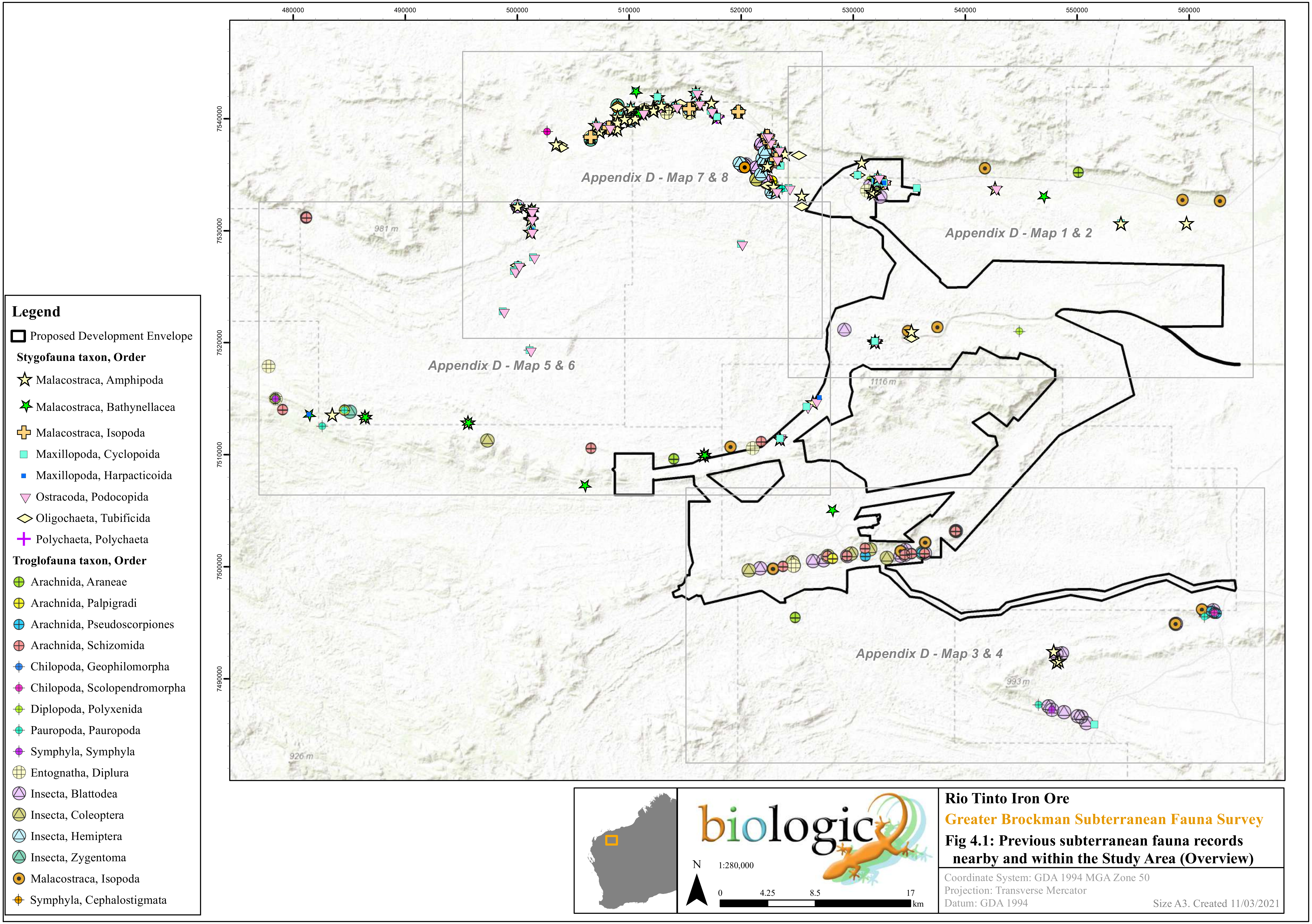
Taxonomy	Likely subterranean status	SRE status where known	Source
Areacandona \`sp. nr *triangulum*\`	Stygobite	Potential SRE	WAM & Biologic
Humphreyscandona woutersi	Stygofauna	Widespread	DBCA
Ilyodromus \`sp. 2\`	Stygofauna	Potential SRE	DBCA
Neocandona novitas (syn. *Areacandona novitas*)	Stygobite	Confirmed SRE	WAM
Ostracoda sp. indet. *	Potential Stygofauna	Uncertain	WAM & DBCA
Cyclopoida			
Diacyclops humphreysi (humphreysi)	Stygoxene	Widespread	WAM & DBCA & Biota (2010)
Diacyclops sobeprolatus	Stygoxene	Widespread	WAM & DBCA & Biota (2010)
Mesocyclops brooksi	Stygoxene	Widespread	Biota (2010)
Orbuscyclops westaustraliensis	Stygofauna	Widespread	WAM
Pescecyclops pilbaricus	Stygofauna	Widespread	Biota (2010)
Diacyclops sp. indet. *	Potential Stygofauna	Uncertain	Biota (2012)
Cyclopoida sp. indet. *	Potential Stygofauna	Uncertain	WAM
Harpacticoida			
Parastenocaris \`sp. B26\`	Stygofauna	Widespread	WAM
Parastenocaris jane	Stygofauna	Widespread	WAM & DBCA
Parastenocaris sp. indet. *	Stygofauna	Uncertain	Biologic
Schizopera roberiverensis	Stygofauna	Widespread	Biota (2010)
Harpacticoida sp. indet. *	Potential Stygofauna	Uncertain	WAM
Bathynellacea (Syncarida)			
Billibathynella sp. indet.	Stygobite	Potential SRE	DBCA
Brevisomabathynella \`sp. A\`	Stygobite	Potential SRE	Biologic
Brevisomabathynella \`sp. B\`	Stygobite	Potential SRE	Biologic
Brevisomabathynella \`sp. C\`	Stygobite	Potential SRE	Biologic
Brevisomabathynella \`sp. B03\`	Stygobite	Potential SRE	WAM & Biologic
Notobathynella sp. indet.	Stygofauna	Uncertain	Biota (2010)
Bathynellacea sp. indet. *	Stygofauna	Uncertain	Biota (2005)
Amphipoda			
Bogidiellidae \`sp. 1\`	Stygofauna	Potential SRE	DBCA
Bogidiella \`sp. B05\`	Stygofauna	Potential SRE	Biologic
Maarrka etheli	Stygofauna	Widespread	Biota (2010)
Melitidae \`sp. B05 (sp. 1 group)\`	Stygofauna	Widespread	WAM
Nedsia hurlberti	Stygofauna	Widespread	Biota (2010)
Nedsia \`sp. B04\`	Stygofauna	Widespread	WAM
Nedsia \`sp. UWA-A\`	Stygofauna	Potential SRE	Biota (2010)
Paramelitidae \`sp. 2 (DEC)\`	Stygofauna	Widespread	Biota (2010)
Paramelitidae \`sp. 6 (DEC)\`	Stygofauna	Widespread	Biota (2010)
Paramelitidae \`sp. B22\`	Stygofauna	Potential SRE	Biota (2012)
Paramelitidae \`sp. B36\`	Stygofauna	Widespread	WAM
Paramelitidae \`sp. B58\`	Stygofauna	Widespread	Biologic
Pilbarus millsi	Stygofauna	Widespread	DBCA & Biota (2010)

Taxonomy	Likely subterranean status	SRE status where known	Source
Nedsia sp. indet. *	Stygofauna	Uncertain	DBCA & Biota (2010)
Paramelitidae sp. indet. *	Stygofauna	Uncertain	Biota (2010)
Isopoda			
Armadillidae \`sp. Helix-I1\` (syn. *Troglarmadillo* \`sp. Helix-I1\`)	Troglobite	Potential SRE	Biota (2016a)
Armadillidae \`sp. Helix-I2\`	Troglobite	Potential SRE	Biota (2016a)
Hanoniscus \`sp. B10\`	Troglofauna	Potential SRE	WAM
Philosciidae \`sp. Helix-I7\` (syn, P. \`sp. Biologic-ISOP001\`)	Defunct OTU, synonym	Potential SRE	Biota (2016b)
Pygolabis paraburdoo	Stygofauna	Widespread	Biota (2010)
Troglarmadillo \`sp. B\`	Troglobite	Potential SRE	WAM & Biota (2013)
Troglarmadillo \`sp. B46\`	Troglofauna	Potential SRE	Biologic
Troglarmadillo \`sp. Helix-I1\` (syn. Armadillidae \`sp. Helix-I1\`)	Troglobite	Potential SRE	Biota (2016b)
Armadillidae sp. indet. *	Potential Troglofauna	Uncertain	WAM
Pygolabis? sp. indet. *	Potential Stygofauna	Uncertain	WAM
Isopoda sp. indet. *	Potential Troglofauna	Uncertain	WAM & Biota (2011, 2013, 2016c)
Scolopendrida			
Cryptops sp. indet.	Troglofauna	Potential SRE	Biota (2014, 2016d)
Polyxenida			
Unixenus sp. indet.	Potential Troglofauna	Uncertain	WAM
Lophoproctidae sp. indet.	Trogloxene	Widespread	WAM
Polyxenida sp. indet. *	Potential Troglofauna	Uncertain	WAM
Geophilida			
Geophilidae sp. indet.	Potential Troglofauna	Potential SRE	Biota (2011)
Pauropoda			
Pauropodidae \`sp. B29\`	Troglofauna	Potential SRE	Biologic
Pauropodidae \`sp. B41\`	Troglofauna	Potential SRE	Biologic
Pauropodidae \`sp. B42\`	Troglofauna	Potential SRE	Biologic
Pauropodidae \`sp. B43\`	Troglofauna	Potential SRE	Biologic
Pauropoda sp. indet. *	Troglofauna	Uncertain	Biota (2012, 2016c)
Diplura			
Campodeidae \`sp. EW\`	Troglofauna	Potential SRE	Biologic
Japygidae \`sp. Helix marra mamba\`	Troglofauna	Potential SRE	Biota (2016a)
Projapygidae \`sp. B14\`	Troglofauna	Potential SRE	Biologic
Projapygidae \`sp. B17\`	Troglofauna	Potential SRE	Biologic
Diplura sp. indet. *	Potential Troglofauna	Uncertain	Biota (2011)
Pseudoscorpiones			
Atemnidae \`sp. WAM-PSE087\`	Troglobite	Potential SRE	Biota (2014)
Chernetidae \`sp. Helix marra mamba\`	Troglobite	Potential SRE	Biota (2016a)
Chthoniidae \`sp. Helix marra mamba\`	Troglobite	Potential SRE	Biota (2016b)
Chthoniidae \`sp. WAM-PSE088\`	Troglobite	Potential SRE	Biota (2014)
Troglochernes sp. indet.	Troglobite	Potential SRE	WAM

Taxonomy	Likely subterranean status	SRE status where known	Source
Palpigradi			
Palpigradi sp. indet.	Potential Troglofauna	Uncertain	WAM & Biologic & Biota (2016a)
Schizomida			
Paradraculoides `sp. Helix lineage S1` (syn. *Paradraculoides* `sp. Helix marra mamba`)	Defunct OTU, synonym	Potential SRE	WAM
Paradraculoides `sp. Helix lineage S2` (syn. *Paradraculoides* `sp. Helix marra mamba`)	Defunct OTU, synonym	Potential SRE	WAM
Paradraculoides `sp. Helix lineage S3` (syn. *Paradraculoides* `sp. Helix marra mamba`)	Defunct OTU, synonym	Potential SRE	WAM
Paradraculoides `sp. Helix marra mamba`	Troglobite	Potential SRE	Biota (2016a, 2016b)
Paradraculoides `sp. Helix-D`	Troglobite	Potential SRE	Biota (2011)
Paradraculoides `sp. B11`	Troglobite	Potential SRE	WAM
Paradraculoides `sp. B12`	Troglobite	Potential SRE	WAM
Paradraculoides `sp. B12A`	Troglobite	Potential SRE	Biologic
Paradraculoides `sp. new 2`	Troglobite	Potential SRE	Biologic
Hubbardiidae sp. indet. (juvenile)*	Likely troglofauna	Uncertain	WAM
Schizomida sp. indet. *	Likely troglofauna	Uncertain	Biota (2011)
Araneae			
Anapistula `sp. EW`	Troglobite	Potential SRE	Biologic
Prethopalpus `sp. MW21`	Troglobite	Potential SRE	Biologic
Theridiidae sp. indet.	Potential Troglofauna	Uncertain	WAM
Oonopidae sp. indet. (juvenile) *	Potential Troglofauna	Uncertain	WAM
Symphyla			
Symphyella `sp. EW`	Troglofauna	Potential SRE	Biologic
Symphyla sp. indet. *	Troglofauna	Uncertain	Biota (2012)
Zygentoma			
Lepidospera `sp. B10`	Troglofauna	Potential SRE	Biologic
Nicoletiidae `sp. Helix marra mamba` (syn. Nicoletiidae `sp. Biologic-ZYGE007`)	Defunct OTU, synonym	Potential SRE	Biota (2016a)
Blattodea			
Nocticolidae `sp. Helix-A`	Troglofauna	Potential SRE	Biota (2011)
Nocticolidae `sp. Helix-BNA`	Troglofauna	Potential SRE	Biota (2012)
Nocticolidae `sp. Helix-BNR`	Troglofauna	Potential SRE	Biota (2012)
Nocticolidae sp. indet. *	Troglofauna	Uncertain	Biota (2012)
Blattodea sp. indet. *	Potential Troglofauna	Uncertain	Biota (2011, 2014, 2016a, 2016b, 2016c, 2016d)
Hemiptera			
Hemiptera sp. indet.	Potential Troglofauna	Potential SRE	Biota (2012)
Coleoptera			
Carabidae `sp. Helix-C1` (syn. Carabidae `sp. Biologic-COLE001`)	Defunct OTU, synonym	Unlikely SRE	Biota (2016a)
Carabidae `sp. Helix-C2`	Troglofauna	Potential SRE	Biota (2016b)

Taxonomy	Likely subterranean status	SRE status where known	Source
Carabidae `sp. Helix-C3`	Troglofauna	Potential SRE	Biota (2016b)
Carabidae `sp. Helix-C4`	Troglofauna	Potential SRE	Biota (2016b)
Macranillus `sp. 'EW`	Troglofauna	Potential SRE	Biologic
Staphylinidae `sp. Helix-C5`	Troglofauna	Potential SRE	Biota (2016b)
Staphylinidae `sp. Helix-C6`	Troglofauna	Potential SRE	Biota (2016b)

* indicates indeterminate taxa such as ‘Blattodea sp. indet.’ which are not included in species counts as they represent specimens that cannot be identified to species level (due to age or quality issues) and may represent a previously listed species. Defunct OTUs and synonyms are also not included in species counts.



biologic

Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Fig 4.1: Previous subterranean fauna records nearby and within the Study Area (Overview)

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994
Size A3. Created 11/03/2021

4.2 Previous survey results

Reports from subterranean fauna surveys within and immediately surrounding the Greater Brockman Study Area were reviewed for local and regional context (see Table 4.2 and 4.3 for overviews).

4.2.1 Brockman Syncline 4 (BS4)

Four subterranean fauna surveys have been conducted at BS4 between 2005 and 2016 (Biota, 2005, 2007, 2016b, 2016e), and a further two surveys were conducted in the nearby Beasley River (Biota, 2009) and Boolgeeda Creek (WRM, 2016).

Biota's survey work at BS4 and surrounding area (*i.e.* Beasley River), which comprised the sampling of 113 boreholes over the course of five surveys (Biota, 2005, 2007, 2009, 2016b, 2016e), revealed a depauperate stygofauna assemblage. Only one stygofauna specimen, a bathynellid, was collected in the 2005 survey from a total sample effort of 54 sampling events at 27 sites over two phases (Biota, 2005).

WRM's 2016 aquatic survey, which sampled 11 sites in Boolgeeda Creek (10 – 40 km west of BS4), recorded a combined total of 84 taxa from hyporheic Karaman-Chappuis samples (WRM, 2016). The 84 taxa included cyclopoid and harpacticoid copepods, ostracods, oligochaetes and syncarids. Whilst the majority of the taxa were considered stygoxene or stygophile, one unidentified syncarid was considered stygobitic (WRM, 2016).

Subterranean fauna surveys undertaken at the BS4 Marra Mamba area (southern side of BS4) and Beasley River recorded a diverse troglofauna assemblage (Biota, 2009, 2016b, 2016e). The two 2016 surveys, which sampled a combined total of 71 sites for troglofauna, recorded 63 potential troglofauna specimens. Molecular analysis revealed that the specimens represented 15 species from eight orders, comprising Pseudoscorpiones, Schizomida, Palpigradi, Coleoptera, Zygentoma, Diplura, Isopoda and Blattodea. The troglofauna recorded were associated with Marra Mamba BIF and colluvium habitats. Limited troglofauna sampling at Beasley River (five sites) recorded 14 potential troglofauna specimens from two orders (Polyxenida and Araneae) (Biota, 2009).

4.2.2 B2/ Nammuldi

Between 1998 and 2001, Biota completed an extensive stygofauna sampling program at Nammuldi (Biota, 2003), consisting of five phases of sampling. Seventeen of the 22 boreholes (77%) yielded no stygofauna during the five phases of sampling. The only stygofauna recorded were four singletons, collected from single sample sites on separate occasions. All the specimens were either immature, too small for identification and/ or lacked taxonomic resolution. Considering that only four specimens from a total of 110 bore-sampling events were recorded, Biota concluded there was no indication of a significant stygofauna community within the orebody aquifer at Nammuldi (Biota, 2003). It was suggested that the lack of a large alluvial drainage system in the

Nammuldi Study Area may have contributed to low stygofauna sampling success (Biota, 2003). Similarly, no additional stygofauna specimens were collected at Nammuldi in a 2010 survey (Biota, 2010). It was concluded that there was little evidence to suggest a significant stygal community is present at Nammuldi (Biota, 2010).

The only previous troglofauna survey conducted at Nammuldi sampled 30 sites over the course of two phases, recording 14 troglobitic specimens belonging to two orders (Polyxenida and Blattodea) (Biota, 2011).

4.2.3 Silvergrass and Caves Creek

Previous subterranean fauna surveys undertaken at Silvergrass revealed a rich stygofauna assemblage (Biota, 2010). A total of 458 stygobitic specimens were collected from 24 of the 41 sites, comprising 18 taxa belonging to eight orders. The assessment concluded that most of the stygofauna taxa recorded at Silvergrass were distributed at least at the scale of the contemporary Caves Creek (at least 30 km), with the majority also known to be regionally widespread (Biota, 2010). The same survey collected 25 troglobitic specimens at Silvergrass, though no specimens were identified to species level due to taxonomic constraints (Biota, 2010). The troglofauna at Silvergrass were primarily recorded in low hills of Marra Mamba Formation; however, due to the low taxonomic resolution of the higher-level identifications, their distributions remained uncertain.

A second troglofauna survey, sampling 74 sites at Silvergrass, recorded 140 troglobitic specimens belonging to the following five orders: Schizomida, Geophilida, Polyxenida, Diplura and Blattodea (Biota, 2011). The assessment concluded only a single troglobitic taxon could be regarded as of conservation significance owing to its locally restricted distribution; *Paradraculoides* sp. Helix-D (later regarded as Hubbardiidae sp. indet. (juvenile)).

A third subterranean fauna survey was recently undertaken by Biologic (2020, unpublished data). A total of 184 bores and holes were sampled over two phases (dry season 2018, wet season 2019), resulting in 259 troglofauna samples and 161 stygofauna samples. Taxonomic comparisons are ongoing, but preliminary results suggest a rich stygofauna and troglofauna species assemblage occurring in the Caves Creek Paleochannel. Using molecular and morphological identification methods, 47 stygofauna taxa belonging to eight orders were identified from the 2966 stygobitic specimens collected. The survey also collected 108 troglobitic specimens, comprising 29 taxa from 14 higher orders. None of these stygofauna and troglofauna species are listed or recognised as conservation priorities under state or federal legislation

4.2.4 West Turner Syncline

Four subterranean fauna surveys have been conducted at West Turner Syncline (located approximately 30 km west of Tom Price) between 2012 and 2016 (Biota, 2012, 2014, 2016c, 2016d).

Biota’s survey work at West Turner Syncline revealed a depauperate stygofauna assemblage (Biota, 2012, 2014, 2016d), with only a single survey recording stygofauna. This survey (Biota, 2012) recorded 16 stygofauna specimens belonging to two morphospecies; Paramelitidae sp. B22 and *Diacyclops* sp. indet. It was concluded that these results collectively indicate that no significant groundwater fauna occurs at West Turner Syncline, and there was minimal risk of any short-range spatial restrictions in the stygofauna found at this location (Biota, 2012).

Similarly, Biota’s four troglofauna surveys (Biota, 2012, 2014, 2016c, 2016d) indicated that troglofauna occur in low densities and limited diversity at West Turner Syncline, considering the sample effort. The 2012 survey, sampling 61 holes over two phases, recorded 77 troglofauna specimens from five orders (Polyxenida, Blattodea, Hemiptera, Pauropoda, Symphyla), none of which were considered true troglobites. Further survey work in 2014, which sampled 20 sites, recorded five morphospecies, comprising two pseudoscorpions (*Tyrannochthonius* \`sp. PSE088\` and Atemnidae \`sp. PSE087\`), and single records of scolopendrid (*Cryptops* sp. indet.), polyxenid (Polyxenida sp. indet.) and a cockroach (Blattodea sp. indet.). Of these, only *Tyrannochthonius* \`sp. PSE088\` and *Cryptops* sp. indet. were considered to be troglobitic (Biota, 2014). The two surveys in 2016 (Biota, 2016c, 2016d) recorded troglofauna belonging to four orders: Blattodea, Pauropoda, Isopoda and Scolopendrida.

Table 4.2: Summary of previous subterranean fauna survey effort and results within and immediately surrounding the Study Area (BS4 & Nammuldi / Silvergrass)

Previous survey	Brockman Syncline 4 Project - Baseline Stygofauna Assessment	Brockman Syncline 4 Boolgeeda Creek Stygofauna Survey	Brockman Syncline 4 Marra Mambas Subterranean Fauna Assessment	BS4 Marra Mambas Troglobitic Fauna Addendum Report	Beasley River Subterranean Fauna Survey 2009	BS4 Baseline Aquatic Biota and Water Quality Surveys of Boolgeeda Creek	Nammuldi Stygofauna Assessment Programme	Nammuldi - Silvergrass Subterranean Fauna Assessment	Nammuldi - Silvergrass Troglobitic Fauna Assessment
Author, year	**Biota 2005**	**Biota 2007**	**Biota 2016a**	**Biota 2016b**	**Biota 2009**	**WRM 2016**	**Biota 2003**	**Biota 2010**	**Biota 2011**
Distance from Study Area	0 km	0 - 0.5 km	0 km	0 km	0 - 5 km	10 - 40 km	~15 km	~15 km	~15 km
Geology	Goethite-hematite BIF, clay, weathered shales; minor alluvials, calcrete and dolerite	Superficial alluvial aquifers	Goethite-hematite BIF, chert, colluvium, minor alluvials and calcrete	Goethite-hematite BIF, chert, colluvium, minor alluvials and calcrete	Not discussed	Alluvial gravels in dry streambed	Alluvials, detritals, calcrete	Goethite-hematite BIF, Calcrete deposits, alluvials (sands, clays, ironstone rubble)	Goethite-hematite BIF, Calcrete deposits, alluvials (sands, clays, ironstone rubble)
Fauna targeted	Stygofauna	Stygofauna	Troglofauna & Stygofauna	Troglofauna	Troglofauna & Stygofauna	Aquatic fauna, including stygofauna	Stygofauna	Troglofauna & Stygofauna	Troglofauna
Areas sampled	BS4	BS4	BS4	BS4	Beasley River	BS4	Nammuldi	Nammuldi, Silvergrass	Nammuldi, Silvergrass
Bores sampled	27	9	48	23	6	11	22	78	104
Bores sampled within Study Area	27	7	48	23	1	0	22	62	104
Sampling methods	Net hauling	Net hauling	Trapping, Scraping, Net hauling	Trapping, Scraping	Trapping, Net hauling	Karaman-Chappuis	Net hauling	Trapping, Net hauling	Trapping
Identification methods	Morpho	Morpho	Morpho & DNA	Morpho & DNA	Morpho	Morpho	Morpho	Morpho	Morpho & DNA

Previous survey	Brockman Syncline 4 Project - Baseline Stygofauna Assessment	Brockman Syncline 4 Boolgeeda Creek Stygofauna Survey	Brockman Syncline 4 Marra Mambas Subterranean Fauna Assessment	BS4 Marra Mambas Troglobitic Fauna Addendum Report	Beasley River Subterranean Fauna Survey 2009	BS4 Baseline Aquatic Biota and Water Quality Surveys of Boolgeeda Creek	Nammuldi Stygofauna Assessment Programme	Nammuldi - Silvergrass Subterranean Fauna Assessment	Nammuldi - Silvergrass Troglobitic Fauna Assessment
Author, year	**Biota 2005**	**Biota 2007**	**Biota 2016a**	**Biota 2016b**	**Biota 2009**	**WRM 2016**	**Biota 2003**	**Biota 2010**	**Biota 2011**
Trog collected	No	No	Yes	Yes	Yes	No	No	Yes	Yes
Araneae					●				
Blattodea			●	●				●	●
Coleoptera			●	●					
Diplura			●						●
Geophilida									●
Isopoda			●	●					
Palpigradi			●						
Polyxenida					●			●	●
Pseudoscorpiones			●	●					
Schizomida			●	●				●	●
Zygentoma			●						
Stygo collected	Yes	No	No	No	No	Yes	Yes	Yes	No
Amphipoda							●	●	
Copepoda						●	●	●	
Isopoda								●	
Nematoda								●	
Oligochaeta						●	●	●	
Ostracoda						●		●	
Platyhelminthes								●	
Bathynellacea	●					●		●	

Table 4.3: Summary of previous subterranean fauna survey effort and results within and immediately surrounding the Study Area (West Turner Syncline & Homestead)

Previous survey	Silvergrass and Caves Creek Subterranean Fauna Assessment	Rio Tinto Regional Troglobitic Fauna Study	West Turner Syncline Stage 2 B1 and Section 17 Deposits Subterranean Fauna Survey	Western Turner Syncline Section 10 BWT and Satellite Ore Bodies Subterranean Fauna Survey	West Turner Syncline S10 Hub Subterranean Fauna Assessment Addendum Report	Western Turner Syncline Section 10 Hub Subterranean Fauna Assessment
Author, year	**Biologic 2020 (unpublished data)**	**Biota 2013**	**Biota 2012**	**Biota 2014**	**Biota 2016c**	**Biota 2016d**
Distance from Study Area	2-40 km	6 - 202 km	13 - 20 km	19 - 22 km	20 - 21 km	19 - 22 km
Geology	BrIF, MMIF, detritals, calcrete, Wittenoom Dolomite	BIF, alluvium, colluvium	Colluvium, BIF	Colluvium, BIF, minor alluvium, chert and calcrete	Not discussed	Colluvium, BIF, minor alluvium, chert and calcrete
Fauna targeted	Troglofauna & Stygofauna	Troglofauna	Troglofauna & Stygofauna	Troglofauna & Stygofauna	Troglofauna	Troglofauna & Stygofauna
Areas sampled	Homestead, Silvergrass, Caves Creek	Homestead, West Angelas, Rhodes Ridge	West Turner Syncline	West Turner Syncline	West Turner Syncline	West Turner Syncline
Bores sampled	184	169	78	24	32	45
Bores sampled within Study Area	0	0	0	0	0	0
Sampling methods	Trapping, Scraping, Net hauling, Karaman, Pumping, Creek flow	Trapping, Scraping, Net hauling	Trapping, Net hauling	Trapping, Net hauling	Trapping	Trapping, Net hauling
Identification methods	Morpho & DNA	Morpho & DNA	Morpho & DNA	Morpho	Morpho	Morpho
Trog collected	Yes	Yes	Yes	Yes	Yes	Yes
Araneae	●	●				
Blattodea	●	●	●	●	●	●
Chilopoda	●					
Coleoptera	●					
Diplura	●	●				
Geophilida		●				
Hemiptera	●	●	●			
Isopoda	●	●			●	
Palpigradi	●					
Pauropoda	●		●		●	
Polyxenida	●	●	●	●		
Pseudoscorpiones	●	●		●		
Schizomida	●	●				
Scolopendrida				●		●
Symphyla	●		●			
Zygentoma	●	●				

Previous survey	Silvergrass and Caves Creek Subterranean Fauna Assessment	Rio Tinto Regional Troglobitic Fauna Study	West Turner Syncline Stage 2 B1 and Section 17 Deposits Subterranean Fauna Survey	Western Turner Syncline Section 10 BWT and Satellite Ore Bodies Subterranean Fauna Survey	West Turner Syncline S10 Hub Subterranean Fauna Assessment Addendum Report	Western Turner Syncline Section 10 Hub Subterranean Fauna Assessment
Author, year	**Biologic 2020 (unpublished data)**	**Biota 2013**	**Biota 2012**	**Biota 2014**	**Biota 2016c**	**Biota 2016d**
Stygo collected	Yes	No	Yes	No	No	No
Amphipoda	●		●			
Bathynellacea	●					
Cyclopoida	●		●			
Harpacticoida	●					
Isopoda	●					
Oligochaeta	●					
Polychaeta	●					
Ostracoda	●					

5. TROGLOFAUNA RESULTS

5.1 Troglofauna habitats

Suitable AWT habitats for troglofauna (*i.e.* caves, cavities, fractures, vugs, and pore spaces) occur widely throughout the Study Area within a variety of geological settings. Two of the most common geologies that provide suitable habitat are the Brockman Iron Formation (BrIF) and Marra Mamba Iron Formation (MMIF), where the supergene weathering processes that have enriched the mineralised zone have created troglofauna habitat by dissolving cavities, vugs, and pore spaces, and opening cracks and fractures within the rock. Habitats created by secondary weathering processes are prevalent throughout the hematite-goethite-martite hardcap (also pisolitic duricrust) on the tops and flanks of the ranges, as well as Robe Pisolite (CID), karstic calcrete, and weathered dolomite deposits in the valleys. Faults and fracture zones throughout these formations and parts of the otherwise massive/ fresh bedrock (particularly where deformed near the surface) can interconnect to form vast networks of suitable AWT habitat. Fractured and weathered rock habitats are prevalent AWT within the BrIF, MMIF and Wittenoom Dolomite Formation (WDF), especially near the numerous faults throughout the Brockman Syncline.

Unconsolidated alluvial and colluvial layers in valleys, adjacent drainage lines, and flanking the main ranges may also provide moderately to highly suitable habitats for troglofauna where sufficient pore spaces occur. AWT habitat in these types of deposits (and the WDF underlying them in the synclinal valleys) may be constrained by near surface groundwater tables, and where adjacent to major drainage lines, as there may be periodic inundation from floods. Nevertheless, such deposits can still provide highly suitable AWT habitats for troglofauna.

Figures 5.1 and 5.2 show modelled AWT habitats throughout the Study Area in relation to surface geological mapping (GSWA 1:250,000), and locations of troglofauna sampled during the survey. Details regarding AWT habitats for each major survey area are noted further below.

5.1.1 BS2 and BS3

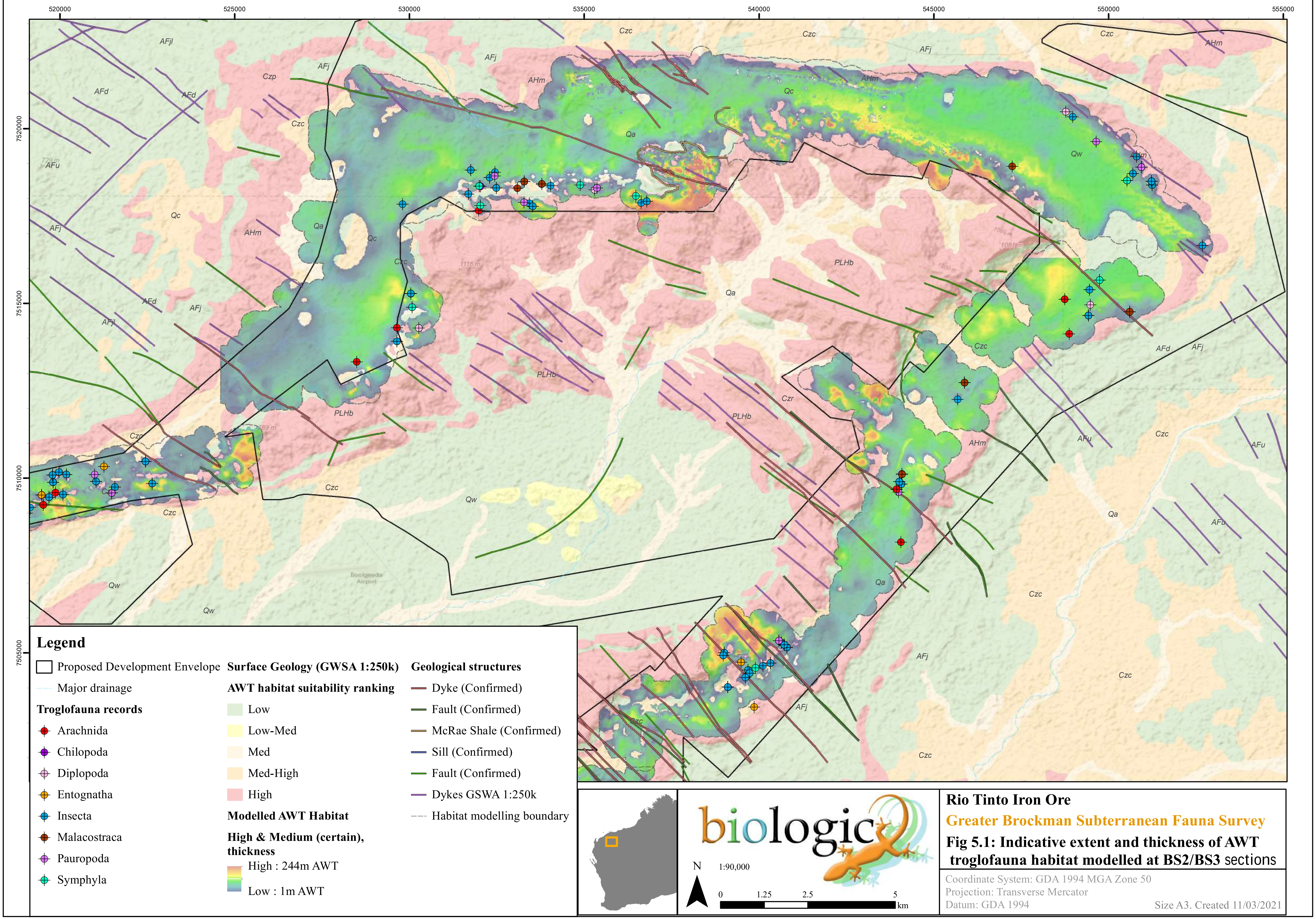
Figure 5.1 shows the thickness of high and medium (certain) AWT habitat surrounding the Brockman Syncline from BS2 (north and west) to BS3 (south and east). High and medium (certain) suitability habitats were mainly modelled within the BrIF and MMIF of the major ranges, as well as in the WD, detritals and calcrete in the Synclinal valley (where above water table) (refer section 3.5 and Biologic 2020). The resultant modelling shows moderately to highly thick, nearly continuous AWT habitat along the flanks of the Brockman Range. Some patchiness in habitat continuity occurs where Mt McRae Shales are prominent along the flanks of the Brockman Range, but the wider extent of AWT habitat around these patches is well connected.

Meanwhile a medium thickness of AWT habitat is shown throughout the detrital valley and in the surrounding MMIF ridge. The gaps in the modelled AWT habitats in the eastern part of the syncline are attributed to the sparsity of drilling in this area (as observed by discontinuities in the modelling boundary), rather than actual patchiness of habitat. Extrapolation between these patches, within the BrIF, MMIF, or valley detritals suggests connected habitats, as seen in northern parts.

The thickest areas of modelled habitat occur high on the flanks of the Brockman Range (shown in red in Figure 5.1). In some areas, the modelling may be overestimating the maximum depth of the habitable zone (particularly in the thickness of 'medium' certain geologies), as high pressures and infill from fine sediments may reduce aperture spaces in ironstone formation at depths beyond approximately 150 mbgl (J. Barnett pers. comm. 2017). Diamond core drilling throughout the Brockman Syncline was relatively sparse, but visual inspection of drill cores from Nammuldi and Lens G showed the occurrence of vuggy, porous, and well-developed fractures that would be suitable for troglofauna down to depths of at least 96 mbgl. Even if areas of suitable habitat modelled deeper than 150 mbgl were ignored (i.e. the red and orange colours in Figure 5.1), the habitat modelling still shows extensive areas of AWT habitat in upland parts of the Brockman Range, up to approx. 150 m from surface (i.e. yellow coloured areas).

Structural elements such as faults and folds are very common throughout the Brockman Syncline zone, mainly striking in a north west to south east direction, perpendicular to the strike of the ridge in western and eastern parts. Very few of these structures appear to extend throughout the modelled AWT habitats, and hydrogeological reports suggested that the faults and dykes are restricted to the bedrock geologies only (i.e. BrIF, MMIF, and WD) (Rio Tinto 2020). Although several confirmed dykes are shown to occur in the western, northern, and eastern parts of the syncline, these structures are not interpreted to form barriers to troglofauna movement for species that can occur in the detrital formations. The modelled connectivity of AWT habitats across these dykes is assumed to be facilitated by high to medium suitability detrital formations on the range flanks and in the valley, which occur above these geological structures.

Concurrently, the high number of faults and associated fracture zones occurring throughout the Syncline may facilitate local habitat connectivity between areas within the habitat modelling boundary and the BrIF/ MMIF geologies beyond the modelling boundary. Categorisation of the surface geology for AWT habitat suitability showed vast areas of high to medium suitability AWT habitat in the centre of the Brockman Syncline, adjacent to and contiguous with the modelled habitat (Figure 5.1). These areas, although subject to the same geological structures, may also facilitate wider habitat connectivity for troglofauna species.



Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Fig 5.1: Indicative extent and thickness of AWT troglofauna habitat modelled at BS2/BS3 sections

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994
Size A3. Created 11/03/2021

5.1.2 BS1, BS4 and Vivash

Figure 5.2 shows the modelled troglofauna habitat at BS1 in the north of the map, and BS4 to Vivash in the south and south west of the map.

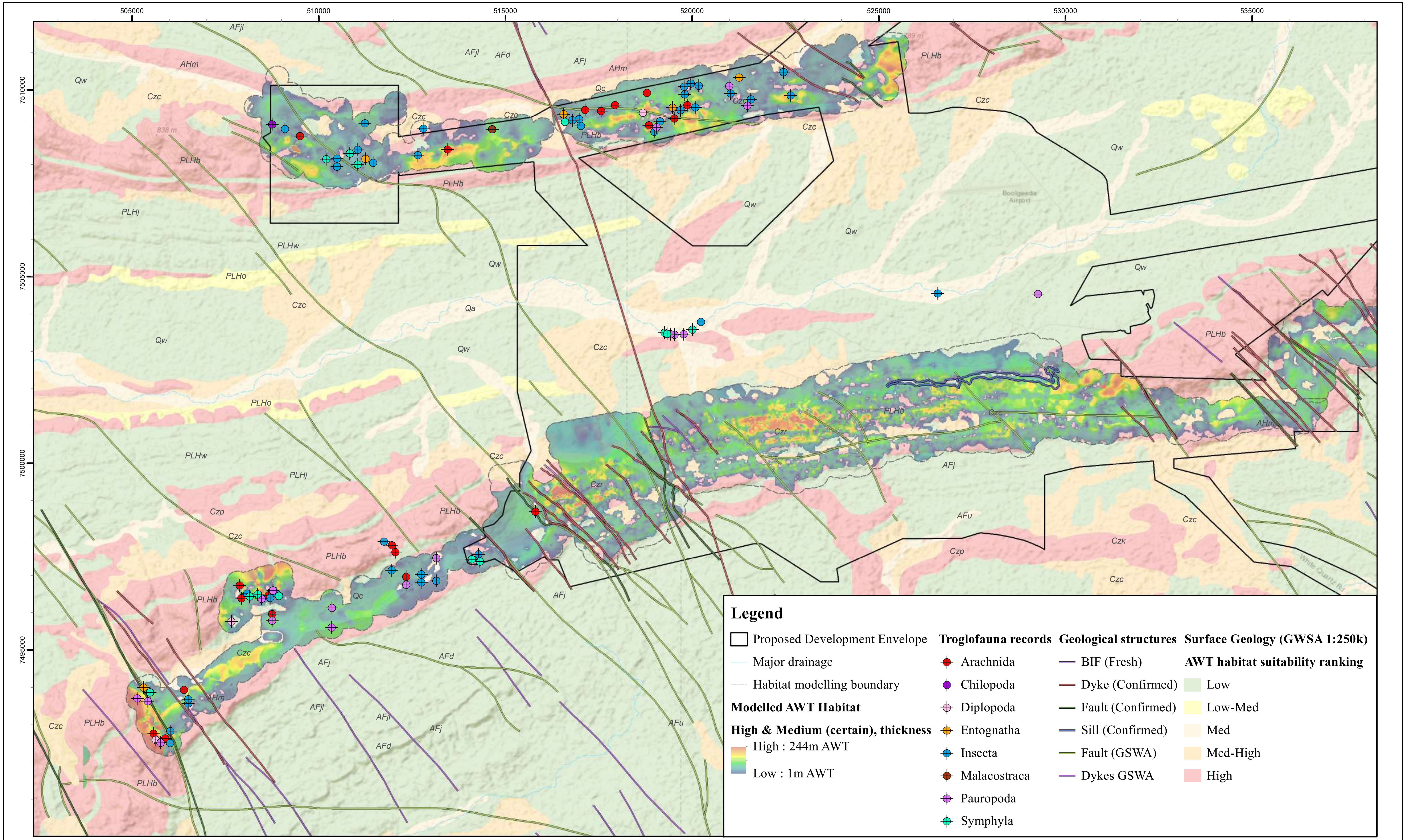
The modelling shows AWT habitats are reasonably continuous along strike of the syncline and synclinal valley, particularly at BS1 and at Vivash. At BS4 AWT habitats are patchier, with a higher degree of localised variability, but the modelling did not reveal any major breaks in the overall continuity of habitat at the landscape scale.

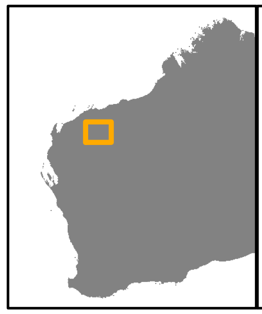
At BS1, thicker patches of AWT habitat are shown in the south and east, associated with the upland areas of the Brockman Range (BrIF, noted as PLHb in Figure 5.2). The synclinal valley at BS1 features a thin to medium thickness of suitable habitat AWT (comprised of detritals and calcrete, shown as blue/ green patches), which is largely continuous along strike and connected to the BrIF on the ranges. The northern side of the synclinal valley is composed of MMIF (AHm in Figure 5.2), which is largely beyond the modelling boundary, but which also provides highly suitable habitats.

The AWT habitat at BS4 and Vivash is hosted within the same geological formations as at BS1, but the size and thickness of the bands is larger, they are closer together in the landscape, and the orientation from north to south is mirrored on the southern limb of the Brockman Syncline. Intense folding, faulting, and deformation has affected this area of the Syncline, bringing the MMIF, WD, and BrIF geologies closer together spatially, and creating numerous complex geological structures.

The detrital formations of this area are not as vast as at BS2 and BS3, but there is a thin layer of detrital material that could facilitate AWT habitat connectivity along strike, above the numerous dykes of the area. In any case, the dykes appear to be subject to the same faulting that creates fracture zones in the bedrock (Rio Tinto, 2020), thereby promoting potential habitat connectivity. Although the AWT habitat modelling at BS4 and Vivash shows a greater degree of localised patchiness and complexity than in other parts of the Brockman Syncline, this may not necessarily translate to habitat discontinuity where the intrusives are as highly faulted and fractured as the surrounding bedrock. The faults also appear to carry on beyond the habitat modelling area into the surrounding BrIF geology north of the far eastern part of BS4, and north of Vivash. These faults and associated fracture zones may facilitate connectivity between highly suitable areas of AWT habitat inside and outside of the modelling boundary.

The current habitat modelling does not extend throughout the Boolgeeda Creek valley in the centre of the Syncline between BS1 and BS4/ Vivash. Nevertheless, the presence of calcrete, Robe Pisolite, and alluvium/ colluvium (shown in red, orange, and yellow in Figure 5.2) indicates that potentially suitable geological formations occur to support troglofauna. Numerous troglofauna were recorded from the few samples that were able to be collected in this area, although these were entirely from cased bores or Karaman samples, which may have affected the ability to detect true troglofauna.





Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Fig 5.2: Indicative extent and thickness of AWT troglofauna habitat modelled at BS1 to BS4

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994
Size A3. Created 11/03/2021

5.2 Troglofauna results (current survey)

The current survey recorded a total of 799 troglofauna specimens. A total of 124 unique species/ OTUs were recorded, representing 16 higher level taxonomic groups comprising Araneae, Palpigradi, Pseudoscorpiones, Schizomida, Scorpiones, Isopoda, Chilopoda, Pauropoda, Polydesmida, Polyxenida, Symphyla, Diplura, Blattodea, Coleoptera, Hemiptera and Zygentoma (Table 5.1 and Table 5.2). A further 28 indeterminate taxa were identified belonging to the aforementioned groups, although these could not be resolved to species-level due to specimens being immature, in poor/damaged condition or the wrong sex for species-level identification (Table 5.3). The locations of subterranean troglofauna collected during the survey are shown in Figure 5.3 (overview) and in Figures 5.4 – 5.9 (detailed).

Table 5.1: Overview of troglofauna species/ OTUs detected from the Study Area (current survey)

Higher taxon	No. species/ OTUs	No specimens
Araneae	9	15
Palpigradi	13	20
Pseudoscorpiones	7	13
Schizomida	4	18
Scorpiones	1	1
Isopoda	7	8
Chilopoda	6	11
Pauropoda	14	16
Polydesmida	1	1
Polyxenida	4	8
Symphyla	15	28
Diplura	16	19
Blattodea	6	41
Coleoptera	6	13
Hemiptera	4	24
Zygentoma	11	20
Indeterminate	/	543
Total	**124**	**799**

Table 5.2: Troglofauna species/ OTUs detected from the Study Area (current survey), taxonomic and distribution comments, known linear ranges and collection locations

Taxonomy	No. spms	Taxonomic certainty and comment	Sub-fauna status, SRE status	Sections	No. sites	Distribution, known linear range
ARACHNIDA						
Araneae						
Araneae `sp. Biologic-ARAN004`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS4	1	Singleton
Araneae `sp. Biologic-ARAN005`	2	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS1	2	Locally restricted (1.7 km)
Gnaphosidae `sp. Biologic-ARAN006`	2	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS2, BS3	2	Locally widespread (15.0 km)
Gnaphosidae `sp. Biologic-ARAN007`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS4	1	Singleton
Prethopalpus `sp. Biologic-ARAN001`	1	High, DNA (unique lineage)	Troglobite, Potential SRE	BS3	1	Singleton
Prethopalpus `sp. Biologic-ARAN002`	1	High, DNA (unique lineage)	Troglobite, Potential SRE	BS2	1	Singleton
Prethopalpus `sp. Biologic-ARAN016`	1	High, DNA (unique lineage)	Troglobite, Potential SRE	BS4	1	Singleton
Prethopalpus `sp. Biologic-ARAN023`	1	High, DNA (unique lineage)	Troglobite, Potential SRE	BS3	1	Singleton
Theridiidae `sp. WAM-ARAN001`	5	High, DNA; external match Paraburdoo (Cullen & Harvey, 2018)	Not troglobite, Widespread	BS1, BS4	2	Regionally widespread (100+ km)
Palpigradi						
Palpigradi `sp. Biologic-PALP002`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS2	1	Singleton
Palpigradi `sp. Biologic-PALP003`	2	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS3	2	Locally restricted (0.2 km)
Palpigradi `sp. Biologic-PALP004`	2	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS3	2	Locally restricted (3.3 km)
Palpigradi `sp. Biologic-PALP006`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS3	1	Singleton
Palpigradi `sp. Biologic-PALP007`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS2	1	Singleton
Palpigradi `sp. Biologic-PALP008`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS4	1	Singleton
Palpigradi `sp. Biologic-PALP009`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS4	1	Singleton
Palpigradi `sp. Biologic-PALP010`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS1	1	Singleton
Palpigradi `sp. Biologic-PALP012`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS3	1	Singleton
Palpigradi `sp. Biologic-PALP013`	6	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS4	2	Locally restricted (7.5 km)
Palpigradi `sp. Biologic-PALP031`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS3	1	Singleton
Palpigradi `sp. Biologic-PALP032`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS3	1	Singleton
Palpigradi `sp. Biologic-PALP033`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS3	1	Singleton
Pseudoscorpiones						
Chthoniidae `sp. Biologic-PSEU004`	4	High, DNA (unique lineage)	Troglobite, Potential SRE	BS1	4	Locally restricted (0.5 km)
Chthoniidae `sp. Biologic-PSEU005`	1	High, DNA (unique lineage)	Troglobite, Potential SRE	BS4	1	Singleton

Taxonomy	**No. spms**	**Taxonomic certainty and comment**	**Sub-fauna status, SRE status**	**Sections**	**No. sites**	**Distribution, known linear range**
Chthoniidae `sp. Biologic-PSEU006`	3	High, DNA (unique lineage)	Troglobite, Potential SRE	BS1	3	Locally restricted (1.0 km)
Chthoniidae `sp. Biologic-PSEU007`	1	High, DNA (unique lineage)	Troglobite, Potential SRE	BS3	1	Singleton
Chthoniidae `sp. Biologic-PSEU008`	1	High, DNA (unique lineage)	Troglobite, Potential SRE	BS4	1	Singleton
Chthoniidae `sp. Biologic-PSEU009`	2	High, DNA (unique lineage)	Troglobite, Potential SRE	BS4	2	Locally restricted (4.3 km)
Indolpium `sp. Biologic-PSEU003`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS1	1	Singleton
Schizomida						
Draculoides `sp. Biologic-SCHI010`	1	High, DNA (unique lineage)	Troglobite, Potential SRE	BS4	1	Singleton
Draculoides `sp. Biologic-SCHI011`	2	High, DNA (unique lineage)	Troglobite, Potential SRE	BS4	2	Locally restricted (3.5 km)
Draculoides `sp. Biologic-SCHI017`	4	High, DNA (unique lineage)	Troglobite, Potential SRE	BS1	3	Locally restricted (2.0 km)
Draculoides `sp. Biologic-SCHI019`	11	High, DNA; external match Eliwana/ Flying Fish (Bennelongia 2015)	Troglobite, Potential SRE	BS1	10	Potentially locally widespread (15.7 km)
Scorpiones						
Scorpiones `sp. Biologic-SCOR002`	1	High, DNA (unique lineage)	Troglobite, Potential SRE	BS3	1	Singleton
MALACOSTRACA						
Isopoda						
Armadillidae `sp. Biologic-ISOP002`	2	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS1	1	Single site
Armadillidae `sp. Biologic-ISOP004`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS4	1	Singleton
Armadillidae `sp. Biologic-ISOP008`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS4	1	Singleton
Buddelundia? `sp. Biologic-ISOP005`	1	High, DNA (unique lineage)	Uncertain troglobite, Potential SRE	BS3	1	Singleton
Buddelundia? `sp. Biologic-ISOP006`	1	High, DNA (unique lineage)	Uncertain troglobite, Potential SRE	BS3	1	Singleton
Isopoda `sp. Biologic-ISOP007`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS3	1	Singleton
Philosciidae `sp. Biologic-ISOP001`	1	High, DNA; external match BS4 (Biota 2016)	Not troglobite, unlikely SRE	BS2	1	Locally widespread (41 km)
MYRIAPODA						
Chilopoda						
Cormocephalus `sp. A`	1	High, DNA; external match Trinity bore, Mesa B (Edgecombe *et al.* 2019)	Not troglobite, Widespread	BS2	1	Regionally widespread (100+ km)
Geophilomorpha `sp. Biologic-CHIL002`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS1	1	Singleton
Geophilomorpha `sp. Biologic-CHIL007`	4	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS1	1	Single site
Scolopendromorpha `sp. Biologic-CHIL005`	1	High, DNA (unique lineage)	Uncertain troglobite, Potential SRE	BS4	1	Singleton
Scolopendromorpha `sp. Biologic-CHIL006`	3	High, DNA (unique lineage)	Not troglobite, Potential SRE	BS4	2	From hyporheic samples only (0.8 km)
Scolopendromorpha `sp. BS1`	1	Morpho; no genetic confirmation	Potential troglobite, Potential SRE	BS1	1	Singleton

Taxonomy	No. spms	Taxonomic certainty and comment	Sub-fauna status, SRE status	Sections	No. sites	Distribution, known linear range
Pauropoda						
Pauropoda `sp. Biologic-PAUR004`	1	High, external match with sequences from Rocklea Station (GenBank)	Not troglobite, uncertain SRE	BS4	1	Locally widespread (45.5 km)
Pauropoda `sp. Biologic-PAUR005`	1	High, DNA (unique lineage)	Uncertain troglobite, Potential SRE	BS2	1	Singleton
Pauropoda `sp. Biologic-PAUR006`	1	High, DNA (unique lineage)	Uncertain troglobite, Potential SRE	BS2	1	Singleton
Pauropoda `sp. Biologic-PAUR007`	2	High, DNA (unique lineage)	Uncertain troglobite, Potential SRE	BS2	2	Locally restricted (1.2 km)
Pauropoda `sp. Biologic-PAUR008`	2	High, DNA; external match SGCCK (Biologic 2020)	Not troglobite, uncertain SRE	BS3, BS4	2	Locally widespread (52.6 km), hyporheic samples only
Pauropoda `sp. Biologic-PAUR009`	1	High, external match with sequences from Rocklea Station (GenBank)	Not troglobite, uncertain SRE	BS1	1	Locally widespread (45.0 km)
Pauropoda `sp. Biologic-PAUR010`	1	High, DNA (unique lineage)	Uncertain troglobite, Potential SRE	BS2	1	Singleton
Pauropoda `sp. Biologic-PAUR011`	1	High, DNA (unique lineage)	Uncertain troglobite, Potential SRE	BS4	1	Singleton
Pauropoda `sp. Biologic-PAUR013`	1	High, DNA (unique lineage)	Uncertain troglobite, Potential SRE	BS3	1	Singleton
Pauropoda `sp. Biologic-PAUR036`	1	High, DNA (unique lineage)	Uncertain troglobite, Potential SRE	BS3	1	Singleton
Pauropoda `sp. Biologic-PAUR037`	1	High, DNA (unique lineage)	Uncertain troglobite, Potential SRE	BS3	1	Singleton
Pauropoda `sp. Biologic-PAUR038`	1	High, DNA (unique lineage)	Uncertain troglobite, Potential SRE	BS3	1	Singleton
Pauropoda `sp. Biologic-PAUR039`	1	High, DNA (unique lineage)	Uncertain troglobite, Potential SRE	BS3	1	Singleton
Pauropoda `sp. Biologic-PAUR040`	1	High, DNA (unique lineage)	Uncertain troglobite, Potential SRE	BS3	1	Singleton
Polydesmida						
Polydesmida `sp. Biologic-POLD002`	1	High, DNA (unique lineage)	Troglobite, Potential SRE	BS3	1	Singleton
Polyxenida						
Polyxenida `sp. Biologic-POLX002`	2	High, DNA; external match Robe Headwaters, Turee Syncline and Western Turner Syncline (Biota 2009, Biota 2013, Biota 2014)	Not troglobite, Widespread	BS3	2	Regionally widespread (100+ km)
Polyxenida `sp. Biologic-POLX003`	4	High, DNA; external match Paraburdoo, Turee Syncline and Mesa G (Biota 2006, Biota 2009, Biota 2013)	Not troglobite, Widespread	BS1, BS2, BS3	4	Regionally widespread (100+ km)
Polyxenida `sp. Biologic-POLX005`	1	High, DNA; external match West Angelas, Angelo River and Rhodes Ridge (Biologic, unpublished dataset)	Not troglobite, Widespread	BS2	1	Regionally widespread (200+ km)
Lophoproctidae `sp. Biologic-POLX006`	1	High, DNA; external match Bungaroo Valley (Helix sequence) and Angelo River (Biologic, unpublished dataset)	Not troglobite, Widespread	BS3	1	Regionally widespread (100+ km)
Symphyla						
Hanseniella `sp. Biologic-SYMP001`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS2	1	Singleton

Taxonomy	No. spms	Taxonomic certainty and comment	Sub-fauna status, SRE status	Sections	No. sites	Distribution, known linear range
Hanseniella `sp. Biologic-SYMP003`	5	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS2, BS3	5	Locally widespread (16.4 km)
Hanseniella `sp. Biologic-SYMP006`	2	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS4	2	Locally restricted (4.3 km)
Hanseniella `sp. Biologic-SYMP031`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS3	1	Singleton
Hanseniella `sp. Biologic-SYMP032`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS3	1	Singleton
Scolopendrellidae `sp. Biologic-SYMP008`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS4	1	Singleton
Scolopendrellidae `sp. Biologic-SYMP014`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS4	1	Singleton
Scutigerellidae `sp. Biologic-SYMP004`	2	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS3, BS2	2	Locally restricted (2.9 km)
Scutigerellidae `sp. Biologic-SYMP005`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS4	1	Singleton, hyporheic sample only
Scutigerellidae `sp. Biologic-SYMP007`	4	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS1, BS4	3	Locally widespread (12 km)
Symphyla `sp. Biologic-SYMP013`	4	High, DNA (unique lineage	Potential troglobite, Potential SRE	BS4	1	Single site, hyporheic sample only
Symphylella `sp. Biologic-SYMP030`	1	High, DNA (unique lineage	Potential troglobite, Potential SRE	BS3	1	Singleton
Symphylella `sp. BS4`	2	Med, Putative unique OTU based on morphology and distribution patterns in the group; no genetic confirmation.	Potential troglobite, Potential SRE	BS4	1	Single site
Symphylella `sp. BS1`	1	Med, Putative unique OTU based on morphology and distribution patterns in the group; no genetic confirmation.	Potential troglobite, Potential SRE	BS1	1	Singleton
Scolopendrellopsis `sp. BS1`	1	High, DNA (unique lineage	Potential troglobite, Potential SRE	BS1	1	Singleton
ENTOGNATHA						
Diplura						
Japygidae `sp. Biologic-DIPL008`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS1	1	Singleton
Japygidae `sp. Biologic-DIPL009`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS4	1	Singleton, collected from water bore
Japygidae `sp. Biologic-DIPL014`	1	High, DNA (unique lineage); close genetic relationship to DIPL015	Potential troglobite, Potential SRE	BS1	1	Singleton
Japygidae `sp. Biologic-DIPL015`	1	High, DNA; external match with sequences from Eliwana (Bennelongia, 2015)	Uncertain troglobite, Potential SRE	BS1	1	Adjacent sampling areas (20 km)
Japygidae `sp. Biologic-DIPL027`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS3	1	Singleton
Japygidae `sp. Biologic-DIPL028`	2	High, DNA; external match with a Helix sequence from BS4	Uncertain troglobite, Potential SRE	BS3, BS4	2	Adjacent sampling areas (27.1 km)
Parajapygidae `sp. Biologic-DIPL007`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS3	1	Singleton
Parajapygidae `sp. Biologic-DIPL018`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS1	1	Singleton
Parajapygidae `sp. Biologic-DIPL029`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS3	1	Singleton

Taxonomy	No. spms	Taxonomic certainty and comment	Sub-fauna status, SRE status	Sections	No. sites	Distribution, known linear range
Projapygidae `sp. Biologic-DIPL003`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS1	1	Singleton
Projapygidae `sp. Biologic-DIPL004`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS3	1	Singleton
Projapygidae `sp. Biologic-DIPL005`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS4	1	Singleton, hyporheic sample only
Projapygidae `sp. Biologic-DIPL013`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS1	1	Singleton
Projapygidae `sp. Biologic-DIPL030`	2	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS3	2	Locally restricted (2.4 km)
Projapygidae `sp. Biologic-DIPL031`	2	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS3	2	Locally restricted (0.6 km)
Projapygidae `sp. Biologic-DIPL032`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS3	1	Singleton
INSECTA						
Blattodea						
Nocticola `sp. Biologic-BLAT005`	4	High, DNA (unique lineage)	Uncertain troglobite, Potential SRE	BS1	4	Locally restricted (1.6 km)
Nocticola `sp. Biologic-BLAT006`	5	High, DNA (unique lineage)	Uncertain troglobite, Potential SRE	BS1	3	Locally restricted (2.0 km)
Nocticola `sp. Biologic-BLAT007`	12	High, DNA (unique lineage)	Not troglobite, unlikely SRE	BS1, BS2, BS4	9	Locally widespread (44 km)
Nocticola `sp. Biologic-BLAT008`	10	High, DNA (unique lineage)	Uncertain troglobite, Potential SRE	BS2, BS3	9	Adjacent sampling areas (18.6 km)
Nocticola `sp. Biologic-BLAT010`	9	High, DNA; external match SGCCK (Biologic 2020)	Not troglobite, unlikely SRE	BS1	3	Locally widespread (33.2 km)
Nocticola `sp. Biologic-BLAT012`	1	High, DNA (unique lineage)	Uncertain troglobite, Potential SRE	BS4	1	Singleton
Coleoptera						
Carabidae `sp. Biologic-COLE001`	2	High, DNA; external match BS4 (Biota 2016)	Not troglobite, unlikely SRE	BS3, BS4	1	Locally widespread (40.7 km)
Coleoptera `sp. Biologic-COLE002`	1	High, DNA (unique lineage)	Uncertain troglobite, Potential SRE	BS3	1	Singleton
Coleoptera `sp. Biologic-COLE003`	1	High, DNA (unique lineage)	Uncertain troglobite, Potential SRE	BS1	1	Singleton
Cryptorhynchinae `sp. Biologic-COLE004`	2	High, DNA (unique lineage)	Uncertain troglobite, Potential SRE	BS4	2	Locally restricted (3.4 km)
Ptinella? `sp. BS1`	4	Med, Putative unique OTU based on morphology and distribution patterns in the group; DNA failed	Uncertain troglobite, Potential SRE	BS1	1	Single site
Staphylinidae? `sp. BS1`	3	Med, Putative unique OTU based on morphology and distribution patterns in the group; DNA failed	Uncertain troglobite, Potential SRE	BS1	1	Single site
Hemiptera						
Meenoplidae `sp. Biologic-HEMI001`	12	High, DNA; external match Hope Downs (Biologic 2019)	Not troglobite, unlikely SRE	BS1, BS2, BS3, BS4	19	Locally widespread (48.2 km)
Meenoplidae `sp. Biologic-HEMI004`	2	High, DNA (unique lineage)	Not troglobite, unlikely SRE	BS4	2	Collected from hyporheic samples only (0.1 km)
Phaconeura `sp. WAM-PHAC001`	1	High, DNA; external match Paraburdoo (Cullen & Harvey, 2018)	Not troglobite, Widespread	BS2	1	Regionally widespread (100+ km)
Phaconeura `sp. WAM-PHAC002`	9	High, DNA; external match Paraburdoo (Cullen & Harvey, 2018)	Not troglobite, Widespread	BS1, BS2, BS3, BS4	9	Regionally widespread (100+ km)

Taxonomy	No. spms	Taxonomic certainty and comment	Sub-fauna status, SRE status	Sections	No. sites	Distribution, known linear range
Zygentoma						
Atelurinae `sp. Biologic-ZYGE008`	6	High, DNA (unique lineage)	Not troglobite, unlikely SRE	BS1, BS3, BS4	5	Locally widespread (35.7 km)
Nicoletiidae `sp. Biologic-ZYGE002`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS4	1	Singleton
Nicoletiidae `sp. Biologic-ZYGE004`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS1	1	Singleton
Nicoletiinae `sp. Biologic-ZYGE005`	3	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS2	3	Locally restricted (2.4 km)
Nicoletiinae `sp. Biologic-ZYGE006`	2	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS3	1	Locally restricted (2.3 km)
Nicoletiinae `sp. Biologic-ZYGE007`	1	High, DNA; external match BS4 (Biota 2016)	Potential troglobite, Potential SRE	BS3	1	Locally restricted (4.5 km)
Nicoletiinae `sp. Biologic-ZYGE015`	2	High, DNA (unique lineage)	Uncertain troglobite, unlikely SRE	BS1, BS4	2	Locally widespread (17.5 km)
Subnicoletiinae `sp. Biologic-ZYGE024`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS3	1	Singleton
Subnicoletiinae `sp. Biologic-ZYGE025`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS3	1	Singleton
Subnicoletiinae `sp. Biologic-ZYGE026`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS4	1	Singleton
Subnicoletiinae `sp. Biologic-ZYGE027`	1	High, DNA (unique lineage)	Potential troglobite, Potential SRE	BS3	1	Singleton

Note: BS1 = Brockman Syncline 1 section, BS2 = Brockman Syncline 2 section, BS3 = Brockman Syncline 3 section, BS4 = Brockman Syncline 4 section (incl. Vivash and Boolgeeda Creek reference areas).

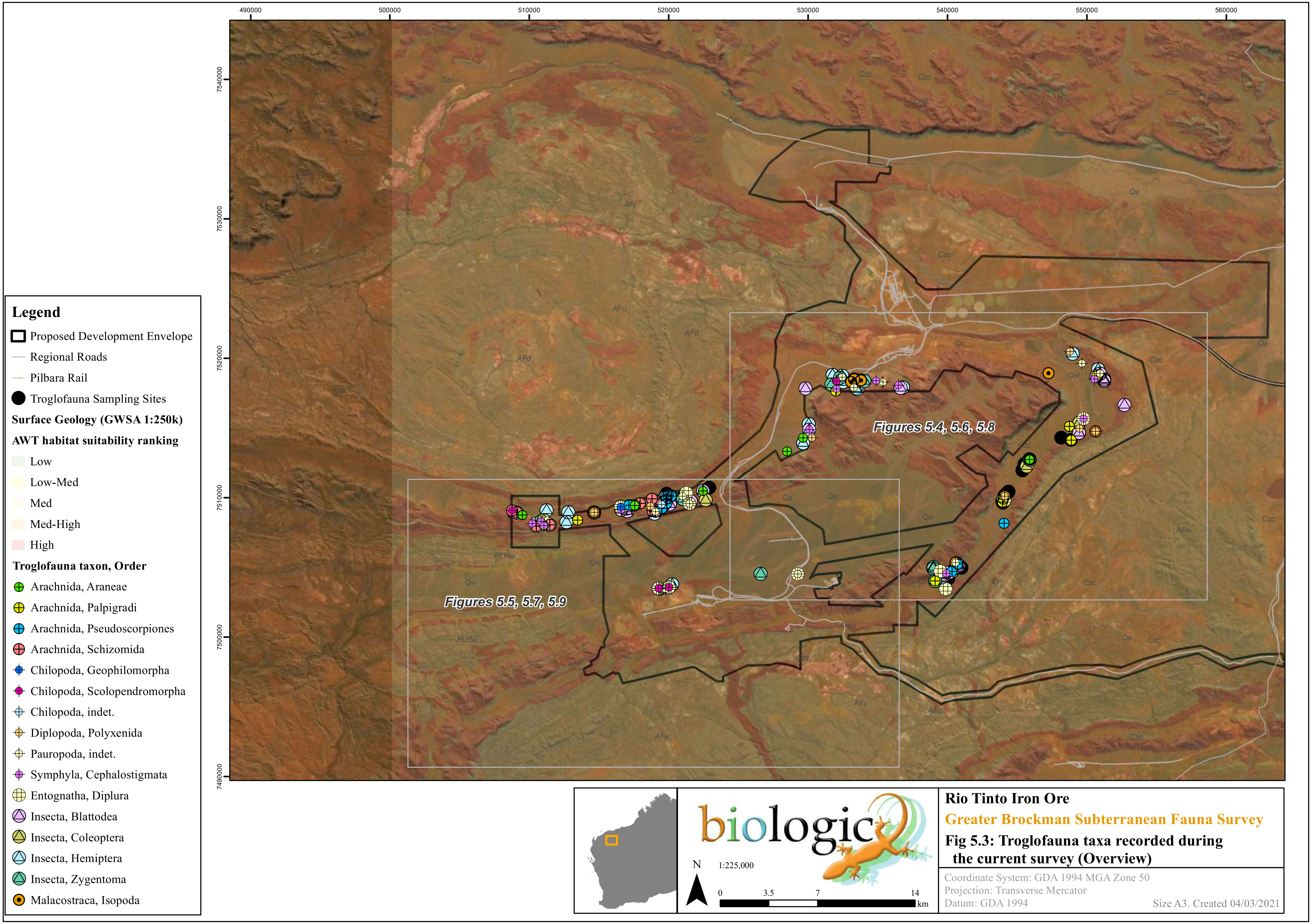
Table 5.3: Higher level troglofauna identifications (morphological) within the Study Area

Taxonomy	No. spms	Taxonomic comments	Subterranean status, SRE status	Sections	No. sites
Araneae sp. indet.	13	Indeterminate higher-level taxon (order). DNA fail (2 specimens) and DNA not tested (8 specimens). May represent other Araneae sp. collected from the Study Area.	Potential Troglofauna, Uncertain	BS1, BS4	6
Armadillidae sp. indet.	4	Indeterminate higher-level taxon (family). DNA fail (1 specimen) and DNA not tested (4 specimens). Likely to represent Armadillidae `sp. Biologic-ISOP002` collected from the same site.	Potential Troglobite, Uncertain	BS1, BS4	2
Atelurinae sp. indet.	19	Indeterminate higher-level taxon (subfamily). DNA fail (4 specimens) and DNA not tested (15 specimens). May represent other Atelurinae sp. recorded from the Study Area, such as Atelurinae `sp. Biologic-ZYGE008` collected from the same site.	Trogloxene/ Troglophile, Uncertain	BS1, BS3	4
Blattidae sp. indet.	2	Indeterminate higher-level taxon (family). DNA not tested. May represent other Blattodea sp. recorded from the Study Area.	Potential Troglofauna, Uncertain	BS3	2
Chilopoda sp. indet	1	Indeterminate higher-level taxon (class). DNA fail. May represent other Chilopoda sp. recorded from the Study Area, such as Geophilomorpha `sp. Biologic-CHIL007` collected from the same site.	Potential Troglofauna, Uncertain	BS1	1
Chthoniidae sp. indet.	1	Indeterminate higher-level taxon (family). DNA not tested. May represent other Chthoniidae sp. recorded from the Study Area, such as Chthoniidae `sp. Biologic-PSEU006` collected from the same site.	Potential Troglobite, Uncertain	BS1	1
Diplopoda sp. indet.	8	Indeterminate higher-level taxon (class). DNA not tested. May represent other Diplopoda sp. collected from the Study Area.	Potential Troglofauna, Uncertain	BS3	1
Geophilida sp. indet.	3	Indeterminate higher-level taxon (order). DNA not tested. May represent other Geophilida sp. collected from the Study Area.	Potential Troglofauna, Uncertain	BS3	1
Geophilomorpha sp. indet.	3	Indeterminate higher-level taxon (order). DNA not tested. Likely to represent Geophilomorpha `sp. Biologic-CHIL007` collected from the same site.	Potential Troglofauna, Uncertain	BS1	1
Hanseniella sp. indet.	15	Indeterminate higher-level taxon (genus). DNA not tested. May represent other Symphyla sp. recorded from the Study Area.	Potential Troglofauna, Uncertain	BS1, BS3, BS4	6
Hemiptera sp. indet.	47	Indeterminate higher-level taxon (order). DNA fail (12 specimens) and DNA not tested 40 specimens). Some immature specimens (nymphs). May represent other Hemiptera sp. collected from the Study Area.	Trogloxene/ Troglophile, Uncertain	BS1, BS2, BS3, BS4	11
Isopoda sp. indet.	4	Indeterminate higher-level taxon (order). DNA fail (3 specimens) and DNA not tested (1 specimen). May represent other Isopoda sp. collected from the Study Area.	Potential Troglofauna, Uncertain	BS2, BS3	4

Taxonomy	No. spms	Taxonomic comments	Subterranean status, SRE status	Sections	No. sites
Japygidae sp. indet.	4	Indeterminate higher-level taxon (family). DNA fail (1 specimen) and DNA not tested (4 specimens). May represent Japygidae `sp. Biologic-DIPL014` collected from the same site.	Potential Troglobite, Uncertain	BS1, BS4	4
Lophoproctidae sp. indet.	9	Indeterminate higher-level taxon (family). DNA not tested. May represent other	Trogloxene/ Troglophile, Uncertain	BS1, BS3	4
Meenoplidae sp. indet.	53	Indeterminate higher-level taxon (family). DNA fail (16 specimens) and DNA not tested (37 specimens). May represent other Meenoplidae sp. from the Study Area.	Trogloxene/ Troglophile, Uncertain	BS1, BS2, BS3, BS4	23
Nicoletiinae sp. indet.	20	Indeterminate higher-level taxon (subfamily). DNA fail (2 specimens) and DNA not tested (18 specimens). May represent other Nicoletiidae sp. recorded from the Study Area.	Potential Troglobite, Uncertain	BS1, BS2, BS4	4
Nocticola sp. indet.	106	Indeterminate higher-level taxon (genus). DNA fail (8 specimens) and DNA not tested (111 specimens). May represent other Nocticola sp. recorded from the Study Area, some of which were collected from the same sites.	Potential Troglobite, Uncertain	BS1, BS2, BS3, BS4	19
Oonopidae sp. indet.	1	Indeterminate higher-level taxon (genus). DNA not tested. Likely to represent Prethopalpus `sp. Biologic-ARAN023 collected from the same site.	Potential Troglobite, Uncertain	BS3	1
Palpigradi sp. indet.	39	Indeterminate higher-level taxon (order). DNA fail (13 specimens) and DNA not tested (26 specimens). May represent other Palpigradi sp. recorded from the Study Area, such as Palpigradi `sp. Biologic-PALP003`, Palpigradi `sp. Biologic-PALP006` and/or Palpigradi `sp. Biologic-PALP013` collected from the same sites.	Potential Troglobite, Uncertain	BS3, BS4	6
Parajapygidae sp. indet.	2	Indeterminate higher-level taxon (family). DNA fail (1 specimen) and DNA not tested (1 specimen). May represent other Parajapygidae sp. collected from the Study Area.	Potential Troglobite, Uncertain	BS1, BS3	2
Pauropoda sp. indet.	86	Indeterminate higher-level taxon (class). DNA fail (12 specimens) and DNA not tested (74 specimens). May represent other Pauropoda sp. from the Study Area.	Potential Troglofauna, Uncertain	BS1, BS3, BS4	25
Philosciidae sp. indet.	2	Indeterminate higher-level taxon (family). DNA not tested.	Potential Troglofauna, Uncertain	BS2	1
Polyxenida sp. indet.	13	Indeterminate higher-level taxon (order). DNA fail (3 specimens) and DNA not tested (10 specimens). May represent other Polyxenida sp. from the Study Area, such as Polyxenida `sp. Biologic-POLX002` and Polyxenida `sp. Biologic-POLX003` collected from the same sites.	Potential Troglofauna, Uncertain	BS1, BS2, BS3, BS4	8
Projapygidae sp. indet.	22	Indeterminate higher-level taxon (family). DNA fail (9 specimens) and DNA not tested (13 specimens). May represent other Projapygidae sp. collected from the Study Area, such as Projapygidae `sp. Biologic-DIPL002`, Projapygidae `sp. Biologic-DIPL003` and Projapygidae `sp. Biologic-DIPL005` collected from the same sites.	Potential Troglobite, Uncertain	BS1, BS3, BS4	5

Taxonomy	No. spms	Taxonomic comments	Subterranean status, SRE status	Sections	No. sites
Pseudoscorpiones sp. indet.	3	Indeterminate higher-level taxon (order). DNA fail (1 specimen) and DNA not tested (2 specimens). May represent other Pseudoscorpiones sp. recorded from the Study Area, such as Chthoniidae `sp. Biologic-PSEU006` collected from the same site.	Potential Troglofauna, Uncertain	BS1, BS3	2
Schizomida sp. indet.	19	Indeterminate higher-level taxon (order). DNA fail (1 specimen) and DNA not tested (35 specimens). May represent other Schizomida sp. collected from the Study Area.	Potential Troglobite, Uncertain	BS1	3
Subnicoletiinae sp. indet.	10	Indeterminate higher-level taxon (subfamily). DNA not tested. Likely represents other Subnicoletiinae sp. collected from Study Area, such as Subnicoletiinae `sp. Biologic-ZYGE025`, Subnicoletiinae `sp. Biologic-ZYGE026`, and Subnicoletiinae `sp. Biologic-ZYGE027` collected from the same sites	Potential Troglofauna, Uncertain	BS3, BS4	3
Symphyla sp. indet.	34	Indeterminate higher-level taxon (class). DNA fail (5 specimens) and DNA not tested (29 specimens). May represent other Symphyla sp. recorded from the Study Area.	Potential Troglofauna, Uncertain	BS1, BS2, BS3, BS4	12

Note: BS1 = Brockman Syncline 1 section, BS2 = Brockman Syncline 2 section, BS3 = Brockman Syncline 3 section, BS4 = Brockman Syncline 4 section (incl. Vivash and Boolgeeda Creek reference areas).

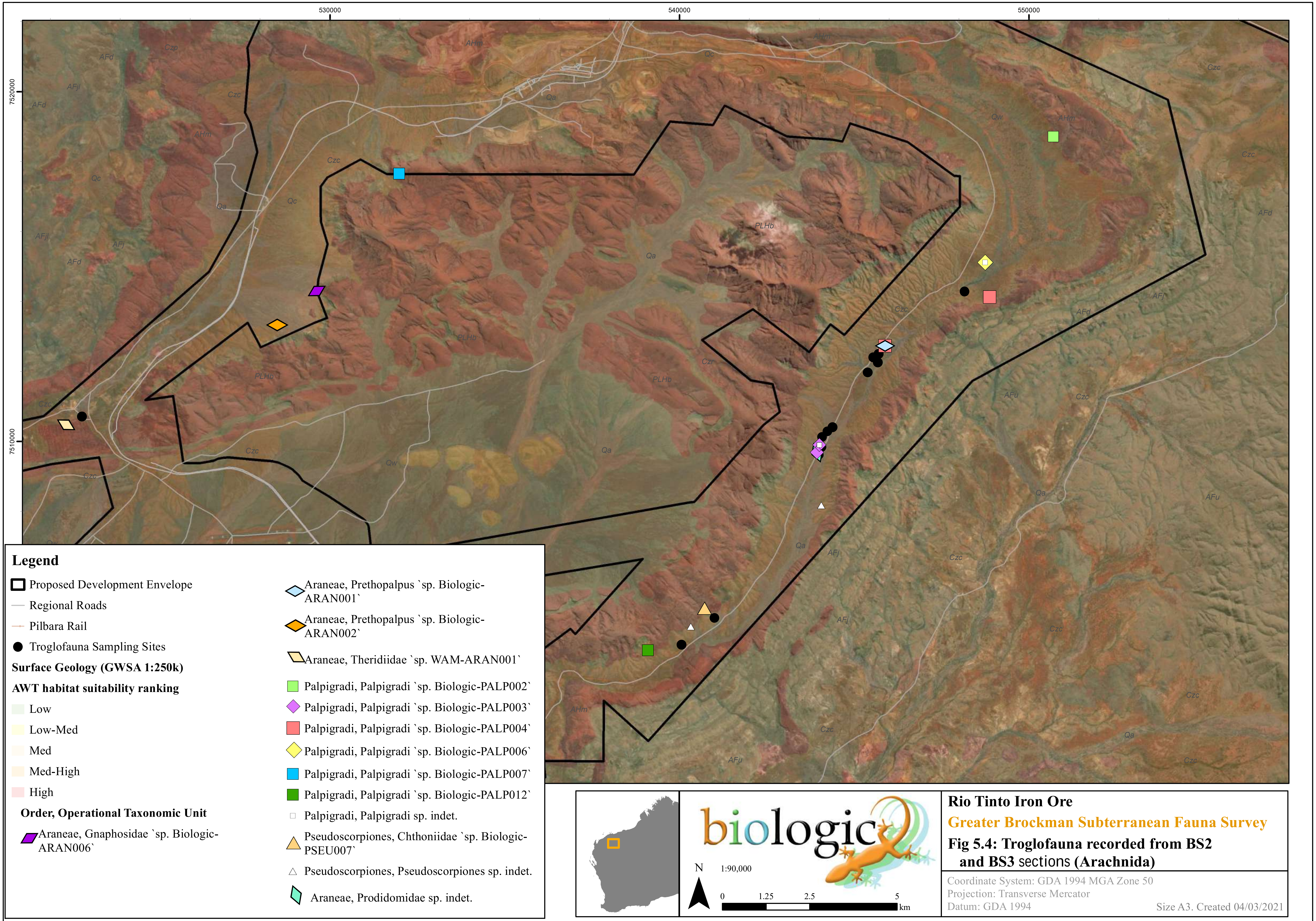


Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Fig 5.3: Troglofauna taxa recorded during the current survey (Overview)

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994
Size A3. Created 04/03/2021



Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Fig 5.4: Troglofauna recorded from BS2 and BS3 sections (Arachnida)

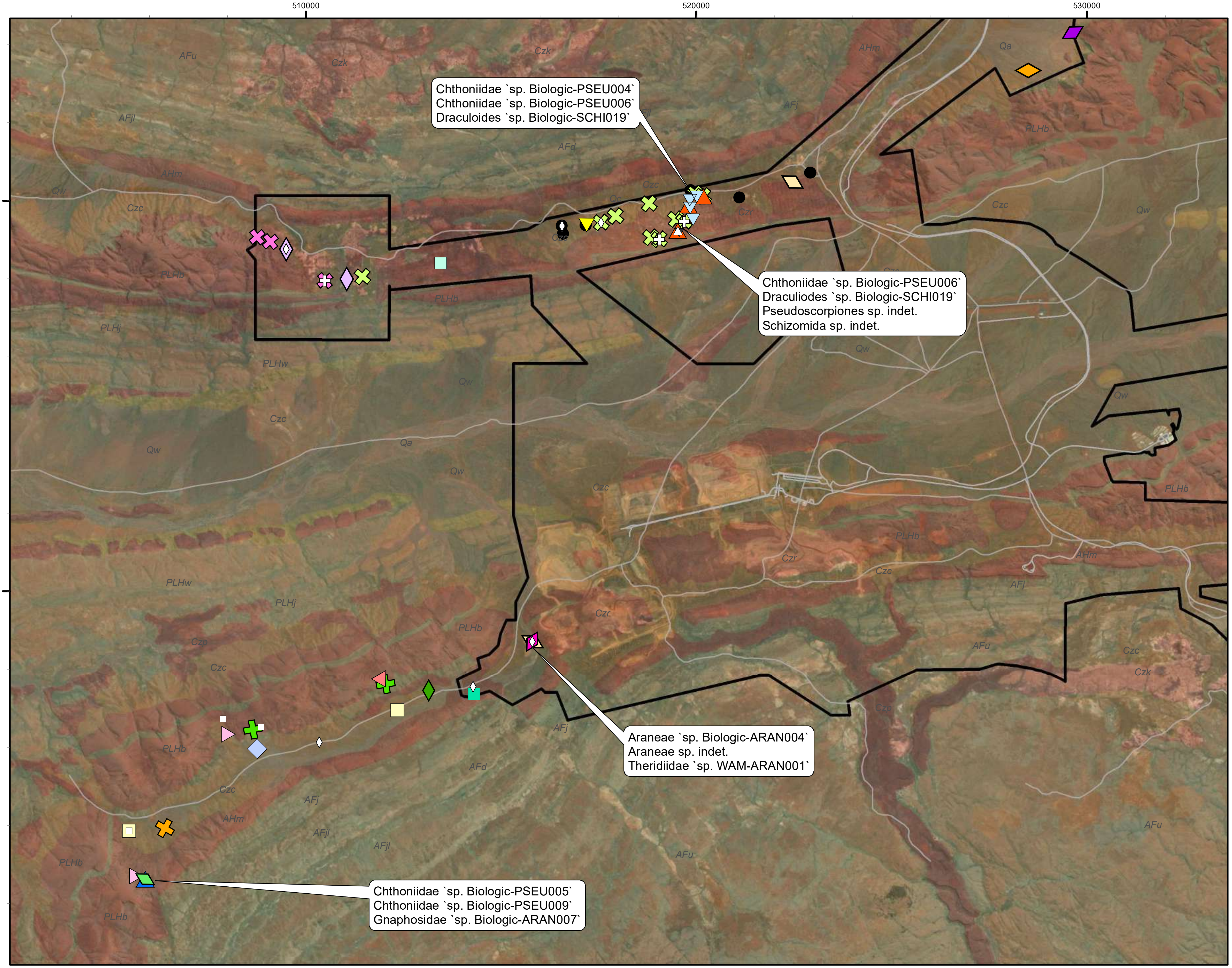
Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994
Size A3. Created 04/03/2021

Legend

- ▭ Proposed Development Envelope
- — Regional Roads
- ● Troglofauna Sampling Sites

Order, Operational Taxonomic Unit

- Araneae, Araneae `sp. Biologic-ARAN004`
- ◇ Araneae, Araneae `sp. Biologic-ARAN005`
- Araneae, Gnaphosidae `sp. Biologic-ARAN006`
- Araneae, Gnaphosidae `sp. Biologic-ARAN007`
- ◆ Araneae, Prethopalpus `sp. Biologic-ARAN002`
- ◆ Araneae, Prethopalpus `sp. Biologic-ARAN016`
- Araneae, Theridiidae `sp. WAM-ARAN001`
- ◇ Araneae, Araneae sp. indet.
- ■ Palpigradi, Palpigradi `sp. Biologic-PALP008`
- ◆ Palpigradi, Palpigradi `sp. Biologic-PALP009`
- ■ Palpigradi, Palpigradi `sp. Biologic-PALP010`
- ■ Palpigradi, Palpigradi `sp. Biologic-PALP013`
- □ Palpigradi, Palpigradi sp. indet.
- ▽ Pseudoscorpiones, Chthoniidae `sp. Biologic-PSEU004`
- ▲ Pseudoscorpiones, Chthoniidae `sp. Biologic-PSEU005`
- ▲ Pseudoscorpiones, Chthoniidae `sp. Biologic-PSEU006`
- ◀ Pseudoscorpiones, Chthoniidae `sp. Biologic-PSEU008`
- ▶ Pseudoscorpiones, Chthoniidae `sp. Biologic-PSEU009`
- ▼ Pseudoscorpiones, Indolpium `sp. Biologic-PSEU003`
- ▼ Pseudoscorpiones, Chthoniidae sp. indet.
- △ Pseudoscorpiones, Pseudoscorpiones sp. indet.
- ✖ Schizomida, Draculoides `sp. Biologic-SCHI010`
- ✚ Schizomida, Draculoides `sp. Biologic-SCHI011`
- ✖ Schizomida, Draculoides `sp. Biologic-SCHI017`
- ✖ Schizomida, Draculoides `sp. Biologic-SCHI019`
- ✚ Schizomida, Schizomida sp. indet.



Chthoniidae `sp. Biologic-PSEU004`
Chthoniidae `sp. Biologic-PSEU006`
Draculoides `sp. Biologic-SCHI019`

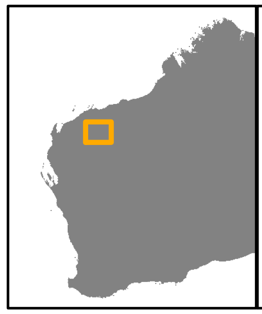
Chthoniidae `sp. Biologic-PSEU006`
Draculiodes `sp. Biologic-SCHI019`
Pseudoscorpiones sp. indet.
Schizomida sp. indet.

Araneae `sp. Biologic-ARAN004`
Araneae sp. indet.
Theridiidae `sp. WAM-ARAN001`

Chthoniidae `sp. Biologic-PSEU005`
Chthoniidae `sp. Biologic-PSEU009`
Gnaphosidae `sp. Biologic-ARAN007`

Surface Geology (GWSA 1:250k)
AWT habitat suitability ranking

- 🟩 Low
- 🟨 Low-Med
- ■ Med
- 🟧 Med-High
- 🟥 High



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1:100,000
0 1.5 3 6 km

Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Fig 5.5: Troglofauna recorded from BS1 and BS4 sections (Arachnida)

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994
Size A3. Created 04/03/2021

Legend

▭ Proposed Development Envelope
— Regional Roads
— Pilbara Rail
● Troglofauna Sampling Sites

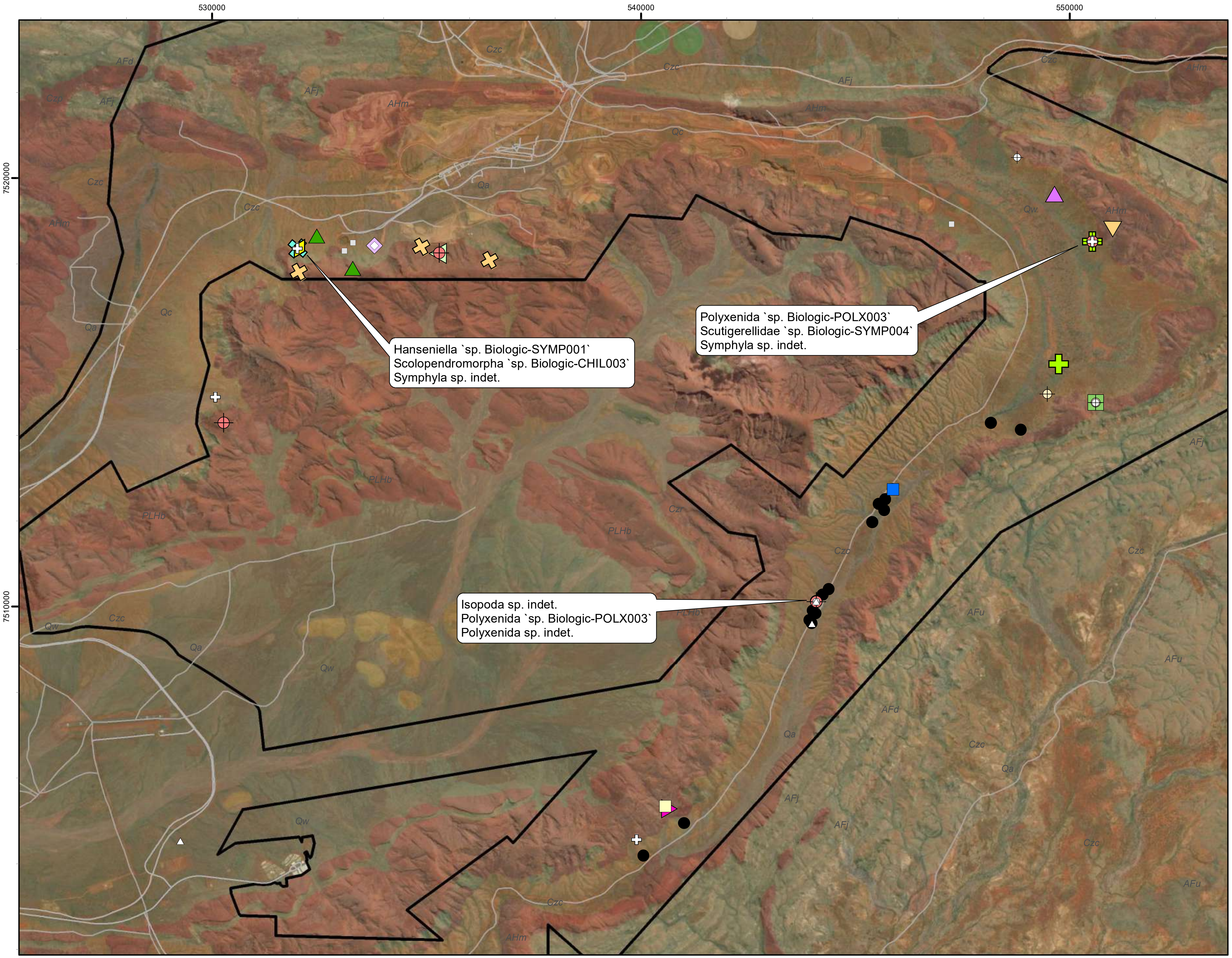
Surface Geology (GWSA 1:250k)

AWT habitat suitability ranking

- ▢ Low
- ▢ Low-Med
- ▢ Med
- ▢ Med-High
- ▢ High

Order, Operational Taxonomic Unit

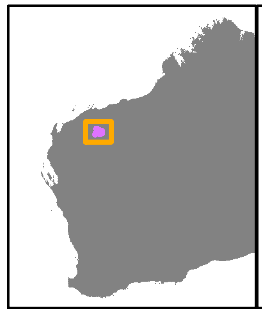
- ▽ Pauropoda, Pauropoda `sp. Biologic-PAUR005`
- ◁ Pauropoda, Pauropoda `sp. Biologic-PAUR006`
- ▲ Pauropoda, Pauropoda `sp. Biologic-PAUR007`
- ▲ Pauropoda, Pauropoda `sp. Biologic-PAUR010`
- ▶ Pauropoda, Pauropoda `sp. Biologic-PAUR013`
- △ Pauropoda, Pauropoda sp. indet.
- ✖ Cephalostigmata, Hanseniella `sp. Biologic-SYMP001`
- ✖ Cephalostigmata, Hanseniella `sp. Biologic-SYMP003`
- ✚ Cephalostigmata, Scutigerellidae `sp. Biologic-SYMP004`
- ✚ Cephalostigmata, Symphyla sp. indet.
- ▰ Scolopendromorpha, Scolopendromorpha `sp. Biologic-CHIL003`
- ⊕ Polyxenida, Polyxenida `sp. Biologic-POLX002`
- ⊕ Polyxenida, Polyxenida `sp. Biologic-POLX003`
- ⊕ Polyxenida, Polyxenida sp. indet.
- 🟩 Isopoda, Buddelundia? `sp. Biologic-ISOP006`
- 🟦 Isopoda, Buddelundia? `sp. Biologic-ISOP005`
- 🟨 Isopoda, Isopoda `sp. Biologic-ISOP007`
- ◇ Isopoda, Philosciidae `sp. Biologic-ISOP001`
- ◇ Isopoda, Philosciidae sp. indet.
- ■ Isopoda, Isopoda sp. indet.



Hanseniella `sp. Biologic-SYMP001`
Scolopendromorpha `sp. Biologic-CHIL003`
Symphyla sp. indet.

Polyxenida `sp. Biologic-POLX003`
Scutigerellidae `sp. Biologic-SYMP004`
Symphyla sp. indet.

Isopoda sp. indet.
Polyxenida `sp. Biologic-POLX003`
Polyxenida sp. indet.



biologic

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0 1.25 2.5 5 km

Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Fig 5.6: Troglofauna recorded from BS2 and BS3 sections (Myriapoda, Crustacea)

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

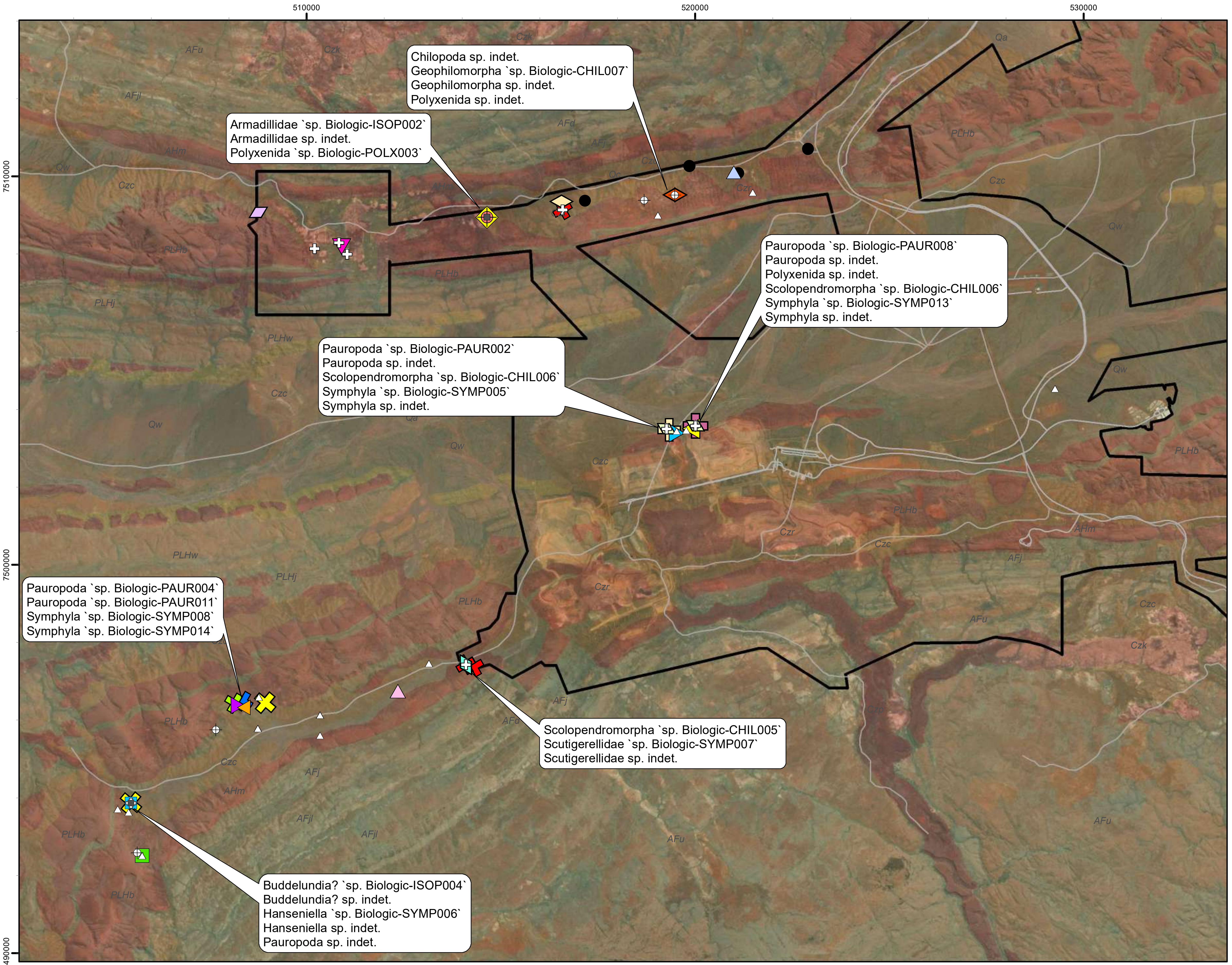
Size A3. Created 04/03/2021

Legend

▭ Proposed Development Envelope
— Regional Roads
● Troglofauna Sampling Sites

Order, Operational Taxonomic Unit

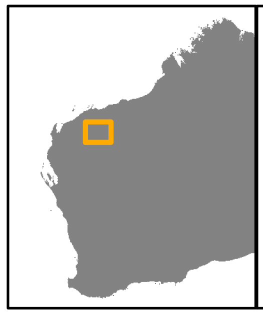
- △ Pauropoda, Pauropoda `sp. Biologic-PAUR001`
- ▶ Pauropoda, Pauropoda `sp. Biologic-PAUR002`
- ▼ Pauropoda, Pauropoda `sp. Biologic-PAUR003`
- ◀ Pauropoda, Pauropoda `sp. Biologic-PAUR004`
- ◀ Pauropoda, Pauropoda `sp. Biologic-PAUR008`
- △ Pauropoda, Pauropoda `sp. Biologic-PAUR009`
- ▶ Pauropoda, Pauropoda `sp. Biologic-PAUR011`
- △ Pauropoda, Pauropoda sp. indet.
- ✕ Cephalostigmata, Hanseniella `sp. Biologic-SYMP006`
- ✕ Cephalostigmata, Scolopendrellidae `sp. Biologic-SYMP008`
- ✕ Cephalostigmata, Scolopendrellidae `sp. Biologic-SYMP014`
- ✚ Cephalostigmata, Scutigerellidae `sp. Biologic-SYMP005`
- ✕ Cephalostigmata, Scutigerellidae `sp. Biologic-SYMP007`
- ✚ Cephalostigmata, Symphyla `sp. Biologic-SYMP013`
- ✚ Cephalostigmata, Symphyla sp. indet.
- ◆ Geophilomorpha, Geophilomorpha `sp. Biologic-CHIL002`
- ◆ Geophilomorpha, Geophilomorpha `sp. Biologic-CHIL007`
- ◇ Geophilomorpha, Geophilomorpha sp. indet.
- ▱ Scolopendromorpha, Scolopendromorpha `sp. BS1`
- ▱ Scolopendromorpha, Scolopendromorpha `sp. Biologic-CHIL005`
- ▱ Scolopendromorpha, Scolopendromorpha `sp. Biologic-CHIL006`
- ◇ Chilopoda, Chilopoda sp. indet
- ⊕ Polyxenida, Polyxenida `sp. Biologic-POLX003`
- ⊕ Polyxenida, Polyxenida sp. indet.
- ■ Isopoda, Armadillidae `sp. Biologic-ISOP004`
- ■ Isopoda, Armadillidae `sp. Biologic-ISOP008`
- ◆ Isopoda, Armadillidae `sp. Biologic-ISOP002`
- ■ Isopoda, Armadillidae sp. indet.



Surface Geology (GWSA 1:250k)

AWT habitat suitability ranking

- 🟩 Low
- 🟨 Low-Med
- ▫ Med
- 🟧 Med-High
- 🟥 High



N

1:100,000

0 1.5 3 6 km

biologic

Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Fig 5.7: Troglofauna recorded from BS1 and BS4 sections (Myriapoda, Crustacea)

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

Size A3. Created 04/03/2021

Legend

▭ Proposed Development Envelope

— Pilbara Rail

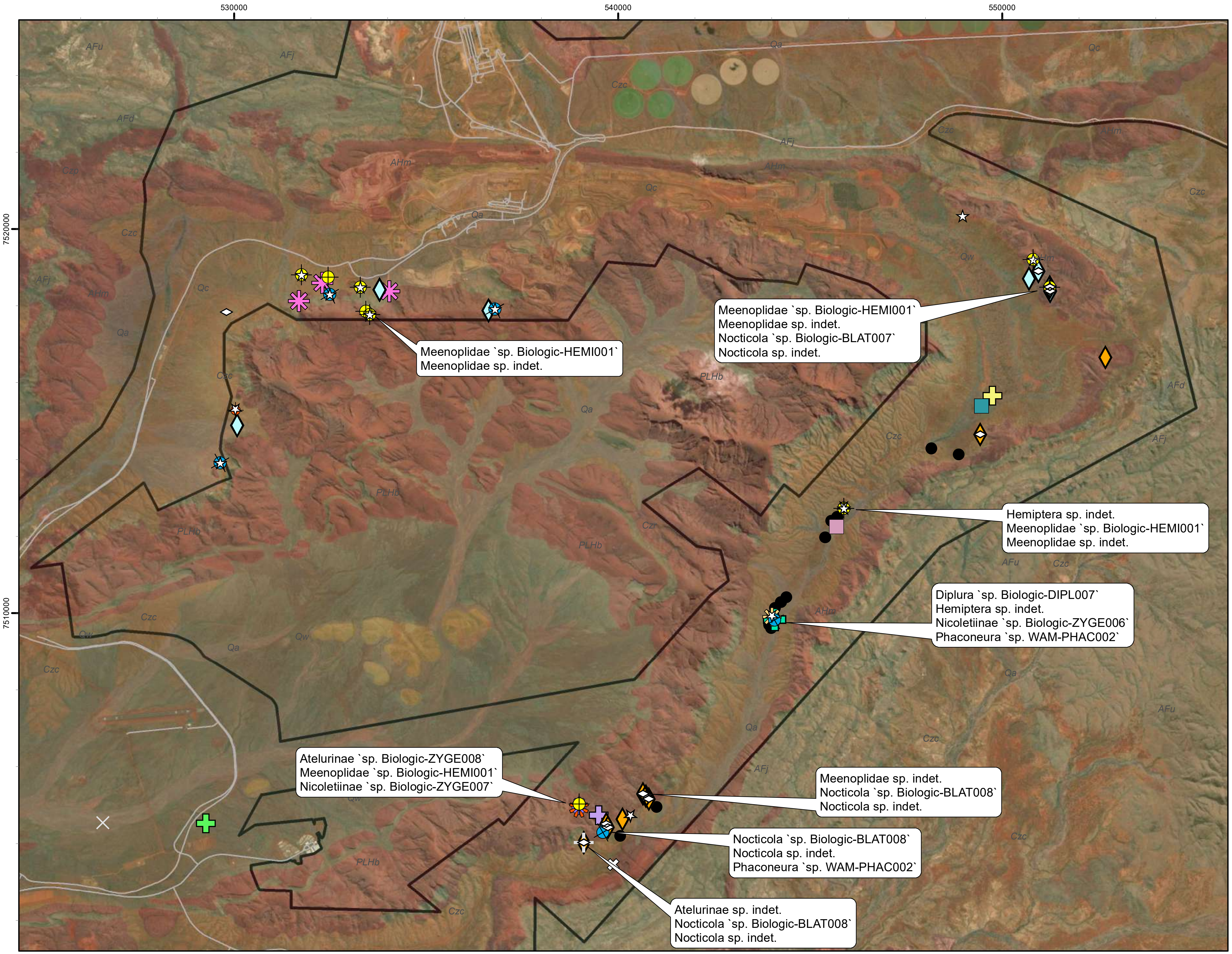
● Troglofauna Sampling Sites

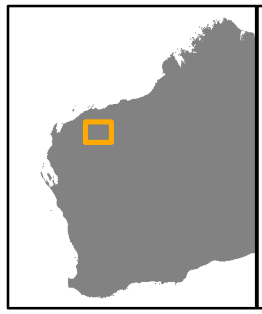
AWT habitat suitability ranking

- Low
- Low-Med
- Med
- Med-High
- High

Order, Operational Taxonomic Unit

- ◆ Blattodea, Nocticola `sp. Biologic-BLAT007`
- ◆ Blattodea, Nocticola `sp. Biologic-BLAT008`
- ◇ Blattodea, Nocticola sp. indet.
- ■ Coleoptera, Coleoptera `sp. Biologic-COLE002`
- ✚ Diplura, Japygidae `sp. Biologic-DIPL009`
- ✚ Diplura, Parajapygidae `sp. Biologic-DIPL007`
- ✚ Diplura, Parajapygidae `sp. Biologic-DIPL011`
- ✚ Diplura, Projapygidae `sp. Biologic-DIPL004`
- ☆ Hemiptera, Hemiptera sp. indet.
- ⊕ Hemiptera, Meenoplidae `sp. Biologic-HEMI001`
- ☆ Hemiptera, Meenoplidae sp. indet.
- ⊕ Hemiptera, Phaconeura `sp. WAM-PHAC001`
- ⊗ Hemiptera, Phaconeura `sp. WAM-PHAC002`
- ✳ Zygentoma, Atelurinae `sp. Biologic-ZYGE008`
- + Zygentoma, Atelurinae sp. indet.
- ✳ Zygentoma, Nicoletiidae `sp. Biologic-ZYGE005`
- ✳ Zygentoma, Nicoletiinae `sp. Biologic-ZYGE006`
- ✳ Zygentoma, Nicoletiinae `sp. Biologic-ZYGE007`
- × Zygentoma, Nicoletiinae sp. indet.
- ■ Coleoptera, Carabidae sp. indet.
- ✧ Diplura, Japygidae sp. indet.





N

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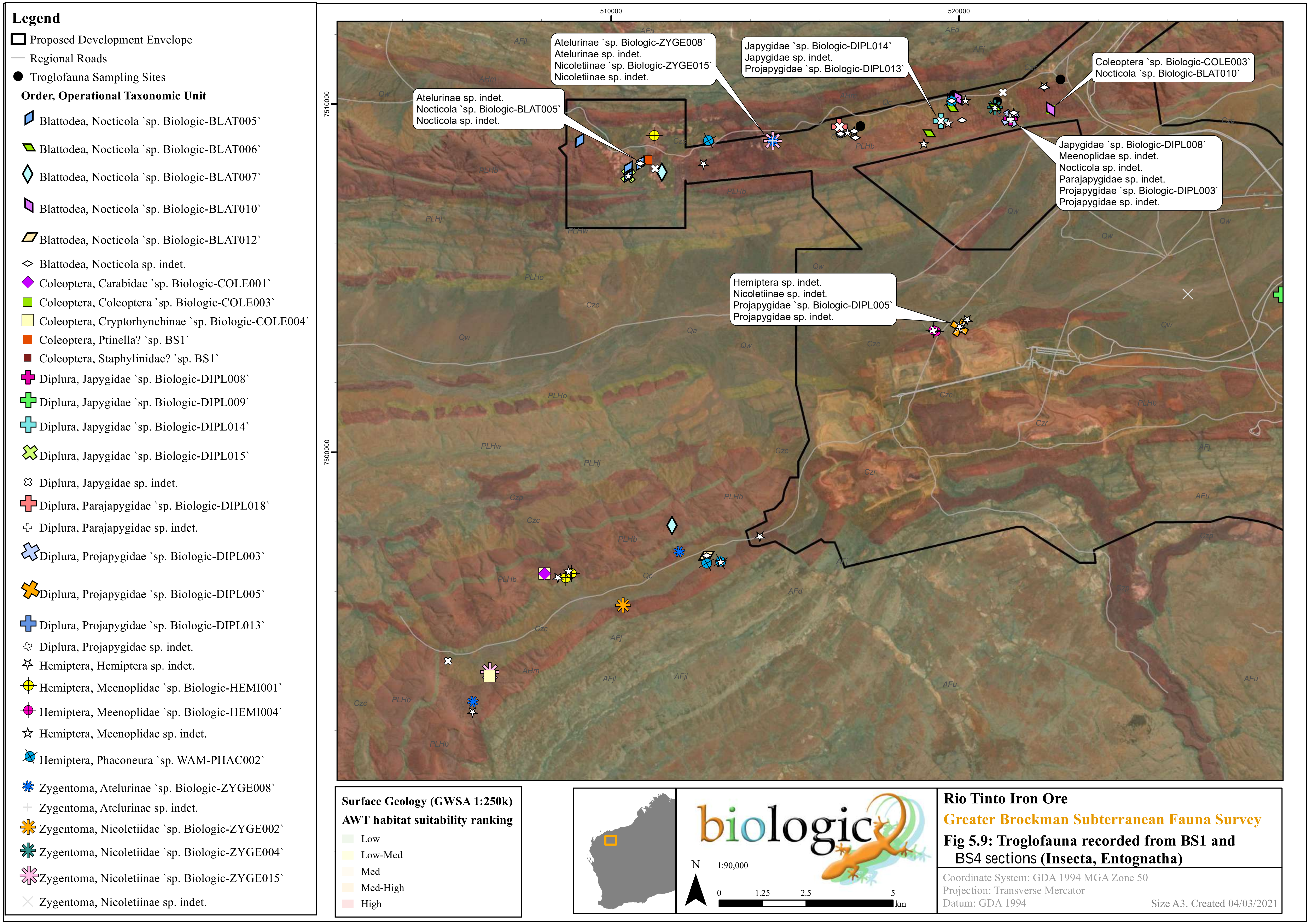
Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Fig 5.8: Troglofauna recorded from BS2 and BS3 sections (Insecta, Entognatha)

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

Size A3. Created 04/03/2021



Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Fig 5.9: Troglofauna recorded from BS1 and BS4 sections (Insecta, Entognatha)

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994
Size A3. Created 04/03/2021

5.3 Species distributions (current and previous surveys)

Appendix H shows all 164 troglofauna taxa that have been found within or near the Development Envelope/ Study Area to date by current and previous surveys.

Based on current occurrence records and taxonomic/ ecological information, these taxa can be broken into four groups according to their distribution patterns (Appendix H):

- Confirmed/ likely widespread throughout the Pilbara region;
- Confirmed/ likely widespread within the Study Area;
- Locally restricted within the Study Area; and
- Known from a single site/ single specimen (singletons).

Within many taxonomic groups, most of the OTUs/ taxa showed similar distribution patterns. This may be attributable to a variety of factors, such as dispersal capabilities/ limitations of the taxonomic group, ecological factors and habitat compartmentalisation/ heterogeneity. For example, most arachnids (spiders, palpigrades, pseudoscorpions and schizomids) were detected only from singletons/ single sites, or from a few sites within localised spatial areas (Appendix H). This fits broadly with the recognised patterns of distribution for troglobitic arachnids, having limited dispersal and high rates of species turnover across geographic distance or between different habitats (Mammola *et al.*, 2018). For this reason, it is considered unlikely that many of the arachnid taxa found within the Study Area are regionally widespread (excluding Theridiidae `sp. WAM-ARAN001`, which is a likely trogloxene spider previously sampled from Paraburdoo). More restricted or putatively restricted taxa such as arachnids (as well as some diplurans, myriapods, isopods, and insects) are identified as key taxa for further consideration in section 8.

Other groups, which are often more vagile and may be able to disperse more widely, such as insects, are more commonly found across the Pilbara as trogloxenic/ troglophilic and soil fauna (Baehr & Main, 2016; Giachino *et al.*, 2021; Halse & Pearson, 2014; Smith & McRae, 2014; Trotter *et al.*, 2017). The distribution patterns for many insect taxa broadly reflected this, with a much higher number of OTUs recorded from multiple sites over large linear ranges between 15 – 65 km, as well as several regionally widespread taxa known from beyond the Study Area (Appendix H). It is therefore considered more likely that singleton insect OTUs (or those recorded only from single sites) may be under-sampled spatially due to sampling artefacts and may be more likely to occur more widely. Nevertheless, this does not exclude the possibility that short-ranging troglobitic species and wider ranging trogloxenic/ troglophilic species may occur within the same genus or taxonomic group. This appears to be the case with the myriapods and isopods, which showed a variety of different linear ranges/ distribution patterns throughout the Study Area.

6. STYGOFAUNA RESULTS

6.1 Stygofauna habitats

The hydrogeological habitats suitable for stygofauna throughout the Study Area are characterised by fractured/ weathered rock aquifers within mineralised MMIF and BrIF, karstic Wittenoom Dolomite, and tertiary detrital aquifers hosted in the valleys (variably porous colluvial and alluvial material, with patchy calcrete and pisolite deposits). Groundwater flows are complicated by lower permeability layers throughout the hydrostratigraphy (such as unmineralized BIF, chert, dolerite, and shales), structural deformities (faults and shear zones), and dolerite intrusives (dykes and sills), particularly around the Brockman Syncline.

Extensive and variably thick superficial aquifers are hosted in the detrital valleys, associated with surface drainage patterns. The major drainage lines of the local area may host a saturated hyporheic zone where near surface groundwater occurs in river gravels and sediments.

The connectivity between these superficial aquifers and the deeper detrital and fractured rock aquifers can be variable due to changes in sediment texture from porous gravels to largely impervious silts and clays. Deeper aquifers (>60–80 mbgl) are typically found to be less suitable for rich stygofauna assemblages throughout the region, owing to their typically lower oxygen and nutrient conditions, and the lack of mixing/ interconnectivity with the surface (Hose *et al.*, 2015). However, rich stygofauna assemblages can be found at greater depths in highly porous/ karstic groundwater environments where greater connectivity with the surface provides for more rapid inputs of dissolved oxygen and nutrients.

Both the variety of hydrogeological settings and their variable interconnectivity may influence the richness of stygofauna assemblages present, and species distributions/ species turnover throughout the Study Area.

Further details regarding BWT habitats for each survey area are noted below.

6.1.1 Brockman Syncline

The hydrogeological setting around the Brockman Syncline is dominated by fractured and weathered rocks of the BrIF (along the Brockman Range) and MMIF (surrounding low hills), as well as a deep tertiary detrital aquifer that occurs in the synclinal valley between them. Despite similar hydrogeological formations to the Caves Creek palaeovalley, this system differs in several important ways, mainly due to the underlying bathymetry of the bedrock, smaller catchment sizes, and the presence of a multitude of dykes and structural controls decentralising groundwater flow patterns. Overall, the Brockman hydrogeological system features much lower recharge from catchment, and slower flow rates than Caves Creek, and despite high storage, considerably less water moves through the system.

The Brockman Syncline zone features a multitude of smaller hydrogeological systems around different parts of the syncline due to spatial differences in the topography and underlying bathymetry. Each system differs slightly in the relative ratios and geometry of the major hydrogeological strata, influencing the surface and groundwater flow patterns, and the degree of segmentation of the local aquifer units due to changes in the bathymetry, in many places dolerite intrusives, and in some cases, faults and disconformities in the bedrock and the dolerite dykes.

The overall pattern is characterised by tall BrIF ranges in a central ring around the syncline, heavily dissected by gorges and gullies which shed surface flows directly to the synclinal valley below. The lower flanks of the BrIF range are draped in variably consolidated colluvium, which provides a recharge area for the fractured/ weathered rocks of the mineralised BrIF and Wittenoom Dolomite below. The synclinal valley is composed of deep colluvial and alluvial sediments forming significant aquifers, and patchy calcrete deposits associated with historical drainage patterns. Present day drainage lines exit the synclinal valley through gullies and gorges in the outer ring of MMIF hills, flowing into several different catchments depending on location and aspect. Most of BS2 drains north to the Duck Creek catchment, BS3 and BS4 mainly drain east and south to the Hardey River catchment, and BS1 and Vivash mainly drain internally through the Brockman Range, into Boolgeeda Creek in the centre of the syncline (which eventually joins Duck Creek approximately 100 km west) (Figure 2.3). Surface flow patterns may provide wider habitat connectivity beyond the syncline for regionally widespread stygofauna species that can use hyporheic zones as dispersal corridors, especially during floods.

Otherwise, groundwater flows and habitat connectivity are highly complicated and variable in different parts of the syncline, due to numerous dykes and structural constraints within the fractured/ weathered rock aquifers. Most of these structural elements run perpendicular or near perpendicular to the strike of the BrIF range, causing compartmentalisation and flow disruptions parallel to strike (e.g. BS3 and BS4/ Vivash). However, the dykes are not considered to restrict flows within the tertiary detrital aquifers, and in many areas, dykes are not considered impermeable due to faults and fracturing, or periodic overtopping through the detritals (Rio Tinto, 2020). Groundwater catchment divides are known to form structural constraints on groundwater flows in the area of BS3 and BS2. Although a major dolerite sill within the BrIF bedrock forms a ‘ring’ around the syncline that generally directs flows outward from the range, at BS1 and Vivash, this barrier is incomplete, and/ or is over-topped, such that groundwater and surface water flows may enter the interior of the syncline to join Boolgeeda Creek (Rio Tinto, 2020).

The conceptual hydrostratigraphy of the Brockman Syncline is characterised by Rio Tinto (2020) as follows, and as shown in Figure 6.1:

- *Where saturated, Tertiary detrital sediments, may be permeable and host groundwater, with the heterogeneity of these sediments (i.e. pisolites, clays) reflected in variable aquifer properties. Saturated Tertiary sediments may be in hydraulic connection with karstic Wittenoom Formation and mineralised Marra Mamba Iron Formation and create a conduit for groundwater to pass across any basement hydraulic barriers.*
- *Karstic dolomite of the Wittenoom Formation presents as a regional aquifer system, with development of secondary permeability through dissolution of dolomite within the Paraburdoo Member. Note that primary permeability of units within the Wittenoom Formation (i.e. shale of the Bee Gorge Member, crystalline dolomite of the Paraburdoo Member) is generally low.*

- *Brockman Iron Formation and Marra Mamba Iron Formation orebodies, where the mineralisation process has increased permeability and porosity. Of note is the Marra Mamba Iron Formation orebodies are often in connection with the Wittenoom Formation and Tertiary detrital aquifers.*
- *The orebody aquifers are flanked by low permeability unmineralised banded iron formation of their respective host units; local permeability may be increased where fracturing and faulting occurs.*
- *Relatively low permeability shales of the Mount McRae Shale and Mount Sylvia Formation acting as an aquitard between the Brockman Iron Formation orebody aquifer and the regional Wittenoom Formation aquifer. However hydraulic connection between these units is observed where faulting has caused occurred, in particular at BS4.*
- *Hydraulic barriers have been identified throughout the Brockman Syncline aquifers, based on changes in groundwater elevations, anomalously steep gradients, or response in monitoring bores to abstraction. The key hydraulic barriers include very low permeability dolerite dykes which intersect the syncline perpendicular to strike and compartmentalises the aquifers. Additionally, differential groundwater levels have been observed across a major Dolerite Sill that has been observed wrapping around the syncline along strike of the Joffre Formation. This sill forms a major hydraulic boundary on the inside of the syncline, however there are a number of locations identified where the sill has been eroded below groundwater level (and infilled with detrital sediments) which allows hydraulic connection with the formations overlying the Brockman Iron Formation at the centre of the syncline.*
- *The system described above is hydraulically isolated from the Fortescue Group (underlying the un-mineralised Marra Mamba Iron Formation), due to the inherent low permeability formations (i.e. unmineralised banded iron formation of the MacLeod and Nammuldi Members, prevalence of shale and dolerite within the Fortescue Group). This hydraulic separation is common across the Pilbara* (Rio Tinto, 2020).

Further details of the hydrogeological setting relevant to each section of the Development Envelope/Study Area are provided below.

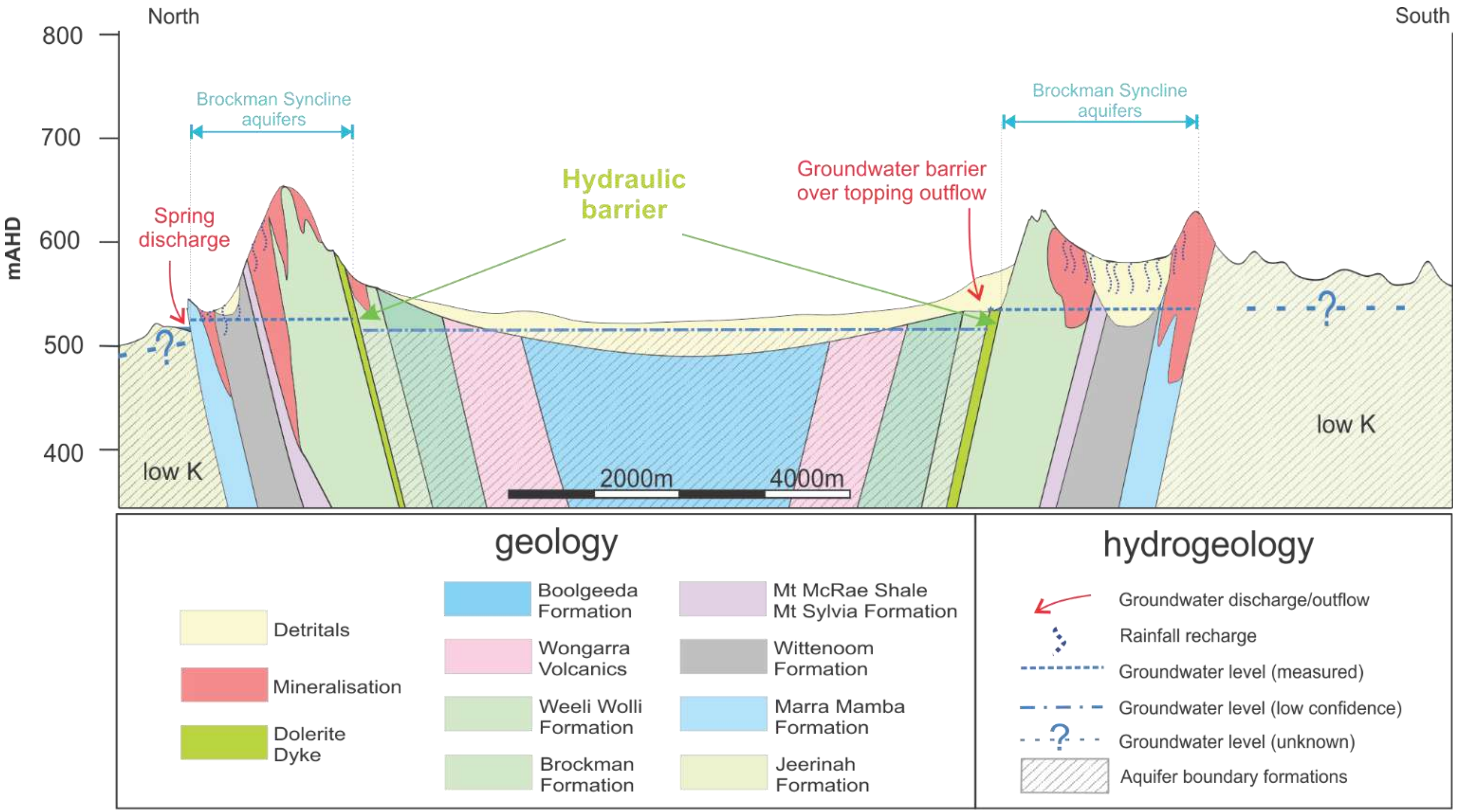


Figure 6.1: Conceptual hydrogeological cross section of the Brockman Syncline. Diagram from Rio Tinto (2020) used with permission.

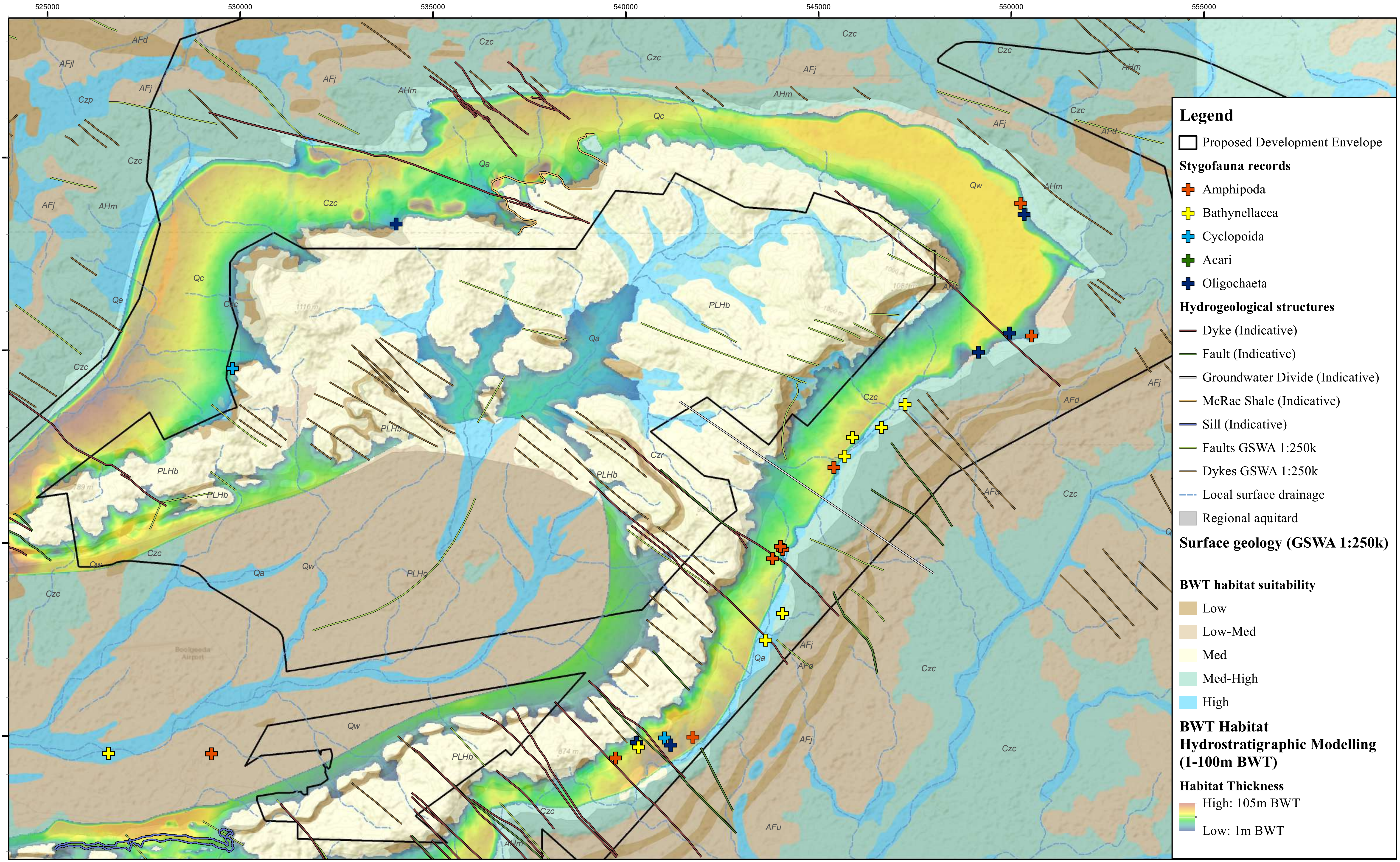
6.1.2 BS2 and BS3

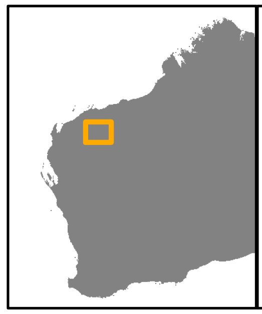
Suitable groundwater habitats at BS2 and BS3 occur in the valley fill detritals and in the fractured/ weathered mineralised zone of the BrIF and MMIF bedrock. Changes in the bathymetry of the bedrock, multiple dykes and two major groundwater divides have strong influences on flows and habitat connectivity at BS2 and BS3 (Figure 6.2). One of these groundwater divides is shown in Figure 6.2 in the eastern part of the Syncline at BS3, while the other occurs opposite this divide in the west at BS2 but is not shown in the spatial data provided.

The majority of the BWT habitat modelled throughout BS2 and BS3 appears to be reasonably extensive, continuous, and moderately to highly thick throughout the synclinal valley fill between the BrIF and MMIF. At a local scale, groundwater flows and habitat connectivity in the detritals is likely more variable due to variability in sediment textures and structural influences from the many dykes running approximately north west to south east. In the area of BS2, only one of these dykes appears to pass through the synclinal valley, whereas at BS3 (particularly in the southern section), there are a multitude of dykes (Figure 6.2).

Although these dykes are not interpreted as complete barriers to flow, they are likely to compartmentalise the groundwater system where numerous/ frequent (Figure 6.3), and potentially influence the occurrence of some stygofauna species. However, there is still much that remains uncertain regarding the relative influence of the dykes/ hydrogeological compartments, and the distribution of stygofauna species at BS2 and BS3. Based on current data, there is no obvious or consistent pattern of stygofauna species or assemblage turnover that appears to be related to particular dykes or groundwater compartments, but there does seem to be an increasing likelihood of species turnover with distance around the outside of the Syncline. In areas between the dykes, modelling has shown that hydrogeological habitats can be expected to be generally well-connected, both laterally and vertically throughout the profile (i.e. between detritals and deeper fractured rock aquifers).

‘Plunge Pool’ near BS3 is a small groundwater fed permanent pool in a MMIF gorge south of BS3. The groundwater flows in the surrounding area are constrained by numerous dolerite dykes and variable porosity in the stratigraphic layers (Figure 6.4). Groundwater investigations have determined that the pool is supported by groundwater only from its immediate hydrogeological compartment, although ephemeral surface flows from other nearby compartments, and groundwater periodically overtopping local dykes may also contribute (Rio Tinto, 2020). Owing to these complicated factors, it is difficult to determine the importance of Plunge pool to stygofauna values in the area, although a few records of stygofauna species were collected from bores and drill holes immediately to the north of the pool, in an adjacent hydrogeological compartment.





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Greater Brockman Subterranean Fauna Survey

Fig 6.2: Indicative extent and thickness of BWT stygofauna habitat modelled at BS2 to BS3 sections

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

Size A3. Created 11/03/2021

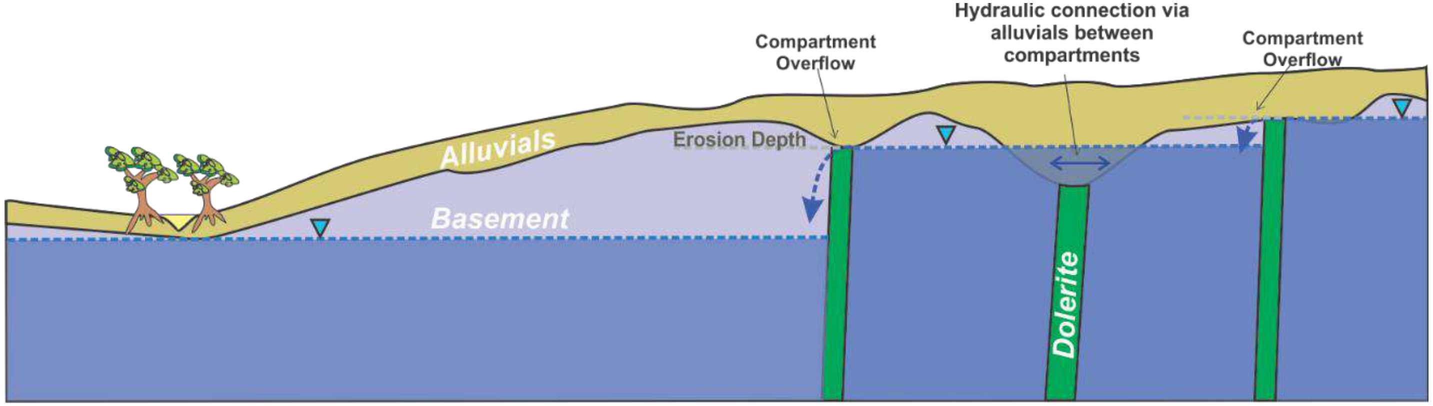


Figure 6.3: Conceptual diagram of geological structures (intrusive dykes) influencing groundwater levels and flows

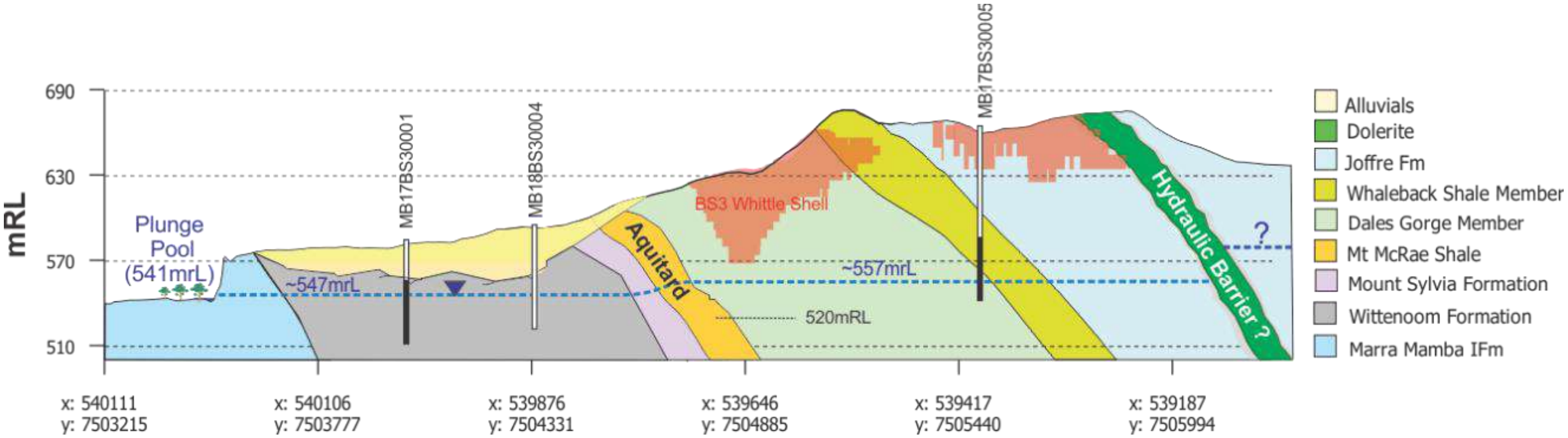


Figure 6.4: Hydrogeological cross section of BS3 south towards ‘Plunge Pool’. Diagram from Rio Tinto (2020) used with permission.

6.1.3 BS1, BS4 and Vivash

The hydrogeological settings at BS1, BS4, and Vivash are influenced by compartmentalisation due to disconformities and intrusives (particularly at BS4, but also Vivash and BS1), and by groundwater flow patterns towards the centre of the syncline and Boolgeeda Creek (at BS1 and Vivash), and externally outside of the syncline at BS4 (Rio Tinto, 2020).

Both the northern (BS1) and southern limbs of the syncline (BS4 and Vivash) feature fractured/ weathered rock aquifers within the mineralised BrIF, MMIF, and karstic Wittenoom Dolomites (Figure 6.5). Tertiary detrital aquifers are present within the alluvial/ colluvial valley fill, but the thickness and spatial extent of the synclinal valley is compressed, especially on the southern limb at BS4. Calcrete and Robe pisolite are present in the central Boolgeeda Valley, at BS1, and to a lesser degree at Vivash and BS4 (Figure 6.5) (Aquaterra, 2005; Rio Tinto, 2014a). The southern limb of the syncline at BS4/ Vivash features a multitude of faults and dykes, and a shearing zone between BS4 and Vivash that has shifted, but not entirely displaced, the east-west connectivity of the major stratigraphic units (Figure 6.6). In combination with variations in aquifer porosity and the prevalence of fractured rock aquifers throughout, this has resulted in aquifer compartmentalisation and highly complicated groundwater flows throughout this area (Rio Tinto, 2020).

The BWT habitat mapping in the BS4 and Vivash areas shows multiple bands of BWT habitat within 100 m from topographic surface, aligning to the northern and southern flank of the BrIF range (Figure 6.6). The variability in the thickness of the BWT habitat, particularly along the southern flank of the range, suggests a patchiness of habitat that may be related to the structural influences described above. The hydrostratigraphic modelling suggests some potential connectivity between northern and southern bands in areas near major faults (Figure 6.6). In the area between BS4 and Vivash, a major shear zone with associated faulting/ fracturing and numerous intrusives complicates the interpretation of groundwater flows. The BWT habitat is thick in this area, where the northern and southern bands of BWT habitat appear to meet and potentially flow either towards the centre of the syncline (*i.e.* towards Boolgeeda Creek), or south towards the Beasley River (Figure 6.6).

On the northern limb of the syncline at BS1, approximately 8 km NW of this location, groundwater connectivity between the northern synclinal valley and the tertiary detrital aquifers of the Boolgeeda Valley has been established by hyporheic flow (Rio Tinto, 2020). Large calcrete deposits and shallow water tables occur in this area, where a major fault intersects a low point in the Brockman Range, and groundwater frequently overtops the regional dolerite sill in the BrIF to drain towards Boolgeeda Creek. Inward drainage and potential habitat connectivity beyond the synclinal valley also occur at the eastern part of BS1 east, where a tributary of Boolgeeda Creek cuts through the Brockman Range. In general, the northern limb valley at BS1 features thicker and more well-connected BWT habitats than the southern limb. Although there is a central dyke that separates the eastern aquifer from the western part, potential habitat connectivity occurs where groundwater overtops this dyke, and more widely throughout the detrital aquifers associated with Boolgeeda Creek, via the hyporheic zone (Figure 6.6).

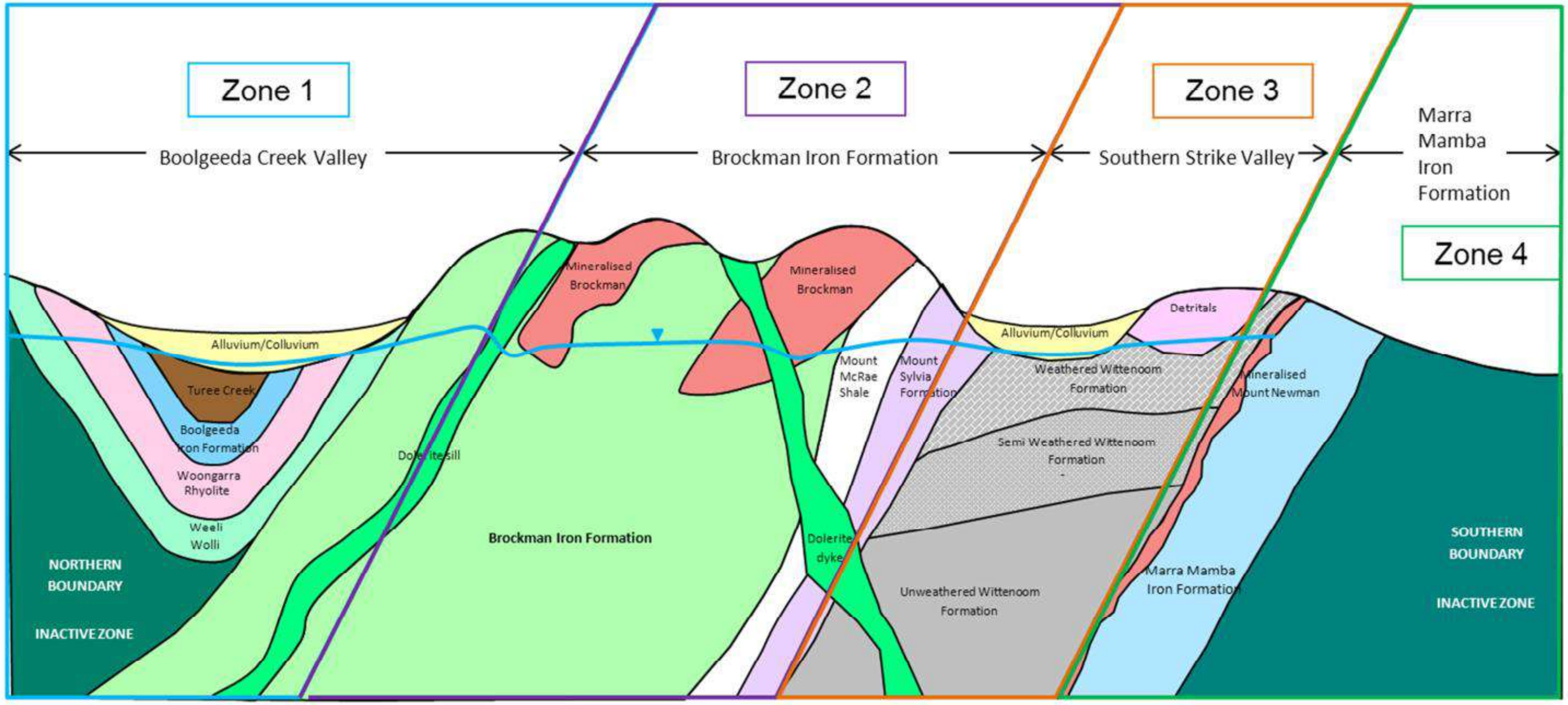
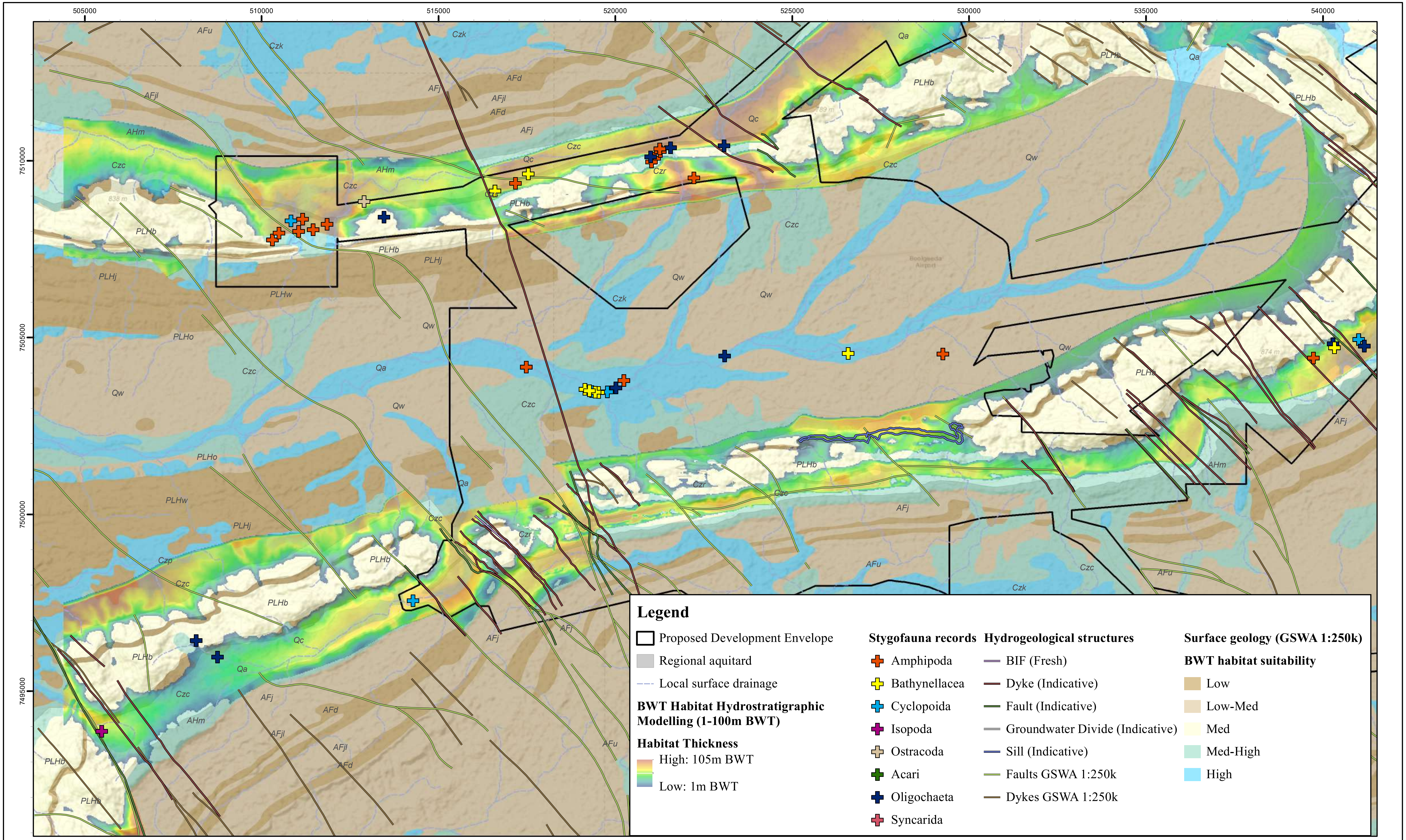


Figure 6.5: Conceptual hydrogeological model of Boolgeeda Creek (Zone 1), and BS4-Vivash (Zones 2-4). Diagram from Rio Tinto (2014a) used with permission.



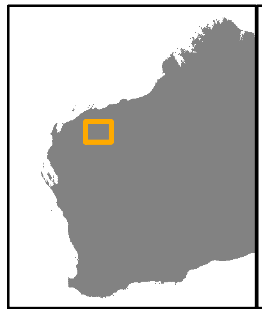


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Fig 6.6: Indicative extent and thickness of BWT stygofauna habitat modelled at BS1 to Vivash

N

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Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

Size A3. Created 11/03/2021

6.2 Groundwater characteristics

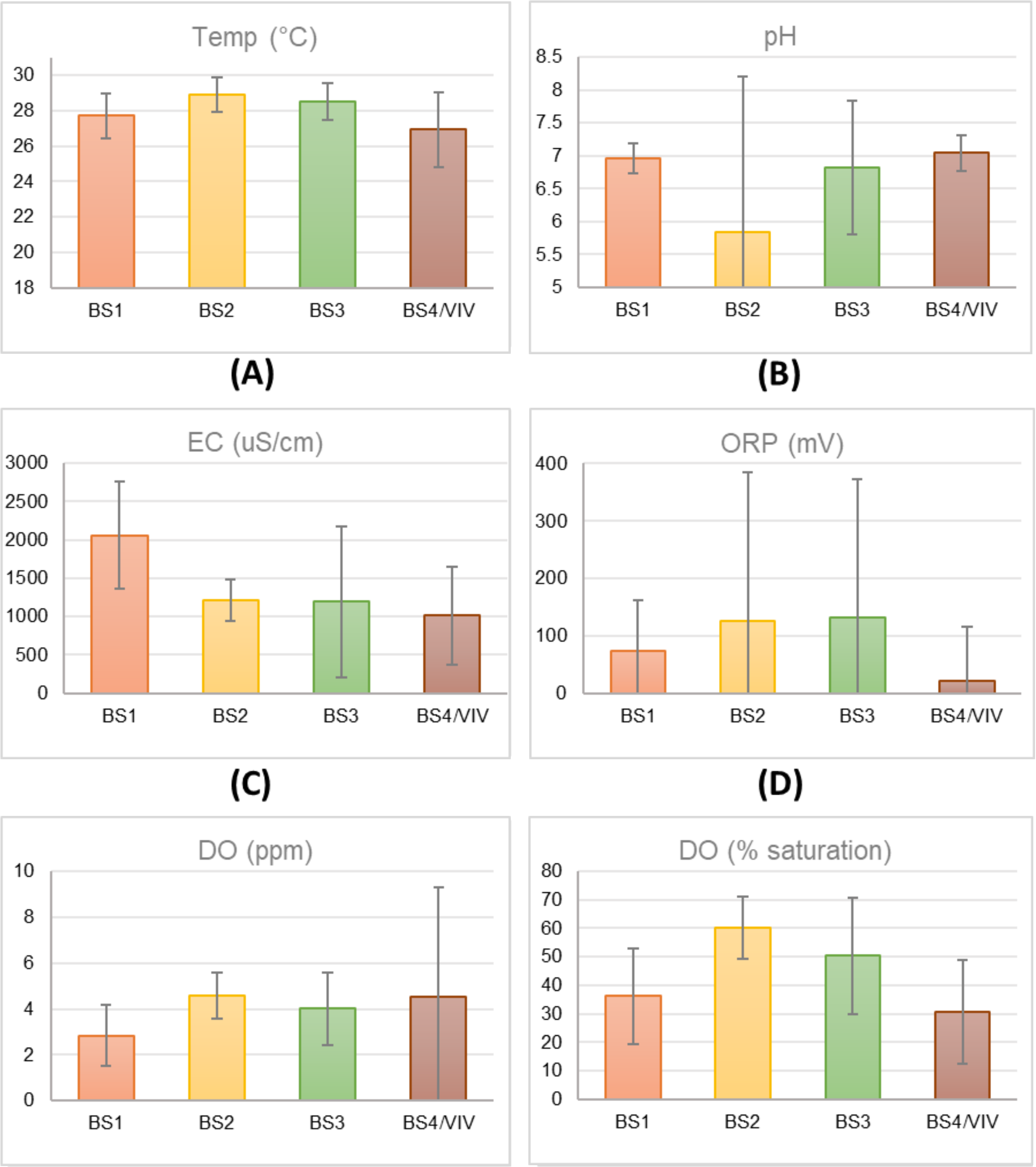
Figures 6.7 A–F show mean (and standard deviation as error bars) temperature, pH, EC (as a representation of salinity), ORP (redox potential) and DO (dissolved oxygen) for bores within Brockman Syncline 1 (BS1), Brockman Syncline 2 (BS2), Brockman Syncline 3 (BS3), and Brockman Syncline 4/ Vivash (BS4/ VIV). The interpretation of these data is somewhat affected by the unequal sample sizes between areas due to differences in the availability of bores that intercepted groundwater. At BS1, 27 bores were sampled, compared to 8 at BS2, 26 at BS3, and 15 at BS4/ VIV (Appendix G). Some bores were sampled multiple times, in which case the average was taken for each environmental variable.

The average groundwater temperature ranged from 27.4 – 28.6 °C and showed little variability across the five sampling areas. The average pH of the groundwater (Figure 6.7B) ranged from 6.57 to 7.26 across all sites, indicating slightly acidic to circum-neutral conditions generally suitable for stygofauna. However, the groundwater of some of the sites within the BS2 / BS3 area was highly acidic (pH = 1 – 3.9) and likely unsuitable for stygofauna.

EC (Figure 6.7C) was low in all five sampling areas, with BS2, BS3, and BS4/ VIV containing mostly fresh water (EC <1,500 uS/cm). These levels are well within the range suitable for stygofauna and can support rich stygofauna assemblages, which are known to occur up to salinities of approximately 10,000 mg/L (TDS) (equivalent to ~EC 18,200 uS/cm) (Halse *et al.*, 2014).

Redox and DO measurements (Figure 6.7D–F) are often variable between sites due to individual bore conditions rather than overall aquifer conditions. All sites contained groundwater with sufficient dissolved oxygen for stygofauna to occur (>1 ppm). The redox potential of groundwater is a measure of the system's capacity to oxidise materials through chemical reactions and has important implications for metal mobility, bio-availability and toxicity (Schuring *et al.*, 1999). Most sites surveyed showed high positive or low positive ORP values, although a few of the deeper bores at each sampling area had anoxic or sulphur- producing conditions (hence negative Redox values), and there were several other cases of biological contamination (*i.e.* dead animals in bores, or decomposing algae in Karaman samples), which produced similar negative redox values and foul odours. These were considered to be the main drivers of the moderate to high variability in redox measurements throughout the survey.

The full range of physicochemical data for all sites (bores, drill holes, and stream bed Karaman samples) measured during the survey can be found in Appendix G.



(A) **(B)**

(C) **(D)**

(E) **(F)**

Figure 6.7: Groundwater physicochemical measurements recorded at each sampling area during the survey: A) temperature; B) pH; C) electrical conductivity; D) oxidation-reduction potential; E) dissolved oxygen in parts per million; and F) dissolved oxygen % saturation. Note: BS4/ VIV includes bores at Boolgeeda Creek. Mean values are shown as bars, standard deviations as error bars.

6.3 Stygofauna results (current survey)

The current survey recorded a total of 2,574 stygofauna and potential stygofauna specimens. A total of 56 unique species/ OTUs were recorded, representing eight higher order groups comprising Oligochaeta, Acari, Ostracoda, Calanoida, Cyclopoida, Bathynellacea, Amphipoda and Isopoda (Table 6.1 and Table 6.2). A further 24 indeterminate taxa were identified which belonged to the aforementioned groups, although these could not be resolved to species-level due to specimens being immature, in poor/damaged condition or the wrong sex for species-level identification (Table 6.3). The locations of subterranean stygofauna collected during the survey are shown in Figure 6.8 (overview) and in Figures 6.9 – 6.15 (detailed).

Amphipods and oligochaetes were the two most abundant groups (Table 6.1), whereas oligochaetes and bathynellids were the most speciose.

Table 6.1: Overview of stygofauna species/ OTUs detected from the Study Area (current survey)

Higher taxon	No. species/ OTUs	No specimens.
Oligochaeta	20	115
Acari	2	4
Ostracoda	3	34
Cyclopoida	7	37
Calanoida	1	1
Bathynellacea	11	76
Amphipoda	10	251
Isopoda	2	36
Indeterminate taxa	/	2020
Total	**56**	**2,574**

Table 6.2: Stygofauna species/ OTUs detected from the Study Area (current survey), taxonomic and distribution comments, known linear ranges and collection locations

Taxonomy	No. spms	ID status Taxonomic comments	Subterranean status, SRE status	Sections	No. sites	Distribution comments, known linear range
OLIGOCHAETA						
Enchytraeidae						
Enchytraeidae `sp. E6`	3	High, DNA; external match with sequences from Rhodes Ridge and McPhee Creek (Biologic internal database)	Stygoxene, Widespread	BS1, BS2, BS4	3	Regionally widespread (300+ km)
Enchytraeidae `sp. E11`	2	High, DNA; external match with sequences from Weelamurra Creek and McPhee Creek (Brown et al., 2015), and West Angelas (Biologic 2020)	Stygoxene, Widespread	BS3, BS4	2	Regionally widespread (300+ km)
Enchytraeidae `sp. Biologic-OLIG004`	9	High, DNA; external match with sequences from Rhodes Ridge and Angelo River (Biologic, unpublished data)	Stygoxene, Widespread	BS1, BS3	3	Regionally widespread (200+ km)
Enchytraeidae `sp. Biologic-OLIG006`	6	High, DNA; external match with sequences from West Angelas (Biologic, unpublished data)	Stygoxene, Widespread	BS3	4	Regionally widespread (160+ km)
Enchytraeidae `sp. Biologic-OLIG016`	15	High, DNA; external match with sequences from the Goldfields (unpublished)	Stygoxene, Widespread	BS3, BS4	3	Regionally widespread (300+ km)
Enchytraeidae `sp. Biologic-OLIG017`	2	High, DNA; external match with sequences from Angelo River (Biologic 2021)	Stygoxene, Widespread	BS3, BS4	2	Regionally widespread (160+ km)
Enchytraeidae `sp. Biologic-OLIG018`	5	High, DNA; external match SGCCK (Biologic 2020)	Stygoxene, unlikely SRE	BS3	1	Locally widespread (48.6 km)
Enchytraeidae `sp. Biologic-OLIG022`	11	High, DNA; external match with sequences from McPhee Creek (Biologic 2020)	Stygoxene, Widespread	BS3	4	Regionally widespread (300+ km)
Enchytraeidae `sp. Biologic-OLIG052`	1	High, DNA (unique lineage)	Stygoxene, uncertain SRE	BS1	1	Singleton
Enchytraeidae `sp. Biologic-OLIG053`	1	High, DNA (unique lineage)	Stygoxene, uncertain SRE	BS4	1	Singleton
Enchytraeidae `sp. Biologic-OLIG055`	1	High, DNA (unique lineage)	Stygoxene, uncertain SRE	BS4	1	Singleton
Naididae						
Pristina aequiseta	6	High, morphologically identified, named species	Stygoxene, Widespread	BS4	1	Regionally widespread (1000+ km)
Pristina leidyi	2	High, morphologically identified, named species	Stygoxene, Widespread	BS4	1	Regionally widespread (1000+ km)
Nais communis	1	High, morphologically identified, named species	Stygoxene, Widespread	BS4	1	Regionally widespread (1000+ km)
Phreodrillidae						
Antarctodrilus `sp. Biologic-OLIG054`	1	High, DNA (unique lineage)	Stygofauna, Potential SRE	BS4	1	Singleton

Taxonomy	**No. spms**	**ID status Taxonomic comments**	**Subterranean status, SRE status**	**Sections**	**No. sites**	**Distribution comments, known linear range**
Phreodrilidae `sp. 12`	25	High, DNA; external match with sequences from the Fortescue River catchment, Black Range Creek and West Angelas (Brown *et al.*, 2015)	Stygofauna, Widespread	BS1, BS3	8	Regionally widespread (300+ km)
Phreodrilidae `sp. Biologic-OLIG001`	1	High, DNA (unique lineage); specimen originated from Karaman sample and may thus represent a stygophile/xene OTU	Stygofauna, Potential SRE	BS4	1	Singleton
Phreodrilidae `sp. Biologic-OLIG002`	1	High, DNA (unique lineage)	Stygofauna, Potential SRE	BS1	1	Singleton
Phreodrilidae `sp. Biologic-OLIG011`	13	High, DNA (unique lineage); specimens originated from Karaman sample and may thus represent a stygophile/xene OTU	Stygofauna, Potential SRE	BS4	2	Locally restricted (0.9 km)
Phreodrilidae `sp. P12`	8	High, DNA; external match with sequences from the Fortescue River catchment and Coondwanna (Brown *et al.*, 2015)	Stygofauna, Widespread	BS1, BS3	5	Regionally widespread (100+ km)
ACARI						
Pezidae						
Pezidae `sp. BGCK`	3	Med, Morpho, Spatial info; no genetic confirmation.	Stygofauna, uncertain SRE	BS4	1	Single site
Pezidae `sp. BS3X`	1	Med, Morpho, Spatial info; no genetic confirmation.	Stygofauna, uncertain SRE	BS3	1	Putative singleton
OSTRACODA						
Candonidae						
Candonopsis tenuis	20	High, morphologically identified, named species	Stygofauna, Widespread	BS4	3	Regionally widespread (360 km)
Cyprididae						
Cypretta seurati	2	High, morphologically identified, named species	Stygoxene, Widespread	BS1	1	Regionally widespread (600+ km)
Limnocytheridae						
Limnocythere `sp. BOS1314`	12	High, morphologically aligned to known morphospecies	Stygofauna, Potential SRE	BS4	1	Locally widespread (41.8 km)
CALANOIDA						
Calanoida `sp. Biologic-CALA002`	1	High, DNA (unique lineage)	Stygofauna, Potential SRE	BS3	1	Single site
CYCLOPOIDA						
Cyclopidae						
Anzcyclops? `sp. BS3`	2	Med, Morpho, Spatial info; no genetic confirmation.	Stygofauna, uncertain SRE	BS3	1	Locally restricted (4.5 km)
Diacyclops humphreysi	19	High, morphologically identified, named species	Stygoxene, Widespread	BS4	1	Regionally widespread (700+ km)
Diacyclops nr hymphreysi	8	Med, Morpho; no genetic confirmation	Stygofauna, unlikely SRE	BS1, BS4		Locally restricted (5.6 km)

Taxonomy	No. spms	ID status Taxonomic comments	Subterranean status, SRE status	Sections	No. sites	Distribution comments, known linear range
Mesocyclops notius	1	High, morphologically identified, named species	Stygoxene, Widespread	BS2	1	Regionally widespread (1000+ km)
Microcyclops varicans	3	High, morphologically identified, named species	Stygoxene, Widespread	BS4	1	Regionally widespread (1000+ km)
Thermocyclops aberrans	2	High, morphologically identified, named species	Stygofauna, Widespread	BS2	1	Regionally widespread (200 km)
Thermocyclops cf aberrans	9	Med, Morpho; no genetic confirmation	Stygofauna, unlikely SRE	BS4		Single site
BATHYNELLACEA						
Bathynellidae						
Bathynellidae `sp. Biologic-BATH001`	1	High, DNA (unique lineage)	Stygobite, Potential SRE	BS4	1	Singleton
Bathynellidae `sp. Biologic-BATH002`	2	High, DNA (unique lineage)	Stygobite, Potential SRE	BS4	2	Locally restricted (4 km)
Bathynellidae `sp. Biologic-BATH003`	8	High, DNA (unique lineage)	Stygobite, Potential SRE	BS4	2	Locally restricted (0.4 km)
Parabathynellidae						
Atopobathynella `sp. BGCK`	1	Med, Morpho, Spatial info; no genetic confirmation	Stygobite, Potential SRE	BS4	1	Single site
Atopobathynella `sp. Biologic-PBAT013`	15	High, DNA (unique lineage)	Stygobite, Potential SRE	BS4	3	Locally restricted (0.13 km)
Atopobathynella `sp. Biologic-PBAT014`	1	High, DNA (unique lineage)	Stygobite, Potential SRE	BS4	1	Singleton
Parabathynellidae `sp. Biologic-PBAT003`	6	High, DNA (unique lineage)	Stygobite, Potential SRE	BS1	1	Single site
Parabathynellidae `sp. Biologic-PBAT004`	22	High, DNA (unique lineage)	Stygobite, Potential SRE	BS3	5	Locally restricted (2 km)
Parabathynellidae `sp. Biologic-PBAT005`	7	High, DNA (unique lineage)	Stygobite, Potential SRE	BS3	2	Locally restricted (0.8 km)
Parabathynellidae `sp. Biologic-PBAT012`	10	High, DNA (unique lineage)	Stygobite, Potential SRE	BS3	4	Locally restricted (1 km)
Parabathynellidae `sp. Biologic-PBAT022`	3	High, DNA (unique lineage)	Stygobite, Potential SRE	BS4	1	Single site
AMPHIPODA						
Bogidiellidae						
Bogidiellidae `sp. Biologic-AMPH011`	3	High, DNA (unique lineage)	Stygofauna, Potential SRE	BS1	3	Likely locally widespread (11.8 km)
Eriopisidae						
Nedsia `sp. Biologic-AMPH003`	125	High, DNA (unique lineage)	Stygofauna, Potential SRE	BS4	1	Single site
Nedsia nanutarra	5	High, DNA; external match with sequence from	Stygofauna, Widespread	BS1	5	Regionally widespread (100+ km)

Taxonomy	No. spms	ID status Taxonomic comments	Subterranean status, SRE status	Sections	No. sites	Distribution comments, known linear range
		Greater Paraburdoo (Cullen & Harvey, 2018)				
Nedsia `sp. Biologic-AMPH052`		High, DNA; external match.	Stygofauna, Widespread	BS1	1	Regionally widespread, LR 100+ km
Paramelitidae						
Paramelitidae `sp. Biologic-AMPH012`	1	High, DNA (unique lineage)	Stygofauna, Potential SRE	BS3	1	Singleton
Paramelitidae `sp. Biologic-AMPH015`	44	High, DNA (unique lineage)	Stygofauna, Potential SRE	BS3	9	Locally restricted (11 km)
Paramelitidae `sp. Helix-AMP037`	9	High, DNA; external match with sequence from Mesa H (Biota, 2018)	Stygofauna, Widespread	BS4, BS1	6	Regionally widespread (100+ km)
Paramelitidae `sp. Biologic-AMPH047`	1	High, DNA (unique lineage)	Stygofauna, Potential SRE	BS3	1	Singleton
Paramelitidae `sp. Biologic-AMPH048`	1	High, DNA (unique lineage)	Stygofauna, Potential SRE	BS3	1	Singleton
Indeterminate						
Amphipoda `sp. Biologic-AMPH009`	56	High, DNA; morphologically 'cf Niphargidae'. Genetically distinct from available Niphargidae sequences (unique lineage)	Stygobite, Potential SRE	BS4	7	Locally restricted (0.9 km)
ISOPODA						
Microcerberidae						
Microcerberidae `sp. Biologic-ISOP026	1	High, DNA (unique lineage)	Stygofauna, Potential SRE	BS3	1	Singleton
Indeterminate						
Isopoda `sp. Biologic-ISOP011`	35	High, DNA (unique lineage). Stygobytic isopod, morphologically distinct from *Pygolabis*	Stygofauna, Potential SRE	BS4	1	Single site

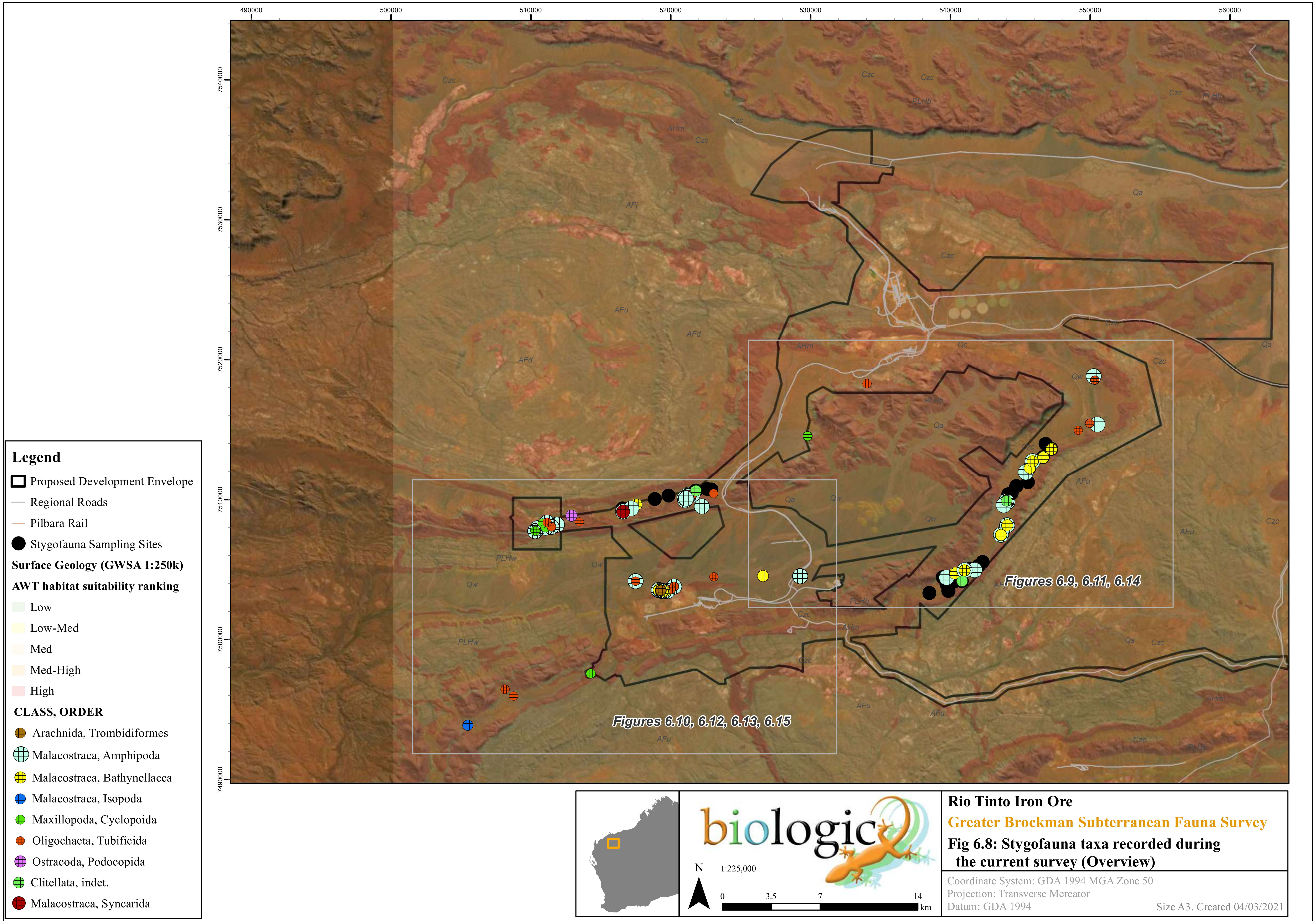
Note: BS1 = Brockman Syncline 1 section, BS2 = Brockman Syncline 2 section, BS3 = Brockman Syncline 3 section, BS4 = Brockman Syncline 4 section (incl. Vivash and Boolgeeda Creek reference areas).

Table 6.3: Higher level stygofauna identifications within the Study Area

Taxonomy	No. spms	Taxonomic comments	Subterranean status, SRE status	Regions	No. sites
Amphipoda sp. indet.	54	Indeterminate higher-level taxon (order). DNA not tested. May represent other Amphipoda sp. collected from the Study Area.	Potential Stygofauna, Uncertain	BS3, BS4	3
Antarctodrilus sp. indet.	7	Indeterminate higher-level taxon (genus). DNA fail (1 specimen) and DNA not tested (6 specimens). May represent other Phreodrilidae sp. recorded from the Study Area.	Potential Stygofauna, Uncertain	BS3, BS4	2
Atopobathynella sp. indet.	14	Indeterminate higher-level taxon (genus). DNA fail (1 specimen) and DNA not tested (13 specimens). May represent other *Atophobathynella* sp. recorded from the Study Area.	Stygobite, Uncertain	BS4	3
Australocamptus sp. indet.	1	Indeterminate higher-level taxon (genus). DNA not tested. May represent other Harpacticoida sp. collected from the Study Area.	Potential Stygofauna, Uncertain	BS3	1
Bathynellidae sp. indet.	16	Indeterminate higher-level taxon (family). DNA not tested. Likely to represent Bathynellidae `sp. Biologic-BATH001`, Bathynellidae `sp. Biologic-BATH002` and/or Bathynellidae `sp. Biologic-BATH003` collected from the same site.	Stygobite, Uncertain	BS4	1
Bogidiellidae sp. indet.	1	Indeterminate higher-level taxon (family). DNA not tested. May represent other Bogidiellidae sp. recorded from the Study Area, such as Bogidiellidae `sp. Biologic-AMPH011` recorded from the same site.	Potential Stygofauna, Uncertain	BS1	1
Copepoda sp. indet.	523	Indeterminate higher-level taxon (subclass). DNA fail (1 specimen) and DNA not tested (523 specimens). May represent other *Copepoda* sp. recorded from the Study Area.	Potential Stygofauna, Uncertain	BS3, BS4	10
Cyclopoida sp. indet.	667	Indeterminate higher-level taxon (order). DNA not tested. May represent other Cyclopoida sp. collected from the Study Area.	Potential Stygofauna, Uncertain	BS1, BS2, BS3, BS4	24
Diacyclops nr humprheysi	10	Indeterminate higher-level taxon (genus). DNA fail. May represent other *Diacyclops* sp. collected from the Study Area.	Potential Stygofauna, Uncertain	BS1, BS4	4
Enchytraeidae sp. indet.	201	Indeterminate higher-level taxon (family). DNA fail (1 specimen) and DNA not tested (200 specimens). May represent other Enchytraeidae sp. recorded from the Study Area.	Potential Stygofauna, Uncertain	BS1, BS2, BS3, BS4	15
Harpacticoida sp. indet.	7	Indeterminate higher-level taxon (order). DNA not tested. May represent other Harpacticoida sp. collected from the Study Area.	Potential Stygofauna, Uncertain	BS4	2
Naididae sp. indet.	1	Indeterminate higher-level taxon (family). DNA not tested.	Potential Stygofauna, Uncertain	BS2	1
Nedsia sp. indet.	102	Indeterminate higher-level taxon (genus). DNA fail (1 specimen) and DNA not tested (101 specimens). May represent other *Nedsia* sp. recorded from the Study Area.	Potential Stygofauna, Uncertain	BS1, BS4	11
Nematoda sp. indet.	5	Indeterminate higher-level taxon (phylum). DNA not tested.	Potential Stygofauna, Uncertain	BS1, BS3	3
Oligochaeta sp. indet.	27	Indeterminate higher-level taxon (class). DNA fail (4 specimens) and DNA not tested (23 specimens). May represent other *Ostracoda* sp. recorded from the Study Area.	Potential Stygofauna, Uncertain	BS1, BS4	9
Ostracoda sp. indet.	56	Indeterminate higher-level taxon (class). DNA not tested. May represent other Ostracoda sp. collected from the Study Area.	Potential Stygofauna, Uncertain	BS1, BS3, BS4	6
Parabathynellidae nr. Brevisomabathynella sp. indet.	47	Indeterminate higher-level taxon (family). DNA fail (6 specimens) and DNA not tested (41 specimens). May represent other Parabathynellidae sp. recorded from the Study Area.	Stygobite, Uncertain	BS3	3
Parabathynellidae sp. indet.	41	Indeterminate higher-level taxon (family). DNA fail (6 specimens) and DNA not tested (35 specimens). May represent other Parabathynellidae sp. recorded from the Study Area.	Stygobite, Uncertain	BS1, BS3, BS4	4

Taxonomy	No. spms	Taxonomic comments	Subterranean status, SRE status	Regions	No. sites
Paramelitidae sp. indet.	213	Indeterminate higher-level taxon (family). DNA fail (5 specimens) and DNA not tested (207 specimens). May represent other Paramelitidae sp. recorded from the Study Area.	Potential Stygofauna, Uncertain	BS1, BS2, BS3, BS4	19
Pescecyclops sp. indet.	4	Indeterminate higher-level taxon (genus). DNA not tested. May represent other Cyclopoida sp. collected from the Study Area.	Potential Stygofauna, Uncertain	BS3, BS4	2
Phreodrilidae sp. indet.	23	Indeterminate higher-level taxon (family). DNA not tested. May represent other Phreodrilidae sp. collected from the Study Area	Potential Stygofauna, Uncertain	BS1, BS3, BS4	4

Note: BS1 = Brockman Syncline 1 section, BS2 = Brockman Syncline 2 section, BS3 = Brockman Syncline 3 section, BS4 = Brockman Syncline 4 section (incl. Vivash and Boolgeeda Creek reference areas).



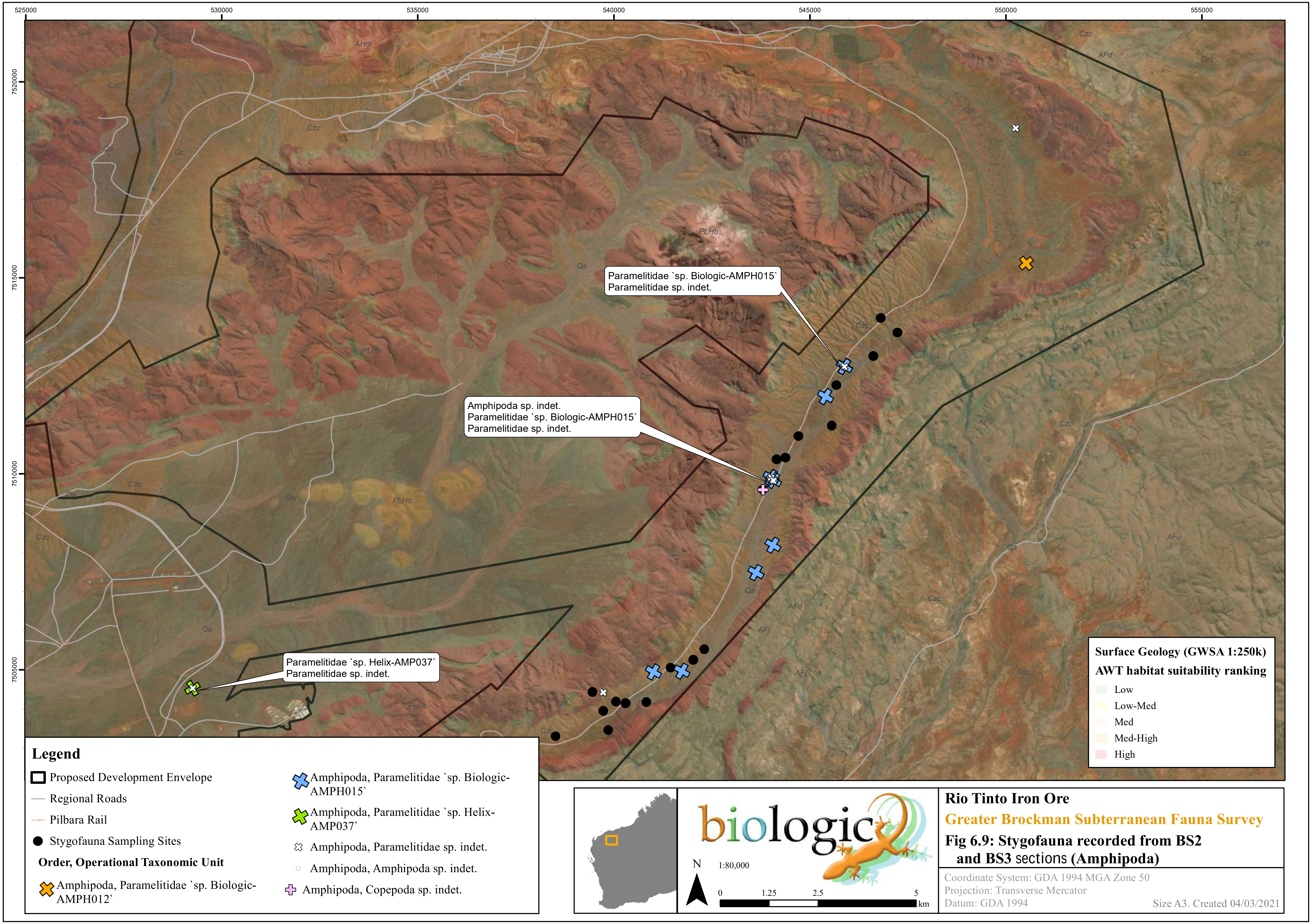
Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Fig 6.8: Stygofauna taxa recorded during the current survey (Overview)

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

Size A3. Created 04/03/2021



Rio Tinto Iron Ore

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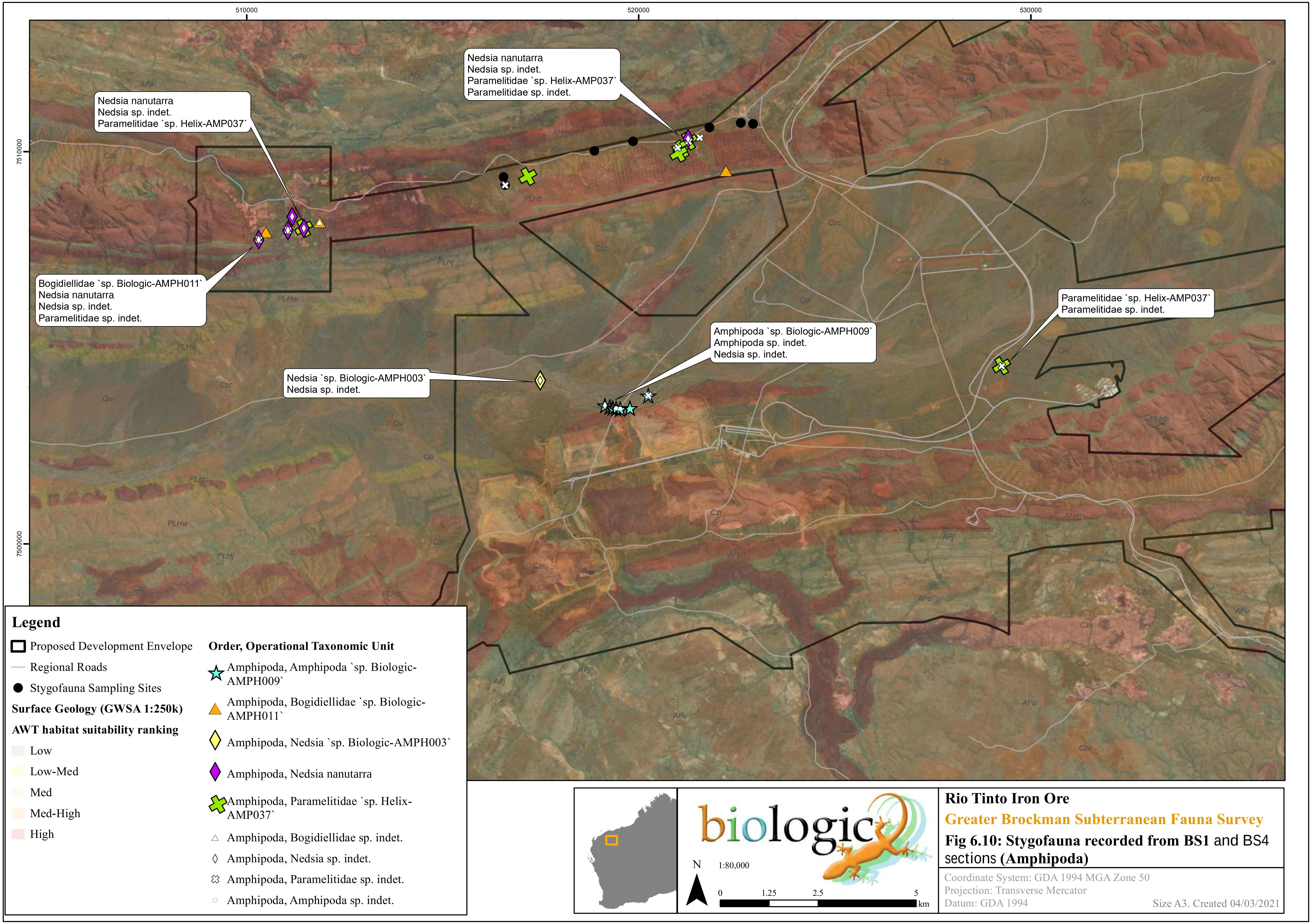
Fig 6.9: Stygofauna recorded from BS2 and BS3 sections (Amphipoda)

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994
Size A3. Created 04/03/2021



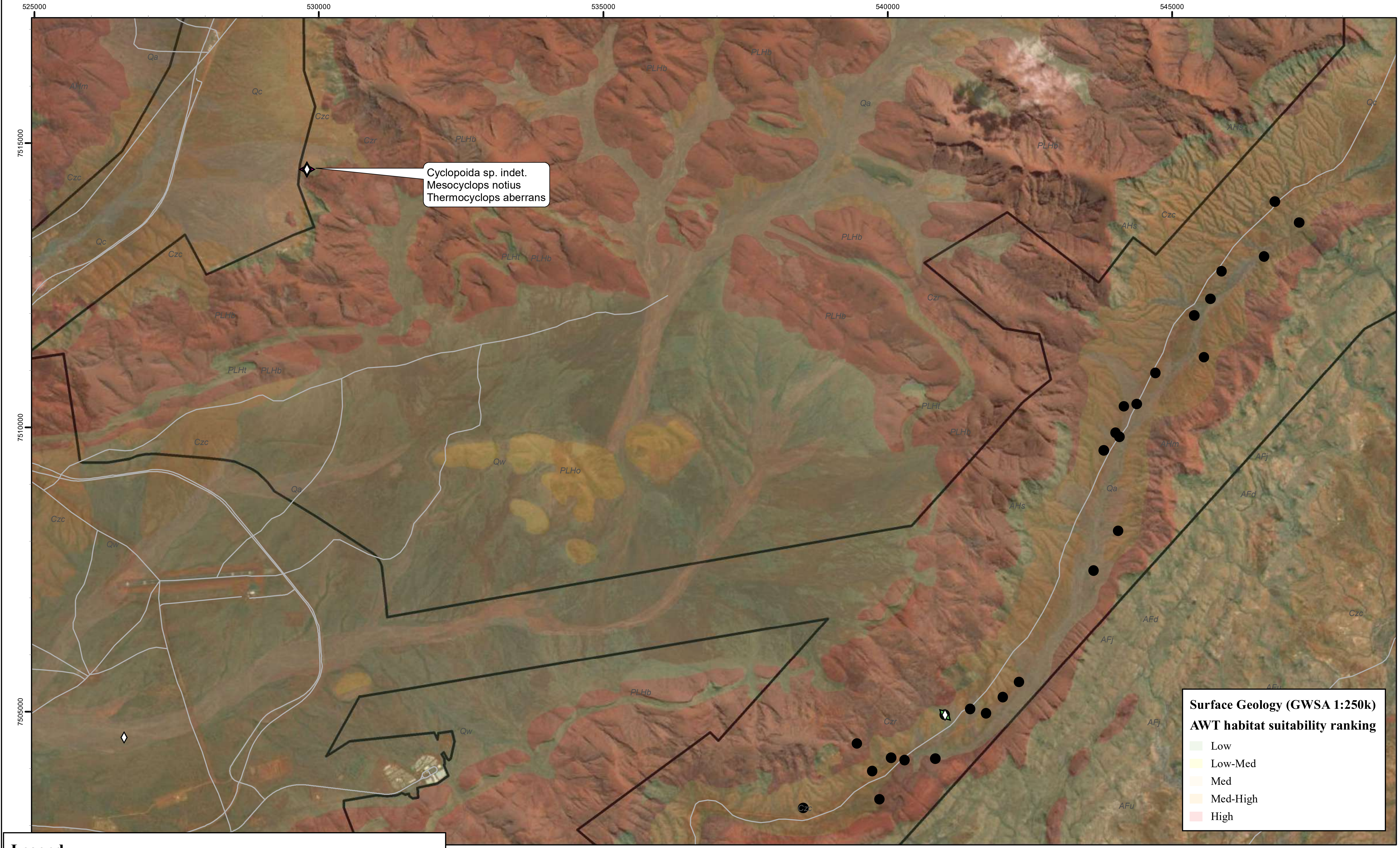
Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Fig 6.10: Stygofauna recorded from BS1 and BS4 sections (Amphipoda)

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

Size A3. Created 04/03/2021



Cyclopoida sp. indet.
Mesocyclops notius
Thermocyclops aberrans

Surface Geology (GWSA 1:250k)

AWT habitat suitability ranking

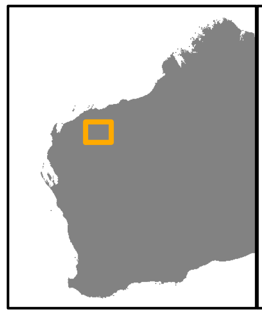
- 🟩 Low
- 🟨 Low-Med
- ▢ Med
- 🟧 Med-High
- 🟥 High

Legend

- ▢ Proposed Development Envelope
- — Regional Roads
- ● Stygofauna Sampling Sites

Order, Operational Taxonomic Unit

- ◆ Cyclopoida, Anzcyclops? `sp. BS3`
- ◆ Cyclopoida, Mesocyclops notius
- ◆ Cyclopoida, Thermocyclops aberrans
- ◇ Cyclopoida, Cyclopoida sp. indet.



biologic

N

1:60,000

0 0.75 1.5 3 km

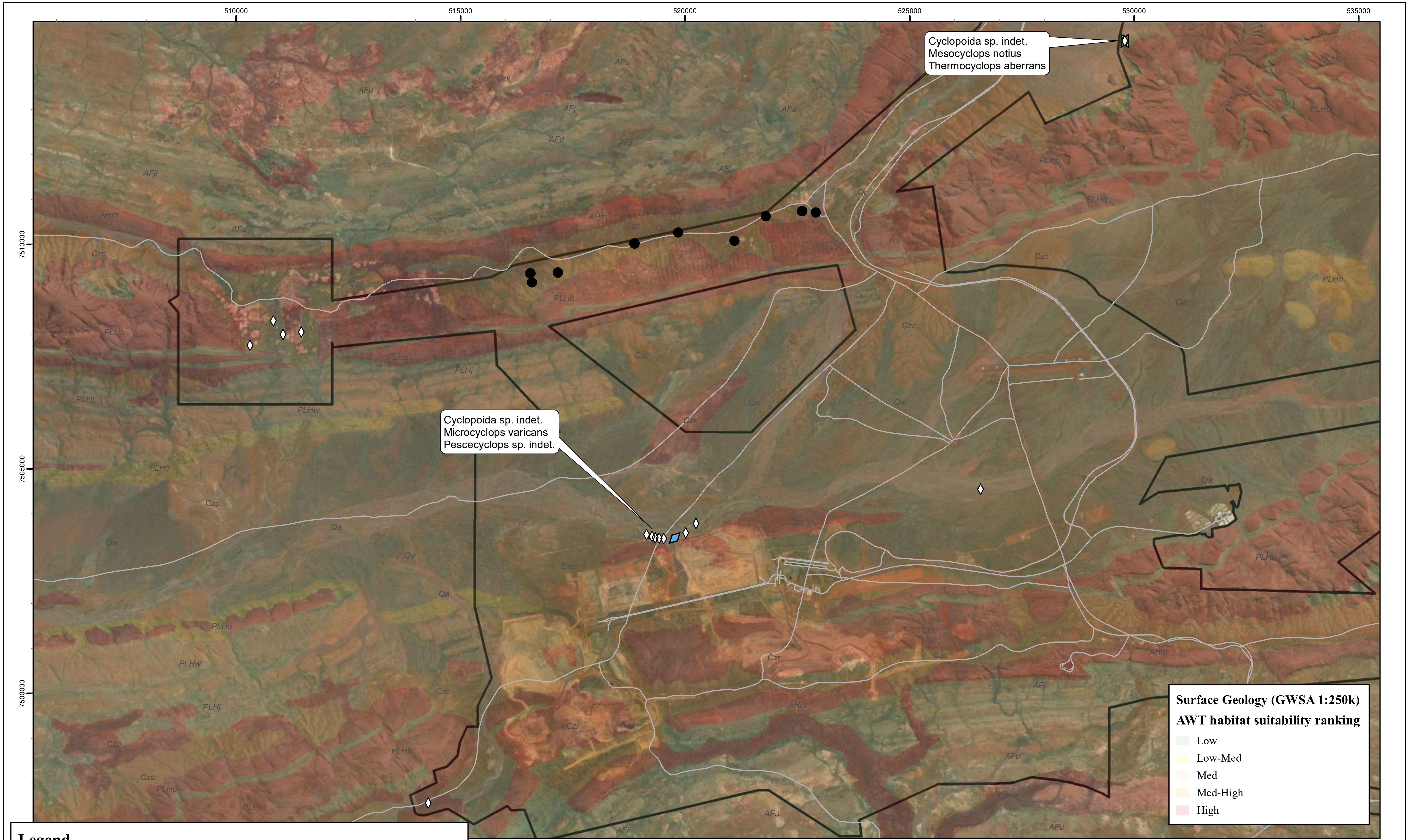
Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Fig 6.11: Stygofauna recorded from BS2 and BS3 sections (Copepoda)

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

Size A3. Created 04/03/2021



Surface Geology (GWSA 1:250k)

AWT habitat suitability ranking

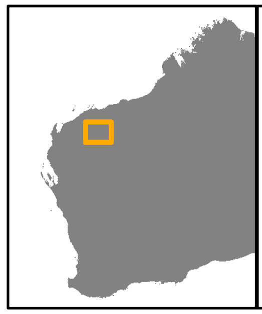
▢	Low
▢	Low-Med
▢	Med
▢	Med-High
▢	High

Legend

▢	Proposed Development Envelope
—	Regional Roads
●	Stygofauna Sampling Sites

Order, Operational Taxonomic Unit

◆	Cyclopoida, Diacyclops humphreysi
◆	Cyclopoida, Mesocyclops notius
◆	Cyclopoida, Microcyclops varicans
◇	Cyclopoida, Pescecyclops sp. indet.
◆	Cyclopoida, Thermocyclops aberrans
◇	Cyclopoida, Cyclopoida sp. indet.



biologic

N

1:75,000

0 1 2 4
km

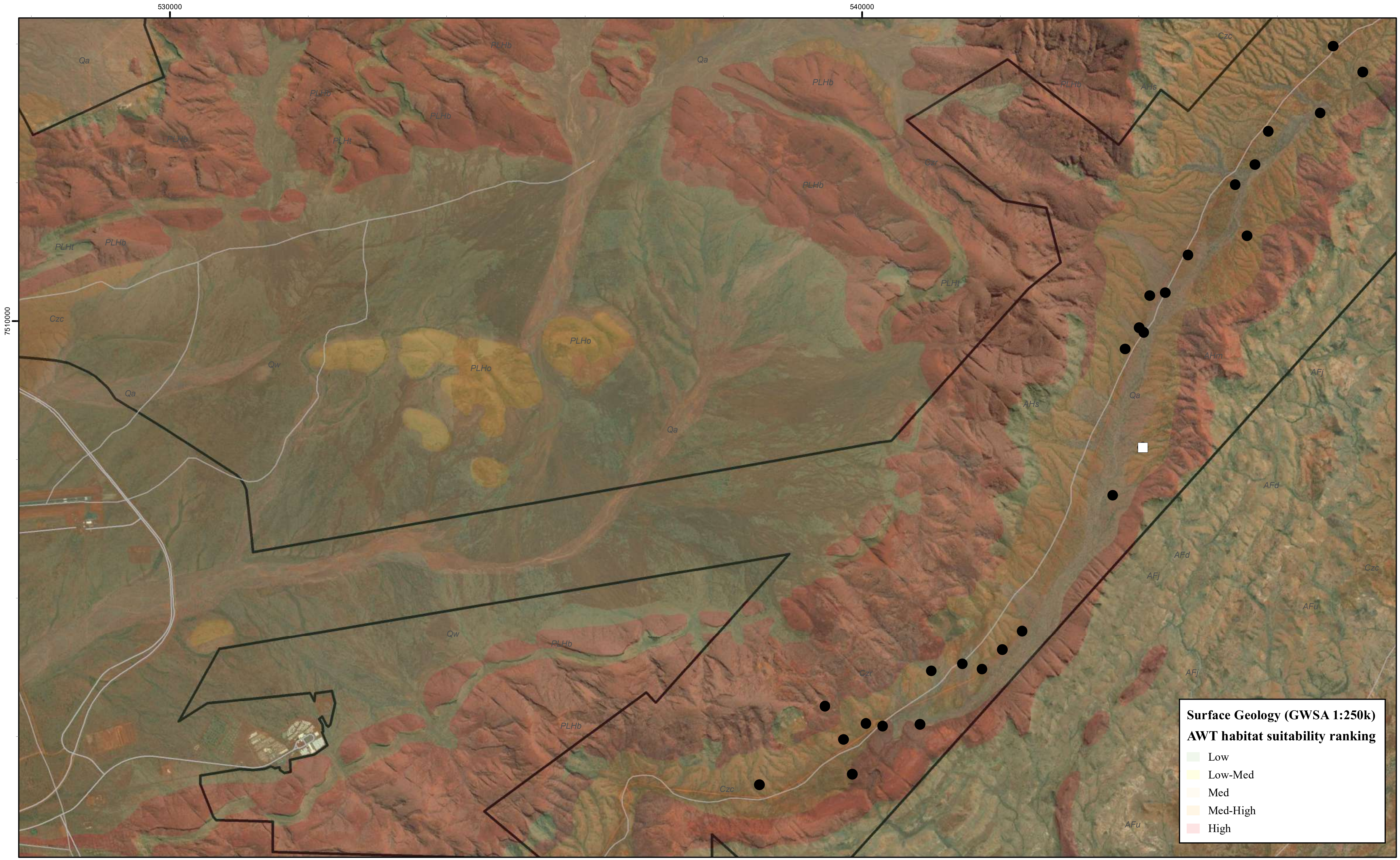
Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Fig 6.12: Stygofauna recorded from BS1 and BS4 sections (Copepoda)

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

Size A3. Created 04/03/2021



Legend

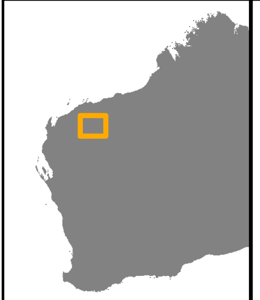
☐ Proposed Development Envelope

— Regional Roads

● Stygofauna Sampling Sites

Order, Operational Taxonomic Unit

☐ Podocopida, Ostracoda sp. indet.



N

1:50,000

0 0.75 1.5 3 km

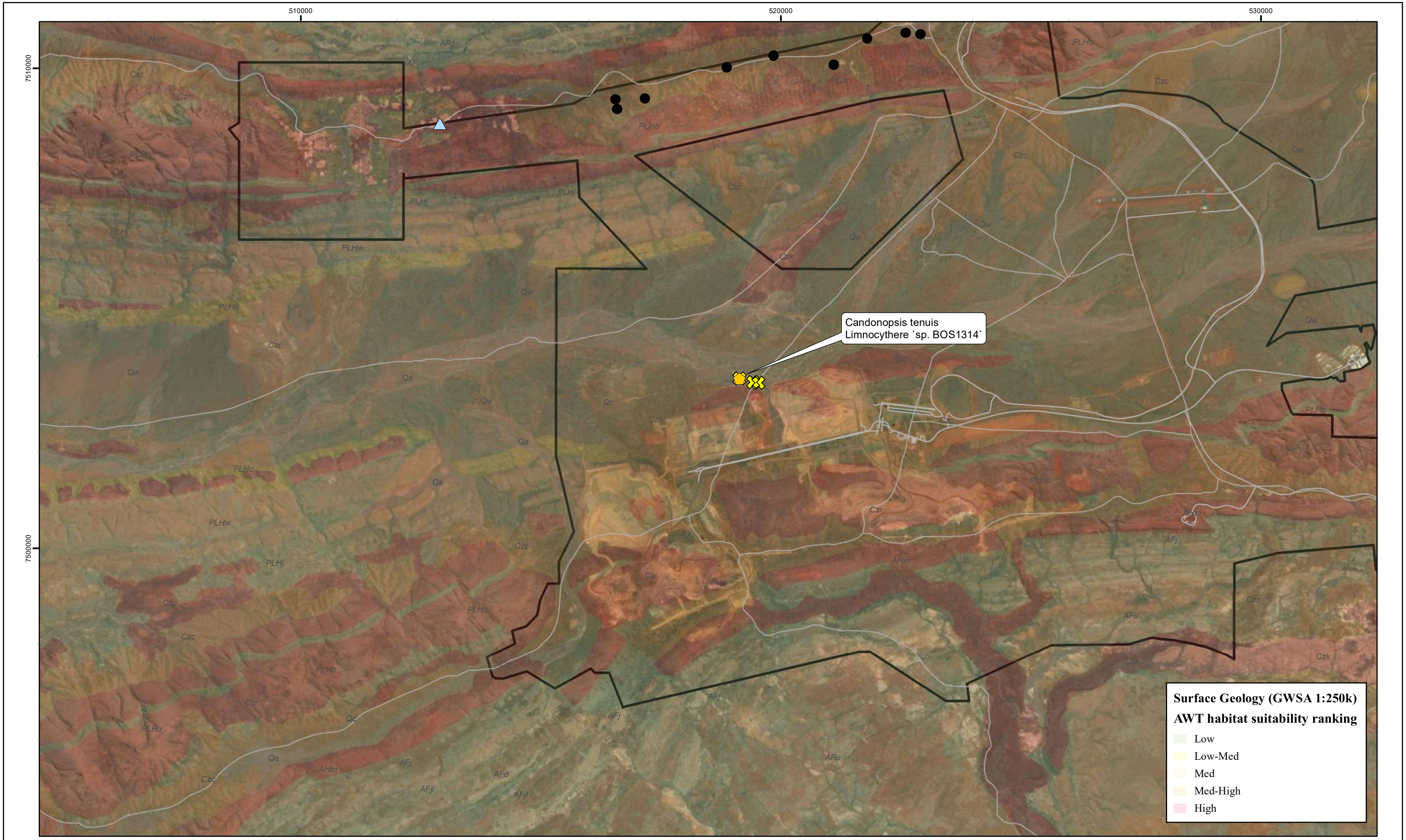
Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Fig 6.13: Stygofauna recorded from BS2 and BS3 sections (Ostracoda)

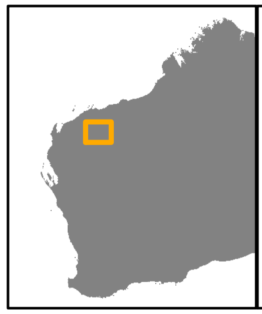
Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

Size A3. Created 04/03/2021



Legend

▭ Proposed Development Envelope	**Order, Operational Taxonomic Unit**
— Regional Roads	✕ Podocopida, Candonopsis tenuis
● Stygofauna Sampling Sites	△ Podocopida, Cypretta seurati
	⬠ Podocopida, Limnocythere `sp. BOS1314`



N

1:70,000

0 1 2 4 km

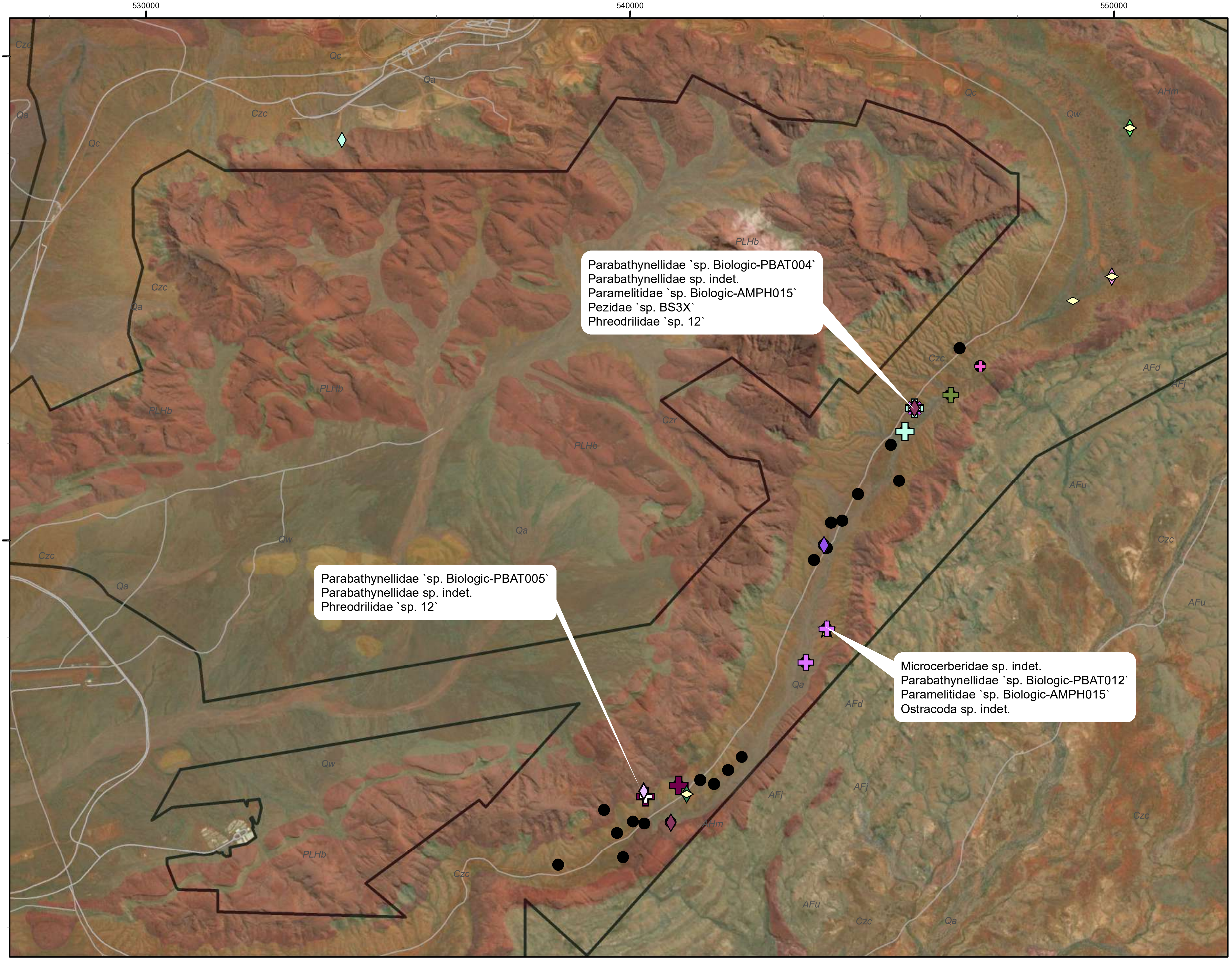
Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Fig 6.14: Stygofauna recorded from BS1 and BS4 sections (Ostracoda)

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

Size A3. Created 04/03/2021



Parabathynellidae `sp. Biologic-PBAT004`
Parabathynellidae sp. indet.
Paramelitidae `sp. Biologic-AMPH015`
Pezidae `sp. BS3X`
Phreodrilidae `sp. 12`

Parabathynellidae `sp. Biologic-PBAT005`
Parabathynellidae sp. indet.
Phreodrilidae `sp. 12`

Microcerberidae sp. indet.
Parabathynellidae `sp. Biologic-PBAT012`
Paramelitidae `sp. Biologic-AMPH015`
Ostracoda sp. indet.

Legend

- ▭ Proposed Development Envelope
- — Regional Roads
- — Pilbara Rail
- ● Stygofauna Sampling Sites

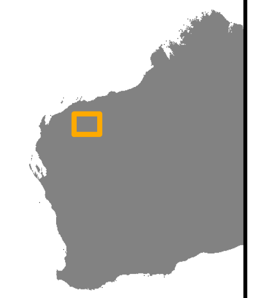
Order, Operational Taxonomic Unit

- ✚ Bathynellacea, Parabathynellidae `sp. Biologic-PBAT004`
- ✚ Bathynellacea, Parabathynellidae `sp. Biologic-PBAT005`
- ✚ Bathynellacea, Parabathynellidae sp. indet.
- ✳ Trombidiformes, Pezidae `sp. BS3X`
- ◆ Tubificida, Enchytraeidae `sp. Biologic-OLIG004`
- ◆ Tubificida, Enchytraeidae `sp. Biologic-OLIG005`
- ◆ Tubificida, Enchytraeidae `sp. Biologic-OLIG017`
- ◆ Tubificida, Enchytraeidae `sp. Biologic-OLIG018`
- ◆ Tubificida, Enchytraeidae sp. indet.
- ◆ Tubificida, Naididae sp. indet.
- ◆ Tubificida, Phreodrilidae `sp. 12`
- ◆ Tubificida, Phreodrilidae sp. indet.
- ✚ Bathynellacea, Parabathynellidae `sp. Biologic-PBAT012`
- ✚ Bathynellacea, Parabathynellidae nr. Brevisoma b.
- ✚ Bathynellacea, Paramelitidae `sp. Biologic-AMPH015`
- ★ Isopoda, Microcerberidae sp. indet.

Surface Geology (GWSA 1:250k)

AWT habitat suitability ranking

- 🟩 Low
- 🟨 Low-Med
- 🟨 Med
- 🟧 Med-High
- 🟥 High



biologic

N

1:80,000

0 1.25 2.5 5 km

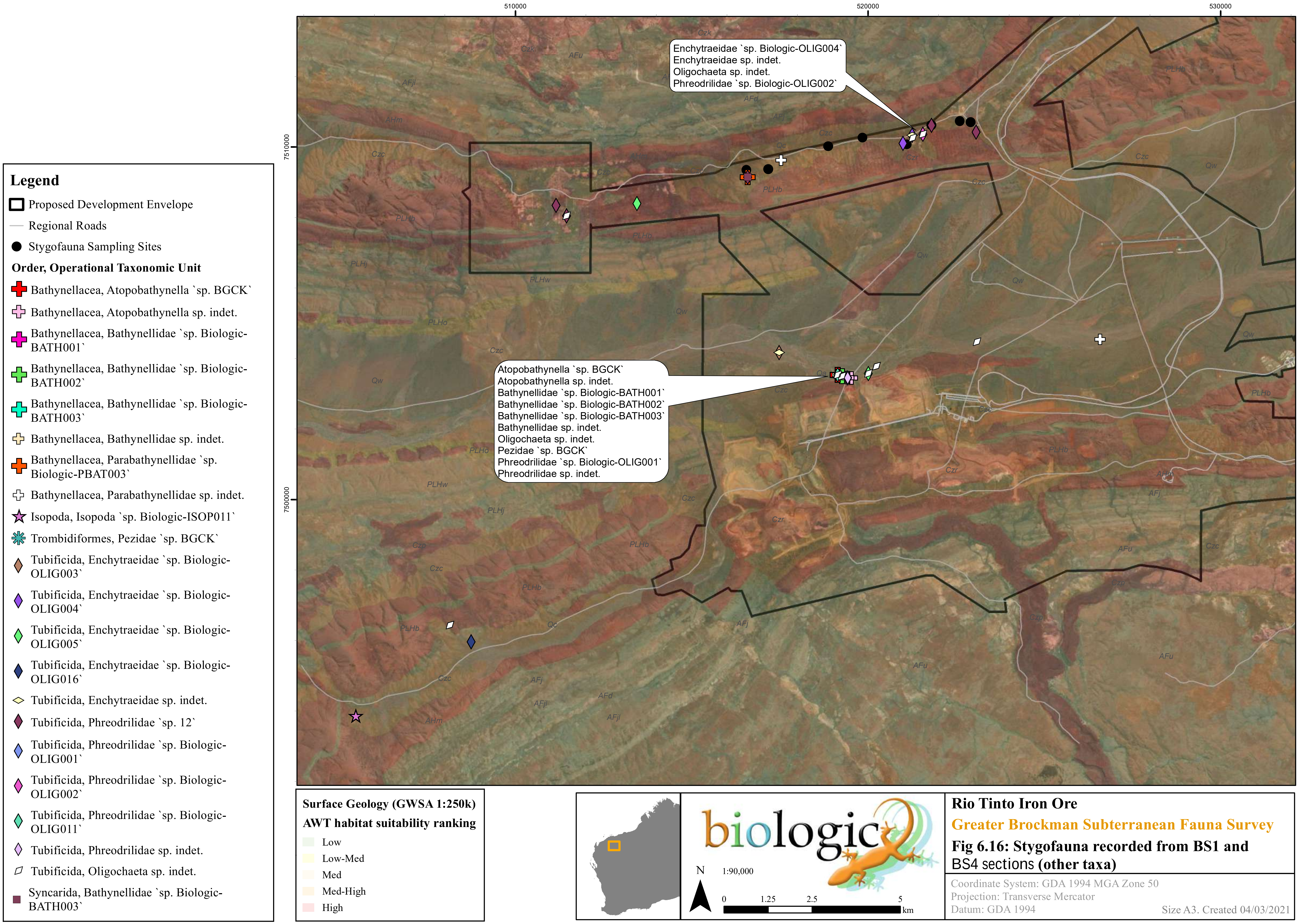
Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Fig 6.15: Stygofauna recorded from BS2 and BS3 sections (other taxa)

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

Size A3. Created 04/03/2021



Enchytraeidae `sp. Biologic-OLIG004`
Enchytraeidae sp. indet.
Oligochaeta sp. indet.
Phreodrilidae `sp. Biologic-OLIG002`

Atopobathynella `sp. BGCK`
Atopobathynella sp. indet.
Bathynellidae `sp. Biologic-BATH001`
Bathynellidae `sp. Biologic-BATH002`
Bathynellidae `sp. Biologic-BATH003`
Bathynellidae sp. indet.
Oligochaeta sp. indet.
Pezidae `sp. BGCK`
Phreodrilidae `sp. Biologic-OLIG001`
Phreodrilidae sp. indet.

Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Fig 6.16: Stygofauna recorded from BS1 and BS4 sections (other taxa)

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994
Size A3. Created 04/03/2021

6.4 Species distributions (current and previous surveys)

Appendix I shows all 76 stygofauna taxa that have been found within or near the Development Envelope/Study Area to date by current and previous surveys.

Based on current occurrence records and taxonomic/ ecological information, these taxa can be broken into four groups according to their distribution (Appendix I):

- Confirmed/likely widespread throughout the Pilbara region;
- Confirmed/likely widespread within the Study Area;
- Locally restricted within the Study Area; and
- Known from a single site/ singleton.

Unlike the troglofauna, there were only a few stygofauna taxonomic groups that had consistent distribution patterns in a local and regional sense.

Bathynellacea (also known as Syncarida) for example, were detected only from singletons/ single sites, or from a few sites within a localised spatial area (Appendix I). The most recent taxonomic studies of Bathynellidae and Parabathynellidae throughout the region (those including significant genetic work) have suggested that most syncarids have very limited dispersal abilities and show high rates of species turnover over geographical distance and different hydrogeological habitats (Abrams *et al.*, 2012; Matthews *et al.*, 2020; Perina *et al.*, 2018, 2019a; Perina *et al.*, 2019b). Therefore, the restricted distributions and high species turnover of syncarid OTUs found in this study are unlikely to be attributed to sampling artefacts, particularly given the high success rate of DNA throughout these groups. More restricted or putatively restricted taxa such as bathynellaceans (as well as some ostracods, amphipods, isopods, and worms) are identified as key taxa for further consideration in section 8.

Other groups, particularly cyclopoid copepods, most harpacticoids, and many amphipods, ostracods, and worms are typically widely distributed throughout catchments or sub-catchments in the Pilbara region (refer distribution comments in Appendix I). Although many stygoxenes and stygophiles occur within these groups (*i.e.* taxa that can also live within surface waters), there are also many true stygobites that are able to disperse throughout catchments or across multiple different hydrogeological habitats via the hyporheic zone of major drainage lines. In the case of copepods and worms, most of the published studies to date suggest the dominant distribution patterns are widespread occurrence regionally or throughout catchments and sub-catchments in the Pilbara region (Brown *et al.* 2015). The results from the Study Area broadly reflect this, with many copepods and oligochaetes representing either regionally or locally widespread taxa (Appendix I). However, comparatively little DNA studies have been undertaken on Pilbara copepods, and the patterns in the Yilgarn region suggest many SRE copepod taxa occur in that region (Karanovic & Cooper, 2011, 2012; Karanovic *et al.*, 2013).

For other groups such as amphipods and ostracods that are known to contain species with a wide variety of distributions (from SRE to locally and regionally widespread) co-occurring within the same habitat, the question of whether singleton records may be attributed to sampling artefacts and the species may actually occur more widely is complicated and must be assessed on a case by case basis.

7. SURVEY ADEQUACY

The total sampling effort undertaken during the current survey (as shown in sections 5.1 and 6.1) exceeds the minimum EPA guidelines for subterranean fauna (2016a, 2016b), even in consideration of the diverse habitat units sampled for troglofauna and stygofauna throughout the four survey areas of the Study Area. Individually, each of the four sampling areas were also sampled in excess of the EPA minimum guidelines (2016a, 2016b).

Table 7.1 provides details of survey strike rates (*i.e.* ratio of samples that detected subterranean fauna *vs.* those that did not) and average species richness per sample. Average species richness calculations were performed only on 'fauna-positive' samples (*i.e.* samples where subterranean fauna were detected), while 'fauna negative' samples were excluded.

The overall strike rate for troglofauna within the Study Area was higher than a recent similar survey at Greater Paraburdoo (Biologic 2019) and the previous Biota surveys in the Study Area (also refer Figure 7.1). Average species richness of troglofauna throughout the Study Area as a whole was comparable with previous surveys at Greater Paraburdoo, Silvergrass and BS4 (between 0.50 and 0.61), but this varied between the survey areas, with the BS2 area being the lowest (0.45) and BS3 being the highest (0.81).

The trends in this data may be attributed to many interacting factors, including characteristics of the troglofauna communities and habitats present in the environment, as well as the sampling intensity for each survey or survey area, the sampling methods used, the degree of taxonomic certainty (based on the state of knowledge at the time of survey), and the variable use of DNA analyses to detect finer scale species differences amongst the fauna. In this sense the previous Nammuldi and Silvergrass surveys (Biota 2011) do not provide particularly useful comparisons with the current data, owing to the order of magnitude greater sampling intensity and greater DNA analyses that have contributed to the current troglofauna results.

Table 7.1: Summary of sampling adequacy statistics comparing the overall Greater Brockman Study Area, with survey areas at BS1, BS2, BS3, and BS4/VIV. Previous surveys at Greater Paraburdoo, Nammuldi, Silvergrass and BS4 are included for comparison.

Project Area	Total samples	Samples by method	Fauna-positive samples†	Species	Strike rate#	Average species richness^
Troglofauna						
Greater Brockman (Total)	**1102**	**Scraping (701), Trapping (401)**	**242**	**124**	**0.22**	**0.51**
BS1	269	Scraping (171), Trapping (98)	68	35	0.25	0.51
BS2	319	Scraping (185), Trapping (134)	47	21	0.15	0.45
BS3	286	Scraping (201), Trapping (85)	62	50	0.22	0.81
BS4	228	Scraping (144), Trapping (84)	65	39	0.29	0.60
Greater Paraburdoo (Biologic 2019)	431	Scraping (288), Trapping (143)	67	39	0.16	0.58
Nammuldi (Biota 2011)	29	Trapping (29)	2	2	0.07	1
Silvergrass (Biota 2011)	75	Trapping (75)	12	6	0.16	0.5
Historical BS4 (Biota 2016a, b, c)	149	Scraping (54), Trapping (95)	28	17	0.19	0.61
Stygofauna						
Greater Brockman (Total)	**320**	**Hauling/ Karaman (320)**	**125**	**54**	**0.39**	**0.43**
BS1	75	Hauling (75)	27	12	0.36	0.44
BS2	35	Hauling (35)	5	3	0.14	0.60
BS3	154	Hauling (154)	64	19	0.42	0.30
BS4	56	Hauling/ Karaman (56)	29	30	0.52	1.03
Greater Paraburdoo (Biologic 2019)	106	Hauling/ Pumping/ Karaman (106)	37	66	0.35	1.78
Nammuldi (Biota 2010)*	23*	Hauling (23)	3	3	0.13	1
Silvergrass (Biota 2010)*	41*	Hauling (41)	24	22	0.59	0.92

Note: † 'fauna-positive' samples are samples where troglofauna or stygofauna were detected. # Strike rate is the ratio of fauna-positive to fauna-negative samples. ^ Average species richness was calculated only for fauna-positive samples. * Nammuldi and Silvergrass stygofauna data Biota (2010) were calculated by site (*i.e.* all samples from a particular bore/ hole) as sample by sample data was not available. Text colour reflects chart colours in Figures below.

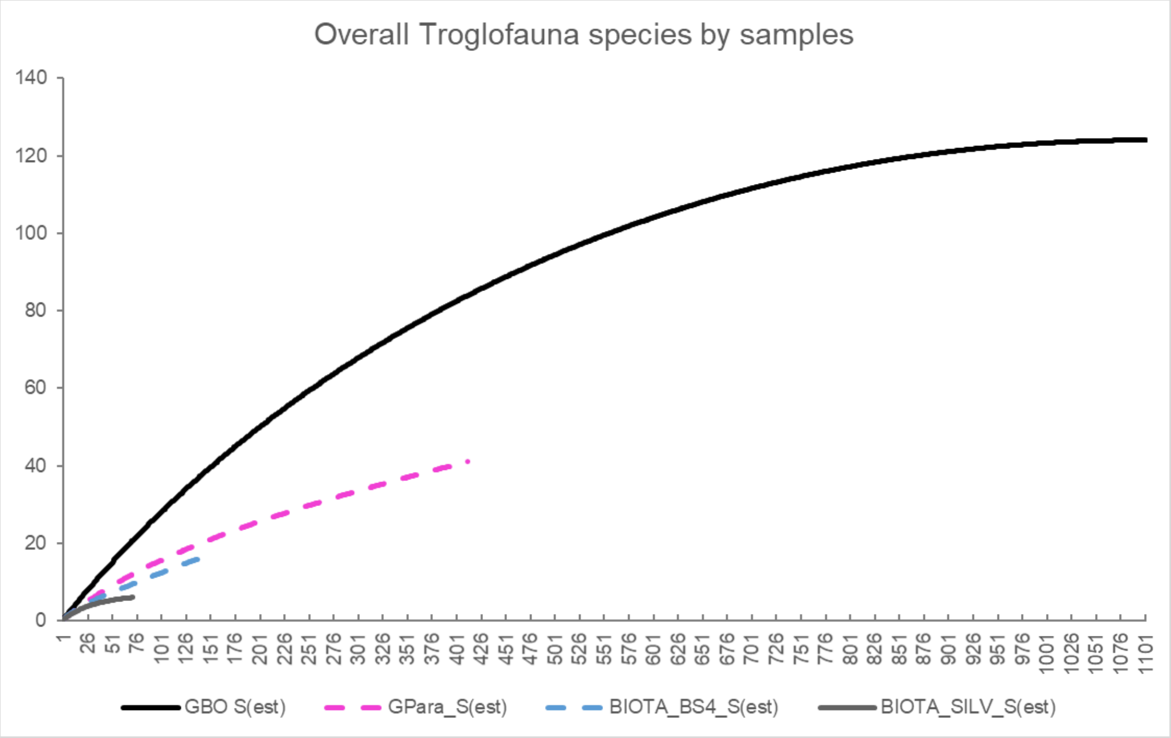


Figure 7.1: Troglofauna species accumulation curves S(est) for overall sampling at Greater Brockman (GBO), and previous surveys at Greater Paraburdoo (GPara), BS4 (BIOTA_BS4), and Silvergrass (BIOTA_SILV).

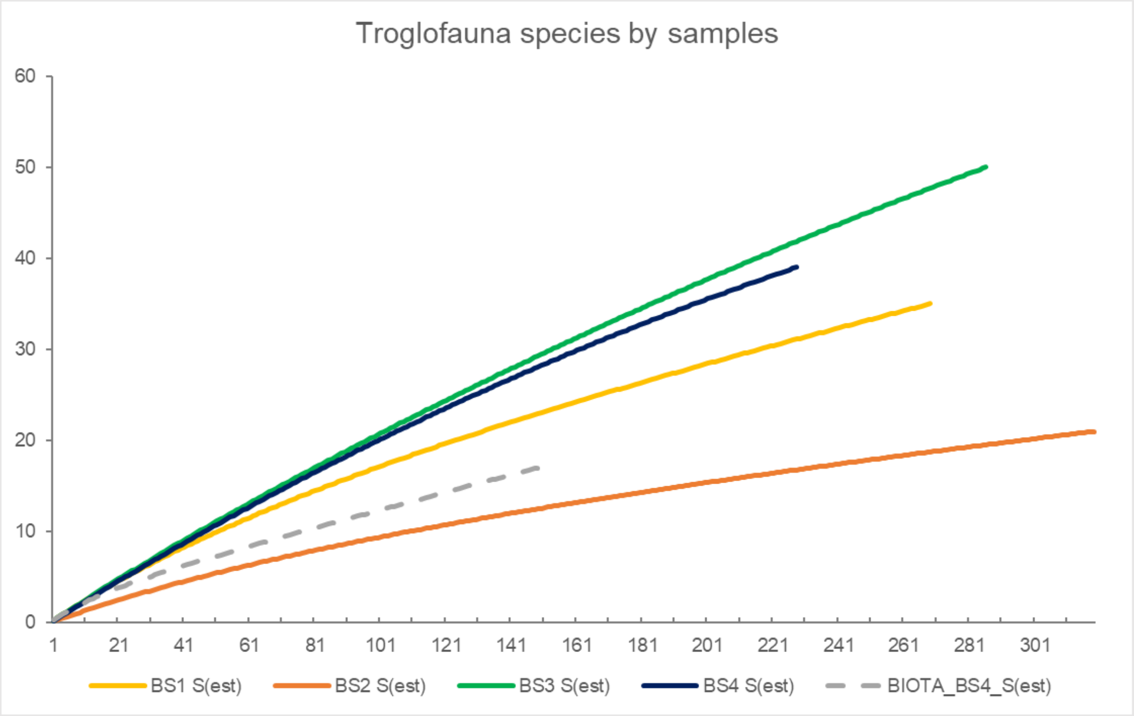


Figure 7.2: Troglofauna species accumulation curves (S(est)) for each sampling area at Greater Brockman (BS1, BS2, BS3 & BS4), and for a previous survey within these sampling areas; *i.e.* BS4 (BIOTA_BS4),

The overall species accumulation curve (S(est)) for troglofauna (Figure 7.1) appears to have reached a plateau, with almost no new species being detected after 1000 samples. This suggests that this survey may have captured a significant proportion of troglofauna species at Greater Brockman. Nevertheless, when broken down into the four sampling areas (Figure 7.2), none of the curves appear to be asymptotic. The BS2 curve is rising most slowly, not only due to a slightly greater sampling effort, but also a lower rate of new species detection in that area, reflected in the lower strike rate (0.15) and moderate species richness per positive sample (0.45) shown in Table 7.1. Compared to the curves from previous surveys, the current survey curves reflect typically greater sampling effort and more species detected (probably as a result of more DNA analyses) for each sampling area.

Comparisons of five species estimator models (Figure 7.3) found considerable variability in the additional species estimated to occur in each sampling area. Analysis of results from BS2 and BS1 revealed that the survey effort to date had detected a high to moderate proportion of the total species richness estimated to occur (60%-79% for BS2, and 58%-78% for BS1), but only when estimators that exceeded the Michaelis-Menten Mean value were excluded (commonly ACE Mean and Chao 1 Mean). In these cases, the Michaelis-Menten Mean value was used as a stopping point, therefore any species estimator results exceeding this value were considered unreliable, as is common practise for this type of analysis (refer section 3.7). In contrast, at BS3 and BS4, the troglofauna survey effort to date has detected a more moderate proportion of the total species richness estimated to occur (35%-76% for BS3 and 45%-77% for BS4), and all species estimator models were regarded as potentially reliable results (Figure 7.3).

Overall, this range of values compares well to the range of estimates generated for previous surveys in the Study Area, namely BS4 (18% to 76%) (Biota, 2016a, 2016b, and 2016c) Nammuldi (51% to 100%) (Biota 2011), and Silvergrass (60% to 86%) (Biota 2011), as well as Greater Paraburdoo (52% to 80%) (Biologic 2019). These comparisons broadly show that the sampling effort at each of the Greater Brockman sampling areas is within the typical/ expected range of results for other troglofauna surveys in the same or similar habitat settings. Within the inherent constraints of estimating troglofauna species richness (discussed in section 3.7 and 3.8), the results from species accumulation and richness estimator models provide confidence that the current survey has met or exceeded sampling adequacy expectations for troglofauna surveys in similar settings in the region.

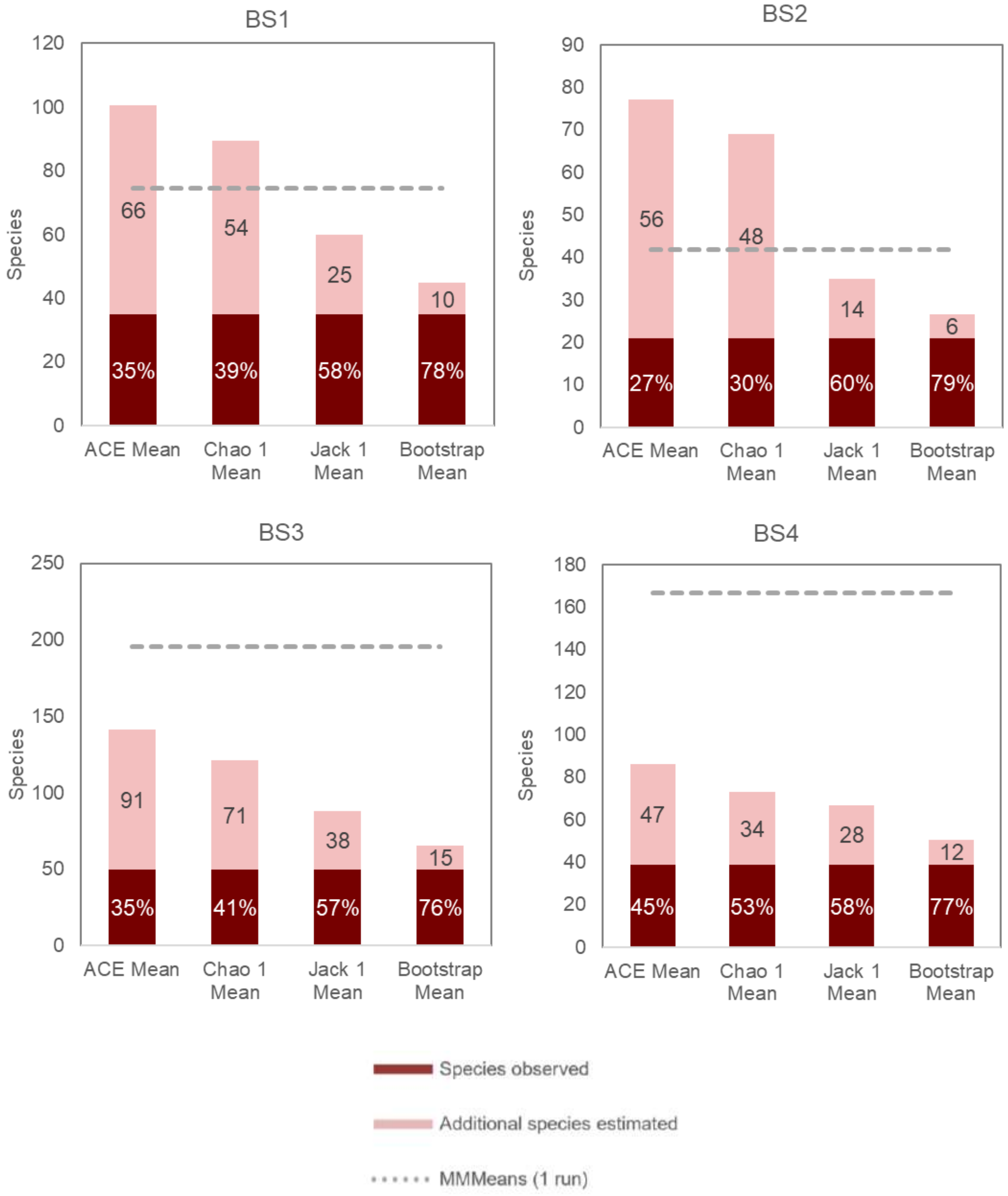


Figure 7.3: Observed troglofauna species richness compared to total species richness estimated by four models in EstimateS (ACE, Chao 1, Jackknife 1, and Bootstrap). Dotted line indicates Michaelis-Menten Mean (stopping point); species estimator values above this value are considered invalid. Data labels indicate number of additional undetected species predicted to occur (black font) and percentage of total estimated species that the observed species represents (white font), under each model.

Stygofauna strike rates (Table 7.1) were highly variable between different sampling areas and different surveys, with BS2 showing a low (0.14) low strike rate, while BS1, BS3 and and BS4 had rates higher than the overall strike rate for Greater Paraburdoo (Table 7.1).

Relative to the strike rate, the average species richness for stygofauna-positive samples was highly variable between areas and surveys, with values ranging from 0.30 (at BS3) to 1.03 (at BS4) (Table 7.1). Nevertheless, much of this can be attributed to differences in sampling intensity which was constrained by the number of available bores and holes intercepting groundwater, particularly at BS2, but also in some areas of BS4, BS1, and BS3. Surveys/ areas which had very few fauna positive samples such as BS2 and Nammuldi (Biota 2010) showed high average species richness values (probably a statistical artefact), while the relatively high values shown at Greater Paraburdoo (Biologic 2019) and BS4 could be attributed to the high richness of stygofauna collected mainly from a few bores/ Karaman samples in particular areas such as Seven-Mile Creek at Paraburdoo, and Boolgeeda Creek at BS4/VIV (S. Callan pers. obs.).

The overall species accumulation curve (S(est)) for stygofauna (Figure 7.4) from the current survey appears to be rising slowly but steadily, with no indication of an asymptote or plateau. This is also the case for the two comparison curves included in Figure 7.4, from Greater Paraburdoo (Biologic, 2019), and Nammuldi-Silvergrass (Biota, 2010), although the latter is less useful as a comparison, as the species data were recorded per site, not per sample as in the other curves.

Figure 7.5 shows that the species accumulation curves for BS1, and BS3 appear to be approaching an asymptote, while the curves for BS2 and BS4 appear to be rising steadily at the end of their respective sampling efforts.

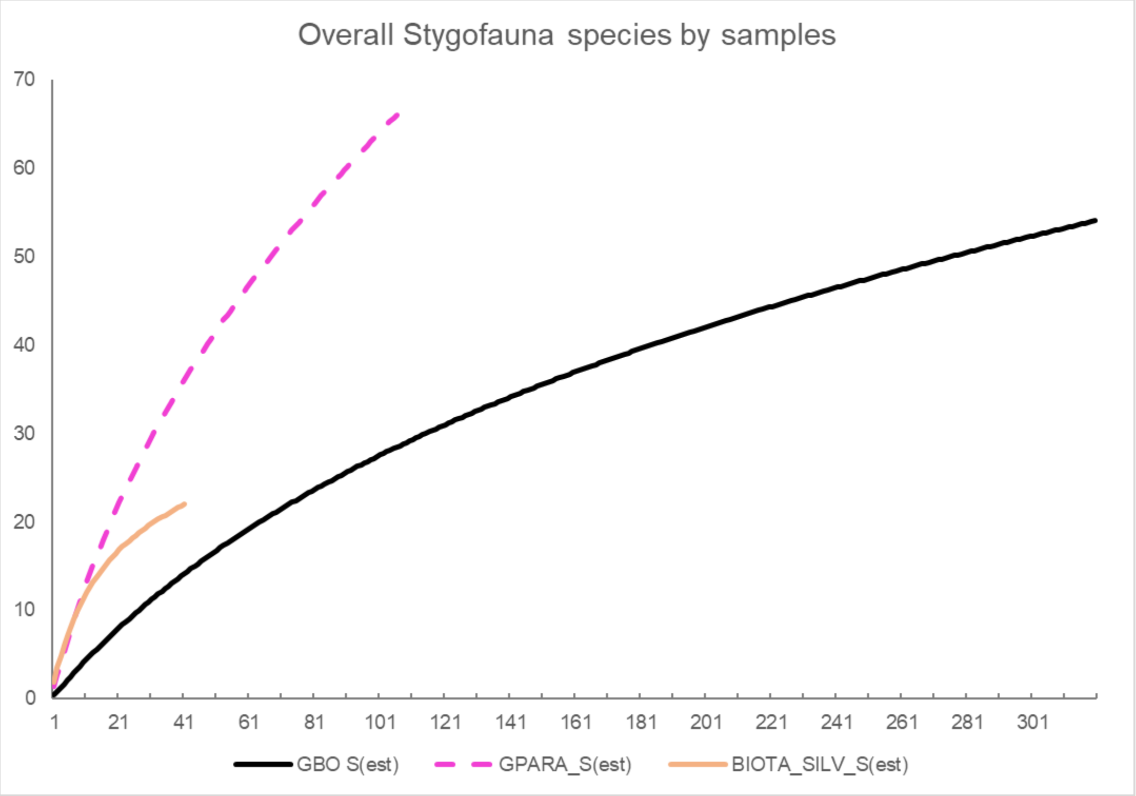


Figure 7.4: Overall stygofauna species accumulation curves (S(est)) for surveys at Greater Brockman (GBO), and previous surveys at Greater Paraburdoo (GPara), and Silvergrass (BIOTA_SILV).

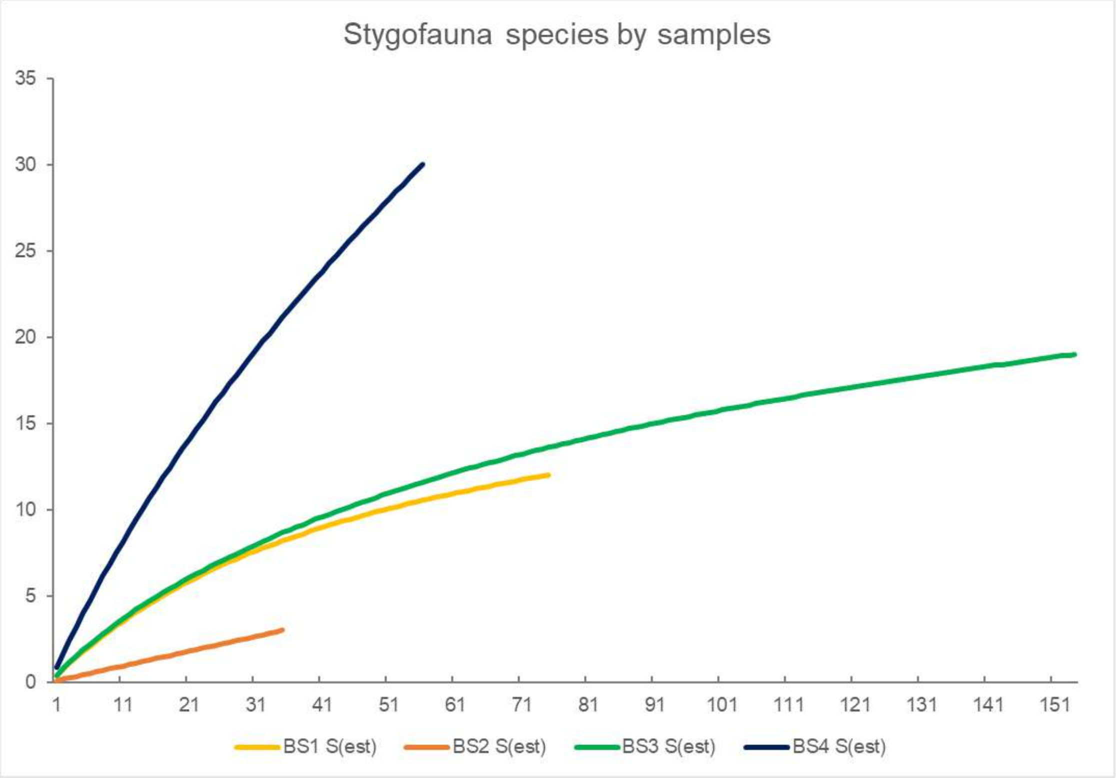


Figure 7.5: Stygofauna species accumulation curves (S(est)) for sampling at Greater Brockman survey areas BS1, BS2, BS3 & BS4.

The five species estimator models for stygofauna (Figure 7.6) found considerable variability in the additional species estimated to occur in each sampling area. The results from BS2 are considered unreliable as there were only three species recorded from three samples (Table 7.1), thus insufficient data to analyse (all estimates are shown in excess of the Michaelis-Menten stopping point). Analysis of BS1 showed that the survey effort to date had detected a relatively high proportion of the total species richness estimated to occur (71%-85%) (Figure 7.6). Sampling at BS3 and BS4 was estimated to have detected a moderate to high proportion of the total estimated species richness (40%-84% at BS3 and 42%-78% at BS4), and all species models were regarded as reliable results (Figure 7.6).

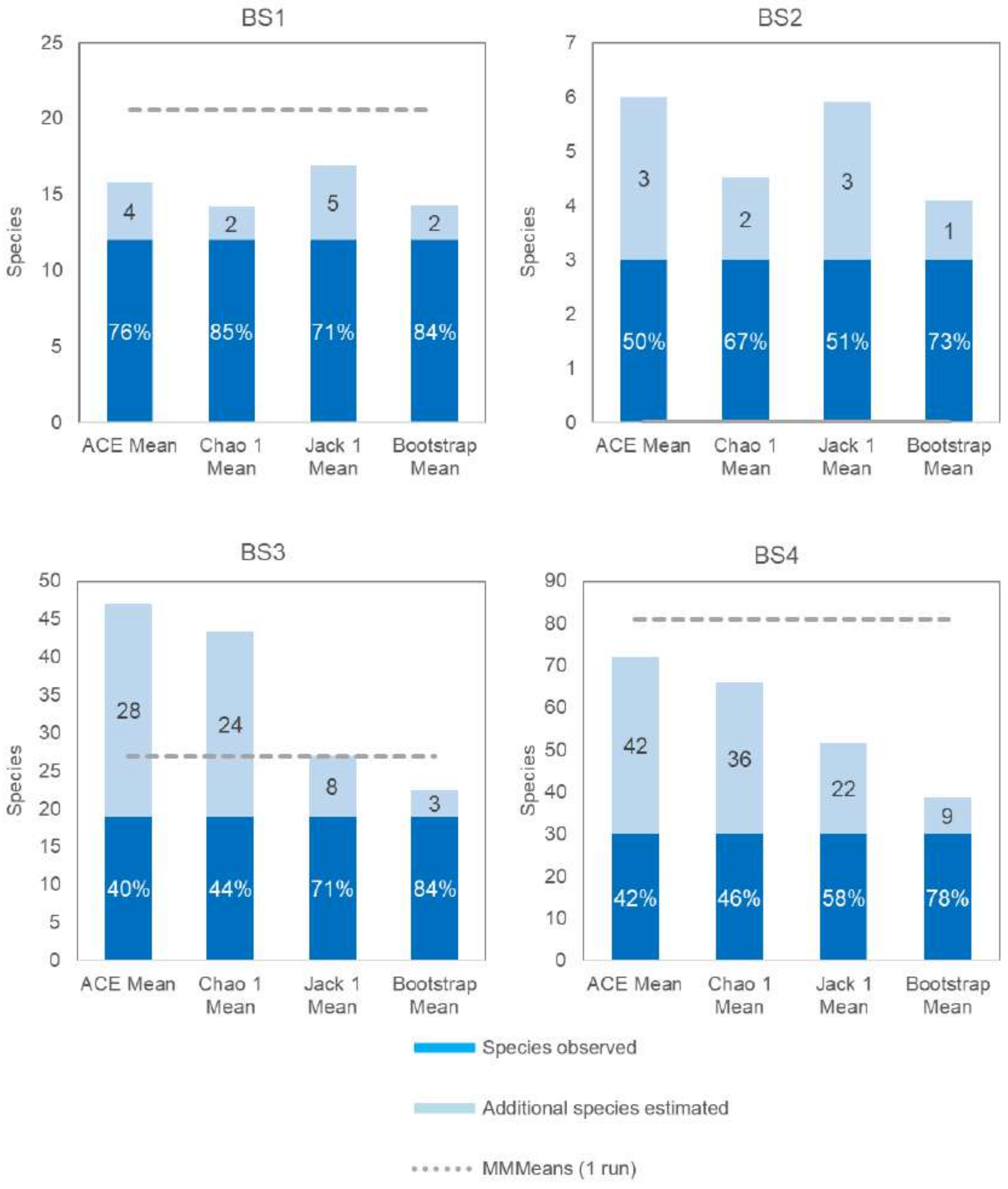


Figure 7.6: Observed stygofauna species richness compared to total species richness estimated by four models in EstimateS (ACE, Chao 1, Jackknife 1, and Bootstrap). Dotted line indicates stopping point estimated by Michaelis-Menten. Data labels indicate number of additional undetected species and percentage of total estimated species that the observed species represents, estimated to occur by each model.

Overall, these values compare well against previous surveys at Greater Paraburdoo (57% to 80%) (Biologic, 2019), Silvergrass (74% to 86%) and Nammuldi (51% to 74%) (Biota, 2010). These comparisons show that in most of the survey areas, the stygofauna sampling effort produced results within the typical range for other similar surveys. Within the constraints of suitable numbers of bores/ holes intercepting groundwater, the species accumulation curves, and richness estimator models provide confidence that the current sampling effort has met or exceeded sampling adequacy expectations for stygofauna surveys in the same or similar habitats.

The cumulative sampling effort undertaken to date for stygofauna and troglofauna within each Greater Brockman sampling area (i.e. including all previous and current surveys) has met or exceeded the EPA (2016b, 2016c) minimum guidelines. The overall troglofauna species accumulation curve has reached a plateau, suggesting that the survey captured a significant proportion of the regional troglofauna species diversity. Nevertheless, none of the troglofauna species accumulation curves of the four sampling areas appear to be asymptotic, and few of the stygofauna curves have reached an asymptote. Steadily rising curves and the lack of an apparent asymptote are commonly observed for subterranean fauna surveys; particularly for troglofauna, which are recognised as occurring rarely/ sparsely within most geological habitats, despite the diversity of species present, and are thus difficult to detect in sufficient quantities/ frequency of occurrence to produce an asymptote in the species curves.

8. DISCUSSION

8.1 Troglofauna

A total of 164 troglofauna taxa have been collected to date by current and previous surveys (Appendix H). None of these troglofauna species, nor the community, are listed or recognised as conservation priorities under state or federal legislation.

From the 164 taxa recorded to date, 95 key troglofauna species/ OTUs within 14 taxonomic orders were identified (Table 8.1). These key species were only found inside the Study Area where they were either detected from single sites/ singletons or from a few sites within a localised spatial area.

Table 8.1: Key troglofauna species/ OTUs (current and previous surveys)

Arachnida	**Myriapoda**	**Insecta**
Araneae `sp. Biologic-ARAN004`	Geophilomorpha `sp. Biologic-CHIL002`	*Nocticola* `sp. Biologic-BLAT005`
Araneae `sp. Biologic-ARAN005`	Geophilomorpha `sp. Biologic-CHIL007`	*Nocticola* `sp. Biologic-BLAT006`
Prethopalpus `sp. Biologic-ARAN001`	Polydesmida `sp. Biologic-POLD002`	Coleoptera `sp. Biologic-COLE002`
Prethopalpus `sp. Biologic-ARAN002`	Scolopendromorpha `sp. Biologic-CHIL005`	Coleoptera `sp. Biologic-COLE003`
Prethopalpus `sp. Biologic-ARAN023`	Scolopendromorpha `sp. Biologic-CHIL006`	*Ptinella*? `sp. BS1`
Palpigradi `sp. Biologic-PALP002`	Scolopendromorpha `sp. BS1`	Staphylinidae? `sp. BS1`
Palpigradi `sp. Biologic-PALP003`	Pauropoda `sp. Biologic-PAUR005`	Carabidae `sp. Helix-C2`
Palpigradi `sp. Biologic-PALP004`	Pauropoda `sp. Biologic-PAUR006`	Carabidae `sp. Helix-C3`
Palpigradi `sp. Biologic-PALP006`	Pauropoda `sp. Biologic-PAUR007`	Carabidae `sp. Helix-C4`
Palpigradi `sp. Biologic-PALP007`	Pauropoda `sp. Biologic-PAUR009`	Staphylinidae `sp. Helix-C5`
Palpigradi `sp. Biologic-PALP008`	Pauropoda `sp. Biologic-PAUR010`	Staphylinidae `sp. Helix-C6`
Palpigradi `sp. Biologic-PALP010`	Pauropoda `sp. Biologic-PAUR013`	Nicoletiidae `sp. Biologic-ZYGE004`
Palpigradi `sp. Biologic-PALP012`	Pauropoda `sp. Biologic-PAUR036`	Nicoletiinae `sp. Biologic-ZYGE005`
Palpigradi `sp. Biologic-PALP031`	Pauropoda `sp. Biologic-PAUR037`	Nicoletiinae `sp. Biologic-ZYGE006`
Palpigradi `sp. Biologic-PALP032`	Pauropoda `sp. Biologic-PAUR038`	Nicoletiinae `sp. Biologic-ZYGE007`
Palpigradi `sp. Biologic-PALP033`	Pauropoda `sp. Biologic-PAUR039`	*Subnicoletiinae* `sp. Biologic-ZYGE024`
Chthoniidae `sp. Biologic-PSEU004`	Pauropoda `sp. Biologic-PAUR040`	*Subnicoletiinae* `sp. Biologic-ZYGE025`
Chthoniidae `sp. Biologic-PSEU006`	Polydesmida `sp. Biologic-POLD002`	*Subnicoletiinae* `sp. Biologic-ZYGE026`
Chthoniidae `sp. Biologic-PSEU007`	*Hanseniella* `sp. Biologic-SYMP001`	*Subnicoletiinae* `sp. Biologic-ZYGE027`
Indolpium `sp. Biologic-PSEU003`	*Hanseniella* `sp. Biologic-SYMP003``	**Diplura**
Chernetidae `sp. Helix marra mamba`	*Hanseniella* `sp. Biologic-SYMP031`	Japygidae `sp. Biologic-DIPL008`
Chthoniidae `sp. Helix marra mamba`	*Hanseniella* `sp. Biologic-SYMP032`	Japygidae `sp. Biologic-DIPL009`
Troglochernes sp. indet.	Scutigerellidae `sp. Biologic-SYMP004`	Japygidae `sp. Biologic-DIPL014`
Draculoides `sp. Biologic-SCHI017`	Scutigerellidae `sp. Biologic-SYMP005`	Japygidae `sp. Biologic-DIPL027`
Scorpiones `sp. Biologic-SCOR002`	Symphyla `sp. Biologic-SYMP013`	Japygidae `sp. Helix marra mamba`
Isopoda	*Symphylella* `sp. Biologic-SYMP030`	Parajapygidae `sp. Biologic-DIPL007`
Armadillidae `sp. Biologic-ISOP002`	*Symphylella* `sp. BS4`	Parajapygidae `sp. Biologic-DIPL018`
Buddelundia? `sp. Biologic-ISOP005`	*Symphylella* `sp. BS1`	Parajapygidae `sp. Biologic-DIPL029`
Buddelundia? `sp. Biologic-ISOP006`	*Scolopendrellopsis* `sp. BS1`	Projapygidae `sp. Biologic-DIPL003`
Isopoda `sp. Biologic-ISOP007`		Projapygidae `sp. Biologic-DIPL004`
Armadillidae `sp. Helix-I1`		Projapygidae `sp. Biologic-DIPL005`
Armadillidae `sp. Helix-I2`		Projapygidae `sp. Biologic-DIPL013`
Troglarmadillo `sp. Helix-I1`		Projapygidae `sp. Biologic-DIPL030`
		Projapygidae `sp. Biologic-DIPL031`
		Projapygidae `sp. Biologic-DIPL032`

Not all troglofauna singletons or species/ OTUs recorded from small spatial areas have the same likelihood of representing truly range-restricted troglobitic species, due to differences in their ecology and dispersal capabilities. It is also important to note that, owing to the difficulties in sampling troglofauna species throughout their full distribution range, even for taxa that are dispersal limited and range-restricted, there is a reasonable likelihood that species/ OTUs known only from single sites may occur more widely throughout the immediate local extent of their habitat (*i.e.* locally beyond their known sampling location) (Halse & Pearson, 2014).

Important contextual information for each of the key taxonomic groups in Table 8.1 is discussed below. This information incorporates; a) the current state of taxonomic certainty and ability to undertake regional comparisons using genetic or morphological information, b) the current state of ecological knowledge of the taxon, c) the known distributions of other species within the group (based on regional information), and d) local habitat factors that may increase or decrease the likelihood that the taxa occurs more widely. As the Hemiptera and Polyxenida contain almost entirely widespread trogloxenic/ troglophilic taxa (refer Appendix H), these were omitted from further discussion.

Arachnida

Troglobitic arachnids are known to be highly range-restricted and there is a high likelihood of SRE taxa occurring in this group, as is reflected in the current results. Of the 48 arachnid taxa found within or near the Development Envelope to date, 25 species were detected only from singletons/ single sites, or from a few sites within localised spatial areas (Table 8.1, Appendix H). Unsurprisingly, very few of the available regional genetic sequences matched arachnid specimens from the survey (Appendix C), and high rates of species turnover were observed in four arachnid groups (Araneae, Pseudoscorpiones, Palpigradi and Schizomida) within and between sampling areas.

Troglobitic spiders, palpigrades and pseudoscorpions in particular tend to have very limited dispersal capabilities (*e.g.* Mammola & Isaia, 2017; Ribera *et al.*, 2018) and are commonly recorded only from single habitats or single sites, whilst some schizomids have shown distributions over a few kilometres linear range (refer Appendix H). Therefore, there is a relatively low likelihood that the 25 key arachnid species/ OTUs are regionally or even locally widespread. One regionally widespread Theridiidae spider was detected, but this was considered a potential trogloxene or possibly soil fauna and is not a key species (individuals were pale and slender with reduced eyes, but not completely eyeless). In a few cases, such as *Troglochernes* sp. indet., OTUs from previous surveys were regarded as distinct as a precaution, based on available taxonomic information and the spatial pattern of species turnover throughout the group, despite direct morphological or genetic comparisons not being possible.

Isopoda

Of the 12 isopod taxa collected within the Study Area (Appendix H), seven species/ OTUs were detected only from singletons/ single sites, or from a few sites within localised spatial areas (Table 8.1). Most of these belonged to the family Armadillidae (Table 8.1) which is known to include highly restricted troglobitic species throughout the Pilbara region, and many dispersal-limited subterranean (and even terrestrial SRE) species (S. Judd pers. comm. 2019). Some of the isopod taxa from the survey have been found to be locally widespread, and there was some residual taxonomic uncertainty around taxa recorded as ‘*Buddelundia*?’, as this is typically a terrestrial, rather than troglobitic genus. Nevertheless, as a precaution, the six taxa listed in Table 8.1 are considered potentially range-restricted, based on current sampling records.

Myriapoda

Of the 41 myriapod taxa (centipedes, pauropods, symphylans, and millipedes) collected within the Study Area to date (Appendix H), 28 species/ OTUs were detected only from single sites, or from a few sites within localised spatial areas (Table 8.1).

The ecological categorisation of myriapods can be difficult to determine, as eyelessness and pale colouration are prevalent throughout many members of the group and apparent troglomorphy is not necessarily an indication of ecological adaptation to subterranean habitats. Consequently, certain taxa that were recorded only from Karaman sampling (*i.e.* from holes dug <1 m deep in river gravels) (Table 5.2) were excluded from the key species list as they probably represent soil fauna/ trogloxenes or epigean forms.

There is also a chance that some of the OTUs collected from drill hole sampling represent soil fauna/ trogloxenes and may occur more widely throughout the local or regional area than currently recognised. However, previous studies throughout the Pilbara region have shown that highly restricted troglobitic species are also known to occur within the Geophilomorpha, Scolopendromorpha, Symphyla, and Pauropoda. Recent genetic research has revealed a number of highly divergent lineages from the Pilbara and Yilgarn regions (Edgecombe *et al.*, 2019), and unpublished information suggests that even terrestrial and soil dwelling geophilomorphs and scolopendromorphs (*e.g. Cryptops*) can be SRE (E. Volschenk pers. comm., 2019). DNA results from the current OTUs showed strong patterns of species turnover within and between sampling areas in both centipede groups, and among some of the Pauropoda and Symphyla. As a precaution, all singleton/ single site myriapod OTUs are considered key species and may be potentially restricted. Four OTUs, Scolopendromorpha `sp. BS1`, *Symphylella* `sp. BS4`, *Symphylella* `sp. BS1`, and *Scolopendrellopsis* `sp. BS1` were considered distinct as a precaution, based on available taxonomic information and the spatial pattern of species turnover throughout each respective group, despite direct morphological or genetic comparisons not being possible.

Diplura

Diplura are a poorly studied group of hexapods that are always small, eyeless, and pale, therefore apparent troglomorphy does not confirm ecological adaptation to subterranean habitats. As with Myriapoda, any OTUs that were recorded from Karaman sampling were excluded as they are likely to represent potential soil fauna/ trogloxenes (Table 5.2). There is a chance that some of the remaining key Diplura OTUs may represent additional soil/ trogloxene forms. However, the group as a whole showed a high rate of species turnover within and between sampling areas (Appendix H), and as a precaution, singleton/ single site Diplura OTUs are therefore considered key species and may be potentially restricted.

Insecta

The assessment of subterranean status in some of the insect groups can be difficult, as both troglobitic and trogloxenic/ soil fauna forms are regularly found throughout the region. Many troglobitic insect taxa are more highly vagile than other troglofauna and have relatively wide distributions, although still be within the nominal limits for SRE species (following Harvey, 2002). For example, approximately half of the eight *Nocticola* OTUs from the survey were found widely throughout the local area (linear ranges 18-44 km), and some across multiple geological habitats. It is therefore considered likely that the remaining two *Nocticola* OTUs (key species identified in Table 8.1) from single sites/ limited spatial areas may be under-sampled and could occur more widely throughout suitable, connected habitats.

Similarly, some troglofaunal beetles (Coleoptera) are known to have moderate distribution ranges – still within the nominal limits of an SRE, but not as highly restricted to single geological habitats as troglofaunal arachnids or myriapods. While nine key beetle species/ OTUs are currently known only from single sites (Table 8.1) (including two taxa putatively regarded as distinct OTUs as a precaution), there is a chance that some of these taxa could occur more widely throughout the local extent of their habitat. Troglomorphy within the Coleoptera takes many forms depending on the taxonomic group (*e.g.* eyelessness, partial eyelessness, elongated sensory hairs, and body shape adaptations, but rarely cuticle thinning or depigmentation); therefore, the identification of troglobitic forms from soil fauna/ trogloxenic forms is not straightforward.

In the Zygentoma, the subfamily Atelurinae is typically regarded as soil fauna or trogloxenic due to its habitation of termite and ant nests, although these silverfish are commonly collected from bores and drill holes (Smith & McRae, 2014). A related subfamily, the Nicoletiinae, are more commonly regarded as range restricted troglobites when eyeless and pale (Smith *et al.*, 2012; Smith *et al.*, 2019), and this broadly fits with the recorded patterns of species distribution/ turnover amongst these two groups within the Study Area. Nevertheless, several Nicoletiinae OTUs were recorded reasonably widely (linear ranges 2.4 km to 17.5 km) throughout the Study Area, and there is a chance that some of the remaining four key species of Nicoletiinae (Table 8.1) also occur more widely throughout the connected extent of their habitats.

8.2 Stygofauna

A total of 76 stygofauna species/OTUs have been collected within and in the immediate vicinity of the Study Area by all surveys to date. Taxonomic and ecological details for these taxa are provided in Appendix I.

From the 76 taxa recorded to date, 38 key stygofauna species/ OTUs within eight taxonomic orders were identified (Table 8.2). These key species were only found inside the Study Area, where they were either detected from single sites/ singletons or from a few sites within a localised spatial area.

Table 8.2: Key stygofauna species/ OTUs

<table>
<tr><th>Bathynellacea</th><th>Amphipoda</th><th>Oligochaeta</th></tr>
<tr><td rowspan="5"><i>Atopobathynella</i> `sp. BGCK`
<i>Atopobathynella</i> `sp. Biologic-PBAT013`
<i>Atopobathynella</i> `sp. Biologic-PBAT014`
Bathynellidae `sp. Biologic-BATH001`
Bathynellidae `sp. Biologic-BATH002`
Bathynellidae `sp. Biologic-BATH003`
<i>Billibathynella</i> sp. indet.
<i>Brevisomabathynella</i> `sp. B03`
Parabathynellidae `sp. Biologic-PBAT003`
Parabathynellidae `sp. Biologic-PBAT004`
Parabathynellidae `sp. Biologic-PBAT005`
Parabathynellidae `sp. Biologic-PBAT012`
Parabathynellidae `sp. Biologic-PBAT022`</td><td>Amphipoda `sp. Biologic-AMPH009`
<i>Bogidiella</i> `sp. B05`
Bogidiellidae `sp. Biologic-AMPH011`
<i>Nedsia</i> `sp. Biologic-AMPH003`
Paramelitidae `sp. Biologic-AMPH012`
Paramelitidae `sp. Biologic-AMPH015`
Paramelitidae `sp. Biologic-AMPH047`
Paramelitidae `sp. Biologic-AMPH048`</td><td>Enchytraeidae `sp. Biologic-OLIG052`
Enchytraeidae `sp. Biologic-OLIG053`
Enchytraeidae `sp. Biologic-OLIG055`
Antarctodrilus `sp. Biologic-OLIG054`
Phreodrilidae `sp. Biologic-OLIG001`
Phreodrilidae `sp. Biologic-OLIG002`
Phreodrilidae `sp. Biologic-OLIG011`</td></tr>
<tr><th>Acari</th><th>Ostracoda</th></tr>
<tr><td>Pezidae `sp. BGCK`
Pezidae `sp. BS3X`</td><td><i>Areacandona nammuldi</i>
<i>Areacandona</i> `sp. BOS1020`
<i>Areacandona</i> nr <i>triangulum</i></td></tr>
<tr><th>Isopoda</th><th>Copepoda</th></tr>
<tr><td>Microcerberidae `sp. Biologic-ISOP026</td><td>Anzcyclops? `sp. BS3`<br>Calanoida `sp. Biologic-CALA002`<br><i>Diacyclops</i> `sp. Biologic-CYCL029`
<i>Thermocyclops</i> cf <i>aberrans</i></td></tr>
</table>

Not all singletons or species/ OTUs recorded from small spatial areas have the same likelihood of being truly restricted in range, due to differences in their ecology and dispersal capabilities. Even for singleton/ single site taxa that are dispersal-limited, there is a reasonable likelihood that they may occur more widely throughout the immediate local extent of their habitat beyond their only known sampling location.

Important contextual information for each of the key taxonomic groups in Table 8.2 is discussed below.

<u>Bathynellacea (Syncarida)</u>

Syncarids are entirely stygobitic, and despite the limitations to species-level taxonomy (particularly within the Bathynellidae), many range-restricted species and morphospecies are known to occur in the region (Perina *et al.*, 2018, 2019a; Perina *et al.*, 2019b). Representatives of this order are known to have limited dispersal abilities due to their habit of crawling over the sub-strata as opposed to free-swimming within water-filled subterranean cavities (Coineau & Camacho, 2013;

Schminke, 1974). Consequently, species turnover can be high over smaller distances than some of the more vagile, free-swimming stygofaunal groups including cyclopoid copepods, ostracods, and amphipods. This is reflected in the results of this study, as the majority of syncarid taxa were detected only from singletons or single sites (Appendix I), and a high degree of species turnover was evident over relatively small geographical areas. Only one taxon from a previous third-party survey *Brevisomabathynella* `sp. A` (Biologic 2019) was found to occur throughout a moderate linear range (10 km) (Appendix I). Based on the current patterns of species turnover and the results of recent published studies (Matthews *et al.*, 2020; Perina, 2019; Perina *et al.*, 2018; Perina *et al.*, 2019) it is considered highly unlikely that any of the syncarid species/ OTUs collected from the Study Area are regionally widespread. For this reason, the indeterminate taxon that could not be directly compared to the other OTUs (*Atopobathynella* `sp. BGCK`) was considered likely to be unique based on available morphological information and spatial distance/ different habitats to the remaining OTUs.

Interestingly, all three species of Bathynellidae from the Study Area were collected from Karaman sampling in Boolgeeda Creek. Although bathynellid syncarids are known to occur occasionally within the hyporheic zone, the detection of three widely divergent OTUs within the same sample is unusual. This sampling site was downstream of the excess water discharge point from current operations at BS4, but the good physical quality of the live-taken specimens indicates that they were unlikely to have originated elsewhere and been transported to Boolgeeda Creek by high-pressure pumping. Nevertheless, the water discharge may have elevated groundwater levels within Boolgeeda Creek, resulting in an increase in stygofauna activity, and the extent and interconnectivity of the available habitat downstream.

Ostracoda

The distributions of stygobitic ostracods within the Pilbara region range from widespread to highly range-restricted (Reeves *et al.*, 2007). Three of the ostracod species/ OTUs collected to date were regionally or locally widespread, with large linear ranges throughout continuous hydrogeological habitats or across multiple catchments (Appendix I). Although locally widespread species are not known to occur regionally, and thus their current distributions are within the nominal limits for SRE species (following Harvey 2002), it is highly likely that many of these may occur beyond the Study Area within the wider catchment areas.

Nevertheless, three ostracod taxa were collected only from single sites or small spatial areas and were thus considered key species (Table 8.2). Due to the variable distributions of ostracods within different taxonomic groups, it is unclear whether these taxa may occur more widely than currently recorded throughout the region.

Oligochaeta

Aquatic oligochaetes have inherent morphological features resembling stygobites (pale colouration, eyelessness, elongate body form), which makes it difficult to assess their subterranean status based on morphological features alone. The Naididae and Phreodrillidae include species known to occur in surface waters as well as subterranean habitats, while the Enchytraeidae are regularly detected from troglofauna traps, as they can move through water films within air-filled subterranean cavities as well as groundwater (Brown *et al.*, 2015).

Recent studies indicate that most Pilbara oligochaetes occur throughout large sub-catchments or entire catchments, with a number of regionally widespread taxa (Brown *et al.*, 2015). These types of patterns were reflected in the results of the current study, with more than half of the taxa recorded representing either regionally or locally widespread species (Appendix I). It is therefore considered likely that the remaining oligochaete taxa from single sites/ singleton records (7 OTUs) occur more widely, at least within the wider local area.

There was one identification of Phreodrillidae from previous surveys that is not considered valid species-level identifications (`Phreodrillid with dissimilar ventral chaetae`) owing to improvements in the morphological and genetic taxonomy of this group since the time of survey.

Amphipoda

Subterranean amphipods are highly diverse at multiple taxonomic levels and contain some highly vagile and widespread stygofauna species, as well as many moderately and locally restricted species. The distributions of amphipods within the Study Area reflected this, with six taxa regionally or locally widespread (Appendix I), and eight OTUs from singleton records/ single sites or restricted distributions, which are considered to be among the key stygofauna species (Table 8.2).

For the most part, sufficient DNA studies had been conducted throughout the Study Area to enable local direct comparisons of previous OTUs; however, some of the previous DNA information was not available for comparisons, and some of the third party records were not identified using genetic analyses. In addition, amphipod taxonomy has changed much over the years and some of the previous identifications are unable to be resolved against the current OTUs; therefore, there may be some unavoidable synonyms or duplicates in the combined list of taxa.

Acari

Although subterranean water mites are classed as stygobites, they have their highest biodiversity within the hyporheic zones and are classed as members of the ‘permanent hyporheos’ or the community that occurs within the deep sand and gravel beds associated with areas of groundwater discharge (Gilbert, 1994). They typically characterize the transition zone between the temporary or shallow hyporheic ecozone and the groundwater hypogean environment (Boulton & Hancock, 2006, Gilbert, 1994, Humphreys, 2006, Serov et al, 2011).

Two Pezidae OTUs, Pezidae `sp. BGCK` and Pezidae `sp. BS3X` were detected from single sites at Boolgeeda Creek and BS3, respectively. The specimens were indeterminate morphologically due to poor condition and/or immature, and DNA analyses failed to provide viable sequences. As a precaution, because the specimens were collected in different, disconnected hydrogeological settings, these records were treated as two distinct OTUs. Nevertheless, current information is insufficient to exclude the chance that these mites could represent a single, locally, or regionally widespread taxon.

9. CONCLUDING REMARKS

The Greater Brockman Subterranean Fauna Survey represents one of the largest and most comprehensive stygofauna and troglofauna surveys undertaken throughout the Pilbara region to date, having collected 1,468 subterranean fauna samples from 683 bores and drill holes throughout the Study Area over five phases. The sample effort satisfied and exceeded current EPA guidelines.

The survey revealed highly diverse assemblages comprising 124 troglofauna species/ OTUs and 56 stygofauna species/ OTUs identified by a combination of morphological and genetic analysis, and regional comparisons based on available information.

The habitat modelling revealed a diversity of AWT/BWT habitats throughout the Study Area, of varying thickness and connectivity due to local geological, hydrogeological, and structural factors. These local habitat factors were taken into consideration in the assessment of wider potential distributions and conservation significance of the fauna detected.

The overall diversity of species and assemblages was considered to appropriately reflect the large size of the Study Area and the complexity of subterranean habitats present above and below water table. Species turnover was evident in some fauna groups due to geographical distance and habitat heterogeneity/ potential fragmentation. Many other groups were diverse within the same connected habitats, which suggested a variety of possible species distribution patterns.

The current results may be affected by sampling artefacts, and there may be additional records or additional cryptic taxa, within the remaining indeterminate specimens (n = 2563). These artefacts are due to a) the complexity of habitats throughout the Study Area, b) the necessary sub-sampling for genetic analysis, and c) the rarity/ inherent difficulties in detecting some groups (particularly troglofauna) during survey.

In combination with previous records, a total of 164 troglofauna species/ OTUs and 76 stygofauna species/ OTUs are known to occur within or near the Study Area to date. Species identifications and regional comparisons revealed many locally and regionally widespread taxa, particularly amongst the stygofauna. Nevertheless, 95 troglofauna taxa recorded from the Study Area to date were detected from single sites or from a few sites within a localised spatial area, comprising Arachnida (25 OTUs), Isopoda (7 OTUs), Myriapoda (29 OTUs), Diplura (15 OTUs) and Insecta (19 OTUs). Of the stygofauna, 38 stygofauna taxa were detected only from single sites, or from a few sites within localised spatial areas, comprising Oligochaeta (7 OTUs), Acari (2 OTUs), Ostracoda (3 OTUs), Copepoda (4 OTUs), Bathynellacea (13 OTUs), Amphipoda (8 OTUs) and Isopoda (1 OTU).

10. REFERENCES

Abrams, K. M., Guzik, M. T., Cooper, S. J. B., Humphreys, W. F., King, R. A., Cho, J. L., & Austin, A. D. (2012). What lies beneath: molecular phylogenetics and ancestral state reconstruction of the ancient subterranean Australian Parabathynellidae (Syncarida, Crustacea). *Mol Phylogenet Evol, 64*(1), 130-144.

Aquaterra. (2005). *West Angelas Dewatering: Model Review*. Unpublished memo prepared for Pilbara Iron.

Baehr, M., & Main, D. (2016). New genera and species of subterranean Anilline Bembidiini from the Pilbara, northwestern Australia (Insecta: Coleoptera: Carabidae: Bembidiini: Anillina). *Records of the Western Australian Museum, 31*(2), 59-89.

Bastin, G. (2008). *Rangelands 2008 - Taking the pulse*. Canberra, Australian Capital Territory: National Land & Water Resources Audit.

Bennelongia. (2010). *Troglofauna Assessment for the Solomon Project: Firetail Deposits*. Jolimont, WA:

Bennelongia. (2011). *Pilbara Iron Ore Project: Blacksmith subterranean fauna surveys*. Jolimont, WA:

Bennelongia. (2013). *Solomon Iron Ore Project: Troglofauna survey at Zion Deposit*. Jolimont, WA:

Biologic. (2019). *Greater Paraburdoo Subterranean Fauna Survey*. East Perth, WA:

Biologic. (2022). *Greater Brockman. Subterranean Fauna Habitat Modelling and Assessment*. East Perth, WA:

Biota. (2003). *Nammuldi Stygofauna Assessment Programme. January 2013. Report to Hamersley Iron*. Leederville, WA:

Biota. (2005). *Brockman Syncline 4 Project Baseline Stygofauna Assessment*. Leederville, WA:

Biota. (2006). *Mesa A and Robe Valley Mesas Troglobitic Fauna Survey*. Leederville, WA:

Biota. (2007). *Brockman Syncline 4 Bolgeeda Creek Stygofauna Survey. Unpublished Report prepared for Pilbara Iron. May 2007*. Leederville, WA:

Biota. (2008a). *Marandoo Mine Phase 2 Subterranean Fauna Assessment. Report prepared for Pilbara Iron Ltd*. Leederville, WA:

Biota. (2008b). *West Turner Syncline Section 10 Subterranean Fauna Assessment*. Leederville, WA:

Biota. (2009). *Beasley River Subterranean Fauna Survey 2009. Unpublished report prepared for Rio Tinto Iron Ore. December 2009*. Leederville, WA:

Biota. (2010). *Nammuldi - Silvergrass Subterranean Fauna Assessment*. Leederville, WA:

Biota. (2011). *Nammuldi - Silvergrass Troglobitic Fauna Assessment*. Leederville, WA:

Biota. (2012). *West Turner Syncline Stage 2 B1 and Section 17 Deposits Subterranean Fauna Survey. September 2012. Report prepared for Rio Tinto Iron Ore*. Leederville, WA:

Biota. (2013). *Rio Tinto regional troglobitic fauna study*. Leederville, WA:

Biota. (2014). *Western Turner Syncline Section 10 Below Water Table and Satellite Ore Bodies Subterranean Fauna Survey*. Leederville, WA:

Biota. (2016a). *Brockman Syncline 4 Marra Mambas Subterranean Fauna Assessment*. Leederville, WA:

Biota. (2016b). *BS4 Marra Mambas Troglobitic Fauna Addendum Report*. Leederville, WA:

Biota. (2016c). *Western Turner Syncline S10 Hub Subterranean Fauna Assessment Addendum Report. Report prepared for Rio Tinto Iron Ore. February 2016*. Leederville, WA:

Biota. (2016d). *Western Turner Syncline Section 10 Hub Subterranean Fauna Assessment. Report prepared for Rio Tinto Iron Ore. February 2016*. Leederville, WA:

Biota, Environmental Sciences. (2016e). *Brockman Syncline 4 Marra Mambas Subterranean Fauna Assessment. Unpublished report prepared for Rio Tinto Iron Ore. October 2016*.

Blatnik, M., Culver, D. C., Gabrovsek, F., Knez, M., Kogovsek, B., Kogovsek, J., . . . Hajna, N. Z. (2020). Changing perspectives on subterranean habitats. In M. Knez, B. Otonicar, M. Petric, T. Pipan, & T. Slabe (Eds.), *Karstology in the classical Karst*.

BoM, Bureau of Meteorology. (2019). Climate Data Online. Retrieved 2019, from Bureau of Meteorology http://www.bom.gov.au./climate/data/index.shtml

BoM, Bureau of Meteorology. (2021). Climate Data Online. Retrieved 2021 http://www.bom.gov.au./climate/data/index.shtml

Brown, L., Finston, T., Humphreys, G., Eberhard, S., & Pinder, A. (2015). Groundwater oligochaetes show complex genetic patterns of distribution in the Pilbara region of Western Australia. *Invertebrate Systematics, 29*(5), 405-420.

Christiansen, K. A. (2005). Morphological adaptations. In D. C. Culver & D. B. White (Eds.), *Encyclopedia of Caves*: Elsevier.

Coineau, N., & Camacho, A. I. (2013). Superorder Syncarida Packard, 1885. In M. von Vaupel Klein, M. Charmantier-Daures, & F. R. Schram (Eds.), *The Crustacea - Treatise on Zoology - Anatomy, Taxonomy, Biology* (Vol. 4, pp. 357-449). Brill, Leiden/Boston.

Colwell, R. K. (2013). EstimateS: Statistical estimation of species richness and shared species from samples. Version 9: User's Guide and application published at: http://purl.oclc.org/estimates.

Eberhard, S. M., Halse, S. A., & Humphreys, W. F. (2005). Stygofauna in the Pilbara region, north-west Western Australia: A review. *Journal of the Royal Society of Western Australia, 88*(4), 167-176.

Eberhard, S. M., Halse, S. A., Williams, M. R., Scanlon, M. D., Cocking, J., & Barron, H. J. (2009). Exploring the relationship between sampling efficiency and short-range endemism for groundwater fauna in the Pilbara region, Western Australia. *Freshwater Biology, 54*, 885-901.

Edgecombe, G. D., Huey, J. A., Humphreys, W. F., Hillyer, M., Burger, M. A., Volschenk, E. S., & Waldock, J. M. (2019). Blind scolopendrid centipedes of the genus *Cormocephalus* from subterranean habitats in Western Australia (Myriapoda: Scolopendromorpha: Scolopendridae). *Invertebrate Systematics, 3*(6), 807-824.

EPA, Environmental Protection Authority. (2013). *Draft Environmental Assessment Guideline for Consideration of Subterranean fauna in Environmental Impact Assessment in Western Australia*. Perth, Western Australia: Environmental Protection Authority.

EPA, Environmental Protection Authority. (2016a). *Environmental Factor Guideline: Subterranean Fauna*. Perth, Western Australia: Environmental Protection Authority.

EPA, Environmental Protection Authority. (2016b). *Technical Guidance: Sampling Methods for Subterranean Fauna*. Perth, Western Australia: Environmental Protection Authority.

EPA, Environmental Protection Authority. (2016c). *Technical Guidance: Subterranean Fauna Survey*. Perth, Western Australia: Environmental Protection Authority.

EPA, Environmental Protection Authority. (2021). *Technical Guidance: Subterranean Fauna Surveys for Environmental Impact Assessment*. Perth, Western Australia: Environmental Protection Authority.

Giachino, P. M., Eberhard, S., & Perina, G. (2021). A rich fauna of subterranean short-range endemic Anillini (Coleoptera, Carabidae, Trechinae) from semi-arid regions of Western Australia. *ZooKeys, 1044*, 269-337.

Gibert, J., & Deharveng, L. (2002). Subterranean ecosystems: A truncated functional biodiversity. *BioScience, 52*(6), 473-481.

Hahn, H. J. (2009). A proposal for an extended typology of groundwater habitats. *Hydrogeology Journal, 17*, 77-81.

Hahn, H. J., & Fuchs, A. (2009). Distribution patterns of groundwater communities across aquifer types in south-western Germany. *Freshwater Biology*(54), 848-860.

Halse, S. A., & Pearson, G. B. (2014). Troglofauna in the vadose zone: comparison of scraping and trapping results and sampling adequacy. *Subterranean Biology, 13*, 17-34.

Halse, S. A., Scanlon, M. D., Cocking, J. S., Barron, H. J., Richardson, J. B., & Eberhard, S. (2014). Pilbara stygofauna: deep groundwater of an arid landscape contains globally significant radiation of biodiversity. *Records of the Western Australian Museum, Supplement, 78*, 443-483.

Harvey, M. S. (2002). Short range endemism in the Australian fauna: some examples from non-marine environments. *Invertebrate Systematics, 16*, 555-570.

Hose, G. C., Sreekanth, J., Barron, O., & Pollino, C. (2015). *Stygofauna in Australian groundwater systems: extent of knowledge*.

Howarth, F. G. (1983). Ecology of cave arthropods. *Annual Review of Entomology, 28*(1), 365-389.

Humphreys, W. F. (1999). The distribution of Australian cave fishes. *Records of the Western Australian Museum, 19*, 469-472.

Humphreys, W. F. (2006). Aquifers: the ultimate ground-water dependent ecosystems. *Australian Journal of Botany, 54*, 115-132.

Humphreys, W. F. (2008). Rising from Down Under: developments in subterranean biodiversity in Australia from a groundwater fauna perspective. *Invertebrate Systematics, 22*, 85-101.

Karanovic, T., & Cooper, S. J. B. (2011). Third genus of parastenocaridid copepods from Australia supported by molecular evidence (Copepoda, Harpacticoida). *Crustaceana Monographs, 16*, 293-337.

Karanovic, T., & Cooper, S. J. B. (2012). Explosive radiation of the genus *Schizopera* on a small subterranean island in Western Australia (Copepoda : Harpacticoida): unravelling the cases of cryptic speciation, size differentiation and multiple invasions. *Invertebrate Systematics, 26*(2), 115-192.

Karanovic, T., Eberhard, S. M., Perina, G., & Callan, S. (2013). Two new subterranean ameirids (Crustacea: Copepoda: Harpacticoida) expose weaknesses in the conservation of short-range endemiocs threatened by mining developments in Western Australia. *Invertebrate Systematics, 27*, 540-566.

Kendrick, P. (2001). Pilbara 3 (PIL3 - Hamersley subregion). In J. May & N. McKenzie (Eds.), *A biodiversity audit of Western Australia's 53 biogeographical subregions in 2002* (pp. 568-580). Kensington, Western Australia: Department of Conservation and Land Management.

Leighton, K. A. (2004). Climate. In A. M. E. van Vreeswyk, A. L. Payne, K. A. Leighton, & P. Hennig (Eds.), *An inventory and condition survey of the Pilbara region, Western Australia* (Vol. Technical bulletin No. 92). Perth, Western Australia: Western Australian Department of Agriculture.

Malard, F., & Hervant, F. (1999). Oxygen supply and the adaptations of animals in groundwater. *Freshwater Biology, 41*, 1-30.

Mammola, S., Goodacre, S. L., & Isaia, M. (2018). Climate change may drive cave spiders to extinction. *Ecography, 41*(1), 233-243. doi:10.1111/ecog.02902

Mammola, S., & Isaia, M. (2017). Spiders in caves. *Proceeding of the Royal Society B, 284*(1853).

Matthews, E. F., Abrams, K. M., Cooper, S. J. B., Huey, J. A., Hillyer, M. J., Humphreys, W. F., . . . Guzik, M. T. (2020). Scratching the surface of subterranean biodiversity: Molecular analysis reveals a diverse and previously unknown fauna of Parabathynellidae (Crustacea: Bathynellacea) from the Pilbara, Western Australia. *Molecular Phylogenetics and Evolution, 142*, 106643.

McKenzie, N. L., van Leeuwen, S., & Pinder, A. M. (2009). Introduction to the Pilbara biodiversity survey, 2002-2007. *Records of the Western Australian Museum Supplement, 78*, 3-89.

Perina, G., Camacho, A. I., Huey, J., Horwitz, P., & Koenders, A. (2018). Understanding subterranean variability: the first genus of Bathynellidae (Bathynellacea, Crustacea) from Western Australia described through a morphological and multigene approach. *Invertebrate Systematics, 32*, 423-447.

Perina, G., Camacho, A. I., Huey, J., Horwitz, P., & Koenders, A. (2019a). New Bathynellidae (Crustacea) taxa and their relationships in the Fortescue catchment aquifers of the Pilbara region, Western Australia. *Systematics and Biodiversity, 17*(2), 148-164.

Perina, G., Camacho, A. I., Huey, J., Horwitz, P., & Koenders, A. (2019b). The role of allopatric speciation and ancient origins of Bathynellidae (Crustacea) in the Pilbara (Western Ausralia): two new genera from the De Grey River catchment. *Contributions to Zoology, 88*(4), 452-497.

Poulson, T. L., & Lavoie, K. H. (2000). The trophic basis of subterranean ecosystems. In H. Wilkens, D. C. Culver, & W. F. Humphries (Eds.), *Ecosystems of the World - Subterranean Ecosystems* (pp. 231-249). Amsterdam: Elsevier.

Reeves, J. M., De Deckker, P., & Halse, S. (2007). Groundwater ostracods from the arid Pilbara region of northwestern Australia: Distribution and water chemistry. *Hydrobiologia, 585*, 99-118.

Ribera, I., Cieslak, A., Faille, A., & Fresneda, J. (2018). Historical and ecological factors determining cave diversity. In *Cave Ecology* (Vol. 235).

Rio Tinto. (2010). *Baseline Hydrology Assessment for Caves Creek Discharge. December 2010*. Perth, WA:

Rio Tinto. (2011). *Baseline Hydrology Assessment for Duck Creek Discharge. March 2011*. Perth, WA:

Rio Tinto. (2014a). *Brockman Syncline 4 - Revised Proposal. Assessment on Proponent Information. Environmental Review Document*. Perth, WA:

Rio Tinto. (2014b). *Brockman Syncline 4 Revised Proposal. Monitoring and Management Plan. August 2014*. Perth, WA:

Rio Tinto. (2020). *Brockman Syncline: Hydrogeological Assessment v2.0 (January 2020). Rio Tinto Iron Ore Resource Development, Water Resource Evaluation Report. Perth, WA*. Perth, WA:

Saccò, M., Blyth, A., Humphreys, W. F., Karasiewicz, S., Meredith, T., Laini, A., . . . Grice, K. (2020a). Stygofaunal community trends along varied rainfall conditions: Deciphering ecological niche dynamics of a shallow calcrete in Western Australia. *Ecohydrology, 13*, e2150. doi:https://doi.org/10.1002/eco.2150

Saccò, M., Blyth, A. J., Humphreys, W. F., Karasiewicz, S., Meredith, K. T., Laini, A., . . . Grice, K. (2020b). Stygofaunal community trends along varied rainfall conditions: Deciphering ecological niche dynamics of a shallow calcrete in Western Australia. *Ecohydrology, 13*(1). doi:10.1002/eco.2150

Schminke, H. K. (1974). Mesozoic intercontinental relationships as evidenced by bathynellid Crustacea (Syncarida: Malacostraca). *Systematic Zoology, 23*(2), 157-164.

Schuring, J., Schulz, H. D., Fischer, W. R., Böttcher, J., & Duijnisveld, W. H. M. (1999). *Redox: Fundamentals, Processes and Applications*. Berlin, Heidelberg, New York: Springer-Verlag.

Smith, G. B., Eberhard, S. M., Perina, G., & Finston, T. (2012). New species of short range endemic troglobitic silverfish (Zygentoma: Nicoletiidae) from subterranean habitats in Western Australia's semi-arid Pilbara region. *Records of the Western Australian Museum, 27*, 101-116.

Smith, G. B., & McRae, J. M. (2014). New species of subterranean silverfish (Zygentoma: Nicoletiidae: Atelurinae) frm Western Australia's semi-arid Pilbara region. *Records of the Western Australian Museum, 29*, 105-127.

Smith, G. B., Mitchell, A. A., Lee, T. R. C., & Espinasa, L. (2019). DNA barcoding and integrative taxonomy of the *Heterolepisma sclerophylla* species complex (Zygentoma: Lepismatidae: Heterolepismatinae) and the description of two new species. *Records of the Australian Museum, 71*(1), 1-32.

Strategen. (2012). *Nammuldi-Silvergrass Expansion Project. Public Environmental Review. June 2012*. Subiaco, WA:

Strayer, D. L. (1994). Limits to biological distributions in groundwater. In J. Gibert, D. L. Danielopol, & J. A. Stanford (Eds.), *Groundwater Ecology* (pp. 287-310). San Diego: Academic Press.

Subterranean Ecology. (2010). *Fortescue Metals Group Solomon Project: Kings Deposits Subterranean Fauna Survey & Assessment*. Greenwood, WA:

Subterranean Ecology. (2011). *Fortescue Metals Group Solomon Project: Regional Subterranean Fauna Survey. February 2011. Report to Fortescue Metals Group Ltd*. Greenwood, WA:

Thackway, R., & Cresswell, I. D. (1995). *An Interim Biogeographical Regionalisation for Australia*. Canberra, Australian Capital Territory: Australian Nature Conservation Agency.

Trotter, A. J., McRae, J. M., Main, D. C., & Finston, T. L. (2017). Speciation in fractured rock landforms: towards understanding the diversity of subterranean cockroaches (Dictyoptera: Nocticolidae: Nocticola) in Western Australia. *Zootaxa, 4250*(2), 143-170.

URS. (2010a). *Modelling Dewatering at Nammuldi. Report prepared for Rio Tinto Iron Ore Expansion Projects. February 2010*. Perth, WA:

URS. (2010b). *Preliminary Groundwater Modelling for Dewatering Design. Silvergrass deposits. Report prepared for Rio Tinto Iron Ore Expansion Projects. April 2010*. Perth, WA:

Watts, C. H. S., & Humphreys, W. F. (2004). Thirteen new Dytiscidae (Coleoptera) of the genera *Boongurrus* Larson, *Tjirtudessus* Watts & Humphreys and *Nirripirti* Watts and Humphreys, from underground waters in Australia. *Transactions of the Royal Society of South Australia, 128*, 99-129.

WRM. (2016). *Brockman Syncline 4 Project: Baseline Aquatic Biota and Water Quality Surveys of Boolgeeda Creek*. Burswood, WA:

APPENDICES

APPENDIX A: Regulation 17 and Regulation 27 licences

DEPARTMENT OF PARKS AND WILDLIFE

Department of Parks and Wildlife

Enquiries: 17 DICK PERRY AVE, KENSINGTON, WESTERN AUSTRALIA
Telephone: 08 9219 9000
Facsimile: 08 9219 8242
Web Site: https://wildlifelicensing.dpaw.wa.gov.au
Correspondance: **Locked Bag 30**
Bentley Delivery Centre WA 6983

Wildlife Conservation Act 1950

REGULATION 17

Regulation 17 – Licence to take fauna for scientific purposes (Regulation 17 - Standard)

The undermentioned person may take fauna for research or other scientific purposes and where authorised, keep it in captivity, subject to the following and attached conditions, which may be added to, suspended or otherwise varied as considered fit.

Director General

Conditions

1 The licensee must comply with the provisions of the Wildlife Conservation Act 1950, Wildlife Conservation Regulations 1970 and any Notices in force under this legislation.

2 The licensee shall take fauna only in the manner stated on the endorsed Regulation 17 licence application form and endorsed related correspondence.

3 Unless specifically authorised in the conditions of this Licence or otherwise in writing by the Director General, species of fauna declared as likely to become extinct, rare or otherwise in need of special protection shall not be taken.

4 Any by-catch of fauna, which is declared to be rare, likely to become extinct, or otherwise in need of special protection shall be released immediately at the point of capture. Where such fauna taken under this licence is injured or deceased, the licensee shall contact the Department's Wildlife Licensing Section for advice on disposal. Records must be kept of any such fauna so captured and details are to be included in the report required under further condition below.

5 Any interaction involving Gazetted Threatened Fauna that may be harmful to the fauna and/or invasive may require approval from the Commonwealth Department of the Environment ph 02 6274 1111. Interaction with such species is controlled by the Commonwealth Environment Protection and Biodiversity Conservation Act 1999 and Environment Protection and Biodiversity Conservation Regulations 2000 as well as the Wildlife Conservation Act 1950 and Wildlife Conservation Regulations 1970.

6 No fauna shall be taken in areas where it would impinge on pre-existing scientific research programs.

7 Except in the case of approved lethal traps, the licensee shall ensure that measures are taken in the capture and handling of fauna to prevent injury or mortality resulting from that capture or handling. Where traps or other mechanical means or devices are used to capture fauna these shall be deployed so as to prevent exposure of trapped animals to ants and debilitating weather conditions and inspected at regular intervals throughout each day of their use. At the conclusion of research all markers used, and signs and structures erected by the licensee shall be removed and the environment returned to its original condition.

8 Not more than ten specimens of any one protected species of fauna shall be taken and removed from any location less than 20km apart. Where exceptional circumstances make it necessary to take a larger number of specimens from a particular location in order to obtain adequate statistical data, the collector must proceed with circumspection and justify their actions to the Director General in advance.

9 The licensee shall not release any fauna or their progeny in any area where it does not naturally occur, nor hand such fauna over to any other person or authority unless approved by the Director General, nor dispose of the remains of such fauna in any manner likely to confuse the natural or present day distribution of the species.

10 Bioprospecting involving the removal of sample aquatic and terrestrial organisms for chemical extraction and bioactivity screening shall not be conducted without specific written approval by the Director General.

11 No fauna is to be taken from any CALM land, as defined in the Conservation and Land Management Regulations 2002, without prior written approval of the Director General. No fauna is to be taken from any public land without the prior written approval of the Government Authority managing that land.

12 The licensee must not enter upon any private property or pastoral lease for the purposes of this licence, nor take any fauna from any private land or pastoral lease without the prior consent in writing of the owner or occupier. Similarly, in the case of Aboriginal lands, the licensee must not enter upon or take fauna from such lands without the written approval of the Department of Aboriginal Affairs and/or the relevant native title holders or applicants.

13 Copies of this licence and any written approval or consent required by conditions of this licence must be carried by the licensee and any person/s authorised under the licence at all times when conducting activities relevant to the licence and must be presented to an authorised officer of the Department upon request.

14 All holotypes and syntypes and a half share of paratypes of species or subspecies permitted to be permanently taken under this licence shall be donated to the Western Australian Museum. Duplicates (one pair in each case) of any species collected, which represents a significant extension of geographic range shall upon request be donated to the Western Australian Museum.

15 To prevent any unnecessary collecting in this State, all specimens and material taken and retained under the authority of this license shall, upon request, be loaned to the Western Australian Museum. Any unused portion or portions of any specimen collected under the authority of this license shall be offered to the Western Australian Museum for inclusion in its collection or made available to other scientific workers if so required.

16 Within one month of the expiration of this licence, the holder shall submit an electronic return into the department’s Wildlife Licensing System, detailing the locality, site, geocode, date and number of each species of fauna captured, sighted or vouchered during the currency of the licence. A copy of any paper, report or thesis resulting from the research shall upon completion be lodged with the Director General.

Purpose

Subterranean (Troglofauna and Stygofauna) survey via PVC troglofauna traps and stygofauna plankton net hauls in accordance with EPA (2016) guidance statement for Rio Tinto Brockman 2 / Greater Nammuldi sites.

Locations

Brockman 2 / Greater Nammuldi sites approximately 60km north-west of Tom Price.

Authorised Person

Surname	**Given name(s)**
Callan	Shae
Durrant	Bradley
Main	Dean
Gunawardene	Nihara
Rudin	Fabian
de Silva	Thomas
Slabber	Arnold

Date of Issue 03/09/2018
Valid From 01/10/2018
Date of Expiry 30/09/2019

Licensee: Mr Syngeon Michael Rodman
Address Biologic Environmental
Office G, 162 Rokeby Rd
Subiaco WA 6008
Australia

Issued by a Wildlife Licensing Officer of the Department of Parks and Wildlife under delegation from the Minister for Environment pursuant to section 133(1) of the Conservation and Land Management Act 1984.

FAUNA TAKING (BIOLOGICAL ASSESSMENT) LICENCE

Regulation 27, Biodiversity Conservation Regulations 2018

Licence Number:	BA27000038
Licence Holder:	Mr Syngeon Michael Rodman Biologic Environmental Office G, 162 Rokeby Road Subiaco WA 6008
Date of Issue:	05/04/2019
Date Valid From:	05/04/2019
Date of Expiry:	04/04/2020

LICENSED ACTIVITIES

Subject to the terms and conditions on this licence, the licence holder may –

1. Take and disturb fauna for Greater Brockman Syncline 4 (BS4) Sustaining Tonnes Project - Level 2 Subterranean (stygofauna and troglofauna) fauna survey using net hauling, scraping and litter trapping. Captured subterranean fauna will be retained as specimens

LOCATIONS

1. The Brockman Syncline 4 (BS4) locality in the Pilbara region of Western Australia, approximately 50km north-west of Tom Price.

AUTHORISED PERSONS

The following persons or persons of the specified class may assist in carrying out the licensed activities:

1. Shae Callan
2. Dean Main
3. Nihara Gunawardene
4. Fabian Rudin
5. Lythe Morgan
6. Phillip Runham

CONDITIONS

1. Fauna must not be taken on CALM land, (as defined in the Conservation and Land Management Regulations 2002*),* unless authorised by a written notice of a lawful authority issued under regulations 4 and 8 of the Conservation and Land Management Regulations 2002.
2. If persons, other than the licence holder, are authorised to carry out/assist in carrying out the activities under the licence, the licence holder must ensure those persons have read and understand the licence terms and conditions.
3. The written authorisation of the person in possession or occupation of the land accessed and upon which fauna is taken, as required under regulation 101(2) and referred to in "Additional information" below, must:
   a) state location details (including lot or location number, street/road, suburb and local government authority);

   b) state land owner or occupier name, and contact phone number;
   c) specify the time period that the authorisation is valid for;
   d) be signed and dated; and
   e) be attached to this licence at all times.

4. This licence, and any written authorisation or lawful authority which authorises the take of fauna on specified locations must be carried at all times while conducting licensed activities and be produced on demand by a wildlife officer.
5. If a species of fauna listed as a threatened species under Section 19 of the *Biodiversity Conservation Act 2016* is inadvertently captured, that species is to be released immediately at the point of capture. If the fauna is injured or deceased, the licence holder shall contact the DBCA Wildlife Licensing Section (wildlifelicensing@dbca.wa.gov.au) for advice on treatment or disposal. Details of any capture of threatened fauna must be included in the “Return of Fauna Taken.”
6. The licence holder must not:
   a) release any fauna in any area where it does not naturally occur;
   b) transfer fauna to any other person or authority (other than the Western Australian Museum) unless approved in writing by the CEO; or
   c) dispose of the remains of fauna in any manner likely to interfere the natural or present day distribution of the species.
7. The licence holder must not take and remove more than ten specimens of any one protected species of fauna from any location less than 20km apart. Where exceptional circumstances make it necessary to take a larger number of specimens from a particular location in order to obtain adequate statistical data, the collector must proceed with circumspection and justify their actions to the Director General in advance.
8. All holotypes and syntypes and a half share of paratypes of species or subspecies permitted to be permanently taken under this licence must be donated to the Western Australian Museum. Duplicates (one pair in each case) of any species collected, which represents a significant extension of geographic range must be offered to the Western Australian Museum.
9. All specimens and material retained under the authority of this licence must be offered to the Western Australian Museum for loan, for inclusion in its collection, or on request be made available to other persons involved in relevant scientific studies.
10. The licence holder must create, compile and maintain records and information as required in a DBCA approved “Return of Fauna Taken” of all fauna taking activities as they occur.
11. A DBCA approved “Return of Fauna Taken” must be completed in full (including nil taking details) and submitted to DBCA Wildlife Licensing Section (wildlifelicensing@dbca.wa.gov.au) prior to the end of each annual period of the licence (from the valid from date) (refer to “Additional Information” section below).

Danny Stefoni
LICENSING OFFICER
WILDLIFE PROTECTION BRANCH

Delegate of CEO

ADDITIONAL INFORMATION

1. It is an offence to take any species of fauna listed as a threatened species under Section 19 of the *Biodiversity Conservation Act 2016* unless the person is authorised under Section 40. The penalty ranges between $300 000 and $500 000; Section 150 Biodiversity Conservation Act 2016.
2. Regulation 82 empowers the CEO to add, substitute or delete a term or condition of a licence or to correct errors. Such power may be exercised on application of a licence holder or by the CEO's own initiative. If an amendment to a licence term or condition is required, please contact the CEO or the Licensing Section on wildlifelicensing@dbca.wa.gov.au in the first instance. The licence holder, if adversely affected by a condition imposed in this licence, may apply to the State Administrative Tribunal for review of the decision of the CEO to impose that condition on a licence: regulation 89(2) Biodiversity Conservation Regulations 2018.
3. A person must not contravene a condition of a licence. The penalty for an offence involving the contravention of a condition of a licence is a fine of $10 000: regulation 84 of the Biodiversity Conservation Regulations 2018.
4. It is an offence for persons authorised by this licence to enter land that is not in their possession or under their control without first having the *prior* written authorisation of the current owner or occupier of the land to:

   a) enter the land; and

   b) carry out the activity authorised by this licence.

   The penalty for this offence is a fine of $5 000: regulation 101(2) of the Biodiversity Conservation Regulations 2018.
5. The licence holder must be able to produce for inspection upon request any information or records required by regulation 85(2) of the Biodiversity Conservation Regulations 2018 Penalty $10 000. It is an offence to knowingly include false or misleading information or make statements in records: regulation 85(3) of the Biodiversity Conservation Regulations 2018 Penalty $10 000. It is an offence to include any information or make any statement in a return that the licence holder knows to be false or misleading in a material particular: regulation 86 (2) of the Biodiversity Conservation Regulations 2018 Penalty $10 000.
6. The approved DBCA "Return of Fauna Taken" data file can be downloaded from the DBCA webpage (https://www.dpaw.wa.gov.au/plants-and-animals/licences-and-authorities).
7. The issuing of a licence under the Biodiversity Conservation Regulations 2018 does not constitute an animal ethics approval or a licence to use animals for scientific purposes as required under the *Animal Welfare Act 2002,* Animal Welfare (Scientific Purposes) Regulations 2003. It is the responsibility of a licence applicant / licence holder to ensure that they comply with the requirements of all applicable legislation. Enquiries relating to the Animal Welfare Act licences and animal ethics approvals are to be directed to the Department of Primary Industries and Regional Development (https://www.agric.wa.gov.au/animalwelfare).
8. Threatened fauna can only be taken under a *Biodiversity Conservation Act 2016* Section 40 authorisation, Occurrences of threatened species must be reported to the CEO. For more information please see https://www.dpaw.wa.gov.au/plants-and-animals/threatened-species-and-communities/threatened-animals.
9. Any interaction involving Nationally Listed Threatened Fauna that may be invasive and/or harmful to the fauna may require approval from the Commonwealth Department of the Environment and Energy http://www.environment.gov.au/about-us/business-us/permits-assessments-licences. Interaction with such species is controlled by the Commonwealth *Environment Protection and Biodiversity Conservation Act 1999* and Environment Protection and Biodiversity Conservation Regulations 2000 as well as the *Biodiversity Conservation Act 2016* and Biodiversity Conservation Regulations 2018.

APPENDIX B: Bores and drill holes visited during the survey

Note: The above appendix has been provided to the client in Excel Spreadsheet format.

File name: “GBO_SUBF_Appendices B, E and F.xlsx”.

APPENDIX C: Molecular Systematics Analysis Report

Greater Brockman
Subterranean Fauna Survey
Molecular Systematics Analysis

Biologic Environmental Survey

Report to Rio Tinto Iron Ore

July 2020

DOCUMENT STATUS				
Version No.	**Authors**	**Review / Approved for Issue**	**Approved for Issue to**	
			Name	**Date**
1	N. Gunawardene, S. Callan, S. Floeckner, F. Rudin	B. Durrant	T. Savage (Rio Tinto)	20/12/2019
2	N. Gunawardene, S. Callan, J. Huey, S. Floeckner, F. Rudin	B. Durrant	T. Savage (Rio Tinto)	15/04/2020
3	N. Gunawardene, S. Callan, J. Huey, S. Floeckner, F. Rudin	B. Durrant	T. Savage (Rio Tinto)	24/07/2020

GLOSSARY

12S/16S	Mitochondrially encoded 12S/16S ribosomal RNA, a component of the small subunit of the mitochondrial ribosome, which is useful in phylogenetic studies
BGCK	Boolgeeda Creek
BLAST	Basic Local Alignment Search Tool, an algorithm for comparing primary biological sequence information
BS1	Brockman Syncline 1
BS2	Brockman Syncline 2 Extension
BS3	Brockman Syncline 3
BS4/ VIV	Brockman Syncline 4/ Vivash (includes Boolgeeda Creek)
COI	Cytochrome Oxidase subunit 1, a mitochondrial gene commonly used in phylogenetic studies and as a DNA barcode to identify species
GenBank	Annotated open access sequence database of all publicly available nucleotide sequences and their protein translations
HSTD	Homestead
OTU	Operational taxonomic unit – species-equivalent taxonomic unit based on COI or 12S/16S cluster similarity
SGW	Silvergrass West
WAM MSU	Western Australian Museum – Molecular Systematics Unit

1 INTRODUCTION

Rio Tinto Iron Ore (Rio Tinto) commissioned Biologic Environmental Survey (Biologic) to undertake a molecular systematics analysis (DNA barcoding) of 600 subterranean fauna (stygofauna and troglofauna) specimens collected from Rio Tinto's Greater Brockman Project (the Study Area). This Project comprises the following survey areas: Silvergrass and Caves Creek (SGCCK; includes the deposits SGW and HSTD), Brockman Syncline 2 Extension/ Brockman 3 (BS2/ BS3; includes the deposits LENSG, BS2W, BS2SW, MAYB, DSM, BS3, and BS3X), and Brockman Syncline 4/ Vivash (BS4/ VIV; includes deposits BS1, VIV, and BGCK). A subset of specimens (70 Arachnida) was selected for molecular analysis by the Western Australian Museum Molecular Systematics Unit (WAM MSU).

1.1 Aims and objectives

The aims and objectives of the molecular systematics analysis were to:

- Undertake DNA sequencing of 600 subterranean fauna specimens to obtain barcoding sequences of the mitochondrial gene Cytochrome Oxidase I (COI; Hebert *et al.*, 2003b), the nuclear gene 12S for Zygentoma specimens, and a combination of COI and 16S for *Nedsia* specimens;
- Investigate the interspecific and intraspecific relationships between sequences of each higher taxonomic group (*i.e.* use the results of the DNA analysis to indicate how many different species-level Operational Taxonomic Units (OTUs) are likely to occur within each genus or relevant higher taxon, based on relevant species thresholds);
- Investigate the relationships between sequences from the Study Area and relevant sequences from the wider Pilbara region, using available DNA databases (*i.e.* compare the results of the current analysis with accessible DNA databases to assess whether any of the species/ OTUs from the Study Area have been collected previously or more widely beyond the Study Area); and
- Incorporate results from WAM MSU analysis of the subset of Arachnida specimens.

This document reports the methods and results of the molecular systematics analysis (including WAM MSU results). All sequence data will be provided to Rio Tinto for inclusion in the molecular sequence database and uploaded to GenBank (https://www.ncbi.nlm.nih.gov/genbank/) as per Rio Tinto requirements.

2 METHODS

2.1 Sub-sample preparation

A total of 600 subterranean fauna specimens collected from the Study Area by Biologic were selected for molecular systematics analysis. The specimens were chosen based on their parataxonomic identification and geographic spread across the Study Area to assist with understanding species distributions of stygofauna and troglofauna. Adequate redundancy in specimen selection was incorporated to account for any potential sequence generation failure. Specimens in good condition were chosen to increase their DNA extraction potential.

Morphological identification was also undertaken by in-house parataxonomists using available keys. Specimens were identified to the lowest taxonomic classification practicable, with Amphipoda and Bathynellaceae being identified to species or morphospecies by specialist taxonomist Dr Giulia Perina. This resulted in the 600 specimens being classified into nine different classes comprised of 18 orders (Table 2.1).

Where whole specimens were available, tissue preparation was undertaken by removing a leg or other body material that was unimportant for morphological taxonomy, briefly drying off ethanol, and placing the tissue in ATL buffer. In some instances, for very small and/or juvenile specimens, the entire animal was utilised. Greatest care was taken to decontaminate all tools and equipment between samples, using 10% bleach and repeated rinsing in deionised water. Table 2.1 provides details of the taxonomic orders chosen for molecular analysis. Further taxonomic clarification for each specimen included in the analysis can be found in Appendix 1.

Table 2.1: Taxonomic orders and total number of individuals from the Study Area included in the analysis.

Taxon	SGCCK	BS2/ BS3	BS4/ VIV	Total
Arachnida				
Acari			7	**7**
Araneae	2	3	11	**16**
Palpigradi	1	8	8	**17**
Pseudoscorpiones	1	2	12	**15**
Schizomida	23		18	**41**
Chilopoda				
Chilopoda	1	1	8	**10**
Diplopoda				
Polyxenida	1	6	4	**11**
Entognatha				
Diplura	6	3	15	**24**
Insecta				
Blattodea	13	19	21	**53**
Coleoptera	1	1	5	**7**
Hemiptera	9	21	17	**47**
Zygentoma	2	12	15	**29**
Malacostraca				
Amphipoda	140	17	30	**187**

Bathynellacea	6	11	14	**31**
Isopoda	5	8	6	**19**
Oligochaeta				
Tubificida	9	7	17	**33**
Pauropoda				
Pauropoda	3	6	16	**25**
Symphyla				
Cephalostigmata	3	8	17	**28**
Grand Total	**226**	**133**	**241**	**600**

2.2 DNA extraction, amplification and sequencing

DNA extraction and sequencing methods followed Cullen and Harvey (2017, 2018), as follows:

Subsampled tissue/specimen was placed directly into ATL buffer for extraction using the *QIAGEN DN-easy* Blood and Tissue extraction kit, and DNA extraction followed the manufacturer's protocols. DNA extractions were amplified by Polymerase Chain Reaction (PCR) using Folmer PCR primers (LCO1490, HCO2198; Folmer *et al.*, 1994) to assess the variability of COI. Zygentoma samples were amplified using 12S primers (12Sai, 12Sbi; Simon *et al.*, 1994) when COI primers failed to produce viable results.

The resulting PCR product was cleaned up and Sanger sequenced by the Australian Genomic Research Facility (AGRF) Perth node. Molecular laboratory workflows were managed using GENEIOUS v 10.1.2 (Kearse *et al.*, 2012) with the Biocode plugin (http://www.mooreabiocode.org).

2.3 Analysis of sequence alignments/ divergence

Raw sequence data were edited and assembled in GENEIOUS. Consensus sequences were compared against GenBank using the BLAST plugin in GENEIOUS to determine nearest matches within the target higher taxonomic group. The consensus sequences were then aligned using the MAFFT (Multiple Alignment using Fast Fourier Transform) algorithm (Katoh *et al.*, 2002). Trees were constructed on resulting alignments using the GENEIOUS Tree Builder, applying Tamura-nei Genetic Distance Model and Neighbour-joining as the Tree Build Method. To test the robustness of the resulting Consensus Tree, the tree was re-sampled 1000 times using the Bootstrap method. Numbers on tree nodes represent bootstrap values and are out of 100. That is, values of 100 indicate that node is recovered in 100% of the resampled trees and is highly supported. Regional sequences, available as of December 2019, were obtained from Rio Tinto's molecular sequence database as well as genetic data from accessible reports and publications (*e.g.* Helix Molecular Solutions). Only relevant sequences per taxon group were included in the tree building analyses.

DNA comparisons were typically conducted at the order level (Table 2.1), except for Bathynellaceae which was analysed at the family level (Bathynellidae and Parabathynellidae). In cases where there was an abundance of sequences (*e.g.* Amphipoda), secondary comparisons were also undertaken at the family level. For groups where taxonomic clarification at the order level was not possible due to low numbers of specimens, comparisons between sequences remained at the class level (*e.g.* Chilopoda, Pauropoda, Symphyla).

To delimit taxonomic units using molecular data, we combined a genetic distance-based threshold method with our morphological identifications. Wherever possible, fauna-specific genetic distance thresholds for delimiting species and OTUs were used, based on published literature and available previous reports. Where these thresholds were not available, the assessment used average divergence thresholds for related groups or higher taxa developed by broad-level studies (*e.g.* Hebert *et al.*, 2003a).

2.4 Constraints and Limitations

The analysis was constrained by the breadth of data available to undertake comparisons, the accessibility of pre-existing regional sequences, and the success rate of genetic sequencing, which can be affected by specimen collection, preservation, storage methods and contamination. Best practises were followed during specimen collection, preservation, and storage, prior to specimens arriving at Biologic's laboratories. All care was taken to ensure that the risks of laboratory contamination, data handling issues, and specimen management issues were minimised within Biologic's laboratories throughout the subsampling, processing, and genetic analysis.

The databases used for regional comparisons were limited to GenBank (no sequences uploaded to GenBank after December 2019 have been included in the analyses), the Rio Tinto Molecular Sequence Database, and publicly available data from published genetic reports including those conducted for Rio Tinto (by Helix Molecular Solutions). While these sequence databases, in combination, comprise a large portion of the subterranean fauna genetic work undertaken for Rio Tinto in the Pilbara region, it is acknowledged that there may be many other relevant sequences from third party project areas nearby or elsewhere in the region that were not available for comparison at the time of the study.

DNA barcoding using the mitochondrial gene COI, while useful for explaining genetic differences among closely related species, is limited in its ability to resolve deeper phylogenetic relationships among taxa at higher taxonomic levels (*e.g.* Genus, Family, Order). In the current study, phylogenetic relationships among species/OTUs at >25% COI divergence are treated with caution. If further resolution of deeper nodes in the phylogeny is important for project goals, this could be investigated using a multiple gene approach.

3 RESULTS AND DISCUSSION

A total of 530 specimens were processed for sequencing by Biologic, 44 by the WAM MSU, and 26 by both WAM MSU and Biologic. Sequences were successfully derived for 546 of these specimens (91% of specimens), with 54 failing to produce a PCR product. Of these 546 sequences, 96 did not produce a high-quality sequence (less than 80% of untrimmed bases in the sequence were of high quality) or were subject to contamination. This left 450 high quality sequences for analysis (75% of sequences). The orders of the sequences are tabulated in Table 3.1.

Table 3.1: Number of specimens with high quality sequences used in the analysis.

Taxon	SGCCK	BS2/ BS3	BS4/ VIV	Total
Arachnida				
Araneae	2	3	9	14
Palpigradi	1	8	5	14
Pseudoscorpiones	1	1	12	14
Schizomida	22		18	40
Chilopoda				
Geophilomorpha			2	2
Scolopendromorpha	1	1	4	6
Diplopoda				
Polyxenida	1	6	1	8
Entognatha				
Diplura	5	2	9	16
Insecta				
Blattodea	11	18	16	45
Coleoptera		1	4	5
Hemiptera	9	15	9	33
Zygentoma	1	7	7	15
Malacostraca				
Amphipoda	110	10	24	144
Bathynellacea	5	6	9	20
Isopoda	3	4	6	13
Oligochaeta				
Tubificida	8	6	13	27
Pauropoda				
Pauropoda	3	6	7	16
Symphyla				
Cephalostigmata	2	6	10	18
Grand Total	**185**	**100**	**165**	**450**

In total, 154 OTUs have been designated to specimens from the Study Area. In general, ~8% COI divergence is seen as an appropriate species-level threshold for OTUs in the absence of other published species thresholds (Hebert *et al.*, 2003a), however, higher or lower divergences are sometimes justified depending on the organism studied. Unless otherwise stated, the current analysis considered sequences that exhibited COI divergences <8% to belong to the same OTU. The results of each order's analysis are described in the subsequent sections and the full list of OTUs per order can be found in Appendix 1. All distance matrices for each order can be found in Appendices B-J.

4 TROGLOFAUNA

4.1 Arachnida

4.1.1 Araneae

Nine Araneae OTUs were determined from the Study Area (Figure 4.1). Interspecific divergences range from 9 to 30% (Appendix 2). The morphology of the two Biologic-ARAN003 specimens indicated potentially troglobytic *Anapistula* (Symphytognathidae), and the molecular analysis provided no further clarity on the taxonomy of this OTU. It was therefore named Symphytognathidae? `sp. Biologic-ARAN003` with caution. The intraspecific divergence of GBO sequences within Theridiidae `sp. WAM-ARAN001` was 1.4%, and these sequences aligned with a regional sequence from Greater Paraburdoo at 1.7% divergence. The intraspecific divergence of Araneae `sp. Biologic-ARAN005 was 6.8%. The remaining OTUs were singletons found at various deposits throughout the Study Area.

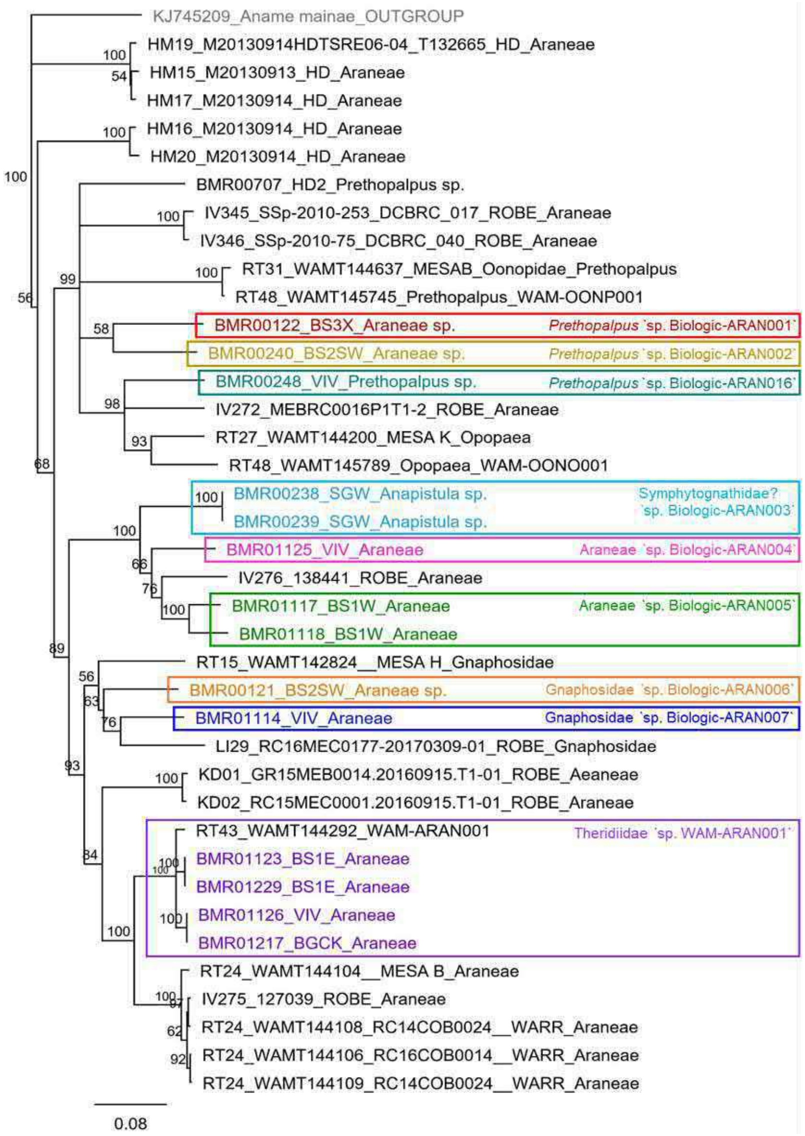


Figure 4.1: Neighbour-joining tree of Araneae haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text.

4.1.2 Palpigradi

Eleven palpigrade OTUs were designated to specimens from the Study Area (Figure 4.2). Interspecific divergences were all generally high between lineages, ranging between 10 and 34% (Appendix 3). Three OTUs were represented by two sequences and these exhibited the following intraspecific divergences: Palpigradi `sp. Biologic-PALP003`: 0.6%, Palpigradi `sp. Biologic-PALP004`: 6.9% Palpigradi `sp. Biologic-PALP013`: 7.2%. All other OTUs were singletons. Morphological taxonomy of the group is poorly resolved, although the groupings within the COI tree suggested that all OTUs could represent species of *Eukoenenia*.

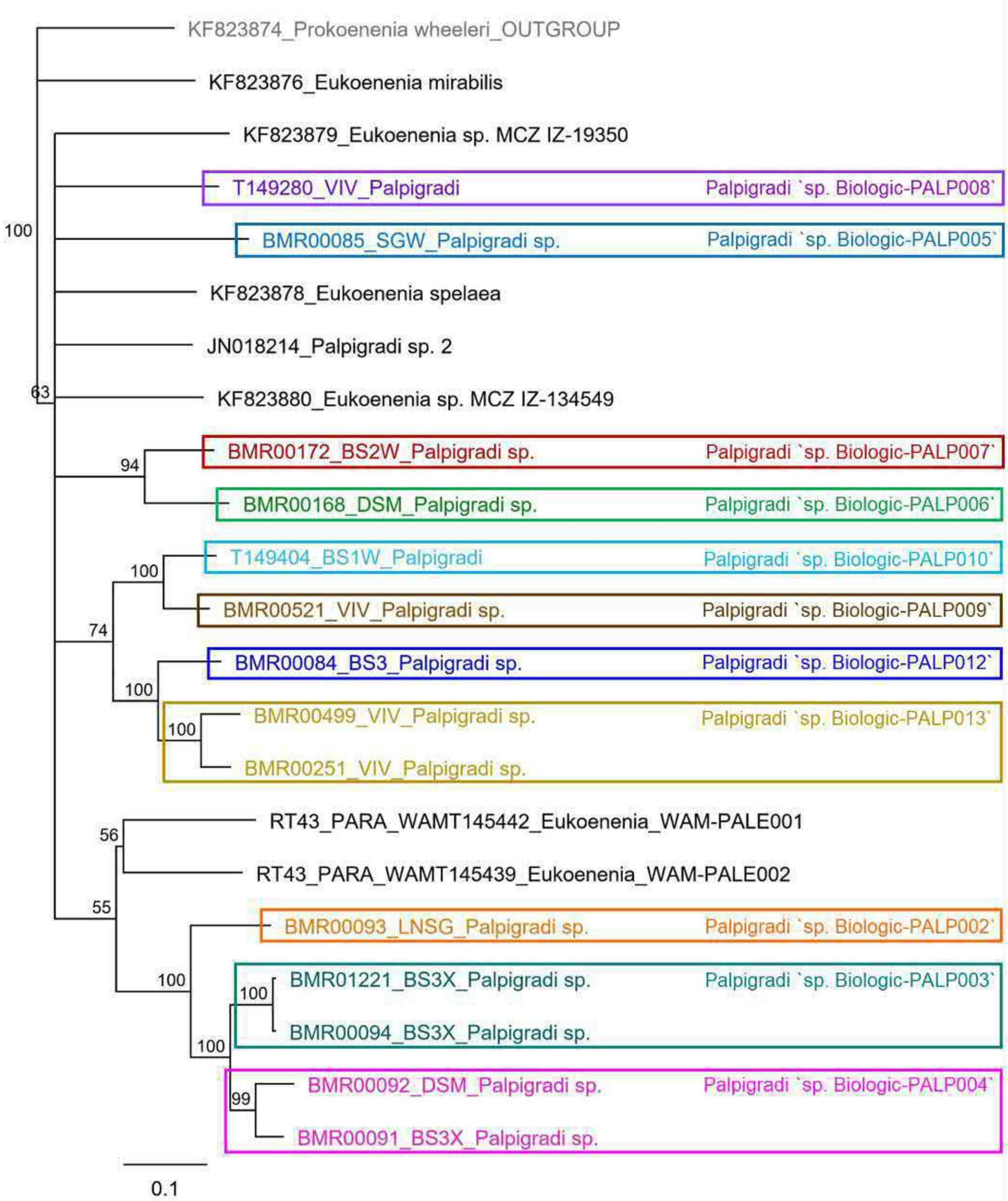


Figure 4.2: Neighbour-joining tree of Palpigradi haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text.

4.1.3 Pseudoscorpiones

Eight OTUs were detected from the Study Area (Figure 4.3, Appendix 4), with six OTUs falling well within sequences of the family Chthoniidae from the region and two falling withing the Olpiidae. None of the GBO sequences aligned with regional sequences. Chthoniidae `sp. Biologic-PSEU004`, represented by four specimens from BS1E, exhibited an intraspecific divergence of 1.5%. Chthoniidae `sp. Biologic-PSEU005` had an intraspecific divergence of 0.3% (three specimens also from BS1E). Both specimens within Chthoniidae `sp. Biologic-PSEU009` were from Vivash and their intraspecific divergence was 5.3%. All other OTUs were singletons and interspecific divergences were moderate to high, ranging from 10 – 32%.

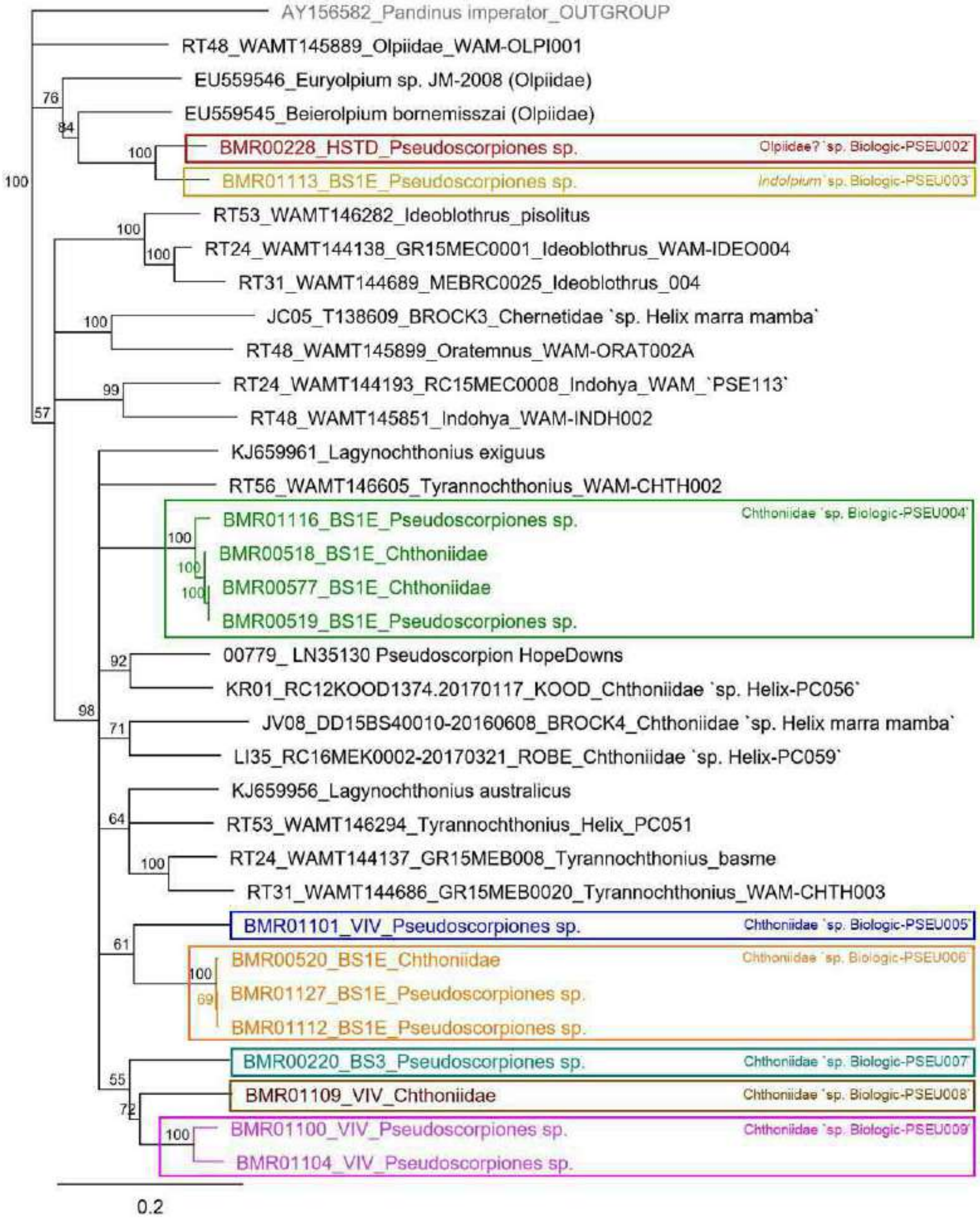


Figure 4.3: Neighbour-joining tree of Pseudoscorpiones haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text.

4.1.4 Schizomida

Ten Schizomida OTUs were detected (Figure 4.4). Based on a study by Abrams *et al.* (2019), a conservative divergence threshold of 6% was used to determine OTUs. However, *Draculoides* `sp. Biologic-SCHI012` and *Draculoides* `sp. Biologic-SCHI013` could represent the same OTU (Clade A; all specimens from Homestead) when using a less conservative threshold of 8%. Similarly, *Draculoides* `sp. Biologic-SCHI015` and *Draculoides* `sp. Biologic-SCHI016` aligned with regional sequences collected from Silvergrass (Biota, 2011) and, together with *Draculoides* `sp. Biologic-SCHI014`, could form an OTU when using the less conservative threshold of 8% (Clade B). All GBO specimens within these three OTUs were found at Silvergrass. Draculoides `sp. Biologic-SCHI019` (intraspecific divergence 1.9%), recorded from deposits BS1E/W, aligned with *Draculoides* sequences collected from Eliwana and Flying Fish (Bennelongia, 2015), to the immediate north of Brockman Syncline (<5% COI). Interspecific divergences between OTUs ranged from 11 to 33% (Appendix 5).

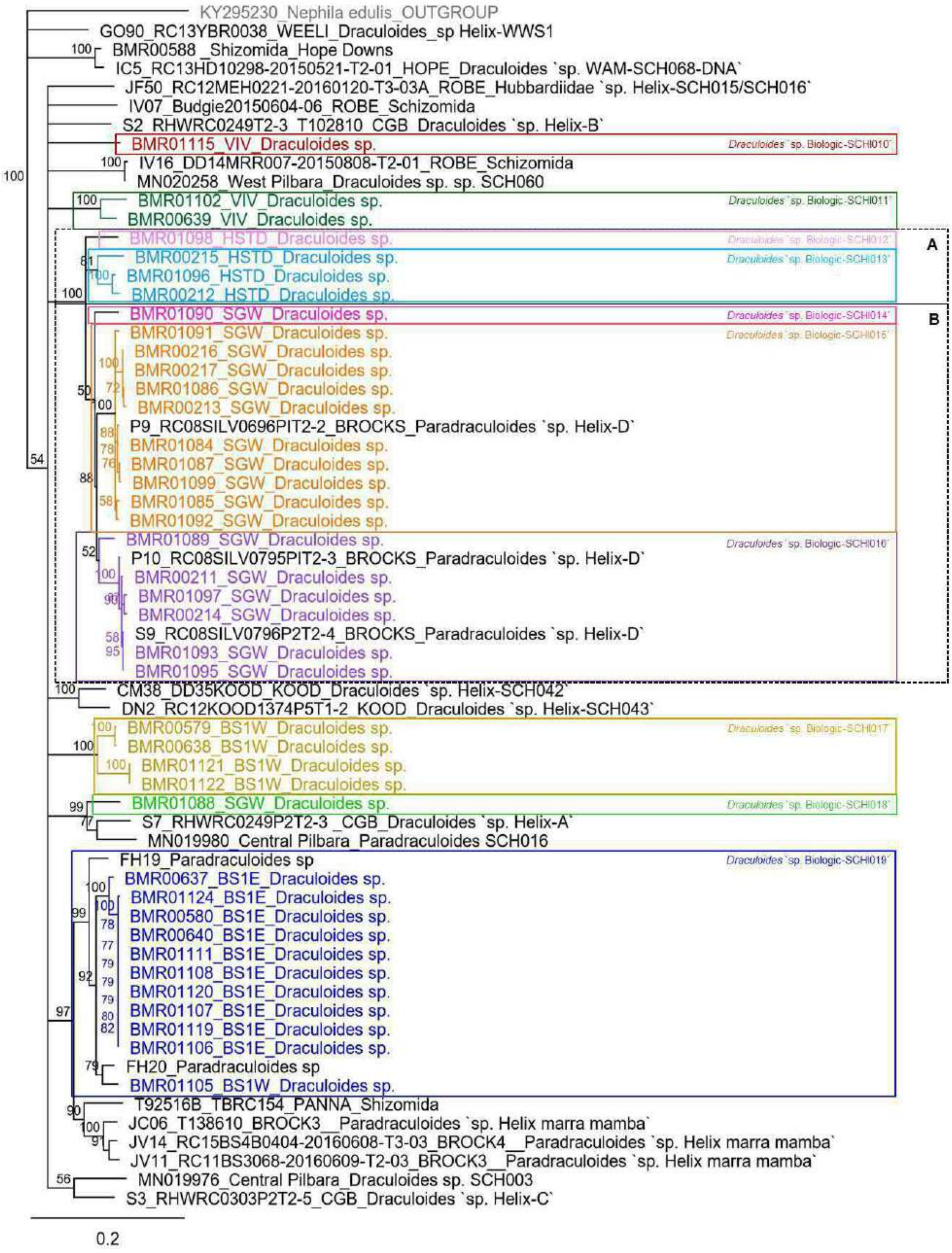


Figure 4.4: Neighbour-joining tree of Schizomida haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text. NB. *Paradraculoides* is now a junior synonym of *Draculoides* (Abrams *et al.*, 2019).

4.2 Myriapoda

4.2.1 Chilopoda

Six OTUs were detected from the Study Area (Figure 4.5). The interspecific divergences between these OTUs ranged from 17 to 29%. Three sequences from Boolgeeda Creek had <1% COI divergence (Scolopendromorpha `sp. Biologic-CHIL006`, Appendix 6). Scolopendromorpha `sp. Biologic-CHIL006` is well nested within *Cryptops*, and as one specimen was identified morphologically as *Cryptops*, it is likely to represent this genus. Likewise, Scolopendromorpha `sp. Biologic-CHIL005` is nested within *Cryptops* and may also represent this genus. None of the Study Area specimens aligned with any of the available regional sequences, suggesting unique species represented by single individuals collected from the various deposits.

Scolopendromorpha `sp. Biologic-CHIL004` was morphologically identified as a scolopendromorph centipede, and aligned closest to other scolopendromorph sequences, including *Cryptops*. Nevertheless, at such high levels of divergence from other available *Cryptops* sequences, the current analysis does not indicate *Cryptops* as the likely genus of this sequence.

BMR00210 was well nested within a lineage containing *Cormocephalus* sequences. A number of troglobitic *Cormocephalus* centipedes have recently been described from the Pilbara region (Edgecombe *et al.*, 2019). BMR00210 had an average divergence of 9.3% from *Cormocephalus* `sp. A`, one of the *Cormocephalus* identified by Edgecombe *et al.* (2019). Based on the high intraspecific divergences found by Edgecombe *et al.* (2019) and the current species concepts in subterranean *Cormocephalus*, BMR00210 has been placed within *Cormocephalus* `sp. A`.

Scolopendromorpha `sp. Biologic-CHIL002` and `sp. Biologic-CHIL007` were morphologically identified as geophilomorph centipedes, and although highly divergent from each other (25% COI), both have aligned closest to other geophilomorph sequences.

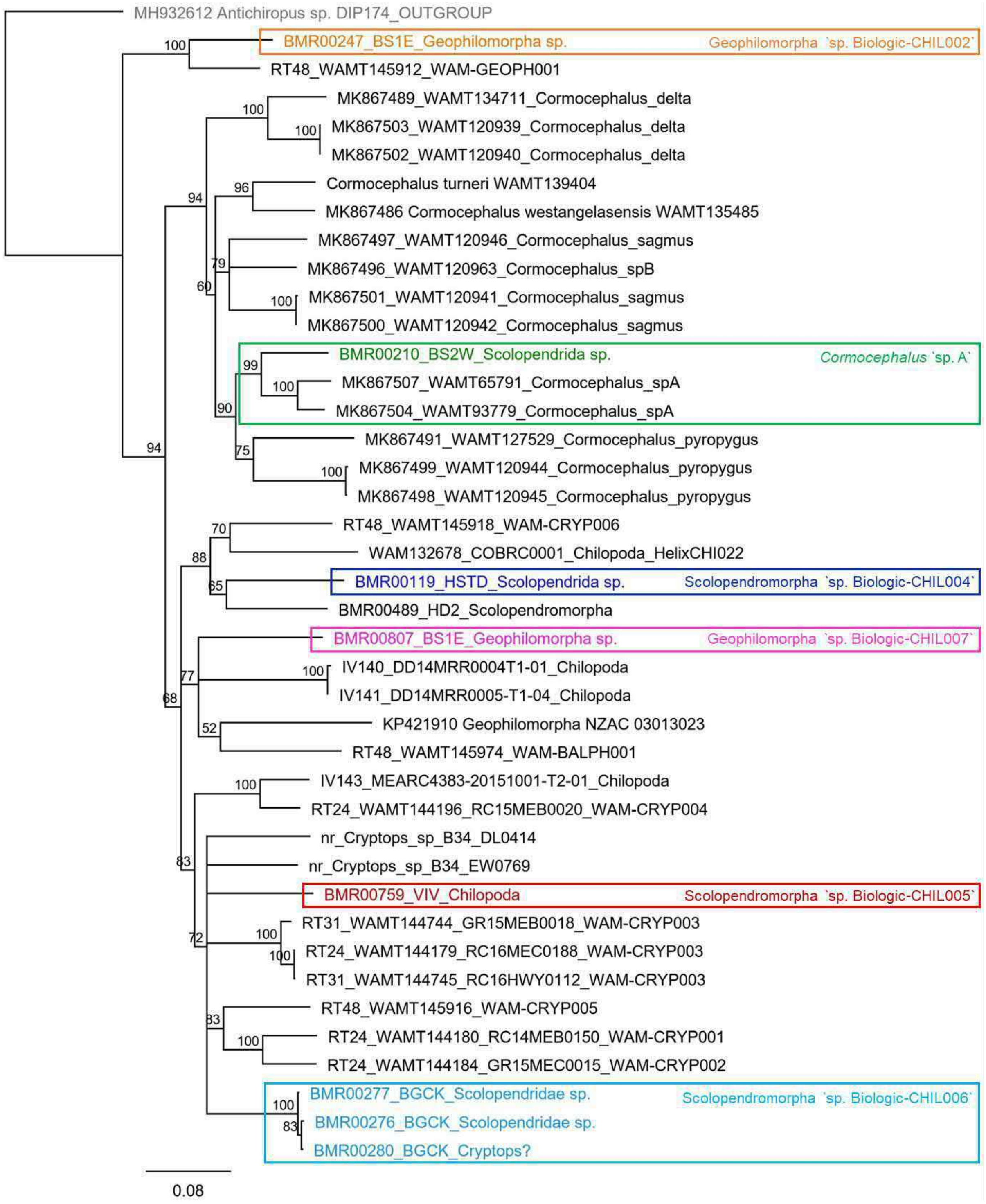


Figure 4.5: Neighbour-joining tree of Chilopoda haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text.

4.2.2 Diplopoda

Two Polyxenida OTUs were determined from the Study Area sequences (Figure 4.6). The divergence between the two GBO specimens within `sp. Biologic-POLX002` was 0.2%, and these aligned (3.7% COI) with regional sequences from Silvergrass, Nammuldi, Robe Headwaters, Turee Syncline, and Western Turner Syncline (Biota, 2009, 2013, 2014). Polyxenida `sp. Biologic-POLX003` had 4.5% divergence between Study Area sequences and diverged from regional sequences (which included sequences from Silvergrass Mesa G, Western Range, and Turee Syncline; Biota, 2009, 2013; Biota, 2006) by 6.6% (Appendix 7). Divergences between Polyxenida `sp. Biologic-POLX002` and `sp. Biologic-POLX003` ranged from 9.5% to 13%.

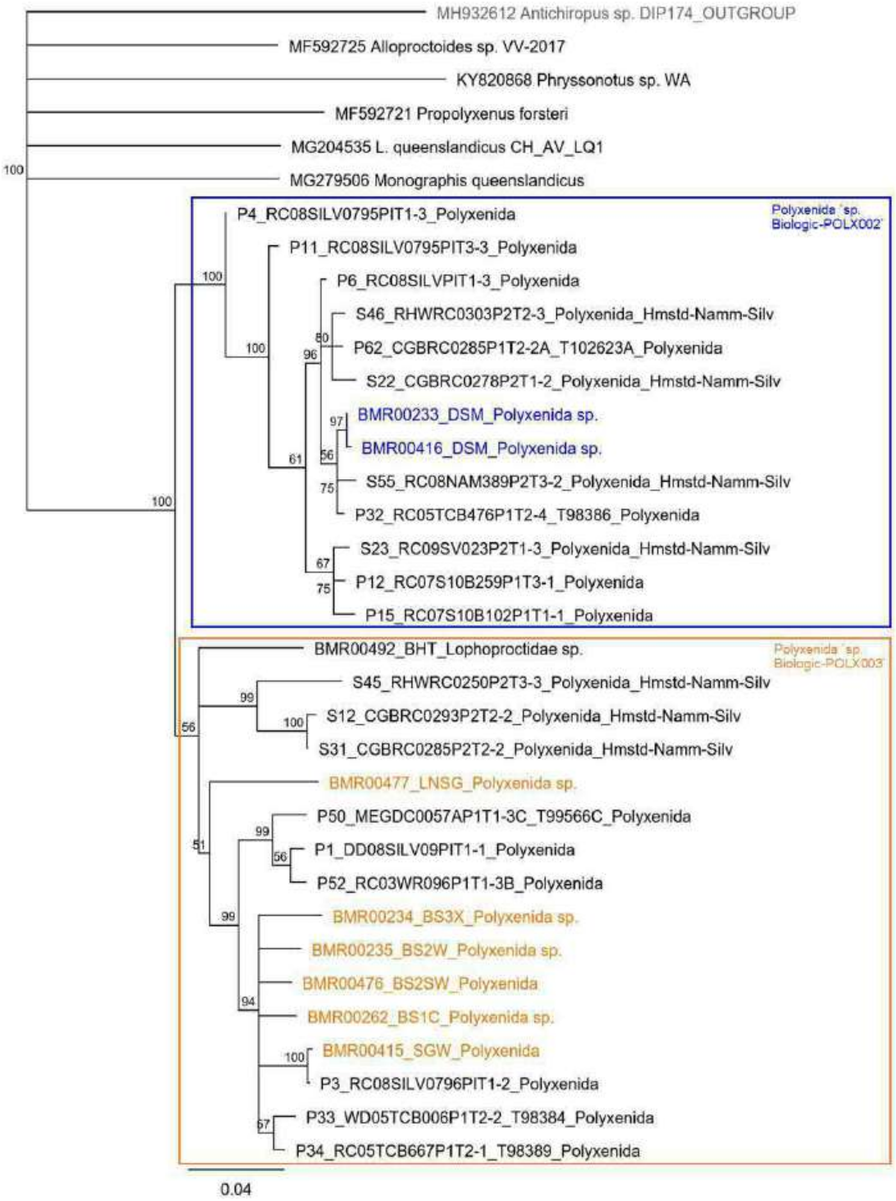


Figure 4.6: Neighbour-joining tree of Polyxenida haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text.

4.2.3 Pauropoda

Fourteen Pauropoda OTUs were detected (Figure 4.7). Owing to the low diversity of available regional sequences for alignment, the Neighbour-joining tree did not suggest any consistent groupings by higher taxon, although several of the OTUs may represent the genus *Decapauropus*. Sequence BMR00089, collected from Silvergrass West, matched a *Decapauropus* sequence from Paraburdoo (*Decapauropus* WAM-PAUD002; Cullen & Harvey, 2018) (5% COI), and this species is therefore regarded as regionally widespread. Interspecific divergences ranged from approximately 11 to 34%. Intraspecific divergences were moderately low for the OTUs where multiple sequences were available (3% for Pauropoda sp. Biologic-PAUR007 and 6% for Pauropoda `sp. Biologic-PAUR008`) (Appendix 8).

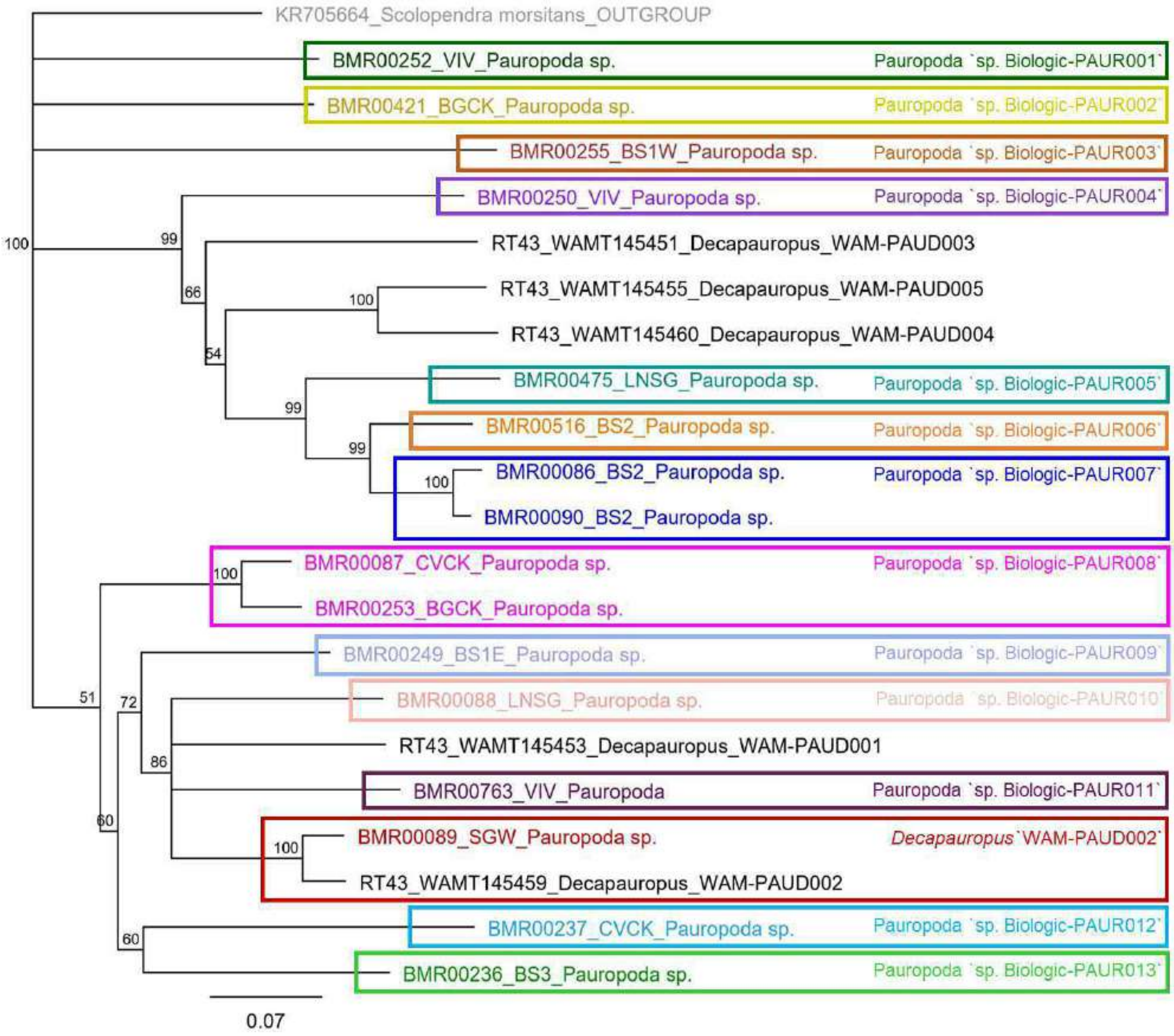


Figure 4.7: Neighbour-joining tree of Pauropoda haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text.

4.2.4 Symphyla

Eleven Symphyla OTUs were detected from the analysis (Figure 4.8, Appendix 9). In most instances, morphological identifications were used to indicate genera, as the Neighbour-joining tree did not suggest any consistent groupings by higher taxon. However, Symphyla `sp. Biologic-SYMP008` and Symphyla `sp. Biologic-SYMP014` were situated within a clade containing other *Symphyella*, so it is likely that these represent the *Symphyella* genus. The other nine sequences fell within Scutigerellidae sequences and likely represent this family. Five of these have been morphologically identified as *Hanseniella*.

Four OTUs were represented by more than one sequence, and their intraspecific divergences were as follows: Scutigerellidae `sp. Biologic-SYMP004`, 8,6% COI; *Hanseniella* `sp. Biologic-SYMP003`, 6.4% COI; *Hanseniella* `sp. Biologic-SYMP006`, 2.8% COI; Scutigerellidae `sp. Biologic-SYMP007`, 2.0%. Both Scutigerellidae `sp. Biologic-SYMP004` and *Hanseniella* `sp. Biologic-SYMP003` comprised specimens which were approximately 3 km apart within connected habitats. Despite moderate COI divergences, they have been treated as single OTUs with caution.

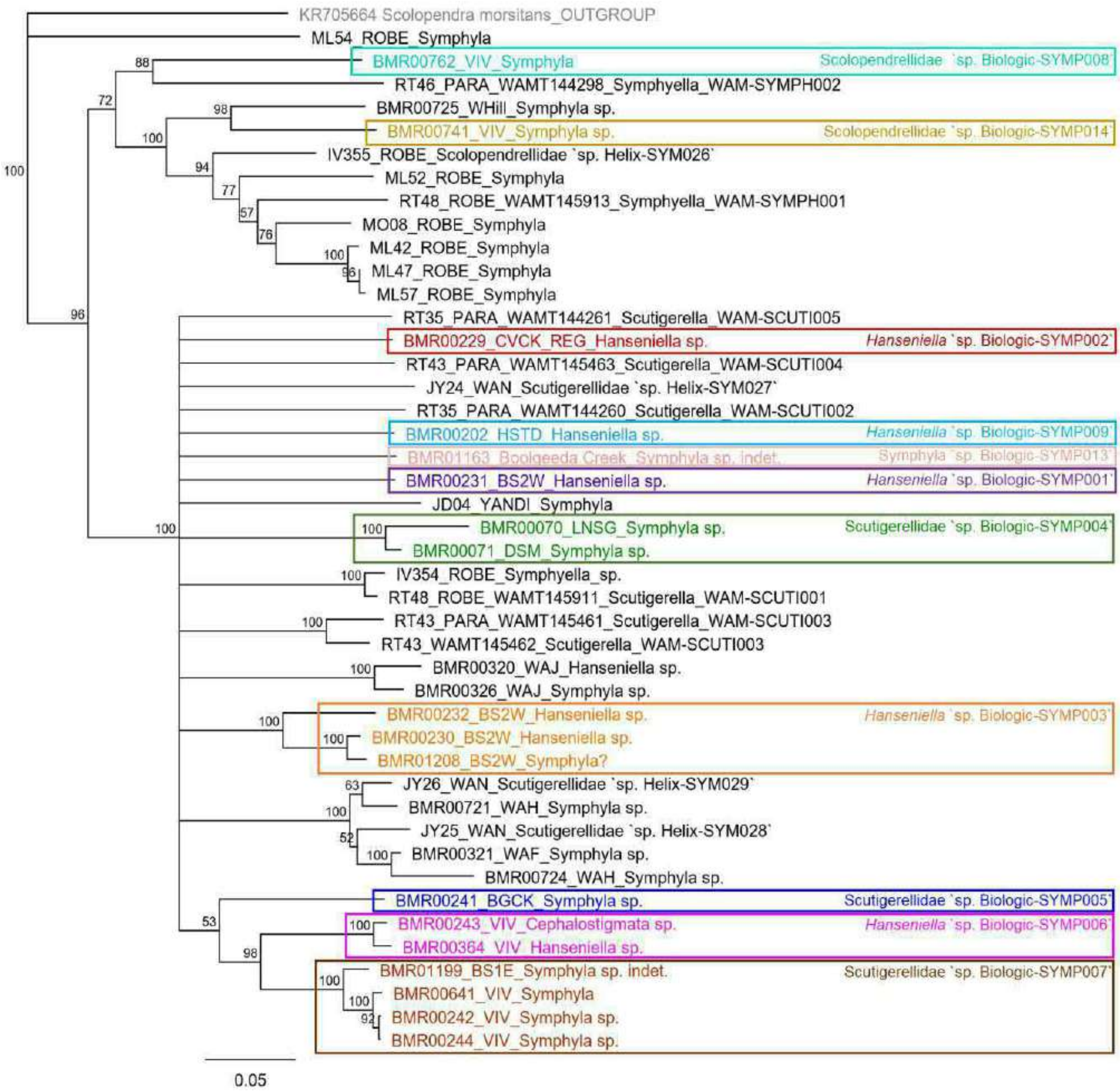


Figure 4.8: Neighbour-joining tree of Symphyla haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text.

4.3 Entognatha – Diplura

Fourteen OTUs were derived from the dipluran sequences in the Study Area (Figure 4.9). None of the Study Area specimens (except BMR00207 from BS1W, which aligned with a japygid from Eliwana at 4.2% COI) aligned with any of the available regional sequences, suggesting 14 potentially unique sequences represented by one or two individuals collected from various survey areas. Intraspecific divergences within Projapygidae `sp. Biologic-DIPL002` and Japygidae `sp. Biologic-DIPL14` were 1.1% and <0.01% respectively. Japygidae `sp. Biologic-DIPL14` and Japygidae `sp. Biologic-DIPL15` diverged from each other by 8.6% and could represent the same species or sister-species (Clade A) but are treated as separate OTUs with caution. The relatively high divergence between Study Area sequences (10 – 27% COI) is of the same order as that between regional sequences, *i.e.* most of the available dipluran sequences from the wider region were similarly highly divergent from one another, and from the Study Area sequences (Appendix 10).

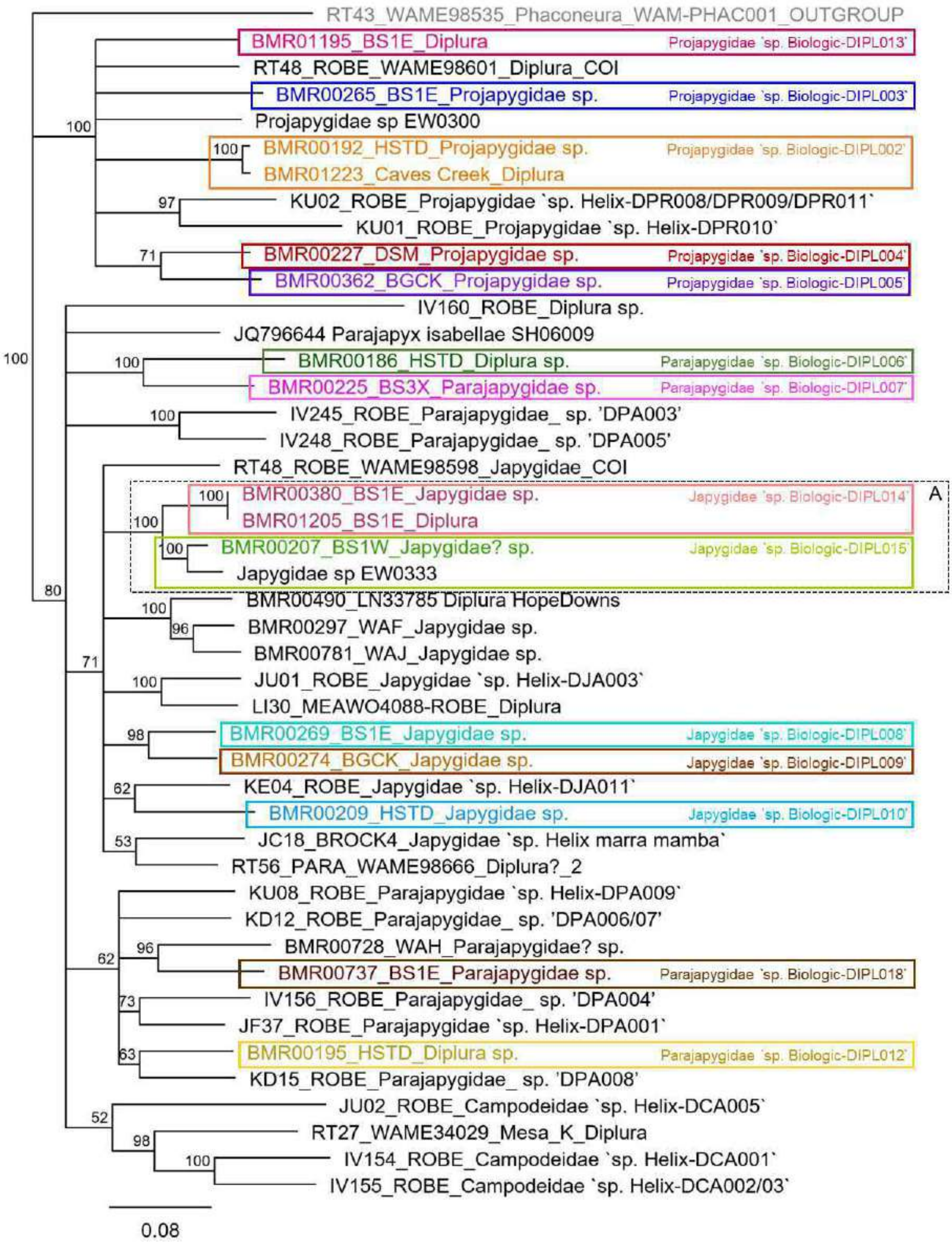


Figure 4.9: Neighbour-joining tree of Diplura haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text.

4.4 Malacostraca - Isopoda

Eight isopod OTUs were derived from the Study Area sequences (Figure 4.10). Six of these belong to the family Armadillidae, according to their morphology and/or their location in the tree. Isopoda `sp. Biologic-ISOP007` is likely to be an armadillid, possibly of the genus *Buddelundia*, because it is in the same branch as two other Aramdillidae whose morphology indicated *Buddelundia*. Intraspecific divergence between the two Armadillidae `sp. Biologic-ISOP002` sequences was <0.01% (Appendix 11). The intraspecific divergence between the GBO sequences within Philoscidae `sp. Biologic-ISOP001` was 5.9%, and these aligned with a regional sequence (Philosciidae `sp. Helix-I7` found at BS4; Biota, 2016b) at 4.8% COI. All other OTUs are singletons found at various deposits across the Study Area. Interspecific divergences range from 15 to 26%.

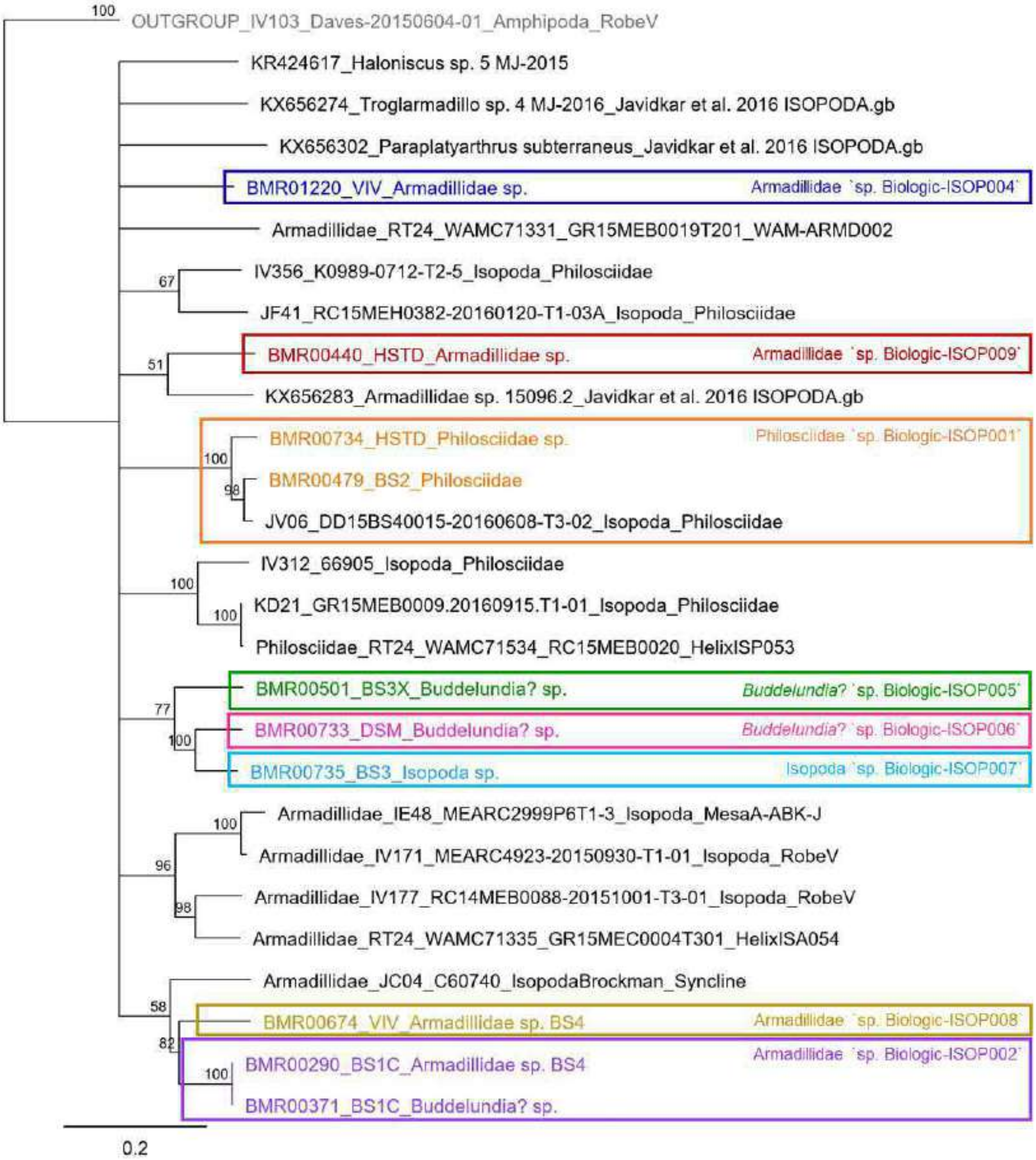


Figure 4.10: Neighbour-joining tree of Isopoda haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text.

4.5 Insecta

4.5.1 Blattodea

Eight Blattodea OTUs were detected (Figure 4.11), all belonging to the genus *Nocticola*. A 4% species/ OTU threshold was used based on a recent molecular study by Trotter *et al*. (2017) which found 3 - 4% divergences between *Nocticola* species. Average intraspecific divergences within Biologic-BLAT005, Biologic-BLAT006, Biologic-BLAT007, Biologic-BLAT008, Biologic-BLAT009, and Biologic-BLAT010 are all <3% (Appendix 12). Average divergences between Biologic-BLAT005, Biologic-BLAT006 and Biologic-BLAT007 were all <7%. Likewise, average divergences between Biologic-BLAT008, Biologic-BLAT009 and Biologic-BLAT010 were all <7%. Interspecific divergences between Biologic-BLAT008 and Biologic-BLAT011, as well as between Biologic-BLAT008 and Biologic-BLAT012, were <8%. Regional sequences (all from Western Turner Syncline) diverge from Greater Brockman OTUs by 7.2%. All specimens within Biologic-BLAT005 were from BS1W, while all specimens within Biologic-BLAT006 were from BS1E. Other OTUs were represented by more than one deposit. Average divergence across all sequences was relatively low at 6.5%, ranging from 0 to 9%.

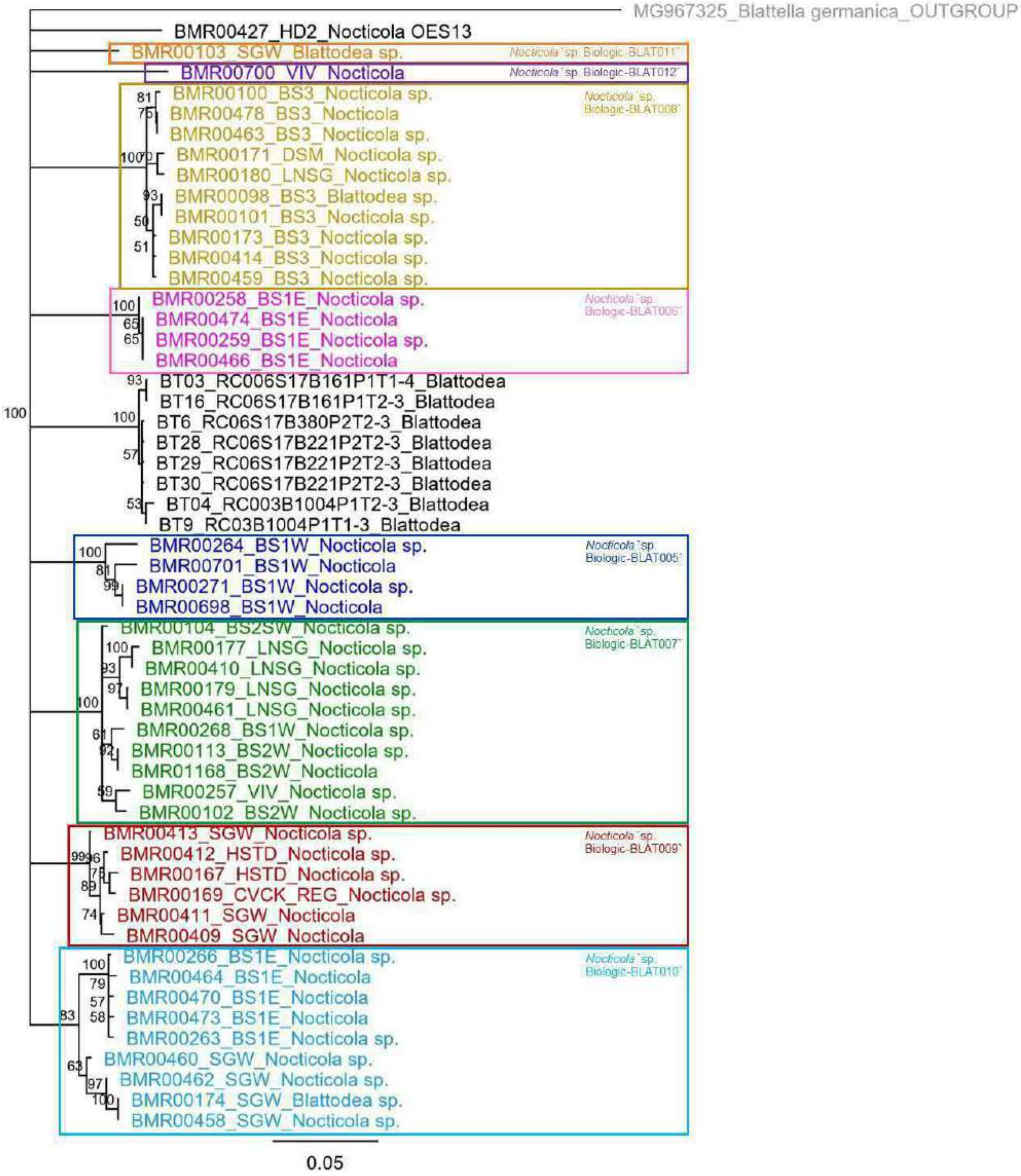


Figure 4.11: Neighbour-joining tree of Blattodea haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text.

4.5.2 Coleoptera

Four Coleoptera OTUs were detected from the analysis (Figure 4.12, Appendix 13). Carabidae `sp. Biologic-COLE001`, recorded from Vivash, aligned with Coleoptera sequences – one of which was also identified as a Carabidae – found at BS4 previously (Biota, 2016a) (intraspecific divergence <3%). Biologic-COLE002 and Biologic-COLE003 were only recorded from single sites and diverged from all other sequences (and each other) by >19%. Curculionidae `sp. Biologic-COLE004` was recorded from two sequences at Vivash (intraspecific divergence 7.4%). Interspecific divergences between OTUs were all >20%.

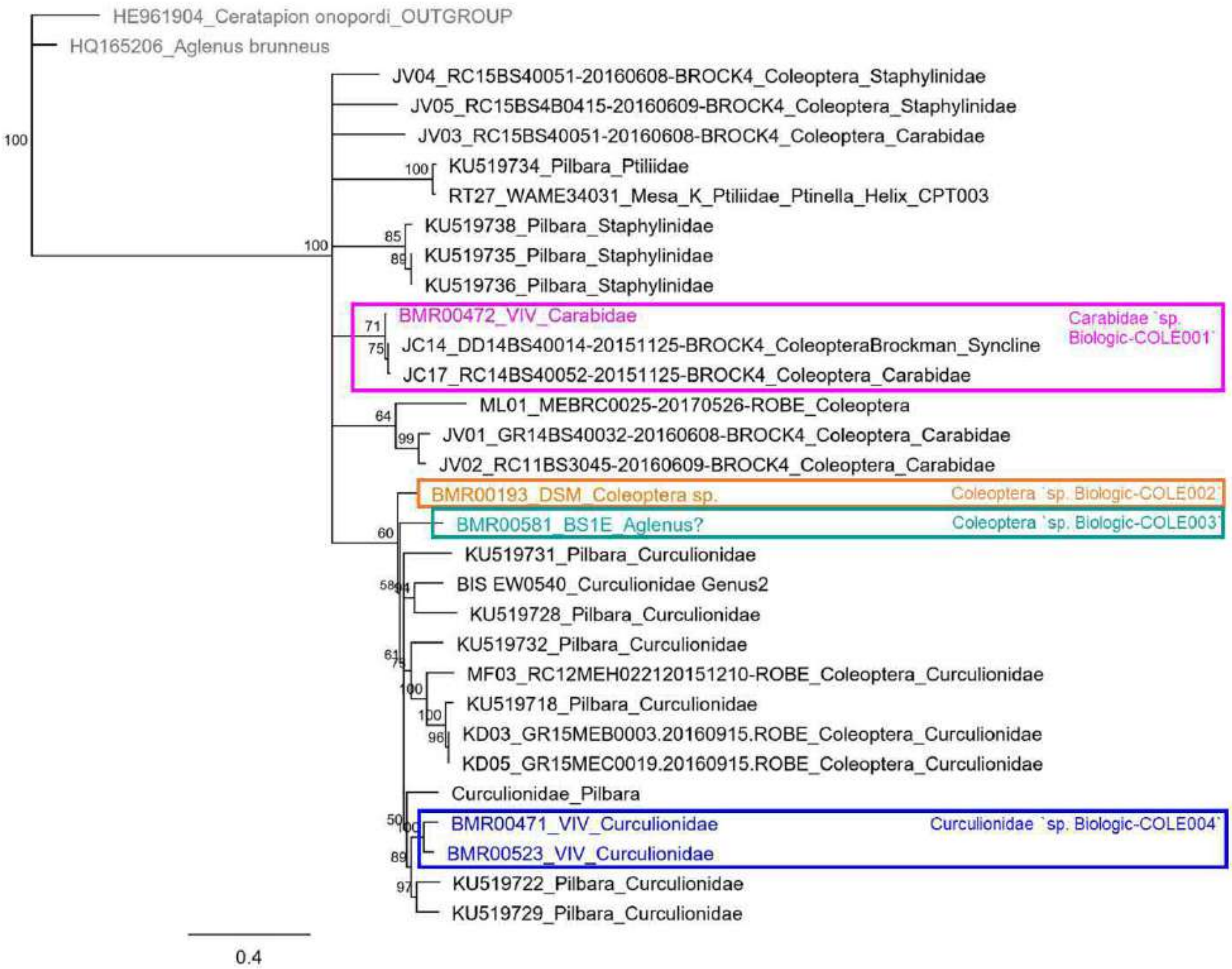


Figure 4.12: Neighbour-joining tree of Coleoptera haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text.

4.5.3 Hemiptera

Four Hemiptera lineages were well-supported (Figure 4.13). The intraspecific divergence of Greater Brockman sequences within *Phaconeura* `sp. WAM-PHAC001` was 3.5%, and these two sequences aligned with sequences from Greater Paraburdoo (Cullen & Harvey, 2018) (Appendix 14). The Greater Brockman sequences within WAM-PHAC002 (intraspecific divergence 0.6%) aligned with sequences found at Greater Brockman (0.7% COI). Within Meenoplidae `sp. Biologic-HEMI001`, the divergence between Hope Downs sequences and Greater Brockman sequences was 4.1%, compared to 0.8% between Greater Brockman sequences. Meenoplidae `sp. Biologic-HEMI004` is only known from two Boolgeeda Creek specimens. Interspecific divergences between OTUs were all >15%.

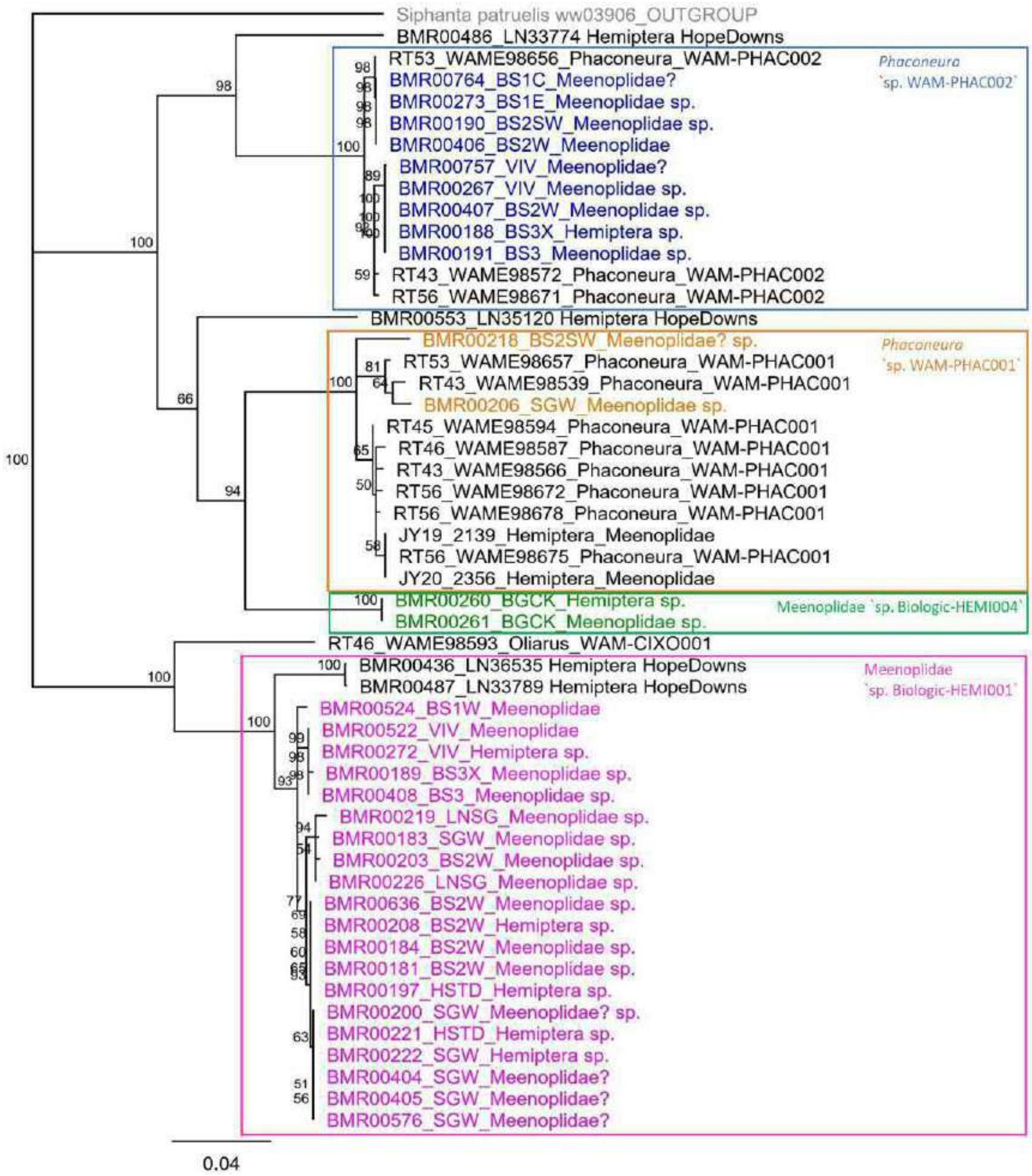


Figure 4.13: Neighbour-joining tree of Hemiptera haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text.

4.5.4 Zygentoma

Based on the COI gene, six OTUs were found in the Study Area. Divergence between Nicoletiidae `sp. Biologic-ZYGE002`, ZYGE003, ZYGE004, ZYGE006 and regional sequences ranged between 13 and 31% and were all considered separate OTUs (Figure 4.14, Appendix 15). The three sequences designated as Nicoletiinae `sp. Biologic-ZYGE005` had an average divergence of 0.6%. These three specimens were all recorded from BS2W and exhibited a divergence ranging from 15 to 30% from all other sequences. Only Nicoletiinae `sp. Biologic-ZYGE007` aligned with a regional sequence from BS4 (named Nicoletiidae `sp. Helix marra mamba`; Biota, 2016a) with a divergence of 4.2%. Both ZYGE005 and ZYGE006 were morphologically identified as Nicoltiinae sp.

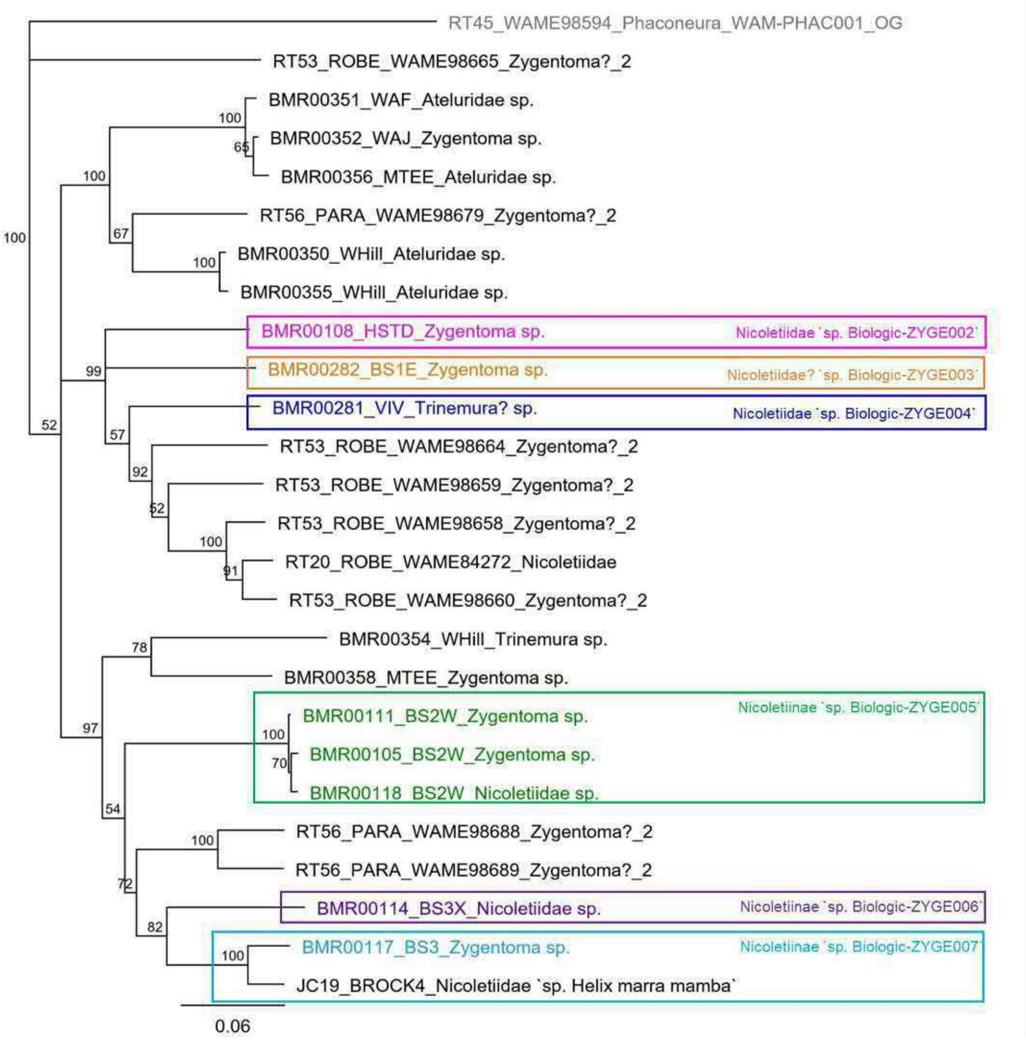


Figure 4.14: Neighbour-joining tree of Zygentoma (COI) haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text.

Analysis of sequences derived at the 12S locus revealed two OTUs (Figure 4.15). For Zygentoma analyses using the 12S primer, ~6% appears to be an appropriate threshold for determining species given Smith *et al*. (2012) reported a divergence of 6.2 – 6.5% between two species of *Trinemura*.

Nicoletiinae `sp. Biologic-ZYGE015`, with an intraspecific divergence of 5.2%, was found at Vivash and BS1C. Atelurinae `so. Biologic-ZYGE008` was found at BS1C, Vivash and BS3 and exhibited an intraspecific divergence of 5% (Appendix 16). Interspecific divergence between these two OTUs was 35.5% and their divergences from all other (regional) sequences was 15 – 41%.

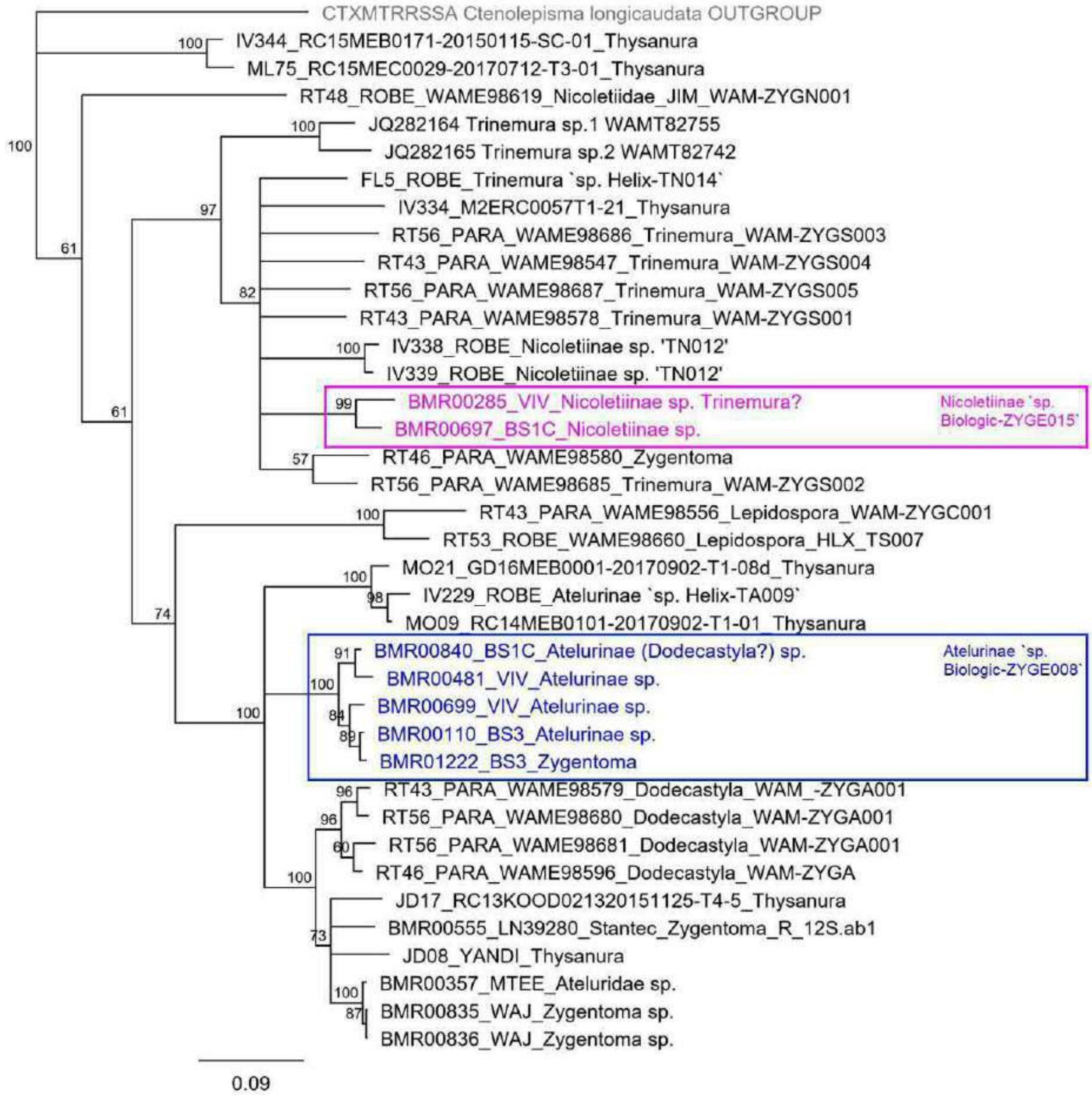


Figure 4.15: Neighbour-joining tree of Zygentoma (12S) haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text.

5 STYGOFAUNA

5.1 Malacostraca

5.1.1 Amphipoda

Melitdae

Three melitid OTUs were detected in the current study using a combination of analyses at the COI and 16S locus (Figure 5.1 and 5.2, Appendices 17 and 18). The intraspecific divergence within *Nedsia* `sp. Biologic-AMPH008` (all from the Homestead/ Caves Creek/ Silvergrass area) was 5.3% at the COI level and 3.6% when concatenating COI and 16S. The intraspecific divergence within *Nedsia* `sp. Biologic-AMPH003` (all from Boolgeeda Creek) was 0.1% COI and <0.01% when concatenating COI and 16S. Five GBO sequences aligned with a sequence from Greater Paraburdoo (Cullen & Harvey, 2018), *Nedsia* `sp. WAM-AMPE003`, at 3.4% COI. The intraspecific divergence of GBO sequences within *Nedsia* `sp. WAM-AMPE003` was 3.7% COI and 4.1% when concatenating COI and 16S.

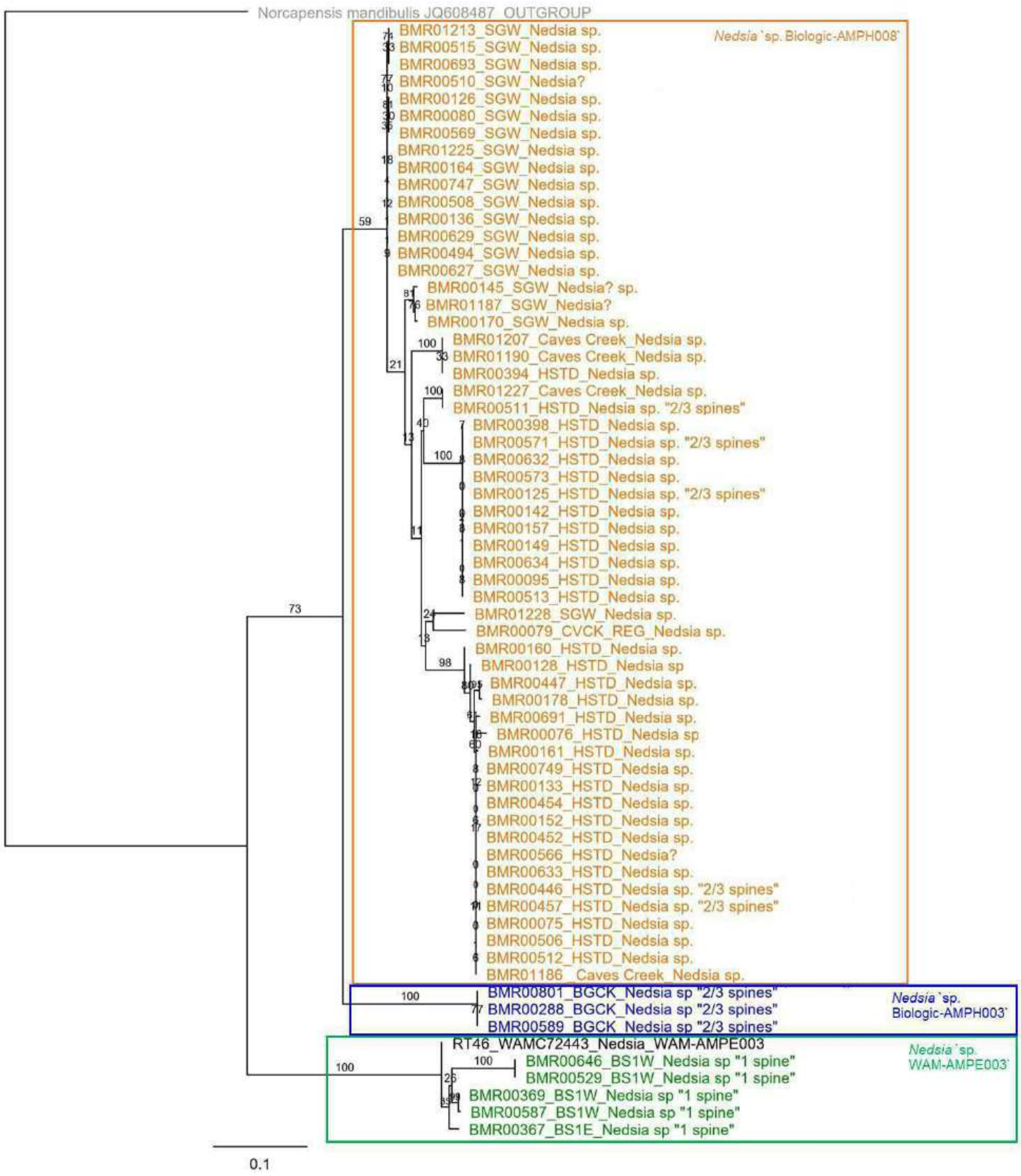


Figure 5.1: RAxML tree of Melitidae (COI) haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text.

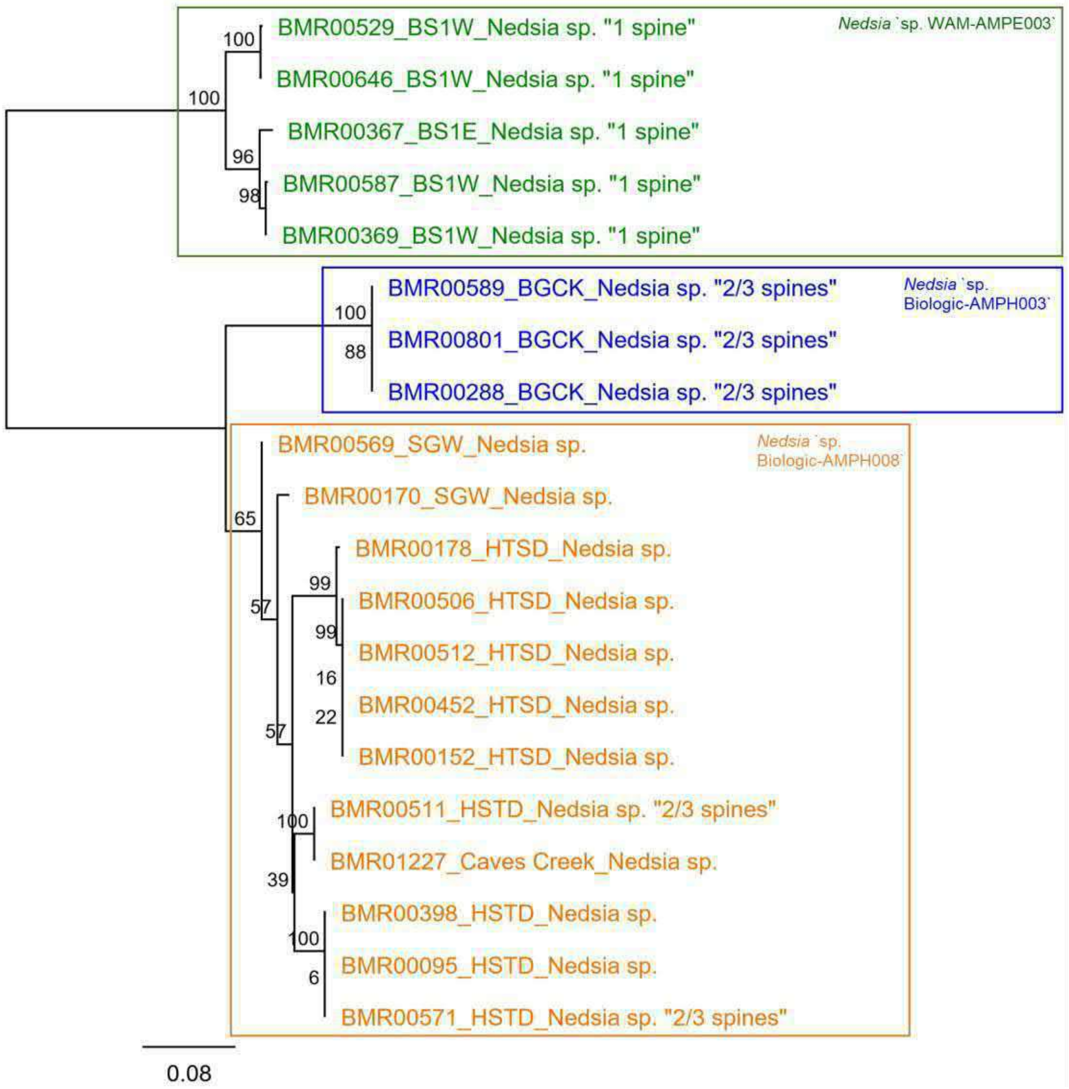


Figure 5.2: RAxML tree of Melitidae (concatenated 16S/ COI) haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text.

Bogidiellidae and Niphargidae

Within the Bogidiellidae and Niphargidae, three OTUs were detected (Figure 5.3, Appendix 19). Amphipoda `sp. Biologic-AMPH009` (intraspecific divergence 0.1% COI) diverges from other Greater Brockman OTUs and other sequences by 23 - 31%. All were recorded from Boolgeeda Creek. Bogidiellidae `sp. Biologic-AMPH010` (intraspecific divergence 1.7%) diverges from AMPH011 by 10.8%, from AMPH009 by 23.0%, and from all other sequences by 18 - 35%. Biologic-AMPH010 was recorded from Silvergrass West, Homestead, and Caves Creek. Biologic-AMPH011 (intraspecific divergence 0.7%) diverges from Biologic-AMPH010 by 10.8%, from Biologic-AMPH009 by 23.5% and from all other sequences by 17 - 33%. Biologic-AMPH011 was recorded from BS1 West and BS1 East. There appears to be a small amount of population structuring within Biologic-AMPH010; intraspecific divergences of the Silvergrass West 'clade' (intraspecific divergence 0.8%) and the Caves Creek/Homestead 'clade' (intraspecific divergence 1.0%) are less than the divergence between the two 'clades' (2.3% divergence).

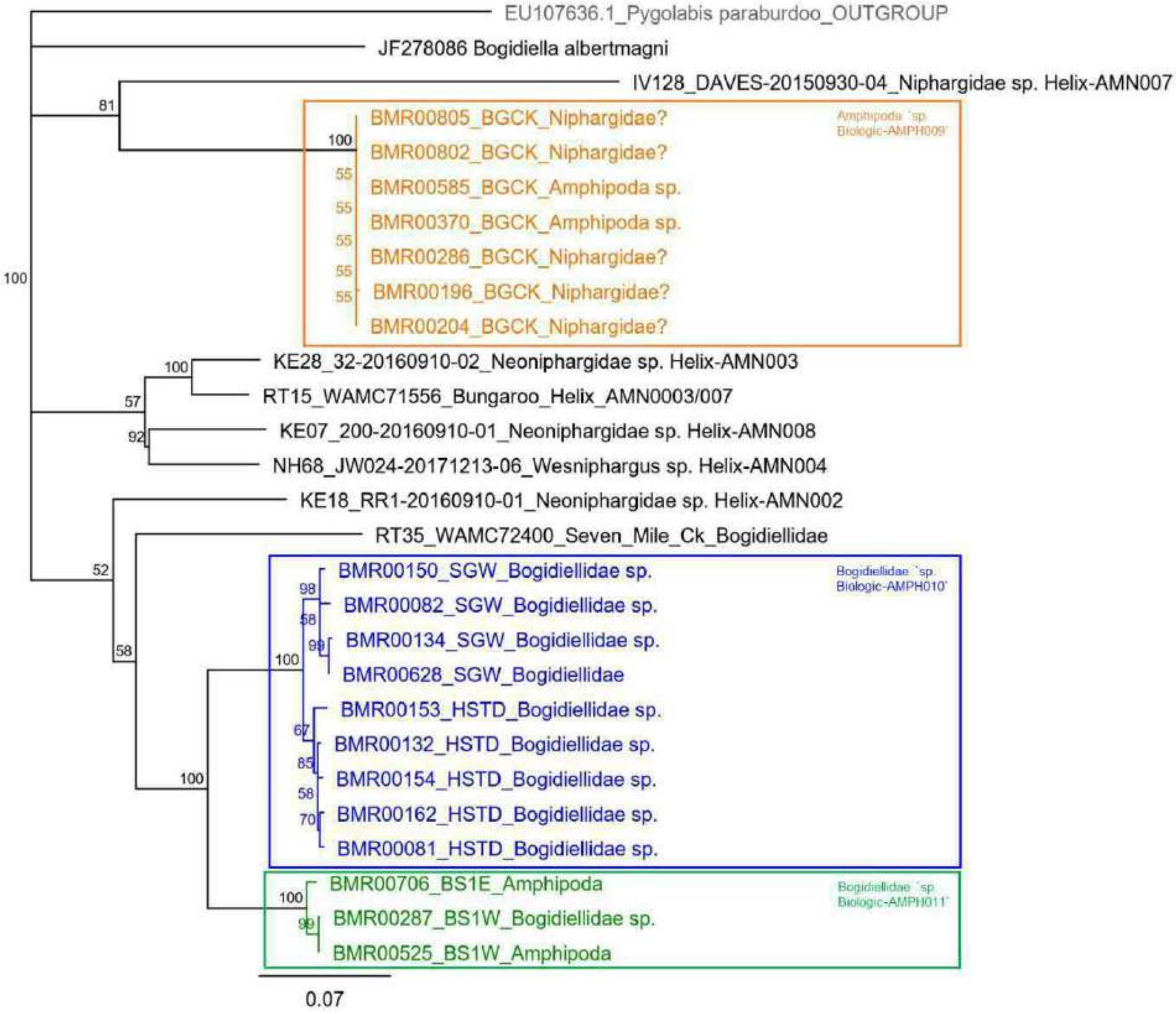


Figure 5.3: Neighbour-joining tree of Amphipoda (Niphargidae and Bogidiellidae) haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text.

Paramelitidae

Six OTUs were detected within the Paramelitidae (Figure 5.4, Appendices 20 and 21), using a 6% threshold for species, which was the lower boundary reported in Finston *et al*. (2007) for this family. One OTU, within which most of the specimens were morphologically identified as *Pilbarus* sp., had an intraspecific divergence of 2.2%, while diverging from *Pilbarus* `sp. F` from Finston *et al*. (2007) by only 2.0% (Figure 5.5). The Greater Brockman specimens were all from Caves Creek, Silvergrass West and Homestead. No clear population structuring was detected. The Finston *et al*. (2007) specimens were from Caves Creek and Hardey River (approximately 95 km southwest of Caves Creek).

The other five paramelitid OTUs were clearly distinct from *Pilbarus* sp. F (Figure 5.6). Paramelitidae `sp. Biologic-AMPH012` diverges from all other sequences by an average of 20.5%. Biologic-AMPH013 (intraspecific divergence 0.1%) were all morphologically identified as *Maarrka* sp. This OTU diverges from another *Maarrka* sp. on GenBank by ~22%. Biologic-AMPH014 (intraspecific divergence 1.9%) was of uncertain identification and diverges from all other sequences by 17 - 33%. Biologic-AMPH015 (intraspecific divergence 2.8%) diverges from two *Yilgarus* sequences from Paraburdoo (Cullen & Harvey, 2018) by 12.0%, and from all other sequences by 19.5%.

The last OTU was a match for NH53 (Paramelitidae `sp. Helix-AMP037`) (Biota, 2018). The Greater Brockman sequences exhibited an intraspecific divergence of 1.8%, and these sequences diverged from NH53 (Helix-AMP037) by 3.8%. NH53 was collected from Mesa H, 90 km NW of Caves Creek. Divergence of this OTU from all other sequences was 14 – 31%.

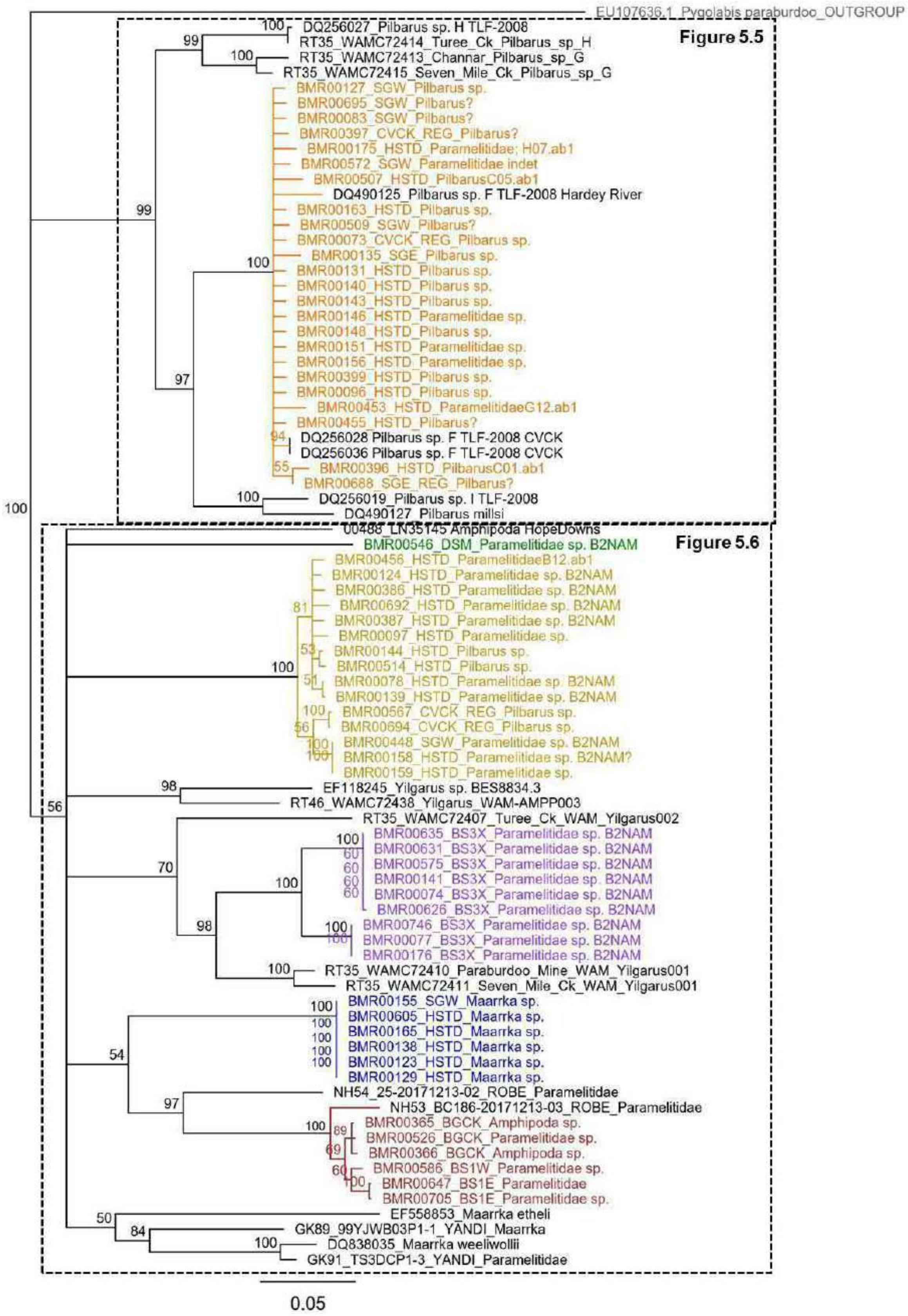


Figure 5.4: Neighbour-joining tree (overview) of Amphipoda (Paramelitidae) haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text.

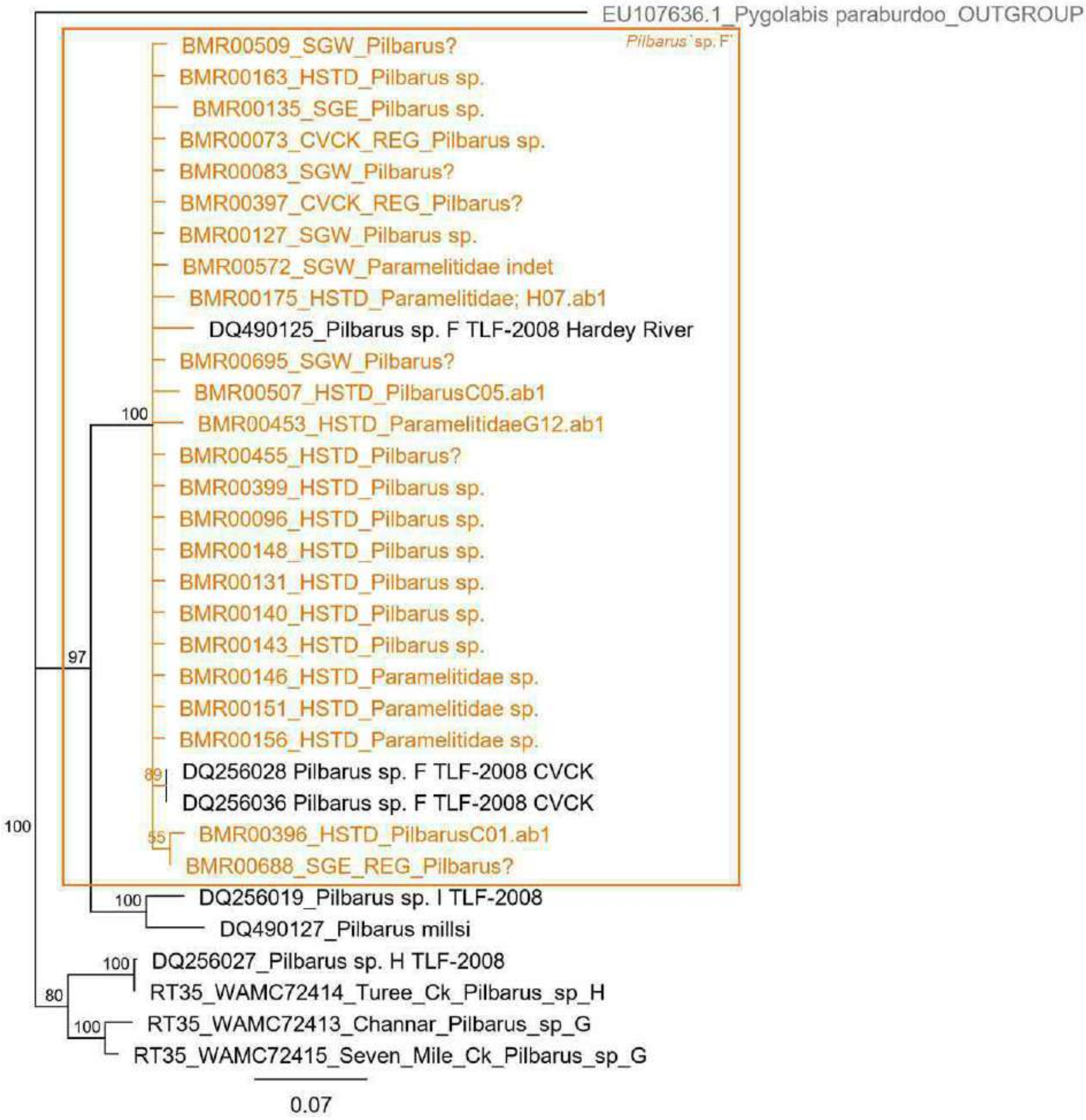


Figure 5.5: Neighbour-joining tree of Amphipoda (*Pilbarus*) haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text

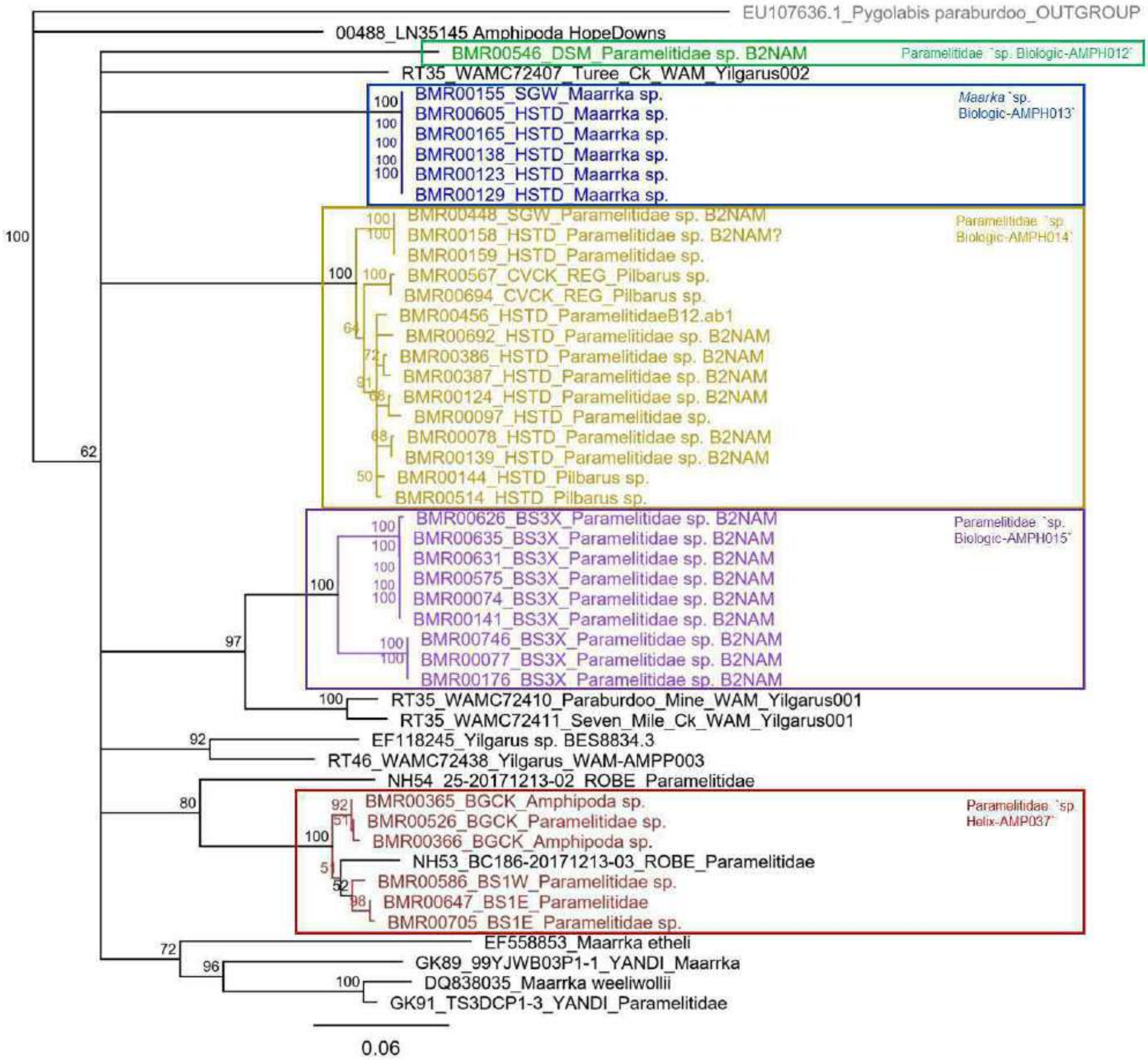


Figure 5.6: Neighbour-joining tree of Amphipoda (Paramelitidae) haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text.

5.1.2 Bathynellaceae

Bathynellidae

Three OTUs within Bathynellidae were recorded from the Study Area (Figure 5.7). Bathynellidae `sp. Biologic-BATH003` contained multiple sequences with an intraspecific divergence of 0.5% (Appendix 22). Interspecific divergences were between 11% and 26%. Bathynellidae `sp. Biologic-BATH002` and BATH003 were divergent by 11%; this is potentially indicative of sister species of the same genus. Bathynellidae `sp. Biologic BATH001` was more highly divergent at 23% from Bathynellidae `sp. Biologic-BATH002` and Bathynellidae `sp. Biologic-BATH003`.

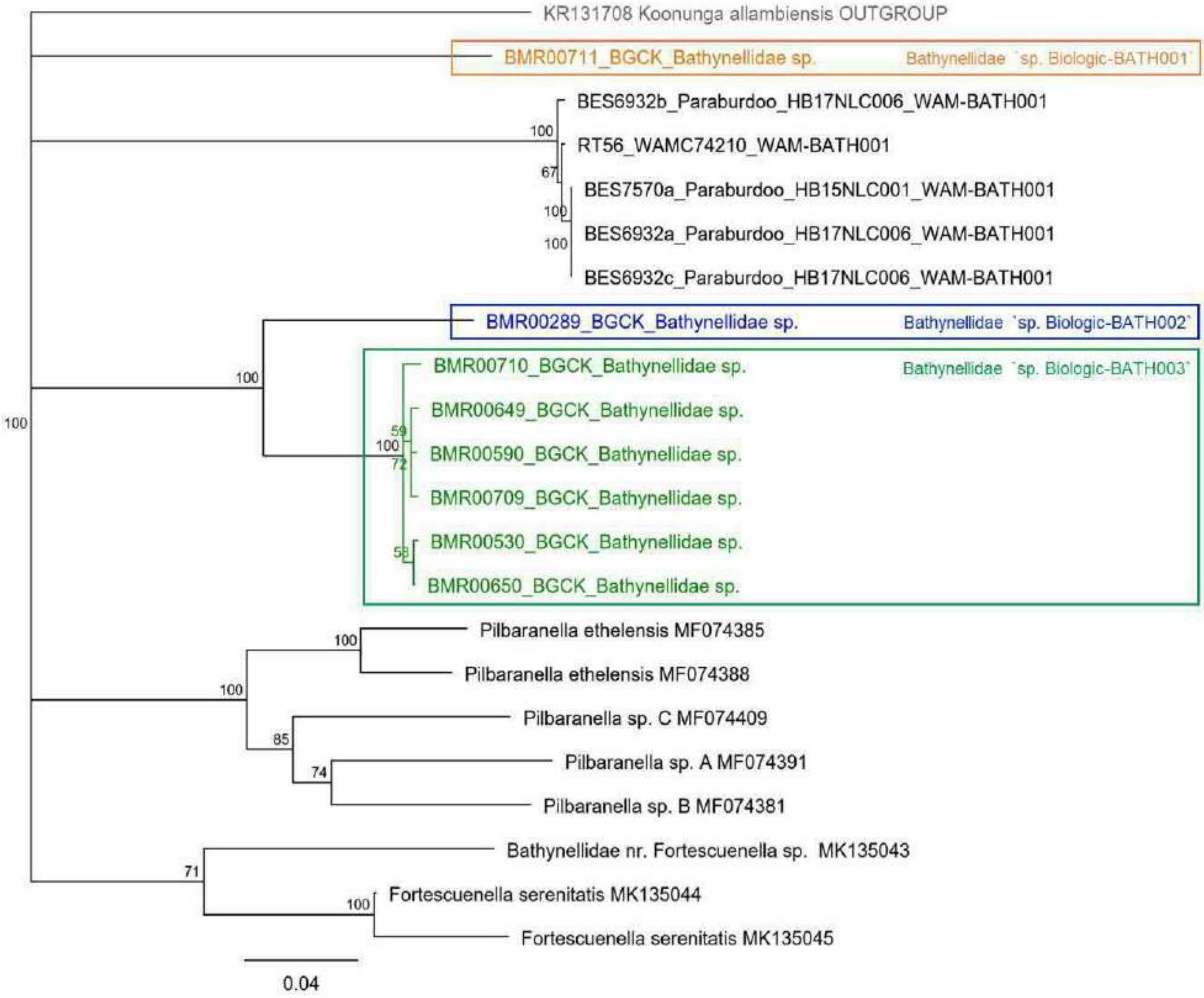


Figure 5.7: Neighbour-joining tree of Bathynellacea (Bathynellidae) haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text.

Parabathynellidae

Six OTUs were detected; five Parabathynellidae OTUs and one Atopobathynellidae OTU (Figure 5.8, Appendix 23). Intraspecific divergences for OTUs that had more than one sequence were <4% (Biologic-PBAT002 = 0.6%; Biologic-PBAT004 = 0.5%; Biologic-PBAT005 = 0.2%; Biologic-PBAT006 = 3.7%). The average divergence between the Study Area lineages was 16.7% (13 – 22%). The average divergence between *Atopobathynella* `sp. Biologic-PBAT006` and Study Area Parabathynellidae lineages was 23%.

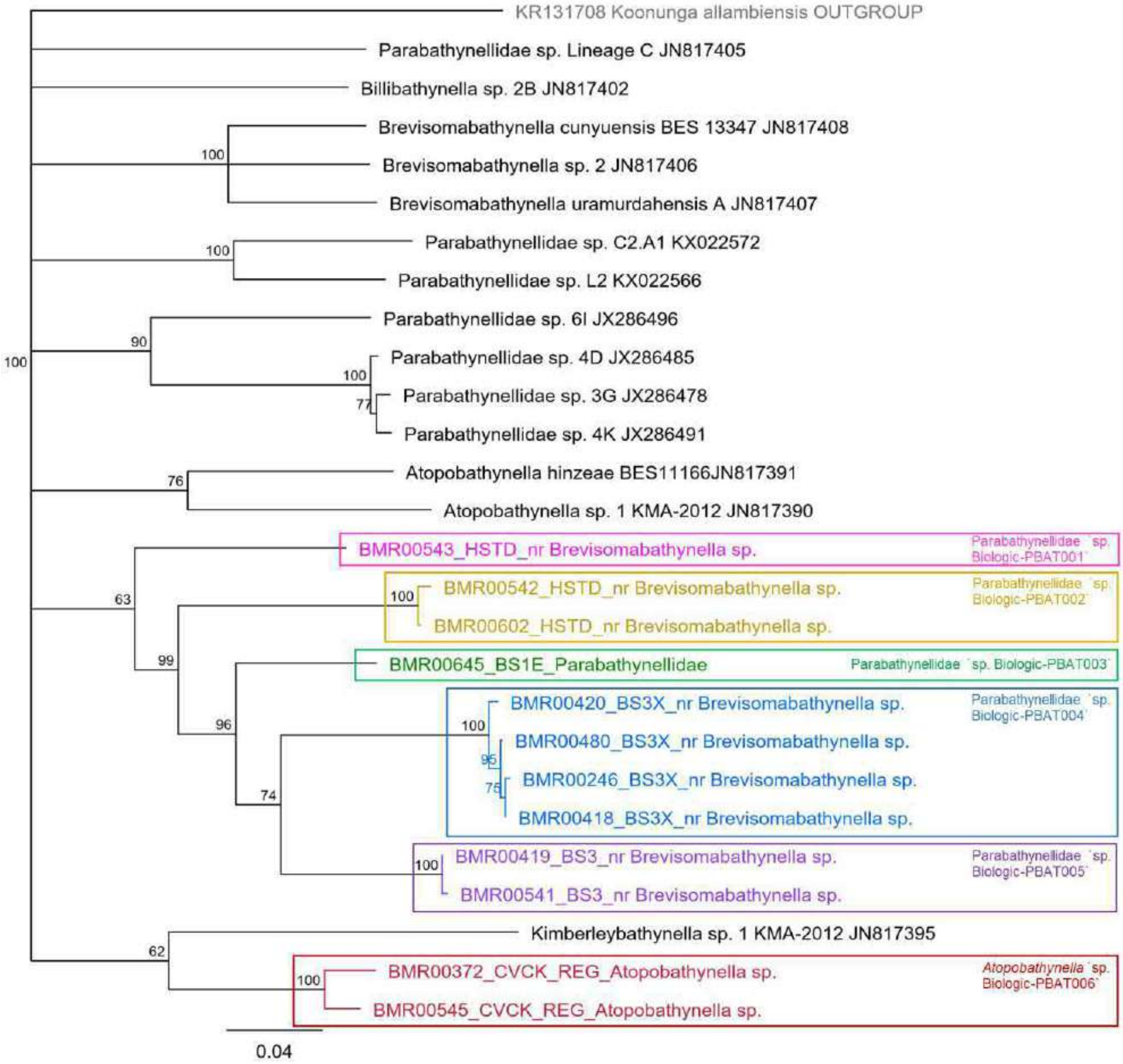


Figure 5.8: Neighbour-joining tree of Bathynellacea (Parabathynellidae) haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text.

5.1.3 Isopoda

Two aquatic Isopoda OTUs were determined from the Study Area (Figure 5.9, Appendix 24). Isopoda \`sp. Biologic-ISOP011\` from Vivash had an intraspecific divergence of <0.01% and diverged from all other sequences by 25 – 29%. The morphology of *Pygolabis* \`sp. Biologic-ISOP012\` strongly indicated this specimen to be a *Pygolabis*, however, it is not nested within other known *Pygolabis* sequences (average divergence ~19% COI).

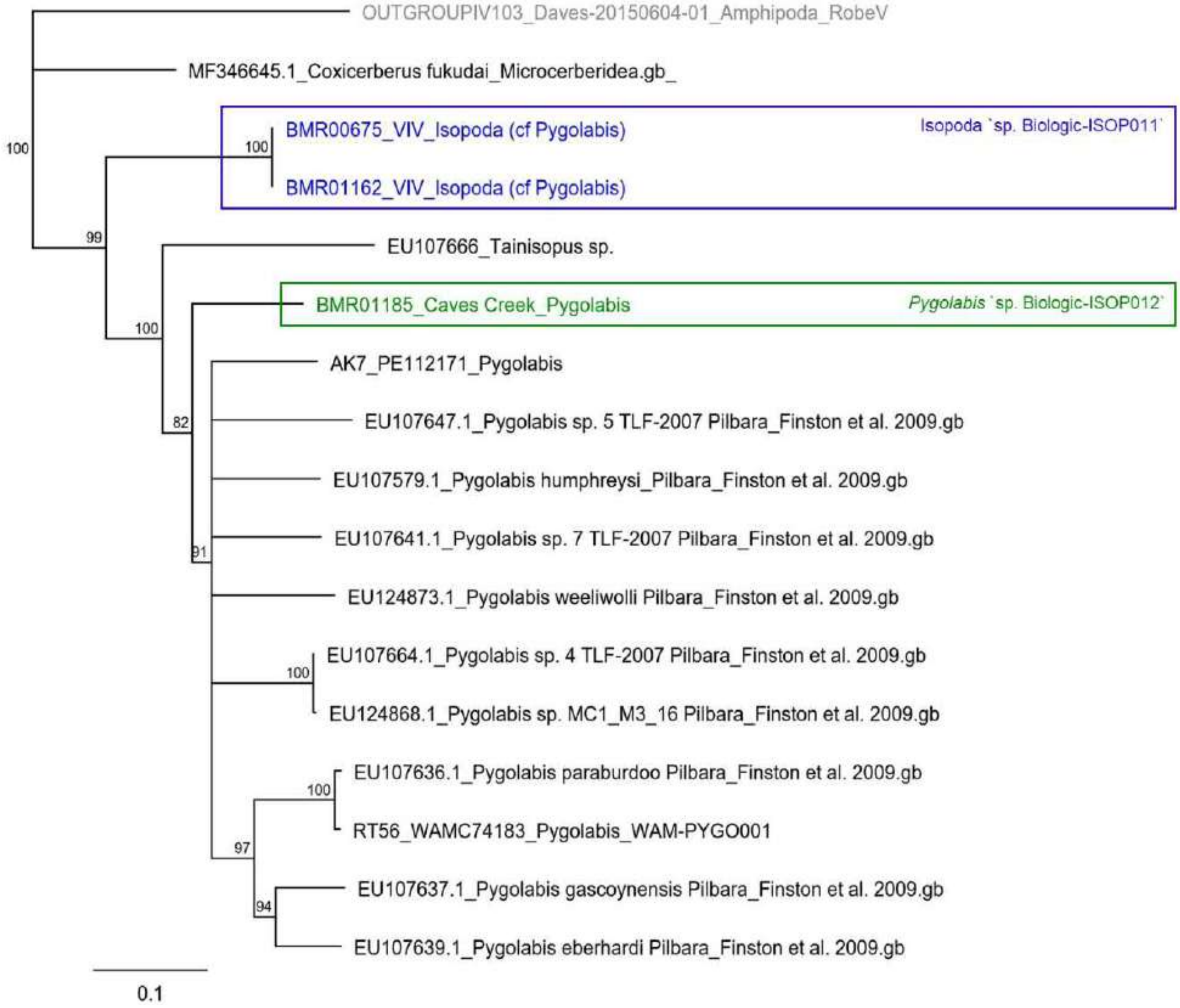


Figure 5.9: Neighbour-joining tree of aquatic Isopoda haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text.

5.2 Oligochaeta

Enchytraeidae

Seven Enchytraeidae OTUs were detected from the analysis (Figure 5.10, Appendix 25). Enchytraeidae `sp. Biologic-OLIG004`, found at BS1E and BS3X, had an intraspecific divergence of 3.6%. Enchytraeidae `sp. Biologic-OLIG003`, recorded from a Karaman sample in Boolgeeda Creek, aligned with Enchytraeidae sp. E13 and Enchytraeidae sp. E11 sequences from McPhee Creek and Weelumurra Creek, respectively (Brown *et al.*, 2015) (<5% COI). The GBO sequences within Enchytraeidae `sp. Biologic-OLIG005` exhibited an intraspecific divergence of 5.6% and aligned with several regional sequences at 6.5% COI divergence: Enchytraeidae `sp. E6 (2-4)` sequences from Greater Paraburdoo (Cullen & Harvey, 2018), previous sequences from West Angelas (Biologic, 2016), and Enchytraeidae sp. 6 (Brown *et al.*, 2015).

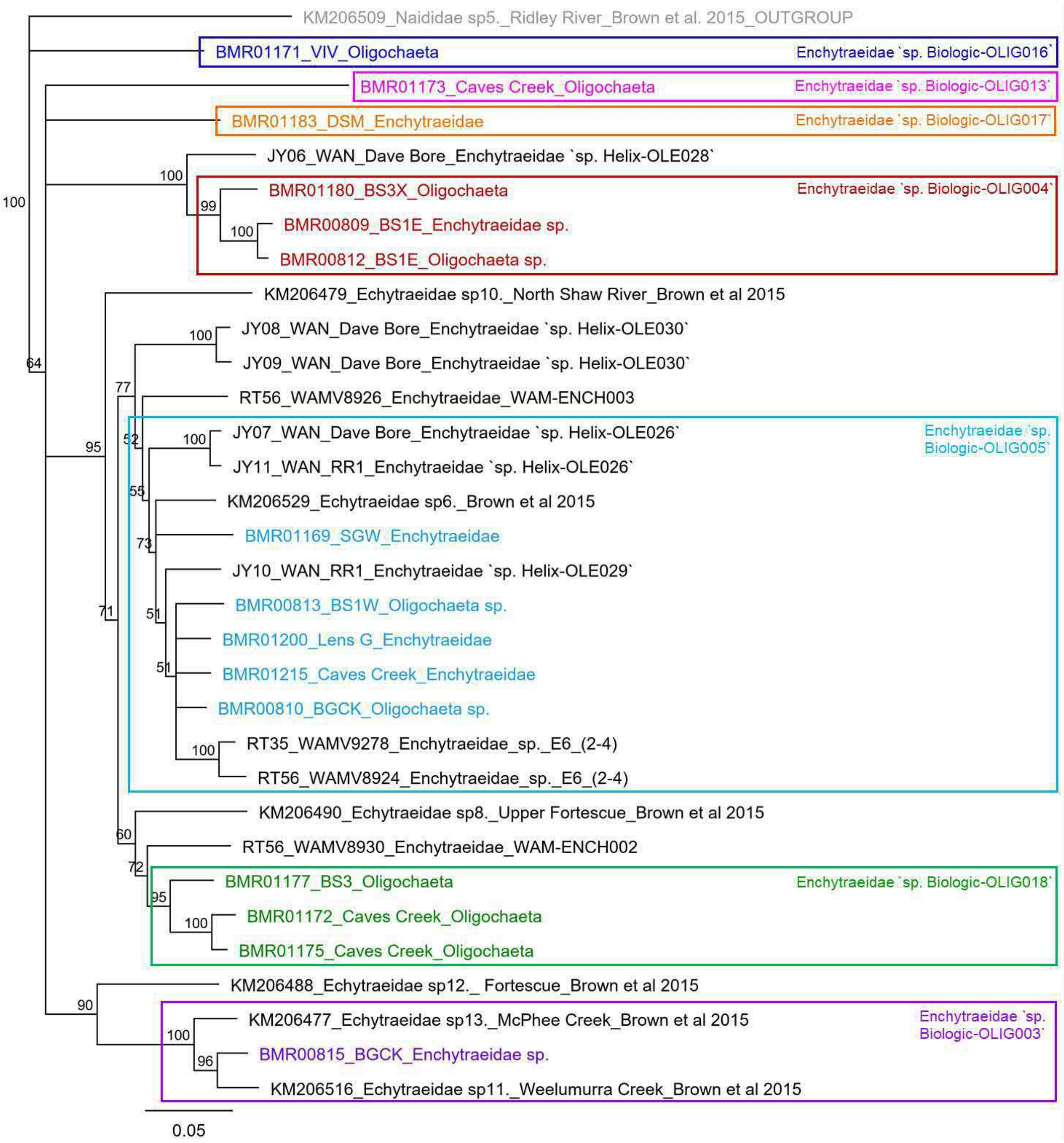


Figure 5.10: Neighbour-joining tree of Oligochaeta (Enchytraeidae) haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text.

Phreodrilidae

Seven phreodrilid OTUs were detected from the Study Area (Figure 5.11, Appendix 26). Interspecific divergences were moderate to high, ranging from 12.8% to 24.2%. The intraspecific divergence of GBO sequences within Phreodrilidae `sp. 12` was 3.1%, and these aligned with sequences from Deposit D at West Angelas (Biologic, 2016) and Fortescue (Brown *et al.*, 2015). The remaining five OTUs were singletons from various deposits across the Study Area.

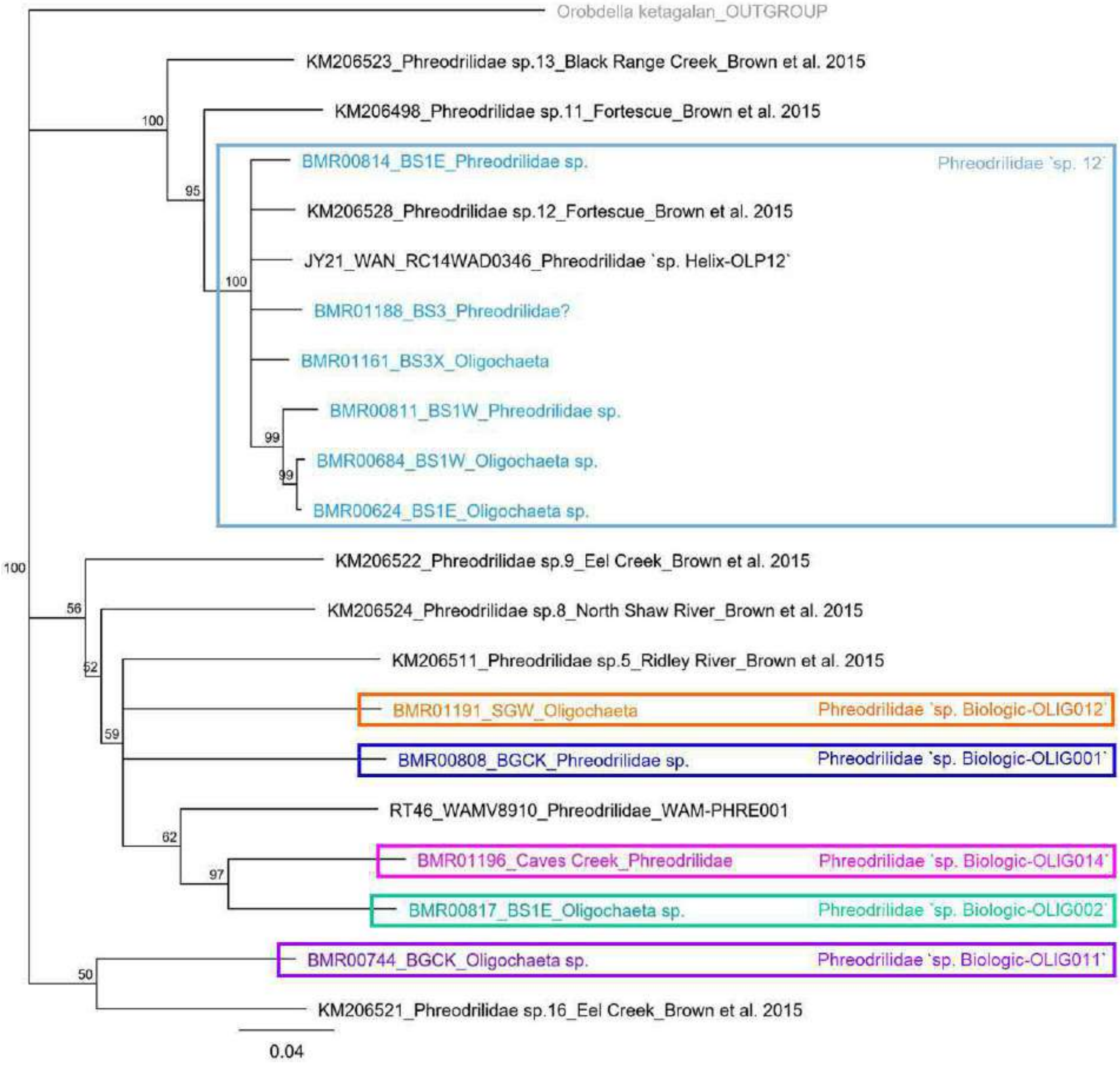


Figure 5.11: Neighbour-joining tree of Oligochaeta (Phreodrilidae) haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text.

Naididae

One Naididae OTU, Naididae `sp. Biologic-OLIG015`, was detected from the analysis (Figure 5.12, Appendix 27) and did not align with any known sequences. It diverged from other Naididae sequences by 15 – 20%.

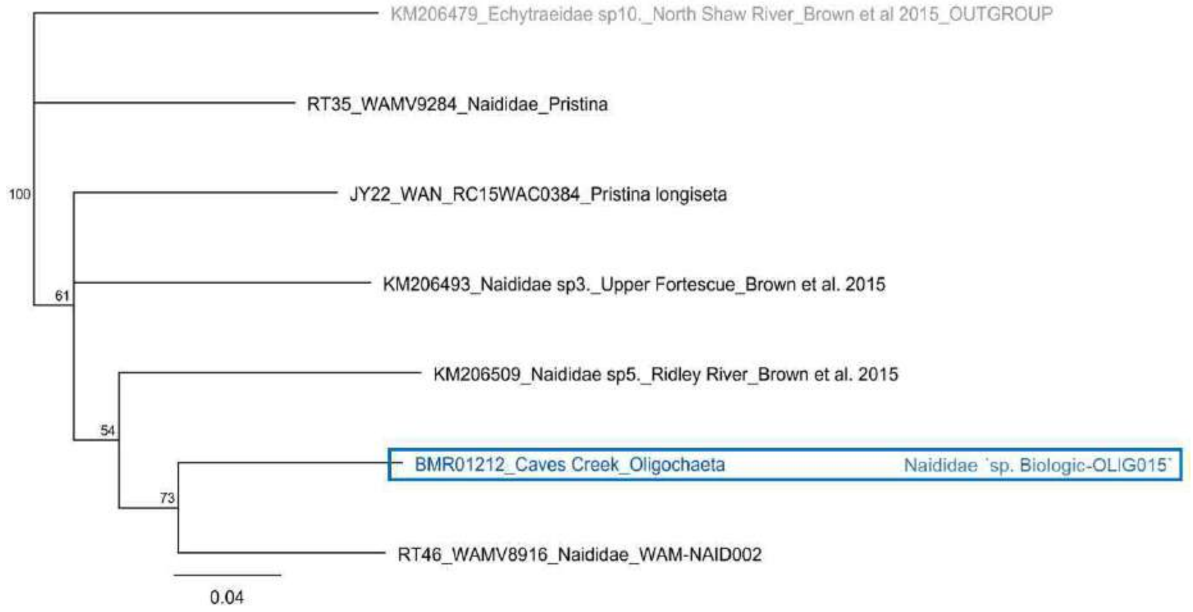


Figure 5.12: Neighbour-joining tree of Oligochaeta (Naididae) haplotypes included in the analysis. Lineages from the Study Area are indicated by coloured text.

6 SUMMARY

Using well-established DNA extraction and sequencing methods, this molecular systematics analysis designated 154 distinct species/ OTUs to 450 high quality sequences from the Study Area. Of these, 185 specimens were from SGCCK, 100 from BS2/ BS3, and 165 from BS4/ VIV. All OTUs, the areas in which they were found, and the specimen numbers per OTU are shown in Appendix 1. The following are the key findings at the species/ OTU level:

- Araneae (COI): 9 OTUs, 8 unique lineages, 1 matching with external sequences,
- Palpigradi (COI): 11 OTUs, all unique lineages,
- Pseudoscorpiones (COI): 8 OTUs, all unique lineages,
- Schizomida (COI): 10 OTUs, 7 unique lineages, 3 matching with external sequences,
- Chilopoda (COI): 6 OTUs, 5 unique lineages, 1 matching with external sequences,
- Diplopoda (COI): 2 OTUs, both matching with external sequences,
- Pauropoda (COI): 14 OTUs, 13 unique lineages, 1 matching with external sequences,
- Symphyla (COI): 11 OTUs, all unique lineages,
- Entognatha – Diplura (COI): 14 OTUs, 13 unique lineages, 1 matching with external sequences,
- Isopoda (troglofaunal) (COI): 8 OTUs, 7 unique lineage, 1 matching with external sequences,
- Blattodea (COI): 8 OTUs, all unique lineages,
- Coleoptera (COI): 4 OTUs, 3 unique lineages, 1 matching with external sequences,
- Hemiptera (COI): 4 OTUs, 1 unique lineage, 3 matching with external sequences,
- Zygentoma:
    - COI: 6 OTUs, 5 unique lineages, 1 matching with external sequences,
    - 12S: 2 OTUs, both unique lineages,
- Amphipoda:
    - Melitidae (COI/ 16S): 3 OTUs, 2 unique lineages, 1 matching with external sequences,
    - Bogidiellidae (COI): 2 OTUs, both unique lineages,
    - Paramelitidae: 6 OTUs, 4 unique lineages, 2 matching external sequences,
    - Indeterminate (likely Niphargidae; COI): 1 OTU, unique lineage,
- Bathynellidae (COI): 3 OTUs, all unique lineages,
- Parabathynellidae (COI): 6 OTUs, all unique lineages,
- Isopoda (stygofauna) (COI): 2 OTUs, both unique lineages,
- Oligochaeta (COI):
    - Enchytraeidae: 7 OTUs, 5 unique lineages, 2 matching with external sequences,
    - Phreodrilidae: 6 OTUs, 5 unique lineages, 1 matching with external sequences,
    - Naididae: 1 OTU, unique lineage.

7 REFERENCES

Abrams, K. M., Huey, J. A., Hillyer, M. J., Humphreys, W. F., Didham, R. K., & Harvey, M. S. (2019). Too hot to handle: Cenozoic aridification drives multiple independent incursions of Schizomida (Hubbardiidae) into hypogean environments. *Molecular Phylogenetics and Evolution, 139*, 106532. doi:https://doi.org/10.1016/j.ympev.2019.106532

Bennelongia, Environmental Consultants. (2015). *Western Hub baseline subterranean fauna assessment*.

Biologic, Environmental Survey. (2016). *West Angelas Deposits C, D & G Subterranean Fauna Survey 2016*.

Biota, Environmental Sciences. (2009). *Turee Syncline Troglofauna Preliminary Assessment*.

Biota, Environmental Sciences. (2011). *Nammuldi - Silvergrass Troglobitic Fauna Assessment*. Unpublished report prepared for Rio Tinto Iron Ore.

Biota, Environmental Sciences. (2013). *Rio Tinto Regional Troglobitic Fauna Study*. Report prepared for Rio Tinto Iron Ore. March 2013.

Biota, Environmental Sciences. (2014). *Western Turner Syncline Section 10 Below Water Table and Satellite Ore Bodies Subterranean Fauna Survey.* Report prepared for Rio Tinto Iron Ore. December 2014.

Biota, Environmental Sciences. (2016a). *Brockman Syncline 4 Marra Mambas Subterranean Fauna Assessment*. Unpublished report prepared for Rio Tinto Iron Ore. October 2016.

Biota, Environmental Sciences. (2016b). *BS4 Marra Mambas Troglobitic Fauna Addendum Report.* Unpublished report prepared for Rio Tinto Iron Ore. September 2016.

Biota, Environmental Sciences. (2018). *Mesa H Subterranean Fauna Assessment.* Report prepared for Rio Tinto Iron Ore. February 2019.

Biota, Environmental Sciences,. (2006). *Mesa A and Robe Valley Mesas Troglobitic Fauna Survey.* Report prepared to Pilbara Iron Ltd. March 2006.

Brown, L., Finston, T., Humphreys, G., Eberhard, S., & Pinder, A. (2015). Groundwater oligochaetes show complex genetic patterns of distribution in the Pilbara region of Western Australia. *Invertebrate Systematics, 29*(5), 405-420.

Cullen, K., & Harvey, M. (2017). *Molecular systematics of subfauna from Mesa B, C, and Warramboo, Western Australia.* Unpublished report prepared for Rio Tinto. December 2017.

Cullen, K., & Harvey, M. (2018). *Molecular systematics of subfauna from Greater Paraburdoo – Final Report.* Unpublished report prepared for Rio Tinto. December 2018.

Edgecombe, G. D., Huey, J. A., Humphreys, W. F., Hillyer, M., Burger, M. A., Volschenk, E. S., *et al.* (2019). Blind scolopendrid centipedes of the genus *Cormocephalus* from subterranean habitats in Western Australia (Myriapoda: Scolopendromorpha: Scolopendridae). *Invertebrate Systematics, 3*(6), Page 807-Page 824.

Finston, T. L., Johnson, M. S., Humphreys, W. F., Eberhard, S. M., & Halse, S. A. (2007). Cryptic speciation in two widespread subterranean amphipod genera reflects historical drainage patterns in an ancient landscape. *Molecular Ecology, 16*(2), 355-365. doi:http://doi.org/10.1111/j.1365-294X.2006.03123.x

Folmer, O., Black, M. B., Hoeh, W., Lutz, R., & Vrijenhoek, R. C. (1994). DNA primers for amplification of mitochondrial cytochrome c oxidase subunit I from diverse metazoan invertebrates. *Molecular Marine Biology and Biotechnology, 3*(5), 294-299.

Hebert, P. D., Cywinska, A., Ball, S. L., & deWaard, J. R. (2003a). Biological identifications through DNA barcodes. *Proc Biol Sci, 270*(1512), 313-321.

Hebert, P. D., Ratnasingham, S., & deWaard, J. R. (2003b). Barcoding animal life: cytochrome c oxidase subunit 1 divergences among closely related species. *Proc Biol Sci, 270 Suppl 1*, S96-99.

Katoh, K., Misawa, K., Kuma, K., & Miyata, T. (2002). MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. *Nucleic Acids Res, 30*(14), 3059-3066.

Kearse, M., Moir, R., Wilson, A., Stones-Havas, S., Cheung, M., Sturrock, S.*, et al.* (2012). Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics, 28*(12), 1647-1649.

Simon, C., Frati, F., Beckenbach, A., Crespi, B., Liu, H., & Flook, P. (1994). Evolution, Weighting, and Phylogenetic Utility of Mitochondrial Gene Sequences and a Compilation of Conserved Polymerase Chain Reaction Primers. *Annals of the Entomological Society of America, 87*(6), 651-701.

Smith, G. B., Eberhard, S. M., Perina, G., & Finston, T. (2012). New species of short range endemic troglobitic silverfish (Zygentoma: Nicoletiidae) from subterranean habitats in Western Australia's semi-arid Pilbara region. *Records of the Western Australian Museum, 27*, 101-116.

Trotter, A. J., McRae, J. M., Main, D. C., & Finston, T. L. (2017). Speciation in fractured rock landforms: towards understanding the diversity of subterranean cockroaches (Dictyoptera: Nocticolidae: *Nocticola*) in Western Australia. *Zootaxa, 4250*(2), 143-170.

8 APPENDICES

Appendix 1: All Operational Taxonomic Units (OTUs) found in the Study Area and the number of sequenced specimens assigned to those OTUs.

Taxon	**OTU_Name**	**SG CCK**	**BS2 BS3**	**BS4 VIV**	**Total**
Arachnida					
Araneae	Araneae `sp. Biologic-ARAN004`			1	1
	Araneae `sp. Biologic-ARAN005`			2	2
	Gnaphosidae `sp. Biologic-ARAN006`		1		1
	Gnaphosidae `sp. Biologic-ARAN007`			1	1
	Prethopalpus `sp. Biologic-ARAN001`		1		1
	Prethopalpus `sp. Biologic-ARAN002`		1		1
	Prethopalpus `sp. Biologic-ARAN016`		1		1
	Symphytognathidae? `sp. Biologic-ARAN003`	2			2
	Theridiidae `sp. WAM-ARAN001`			4	4
Palpigradi	*Palpigradi* `sp. Biologic-PALP002`		1		1
	Palpigradi `sp. Biologic-PALP003`		2		2
	Palpigradi `sp. Biologic-PALP004`		2		2
	Palpigradi `sp. Biologic-PALP005`			1	1
	Palpigradi `sp. Biologic-PALP006`			1	1
	Palpigradi `sp. Biologic-PALP007`		1		1
	Palpigradi `sp. Biologic-PALP008`			1	1
	Palpigradi `sp. Biologic-PALP009`			1	1
	Palpigradi `sp. Biologic-PALP010`	1			1
	Palpigradi `sp. Biologic-PALP012`		1		1
	Palpigradi `sp. Biologic-PALP013`			2	2
Pseudoscorpiones	Chthoniidae `sp. Biologic-PSEU004`			4	4
	Chthoniidae `sp. Biologic-PSEU005`			1	1
	Chthoniidae `sp. Biologic-PSEU006`			3	3
	Chthoniidae `sp. Biologic-PSEU007`		1		1
	Chthoniidae `sp. Biologic-PSEU008`			1	1
	Chthoniidae `sp. Biologic-PSEU009`			2	2
	Indolpium `sp. Biologic-PSEU003`			1	1
	Olpiidae? `sp. Biologic-PSEU002`	1			1
Schizomida	*Draculoides* `sp. Biologic-SCHI010`			1	1
	Draculoides `sp. Biologic-SCHI011`			2	2
	Draculoides `sp. Biologic-SCHI012`	1			1
	Draculoides `sp. Biologic-SCHI013`	3			3
	Draculoides `sp. Biologic-SCHI014`	1			1
	Draculoides `sp. Biologic-SCHI015`	10			10
	Draculoides `sp. Biologic-SCHI016`	6			6
	Draculoides `sp. Biologic-SCHI017`			4	4
	Draculoides `sp. Biologic-SCHI018`	1			1
	Draculoides `sp. Biologic-SCHI019`			11	11
Chilopoda					
Geophilomorpha	Geophilomorpha `sp. Biologic-CHIL002`			1	1
	Geophilomorpha `sp. Biologic-CHIL007`			1	1
Scolopendromorpha	Cormocephalus `sp. A`		1		1
	Scolopendromorpha `sp. Biologic-CHIL004`		1		1
	Scolopendromorpha `sp. Biologic-CHIL005`			1	1
	Scolopendromorpha `sp. Biologic-CHIL006`			3	3
Diplopoda					
Polyxenida	Polyxenida `sp. Biologic-POLX002`		2		2

Taxon	OTU_Name	SG CCK	BS2 BS3	BS4 VIV	Total
	Polyxenida `sp. Biologic-POLX003`		5	1	6
Pauropoda					
	Pauropoda `sp. Biologic-PAUR001`			1	1
	Pauropoda `sp. Biologic-PAUR002`			1	1
	Pauropoda `sp. Biologic-PAUR003`			1	1
	Pauropoda `sp. Biologic-PAUR004`			1	1
	Pauropoda `sp. Biologic-PAUR005`		1		1
	Pauropoda `sp. Biologic-PAUR006`		1		1
	Pauropoda `sp. Biologic-PAUR007`		2		2
	Pauropoda `sp. Biologic-PAUR008`	1		1	2
	Pauropoda `sp. Biologic-PAUR009`			1	1
	Pauropoda `sp. Biologic-PAUR010`		1		1
	Pauropoda `sp. Biologic-PAUR011`			1	1
	Pauropoda `sp. Biologic-PAUR012`	1			1
	Pauropoda `sp. Biologic-PAUR013`		1		1
	Pauropoda `sp. WAM-PAUD002`	1			1
Symphyla					
Cephalostigmata	*Hanseniella* `sp. Biologic-SYMP001`		1		1
	Hanseniella `sp. Biologic-SYMP002`	1			1
	Hanseniella `sp. Biologic-SYMP003`		3		3
	Hanseniella `sp. Biologic-SYMP006`			2	2
	Hanseniella `sp. Biologic-SYMP009`	1			1
	Scolopendrellidae `sp. Biologic-SYMP008`			1	1
	Scolopendrellidae `sp. Biologic-SYMP014`			1	1
	Scutigerellidae `sp. Biologic-SYMP004`		2		2
	Scutigerellidae `sp. Biologic-SYMP005`			1	1
	Scutigerellidae `sp. Biologic-SYMP007`			4	4
	Symphyla `sp. Biologic-SYMP013`			1	1
Entognatha					
Diplura	Japygidae `sp. Biologic-DIPL008`			1	1
	Japygidae `sp. Biologic-DIPL009`			1	1
	Japygidae `sp. Biologic-DIPL010`	1			1
	Japygidae `sp. Biologic-DIPL014`			2	2
	Japygidae `sp. Biologic-DIPL015`			1	1
	Parajapygidae `sp. Biologic-DIPL006`	1			1
	Parajapygidae `sp. Biologic-DIPL007`		1		1
	Parajapygidae `sp. Biologic-DIPL012`	1			1
	Parajapygidae `sp. Biologic-DIPL018`			1	1
	Projapygidae `sp. Biologic-DIPL002`	2			2
	Projapygidae `sp. Biologic-DIPL003`			1	1
	Projapygidae `sp. Biologic-DIPL004`		1		1
	Projapygidae `sp. Biologic-DIPL005`			1	1
	Projapygidae `sp. Biologic-DIPL013`			1	1
Insecta					
Blattodea	*Nocticola* `sp. Biologic-BLAT005`			4	4
	Nocticola `sp. Biologic-BLAT006`			4	4
	Nocticola `sp. Biologic-BLAT007`		8	2	10
	Nocticola `sp. Biologic-BLAT008`		10		10
	Nocticola `sp. Biologic-BLAT009`	6			6
	Nocticola `sp. Biologic-BLAT010`	4		5	9
	Nocticola `sp. Biologic-BLAT011`	1			1
	Nocticola `sp. Biologic-BLAT012`			1	1
Coleoptera	Carabidae `sp. Biologic-COLE001`			1	1

Taxon	**OTU_Name**	**SG CCK**	**BS2 BS3**	**BS4 VIV**	**Total**
	Coleoptera `sp. Biologic-COLE002`		1		1
	Coleoptera `sp. Biologic-COLE003`			1	1
	Curculionidae `sp. Biologic-COLE004`			2	2
Hemiptera	Meenoplidae `sp. Biologic-HEMI001`	8	9	3	20
	Meenoplidae `sp. Biologic-HEMI004`			2	2
	Phaconeura `sp. WAM-PHAC001`	1	1		2
	Phaconeura `sp. WAM-PHAC002`		5	4	9
Zygentoma	Atelurinae `sp. Biologic-ZYGE008`		2	3	5
	Nicoletiidae `sp. Biologic-ZYGE002`	1			1
	Nicoletiidae? `sp. Biologic-ZYGE003`			1	1
	Nicoletiidae `sp. Biologic-ZYGE004`			1	1
	Nicoletiinae `sp. Biologic-ZYGE005`		3		3
	Nicoletiinae `sp. Biologic-ZYGE006`		1		1
	Nicoletiinae `sp. Biologic-ZYGE007`		1		1
	Nicoletiinae `sp. Biologic-ZYGE015`			2	2
Malacostraca					
Amphipoda	Amphipoda `sp. Biologic-AMPH009`			7	7
	Bogidiellidae `sp. Biologic-AMPH010`	9			9
	Bogidiellidae `sp. Biologic-AMPH011`			3	3
	Maarrka `sp. Biologic-AMPH013`	6			6
	Nedsia `sp. Biologic-AMPH003`			3	3
	Nedsia `sp. Biologic-AMPH008`	56			56
	Nedsia `sp. WAM-AMPE003`			5	5
	Paramelitidae `sp. Biologic-AMPH012`		1		1
	Paramelitidae `sp. Biologic-AMPH014`	15			15
	Paramelitidae `sp. Biologic-AMPH015`		9		9
	Paramelitidae `sp. Helix-AMP037`			6	6
	Pilbarus `sp. F`	24			24
Bathynellacea	*Atopobathynella* `sp. Biologic-PBAT006`	2			2
	Bathynellidae `sp. Biologic-BATH001`			1	1
	Bathynellidae `sp. Biologic-BATH002`			1	1
	Bathynellidae `sp. Biologic-BATH003`			6	6
	Parabathynellidae `sp. Biologic-PBAT001`	1			1
	Parabathynellidae `sp. Biologic-PBAT002`	2			2
	Parabathynellidae `sp. Biologic-PBAT003`			1	1
	Parabathynellidae `sp. Biologic-PBAT004`		4		4
	Parabathynellidae `sp. Biologic-PBAT005`		2		2
Isopoda	Armadillidae `sp. Biologic-ISOP002`			2	2
	Armadillidae `sp. Biologic-ISOP004`			1	1
	Armadillidae `sp. Biologic-ISOP008`			1	1
	Armadillidae `sp. Biologic-ISOP009`	1			1
	Buddelundia? `sp. Biologic-ISOP005`		1		1
	Buddelundia? `sp. Biologic-ISOP006`		1		1
	Isopoda `sp. Biologic-ISOP007`		1		1
	Isopoda `sp. Biologic-ISOP011`			2	2
	Philosciidae `sp. Biologic-ISOP001`	1	1		2
	Pygolabis `sp. Biologic-ISOP012`	1			1
Oligochaeta					
Tubificida	Enchytraeidae `sp. Biologic-OLIG003`			1	1
	Enchytraeidae `sp. Biologic-OLIG004`		1	2	3
	Enchytraeidae `sp. Biologic-OLIG005`	2	1	2	5
	Enchytraeidae `sp. Biologic-OLIG013`	1			1
	Enchytraeidae `sp. Biologic-OLIG016`			1	1

Taxon	OTU_Name	SG CCK	BS2 BS3	BS4 VIV	Total
	Enchytraeidae `sp. Biologic-OLIG017`		1		1
	Enchytraeidae `sp. Biologic-OLIG018`	2	1		3
	Naididae `sp. Biologic-OLIG015`	1			1
	Phreodrilidae `sp. 12`		2	4	6
	Phreodrilidae `sp. Biologic-OLIG001`			1	1
	Phreodrilidae `sp. Biologic-OLIG002`			1	1
	Phreodrilidae `sp. Biologic-OLIG011`			1	1
	Phreodrilidae `sp. Biologic-OLIG012`	1			1
	Phreodrilidae `sp. Biologic-OLIG014`	1			1
Grand total		**185**	**100**	**165**	**450**

Appendix 2: Distance matrix of Araneae sequences/ lineages included in the analysis

COI divergences (%) of Araneae (regional comparisons)	O.G.	HM19	HM15	HM17	HM16	HM20	BMR 00707	IV345	IV346	WAMT 144637	WAMT 145745	BMR 00122	BMR 00240	BMR 00248	IV272	WAMT 144200	WAMT 145789	BMR 00238	BMR 00239	BMR 01125	IV276	BMR 01117	BMR 01118	RT15	BMR 00121	BMR 01114	LI29	KD01	KD02	WAMT 144292	BMR 01123	BMR 01229	BMR 01126	BMR 01217	WAMT 144104	IV275	WAMT 144108	WAMT 144106	WAMT 144109
KJ745209_Aname mainae_OUTGROUP		18.1	20.2	19.9	19.0	19.3	22.2	21.7	22.0	27.3	26.7	24.6	22.3	22.2	22.0	23.3	26.1	26.0	26.0	25.7	26.5	24.9	25.8	24.2	21.7	21.3	25.1	22.5	21.9	23.6	23.6	23.6	23.9	23.9	23.3	23.6	23.3	23.4	23.6
HM19_M20130914HDTSRE06-04_T132665_HD_Araneae	18.1		0.5	0.7	16.9	16.9	22.7	21.7	21.5	27.4	26.5	23.9	23.6	21.7	22.4	21.5	24.3	23.2	23.2	23.4	24.8	23.9	23.6	21.7	24.1	20.3	21.2	22.0	21.7	22.9	23.6	23.6	23.6	23.6	21.7	22.4	22.2	22.4	22.7
HM15_M20130913_HD_Araneae	20.2	0.5		0.3	18.3	18.6	22.9	22.1	21.9	26.7	26.6	23.4	23.2	22.6	22.8	21.1	24.8	24.8	24.8	25.3	23.2	24.4	24.2	20.4	22.0	21.3	22.0	23.6	23.7	23.2	23.7	23.7	23.7	23.7	22.4	22.4	22.1	22.8	22.8
HM17_M20130914_HD_Araneae	19.9	0.7	0.3		18.2	18.5	22.6	21.3	21.0	27.0	26.4	22.8	22.8	22.0	22.2	20.9	24.2	24.3	24.3	24.8	23.6	24.2	24.2	20.4	22.0	21.3	21.9	23.3	23.4	23.3	23.6	23.6	23.7	23.7	22.2	22.0	21.7	22.3	22.3
HM16_M20130914_HD_Araneae	19.0	16.9	18.3	18.2		1.5	22.9	23.2	22.9	27.6	27.6	21.3	21.4	22.3	21.6	21.7	23.7	23.9	23.9	23.6	24.4	24.6	24.0	20.4	20.4	22.0	22.8	18.5	18.4	20.2	19.8	19.8	20.1	20.1	20.1	20.2	20.2	20.1	20.2
HM20_M20130914_HD_Araneae	19.3	16.9	18.6	18.5	1.5		23.6	22.7	22.5	27.4	27.5	22.0	21.9	22.9	21.3	21.7	24.2	23.7	23.7	24.8	24.7	25.1	24.9	20.4	20.8	22.5	22.9	19.3	18.8	20.5	19.8	19.8	20.1	20.1	20.5	20.7	20.7	20.4	20.5
BMR00707_HD2_Prethopalpus sp.	22.2	22.7	22.9	22.6	22.9	23.6		15.8	15.6	21.2	21.8	17.8	18.2	18.8	18.2	18.5	19.9	25.5	25.5	25.8	26.5	24.9	24.9	22.6	22.0	22.5	24.9	21.9	21.9	22.6	23.4	23.4	22.9	22.9	21.4	21.9	21.9	22.2	22.0
IV345_SSp-2010-253_DCBRC_017_ROBE_Araneae	21.7	21.7	22.1	21.3	23.2	22.7	15.8		1.4	23.0	23.6	19.9	17.7	20.1	18.2	19.4	22.0	24.6	24.6	23.4	26.9	24.3	24.6	23.2	22.2	24.6	24.3	22.2	22.5	24.6	24.6	24.6	24.6	24.6	23.9	24.3	24.3	24.8	24.8
IV346_SSp-2010-75_DCBRC_040_ROBE_Araneae	22.0	21.5	21.9	21.0	22.9	22.5	15.6	1.4		22.3	22.7	18.9	17.0	20.1	17.5	19.4	21.5	24.3	24.3	22.9	26.6	23.4	24.1	22.5	22.2	24.6	23.4	22.5	22.7	23.9	23.9	23.9	23.9	23.9	23.9	24.3	24.3	24.8	24.8
RT31_WAMT144637_MESAB_Oonopidae_Prethopalpus	27.3	27.4	26.7	27.0	27.6	27.4	21.2	23.0	22.3		1.5	23.8	23.2	25.0	24.4	23.5	25.0	29.1	29.1	29.3	28.9	26.4	28.2	26.4	25.0	26.8	28.0	26.4	26.2	27.0	27.3	27.3	27.9	27.9	27.6	28.2	28.0	28.5	28.5
RT48_WAMT145745_Prethopalpus_WAM-OONP001	26.7	26.5	26.6	26.4	27.6	27.5	21.8	23.6	22.7	1.5		24.0	23.0	24.5	24.3	23.3	24.9	29.1	29.1	29.3	29.4	26.6	28.1	26.1	25.2	26.4	27.8	26.3	26.1	27.0	27.3	27.3	27.9	27.9	27.3	27.9	27.8	28.2	28.2
BMR00122_BS3X_Araneae sp.	24.6	23.9	23.4	22.8	21.3	22.0	17.8	19.9	18.9	23.8	24.0		16.6	22.8	20.7	20.9	23.7	26.1	26.1	27.5	28.2	26.3	26.7	21.3	21.7	23.1	24.9	22.5	22.6	23.4	23.3	23.3	23.3	23.3	23.4	23.4	23.4	23.4	23.4
BMR00240_BS2SW_Araneae sp.	22.3	23.6	23.2	22.8	21.4	21.9	18.2	17.7	17.0	23.2	23.0	16.6		19.0	19.0	19.5	20.7	28.7	28.7	26.4	27.7	27.2	26.9	22.0	22.3	21.7	23.9	24.3	24.6	22.9	23.1	23.1	23.1	23.1	23.4	24.0	24.0	23.9	23.9
BMR00248_VIV_Prethopalpus sp.	22.2	21.7	22.6	22.0	22.3	22.9	18.8	20.1	20.1	25.0	24.5	22.8	19.0		14.3	14.6	14.9	26.6	26.6	26.4	27.2	26.4	25.4	23.6	22.3	23.9	24.6	22.2	22.5	23.4	23.3	23.3	23.6	23.6	22.6	23.1	23.1	23.3	23.1
IV272_MEBRC0016P1T1-2_ROBE_Araneae	22.0	22.4	22.8	22.2	21.6	21.3	18.2	18.2	17.5	24.4	24.3	20.7	19.0	14.3		14.2	16.4	25.2	25.2	25.5	25.9	24.9	25.8	25.4	23.6	23.6	23.7	22.3	21.9	23.9	23.4	23.4	23.9	23.9	24.3	24.8	24.8	24.3	24.5
RT27_WAMT144200_MESA K_Opopaea	23.3	21.5	21.1	20.9	21.7	21.7	18.5	19.4	19.4	23.5	23.3	20.9	19.5	14.6	14.2		12.2	27.2	27.2	26.1	27.5	25.9	26.6	23.3	21.0	22.9	23.7	22.0	21.4	24.2	24.1	24.1	24.5	24.5	23.7	24.1	24.2	24.4	24.4
RT48_WAMT145789_Opopaea_WAM-OONO001	26.1	24.3	24.8	24.2	23.7	24.2	19.9	22.0	21.5	25.0	24.9	23.7	20.7	14.9	16.4	12.2		29.9	29.9	28.0	29.6	28.3	27.7	25.8	24.0	24.9	24.0	24.3	23.7	26.6	26.3	26.3	26.3	26.3	26.1	26.1	26.3	26.4	26.4
BMR00238_SGW_Anapistula sp.	26.0	23.2	24.8	24.3	23.9	23.7	25.5	24.6	24.3	29.1	29.1	26.1	28.7	26.6	25.2	27.2	29.9		0.0	13.8	14.7	15.0	16.3	23.6	24.9	24.2	26.1	24.2	23.6	23.3	22.9	22.9	22.8	22.8	23.7	23.7	23.7	23.6	23.7
BMR00239_SGW_Anapistula sp.	26.0	23.2	24.8	24.3	23.9	23.7	25.5	24.6	24.3	29.1	29.1	26.1	28.7	26.6	25.2	27.2	29.9	0.0		13.8	14.7	15.0	16.3	23.6	24.9	24.2	26.1	24.2	23.6	23.3	22.9	22.9	22.8	22.8	23.7	23.7	23.7	23.6	23.7
BMR01125_VIV_Araneae	25.7	23.4	25.3	24.8	23.6	24.8	25.8	23.4	22.9	29.3	29.3	27.5	26.4	26.4	25.5	26.1	28.0	13.8	13.8		13.3	12.3	13.2	22.9	21.3	24.2	26.0	23.1	22.5	22.0	22.0	22.0	22.3	22.3	22.6	22.8	22.8	22.5	22.6
IV276_138441_ROBE_Araneae	26.5	24.8	23.2	23.6	24.4	24.7	26.5	26.9	26.6	28.9	29.4	28.2	27.7	27.2	25.9	27.5	29.6	14.7	14.7	13.3		11.8	12.8	21.8	23.7	24.2	24.5	24.2	23.9	24.1	24.4	24.4	24.4	24.4	23.2	23.6	23.6	23.2	23.4
BMR01117_BS1W_Araneae	24.9	23.9	24.4	24.2	24.6	25.1	24.9	24.3	23.4	26.4	26.6	26.3	27.2	26.4	24.9	25.9	28.3	15.0	15.0	12.3	11.8		6.8	21.3	22.3	23.9	24.0	23.6	22.9	23.4	23.4	23.4	23.6	23.6	23.7	24.2	24.2	24.6	24.8
BMR01118_BS1W_Araneae	25.8	23.6	24.2	24.2	24.0	24.9	24.9	24.6	24.1	28.2	28.1	26.7	26.9	25.4	25.8	26.6	27.7	16.3	16.3	13.2	12.8	6.8		21.1	23.3	24.2	22.6	23.3	22.9	23.7	23.6	23.6	24.6	24.6	25.2	25.4	25.4	25.2	25.4
RT15_WAMT142824__MESA H_Gnaphosidae	24.2	21.7	20.4	20.4	20.4	20.4	22.6	23.2	22.5	26.4	26.1	21.3	22.0	23.6	25.4	23.3	25.8	23.6	23.6	22.9	21.8	21.3	21.1		16.0	17.0	18.1	19.1	19.3	18.2	18.5	18.5	18.2	18.2	18.5	19.0	19.0	19.1	19.1
BMR00121_BS2SW_Araneae sp.	21.7	24.1	22.0	22.0	20.4	20.8	22.0	22.2	22.2	25.0	25.2	21.7	22.3	22.3	23.6	21.0	24.0	24.9	24.9	21.3	23.7	22.3	23.3	16.0		12.8	16.6	17.5	17.6	16.7	16.9	16.9	17.0	17.0	16.4	16.4	16.4	16.4	16.4
BMR01114_VIV_Araneae	21.3	20.3	21.3	21.3	22.0	22.5	22.5	24.6	24.6	26.8	26.4	23.1	21.7	23.9	23.6	22.9	24.9	24.2	24.2	24.2	24.2	23.9	24.2	17.0	12.8		14.3	18.7	18.5	17.3	17.5	17.5	17.3	17.3	15.8	16.4	16.4	16.3	16.3
LI29_RC16MEC0177-20170309-01_ROBE_Gnaphosidae	25.1	21.2	22.0	21.9	22.8	22.9	24.9	24.3	23.4	28.0	27.8	24.9	23.9	24.6	23.7	23.7	24.0	26.1	26.1	26.0	24.5	24.0	22.6	18.1	16.6	14.3		19.5	19.5	17.9	18.1	18.1	18.4	18.4	19.1	19.5	19.5	19.5	19.5
KD01_GR15MEB0014.20160915.T1-01_ROBE_Aeaneae	22.5	22.0	23.6	23.3	18.5	19.3	21.9	22.2	22.5	26.4	26.3	22.5	24.3	22.2	22.3	22.0	24.3	24.2	24.2	23.1	24.2	23.6	23.3	19.1	17.5	18.7	19.5		0.9	15.3	15.2	15.2	15.3	15.3	17.0	16.6	16.6	16.3	16.4
KD02_RC15MEC0001.20160915.T1-01_ROBE_Araneae	21.9	21.7	23.7	23.4	18.4	18.8	21.9	22.5	22.7	26.2	26.1	22.6	24.6	22.5	21.9	21.4	23.7	23.6	23.6	22.5	23.9	22.9	22.9	19.3	17.6	18.5	19.5	0.9		15.3	15.2	15.2	15.3	15.3	16.7	16.6	16.6	16.3	16.4
RT43_WAMT144292_WAM-ARAN001	23.6	22.9	23.2	23.3	20.2	20.5	22.6	24.6	23.9	27.0	27.0	23.4	22.9	23.4	23.9	24.2	26.6	23.3	23.3	22.0	24.1	23.4	23.7	18.2	16.7	17.3	17.9	15.3	15.3		1.4	1.4	2.0	2.0	10.3	10.2	10.2	10.3	10.5
BMR01123_BS1E_Araneae	23.6	23.6	23.7	23.6	19.8	19.8	23.4	24.6	23.9	27.3	27.3	23.3	23.1	23.3	23.4	24.1	26.3	22.9	22.9	22.0	24.4	23.4	23.6	18.5	16.9	17.5	18.1	15.2	15.2	1.4		0.0	1.8	1.8	10.3	10.2	10.2	10.3	10.5
BMR01229_BS1E_Araneae	23.6	23.6	23.7	23.6	19.8	19.8	23.4	24.6	23.9	27.3	27.3	23.3	23.1	23.3	23.4	24.1	26.3	22.9	22.9	22.0	24.4	23.4	23.6	18.5	16.9	17.5	18.1	15.2	15.2	1.4	0.0		1.8	1.8	10.3	10.2	10.2	10.3	10.5
BMR01126_VIV_Araneae	23.9	23.6	23.7	23.7	20.1	20.1	22.9	24.6	23.9	27.9	27.9	23.3	23.1	23.6	23.9	24.5	26.3	22.8	22.8	22.3	24.4	23.6	24.6	18.2	17.0	17.3	18.4	15.3	15.3	2.0	1.8	1.8		0.0	10.5	10.3	10.3	10.5	10.6
BMR01217_BGCK_Araneae	23.9	23.6	23.7	23.7	20.1	20.1	22.9	24.6	23.9	27.9	27.9	23.3	23.1	23.6	23.9	24.5	26.3	22.8	22.8	22.3	24.4	23.6	24.6	18.2	17.0	17.3	18.4	15.3	15.3	2.0	1.8	1.8	0.0		10.5	10.3	10.3	10.5	10.6
RT24_WAMT144104__MESA B_Araneae	23.3	21.7	22.4	22.2	20.1	20.5	21.4	23.9	23.9	27.6	27.3	23.4	23.4	22.6	24.3	23.7	26.1	23.7	23.7	22.6	23.2	23.7	25.2	18.5	16.4	15.8	19.1	17.0	16.7	10.3	10.3	10.3	10.5	10.5		1.2	1.2	2.0	1.8
IV275_127039_ROBE_Araneae	23.6	22.4	22.4	22.0	20.2	20.7	21.9	24.3	24.3	28.2	27.9	23.4	24.0	23.1	24.8	24.1	26.1	23.7	23.7	22.8	23.6	24.2	25.4	19.0	16.4	16.4	19.5	16.6	16.6	10.2	10.2	10.2	10.3	10.3	1.2		0.3	1.4	1.2
RT24_WAMT144108_RC14COB0024__WARR_Araneae	23.3	22.2	22.1	21.7	20.2	20.7	21.9	24.3	24.3	28.0	27.8	23.4	24.0	23.1	24.8	24.2	26.3	23.7	23.7	22.8	23.6	24.2	25.4	19.0	16.4	16.4	19.5	16.6	16.6	10.2	10.2	10.2	10.3	10.3	1.2	0.3		1.4	1.2
RT24_WAMT144106_RC16COB0014__WARR_Araneae	23.4	22.4	22.8	22.3	20.1	20.4	22.2	24.8	24.8	28.5	28.2	23.4	23.9	23.3	24.3	24.4	26.4	23.6	23.6	22.5	23.2	24.6	25.2	19.1	16.4	16.3	19.5	16.3	16.3	10.3	10.3	10.3	10.5	10.5	2.0	1.4	1.4		0.2
RT24_WAMT144109_RC14COB0024__WARR_Araneae	23.6	22.7	22.8	22.3	20.2	20.5	22.0	24.8	24.8	28.5	28.2	23.4	23.9	23.1	24.5	24.4	26.4	23.7	23.7	22.6	23.4	24.8	25.4	19.1	16.4	16.3	19.5	16.4	16.4	10.5	10.5	10.5	10.6	10.6	1.8	1.2	1.2	0.2	

Appendix 3: Distance matrix of *Palpigradi* sequences/ lineages included in the analysis

COI divergence (%) of Palpigradi (regional comparisons)	O.G.	KF823876	JN018214	KF823879	KF823878	KF823880	T149280	BMR 00085	BMR 00172	BMR 00168	T149404	BMR 00521	BMR 00084	BMR 00499	BMR 00251	BMR 00093	BMR 01221	BMR 00094	BMR 00092	BMR 00091	WAMT 145439	WAMT 145442
KF823874_Prokoenenia wheeleri_OUTGROUP		26.9	26.6	29.7	28.7	26.9	26.6	32.4	28.0	30.1	25.2	26.5	26.1	26.5	25.8	35.7	36.4	36.4	36.4	36.5	31.8	31.8
KF823876_Eukoenenia mirabilis	26.9		25.5	28.5	25.2	28.4	29.8	32.7	31.0	32.9	27.2	28.4	30.0	29.5	30.3	31.2	32.4	32.4	33.5	33.9	31.2	32.0
JN018214_Palpigradi sp. 2	26.6	25.5		28.2	21.1	24.5	28.4	29.9	27.0	27.8	26.0	26.4	29.2	27.8	27.3	28.2	29.0	29.0	30.8	31.1	25.8	27.4
KF823879_Eukoenenia sp. MCZ IZ-19350	29.7	28.5	28.2		26.2	27.0	29.3	31.4	30.2	30.8	28.7	28.1	28.2	31.0	30.4	31.5	31.4	31.6	31.1	31.0	30.8	29.9
KF823878_Eukoenenia spelaea	28.7	25.2	21.1	26.2		19.0	27.2	25.8	24.8	23.5	26.5	26.6	30.1	30.3	30.3	24.1	23.4	23.5	25.5	24.6	24.0	26.6
KF823880_Eukoenenia sp. MCZ IZ-134549	26.9	28.4	24.5	27.0	19.0		24.5	25.4	22.5	24.5	28.3	27.4	27.2	28.9	27.8	25.2	25.4	25.5	23.7	23.9	24.6	27.4
T149280_VIV_Palpigradi	26.6	29.8	28.4	29.3	27.2	24.5		25.2	19.4	22.3	24.6	24.7	21.2	23.8	22.6	29.5	29.6	29.3	30.7	30.4	26.7	28.2
BMR00085_SGW_Palpigradi sp.	32.4	32.7	29.9	31.4	25.8	25.4	25.2		24.1	22.4	29.8	27.9	28.4	30.2	29.3	29.8	27.0	27.0	28.4	27.2	26.4	28.1
BMR00172_BS2W_Palpigradi sp.	28.0	31.0	27.0	30.2	24.8	22.5	19.4	24.1		15.7	24.9	24.6	22.9	23.8	23.4	28.9	28.4	28.4	29.6	28.2	26.6	26.4
BMR00168_DSM_Palpigradi sp.	30.1	32.9	27.8	30.8	23.5	24.5	22.3	22.4	15.7		26.1	24.6	24.3	25.6	24.9	28.6	29.5	29.5	30.7	30.2	26.7	29.3
T149404_BS1W_Palpigradi	25.2	27.2	26.0	28.7	26.5	28.3	24.6	29.8	24.9	26.1		10.1	22.9	22.6	22.3	31.8	31.8	31.8	32.5	32.2	27.8	31.0
BMR00521_VIV_Palpigradi sp.	26.5	28.4	26.4	28.1	26.6	27.4	24.7	27.9	24.6	24.6	10.1		21.4	24.3	22.3	31.2	30.7	30.7	31.3	30.2	27.0	30.2
BMR00084_BS3_Palpigradi sp.	26.1	30.0	29.2	28.2	30.1	27.2	21.2	28.4	22.9	24.3	22.9	21.4		14.8	13.3	33.5	33.4	33.3	34.0	33.1	29.0	29.9
BMR00499_VIV_Palpigradi sp.	26.5	29.5	27.8	31.0	30.3	28.9	23.8	30.2	23.8	25.6	22.6	24.3	14.8		7.2	34.9	35.1	35.1	35.7	34.8	30.2	32.1
BMR00251_VIV_Palpigradi sp.	25.8	30.3	27.3	30.4	30.3	27.8	22.6	29.3	23.4	24.9	22.3	22.3	13.3	7.2		34.6	34.7	34.5	35.7	35.1	29.9	30.5
BMR00093_LNSG_Palpigradi sp.	35.7	31.2	28.2	31.5	24.1	25.2	29.5	29.8	28.9	28.6	31.8	31.2	33.5	34.9	34.6		15.9	15.6	17.0	16.4	28.3	27.2
BMR01221_BS2_3_Palpigradi sp.	36.4	32.4	29.0	31.4	23.4	25.4	29.6	27.0	28.4	29.5	31.8	30.7	33.4	35.1	34.7	15.9		0.6	11.1	10.2	24.6	26.3
BMR00094_BS3X_Palpigradi sp.	36.4	32.4	29.0	31.6	23.5	25.5	29.3	27.0	28.4	29.5	31.8	30.7	33.3	35.1	34.5	15.6	0.6		10.8	10.2	24.6	26.4
BMR00092_DSM_Palpigradi sp.	36.4	33.5	30.8	31.1	25.5	23.7	30.7	28.4	29.6	30.7	32.5	31.3	34.0	35.7	35.7	17.0	11.1	10.8		6.9	27.6	28.5
BMR00091_BS3X_Palpigradi sp.	36.5	33.9	31.1	31.0	24.6	23.9	30.4	27.2	28.2	30.2	32.2	30.2	33.1	34.8	35.1	16.4	10.2	10.2	6.9		27.0	27.3
RT43_PARA_WAMT145439_Eukoenenia_WAM-PALE002	31.8	31.2	25.8	30.8	24.0	24.6	26.7	26.4	26.6	26.7	27.8	27.0	29.0	30.2	29.9	28.3	24.6	24.6	27.6	27.0		24.3
RT43_PARA_WAMT145442_Eukoenenia_WAM-PALE001	31.8	32.0	27.4	29.9	26.6	27.4	28.2	28.1	26.4	29.3	31.0	30.2	29.9	32.1	30.5	27.2	26.3	26.4	28.5	27.3	24.3	

Appendix 4: Distance matrix of Pseudoscorpiones sequences/ lineages included in the analysis

COI divergences (%) of Pseudoscorpiones (regional comparisons)	O.G.	WAMT 145899	EU55 9546	EU55 9545	BMR 00228	T149 297	WAMT 146282	WAMT 144138	WAMT 144689	JC05	WAMT 145889	WAMT 144193	WAMT 145851	KJ65 9961	WAMT 146605	T149 298	T149 397	T149 396	T149 398	BMR 00779	KR01	JV08	LI35	KJ65 9956	WAMT 146294	WAMT 144137	WAMT 144686	T149 291	T149 395	T149 299	T149 296	T149 295	T149 293	T149 290	T149 292
AY156582_Pandinus imperator_OUTGROUP		33.8	30.7	31.3	30.9	33.3	30.4	30.2	32.9	35.4	29.6	30.9	35.0	32.3	32.2	30.2	29.9	29.5	29.5	32.2	32.1	33.9	33.7	31.0	31.9	30.4	33.1	31.9	31.6	31.6	31.8	32.4	31.6	33.9	34.5
RT48_WAMT145899_Oratemnus_WAM-ORAT002A	33.8		28.6	28.2	28.8	30.5	26.3	25.6	26.2	22.8	24.3	28.3	30.3	27.4	28.9	27.7	28.5	28.8	28.8	28.2	26.4	30.1	29.3	27.3	29.0	28.2	29.1	27.4	28.0	28.0	28.2	28.2	30.2	29.7	30.0
EU559546_Euryolpium sp. JM-2008 (Olpiidae)	30.7	28.6		22.4	22.9	24.3	26.0	26.1	28.7	30.2	22.3	27.6	28.5	28.6	29.3	27.4	27.2	27.7	27.7	27.1	26.4	30.4	29.0	28.5	29.9	27.5	27.5	29.5	28.0	27.8	27.8	29.3	29.0	29.5	28.6
EU559545_Beierolpium bornemisszai (Olpiidae)	31.3	28.2	22.4		20.2	21.3	26.7	26.0	27.5	29.2	24.3	26.9	27.3	28.6	26.7	26.0	25.8	26.0	26.0	26.4	28.0	28.4	25.8	25.0	26.1	25.8	26.4	26.3	26.6	26.7	26.7	28.4	28.4	27.2	26.9
BMR00228_HSTD_Pseudoscorpiones sp.	30.9	28.8	22.9	20.2		10.8	27.2	27.2	29.4	29.9	25.0	29.3	27.6	29.6	30.4	28.9	28.6	28.7	28.7	29.0	27.1	30.1	29.6	29.0	28.6	30.1	29.8	28.7	29.9	29.9	29.9	31.3	31.6	31.2	31.9
BMR01113_BS1E_Pseudoscorpiones	33.3	30.5	24.3	21.3	10.8		26.0	25.4	29.7	30.5	24.9	28.0	29.3	30.8	30.1	29.2	29.3	29.3	29.3	29.5	27.8	31.0	31.2	30.4	29.6	29.3	29.6	26.7	29.6	29.6	29.6	31.2	31.0	30.9	31.3
RT53_WAMT146282_Ideoblothrus_pisolitus	30.4	26.3	26.0	26.7	27.2	26.0		9.7	13.1	29.8	22.8	23.4	25.2	23.9	27.7	25.8	25.5	25.8	25.8	27.2	24.2	26.0	26.3	26.3	28.1	25.2	28.3	27.2	27.1	27.1	27.1	28.1	28.7	28.3	29.5
RT24_WAMT144138_GR15MEC0001_Ideoblothrus_WAM-IDEO004	30.2	25.6	26.1	26.0	27.2	25.4	9.7		6.8	27.4	23.4	23.8	26.3	26.6	24.9	26.0	25.8	26.3	26.3	23.4	21.6	24.7	24.1	28.5	26.7	22.9	25.6	26.0	25.6	25.8	25.8	26.3	27.4	26.7	26.9
RT31_WAMT144689_MEBRC0025_Ideoblothrus_004	32.9	26.2	28.7	27.5	29.4	29.7	13.1	6.8		29.2	25.5	23.6	28.5	26.6	28.7	27.5	27.0	27.3	27.3	28.0	27.0	27.6	27.6	29.3	29.5	27.5	29.5	28.6	29.1	29.1	29.2	30.4	31.2	29.1	29.6
JC05_T138609_BROCK3_Chernetidae `sp. Helix marra mamba`	35.4	22.8	30.2	29.2	29.9	30.5	29.8	27.4	29.2		26.1	32.2	30.4	28.6	28.1	27.5	27.5	27.7	27.7	29.6	28.2	27.4	29.4	29.4	30.6	29.8	30.2	31.0	29.6	29.6	29.6	30.1	31.5	29.8	28.9
RT48_WAMT145889_Olpiidae_WAM-OLPI001	29.6	24.3	22.3	24.3	25.0	24.9	22.8	23.4	25.5	26.1		27.8	28.8	24.9	26.3	24.3	23.9	24.3	24.3	26.7	25.1	27.9	27.0	25.9	25.1	24.9	27.1	26.3	27.4	27.4	27.4	27.5	27.7	25.7	26.1
RT24_WAMT144193_RC15MEC0008_Indohya_WAM_`PSE113`	30.9	28.3	27.6	26.9	29.3	28.0	23.4	23.8	23.6	32.2	27.8		18.5	26.1	25.6	26.9	26.3	26.9	26.9	26.7	25.6	28.2	26.1	25.3	26.3	26.3	28.0	27.8	25.4	25.2	25.2	26.3	26.0	27.2	27.1
RT48_WAMT145851_Indohya_WAM-INDH002	35.0	30.3	28.5	27.3	27.6	29.3	25.2	26.3	28.5	30.4	28.8	18.5		24.1	27.1	26.7	27.2	27.1	27.1	27.7	25.7	28.5	27.6	25.3	28.1	29.9	29.8	29.3	27.8	27.7	27.7	28.3	29.3	28.0	29.0
KJ659961_Lagynochthonius exiguus	32.3	27.4	28.6	28.6	29.6	30.8	23.9	26.6	26.6	28.6	24.9	26.1	24.1		18.9	18.9	18.9	18.9	18.9	20.4	21.4	25.9	19.2	18.7	18.4	18.7	20.9	19.7	18.9	18.7	18.7	20.6	21.1	17.2	19.7
RT56_WAMT146605_Tyrannochthonius_WAM-CHTH002	32.2	28.9	29.3	26.7	30.4	30.1	27.7	24.9	28.7	28.1	26.3	25.6	27.1	18.9		19.3	18.7	19.0	19.0	19.3	19.7	20.4	19.8	20.1	18.5	19.2	20.9	22.6	18.4	18.4	18.5	21.0	20.7	17.8	18.5
BMR01116_BS1E_Pseudoscorpiones	30.2	27.7	27.4	26.0	28.9	29.2	25.8	26.0	27.5	27.5	24.3	26.9	26.7	18.9	19.3		2.6	2.7	2.7	19.9	17.0	22.9	19.8	18.5	18.4	19.1	21.6	19.1	18.2	17.9	17.9	18.5	21.1	19.1	19.3
BMR00518_BS1E_Chthoniidae	29.9	28.5	27.2	25.8	28.6	29.3	25.5	25.8	27.0	27.5	23.9	26.3	27.2	18.9	18.7	2.6		0.5	0.5	19.0	17.3	22.3	20.2	18.9	17.6	18.5	20.5	18.7	17.9	17.6	17.6	18.1	20.4	18.4	18.7
BMR00577_BS1E_Chthoniidae	29.5	28.8	27.7	26.0	28.7	29.3	25.8	26.3	27.3	27.7	24.3	26.9	27.1	18.9	19.0	2.7	0.5		0.0	19.1	17.8	22.5	20.7	19.5	17.5	18.9	21.0	19.1	18.4	18.1	18.1	18.5	20.7	18.8	19.1
BMR00519_BS1E_Pseudoscorpiones	29.5	28.8	27.7	26.0	28.7	29.3	25.8	26.3	27.3	27.7	24.3	26.9	27.1	18.9	19.0	2.7	0.5	0.0		19.1	17.8	22.5	20.7	19.5	17.5	18.9	21.0	19.1	18.4	18.1	18.1	18.5	20.7	18.8	19.1
BMR00779_ LN35130 Pseudoscorpion HopeDowns (reversed)	32.2	28.2	27.1	26.4	29.0	29.5	27.2	23.4	28.0	29.6	26.7	26.7	27.7	20.4	19.3	19.9	19.0	19.1	19.1		15.2	22.3	18.2	19.1	18.7	19.5	21.0	20.2	19.9	19.9	19.9	20.5	20.8	18.7	19.0
KR01_RC12KOOD1374.20170117_KOOD_Chthoniidae `sp. Helix-PC056`	32.1	26.4	26.4	28.0	27.1	27.8	24.2	21.6	27.0	28.2	25.1	25.6	25.7	21.4	19.7	17.0	17.3	17.8	17.8	15.2		20.9	18.9	21.1	20.8	21.1	21.0	20.1	20.2	20.2	20.2	20.7	21.6	19.3	20.5
JV08_DD15BS40010-20160608_BROCK4_Chthoniidae `sp. Helix marra mamba`	33.9	30.1	30.4	28.4	30.1	31.0	26.0	24.7	27.6	27.4	27.9	28.2	28.5	25.9	20.4	22.9	22.3	22.5	22.5	22.3	20.9		19.0	22.8	19.6	21.8	22.1	23.3	23.7	23.7	23.7	24.2	22.0	22.3	23.3
LI35_RC16MEK0002-20170321_ROBE_Chthoniidae `sp. Helix-PC059`	33.7	29.3	29.0	25.8	29.6	31.2	26.3	24.1	27.6	29.4	27.0	26.1	27.6	19.2	19.8	19.8	20.2	20.7	20.7	18.2	18.9	19.0		19.7	19.8	20.8	21.5	22.6	21.9	21.7	21.7	20.7	21.6	20.2	21.0
KJ659956_Lagynochthonius australicus	31.0	27.3	28.5	25.0	29.0	30.4	26.3	28.5	29.3	29.4	25.9	25.3	25.3	18.7	20.1	18.5	18.9	19.5	19.5	19.1	21.1	22.8	19.7		15.8	15.2	19.5	21.6	19.1	19.3	19.3	20.1	19.7	20.3	21.1
RT53_WAMT146294_Tyrannochthonius_Helix_PC051	31.9	29.0	29.9	26.1	28.6	29.6	28.1	26.7	29.5	30.6	25.1	26.3	28.1	18.4	18.5	18.4	17.6	17.5	17.5	18.7	20.8	19.6	19.8	15.8		15.9	16.6	20.7	19.8	19.8	19.9	19.9	19.1	19.8	20.4
RT24_WAMT144137_GR15MEB008_Tyrannochthonius_basme	30.4	28.2	27.5	25.8	30.1	29.3	25.2	22.9	27.5	29.8	24.9	26.3	29.9	18.7	19.2	19.1	18.5	18.9	18.9	19.5	21.1	21.8	20.8	15.2	15.9		10.8	19.4	20.2	20.3	20.3	20.6	19.8	18.8	18.9
RT31_WAMT144686_GR15MEB0020_Tyrannochthonius_WAM-CHTH003	33.1	29.1	27.5	26.4	29.8	29.6	28.3	25.6	29.5	30.2	27.1	28.0	29.8	20.9	20.9	21.6	20.5	21.0	21.0	21.0	21.0	22.1	21.5	19.5	16.6	10.8		19.6	21.9	21.7	21.7	21.4	18.7	19.3	19.1
BMR01101_VIV_Pseudoscorpiones	31.9	27.4	29.5	26.3	28.7	26.7	27.2	26.0	28.6	31.0	26.3	27.8	29.3	19.7	22.6	19.1	18.7	19.1	19.1	20.2	20.1	23.3	22.6	21.6	20.7	19.4	19.6		17.3	17.5	17.6	20.8	19.5	18.7	18.7
BMR00520_BS1E_Chthoniidae	31.6	28.0	28.0	26.6	29.9	29.6	27.1	25.6	29.1	29.6	27.4	25.4	27.8	18.9	18.4	18.2	17.9	18.4	18.4	19.9	20.2	23.7	21.9	19.1	19.8	20.2	21.9	17.3		0.3	0.5	19.6	19.3	19.8	19.1
BMR01127_BS1E_Pseudoscorpiones	31.6	28.0	27.8	26.7	29.9	29.6	27.1	25.8	29.1	29.6	27.4	25.2	27.7	18.7	18.4	17.9	17.6	18.1	18.1	19.9	20.2	23.7	21.7	19.3	19.8	20.3	21.7	17.5	0.3		0.2	19.6	19.3	19.8	19.1
BMR01112_BS1E_Pseudoscorpiones	31.8	28.2	27.8	26.7	29.9	29.6	27.1	25.8	29.2	29.6	27.4	25.2	27.7	18.7	18.5	17.9	17.6	18.1	18.1	19.9	20.2	23.7	21.7	19.3	19.9	20.3	21.7	17.6	0.5	0.2		19.8	19.3	19.8	19.1
BMR00220_BS3_Pseudoscorpiones sp.	32.4	28.2	29.3	28.4	31.3	31.2	28.1	26.3	30.4	30.1	27.5	26.3	28.3	20.6	21.0	18.5	18.1	18.5	18.5	20.5	20.7	24.2	20.7	20.1	19.9	20.6	21.4	20.8	19.6	19.6	19.8		18.5	17.9	18.2
BMR01109_VIV_Chthoniidae	31.6	30.2	29.0	28.4	31.6	31.0	28.7	27.4	31.2	31.5	27.7	26.0	29.3	21.1	20.7	21.1	20.4	20.7	20.7	20.8	21.6	22.0	21.6	19.7	19.1	19.8	18.7	19.5	19.3	19.3	19.3	18.5		16.0	16.4
BMR01100_VIV_Pseudoscorpiones	33.9	29.7	29.5	27.2	31.2	30.9	28.3	26.7	29.1	29.8	25.7	27.2	28.0	17.2	17.8	19.1	18.4	18.8	18.8	18.7	19.3	22.3	20.2	20.3	19.8	18.8	19.3	18.7	19.8	19.8	19.8	17.9	16.0		5.3
BMR01104_VIV_Pseudoscorpiones	34.5	30.0	28.6	26.9	31.9	31.3	29.5	26.9	29.6	28.9	26.1	27.1	29.0	19.7	18.5	19.3	18.7	19.1	19.1	19.0	20.5	23.3	21.0	21.1	20.4	18.9	19.1	18.7	19.1	19.1	19.1	18.2	16.4	5.3	

Appendix 5: Distance matrix of Schizomida sequences/ lineages included in the analysis

COI divergences (%) of Schizomida (regional comparisons)	O.G.	GO90	BMR0 0588	IC5	JF50	IV07	S2	T149 334	IV16	MN02 0258	T149 319	T149 402	T149 305	T149 304	T149 322	T149 317	T149 312	T149 313	T149 306	T149 309	T149 302	T149 310	P9	T149 300	T149 303	T149 320	T149 301	T149 314	T149 311	P10	T149 316	T149 329	T149 307	S9	T149 315	T149 321	CM38	DN2	T149 401	T149 405	T149 330	T149 331	T149 308	S7	MN01 9980	FH19	T149 403	T149 333	T149 324	T149 325	T149 326	T149 327	T149 328	T149 332	T149 399	T149 400	FH20	T149 323	T925 16B	JC06	JV14	JV11	MN01 9976	S3
KY295230_Nephila edulis_OUTGROUP		23.3	23.6	23.4	26.0	25.0	27.1	26.1	25.6	25.8	26.6	24.5	26.4	27.1	25.8	26.0	25.4	25.5	25.4	25.4	25.4	25.7	25.7	25.4	25.5	25.7	25.7	25.5	25.7	26.2	25.8	26.1	25.8	26.0	26.0	26.0	25.7	24.5	26.6	26.6	28.3	28.3	26.9	43.8	25.2	24.9	24.8	24.9	24.9	24.9	24.9	24.9	24.9	24.9	24.9	24.9	25.2	25.5	28.3	25.1	25.0	25.0	28.4	26.4
GO90_RC13YBR0038_WEELI_Draculoides_sp Helix-WWS1	23.3		12.5	12.3	13.5	14.2	13.7	15.0	15.6	15.5	15.3	15.1	14.3	14.9	15.3	15.5	16.3	15.3	15.3	15.3	15.3	15.3	15.2	15.3	15.5	15.3	15.0	15.0	14.1	16.3	16.3	16.6	16.4	15.9	16.3	16.3	13.2	12.9	14.7	14.7	16.1	16.1	13.4	31.9	15.3	14.3	14.3	14.9	14.7	14.7	14.7	14.7	14.7	14.7	14.7	14.7	14.3	15.0	14.2	13.0	14.4	15.0	15.2	13.1
BMR00588 _Shizomida_Hope Downs	23.6	12.5		1.8	14.7	16.3	15.9	16.4	17.2	16.7	17.0	15.6	17.9	16.9	17.6	17.6	18.1	17.6	17.8	17.8	17.8	17.9	17.7	17.3	17.5	17.3	17.8	17.6	17.9	19.2	19.1	19.3	19.5	19.3	19.3	19.3	14.1	13.6	15.5	15.5	15.8	15.8	15.8	33.6	16.0	18.4	16.9	17.5	17.3	17.3	17.3	17.3	17.3	17.3	17.3	17.3	17.8	17.0	18.1	17.4	18.0	18.2	16.7	17.3
IC5_RC13HD10298_HOPE_Draculoides `sp. WAM-SCH068-DNA`	23.4	12.3	1.8		14.3	16.1	16.2	15.7	17.8	18.0	16.5	15.3	18.3	16.9	18.3	18.3	18.5	17.8	18.1	18.1	18.1	18.3	18.0	17.7	17.8	17.7	18.1	18.0	18.1	19.3	19.1	19.1	19.3	19.1	19.3	19.3	14.2	13.5	15.6	15.6	15.7	15.7	15.9	29.7	15.4	18.4	17.5	18.1	18.0	18.0	18.0	18.0	18.0	18.0	18.0	18.0	18.2	17.7	18.3	17.3	18.1	18.3	17.3	16.6
JF50_RC12MEH0221_ROBE_Hubbardiidae `sp. Helix-SCH015/SCH016`	26.0	13.5	14.7	14.3		12.6	13.9	13.5	17.0	16.6	16.6	16.5	15.0	15.2	14.7	15.0	15.3	15.6	16.1	16.1	16.1	16.3	16.3	15.8	16.0	16.1	15.8	15.8	15.2	17.3	16.7	16.6	16.6	16.8	16.7	16.7	13.0	13.0	13.0	13.1	14.2	14.2	14.6	28.3	17.4	15.6	15.3	15.6	15.6	15.6	15.6	15.6	15.6	15.6	15.6	15.6	15.5	16.1	16.7	14.9	15.3	15.4	15.2	14.7
IV07_Budgie20150604-06_ROBE_Schizomida	25.0	14.2	16.3	16.1	12.6		12.8	13.3	14.7	14.9	13.9	13.6	16.0	16.4	17.5	17.5	16.0	16.6	16.4	16.4	16.4	16.6	16.5	16.3	16.1	16.3	16.7	16.6	15.6	17.7	17.4	17.5	17.7	17.1	17.5	17.5	13.7	14.3	12.8	12.8	13.6	13.6	13.9	27.7	14.7	12.6	13.1	13.5	13.3	13.3	13.3	13.3	13.3	13.3	13.3	13.3	11.8	13.0	13.8	13.0	12.1	13.0	13.1	14.4
S2_RHWRC0249T2-3_T102810_CGB_Draculoides `sp. Helix-B`	27.1	13.7	15.9	16.2	13.9	12.8		14.2	15.0	15.9	14.4	13.9	14.8	15.9	15.7	15.5	15.0	15.5	15.7	15.7	15.7	15.5	15.3	15.1	15.3	15.5	15.5	15.3	13.4	15.6	15.5	15.5	15.9	15.7	15.7	15.7	13.0	14.0	13.0	13.0	14.0	14.0	13.0	11.7	14.6	12.5	12.5	13.2	13.0	13.0	13.0	13.0	13.0	13.0	13.0	13.0	12.5	13.6	13.6	13.3	13.1	13.5	13.2	14.9
BMR01115_VIV_Schizomida	26.1	15.0	16.4	15.7	13.5	13.3	14.2		17.2	15.8	13.8	13.2	16.4	16.4	16.9	17.3	16.1	15.3	16.1	16.1	16.1	16.0	15.5	15.2	15.3	15.5	15.7	15.5	15.8	17.1	16.9	17.5	17.5	17.0	17.0	17.0	15.5	13.6	12.9	13.1	13.1	13.1	13.4	33.0	16.3	14.4	14.1	14.1	14.1	14.1	14.1	14.1	14.1	14.1	14.1	14.1	13.8	14.4	16.4	16.0	15.5	14.9	12.9	12.9
IV16_DD14MRR007-20150808-T2-01_ROBE_Schizomida	25.6	15.6	17.2	17.8	17.0	14.7	15.0	17.2		0.0	15.7	16.8	15.3	15.9	16.7	16.9	16.3	16.3	16.1	16.1	16.1	15.9	15.9	15.9	16.1	16.3	16.3	16.1	15.1	16.0	16.1	16.3	16.3	16.0	16.3	16.3	16.8	16.8	17.6	17.8	19.6	19.6	18.2	16.2	17.2	14.0	16.5	17.1	16.9	16.9	16.9	16.9	16.9	16.9	16.9	16.9	14.1	16.7	14.5	13.3	13.7	13.1	15.3	16.0
MN020258_West Pilbara_Draculoides sp. sp. SCH060	25.8	15.5	16.7	18.0	16.6	14.9	15.9	15.8	0.0		15.3	16.2	14.9	14.7	15.2	15.3	15.2	15.7	15.8	15.8	15.8	15.7	15.7	15.3	15.5	15.7	15.8	15.7	14.6	15.6	15.7	16.0	16.0	15.8	15.8	15.8	16.0	18.5	16.4	16.6	17.9	17.9	16.6	35.1	17.2	15.0	15.7	16.0	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.0	16.0	16.4	15.4	15.7	15.1	14.4	16.0
BMR01102_VIV_Schizomida	26.6	15.3	17.0	16.5	16.6	13.9	14.4	13.8	15.7	15.3		5.4	16.3	17.9	17.6	18.1	17.5	17.6	17.6	17.6	17.6	17.6	17.7	17.3	17.5	17.6	17.8	17.6	17.6	17.6	16.9	16.9	16.6	17.0	17.0	17.0	15.5	15.8	14.4	14.4	14.6	14.6	16.3	32.8	16.6	14.6	14.9	15.3	15.3	15.3	15.3	15.3	15.3	15.3	15.3	15.3	14.4	15.2	18.4	14.8	15.7	16.3	14.9	15.8
BMR00639_VIV_Schizomida	24.5	15.1	15.6	15.3	16.5	13.6	13.9	13.2	16.8	16.2	5.4		15.7	17.2	16.8	17.4	16.9	16.3	16.2	16.2	16.2	16.2	16.4	16.0	16.2	16.3	16.5	16.3	16.3	16.7	16.3	16.6	16.3	16.5	16.5	16.5	15.3	15.9	15.0	15.0	15.4	15.4	16.0	33.1	15.1	14.5	14.7	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.8	14.1	15.1	18.7	15.7	15.4	16.0	15.0	16.0
BMR01098_HSTD_Schizomida	26.4	14.3	17.9	18.3	15.0	16.0	14.8	16.4	15.3	14.9	16.3	15.7		7.8	6.4	7.3	7.4	7.4	7.8	7.8	7.8	8.1	7.6	7.4	7.6	7.8	7.3	7.4	6.4	8.4	7.9	8.1	8.1	7.8	7.8	7.8	14.6	15.0	16.6	16.6	18.2	18.2	16.0	34.0	18.2	16.0	16.3	16.4	16.3	16.3	16.3	16.3	16.3	16.3	16.3	16.3	16.1	16.3	15.1	15.6	16.1	15.9	17.2	15.5
BMR00215_HSTD_Schizomida sp.	27.1	14.9	16.9	16.9	15.2	16.4	15.9	16.4	15.9	14.7	17.9	17.2	7.8		5.5	6.1	7.4	7.4	8.5	8.5	8.5	8.8	8.1	7.9	8.1	8.2	7.6	7.6	7.9	9.7	9.0	9.3	9.0	9.0	9.0	9.0	15.3	16.1	14.3	14.3	16.7	16.7	15.8	34.2	17.9	15.2	15.0	15.8	15.7	15.7	15.7	15.7	15.7	15.7	15.7	15.7	15.7	16.1	14.9	16.8	16.5	16.7	16.4	14.0
BMR01096_HSTD_Schizomida	25.8	15.3	17.6	18.3	14.7	17.5	15.7	16.9	16.7	15.2	17.6	16.8	6.4	5.5		1.2	6.4	6.5	7.1	7.1	7.3	7.6	7.0	6.8	7.0	7.1	6.4	6.5	6.1	8.1	7.6	7.4	7.4	7.4	7.4	7.4	15.2	15.6	14.9	14.9	17.2	17.2	15.3	34.3	17.0	15.2	15.5	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	16.1	16.1	16.2	16.0	16.3	16.5	16.7	14.1
BMR00212_HSTD_Schizomida sp.	26.0	15.5	17.6	18.3	15.0	17.5	15.5	17.3	16.9	15.3	18.1	17.4	7.3	6.1	1.2		7.0	7.1	7.8	7.8	7.9	8.2	7.6	7.4	7.6	7.8	7.0	7.1	6.4	8.7	8.2	8.1	8.1	8.1	8.1	8.1	15.6	16.0	15.2	15.2	17.2	17.2	15.0	34.5	16.7	15.5	15.7	15.7	15.7	15.7	15.7	15.7	15.7	15.7	15.7	15.7	16.3	16.4	17.3	16.6	16.9	16.9	16.6	14.0
BMR01090_SGW_Schizomida	25.4	16.3	18.1	18.5	15.3	16.0	15.0	16.1	16.3	15.2	17.5	16.9	7.4	7.4	6.4	7.0		6.7	6.7	6.7	6.8	7.1	7.0	6.7	6.8	7.0	6.8	6.7	6.2	7.7	7.1	7.6	7.3	7.3	7.3	7.3	15.5	16.1	14.4	14.4	16.7	16.7	15.8	34.7	18.1	14.1	15.5	15.5	15.5	15.5	15.5	15.5	15.5	15.5	15.5	15.5	16.1	16.3	15.8	17.8	16.1	16.3	16.7	13.8
BMR01091_SGW_Schizomida	25.5	15.3	17.6	17.8	15.6	16.6	15.5	15.3	16.3	15.7	17.6	16.3	7.4	7.4	6.5	7.1	6.7		1.2	1.2	1.4	1.7	0.9	0.6	0.8	0.9	0.5	0.3	4.9	6.5	5.8	6.5	6.5	5.9	5.9	5.9	16.1	16.9	14.3	14.3	16.9	16.9	16.4	35.3	18.1	15.0	15.7	16.4	16.3	16.3	16.3	16.3	16.3	16.3	16.3	16.3	16.0	16.6	16.4	16.0	15.7	16.1	16.9	16.0
BMR00216_SGW_Schizomida sp.	25.4	15.3	17.8	18.1	16.1	16.4	15.7	16.1	16.1	15.8	17.6	16.2	7.8	8.5	7.1	7.8	6.7	1.2		0.0	0.2	0.5	1.6	1.2	1.4	1.5	1.1	0.9	5.3	7.1	6.4	6.8	6.8	6.5	6.5	6.5	16.7	17.1	15.0	15.0	17.6	17.6	16.9	35.3	18.2	15.0	16.3	17.0	16.9	16.9	16.9	16.9	16.9	16.9	16.9	16.9	16.3	17.2	17.1	16.6	15.7	16.5	17.2	16.0
BMR00217_SGW_Schizomida sp.	25.4	15.3	17.8	18.1	16.1	16.4	15.7	16.1	16.1	15.8	17.6	16.2	7.8	8.5	7.1	7.8	6.7	1.2	0.0		0.2	0.5	1.6	1.2	1.4	1.5	1.1	0.9	5.3	7.1	6.4	6.8	6.8	6.5	6.5	6.5	16.7	17.1	15.0	15.0	17.6	17.6	16.9	35.3	18.2	15.0	16.3	17.0	16.9	16.9	16.9	16.9	16.9	16.9	16.9	16.9	16.3	17.2	17.1	16.6	15.7	16.5	17.2	16.0
BMR01086_SGW_Schizomida	25.4	15.3	17.8	18.1	16.1	16.4	15.7	16.1	16.1	15.8	17.6	16.2	7.8	8.5	7.3	7.9	6.8	1.4	0.2	0.2		0.3	1.7	1.4	1.5	1.7	1.2	1.1	5.5	7.2	6.5	7.0	7.0	6.7	6.7	6.7	16.7	17.1	15.0	15.0	17.6	17.6	16.9	35.3	18.4	15.0	16.3	17.0	16.9	16.9	16.9	16.9	16.9	16.9	16.9	16.9	16.3	17.2	17.1	16.6	15.7	16.5	17.2	16.0
BMR00213_SGW_Schizomida sp.	25.7	15.3	17.9	18.3	16.3	16.6	15.5	16.0	15.9	15.7	17.6	16.2	8.1	8.8	7.6	8.2	7.1	1.7	0.5	0.5	0.3		2.0	1.7	1.8	2.0	1.5	1.4	5.8	7.2	6.5	7.0	7.0	6.7	6.7	6.7	17.1	17.3	15.2	15.2	17.5	17.5	17.0	35.1	18.7	15.3	16.6	17.3	17.2	17.2	17.2	17.2	17.2	17.2	17.2	17.2	16.3	17.5	17.3	16.8	15.9	16.7	17.2	16.3
P9_RC08SILV0696PIT2-2_BROCKS_Paradraculoides `sp. Helix-D`	25.7	15.2	17.7	18.0	16.3	16.5	15.3	15.5	15.9	15.7	17.7	16.4	7.6	8.1	7.0	7.6	7.0	0.9	1.6	1.6	1.7	2.0		0.3	0.5	0.6	1.1	0.9	5.1	6.5	6.0	6.7	6.7	6.0	6.1	6.1	16.2	16.7	15.1	15.1	17.7	17.7	16.6	35.5	18.6	14.8	16.0	16.8	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.0	16.9	15.9	15.7	15.3	15.7	17.1	15.7
BMR01084_SGW_Schizomida	25.4	15.3	17.3	17.7	15.8	16.3	15.1	15.2	15.9	15.3	17.3	16.0	7.4	7.9	6.8	7.4	6.7	0.6	1.2	1.2	1.4	1.7	0.3		0.2	0.3	0.8	0.6	4.9	6.5	5.8	6.5	6.5	5.9	5.9	5.9	16.0	16.5	14.7	14.7	17.3	17.3	16.4	35.0	18.4	14.7	15.7	16.4	16.3	16.3	16.3	16.3	16.3	16.3	16.3	16.3	15.7	16.6	16.2	15.8	15.3	15.7	16.7	15.8
BMR01087_SGW_Schizomida	25.5	15.5	17.5	17.8	16.0	16.1	15.3	15.3	16.1	15.5	17.5	16.2	7.6	8.1	7.0	7.6	6.8	0.8	1.4	1.4	1.5	1.8	0.5	0.2		0.2	0.9	0.8	5.0	6.6	5.9	6.7	6.7	6.1	6.1	6.1	16.1	16.7	14.9	14.9	17.5	17.5	16.6	35.1	18.5	14.9	15.8	16.6	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	15.8	16.7	16.4	16.0	15.1	15.5	16.9	16.0
BMR01099_SGW_Schizomida	25.7	15.3	17.3	17.7	16.1	16.3	15.5	15.5	16.3	15.7	17.6	16.3	7.8	8.2	7.1	7.8	7.0	0.9	1.5	1.5	1.7	2.0	0.6	0.3	0.2		1.1	0.9	5.2	6.8	6.1	6.8	6.8	6.2	6.2	6.2	16.0	16.5	15.0	15.0	17.3	17.3	16.7	35.3	18.7	15.0	16.0	16.7	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.0	16.9	16.2	16.2	15.3	15.7	17.0	16.1
BMR01085_SGW_Schizomida	25.7	15.0	17.8	18.1	15.8	16.7	15.5	15.7	16.3	15.8	17.8	16.5	7.3	7.6	6.4	7.0	6.8	0.5	1.1	1.1	1.2	1.5	1.1	0.8	0.9	1.1		0.2	5.0	6.6	5.9	6.4	6.4	5.8	5.8	5.8	16.3	16.7	14.6	14.6	17.2	17.2	16.4	35.1	18.1	14.7	15.3	16.1	16.0	16.0	16.0	16.0	16.0	16.0	16.0	16.0	16.0	16.6	16.4	16.0	15.5	15.9	16.9	15.8
BMR01092_SGW_Schizomida	25.5	15.0	17.6	18.0	15.8	16.6	15.3	15.5	16.1	15.7	17.6	16.3	7.4	7.6	6.5	7.1	6.7	0.3	0.9	0.9	1.1	1.4	0.9	0.6	0.8	0.9	0.2		4.9	6.5	5.8	6.5	6.5	5.9	5.9	5.9	16.3	16.7	14.4	14.4	17.0	17.0	16.4	35.1	18.1	14.7	15.3	16.1	16.0	16.0	16.0	16.0	16.0	16.0	16.0	16.0	16.0	16.6	16.4	16.0	15.5	15.9	16.7	15.8
BMR01089_SGW_Schizomida	25.7	14.1	17.9	18.1	15.2	15.6	13.4	15.8	15.1	14.6	17.6	16.3	6.4	7.9	6.1	6.4	6.2	4.9	5.3	5.3	5.5	5.8	5.1	4.9	5.0	5.2	5.0	4.9		5.5	4.9	5.5	5.5	5.0	5.0	5.0	14.9	16.0	14.1	14.1	16.7	16.7	14.4	34.3	17.6	15.2	15.8	16.0	15.8	15.8	15.8	15.8	15.8	15.8	15.8	15.8	16.1	15.7	15.8	15.8	15.9	15.7	16.6	14.7
P10_RC08SILV0795PIT2-3_BROCKS_Paradraculoides `sp. Helix-D`	26.2	16.3	19.2	19.3	17.3	17.7	15.6	17.1	16.0	15.6	17.6	16.7	8.4	9.7	8.1	8.7	7.7	6.5	7.1	7.1	7.2	7.2	6.5	6.5	6.6	6.8	6.6	6.5	5.5		1.3	2.1	2.2	1.4	1.4	1.4	16.6	17.9	16.9	16.9	17.2	17.2	16.8	36.2	18.5	14.9	15.9	16.6	16.5	16.5	16.5	16.5	16.5	16.5	16.5	16.5	15.2	15.9	16.4	17.3	17.1	16.9	17.1	16.4
BMR00211_SGW_Schizomida sp.	25.8	16.3	19.1	19.1	16.7	17.4	15.5	16.9	16.1	15.7	16.9	16.3	7.9	9.0	7.6	8.2	7.1	5.8	6.4	6.4	6.5	6.5	6.0	5.8	5.9	6.1	5.9	5.8	4.9	1.3		0.8	0.9	0.2	0.2	0.2	16.7	17.7	16.6	16.6	17.2	17.2	16.4	35.3	18.4	15.2	15.8	16.6	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	15.5	16.1	16.6	16.8	16.5	16.5	16.7	16.3
BMR01097_SGW_Schizomida	26.1	16.6	19.3	19.1	16.6	17.5	15.5	17.5	16.3	16.0	16.9	16.6	8.1	9.3	7.4	8.1	7.6	6.5	6.8	6.8	7.0	7.0	6.7	6.5	6.7	6.8	6.4	6.5	5.5	2.1	0.8		0.5	0.6	0.6	0.6	16.6	17.3	16.9	16.9	17.2	17.2	16.9	35.3	18.8	15.2	16.1	16.9	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	15.8	16.4	17.1	17.0	16.7	16.7	17.2	16.7
BMR00214_SGW_Schizomida sp.	25.8	16.4	19.5	19.3	16.6	17.7	15.9	17.5	16.3	16.0	16.6	16.3	8.1	9.0	7.4	8.1	7.3	6.5	6.8	6.8	7.0	7.0	6.7	6.5	6.7	6.8	6.4	6.5	5.5	2.2	0.9	0.5		0.8	0.8	0.8	16.6	17.5	16.6	16.6	17.2	17.2	16.7	35.1	18.7	15.2	15.8	16.6	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	15.8	16.4	17.1	17.0	16.5	16.7	17.2	16.4
S9_RC08SILV0796P2T2-4_BROCKS_Paradraculoides `sp. Helix-D`	26.0	15.9	19.3	19.1	16.8	17.1	15.7	17.0	16.0	15.8	17.0	16.5	7.8	9.0	7.4	8.1	7.3	5.9	6.5	6.5	6.7	6.7	6.0	5.9	6.1	6.2	5.8	5.9	5.0	1.4	0.2	0.6	0.8		0.0	0.0	16.5	17.6	16.7	16.7	17.3	17.3	16.4	35.4	18.4	14.8	15.8	16.6	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	15.3	16.1	15.9	16.3	16.0	16.0	16.9	15.7
BMR01093_SGW_Schizomida	26.0	16.3	19.3	19.3	16.7	17.5	15.7	17.0	16.3	15.8	17.0	16.5	7.8	9.0	7.4	8.1	7.3	5.9	6.5	6.5	6.7	6.7	6.1	5.9	6.1	6.2	5.8	5.9	5.0	1.4	0.2	0.6	0.8	0.0		0.0	16.7	17.7	16.7	16.7	17.3	17.3	16.4	35.3	18.4	15.2	15.8	16.6	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	15.5	16.1	16.6	16.8	16.5	16.5	16.9	16.3
BMR01095_SGW_Schizomida	26.0	16.3	19.3	19.3	16.7	17.5	15.7	17.0	16.3	15.8	17.0	16.5	7.8	9.0	7.4	8.1	7.3	5.9	6.5	6.5	6.7	6.7	6.1	5.9	6.1	6.2	5.8	5.9	5.0	1.4	0.2	0.6	0.8	0.0	0.0		16.7	17.7	16.7	16.7	17.3	17.3	16.4	35.3	18.4	15.2	15.8	16.6	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	15.5	16.1	16.6	16.8	16.5	16.5	16.9	16.3
CM38_DD35KOOD_KOOD_Draculoides `sp. Helix-SCH042`	25.7	13.2	14.1	14.2	13.0	13.7	13.0	15.5	16.8	16.0	15.5	15.3	14.6	15.3	15.2	15.6	15.5	16.1	16.7	16.7	16.7	17.1	16.2	16.0	16.1	16.0	16.3	16.3	14.9	16.6	16.7	16.6	16.6	16.5	16.7	16.7		6.6	14.6	14.6	15.2	15.2	15.0	28.3	15.6	13.7	13.9	14.4	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.5	15.2	15.4	13.7	14.3	14.8	14.4	13.3
DN2_RC12KOOD1374P5T1-2_KOOD_Draculoides `sp. Helix-SCH043`	24.5	12.9	13.6	13.5	13.0	14.3	14.0	13.6	16.8	18.5	15.8	15.9	15.0	16.1	15.6	16.0	16.1	16.9	17.1	17.1	17.1	17.3	16.7	16.5	16.7	16.5	16.7	16.7	16.0	17.9	17.7	17.3	17.5	17.6	17.7	17.7	6.6		15.2	15.2	17.5	17.5	15.4	14.6	15.8	13.9	14.6	15.0	15.0	15.0	15.0	15.0	15.0	15.0	15.0	15.0	15.2	15.2	14.3	12.8	13.4	14.1	16.3	13.3
BMR00579_BS1W_Schizomida	26.6	14.7	15.5	15.6	13.0	12.8	13.0	12.9	17.6	16.4	14.4	15.0	16.6	14.3	14.9	15.2	14.4	14.3	15.0	15.0	15.0	15.2	15.1	14.7	14.9	15.0	14.6	14.4	14.1	16.9	16.6	16.9	16.6	16.7	16.7	16.7	14.6	15.2		0.2	5.8	5.8	13.2	31.6	14.9	14.7	14.4	14.3	14.3	14.3	14.3	14.3	14.3	14.3	14.3	14.3	13.1	14.1	15.1	15.8	15.7	15.9	12.0	13.5
BMR00638_BS1W_Schizomida	26.6	14.7	15.5	15.6	13.1	12.8	13.0	13.1	17.8	16.6	14.4	15.0	16.6	14.3	14.9	15.2	14.4	14.3	15.0	15.0	15.0	15.2	15.1	14.7	14.9	15.0	14.6	14.4	14.1	16.9	16.6	16.9	16.6	16.7	16.7	16.7	14.6	15.2	0.2		5.9	5.9	13.2	31.6	14.9	14.9	14.4	14.3	14.3	14.3	14.3	14.3	14.3	14.3	14.3	14.3	13.2	14.3	15.1	15.8	15.7	15.9	12.0	13.5
BMR01121_BS1W_Schizomida	28.3	16.1	15.8	15.7	14.2	13.6	14.0	13.1	19.6	17.9	14.6	15.4	18.2	16.7	17.2	17.2	16.7	16.9	17.6	17.6	17.6	17.5	17.7	17.3	17.5	17.3	17.2	17.0	16.7	17.2	17.2	17.2	17.2	17.3	17.3	17.3	15.2	17.5	5.8	5.9		0.0	13.4	32.2	15.2	14.6	13.8	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	12.6	14.0	14.5	17.0	17.2	16.5	12.6	13.7
BMR01122_BS1W_Schizomida	28.3	16.1	15.8	15.7	14.2	13.6	14.0	13.1	19.6	17.9	14.6	15.4	18.2	16.7	17.2	17.2	16.7	16.9	17.6	17.6	17.6	17.5	17.7	17.3	17.5	17.3	17.2	17.0	16.7	17.2	17.2	17.2	17.2	17.3	17.3	17.3	15.2	17.5	5.8	5.9	0.0		13.4	32.2	15.2	14.6	13.8	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	12.6	14.0	14.5	17.0	17.2	16.5	12.6	13.7
BMR01088_SGW_Schizomida	26.9	13.4	15.8	15.9	14.6	13.9	13.0	13.4	18.2	16.6	16.3	16.0	16.0	15.8	15.3	15.0	15.8	16.4	16.9	16.9	16.9	17.0	16.6	16.4	16.6	16.7	16.4	16.4	14.4	16.8	16.4	16.9	16.7	16.4	16.4	16.4	15.0	15.4	13.2	13.2	13.4	13.4		27.7	9.4	13.7	12.6	12.5	12.3	12.3	12.3	12.3	12.3	12.3	12.3	12.3	14.3	13.5	13.6	14.6	13.8	13.8	14.3	14.6
S7_RHWRC0249PT2-3 _CGB_Draculoides `sp. Helix-A`	43.8	31.9	33.6	29.7	28.3	27.7	11.7	33.0	16.2	35.1	32.8	33.1	34.0	34.2	34.3	34.5	34.7	35.3	35.3	35.3	35.3	35.1	35.5	35.0	35.1	35.3	35.1	35.1	34.3	36.2	35.3	35.3	35.1	35.4	35.3	35.3	28.3	14.6	31.6	31.6	32.2	32.2	27.7		28.0	29.9	31.8	32.4	32.2	32.2	32.2	32.2	32.2	32.2	32.2	32.2	28.8	32.7	13.0	13.4	12.9	13.3	31.6	34.5
MN019980_Central Pilbara_Paradraculoides SCH016	25.2	15.3	16.0	15.4	17.4	14.7	14.6	16.3	17.2	17.2	16.6	15.1	18.2	17.9	17.0	16.7	18.1	18.1	18.2	18.2	18.4	18.7	18.6	18.4	18.5	18.7	18.1	18.1	17.6	18.5	18.4	18.8	18.7	18.4	18.4	18.4	15.6	15.8	14.9	14.9	15.2	15.2	9.4	28.0		14.3	14.3	14.3	14.1	14.1	14.1	14.1	14.1	14.1	14.1	14.1	13.7	14.6	14.5	14.4	14.5	14.9	14.3	15.2
FH19_Paradraculoides sp	24.9	14.3	18.4	18.4	15.6	12.6	12.5	14.4	14.0	15.0	14.6	14.5	16.0	15.2	15.2	15.5	14.1	15.0	15.0	15.0	15.0	15.3	14.8	14.7	14.9	15.0	14.7	14.7	15.2	14.9	15.2	15.2	15.2	14.8	15.2	15.2	13.7	13.9	14.7	14.9	14.6	14.6	13.7	29.9	14.3		5.0	5.8	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.2	5.5	9.0	8.4	8.6	8.9	13.8	13.1
BMR00637_BS1E_Schizomida	24.8	14.3	16.9	17.5	15.3	13.1	12.5	14.1	16.5	15.7	14.9	14.7	16.3	15.0	15.5	15.7	15.5	15.7	16.3	16.3	16.3	16.6	16.0	15.7	15.8	16.0	15.3	15.3	15.8	15.9	15.8	16.1	15.8	15.8	15.8	15.8	13.9	14.6	14.4	14.4	13.8	13.8	12.6	31.8	14.3	5.0		1.7	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	4.7	4.4	10.2	9.6	10.1	9.9	14.0	13.7
BMR01124_BS1E_Schizomida	24.9	14.9	17.5	18.1	15.6	13.5	13.2	14.1	17.1	16.0	15.3	14.8	16.4	15.8	15.8	15.7	15.5	16.4	17.0	17.0	17.0	17.3	16.8	16.4	16.6	16.7	16.1	16.1	16.0	16.6	16.6	16.9	16.6	16.6	16.6	16.6	14.4	15.0	14.3	14.3	14.4	14.4	12.5	32.4	14.3	5.8	1.7		0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	5.3	5.2	10.6	10.4	10.9	10.7	13.5	13.2
BMR01119_BS1E_Schizomida	24.9	14.7	17.3	18.0	15.6	13.3	13.0	14.1	16.9	15.8	15.3	14.8	16.3	15.7	15.8	15.7	15.5	16.3	16.9	16.9	16.9	17.2	16.6	16.3	16.4	16.6	16.0	16.0	15.8	16.5	16.4	16.7	16.4	16.4	16.4	16.4	14.2	15.0	14.3	14.3	14.4	14.4	12.3	32.2	14.1	5.6	1.5	0.2		0.0	0.0	0.0	0.0	0.0	0.0	0.0	5.2	5.0	10.4	10.2	10.7	10.5	13.4	13.2
BMR01106_BS1E_Schizomida	24.9	14.7	17.3	18.0	15.6	13.3	13.0	14.1	16.9	15.8	15.3	14.8	16.3	15.7	15.8	15.7	15.5	16.3	16.9	16.9	16.9	17.2	16.6	16.3	16.4	16.6	16.0	16.0	15.8	16.5	16.4	16.7	16.4	16.4	16.4	16.4	14.2	15.0	14.3	14.3	14.4	14.4	12.3	32.2	14.1	5.6	1.5	0.2	0.0		0.0	0.0	0.0	0.0	0.0	0.0	5.2	5.0	10.4	10.2	10.7	10.5	13.4	13.2
BMR01107_BS1E_Schizomida	24.9	14.7	17.3	18.0	15.6	13.3	13.0	14.1	16.9	15.8	15.3	14.8	16.3	15.7	15.8	15.7	15.5	16.3	16.9	16.9	16.9	17.2	16.6	16.3	16.4	16.6	16.0	16.0	15.8	16.5	16.4	16.7	16.4	16.4	16.4	16.4	14.2	15.0	14.3	14.3	14.4	14.4	12.3	32.2	14.1	5.6	1.5	0.2	0.0	0.0		0.0	0.0	0.0	0.0	0.0	5.2	5.0	10.4	10.2	10.7	10.5	13.4	13.2
BMR01120_BS1E_Schizomida	24.9	14.7	17.3	18.0	15.6	13.3	13.0	14.1	16.9	15.8	15.3	14.8	16.3	15.7	15.8	15.7	15.5	16.3	16.9	16.9	16.9	17.2	16.6	16.3	16.4	16.6	16.0	16.0	15.8	16.5	16.4	16.7	16.4	16.4	16.4	16.4	14.2	15.0	14.3	14.3	14.4	14.4	12.3	32.2	14.1	5.6	1.5	0.2	0.0	0.0	0.0		0.0	0.0	0.0	0.0	5.2	5.0	10.4	10.2	10.7	10.5	13.4	13.2
BMR01108_BS1E_Schizomida	24.9	14.7	17.3	18.0	15.6	13.3	13.0	14.1	16.9	15.8	15.3	14.8	16.3	15.7	15.8	15.7	15.5	16.3	16.9	16.9	16.9	17.2	16.6	16.3	16.4	16.6	16.0	16.0	15.8	16.5	16.4	16.7	16.4	16.4	16.4	16.4	14.2	15.0	14.3	14.3	14.4	14.4	12.3	32.2	14.1	5.6	1.5	0.2	0.0	0.0	0.0	0.0		0.0	0.0	0.0	5.2	5.0	10.4	10.2	10.7	10.5	13.4	13.2
BMR01111_BS1E_Schizomida	24.9	14.7	17.3	18.0	15.6	13.3	13.0	14.1	16.9	15.8	15.3	14.8	16.3	15.7	15.8	15.7	15.5	16.3	16.9	16.9	16.9	17.2	16.6	16.3	16.4	16.6	16.0	16.0	15.8	16.5	16.4	16.7	16.4	16.4	16.4	16.4	14.2	15.0	14.3	14.3	14.4	14.4	12.3	32.2	14.1	5.6	1.5	0.2	0.0	0.0	0.0	0.0	0.0		0.0	0.0	5.2	5.0	10.4	10.2	10.7	10.5	13.4	13.2
BMR00640_BS1E_Schizomida	24.9	14.7	17.3	18.0	15.6	13.3	13.0	14.1	16.9	15.8	15.3	14.8	16.3	15.7	15.8	15.7	15.5	16.3	16.9	16.9	16.9	17.2	16.6	16.3	16.4	16.6	16.0	16.0	15.8	16.5	16.4	16.7	16.4	16.4	16.4	16.4	14.2	15.0	14.3	14.3	14.4	14.4	12.3	32.2	14.1	5.6	1.5	0.2	0.0	0.0	0.0	0.0	0.0	0.0		0.0	5.2	5.0	10.4	10.2	10.7	10.5	13.4	13.2
BMR00580_BS1E_Schizomida	24.9	14.7	17.3	18.0	15.6	13.3	13.0	14.1	16.9	15.8	15.3	14.8	16.3	15.7	15.8	15.7	15.5	16.3	16.9	16.9	16.9	17.2	16.6	16.3	16.4	16.6	16.0	16.0	15.8	16.5	16.4	16.7	16.4	16.4	16.4	16.4	14.2	15.0	14.3	14.3	14.4	14.4	12.3	32.2	14.1	5.6	1.5	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0		5.2	5.0	10.4	10.2	10.7	10.5	13.4	13.2
FH20_Paradraculoides sp	25.2	14.3	17.8	18.2	15.5	11.8	12.5	13.8	14.1	15.0	14.4	14.1	16.1	15.7	16.1	16.3	16.1	16.0	16.3	16.3	16.3	16.3	16.0	15.7	15.8	16.0	16.0	16.0	16.1	15.2	15.5	15.8	15.8	15.3	15.5	15.5	14.5	15.2	13.1	13.2	12.6	12.6	14.3	28.8	13.7	5.2	4.7	5.3	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.2		3.6	10.5	10.0	10.3	10.5	13.1	14.1
BMR01105_BS1W_Schizomida	25.5	15.0	17.0	17.7	16.1	13.0	13.6	14.4	16.7	16.0	15.2	15.1	16.3	16.1	16.1	16.4	16.3	16.6	17.2	17.2	17.2	17.5	16.9	16.6	16.7	16.9	16.6	16.6	15.7	15.9	16.1	16.4	16.4	16.1	16.1	16.1	15.2	15.2	14.1	14.3	14.0	14.0	13.5	32.7	14.6	5.5	4.4	5.2	5.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	3.6		10.4	10.0	10.7	10.5	13.4	14.6
T92516B_TBRC154_PANNA_Shizomida	28.3	14.2	18.1	18.3	16.7	13.8	13.6	16.4	14.5	16.4	18.4	18.7	15.1	14.9	16.2	17.3	15.8	16.4	17.1	17.1	17.1	17.3	15.9	16.2	16.4	16.2	16.4	16.4	15.8	16.4	16.6	17.1	17.1	15.9	16.6	16.6	15.4	14.3	15.1	15.1	14.5	14.5	13.6	13.0	14.5	9.0	10.2	10.6	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.5	10.4		8.2	8.5	8.8	15.6	13.6
JC06_T138610_BROCK3_Paradraculoides `sp. Helix marra mamba`	25.1	13.0	17.4	17.3	14.9	13.0	13.3	16.0	13.3	15.4	14.8	15.7	15.6	16.8	16.0	16.6	17.8	16.0	16.6	16.6	16.6	16.8	15.7	15.8	16.0	16.2	16.0	16.0	15.8	17.3	16.8	17.0	17.0	16.3	16.8	16.8	13.7	12.8	15.8	15.8	17.0	17.0	14.6	13.4	14.4	8.4	9.6	10.4	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.0	10.0	8.2		3.1	3.8	14.4	13.0
JV14_RC15BS4B0404_BROCK4_Paradraculoides `sp. Helix marra mamba`	25.0	14.4	18.0	18.1	15.3	12.1	13.1	15.5	13.7	15.7	15.7	15.4	16.1	16.5	16.3	16.9	16.1	15.7	15.7	15.7	15.7	15.9	15.3	15.3	15.1	15.3	15.5	15.5	15.9	17.1	16.5	16.7	16.5	16.0	16.5	16.5	14.3	13.4	15.7	15.7	17.2	17.2	13.8	12.9	14.5	8.6	10.1	10.9	10.7	10.7	10.7	10.7	10.7	10.7	10.7	10.7	10.3	10.7	8.5	3.1		2.2	15.1	13.8
JV11_RC11BS3068_BROCK3_Paradraculoides `sp. Helix marra mamba`	25.0	15.0	18.2	18.3	15.4	13.0	13.5	14.9	13.1	15.1	16.3	16.0	15.9	16.7	16.5	16.9	16.3	16.1	16.5	16.5	16.5	16.7	15.7	15.7	15.5	15.7	15.9	15.9	15.7	16.9	16.5	16.7	16.7	16.0	16.5	16.5	14.8	14.1	15.9	15.9	16.5	16.5	13.8	13.3	14.9	8.9	9.9	10.7	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.5	8.8	3.8	2.2		15.5	14.0
MN019976_Central Pilbara_Draculoides sp. SCH003	28.4	15.2	16.7	17.3	15.2	13.1	13.2	12.9	15.3	14.4	14.9	15.0	17.2	16.4	16.7	16.6	16.7	16.9	17.2	17.2	17.2	17.2	17.1	16.7	16.9	17.0	16.9	16.7	16.6	17.1	16.7	17.2	17.2	16.9	16.9	16.9	14.4	16.3	12.0	12.0	12.6	12.6	14.3	31.6	14.3	13.8	14.0	13.5	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.1	13.4	15.6	14.4	15.1	15.5		10.9
S3_RHWRC0303P2T2-5_CGB_Draculoides `sp. Helix-C`	26.4	13.1	17.3	16.6	14.7	14.4	14.9	12.9	16.0	16.0	15.8	16.0	15.5	14.0	14.1	14.0	13.8	16.0	16.0	16.0	16.0	16.3	15.7	15.8	16.0	16.1	15.8	15.8	14.7	16.4	16.3	16.7	16.4	15.7	16.3	16.3	13.3	13.3	13.5	13.5	13.7	13.7	14.6	34.5	15.2	13.1	13.7	13.2	13.2	13.2	13.2	13.2	13.2	13.2	13.2	13.2	14.1	14.6	13.6	13.0	13.8	14.0	10.9	

Appendix 6: Distance matrix of Chilopoda sequences/ lineages included in the analysis

COI divergence (%) of Chilopoda (regional comparisons)	O.G.	BMR 00247	WAMT 145912	MK86 7489	MK86 7503	MK86 7502	WAMT 139404	WAMT 135485	MK86 7497	MK86 7496	MK86 7501	MK86 7500	BMR 00210	MK86 7507	MK86 7504	MK86 7491	MK86 7499	MK86 7498	WAMT 145918	WAM132 678	BMR 00119	BMR 00489	BMR 00807	IV140	IV141	KP42191 0	WAMT 145974	IV143	WAMT 145912	DL0414	EW0769	BMR 00759	WAMT 144744	WAMT 144179	WAMT 144745	WAMT 145916	WAMT 144180	WAMT 144184	BMR 00277	BMR 00276	BMR 00280
MH932612 Antichiropus sp. DIP174_OUTGROUP		26.3	29.2	33.1	34.3	34.3	29.0	28.7	26.7	28.7	27.4	27.4	26.4	26.1	26.0	30.2	30.4	30.2	32.4	32.2	29.6	31.9	31.1	33.7	33.6	34.7	32.7	28.4	27.5	32.2	30.3	29.3	31.0	32.2	32.2	31.3	31.9	29.6	29.2	29.5	29.5
BMR00247_BS1E_Geophilomorpha sp.	26.3		12.6	29.2	28.1	28.1	24.0	25.5	24.5	24.1	22.4	22.4	22.0	22.6	22.9	26.6	26.1	26.0	29.2	28.4	29.0	28.4	25.2	26.9	26.7	29.8	28.1	25.1	25.4	26.3	24.3	25.7	25.2	26.7	26.7	26.4	27.4	26.9	24.5	24.7	24.8
RT48_WAMT145912_WAM-GEOPH001	29.2	12.6		26.3	25.7	25.7	25.1	24.6	24.0	23.8	24.6	24.6	24.0	23.4	24.3	26.2	24.5	24.6	28.1	27.0	28.9	27.4	24.9	22.0	21.7	25.7	23.6	24.8	24.0	24.8	23.5	26.9	25.2	24.7	24.7	26.4	25.7	25.7	25.6	25.5	25.7
MK867489_WAMT134711_Cormocephalus_delta	33.1	29.2	26.3		9.4	9.4	18.8	18.7	17.5	17.8	19.0	18.8	20.4	21.4	20.4	21.5	18.8	19.0	24.7	26.7	25.8	24.2	25.2	22.9	22.8	25.1	24.2	24.8	25.4	26.1	25.0	24.5	23.9	23.9	23.9	24.2	22.6	23.6	23.7	23.5	23.4
MK867503_WAMT120939_Cormocephalus_delta	34.3	28.1	25.7	9.4		0.0	18.5	18.8	16.3	16.6	17.5	17.6	20.1	20.2	20.2	19.3	17.9	17.8	23.8	27.0	26.1	24.5	24.9	21.9	21.9	25.1	22.0	25.4	26.0	26.1	24.1	24.3	22.8	22.5	22.5	24.3	24.2	24.5	22.8	23.2	22.8
MK867502_WAMT120940_Cormocephalus_delta	34.3	28.1	25.7	9.4	0.0		18.5	18.8	16.3	16.6	17.5	17.6	20.1	20.2	20.2	19.3	17.9	17.8	23.8	27.0	26.1	24.5	24.9	21.9	21.9	25.1	22.0	25.4	26.0	26.1	24.1	24.3	22.8	22.5	22.5	24.3	24.2	24.5	22.8	23.2	22.8
Cormocephalus turneri WAMT139404	29.0	24.0	25.1	18.8	18.5	18.5		10.5	16.7	16.2	15.9	15.7	17.6	17.6	17.2	18.9	19.0	18.8	25.6	27.7	25.5	25.1	26.0	25.1	24.8	28.3	25.1	21.7	22.6	23.6	20.9	22.6	21.7	21.7	21.7	24.2	22.3	22.9	21.8	22.3	22.0
MK867486 Cormocephalus westangelasensis WAMT135485	28.7	25.5	24.6	18.7	18.8	18.8	10.5		15.7	12.7	17.1	16.9	18.5	18.1	17.8	18.3	19.9	20.1	24.9	28.1	25.7	26.1	25.5	24.8	24.6	28.9	24.9	23.4	23.3	22.5	21.3	22.8	22.2	22.3	22.3	23.6	22.6	23.4	21.8	22.0	21.7
MK867497_WAMT120946_Cormocephalus_sagmus	26.7	24.5	24.0	17.5	16.3	16.3	16.7	15.7		12.6	13.1	12.9	16.9	18.1	17.6	18.7	19.1	19.3	25.1	26.7	25.8	24.5	24.2	24.0	23.9	27.4	23.9	24.5	23.3	25.1	23.3	23.6	24.3	24.0	24.0	22.9	23.3	22.9	22.8	22.8	22.5
MK867496_WAMT120963_Cormocephalus_spB	28.7	24.1	23.8	17.8	16.6	16.6	16.2	12.7	12.6		12.0	12.0	16.2	16.2	17.5	18.6	17.6	17.8	26.4	25.7	26.5	24.6	23.7	24.9	24.6	27.4	22.2	23.5	22.3	23.8	22.3	23.3	22.0	22.6	22.6	23.9	21.3	20.4	21.0	21.2	20.9
MK867501_WAMT120941_Cormocephalus_sagmus	27.4	22.4	24.6	19.0	17.5	17.5	15.9	17.1	13.1	12.0		0.2	16.3	16.1	16.0	16.5	18.0	17.9	24.8	24.6	25.4	23.8	23.5	25.4	25.2	29.6	24.9	23.1	22.1	23.5	21.3	22.0	22.6	23.5	23.5	22.6	21.5	21.0	21.9	21.8	21.8
MK867500_WAMT120942_Cormocephalus_sagmus	27.4	22.4	24.6	18.8	17.6	17.6	15.7	16.9	12.9	12.0	0.2		16.1	16.1	15.8	16.3	18.2	18.0	24.6	24.6	25.2	23.7	23.5	25.3	25.2	29.6	25.1	22.9	22.0	23.6	21.3	22.2	22.5	23.4	23.4	22.6	21.4	20.9	21.9	21.8	21.8
BMR00210_BS2W_Scolopendrida sp.	26.4	22.0	24.0	20.4	20.1	20.1	17.6	18.5	16.9	16.2	16.3	16.1		10.6	11.9	16.8	15.8	15.7	28.5	28.1	24.9	27.4	26.4	26.3	26.0	29.2	26.1	23.7	23.6	25.2	23.7	24.2	24.9	26.0	26.0	24.9	24.3	22.3	24.4	24.6	24.3
MK867507_WAMT65791_Cormocephalus_spA	26.1	22.6	23.4	21.4	20.2	20.2	17.6	18.1	18.1	16.2	16.1	16.1	10.6		5.3	16.6	17.5	17.3	29.0	27.7	24.9	27.4	26.7	27.1	26.9	29.5	27.4	24.3	22.5	24.5	22.5	24.0	25.7	26.1	26.1	25.1	22.9	24.0	25.0	25.1	25.1
MK867504_WAMT93779_Cormocephalus_spA	26.0	22.9	24.3	20.4	20.2	20.2	17.2	17.8	17.6	17.5	16.0	15.8	11.9	5.3		16.6	17.9	17.8	27.4	27.2	25.4	25.8	25.4	25.7	25.5	29.9	26.3	22.3	21.6	25.4	22.7	23.6	24.9	25.2	25.2	24.6	22.9	23.1	24.4	24.5	24.5
MK867491_WAMT127529_Cormocephalus_pyropygus	30.2	26.6	26.2	21.5	19.3	19.3	18.9	18.3	18.7	18.6	16.5	16.3	16.8	16.6	16.6		15.9	15.9	28.6	27.8	27.5	28.7	27.8	26.7	26.5	32.5	27.1	25.6	24.1	26.6	24.3	26.4	26.2	25.5	25.5	23.5	25.7	24.7	26.8	26.8	26.8
MK867499_WAMT120944_Cormocephalus_pyropygus	30.4	26.1	24.5	18.8	17.9	17.9	19.0	19.9	19.1	17.6	18.0	18.2	15.8	17.5	17.9	15.9		0.2	27.8	28.4	26.9	25.8	28.0	26.4	26.1	29.0	25.5	23.1	23.1	26.1	25.2	24.8	23.9	23.7	23.7	25.7	24.8	23.9	27.5	27.4	27.1
MK867498_WAMT120945_Cormocephalus_pyropygus	30.2	26.0	24.6	19.0	17.8	17.8	18.8	20.1	19.3	17.8	17.9	18.0	15.7	17.3	17.8	15.9	0.2		27.6	28.4	26.7	25.7	27.8	26.3	26.0	28.9	25.4	22.9	22.9	26.0	25.0	24.6	24.0	23.9	23.9	25.5	24.9	23.7	27.5	27.6	27.2
RT48_WAMT145918_WAM-CRYP006	32.4	29.2	28.1	24.7	23.8	23.8	25.6	24.9	25.1	26.4	24.8	24.6	28.5	29.0	27.4	28.6	27.8	27.6		18.5	20.1	18.0	22.1	22.2	22.3	23.3	23.9	23.0	21.9	23.6	22.9	23.8	22.4	22.0	22.1	19.7	21.6	22.0	23.8	23.8	23.7
WAM132678_COBRC0001_Chilopoda_HelixCHI022	32.2	28.4	27.0	26.7	27.0	27.0	27.7	28.1	26.7	25.7	24.6	24.6	28.1	27.7	27.2	27.8	28.4	28.4	18.5		21.3	20.6	23.8	25.8	25.8	26.0	23.2	23.7	22.5	24.2	25.7	25.3	22.8	23.5	23.5	23.9	23.0	22.5	25.5	25.3	25.8
BMR00119_HSTD_Scolopendrida sp.	29.6	29.0	28.9	25.8	26.1	26.1	25.5	25.7	25.8	26.5	25.4	25.2	24.9	24.9	25.4	27.5	26.9	26.7	20.1	21.3		17.6	25.5	25.5	25.5	27.4	26.4	22.6	21.7	22.8	24.5	22.5	20.7	21.6	21.6	21.4	22.3	23.6	21.9	22.0	21.9
BMR00489_HD2_Scolopendromorpha	31.9	28.4	27.4	24.2	24.5	24.5	25.1	26.1	24.5	24.6	23.8	23.7	27.4	27.4	25.8	28.7	25.8	25.7	18.0	20.6	17.6		22.4	23.3	23.3	26.7	25.1	22.5	21.9	20.7	23.7	23.1	22.0	22.5	22.5	21.7	20.1	20.8	19.6	19.8	19.6
BMR00807_BS1E_Geophilomorpha sp.	31.1	25.2	24.9	25.2	24.9	24.9	26.0	25.5	24.2	23.7	23.5	23.5	26.4	26.7	25.4	27.8	28.0	27.8	22.1	23.8	25.5	22.4		21.7	21.7	21.9	22.9	22.4	22.7	23.2	25.6	23.6	22.1	22.7	22.7	21.7	24.2	23.7	22.1	22.2	22.1
IV140_DD14MRR0004T1-01_Chilopoda	33.7	26.9	22.0	22.9	21.9	21.9	25.1	24.8	24.0	24.9	25.4	25.3	26.3	27.1	25.7	26.7	26.4	26.3	22.2	25.8	25.5	23.3	21.7		0.3	22.5	22.2	22.9	23.7	23.4	23.8	24.5	23.1	22.2	22.4	23.9	23.0	25.0	22.9	22.8	23.1
IV141_DD14MRR0005-T1-04_Chilopoda	33.6	26.7	21.7	22.8	21.9	21.9	24.8	24.6	23.9	24.6	25.2	25.2	26.0	26.9	25.5	26.5	26.1	26.0	22.3	25.8	25.5	23.3	21.7	0.3		22.3	21.9	22.8	23.6	23.2	23.4	24.3	22.8	21.9	22.1	23.9	22.8	24.7	22.9	22.8	23.1
KP421910 Geophilomorpha NZAC 03013023	34.7	29.8	25.7	25.1	25.1	25.1	28.3	28.9	27.4	27.4	29.6	29.6	29.2	29.5	29.9	32.5	29.0	28.9	23.3	26.0	27.4	26.7	21.9	22.5	22.3		21.4	25.8	25.5	24.8	26.2	27.1	26.3	25.2	25.2	24.5	26.0	26.1	28.9	29.1	28.7
RT48_WAMT145974_WAM-BALPH001	32.7	28.1	23.6	24.2	22.0	22.0	25.1	24.9	23.9	22.2	24.9	25.1	26.1	27.4	26.3	27.1	25.5	25.4	23.9	23.2	26.4	25.1	22.9	22.2	21.9	21.4		22.0	22.5	23.2	23.7	23.4	21.2	21.0	21.0	23.5	23.5	23.5	23.9	24.2	23.9
IV143_MEARC4383-20151001-T2-01_Chilopoda	28.4	25.1	24.8	24.8	25.4	25.4	21.7	23.4	24.5	23.5	23.1	22.9	23.7	24.3	22.3	25.6	23.1	22.9	23.0	23.7	22.6	22.5	22.4	22.9	22.8	25.8	22.0		7.7	18.7	18.7	19.0	18.8	18.8	19.0	20.4	18.9	19.7	20.2	20.2	20.1
RT24_WAMT144196_RC15MEB0020_WAM-CRYP004	27.5	25.4	24.0	25.4	26.0	26.0	22.6	23.3	23.3	22.3	22.1	22.0	23.6	22.5	21.6	24.1	23.1	22.9	21.9	22.5	21.7	21.9	22.7	23.7	23.6	25.5	22.5	7.7		19.1	17.5	17.8	17.8	17.9	17.9	18.1	17.5	18.2	19.9	19.8	19.6
nr_Cryptops_sp_B34_DL0414	32.2	26.3	24.8	26.1	26.1	26.1	23.6	22.5	25.1	23.8	23.5	23.6	25.2	24.5	25.4	26.6	26.1	26.0	23.6	24.2	22.8	20.7	23.2	23.4	23.2	24.8	23.2	18.7	19.1		16.4	18.4	16.4	16.3	16.4	17.0	17.8	19.1	18.8	18.8	18.5
nr_Cryptops_sp_B34_EW0769	30.3	24.3	23.5	25.0	24.1	24.1	20.9	21.3	23.3	22.3	21.3	21.3	23.7	22.5	22.7	24.3	25.2	25.0	22.9	25.7	24.5	23.7	25.6	23.8	23.4	26.2	23.7	18.7	17.5	16.4		18.0	15.6	14.9	15.0	17.3	18.4	19.1	15.9	16.3	16.0
BMR00759_VIV_Chilopoda	29.3	25.7	26.9	24.5	24.3	24.3	22.6	22.8	23.6	23.3	22.0	22.2	24.2	24.0	23.6	26.4	24.8	24.6	23.8	25.3	22.5	23.1	23.6	24.5	24.3	27.1	23.4	19.0	17.8	18.4	18.0		16.9	17.2	17.2	17.3	19.0	17.6	17.7	18.1	17.8
RT31_WAMT144744_GR15MEB0018_WAM-CRYP003	31.0	25.2	25.2	23.9	22.8	22.8	21.7	22.2	24.3	22.0	22.6	22.5	24.9	25.7	24.9	26.2	23.9	24.0	22.4	22.8	20.7	22.0	22.1	23.1	22.8	26.3	21.2	18.8	17.8	16.4	15.6	16.9		2.1	2.1	16.4	17.2	17.3	15.5	15.9	15.5
RT24_WAMT144179_RC16MEC0188_WAM-CRYP003	32.2	26.7	24.7	23.9	22.5	22.5	21.7	22.3	24.0	22.6	23.5	23.4	26.0	26.1	25.2	25.5	23.7	23.9	22.0	23.5	21.6	22.5	22.7	22.2	21.9	25.2	21.0	18.8	17.9	16.3	14.9	17.2	2.1		0.0	17.1	18.0	17.9	16.0	16.3	16.0
RT31_WAMT144745_RC16HWY0112_WAM-CRYP003	32.2	26.7	24.7	23.9	22.5	22.5	21.7	22.3	24.0	22.6	23.5	23.4	26.0	26.1	25.2	25.5	23.7	23.9	22.1	23.5	21.6	22.5	22.7	22.4	22.1	25.2	21.0	19.0	17.9	16.4	15.0	17.2	2.1	0.0		17.2	18.1	17.9	16.0	16.3	16.0
RT48_WAMT145916_WAM-CRYP005	31.3	26.4	26.4	24.2	24.3	24.3	24.2	23.6	22.9	23.9	22.6	22.6	24.9	25.1	24.6	23.5	25.7	25.5	19.7	23.9	21.4	21.7	21.7	23.9	23.9	24.5	23.5	20.4	18.1	17.0	17.3	17.3	16.4	17.1	17.2		15.4	13.9	17.3	17.6	17.3
RT24_WAMT144180_RC14MEB0150_WAM-CRYP001	31.9	27.4	25.7	22.6	24.2	24.2	22.3	22.6	23.3	21.3	21.5	21.4	24.3	22.9	22.9	25.7	24.8	24.9	21.6	23.0	22.3	20.1	24.2	23.0	22.8	26.0	23.5	18.9	17.5	17.8	18.4	19.0	17.2	18.0	18.1	15.4		9.2	17.1	16.8	16.6
RT24_WAMT144184_GR15MEC0015_WAM-CRYP002	29.6	26.9	25.7	23.6	24.5	24.5	22.9	23.4	22.9	20.4	21.0	20.9	22.3	24.0	23.1	24.7	23.9	23.7	22.0	22.5	23.6	20.8	23.7	25.0	24.7	26.1	23.5	19.7	18.2	19.1	19.1	17.6	17.3	17.9	17.9	13.9	9.2		17.0	16.8	16.6
BMR00277_BGCK_Scolopendridae sp.	29.2	24.5	25.6	23.7	22.8	22.8	21.8	21.8	22.8	21.0	21.9	21.9	24.4	25.0	24.4	26.8	27.5	27.5	23.8	25.5	21.9	19.6	22.1	22.9	22.9	28.9	23.9	20.2	19.9	18.8	15.9	17.7	15.5	16.0	16.0	17.3	17.1	17.0		0.9	0.8
BMR00276_BGCK_Scolopendridae sp.	29.5	24.7	25.5	23.5	23.2	23.2	22.3	22.0	22.8	21.2	21.8	21.8	24.6	25.1	24.5	26.8	27.4	27.6	23.8	25.3	22.0	19.8	22.2	22.8	22.8	29.1	24.2	20.2	19.8	18.8	16.3	18.1	15.9	16.3	16.3	17.6	16.8	16.8	0.9		0.4
BMR00280_BGCK_Cryptops?	29.5	24.8	25.7	23.4	22.8	22.8	22.0	21.7	22.5	20.9	21.8	21.8	24.3	25.1	24.5	26.8	27.1	27.2	23.7	25.8	21.9	19.6	22.1	23.1	23.1	28.7	23.9	20.1	19.6	18.5	16.0	17.8	15.5	16.0	16.0	17.3	16.6	16.6	0.8	0.4	

Appendix 7: Distance matrix of Polyxenida sequences/ lineages included in the analysis

COI divergence (%) of Polyxenida (regional comparisons)	O.G.	MF59 2725	KY82 0868	MF59 2721	MG20 4535	MG27 9506	P4	P11	P6	S46	P62	S22	BMR 00233	BMR 00416	S55	P32	S23	P12	P15	BMR 00492	S45	S12	S31	BMR 00477	P50	P1	P52	BMR 00234	BMR 00235	BMR 00262	BMR 00415	BMR 00476	P3	P33	P34
MH932612 Antichiropus sp. DIP174_OUTGROUP		20.3	30.0	22.5	21.9	21.3	24.2	23.5	22.4	22.3	22.3	22.8	22.8	22.9	23.0	23.3	23.1	22.9	23.3	22.3	22.5	23.3	22.2	22.2	22.9	22.3	22.6	22.5	22.8	22.9	23.6	22.8	23.8	23.1	23.8
MF592725 Alloproctoides sp. VV-2017	20.3		19.2	17.5	15.7	16.5	19.3	19.3	19.7	18.6	19.0	18.9	18.6	18.8	18.9	18.9	18.2	18.4	18.6	18.2	17.6	18.5	18.5	17.3	18.5	18.0	17.9	16.9	16.9	17.7	17.3	17.1	17.1	17.7	17.4
KY820868 Phryssonotus sp. WA	30.0	19.2		21.1	22.3	22.8	27.9	27.7	19.5	25.6	21.1	21.8	26.2	26.4	25.7	21.6	26.6	21.0	21.4	26.4	25.9	27.0	25.9	26.4	22.6	23.7	23.1	26.1	26.1	26.1	26.7	26.1	24.1	21.1	26.3
MF592721 Propolyxenus forsteri	22.5	17.5	21.1		19.2	18.0	19.7	19.9	20.8	20.0	20.9	20.2	20.3	20.5	20.1	20.2	19.0	19.3	19.9	18.0	20.1	17.7	17.3	16.9	18.3	17.8	17.7	17.7	18.8	18.0	18.2	17.7	18.0	18.4	18.5
MG204535 L. queenslandicus CH_AV_LQ1	21.9	15.7	22.3	19.2		15.1	18.0	17.9	16.2	16.1	16.1	16.3	16.7	16.9	17.2	16.6	17.0	16.4	16.7	16.1	16.5	16.8	16.4	15.5	15.9	15.9	15.6	16.3	16.1	16.4	16.6	16.3	16.0	16.1	16.7
MG279506 Monographis queenslandicus	21.3	16.5	22.8	18.0	15.1		17.6	17.7	15.5	15.8	15.5	15.2	15.9	16.1	16.5	16.1	16.9	15.9	16.2	15.0	16.5	17.4	16.6	15.3	15.4	15.3	15.9	14.8	14.6	14.8	15.0	14.6	14.8	14.8	15.2
P4_RC08SILV0795PIT1-3_Polyxenida	24.2	19.3	27.9	19.7	18.0	17.6		7.4	9.7	8.8	9.3	9.9	8.5	8.7	9.1	9.3	7.3	8.6	8.9	11.3	13.0	12.5	12.0	12.5	11.4	11.1	10.9	11.0	10.2	9.8	10.4	9.8	10.7	9.8	10.2
P11_RC08SILV0795PIT3-3_Polyxenida	23.5	19.3	27.7	19.9	17.9	17.7	7.4		8.6	7.4	7.7	8.4	7.6	7.7	7.8	8.0	5.1	6.5	7.0	11.5	12.6	12.4	11.5	12.0	11.1	11.1	10.8	11.2	10.3	9.8	10.8	9.5	11.0	10.6	10.8
P6_RC08SILVPIT1-3_Polyxenida	22.4	19.7	19.5	20.8	16.2	15.5	9.7	8.6		3.3	3.5	3.8	2.6	2.8	3.3	3.5	5.5	5.6	6.0	10.8	11.1	11.1	11.0	12.9	11.9	11.5	12.1	13.1	12.1	11.4	12.5	11.2	12.3	12.1	11.9
S46_RHWRC0303P2T2-3_Polyxenida_Hmstd-Namm-Silv	22.3	18.6	25.6	20.0	16.1	15.8	8.8	7.4	3.3		1.1	1.2	1.2	1.4	2.5	2.9	4.2	4.5	4.7	10.0	10.6	11.1	10.3	11.9	10.8	10.7	10.5	10.9	10.8	10.0	10.9	9.7	11.0	10.2	10.6
P62_CGBRC0285P1T2-2A_T102623A_Polyxenida	22.3	19.0	21.1	20.9	16.1	15.5	9.3	7.7	3.5	1.1		1.7	1.8	2.0	2.9	3.2	4.4	4.5	4.7	10.4	10.8	11.6	10.8	11.9	11.3	11.1	11.2	11.6	11.1	10.4	11.6	9.9	11.4	11.3	11.1
S22_CGBRC0278P2T1-2_Polyxenida_Hmstd-Namm-Silv	22.8	18.9	21.8	20.2	16.3	15.2	9.9	8.4	3.8	1.2	1.7		1.9	2.0	3.1	3.5	5.0	5.1	5.5	10.7	11.4	11.5	10.9	12.3	11.4	11.3	11.3	11.4	11.2	10.5	11.5	10.0	11.5	11.2	11.3
BMR00233_BS3_Polyxenida sp.	22.8	18.6	26.2	20.3	16.7	15.9	8.5	7.6	2.6	1.2	1.8	1.9		0.2	1.6	2.0	4.0	4.2	4.4	10.0	11.4	11.6	10.8	11.6	11.4	11.2	11.0	11.9	11.2	10.6	11.4	10.3	11.4	10.8	11.1
BMR00416_DSM_Polyxenida sp.	22.9	18.8	26.4	20.5	16.9	16.1	8.7	7.7	2.8	1.4	2.0	2.0	0.2		1.8	2.0	4.1	4.3	4.5	10.2	11.4	11.8	10.9	11.7	11.5	11.4	11.2	12.0	11.4	10.8	11.2	10.5	11.2	10.9	11.2
S55_RC08NAM389P2T3-2_Polyxenida_Hmstd-Namm-Silv	23.0	18.9	25.7	20.1	17.2	16.5	9.1	7.8	3.3	2.5	2.9	3.1	1.6	1.8		1.9	3.9	3.9	4.3	10.6	11.9	11.4	10.5	12.3	12.1	12.0	11.9	12.3	11.7	11.1	11.9	10.8	12.1	11.4	11.7
P32_RC05TCB476P1T2-4_T98386_Polyxenida	23.3	18.9	21.6	20.2	16.6	16.1	9.3	8.0	3.5	2.9	3.2	3.5	2.0	2.0	1.9		4.4	4.7	5.1	11.1	11.8	12.0	11.2	12.4	11.9	11.6	11.8	12.3	11.4	11.1	11.4	10.6	11.4	11.4	11.5
S23_RC09SV023P2T1-3_Polyxenida_Hmstd-Namm-Silv	23.1	18.2	26.6	19.0	17.0	16.9	7.3	5.1	5.5	4.2	4.4	5.0	4.0	4.1	3.9	4.4		2.1	2.9	10.8	12.2	11.8	10.9	12.5	12.5	12.1	11.9	12.0	11.1	10.6	11.6	10.5	11.8	11.3	11.4
P12_RC07S10B259P1T3-1_Polyxenida	22.9	18.4	21.0	19.3	16.4	15.9	8.6	6.5	5.6	4.5	4.5	5.1	4.2	4.3	3.9	4.7	2.1		1.9	10.8	12.1	12.0	11.2	12.5	12.3	11.8	11.8	12.6	11.1	11.1	11.8	10.8	11.7	11.6	11.6
P15_RC07S10B102P1T1-1_Polyxenida	23.3	18.6	21.4	19.9	16.7	16.2	8.9	7.0	6.0	4.7	4.7	5.5	4.4	4.5	4.3	5.1	2.9	1.9		11.2	11.9	12.2	11.2	12.7	12.3	12.0	12.0	13.2	11.3	11.3	12.0	11.0	11.9	11.8	11.7
BMR00492_ LN38435 Diplopoda HopeDowns	22.3	18.2	26.4	18.0	16.1	15.0	11.3	11.5	10.8	10.0	10.4	10.7	10.0	10.2	10.6	11.1	10.8	10.8	11.2		9.7	8.5	8.0	8.8	9.1	8.2	8.8	9.0	8.5	8.5	9.0	8.7	9.2	9.7	8.9
S45_RHWRC0250P2T3-3_Polyxenida_Hmstd-Namm-Silv	22.5	17.6	25.9	20.1	16.5	16.5	13.0	12.6	11.1	10.6	10.8	11.4	11.4	11.4	11.9	11.8	12.2	12.1	11.9	9.7		6.2	5.6	9.9	9.7	9.3	9.6	10.5	10.8	9.9	10.0	10.0	9.8	10.2	10.5
S12_CGBRC0293P2T2-2_Polyxenida_Hmstd-Namm-Silv	23.3	18.5	27.0	17.7	16.8	17.4	12.5	12.4	11.1	11.1	11.6	11.5	11.6	11.8	11.4	12.0	11.8	12.0	12.2	8.5	6.2		0.9	9.3	8.7	8.4	8.7	9.7	9.7	9.0	9.2	9.0	9.0	9.4	9.8
S31_CGBRC0285P2T2-2_Polyxenida_Hmstd-Namm-Silv	22.2	18.5	25.9	17.3	16.4	16.6	12.0	11.5	11.0	10.3	10.8	10.9	10.8	10.9	10.5	11.2	10.9	11.2	11.2	8.0	5.6	0.9		8.8	8.0	7.6	7.9	8.8	8.9	8.0	8.3	8.2	8.3	8.8	8.9
BMR00477_LNSG_Polyxenida sp.	22.2	17.3	26.4	16.9	15.5	15.3	12.5	12.0	12.9	11.9	11.9	12.3	11.6	11.7	12.3	12.4	12.5	12.5	12.7	8.8	9.9	9.3	8.8		9.1	8.7	8.1	8.7	7.8	7.6	9.0	7.1	8.9	8.5	8.5
P50_MEGDC0057AP1T1-3C_T99566C_Polyxenida	22.9	18.5	22.6	18.3	15.9	15.4	11.4	11.1	11.9	10.8	11.3	11.4	11.4	11.5	12.1	11.9	12.5	12.3	12.3	9.1	9.7	8.7	8.0	9.1		3.6	3.0	5.9	5.3	5.4	5.6	5.3	5.6	5.1	5.7
P1_DD08SILV09PIT1-1_Polyxenida	22.3	18.0	23.7	17.8	15.9	15.3	11.1	11.1	11.5	10.7	11.1	11.3	11.2	11.4	12.0	11.6	12.1	11.8	12.0	8.2	9.3	8.4	7.6	8.7	3.6		2.4	5.8	5.5	5.0	5.2	5.3	5.0	5.2	5.5
P52_RC03WR096P1T1-3B_Polyxenida	22.6	17.9	23.1	17.7	15.6	15.9	10.9	10.8	12.1	10.5	11.2	11.3	11.0	11.2	11.9	11.8	11.9	11.8	12.0	8.8	9.6	8.7	7.9	8.1	3.0	2.4		5.6	5.1	5.1	5.3	4.9	5.2	4.9	5.3
BMR00234_BS3_Polyxenida sp.	22.5	16.9	26.1	17.7	16.3	14.8	11.0	11.2	13.1	10.9	11.6	11.4	11.9	12.0	12.3	12.3	12.0	12.6	13.2	9.0	10.5	9.7	8.8	8.7	5.9	5.8	5.6		3.6	3.5	3.2	3.2	3.3	3.7	3.8
BMR00235_BS2_Polyxenida sp.	22.8	16.9	26.1	18.8	16.1	14.6	10.2	10.3	12.1	10.8	11.1	11.2	11.2	11.4	11.7	11.4	11.1	11.1	11.3	8.5	10.8	9.7	8.9	7.8	5.3	5.5	5.1	3.6		2.6	2.3	1.7	2.3	2.9	2.6
BMR00262_BS1C_Polyxenida sp.	22.9	17.7	26.1	18.0	16.4	14.8	9.8	9.8	11.4	10.0	10.4	10.5	10.6	10.8	11.1	11.1	10.6	11.1	11.3	8.5	9.9	9.0	8.0	7.6	5.4	5.0	5.1	3.5	2.6		3.0	2.1	3.1	3.7	3.2
BMR00415_SGW_Polyxenida	23.6	17.3	26.7	18.2	16.6	15.0	10.4	10.8	12.5	10.9	11.6	11.5	11.4	11.2	11.9	11.4	11.6	11.8	12.0	9.0	10.0	9.2	8.3	9.0	5.6	5.2	5.3	3.2	2.3	3.0		2.7	0.3	3.6	3.4
BMR00476_BS2_Polyxenida	22.8	17.1	26.1	17.7	16.3	14.6	9.8	9.5	11.2	9.7	9.9	10.0	10.3	10.5	10.8	10.6	10.5	10.8	11.0	8.7	10.0	9.0	8.2	7.1	5.3	5.3	4.9	3.2	1.7	2.1	2.7		2.8	3.4	3.1
P3_RC08SILV0796PIT1-2_Polyxenida	23.8	17.1	24.1	18.0	16.0	14.8	10.7	11.0	12.3	11.0	11.4	11.5	11.4	11.2	12.1	11.4	11.8	11.7	11.9	9.2	9.8	9.0	8.3	8.9	5.6	5.0	5.2	3.3	2.3	3.1	0.3	2.8		3.4	3.4
P33_WD05TCB006P1T2-2_T98384_Polyxenida	23.1	17.7	21.1	18.4	16.1	14.8	9.8	10.6	12.1	10.2	11.3	11.2	10.8	10.9	11.4	11.4	11.3	11.6	11.8	9.7	10.2	9.4	8.8	8.5	5.1	5.2	4.9	3.7	2.9	3.7	3.6	3.4	3.4		2.7
P34_RC05TCB667P1T2-1_T98389_Polyxenida	23.8	17.4	26.3	18.5	16.7	15.2	10.2	10.8	11.9	10.6	11.1	11.3	11.1	11.2	11.7	11.5	11.4	11.6	11.7	8.9	10.5	9.8	8.9	8.5	5.7	5.5	5.3	3.8	2.6	3.2	3.4	3.1	3.4	2.7	

Appendix 8: Distance matrix of Pauropoda sequences/ lineages included in the analysis

CO1 Divergence (%) of Pauropoda (regional comparisons)	OUT GROUP	BMR 00255	BMR 00252	BMR 00250	WAMT 145451	BMR 00475	BMR 00516	BMR 00086	BMR 00090	WAMT 145455	WAMT 145460	BMR 00087	BMR 00253	BMR 00421	BMR 00237	BMR 00236	BMR 00249	BMR 00763	BMR 00088	WAMT 145453	BMR 00089	WAMT 145459
KR705664_Scolopendra morsitans_OUTGROUP		33.5	26.5	30.1	32.3	31.2	32.6	33	32.9	31.6	32.3	24.5	24.7	23.1	29.8	26.6	27.7	28.3	28.5	28.9	25.4	25.9
BMR00255_BS1W_Pauropoda sp.	33.5		26.6	32.4	33.9	35	31	30.9	30.5	32.4	32.5	29.5	30.4	30.4	37.2	35	29.3	33.9	32.5	33.6	33.1	34.5
BMR00252_VIV_Pauropoda sp.	26.5	26.6		27.8	29.8	31.8	27.8	29	29.4	30.2	28.9	24.5	24.6	21.9	32.1	28.9	24.5	29.6	26.7	29.8	26.6	26.9
BMR00250_VIV_Pauropoda sp.	30.1	32.4	27.8		28.4	31.7	24.2	25.8	26.2	27.4	27.1	29.6	29.3	30.7	33.6	33.5	31.8	33.9	33.3	33	33.4	32.8
RT43_WAMT145451_Decapauropus_WAM-PAUD003	32.3	33.9	29.8	28.4		28.8	25.4	26.6	26	27	28.4	28.4	28.7	33.4	33.4	33.7	31.2	34.3	33	32.2	32.2	31.9
BMR00475_LNSG_Pauropoda sp.	31.2	35	31.8	31.7	28.8		20.5	19.4	20.1	29.7	29.5	30.4	30.7	32.9	36	33.7	34	35.6	35.1	34.7	33.7	34.3
BMR00516_BS2_Pauropoda sp.	32.6	31	27.8	24.2	25.4	20.5		11.1	12.2	25.1	23.1	30.1	30.2	30.4	34.2	34.7	32.1	33.3	33.4	35.4	33.7	33.1
BMR00086_BS2_Pauropoda sp.	33	30.9	29	25.8	26.6	19.4	11.1		3	25.5	24.5	29.9	30.4	30.7	35	33.4	32.8	34.3	34	34.8	35	34.2
BMR00090_BS2_Pauropoda sp.	32.9	30.5	29.4	26.2	26	20.1	12.2	3		25.1	25.3	29.4	30.1	31.5	35.6	33.1	32.2	33.9	33.8	34.4	33.9	33.8
RT43_WAMT145455_Decapauropus_WAM-PAUD005	31.6	32.4	30.2	27.4	27	29.7	25.1	25.5	25.1		12.4	29.2	31	32.4	35.3	34.1	32.5	32.5	33.7	33.5	34.3	34.1
RT43_WAMT145460_Decapauropus_WAM-PAUD004	32.3	32.5	28.9	27.1	28.4	29.5	23.1	24.5	25.3	12.4		30.1	31.8	33	36.3	33.6	34	32.5	35.1	34.9	33.4	34.1
BMR00087_CVCK_Pauropoda sp.	24.5	29.5	24.5	29.6	28.4	30.4	30.1	29.9	29.4	29.2	30.1		6.2	26	29.3	26.9	22.3	26	25.1	24.9	22.9	23.4
BMR00253_BGCK_Pauropoda sp.	24.7	30.4	24.6	29.3	28.7	30.7	30.2	30.4	30.1	31	31.8	6.2		25.8	28.4	27.4	22.8	25.7	25.5	24.9	24.8	24.8
BMR00421_BGCK_Pauropoda sp.	23.1	30.4	21.9	30.7	33.4	32.9	30.4	30.7	31.5	32.4	33	26	25.8		33.9	30.4	27.4	28.7	29	30.5	27.8	27.4
BMR00237_CVCK_Pauropoda sp.	29.8	37.2	32.1	33.6	33.4	36	34.2	35	35.6	35.3	36.3	29.3	28.4	33.9		29.9	30.7	31.8	30.7	30.4	30.1	29.6
BMR00236_BS3_Pauropoda sp.	26.6	35	28.9	33.5	33.7	33.7	34.7	33.4	33.1	34.1	33.6	26.9	27.4	30.4	29.9		25.2	26	25.5	27.4	25.7	26.1
BMR00249_BS1E_Pauropoda sp.	27.7	29.3	24.5	31.8	31.2	34	32.1	32.8	32.2	32.5	34	22.3	22.8	27.4	30.7	25.2		23.4	23.3	23.3	19.9	20.4
BMR00763_VIV_Pauropoda	28.3	33.9	29.6	33.9	34.3	35.6	33.3	34.3	33.9	32.5	32.5	26	25.7	28.7	31.8	26	23.4		22.6	20.8	20.4	20.7
BMR00088_LNSG_Pauropoda sp.	28.5	32.5	26.7	33.3	33	35.1	33.4	34	33.8	33.7	35.1	25.1	25.5	29	30.7	25.5	23.3	22.6		20.2	19.1	19.1
RT43_WAMT145453_Decapauropus_WAM-PAUD001	28.9	33.6	29.8	33	32.2	34.7	35.4	34.8	34.4	33.5	34.9	24.9	24.9	30.5	30.4	27.4	23.3	20.8	20.2		19	17.4
BMR00089_SGW_Pauropoda sp.	25.4	33.1	26.6	33.4	32.2	33.7	33.7	35	33.9	34.3	33.4	22.9	24.8	27.8	30.1	25.7	19.9	20.4	19.1	19		5
RT43_WAMT145459_Decapauropus_WAM-PAUD002	25.9	34.5	26.9	32.8	31.9	34.3	33.1	34.2	33.8	34.1	34.1	23.4	24.8	27.4	29.6	26.1	20.4	20.7	19.1	17.4	5	

Appendix 9: Distance matrix of Symphyla sequences/ lineages included in the analysis

COI divergences (%) of Symphyla (regional comparisons)	O.G.	ML54	WAMT 144261	BMR 00229	WAMT 145463	JY24	WAMT 144260	BMR 00202	BMR 01163	BMR 00231	JD04	BMR 00070	BMR 00071	IV354	WAMT 145911	BMR 00232	BMR 00230	BMR 01208	WAMT 145461	WAMT 145462	BMR 00320	BMR 00326	JY26	BMR 00721	JY25	BMR 00321	BMR 00724	BMR 00241	BMR 01199	BMR 00641	BMR 00242	BMR 00244	BMR 00243	BMR 00364	BMR 00725	BMR 00741	IV355	ML52	WAMT 145913	MO08	ML42	ML47	ML57	BMR 00762	WAMT 144298
KR705664 Scolopendra morsitans_OUTGROUP		23.6	27.1	27.2	25.4	28.6	26.2	25.3	27.2	26.3	30.6	32.6	28.9	27.2	26.6	25.1	25.0	24.7	27.1	26.6	27.9	27.1	26.5	26.5	27.2	26.2	30.8	25.3	25.1	25.9	26.0	26.2	25.4	26.7	26.6	27.1	25.1	27.2	24.6	23.8	23.6	23.8	23.8	27.2	26.5
ML54_ROBE_Symphyla	23.6		27.7	28.6	28.5	26.9	27.7	27.3	28.6	27.9	32.3	30.1	26.9	27.4	27.2	24.7	26.3	26.8	27.4	26.5	27.9	28.6	27.6	27.8	27.8	26.9	31.6	27.4	27.8	28.8	28.9	28.9	27.6	28.4	25.8	27.4	23.6	26.0	25.2	26.2	26.5	26.2	26.4	27.9	26.2
RT35_PARA_WAMT144261_Scutigerella_WAM-SCUTI005	27.1	27.7		18.4	18.5	20.6	19.5	18.2	17.4	16.4	21.6	22.4	17.2	18.9	19.2	18.1	15.8	16.0	16.1	16.4	21.2	19.6	17.8	18.4	18.5	18.8	22.0	19.3	17.6	18.1	18.2	18.2	16.1	17.3	25.7	27.4	23.7	26.3	27.5	25.5	27.0	27.1	27.3	24.6	25.0
BMR00229_CVCK_REG_Hanseniella sp.	27.2	28.6	18.4		16.9	18.8	20.4	18.5	18.6	17.8	22.3	22.7	16.4	19.6	20.0	15.5	15.8	16.0	18.1	16.9	19.5	18.8	16.6	17.2	17.3	16.9	20.3	19.3	16.1	16.1	16.3	16.4	19.1	20.8	26.3	25.8	24.3	26.7	27.1	26.0	26.4	26.5	26.7	24.6	25.1
RT43_PARA_WAMT145463_Scutigerella_WAM-SCUTI004	25.4	28.5	18.5	16.9		18.4	19.1	17.9	18.6	19.0	22.5	23.7	19.3	17.0	17.2	17.5	16.4	16.0	17.1	16.7	20.3	18.4	19.0	19.0	18.4	18.2	23.0	19.9	17.6	18.2	18.1	17.9	19.5	20.4	26.9	26.0	23.3	26.6	25.4	25.0	25.3	25.2	25.5	25.8	25.6
JY24_WAN_Scutigerellidae `sp. Helix-SYM027`	28.6	26.9	20.6	18.8	18.4		18.0	19.5	19.0	19.4	22.0	22.9	17.5	19.8	19.3	16.6	16.9	17.2	20.2	19.4	18.2	17.1	17.1	17.5	17.8	17.4	20.2	19.1	19.8	19.7	19.2	19.1	19.4	21.7	26.7	27.6	24.3	25.9	29.0	27.5	26.9	27.2	27.4	27.4	27.8
RT35_PARA_WAMT144260_Scutigerella_WAM-SCUTI002	26.2	27.7	19.5	20.4	19.1	18.0		18.8	18.9	19.6	23.4	24.7	20.2	18.2	18.3	19.0	17.3	17.3	16.7	16.7	20.2	19.3	19.0	19.5	20.5	19.9	24.0	18.8	17.9	17.9	17.6	17.6	18.7	20.1	26.1	27.8	24.6	24.5	26.3	26.2	25.3	25.3	25.5	25.4	24.7
BMR00202_HSTD_Hanseniella sp.	25.3	27.3	18.2	18.5	17.9	19.5	18.8		19.2	19.0	21.6	25.9	19.8	18.8	19.0	19.8	19.3	19.6	19.5	17.5	19.8	19.1	17.6	18.8	18.8	18.2	23.0	17.5	18.1	19.0	19.0	18.8	19.1	19.6	24.8	26.9	23.4	24.5	26.9	24.5	25.9	25.0	25.2	24.9	26.1
BMR01163_Boolgeeda Creek_Symphyla sp. indet.	27.2	28.6	17.4	18.6	18.6	19.0	18.9	19.2		17.4	20.7	24.2	18.5	18.2	17.7	17.4	16.8	17.4	17.6	18.5	18.9	17.1	16.5	16.9	17.7	17.2	21.2	18.6	18.3	19.2	18.8	18.8	17.9	18.7	27.6	26.2	24.2	27.2	28.3	25.4	26.9	26.9	27.0	26.5	26.4
BMR00231_BS2W_Hanseniella sp.	26.3	27.9	16.4	17.8	19.0	19.4	19.6	19.0	17.4		21.0	25.1	19.9	18.2	18.4	19.5	17.9	17.8	19.0	18.5	18.0	17.6	18.1	18.5	19.0	19.0	22.1	18.1	18.8	19.5	19.5	19.5	19.5	20.4	26.3	26.7	23.4	24.7	27.4	24.4	25.2	25.7	26.0	24.0	24.0
JD04_YANDI_Symphyla	30.6	32.3	21.6	22.3	22.5	22.0	23.4	21.6	20.7	21.0		25.6	22.1	22.0	21.2	21.2	20.8	21.0	22.3	22.7	23.3	22.7	23.4	23.2	23.6	23.1	23.1	23.6	23.6	24.0	24.0	24.0	22.3	22.5	26.6	29.7	27.2	29.0	30.8	28.6	29.3	29.2	29.5	29.2	30.1
BMR00070_LNSG_Symphyla sp.	32.6	30.1	22.4	22.7	23.7	22.9	24.7	25.9	24.2	25.1	25.6		8.6	24.2	24.1	22.4	22.1	22.1	23.4	23.1	25.2	24.4	23.8	22.5	23.2	24.0	24.9	23.4	22.8	24.0	24.0	24.0	23.7	23.2	30.6	32.6	29.6	31.7	32.1	31.4	30.1	29.9	30.3	30.9	31.2
BMR00071_DSM_Symphyla sp.	28.9	26.9	17.2	16.4	19.3	17.5	20.2	19.8	18.5	19.9	22.1	8.6		19.0	18.6	17.2	16.6	17.0	17.6	16.9	19.8	19.3	17.8	17.0	17.6	17.8	21.6	18.1	17.2	18.5	18.4	18.4	19.0	19.9	24.6	25.7	23.6	27.4	26.4	25.4	24.5	24.7	25.0	25.1	26.9
IV354_ROBE_Symphyella_sp.	27.2	27.4	18.9	19.6	17.0	19.8	18.2	18.8	18.2	18.2	22.0	24.2	19.0		1.7	17.6	18.2	18.1	18.0	16.9	19.5	18.2	16.9	17.2	17.9	17.8	22.3	17.5	17.3	17.8	17.6	17.5	18.8	20.2	24.5	24.8	22.4	25.5	25.8	25.3	25.5	25.2	25.5	24.3	24.4
RT48_ROBE_WAMT145911_Scutigerella_WAM-SCUTI001	26.6	27.2	19.2	20.0	17.2	19.3	18.3	19.0	17.7	18.4	21.2	24.1	18.6	1.7		16.9	17.7	17.5	18.1	17.2	18.8	17.8	16.4	16.4	17.5	17.2	21.2	17.1	17.2	17.2	17.1	16.9	18.9	20.4	24.3	24.3	22.1	25.3	25.7	24.7	25.0	24.7	25.0	23.8	24.6
BMR00232_BS2W_Hanseniella sp.	25.1	24.7	18.1	15.5	17.5	16.6	19.0	19.8	17.4	19.5	21.2	22.4	17.2	17.6	16.9		8.5	9.0	17.9	17.3	19.0	17.8	18.4	18.4	18.7	18.2	21.3	18.7	17.6	17.6	17.6	17.6	17.2	18.0	23.4	24.0	22.1	25.2	25.2	23.9	24.0	24.5	24.7	23.1	26.1
BMR00230_BS2W_Hanseniella sp.	25.0	26.3	15.8	15.8	16.4	16.9	17.3	19.3	16.8	17.9	20.8	22.1	16.6	18.2	17.7	8.5		1.7	15.2	16.0	19.0	17.8	18.1	17.9	17.8	17.6	20.3	18.2	16.3	16.4	16.3	16.3	16.9	17.7	24.6	25.7	22.7	24.7	23.7	23.7	24.0	24.7	24.9	24.2	25.5
BMR01208_BS2W_Symphyla?	24.7	26.8	16.0	16.0	16.0	17.2	17.3	19.6	17.4	17.8	21.0	22.1	17.0	18.1	17.5	9.0	1.7		15.5	16.1	19.0	17.8	18.1	17.9	17.8	17.8	20.3	18.7	16.6	16.6	16.7	16.7	16.9	17.8	24.6	25.2	22.9	24.9	23.7	23.5	23.9	24.7	24.7	24.5	26.3
RT43_PARA_WAMT145461_Scutigerella_WAM-SCUTI003	27.1	27.4	16.1	18.1	17.1	20.2	16.7	19.5	17.6	19.0	22.3	23.4	17.6	18.0	18.1	17.9	15.2	15.5		5.3	19.8	19.3	17.6	17.8	18.8	18.7	22.5	18.2	16.7	17.0	16.7	16.7	16.9	18.9	26.0	26.3	25.1	26.5	25.8	25.5	26.0	26.2	26.5	25.1	25.1
RT43_WAMT145462_Scutigerella_WAM-SCUTI003	26.6	26.5	16.4	16.9	16.7	19.4	16.7	17.5	18.5	18.5	22.7	23.1	16.9	16.9	17.2	17.3	16.0	16.1	5.3		20.0	19.5	17.0	17.3	18.2	17.3	21.2	17.8	16.3	16.6	16.3	16.3	17.0	18.3	24.2	25.2	24.5	26.2	25.7	24.7	24.8	25.0	25.3	24.0	24.9
BMR00320_WAJ_Hanseniella sp.	27.9	27.9	21.2	19.5	20.3	18.2	20.2	19.8	18.9	18.0	23.3	25.2	19.8	19.5	18.8	19.0	19.0	19.0	19.8	20.0		4.1	16.9	17.3	18.1	17.6	22.4	19.0	18.5	19.0	19.1	19.1	20.2	21.0	27.4	25.7	27.5	27.6	28.1	28.7	28.2	27.8	28.2	26.6	27.2
BMR00326_WAJ_Symphyla sp.	27.1	28.6	19.6	18.8	18.4	17.1	19.3	19.1	17.1	17.6	22.7	24.4	19.3	18.2	17.8	17.8	17.8	17.8	19.3	19.5	4.1		16.6	16.9	17.3	17.0	21.9	17.9	18.1	18.5	18.1	18.1	19.1	20.0	26.9	25.5	25.8	27.9	28.0	27.5	27.2	27.0	27.4	25.2	26.6
JY26_WAN_Scutigerellidae `sp. Helix-SYM029`	26.5	27.6	17.8	16.6	19.0	17.1	19.0	17.6	16.5	18.1	23.4	23.8	17.8	16.9	16.4	18.4	18.1	18.1	17.6	17.0	16.9	16.6		3.6	5.0	4.6	9.4	18.7	17.2	17.8	17.9	17.9	19.1	21.4	25.8	23.1	24.5	26.9	26.4	25.4	25.7	25.4	25.7	24.3	26.4
BMR00721_WAH_Symphyla sp.	26.5	27.8	18.4	17.2	19.0	17.5	19.5	18.8	16.9	18.5	23.2	22.5	17.0	17.2	16.4	18.4	17.9	17.9	17.8	17.3	17.3	16.9	3.6		5.3	5.0	9.0	19.0	17.5	17.8	17.8	17.8	19.1	20.3	26.0	24.0	25.0	26.7	26.3	24.9	24.4	24.2	24.5	24.8	27.8
JY25_WAN_Scutigerellidae `sp. Helix-SYM028`	27.2	27.8	18.5	17.3	18.4	17.8	20.5	18.8	17.7	19.0	23.6	23.2	17.6	17.9	17.5	18.7	17.8	17.8	18.8	18.2	18.1	17.3	5.0	5.3		5.0	9.4	20.1	18.2	18.7	18.4	18.4	19.0	20.7	26.1	24.6	24.7	27.4	26.7	24.7	25.4	25.0	25.4	26.4	27.2
BMR00321_WAF_Symphyla sp.	26.2	26.9	18.8	16.9	18.2	17.4	19.9	18.2	17.2	19.0	23.1	24.0	17.8	17.8	17.2	18.2	17.6	17.8	18.7	17.3	17.6	17.0	4.6	5.0	5.0		5.7	19.0	17.8	17.9	17.9	17.9	18.8	20.5	25.8	24.5	25.2	26.7	26.4	24.7	25.0	24.7	25.0	24.3	26.4
BMR00724_WAH_Symphyla sp.	30.8	31.6	22.0	20.3	23.0	20.2	24.0	23.0	21.2	22.1	23.1	24.9	21.6	22.3	21.2	21.3	20.3	20.3	22.5	21.2	22.4	21.9	9.4	9.0	9.4	5.7		23.8	21.1	20.9	21.1	21.1	22.6	23.8	31.2	30.2	29.8	29.4	30.4	27.9	28.9	28.9	29.1	27.4	30.8
BMR00241_BGCK_Symphyla sp.	25.3	27.4	19.3	19.3	19.9	19.1	18.8	17.5	18.6	18.1	23.6	23.4	18.1	17.5	17.1	18.7	18.2	18.7	18.2	17.8	19.0	17.9	18.7	19.0	20.1	19.0	23.8		15.3	15.7	15.8	15.7	16.1	18.0	24.6	24.0	22.3	23.9	25.7	23.9	24.4	24.4	24.7	25.7	26.4
BMR01199_BS1E_Symphyla sp. indet.	25.1	27.8	17.6	16.1	17.6	19.8	17.9	18.1	18.3	18.8	23.6	22.8	17.2	17.3	17.2	17.6	16.3	16.6	16.7	16.3	18.5	18.1	17.2	17.5	18.2	17.8	21.1	15.3		3.2	3.3	3.5	11.9	12.3	24.3	24.9	21.4	25.0	25.1	23.7	24.0	24.2	24.4	24.2	25.4
BMR00641_VIV_Symphyla	25.9	28.8	18.1	16.1	18.2	19.7	17.9	19.0	19.2	19.5	24.0	24.0	18.5	17.8	17.2	17.6	16.4	16.6	17.0	16.6	19.0	18.5	17.8	17.8	18.7	17.9	20.9	15.7	3.2		0.8	0.9	12.0	12.9	25.4	25.4	23.0	25.4	25.8	24.4	25.4	25.5	25.7	24.8	26.7
BMR00242_VIV_Symphyla sp.	26.0	28.9	18.2	16.3	18.1	19.2	17.6	19.0	18.8	19.5	24.0	24.0	18.4	17.6	17.1	17.6	16.3	16.7	16.7	16.3	19.1	18.1	17.9	17.8	18.4	17.9	21.1	15.8	3.3	0.8		0.2	12.2	13.0	25.4	25.2	23.0	25.2	25.8	24.2	24.9	25.0	25.2	25.1	26.3
BMR00244_VIV_Symphyla sp.	26.2	28.9	18.2	16.4	17.9	19.1	17.6	18.8	18.8	19.5	24.0	24.0	18.4	17.5	16.9	17.6	16.3	16.7	16.7	16.3	19.1	18.1	17.9	17.8	18.4	17.9	21.1	15.7	3.5	0.9	0.2		12.0	13.0	25.4	25.2	23.0	25.2	25.8	24.2	24.9	25.0	25.2	25.1	26.3
BMR00243_VIV_Cephalostigmata sp.	25.4	27.6	16.1	19.1	19.5	19.4	18.7	19.1	17.9	19.5	22.3	23.7	19.0	18.8	18.9	17.2	16.9	16.9	16.9	17.0	20.2	19.1	19.1	19.1	19.0	18.8	22.6	16.1	11.9	12.0	12.2	12.0		2.8	25.1	25.7	22.1	24.2	25.8	23.5	25.4	25.4	25.5	24.6	26.0
BMR00364_VIV_Hanseniella sp.	26.7	28.4	17.3	20.8	20.4	21.7	20.1	19.6	18.7	20.4	22.5	23.2	19.9	20.2	20.4	18.0	17.7	17.8	18.9	18.3	21.0	20.0	21.4	20.3	20.7	20.5	23.8	18.0	12.3	12.9	13.0	13.0	2.8		27.0	28.3	22.9	26.1	27.0	24.7	26.4	26.4	26.6	26.2	27.7
BMR00725_WHill_Symphyla sp.	26.6	25.8	25.7	26.3	26.9	26.7	26.1	24.8	27.6	26.3	26.6	30.6	24.6	24.5	24.3	23.4	24.6	24.6	26.0	24.2	27.4	26.9	25.8	26.0	26.1	25.8	31.2	24.6	24.3	25.4	25.4	25.4	25.1	27.0		13.5	17.2	15.8	17.5	15.6	14.8	14.8	14.9	23.4	23.1
BMR00741_VIV_Symphyla sp.	27.1	27.4	27.4	25.8	26.0	27.6	27.8	26.9	26.2	26.7	29.7	32.6	25.7	24.8	24.3	24.0	25.7	25.2	26.3	25.2	25.7	25.5	23.1	24.0	24.6	24.5	30.2	24.0	24.9	25.4	25.2	25.2	25.7	28.3	13.5		18.9	19.4	19.8	17.6	17.9	18.1	18.1	22.5	26.1
IV355_ROBE_Scolopendrellidae `sp. Helix-SYM026`	25.1	23.6	23.7	24.3	23.3	24.3	24.6	23.4	24.2	23.4	27.2	29.6	23.6	22.4	22.1	22.1	22.7	22.9	25.1	24.5	27.5	25.8	24.5	25.0	24.7	25.2	29.8	22.3	21.4	23.0	23.0	23.0	22.1	22.9	17.2	18.9		11.7	14.2	12.1	13.1	13.3	13.3	19.4	23.0
ML52_ROBE_Symphyla	27.2	26.0	26.3	26.7	26.6	25.9	24.5	24.5	27.2	24.7	29.0	31.7	27.4	25.5	25.3	25.2	24.7	24.9	26.5	26.2	27.6	27.9	26.9	26.7	27.4	26.7	29.4	23.9	25.0	25.4	25.2	25.2	24.2	26.1	15.8	19.4	11.7		14.1	10.9	12.3	12.3	12.5	22.4	25.0
RT48_ROBE_WAMT145913_Symphyella_WAM-SYMPH001	24.6	25.2	27.5	27.1	25.4	29.0	26.3	26.9	28.3	27.4	30.8	32.1	26.4	25.8	25.7	25.2	23.7	23.7	25.8	25.7	28.1	28.0	26.4	26.3	26.7	26.4	30.4	25.7	25.1	25.8	25.8	25.8	25.8	27.0	17.5	19.8	14.2	14.1		12.2	11.3	11.8	11.8	23.4	25.6
MO08_ROBE_Symphyla	23.8	26.2	25.5	26.0	25.0	27.5	26.2	24.5	25.4	24.4	28.6	31.4	25.4	25.3	24.7	23.9	23.7	23.5	25.5	24.7	28.7	27.5	25.4	24.9	24.7	24.7	27.9	23.9	23.7	24.4	24.2	24.2	23.5	24.7	15.6	17.6	12.1	10.9	12.2		7.9	8.2	8.6	21.9	25.3
ML42_ROBE_Symphyla	23.6	26.5	27.0	26.4	25.3	26.9	25.3	25.9	26.9	25.2	29.3	30.1	24.5	25.5	25.0	24.0	24.0	23.9	26.0	24.8	28.2	27.2	25.7	24.4	25.4	25.0	28.9	24.4	24.0	25.4	24.9	24.9	25.4	26.4	14.8	17.9	13.1	12.3	11.3	7.9		1.3	1.3	22.1	24.7
ML47_ROBE_Symphyla	23.8	26.2	27.1	26.5	25.2	27.2	25.3	25.0	26.9	25.7	29.2	29.9	24.7	25.2	24.7	24.5	24.7	24.7	26.2	25.0	27.8	27.0	25.4	24.2	25.0	24.7	28.9	24.4	24.2	25.5	25.0	25.0	25.4	26.4	14.8	18.1	13.3	12.3	11.8	8.2	1.3		0.3	22.4	25.0
ML57_ROBE_Symphyla	23.8	26.4	27.3	26.7	25.5	27.4	25.5	25.2	27.0	26.0	29.5	30.3	25.0	25.5	25.0	24.7	24.9	24.7	26.5	25.3	28.2	27.4	25.7	24.5	25.4	25.0	29.1	24.7	24.4	25.7	25.2	25.2	25.5	26.6	14.9	18.1	13.3	12.5	11.8	8.6	1.3	0.3		22.6	25.2
BMR00762_VIV_Symphyla	27.2	27.9	24.6	24.6	25.8	27.4	25.4	24.9	26.5	24.0	29.2	30.9	25.1	24.3	23.8	23.1	24.2	24.5	25.1	24.0	26.6	25.2	24.3	24.8	26.4	24.3	27.4	25.7	24.2	24.8	25.1	25.1	24.6	26.2	23.4	22.5	19.4	22.4	23.4	21.9	22.1	22.4	22.6		20.4
RT46_PARA_WAMT144298_Symphyella_WAM-SYMPH002	26.5	26.2	25.0	25.1	25.6	27.8	24.7	26.1	26.4	24.0	30.1	31.2	26.9	24.4	24.6	26.1	25.5	26.3	25.1	24.9	27.2	26.6	26.4	27.8	27.2	26.4	30.8	26.4	25.4	26.7	26.3	26.3	26.0	27.7	23.1	26.1	23.0	25.0	25.6	25.3	24.7	25.0	25.2	20.4	

Appendix 10: Distance matrix of Diplura sequences/ lineages included in the analysis

COI divergences (%) of Diplura (regional comparisons)	O.G.	BMR01195	WAME98601	BMR00265	EW0300	BMR00192	BMR01223	KU02	KU01	BMR00227	BMR00362	JU02	IV160	JQ796644	BMR00186	BMR00225	IV245	IV248	WAME34029	IV154	IV155	WAME98598	BMR00380	BMR01205	BMR00207	EW0333	BMR00490	BMR00297	BMR00781	JU01	LI30	BMR00269	BMR00274	JC18	WAME98666	KE04	BMR00209	KU08	KD12	BMR00737	BMR00728	IV156	JF37	BMR00195	KD15
RT43_WAME98535_Phaconeura_WAM-PHAC001_OUTGROUP		27.8	29.5	30.1	27.5	29.3	29.6	30.7	36.3	28.7	32.5	34.7	35.6	29.2	30.4	28.6	30.7	31.2	31.9	30.9	30.8	27.3	27.7	27.7	27.9	28.4	29.5	29.0	28.4	28.8	28.7	28.3	29.5	27.8	26.0	26.3	31.0	29.2	28.2	32.4	30.8	29.7	28.2	30.2	28.7
BMR01195_BS1E_Diplura	27.8		16.4	18.5	17.8	18.7	19.1	18.2	24.2	16.1	17.2	28.0	34.1	24.3	28.3	26.9	25.5	26.1	27.0	28.9	29.0	25.1	24.5	24.5	23.8	25.5	24.5	23.7	23.1	25.2	24.9	24.0	24.0	24.0	23.6	23.6	26.0	25.7	25.8	26.4	27.1	25.7	24.3	25.8	27.1
RT48_ROBE_WAME98601_Diplura_COI	29.5	16.4		18.7	16.4	20.5	20.7	17.6	24.0	19.6	17.8	27.8	31.9	24.0	30.1	27.4	26.1	27.2	27.3	28.5	29.4	23.8	24.5	24.5	21.9	22.9	24.2	25.8	24.8	24.5	24.2	22.8	23.9	22.6	21.7	23.9	26.3	25.8	24.2	26.7	27.7	25.8	24.8	24.6	25.0
BMR00265_BS1E_Projapygidae sp.	30.1	18.5	18.7		16.9	20.5	20.6	18.4	25.3	16.4	16.6	28.0	33.3	25.7	26.9	27.4	28.9	26.6	28.2	30.7	29.1	25.5	25.2	25.2	25.5	25.1	24.2	25.8	25.4	27.2	26.4	24.5	24.6	26.1	25.7	27.4	28.9	26.7	24.9	28.3	28.9	27.8	26.0	26.1	25.8
Projapygidae sp EW0300	27.5	17.8	16.4	16.9		17.0	17.1	16.8	23.4	16.3	16.6	26.4	31.8	24.9	27.2	27.4	27.8	27.1	27.2	26.7	28.4	24.5	24.8	24.8	23.4	21.7	24.2	25.2	24.3	23.8	24.2	24.8	24.3	23.0	22.5	24.9	26.3	25.6	25.3	27.5	26.2	25.5	23.4	26.3	24.9
BMR00192_HSTD_Projapygidae sp.	29.3	18.7	20.5	20.5	17.0		1.1	17.9	26.1	19.5	18.5	26.8	32.0	24.6	27.7	26.9	27.2	26.0	28.2	29.8	29.5	24.9	25.8	25.8	26.3	25.8	24.3	25.1	24.9	26.4	26.1	25.4	25.1	25.4	25.1	25.8	26.4	26.3	26.1	25.8	25.0	26.6	25.4	24.9	25.8
BMR01223_Caves Creek_Diplura	29.6	19.1	20.7	20.6	17.1	1.1		17.9	26.9	19.8	18.8	26.9	31.8	24.5	28.0	26.8	27.3	25.8	28.1	29.6	29.6	25.0	25.9	25.9	26.0	25.8	24.4	25.6	25.5	26.8	26.1	25.6	25.5	25.8	25.0	25.8	26.5	26.1	26.5	25.6	24.7	26.4	25.5	24.7	25.5
KU02_ROBE_Projapygidae `sp. Helix-DPR008/DPR009/DPR011`	30.7	18.2	17.6	18.4	16.8	17.9	17.9		20.5	17.6	15.3	28.6	32.5	25.4	28.4	27.7	30.4	29.7	28.8	28.3	28.8	25.1	26.3	26.3	25.8	25.9	26.7	26.9	27.8	26.9	27.2	27.2	26.7	26.9	25.4	27.0	27.1	24.8	25.8	28.1	26.3	26.4	26.3	27.5	25.2
KU01_ROBE_Projapygidae `sp. Helix-DPR010`	36.3	24.2	24.0	25.3	23.4	26.1	26.9	20.5		24.4	24.8	32.0	39.6	32.5	35.4	34.9	35.7	36.2	33.6	34.0	34.1	31.5	32.7	32.7	32.9	31.4	31.3	30.4	30.7	31.0	33.0	33.0	33.1	32.1	31.6	31.6	34.2	32.0	32.9	34.9	34.9	34.1	32.6	34.2	31.9
BMR00227_DSM_Projapygidae sp.	28.7	16.1	19.6	16.4	16.3	19.5	19.8	17.6	24.4		13.7	26.1	34.3	24.9	27.2	26.9	27.2	26.3	28.3	28.6	28.7	25.4	25.8	25.8	24.4	25.4	24.6	26.7	26.3	25.5	25.5	23.7	25.4	24.2	22.5	26.4	26.7	26.1	24.9	27.1	28.1	25.8	25.4	25.5	26.3
BMR00362_BGCK_Projapygidae sp.	32.5	17.2	17.8	16.6	16.6	18.5	18.8	15.3	24.8	13.7		27.4	32.9	24.2	27.1	28.0	28.4	26.9	27.3	29.5	29.6	25.2	25.4	25.4	24.6	25.5	25.2	26.4	26.3	26.9	27.7	24.3	24.9	26.7	25.1	27.5	26.9	26.3	26.3	26.7	27.1	27.7	27.5	26.6	26.9
JU02_ROBE_Campodeidae `sp. Helix-DCA005`	34.7	28.0	27.8	28.0	26.4	26.8	26.9	28.6	32.0	26.1	27.4		32.3	24.7	26.8	27.1	23.0	22.4	24.1	27.5	26.3	25.3	26.8	26.8	27.7	27.0	23.6	24.0	24.7	24.4	26.1	25.5	26.1	25.2	23.6	26.6	28.8	25.5	24.2	26.0	29.6	25.2	25.6	26.4	25.6
IV160_ROBE_Diplura sp.	35.6	34.1	31.9	33.3	31.8	32.0	31.8	32.5	39.6	34.3	32.9	32.3		28.2	31.6	30.0	30.4	29.1	29.3	32.1	30.2	28.6	28.3	28.3	29.0	27.9	28.7	29.0	30.8	28.4	28.3	29.8	29.3	30.5	30.4	28.9	29.7	29.5	29.4	29.0	28.7	29.8	28.5	29.5	28.0
JQ796644 Parajapyx isabellae SH06009	29.2	24.3	24.0	25.7	24.9	24.6	24.5	25.4	32.5	24.9	24.2	24.7	28.2		24.0	20.7	21.3	21.9	24.1	26.7	25.1	16.9	18.1	18.1	17.0	18.4	17.5	17.8	17.9	18.2	18.8	17.8	17.2	21.3	18.2	18.7	19.3	17.9	17.2	19.8	20.1	18.8	17.3	18.5	19.3
BMR00186_HSTD_Diplura sp.	30.4	28.3	30.1	26.9	27.2	27.7	28.0	28.4	35.4	27.2	27.1	26.8	31.6	24.0		16.3	26.3	25.5	23.2	26.7	26.2	25.5	22.9	22.9	23.8	24.5	24.6	24.3	24.6	25.8	25.5	25.5	25.2	25.1	24.3	24.5	24.9	26.0	26.4	27.5	25.8	26.4	25.7	23.6	25.4
BMR00225_BS3X_Parajapygidae sp.	28.6	26.9	27.4	27.4	27.4	26.9	26.8	27.7	34.9	26.9	28.0	27.1	30.0	20.7	16.3		26.3	26.0	24.7	27.2	25.9	22.9	22.0	22.0	21.4	22.5	23.9	23.1	24.9	23.1	22.9	22.2	22.3	22.6	21.6	22.8	24.0	23.3	23.9	25.4	25.4	26.6	24.8	23.7	23.6
IV245_ROBE_Parajapygidae_ sp. `DPA003`	30.7	25.5	26.1	28.9	27.8	27.2	27.3	30.4	35.7	27.2	28.4	23.0	30.4	21.3	26.3	26.3		12.1	24.7	27.4	26.7	22.3	22.5	22.5	21.7	22.4	23.6	23.1	22.6	21.8	21.5	22.0	23.4	22.1	20.7	22.8	24.3	19.6	18.8	21.1	22.6	20.7	18.1	20.7	20.4
IV248_ROBE_Parajapygidae_ sp. `DPA005`	31.2	26.1	27.2	26.6	27.1	26.0	25.8	29.7	36.2	26.3	26.9	22.4	29.1	21.9	25.5	26.0	12.1		25.7	26.8	26.1	20.1	21.9	21.9	20.8	20.9	21.3	21.9	22.8	21.8	22.1	21.4	21.0	22.9	20.2	22.2	22.2	19.6	19.1	22.0	22.0	19.4	19.1	19.0	19.5
RT27_WAME34029_Mesa_K_Diplura	31.9	27.0	27.3	28.2	27.2	28.2	28.1	28.8	33.6	28.3	27.3	24.1	29.3	24.1	23.2	24.7	24.7	25.7		19.1	20.6	25.0	23.9	23.9	24.2	24.5	26.8	24.4	23.9	24.9	25.0	24.5	24.5	24.9	23.7	22.3	24.5	24.4	26.0	27.5	27.2	27.2	25.4	25.0	25.0
IV154_ROBE_Campodeidae `sp. Helix-DCA001`	30.9	28.9	28.5	30.7	26.7	29.8	29.6	28.3	34.0	28.6	29.5	27.5	32.1	26.7	26.7	27.2	27.4	26.8	19.1		14.4	24.8	27.2	27.2	24.4	25.1	26.7	25.5	26.4	26.1	26.6	25.1	26.3	25.5	25.0	24.3	26.1	25.8	27.3	29.6	29.0	26.1	25.8	26.4	26.4
IV155_ROBE_Campodeidae `sp. Helix-DCA002/03`	30.8	29.0	29.4	29.1	28.4	29.5	29.6	28.8	34.1	28.7	29.6	26.3	30.2	25.1	26.2	25.9	26.7	26.1	20.6	14.4		25.1	26.2	26.2	24.8	24.6	24.2	24.8	25.4	25.4	27.0	23.2	23.5	25.2	24.5	25.7	26.1	24.4	26.6	28.8	27.2	25.6	25.2	25.8	26.1
RT48_ROBE_WAME98598_Japygidae_COI	27.3	25.1	23.8	25.5	24.5	24.9	25.0	25.1	31.5	25.4	25.2	25.3	28.6	16.9	25.5	22.9	22.3	20.1	25.0	24.8	25.1		16.9	16.9	15.5	15.8	17.2	16.4	16.3	16.5	16.7	13.7	13.8	17.9	14.6	16.4	17.5	16.4	17.7	19.0	21.0	16.7	16.0	17.9	17.7
BMR00380_BS1E_Japygidae sp.	27.7	24.5	24.5	25.2	24.8	25.8	25.9	26.3	32.7	25.8	25.4	26.8	28.3	18.1	22.9	22.0	22.5	21.9	23.9	27.2	26.2	16.9		0.0	8.3	8.8	15.8	16.0	15.8	16.6	17.3	14.4	15.0	17.3	14.3	15.5	16.3	18.7	19.6	21.6	19.9	21.6	20.1	19.9	19.8
BMR01205_BS1E_Diplura	27.7	24.5	24.5	25.2	24.8	25.8	25.9	26.3	32.7	25.8	25.4	26.8	28.3	18.1	22.9	22.0	22.5	21.9	23.9	27.2	26.2	16.9	0.0		8.3	8.8	15.8	16.0	15.8	16.6	17.3	14.4	15.0	17.3	14.3	15.5	16.3	18.7	19.6	21.6	19.9	21.6	20.1	19.9	19.8
BMR00207_BS1W_Japygidae? sp.	27.9	23.8	21.9	25.5	23.4	26.3	26.0	25.8	32.9	24.4	24.6	27.7	29.0	17.0	23.8	21.4	21.7	20.8	24.2	24.4	24.8	15.5	8.3	8.3		4.2	15.3	17.0	16.5	16.4	15.6	13.8	14.6	14.1	13.4	14.6	15.8	15.8	17.0	20.6	21.3	20.2	16.5	17.9	17.6
Japygidae sp EW0333	28.4	25.5	22.9	25.1	21.7	25.8	25.8	25.9	31.4	25.4	25.5	27.0	27.9	18.4	24.5	22.5	22.4	20.9	24.5	25.1	24.6	15.8	8.8	8.8	4.2		16.0	17.3	17.0	16.4	16.0	14.7	14.9	13.0	13.9	15.3	16.7	17.4	18.0	20.4	21.5	20.3	17.5	19.6	18.8
BMR00490_LN33785 Diplura HopeDowns	29.5	24.5	24.2	24.2	24.2	24.3	24.4	26.7	31.3	24.6	25.2	23.6	28.7	17.5	24.6	23.9	23.6	21.3	26.8	26.7	24.2	17.2	15.8	15.8	15.3	16.0		9.0	9.0	16.7	18.4	15.5	14.9	17.6	16.0	17.5	18.5	20.4	20.2	22.2	23.3	19.9	20.5	20.7	19.6
BMR00297_WAF_Japygidae sp.	29.0	23.7	25.8	25.8	25.2	25.1	25.6	26.9	30.4	26.7	26.4	24.0	29.0	17.8	24.3	23.1	23.1	21.9	24.4	25.5	24.8	16.4	16.0	16.0	17.0	17.3	9.0		6.4	17.3	17.9	16.9	15.0	18.2	16.0	16.4	18.2	18.2	20.2	22.3	22.1	20.8	20.8	21.1	19.8
BMR00781_WAJ_Japygidae sp.	28.4	23.1	24.8	25.4	24.3	24.9	25.5	27.8	30.7	26.3	26.3	24.7	30.8	17.9	24.6	24.9	22.6	22.8	23.9	26.4	25.4	16.3	15.8	15.8	16.5	17.0	9.0	6.4		17.3	18.5	16.6	16.0	17.8	16.6	17.3	20.1	19.0	20.2	23.4	23.8	20.1	19.9	21.9	20.5
JU01_ROBE_Japygidae `sp. Helix-DJA003`	28.8	25.2	24.5	27.2	23.8	26.4	26.8	26.9	31.0	25.5	26.9	24.4	28.4	18.2	25.8	23.1	21.8	21.8	24.9	26.1	25.4	16.5	16.6	16.6	16.4	16.4	16.7	17.3	17.3		10.8	16.3	16.0	17.8	15.7	15.2	17.8	18.4	19.2	21.6	21.3	20.3	18.5	20.1	19.7
LI30_MEAWO4088-ROBE_Diplura	28.7	24.9	24.2	26.4	24.2	26.1	26.1	27.2	33.0	25.5	27.7	26.1	28.3	18.8	25.5	22.9	21.5	22.1	25.0	26.6	27.0	16.7	17.3	17.3	15.6	16.0	18.4	17.9	18.5	10.8		16.0	16.1	15.8	15.8	14.7	17.5	19.2	18.2	20.7	23.1	19.3	17.7	18.7	18.0
BMR00269_BS1E_Japygidae sp.	28.3	24.0	22.8	24.5	24.8	25.4	25.6	27.2	33.0	23.7	24.3	25.5	29.8	17.8	25.5	22.2	22.0	21.4	24.5	25.1	23.2	13.7	14.4	14.4	13.8	14.7	15.5	16.9	16.6	16.3	16.0		9.6	14.1	14.6	15.3	18.1	18.8	17.8	20.2	21.3	18.8	18.5	17.3	19.8
BMR00274_BGCK_Japygidae sp.	29.5	24.0	23.9	24.6	24.3	25.1	25.5	26.7	33.1	25.4	24.9	26.1	29.3	17.2	25.2	22.3	23.4	21.0	24.5	26.3	23.5	13.8	15.0	15.0	14.6	14.9	14.9	15.0	16.0	16.0	16.1	9.6		14.4	14.6	15.5	16.6	18.8	19.1	21.0	19.4	19.1	18.4	18.8	18.7
JC18_BROCK4_Japygidae `sp. Helix marra mamba`	27.8	24.0	22.6	26.1	23.0	25.4	25.8	26.9	32.1	24.2	26.7	25.2	30.5	21.3	25.1	22.6	22.1	22.9	24.9	25.5	25.2	17.9	17.3	17.3	14.1	13.0	17.6	18.2	17.8	17.8	15.8	14.1	14.4		13.4	14.9	18.4	20.0	18.1	20.1	22.8	20.4	17.9	20.5	19.1
RT56_PARA_WAME98666_Diplura?_2	26.0	23.6	21.7	25.7	22.5	25.1	25.0	25.4	31.6	22.5	25.1	23.6	30.4	18.2	24.3	21.6	20.7	20.2	23.7	25.0	24.5	14.6	14.3	14.3	13.4	13.9	16.0	16.0	16.6	15.7	15.8	14.6	14.6	13.4		14.2	16.1	19.5	17.7	19.8	22.2	19.2	17.4	20.1	18.6
KE04_ROBE_Japygidae `sp. Helix-DJA011`	26.3	23.6	23.9	27.4	24.9	25.8	25.8	27.0	31.6	26.4	27.5	26.6	28.9	18.7	24.5	22.8	22.8	22.2	22.3	24.3	25.7	16.4	15.5	15.5	14.6	15.3	17.5	16.4	17.3	15.2	14.7	15.3	15.5	14.9	14.2		15.2	19.9	20.2	21.0	21.2	19.7	17.5	18.8	18.5
BMR00209_HSTD_Japygidae sp.	31.0	26.0	26.3	28.9	26.3	26.4	26.5	27.1	34.2	26.7	26.9	28.8	29.7	19.3	24.9	24.0	24.3	22.2	24.5	26.1	26.1	17.5	16.3	16.3	15.8	16.7	18.5	18.2	20.1	17.8	17.5	18.1	16.6	18.4	16.1	15.2		21.1	21.4	22.6	21.7	22.0	20.4	19.8	20.1
KU08_ROBE_Parajapygidae `sp. Helix-DPA009`	29.2	25.7	25.8	26.7	25.6	26.3	26.1	24.8	32.0	26.1	26.3	25.5	29.5	17.9	26.0	23.3	19.6	19.6	24.4	25.8	24.4	16.4	18.7	18.7	15.8	17.4	20.4	18.2	19.0	18.4	19.2	18.8	18.8	20.0	19.5	19.9	21.1		14.9	18.7	18.3	15.6	14.7	14.0	16.0
KD12_ROBE_Parajapygidae_ sp. `DPA006/07`	28.2	25.8	24.2	24.9	25.3	26.1	26.5	25.8	32.9	24.9	26.3	24.2	29.4	17.2	26.4	23.9	18.8	19.1	26.0	27.3	26.6	17.7	19.6	19.6	17.0	18.0	20.2	20.2	20.2	19.2	18.2	17.8	19.1	18.1	17.7	20.2	21.4	14.9		16.9	19.6	16.4	15.6	15.2	14.3
BMR00737_BS1E_Parajapygidae sp.	32.4	26.4	26.7	28.3	27.5	25.8	25.6	28.1	34.9	27.1	26.7	26.0	29.0	19.8	27.5	25.4	21.1	22.0	27.5	29.6	28.8	19.0	21.6	21.6	20.6	20.4	22.2	22.3	23.4	21.6	20.7	20.2	21.0	20.1	19.8	21.0	22.6	18.7	16.9		14.9	19.9	17.6	16.9	18.8
BMR00728_WAH_Parajapygidae? sp.	30.8	27.1	27.7	28.9	26.2	25.0	24.7	26.3	34.9	28.1	27.1	29.6	28.7	20.1	25.8	25.4	22.6	22.0	27.2	29.0	27.2	21.0	19.9	19.9	21.3	21.5	23.3	22.1	23.8	21.3	23.1	21.3	19.4	22.8	22.2	21.2	21.7	18.3	19.6	14.9		18.7	17.2	18.7	18.7
IV156_ROBE_Parajapygidae_ sp. `DPA004`	29.7	25.7	25.8	27.8	25.5	26.6	26.4	26.4	34.1	25.8	27.7	25.2	29.8	18.8	26.4	26.6	20.7	19.4	27.2	26.1	25.6	16.7	21.6	21.6	20.2	20.3	19.9	20.8	20.1	20.3	19.3	18.8	19.1	20.4	19.2	19.7	22.0	15.6	16.4	19.9	18.7		13.4	15.7	16.3
JF37_ROBE_Parajapygidae `sp. Helix-DPA001`	28.2	24.3	24.8	26.0	23.4	25.4	25.5	26.3	32.6	25.4	27.5	25.6	28.5	17.3	25.7	24.8	18.1	19.1	25.4	25.8	25.2	16.0	20.1	20.1	16.5	17.5	20.5	20.8	19.9	18.5	17.7	18.5	18.4	17.9	17.4	17.5	20.4	14.7	15.6	17.6	17.2	13.4		14.6	15.0
BMR00195_HSTD_Diplura sp.	30.2	25.8	24.6	26.1	26.3	24.9	24.7	27.5	34.2	25.5	26.6	26.4	29.5	18.5	23.6	23.7	20.7	19.0	25.0	26.4	25.8	17.9	19.9	19.9	17.9	19.6	20.7	21.1	21.9	20.1	18.7	17.3	18.8	20.5	20.1	18.8	19.8	14.0	15.2	16.9	18.7	15.7	14.6		13.5
KD15_ROBE_Parajapygidae_ sp. `DPA008`	28.7	27.1	25.0	25.8	24.9	25.8	25.5	25.2	31.9	26.3	26.9	25.6	28.0	19.3	25.4	23.6	20.4	19.5	25.0	26.4	26.1	17.7	19.8	19.8	17.6	18.8	19.6	19.8	20.5	19.7	18.0	19.8	18.7	19.1	18.6	18.5	20.1	16.0	14.3	18.8	18.7	16.3	15.0	13.5	

Appendix 11: Distance matrix of Isopoda (troglofauna) sequences/ lineages included in the analysis

COI divergences (%) of Isopoda (regional comparisons)	O.G.	WAMC71331	KR424617	KX656274	KX656302	BMR01220	BMR00734	BMR00479	JV06	IV312	KD21	WAMC71534	IE48	IV171	IV177	WAMC71335	BMR00501	BMR00733	BMR00735	IV356	JF41	JC04	BMR00674	BMR00290	BMR00371	BMR00440	KX656283
OUTGROUP_IV103_Daves-20150604-01_Amphipoda_RobeV		33.3	32.6	34.6	36.3	33.3	35.2	36.3	34.3	33.3	32.2	32.4	36.7	33.5	31.6	33.9	33.9	33.0	34.5	32.4	32.6	33.4	34.3	33.4	33.4	34.8	35.4
Armadillidae_RT24_WAMC71331_GR15MEB0019T201_WAM-ARMD002	33.3		24.9	24.0	27.6	26.9	26.5	25.4	25.5	25.0	25.0	25.0	27.8	25.0	24.4	24.6	23.5	21.1	21.6	26.1	27.1	24.6	24.6	22.0	22.0	23.7	24.8
KR424617_Haloniscus sp. 5 MJ-2015	32.6	24.9		23.3	21.9	23.7	21.8	22.1	21.4	22.2	21.4	21.3	22.8	21.7	21.6	22.0	22.8	24.0	23.1	19.8	22.6	25.4	24.2	22.4	22.4	22.6	22.3
KX656274_Troglarmadillo sp. 4 MJ-2016_Javidkar et al. 2016 ISOPODA.gb	34.6	24.0	23.3		24.5	25.0	24.2	24.0	24.1	25.0	23.0	23.4	22.1	21.2	21.7	21.0	20.3	19.2	21.2	24.7	25.6	21.5	21.3	19.4	19.4	24.0	23.2
KX656302_Paraplatyarthrus subterraneus_Javidkar et al. 2016 ISOPODA.gb	36.3	27.6	21.9	24.5		24.4	24.4	24.0	24.2	22.3	22.3	22.5	28.1	26.8	24.9	24.2	24.2	25.9	26.4	20.0	25.0	25.7	24.7	22.5	22.5	25.4	24.7
BMR01220_VIV_Armadillidae sp.	33.3	26.9	23.7	25.0	24.4		23.6	24.3	24.3	23.7	23.6	23.7	25.8	25.4	24.2	24.2	24.3	25.2	23.9	24.6	23.6	24.8	23.3	22.9	22.9	24.9	24.5
BMR00734_HSTD_Philosciidae sp.	35.2	26.5	21.8	24.2	24.4	23.6		5.9	6.8	24.8	23.5	23.5	25.1	24.4	23.9	24.4	25.1	24.0	22.9	20.3	22.9	23.3	24.5	22.4	22.4	24.5	23.9
BMR00479_BS2_Philosciidae	36.3	25.4	22.1	24.0	24.0	24.3	5.9		2.7	24.2	22.3	22.6	24.8	23.9	25.1	24.2	25.2	23.9	22.2	21.0	23.4	22.9	24.5	22.2	22.2	24.5	22.3
JV06_DD15BS40015-20160608-T3-02_Isopoda_Philosciidae	34.3	25.5	21.4	24.1	24.2	24.3	6.8	2.7		23.2	22.7	23.3	24.5	23.0	23.5	24.0	24.4	23.8	22.6	20.1	23.0	22.6	24.3	22.5	22.5	24.3	21.6
IV312_66905_Isopoda_Philosciidae	33.3	25.0	22.2	25.0	22.3	23.7	24.8	24.2	23.2		11.6	11.7	24.9	23.4	23.8	23.3	22.8	24.9	22.3	19.9	20.9	23.5	25.8	22.9	22.9	24.3	22.4
KD21_GR15MEB0009.20160915.T1-01_Isopoda_Philosciidae	32.2	25.0	21.4	23.0	22.3	23.6	23.5	22.3	22.7	11.6		0.3	24.5	22.3	22.0	22.4	22.8	24.9	23.9	17.6	21.8	24.6	24.0	21.1	21.1	23.1	22.3
Philosciidae_RT24_WAMC71534_RC15MEB0020_HelixISP053	32.4	25.0	21.3	23.4	22.5	23.7	23.5	22.6	23.3	11.7	0.3		24.7	22.5	22.2	22.4	22.9	24.9	23.9	17.8	22.1	25.0	24.2	21.3	21.3	23.1	22.1
Armadillidae_IE48_MEARC2999P6T1-3_Isopoda_MesaA-ABK-J	36.7	27.8	22.8	22.1	28.1	25.8	25.1	24.8	24.5	24.9	24.5	24.7		3.8	16.9	18.4	24.7	23.3	23.2	26.4	25.4	24.2	23.6	24.1	24.1	25.5	24.6
Armadillidae_IV171_MEARC4923-20150930-T1-01_Isopoda_RobeV	33.5	25.0	21.7	21.2	26.8	25.4	24.4	23.9	23.0	23.4	22.3	22.5	3.8		16.6	17.8	22.3	20.6	20.7	24.7	23.8	23.0	22.6	22.2	22.2	23.3	23.4
Armadillidae_IV177_RC14MEB0088-20151001-T3-01_Isopoda_RobeV	31.6	24.4	21.6	21.7	24.9	24.2	23.9	25.1	23.5	23.8	22.0	22.2	16.9	16.6		11.3	23.6	23.0	22.8	23.8	25.6	22.4	23.1	21.4	21.4	23.3	21.6
Armadillidae_RT24_WAMC71335_GR15MEC0004T301_HelixISA054	33.9	24.6	22.0	21.0	24.2	24.2	24.4	24.2	24.0	23.3	22.4	22.4	18.4	17.8	11.3		21.6	22.9	21.4	24.7	24.3	21.8	22.0	21.7	21.7	23.6	22.1
BMR00501_BS3X_Buddelundia? sp.	33.9	23.5	22.8	20.3	24.2	24.3	25.1	25.2	24.4	22.8	22.8	22.9	24.7	22.3	23.6	21.6		16.6	16.2	24.7	25.6	19.1	19.1	17.7	17.7	21.3	22.3
BMR00733_DSM_Buddelundia? sp.	33.0	21.1	24.0	19.2	25.9	25.2	24.0	23.9	23.8	24.9	24.9	24.9	23.3	20.6	23.0	22.9	16.6		11.0	24.3	24.7	20.0	20.8	18.3	18.3	20.9	21.5
BMR00735_BS3_Isopoda sp.	34.5	21.6	23.1	21.2	26.4	23.9	22.9	22.2	22.6	22.3	23.9	23.9	23.2	20.7	22.8	21.4	16.2	11.0		22.3	23.4	19.5	19.6	17.9	17.9	19.8	21.5
IV356_K0989-0712-T2-5_Isopoda_Philosciidae	32.4	26.1	19.8	24.7	20.0	24.6	20.3	21.0	20.1	19.9	17.6	17.8	26.4	24.7	23.8	24.7	24.7	24.3	22.3		17.4	24.1	23.9	21.3	21.3	22.8	22.3
JF41_RC15MEH0382-20160120-T1-03A_Isopoda_Philosciidae	32.6	27.1	22.6	25.6	25.0	23.6	22.9	23.4	23.0	20.9	21.8	22.1	25.4	23.8	25.6	24.3	25.6	24.7	23.4	17.4		24.0	25.1	24.8	24.8	24.9	22.0
Armadillidae_JC04_C60740_IsopodaBrockman_Syncline	33.4	24.6	25.4	21.5	25.7	24.8	23.3	22.9	22.6	23.5	24.6	25.0	24.2	23.0	22.4	21.8	19.1	20.0	19.5	24.1	24.0		19.0	18.2	18.2	24.2	23.7
BMR00674_VIV_Armadillidae sp. BS4	34.3	24.6	24.2	21.3	24.7	23.3	24.5	24.5	24.3	25.8	24.0	24.2	23.6	22.6	23.1	22.0	19.1	20.8	19.6	23.9	25.1	19.0		15.2	15.2	22.8	23.2
BMR00290_BS1C_Armadillidae sp. BS4	33.4	22.0	22.4	19.4	22.5	22.9	22.4	22.2	22.5	22.9	21.1	21.3	24.1	22.2	21.4	21.7	17.7	18.3	17.9	21.3	24.8	18.2	15.2		0.0	20.4	21.8
BMR00371_BS1C_Buddelundia? sp.	33.4	22.0	22.4	19.4	22.5	22.9	22.4	22.2	22.5	22.9	21.1	21.3	24.1	22.2	21.4	21.7	17.7	18.3	17.9	21.3	24.8	18.2	15.2	0.0		20.4	21.8
BMR00440_HSTD_Armadillidae sp.	34.8	23.7	22.6	24.0	25.4	24.9	24.5	24.5	24.3	24.3	23.1	23.1	25.5	23.3	23.3	23.6	21.3	20.9	19.8	22.8	24.9	24.2	22.8	20.4	20.4		21.2
KX656283_Armadillidae sp. 15096.2_Javidkar et al. 2016 ISOPODA.gb	35.4	24.8	22.3	23.2	24.7	24.5	23.9	22.3	21.6	22.4	22.3	22.1	24.6	23.4	21.6	22.1	22.3	21.5	21.5	22.3	22.0	23.7	23.2	21.8	21.8	21.2	

Appendix 12: Distance matrix of Blattodea sequences/ lineages included in the analysis

COI divergences (%) of Blattodea (regional comparisons)	O.G.	BMR00 427	BMR00 103	BMR00 700	BMR00 100	BMR00 478	BMR00 463	BMR00 171	BMR00 180	BMR00 098	BMR00 101	BMR00 173	BMR00 414	BMR00 459	BMR00 258	BMR00 474	BMR00 259	BMR00 466	BT03	BT16	BT6	BT28	BT29	BT30	BT04	BT9	BMR00 264	BMR00 701	BMR00 271	BMR00 698	BMR00 104	BMR00 177	BMR00 410	BMR00 179	BMR00 461	BMR00 268	BMR00 113	BMR01 168	BMR00 257	BMR00 102	BMR00 413	BMR00 412	BMR00 167	BMR00 169	BMR00 411	BMR00 409	BMR00 266	BMR00 464	BMR00 470	BMR00 473	BMR00 263	BMR00 460	BMR00 462	BMR00 174	BMR00 458
MG967325_Blattella germanica_OUTGROUP		26.6	25.4	26.6	26.6	26.5	26.5	27.7	26.8	26.6	26.6	26.5	26.5	26.5	26.2	26.3	26.3	26.3	26.6	26.6	26.8	26.8	26.8	26.8	27.3	27.1	25.7	26.2	25.3	25.3	26.3	25.7	25.7	25.6	25.6	26.3	25.6	25.6	25.6	25.3	25.2	24.8	25.1	25.3	25.1	25.3	25.1	25.1	25.0	25.0	25.0	25.4	25.0	25.3	25.3
BMR00427_HD2_Nocticola OES13	26.6		8.3	9.1	8.6	8.5	8.5	9.2	8.9	8.3	8.3	8.3	8.3	8.3	9.1	9.2	9.2	9.2	8.5	8.5	8.3	8.3	8.3	8.3	8.6	8.6	8.5	8.3	8.0	8.0	8.5	8.5	8.2	8.0	8.0	7.6	7.1	7.1	7.4	7.1	7.7	7.9	8.3	8.2	7.9	7.9	8.3	8.6	8.5	8.5	8.5	8.9	8.8	9.1	9.1
BMR00103_SGW_Blattodea sp.	25.4	8.3		8.1	6.8	6.7	6.7	6.3	6.8	6.8	6.8	6.5	6.5	6.5	6.2	6.4	6.4	6.4	7.3	7.3	7.1	7.1	7.1	7.1	7.6	7.1	7.4	7.4	6.7	6.7	7.5	7.0	7.0	7.0	7.0	7.0	6.5	6.5	6.8	7.1	5.0	5.0	5.5	5.3	5.1	5.3	5.2	5.5	5.3	5.3	5.3	3.8	5.8	5.9	5.9
BMR00700_VIV_Nocticola	26.6	9.1	8.1		7.8	7.6	7.6	8.7	8.1	8.1	8.1	7.8	7.8	7.8	9.0	9.1	9.1	9.1	8.2	8.2	8.1	8.1	8.1	8.1	8.5	8.4	8.1	7.8	7.3	7.3	8.7	9.0	9.0	8.4	8.4	8.4	8.2	8.2	8.2	8.5	8.6	8.5	8.4	8.8	8.7	8.5	8.2	8.5	8.4	8.4	8.4	8.9	8.7	9.1	9.1
BMR00100_BS3_Nocticola sp.	26.6	8.6	6.8	7.8		0.2	0.2	1.5	0.9	0.6	0.6	0.6	0.6	0.6	7.6	7.8	7.8	7.8	7.8	7.8	7.6	7.6	7.6	7.6	8.1	7.9	8.7	7.9	7.9	7.9	7.7	9.1	8.8	8.2	8.2	8.2	7.8	7.8	7.8	8.1	7.2	7.6	7.8	7.9	8.0	7.9	7.9	8.2	8.1	8.1	8.1	8.1	8.4	8.4	8.4
BMR00478_BS3_Nocticola	26.5	8.5	6.7	7.6	0.2		0.0	1.4	0.8	0.5	0.5	0.5	0.5	0.5	7.8	7.9	7.9	7.9	7.6	7.6	7.4	7.4	7.4	7.4	7.9	7.8	8.5	8.1	7.8	7.8	7.7	9.0	8.7	8.1	8.1	8.1	7.6	7.6	7.6	7.9	7.0	7.4	7.6	7.8	7.8	7.8	7.8	8.1	7.9	7.9	7.9	8.1	8.4	8.5	8.5
BMR00463_BS3_Nocticola sp.	26.5	8.5	6.7	7.6	0.2	0.0		1.4	0.8	0.5	0.5	0.5	0.5	0.5	7.8	7.9	7.9	7.9	7.6	7.6	7.4	7.4	7.4	7.4	7.9	7.8	8.5	8.1	7.8	7.8	7.7	9.0	8.7	8.1	8.1	8.1	7.6	7.6	7.6	7.9	7.0	7.4	7.6	7.8	7.8	7.8	7.8	8.1	7.9	7.9	7.9	8.1	8.4	8.5	8.5
BMR00171_DSM_Nocticola sp.	27.7	9.2	6.3	8.7	1.5	1.4	1.4		0.9	1.5	1.5	1.5	1.5	1.5	7.9	8.0	8.0	8.0	8.7	8.7	8.7	8.7	8.7	8.7	8.9	8.6	8.2	8.4	8.4	8.4	8.3	8.9	8.6	8.0	8.0	8.2	7.7	7.7	8.0	8.0	7.2	7.7	7.9	8.0	7.6	7.5	8.0	8.4	8.2	8.2	8.2	7.9	8.2	8.6	8.6
BMR00180_LNSG_Nocticola sp.	26.8	8.9	6.8	8.1	0.9	0.8	0.8	0.9		0.9	0.9	0.9	0.9	0.9	7.9	8.1	8.1	8.1	8.1	8.1	7.9	7.9	7.9	7.9	8.4	7.9	8.7	8.2	8.2	8.2	7.9	9.1	8.8	8.2	8.2	8.2	7.8	7.8	8.1	8.1	7.3	7.6	7.8	7.9	8.0	7.9	8.1	8.4	8.2	8.2	8.2	8.4	8.7	9.0	9.0
BMR00098_BS3_Blattodea sp.	26.6	8.3	6.8	8.1	0.6	0.5	0.5	1.5	0.9		0.0	0.3	0.3	0.3	7.9	8.1	8.1	8.1	8.1	8.1	7.9	7.9	7.9	7.9	8.4	7.9	8.7	8.2	8.2	8.2	7.9	9.1	8.8	8.2	8.2	8.2	7.8	7.8	8.1	7.8	7.2	7.6	7.8	7.9	7.8	7.9	7.9	8.2	8.1	8.1	8.1	8.1	8.4	8.7	8.7
BMR00101_BS3_Nocticola sp.	26.6	8.3	6.8	8.1	0.6	0.5	0.5	1.5	0.9	0.0		0.3	0.3	0.3	7.9	8.1	8.1	8.1	8.1	8.1	7.9	7.9	7.9	7.9	8.4	7.9	8.7	8.2	8.2	8.2	7.9	9.1	8.8	8.2	8.2	8.2	7.8	7.8	8.1	7.8	7.2	7.6	7.8	7.9	7.8	7.9	7.9	8.2	8.1	8.1	8.1	8.1	8.4	8.7	8.7
BMR00173_BS3_Nocticola sp.	26.5	8.3	6.5	7.8	0.6	0.5	0.5	1.5	0.9	0.3	0.3		0.0	0.0	7.6	7.8	7.8	7.8	7.8	7.8	7.6	7.6	7.6	7.6	8.1	7.6	8.4	7.9	7.9	7.9	7.5	8.8	8.5	7.9	7.9	7.9	7.4	7.4	7.8	7.8	6.8	7.3	7.4	7.6	7.5	7.6	7.6	7.9	7.8	7.8	7.8	7.8	8.1	8.4	8.4
BMR00414_BS3_Nocticola sp.	26.5	8.3	6.5	7.8	0.6	0.5	0.5	1.5	0.9	0.3	0.3	0.0		0.0	7.6	7.8	7.8	7.8	7.8	7.8	7.6	7.6	7.6	7.6	8.1	7.6	8.4	7.9	7.9	7.9	7.5	8.8	8.5	7.9	7.9	7.9	7.4	7.4	7.8	7.8	6.8	7.3	7.4	7.6	7.5	7.6	7.6	7.9	7.8	7.8	7.8	7.8	8.1	8.4	8.4
BMR00459_BS3_Nocticola sp.	26.5	8.3	6.5	7.8	0.6	0.5	0.5	1.5	0.9	0.3	0.3	0.0	0.0		7.6	7.8	7.8	7.8	7.8	7.8	7.6	7.6	7.6	7.6	8.1	7.6	8.4	7.9	7.9	7.9	7.5	8.8	8.5	7.9	7.9	7.9	7.4	7.4	7.8	7.8	6.8	7.3	7.4	7.6	7.5	7.6	7.6	7.9	7.8	7.8	7.8	7.8	8.1	8.4	8.4
BMR00258_BS1E_Nocticola sp.	26.2	9.1	6.2	9.0	7.6	7.8	7.8	7.9	7.9	7.9	7.9	7.6	7.6	7.6		0.2	0.2	0.2	7.3	7.3	7.1	7.1	7.1	7.1	7.6	7.1	6.5	6.1	6.2	6.2	6.7	7.6	7.3	6.8	6.8	6.7	6.5	6.5	6.5	6.5	6.7	6.7	7.1	6.7	7.1	7.3	6.8	7.1	7.0	7.0	7.0	6.9	5.9	6.4	6.4
BMR00474_BS1E_Nocticola	26.3	9.2	6.4	9.1	7.8	7.9	7.9	8.0	8.1	8.1	8.1	7.8	7.8	7.8	0.2		0.0	0.0	7.4	7.4	7.3	7.3	7.3	7.3	7.8	7.3	6.7	6.2	6.4	6.4	6.8	7.8	7.4	7.0	7.0	6.8	6.7	6.7	6.7	6.7	6.9	6.8	7.3	6.8	7.2	7.4	7.0	7.3	7.1	7.1	7.1	7.1	6.1	6.5	6.5
BMR00259_BS1E_Nocticola sp.	26.3	9.2	6.4	9.1	7.8	7.9	7.9	8.0	8.1	8.1	8.1	7.8	7.8	7.8	0.2	0.0		0.0	7.4	7.4	7.3	7.3	7.3	7.3	7.8	7.3	6.7	6.2	6.4	6.4	6.8	7.8	7.4	7.0	7.0	6.8	6.7	6.7	6.7	6.7	6.9	6.8	7.3	6.8	7.2	7.4	7.0	7.3	7.1	7.1	7.1	7.1	6.1	6.5	6.5
BMR00466_BS1E_Nocticola	26.3	9.2	6.4	9.1	7.8	7.9	7.9	8.0	8.1	8.1	8.1	7.8	7.8	7.8	0.2	0.0	0.0		7.4	7.4	7.3	7.3	7.3	7.3	7.8	7.3	6.7	6.2	6.4	6.4	6.8	7.8	7.4	7.0	7.0	6.8	6.7	6.7	6.7	6.7	6.9	6.8	7.3	6.8	7.2	7.4	7.0	7.3	7.1	7.1	7.1	7.1	6.1	6.5	6.5
BT03_RC006S17B161P1T1-4_Blattodea	26.6	8.5	7.3	8.2	7.8	7.6	7.6	8.7	8.1	8.1	8.1	7.8	7.8	7.8	7.3	7.4	7.4	7.4		0.0	0.4	0.4	0.4	0.4	0.9	0.7	7.6	7.8	6.7	6.7	6.5	7.1	6.8	6.7	6.7	6.2	6.1	6.1	6.7	6.4	6.8	7.1	7.6	7.4	7.1	7.4	6.4	6.4	6.5	6.5	6.5	7.7	7.3	7.3	7.3
BT16_RC06S17B161P1T2-3_Blattodea	26.6	8.5	7.3	8.2	7.8	7.6	7.6	8.7	8.1	8.1	8.1	7.8	7.8	7.8	7.3	7.4	7.4	7.4	0.0		0.4	0.4	0.4	0.4	0.9	0.7	7.6	7.8	6.7	6.7	6.5	7.1	6.8	6.7	6.7	6.2	6.1	6.1	6.7	6.4	6.8	7.1	7.6	7.4	7.1	7.4	6.4	6.4	6.5	6.5	6.5	7.7	7.3	7.3	7.3
BT6_RC06S17B380P2T2-3_Blattodea	26.8	8.3	7.1	8.1	7.6	7.4	7.4	8.7	7.9	7.9	7.9	7.6	7.6	7.6	7.1	7.3	7.3	7.3	0.4	0.4		0.0	0.0	0.0	0.4	0.3	7.4	7.3	6.2	6.2	6.5	7.0	6.7	6.5	6.5	6.1	5.9	5.9	6.5	6.2	6.8	7.0	7.4	7.3	6.9	7.3	6.2	6.2	6.4	6.4	6.4	7.5	7.1	7.1	7.1
BT28_RC06S17B221P2T2-3_Blattodea	26.8	8.3	7.1	8.1	7.6	7.4	7.4	8.7	7.9	7.9	7.9	7.6	7.6	7.6	7.1	7.3	7.3	7.3	0.4	0.4	0.0		0.0	0.0	0.4	0.3	7.4	7.3	6.2	6.2	6.5	7.0	6.7	6.5	6.5	6.1	5.9	5.9	6.5	6.2	6.8	7.0	7.4	7.3	6.9	7.3	6.2	6.2	6.4	6.4	6.4	7.5	7.1	7.1	7.1
BT29_RC06S17B221P2T2-3_Blattodea	26.8	8.3	7.1	8.1	7.6	7.4	7.4	8.7	7.9	7.9	7.9	7.6	7.6	7.6	7.1	7.3	7.3	7.3	0.4	0.4	0.0	0.0		0.0	0.4	0.3	7.4	7.3	6.2	6.2	6.5	7.0	6.7	6.5	6.5	6.1	5.9	5.9	6.5	6.2	6.8	7.0	7.4	7.3	6.9	7.3	6.2	6.2	6.4	6.4	6.4	7.5	7.1	7.1	7.1
BT30_RC06S17B221P2T2-3_Blattodea	26.8	8.3	7.1	8.1	7.6	7.4	7.4	8.7	7.9	7.9	7.9	7.6	7.6	7.6	7.1	7.3	7.3	7.3	0.4	0.4	0.0	0.0	0.0		0.4	0.3	7.4	7.3	6.2	6.2	6.5	7.0	6.7	6.5	6.5	6.1	5.9	5.9	6.5	6.2	6.8	7.0	7.4	7.3	6.9	7.3	6.2	6.2	6.4	6.4	6.4	7.5	7.1	7.1	7.1
BT04_RC003B1004P1T2-3_Blattodea	27.3	8.6	7.6	8.5	8.1	7.9	7.9	8.9	8.4	8.4	8.4	8.1	8.1	8.1	7.6	7.8	7.8	7.8	0.9	0.9	0.4	0.4	0.4	0.4		0.4	7.9	7.8	6.7	6.7	6.7	7.4	7.1	7.0	7.0	6.5	6.4	6.4	7.0	6.7	7.0	7.4	7.9	7.8	7.4	7.8	6.7	6.7	6.8	6.8	6.8	7.8	7.6	7.6	7.6
BT9_RC03B1004P1T1-3_Blattodea	27.1	8.6	7.1	8.4	7.9	7.8	7.8	8.6	7.9	7.9	7.9	7.6	7.6	7.6	7.1	7.3	7.3	7.3	0.7	0.7	0.3	0.3	0.3	0.3	0.4		7.4	7.3	6.5	6.5	6.3	7.0	6.7	6.5	6.5	6.1	5.9	5.9	6.8	6.2	6.8	7.0	7.4	7.3	6.9	7.3	6.5	6.5	6.7	6.7	6.7	7.7	7.3	7.4	7.4
BMR00264_BS1W_Nocticola sp.	25.7	8.5	7.4	8.1	8.7	8.5	8.5	8.2	8.7	8.7	8.7	8.4	8.4	8.4	6.5	6.7	6.7	6.7	7.6	7.6	7.4	7.4	7.4	7.4	7.9	7.4		2.6	2.4	2.4	7.3	6.7	6.7	6.2	6.2	6.4	5.9	5.9	6.8	6.8	7.0	7.0	7.4	7.3	7.2	7.3	7.8	8.1	7.9	7.9	7.9	8.4	7.7	8.4	8.4
BMR00701_BS1W_Nocticola	26.2	8.3	7.4	7.8	7.9	8.1	8.1	8.4	8.2	8.2	8.2	7.9	7.9	7.9	6.1	6.2	6.2	6.2	7.8	7.8	7.3	7.3	7.3	7.3	7.8	7.3	2.6		1.4	1.4	7.3	7.1	6.8	6.4	6.4	6.5	6.4	6.4	7.0	7.0	6.7	6.8	7.0	7.1	7.1	7.1	8.1	8.4	8.2	8.2	8.2	8.2	7.2	7.8	7.8
BMR00271_BS1W_Nocticola sp.	25.3	8.0	6.7	7.3	7.9	7.8	7.8	8.4	8.2	8.2	8.2	7.9	7.9	7.9	6.2	6.4	6.4	6.4	6.7	6.7	6.2	6.2	6.2	6.2	6.7	6.5	2.4	1.4		0.0	6.9	6.5	6.2	5.8	5.8	5.9	5.8	5.8	6.4	6.4	6.4	6.7	7.1	7.0	6.8	7.0	7.0	7.3	7.1	7.1	7.1	7.4	6.8	7.3	7.3
BMR00698_BS1W_Nocticola	25.3	8.0	6.7	7.3	7.9	7.8	7.8	8.4	8.2	8.2	8.2	7.9	7.9	7.9	6.2	6.4	6.4	6.4	6.7	6.7	6.2	6.2	6.2	6.2	6.7	6.5	2.4	1.4	0.0		6.9	6.5	6.2	5.8	5.8	5.9	5.8	5.8	6.4	6.4	6.4	6.7	7.1	7.0	6.8	7.0	7.0	7.3	7.1	7.1	7.1	7.4	6.8	7.3	7.3
BMR00104_BS2SW_Nocticola sp.	26.3	8.5	7.5	8.7	7.7	7.7	7.7	8.3	7.9	7.9	7.9	7.5	7.5	7.5	6.7	6.8	6.8	6.8	6.5	6.5	6.5	6.5	6.5	6.5	6.7	6.3	7.3	7.3	6.9	6.9		2.7	2.3	2.1	2.1	1.7	1.7	1.7	2.5	2.2	6.6	6.2	6.7	6.7	6.1	6.6	6.4	6.7	6.6	6.6	6.6	7.1	6.6	6.7	6.7
BMR00177_LNSG_Nocticola sp.	25.7	8.5	7.0	9.0	9.1	9.0	9.0	8.9	9.1	9.1	9.1	8.8	8.8	8.8	7.6	7.8	7.8	7.8	7.1	7.1	7.0	7.0	7.0	7.0	7.4	7.0	6.7	7.1	6.5	6.5	2.7		0.3	1.2	1.2	1.8	1.7	1.7	2.6	2.3	5.9	5.8	6.2	6.1	5.4	5.8	6.5	6.8	6.7	6.7	6.7	6.8	6.6	6.5	6.5
BMR00410_LNSG_Nocticola sp.	25.7	8.2	7.0	9.0	8.8	8.7	8.7	8.6	8.8	8.8	8.8	8.5	8.5	8.5	7.3	7.4	7.4	7.4	6.8	6.8	6.7	6.7	6.7	6.7	7.1	6.7	6.7	6.8	6.2	6.2	2.3	0.3		0.9	0.9	1.5	1.4	1.4	2.3	2.0	5.6	5.5	5.9	5.8	5.1	5.5	6.2	6.5	6.4	6.4	6.4	6.7	6.3	6.2	6.2
BMR00179_LNSG_Nocticola sp.	25.6	8.0	7.0	8.4	8.2	8.1	8.1	8.0	8.2	8.2	8.2	7.9	7.9	7.9	6.8	7.0	7.0	7.0	6.7	6.7	6.5	6.5	6.5	6.5	7.0	6.5	6.2	6.4	5.8	5.8	2.1	1.2	0.9		0.0	1.4	1.2	1.2	2.1	1.8	5.7	5.9	6.4	6.2	5.7	6.1	5.8	6.1	5.9	5.9	5.9	6.5	6.3	6.2	6.2
BMR00461_LNSG_Nocticola sp.	25.6	8.0	7.0	8.4	8.2	8.1	8.1	8.0	8.2	8.2	8.2	7.9	7.9	7.9	6.8	7.0	7.0	7.0	6.7	6.7	6.5	6.5	6.5	6.5	7.0	6.5	6.2	6.4	5.8	5.8	2.1	1.2	0.9	0.0		1.4	1.2	1.2	2.1	1.8	5.7	5.9	6.4	6.2	5.7	6.1	5.8	6.1	5.9	5.9	5.9	6.5	6.3	6.2	6.2
BMR00268_BS1W_Nocticola sp.	26.3	7.6	7.0	8.4	8.2	8.1	8.1	8.2	8.2	8.2	8.2	7.9	7.9	7.9	6.7	6.8	6.8	6.8	6.2	6.2	6.1	6.1	6.1	6.1	6.5	6.1	6.4	6.5	5.9	5.9	1.7	1.8	1.5	1.4	1.4		0.8	0.8	1.7	1.7	5.9	5.8	6.2	6.1	5.7	6.1	6.1	6.4	6.2	6.2	6.2	6.7	6.5	6.7	6.7
BMR00113_BS2W_Nocticola sp.	25.6	7.1	6.5	8.2	7.8	7.6	7.6	7.7	7.8	7.8	7.8	7.4	7.4	7.4	6.5	6.7	6.7	6.7	6.1	6.1	5.9	5.9	5.9	5.9	6.4	5.9	5.9	6.4	5.8	5.8	1.7	1.7	1.4	1.2	1.2	0.8		0.0	1.5	1.5	5.4	5.3	5.8	5.6	5.2	5.6	5.9	6.2	6.1	6.1	6.1	6.3	6.1	6.2	6.2
BMR01168_BS2W_Nocticola	25.6	7.1	6.5	8.2	7.8	7.6	7.6	7.7	7.8	7.8	7.8	7.4	7.4	7.4	6.5	6.7	6.7	6.7	6.1	6.1	5.9	5.9	5.9	5.9	6.4	5.9	5.9	6.4	5.8	5.8	1.7	1.7	1.4	1.2	1.2	0.8	0.0		1.5	1.5	5.4	5.3	5.8	5.6	5.2	5.6	5.9	6.2	6.1	6.1	6.1	6.3	6.1	6.2	6.2
BMR00257_VIV_Nocticola sp.	25.6	7.4	6.8	8.2	7.8	7.6	7.6	8.0	8.1	8.1	8.1	7.8	7.8	7.8	6.5	6.7	6.7	6.7	6.7	6.7	6.5	6.5	6.5	6.5	7.0	6.8	6.8	7.0	6.4	6.4	2.5	2.6	2.3	2.1	2.1	1.7	1.5	1.5		1.5	5.9	5.6	6.1	5.9	6.0	6.2	6.5	6.8	6.7	6.7	6.7	7.2	6.8	7.1	7.1
BMR00102_BS2W_Nocticola sp.	25.3	7.1	7.1	8.5	8.1	7.9	7.9	8.0	8.1	7.8	7.8	7.8	7.8	7.8	6.5	6.7	6.7	6.7	6.4	6.4	6.2	6.2	6.2	6.2	6.7	6.2	6.8	7.0	6.4	6.4	2.2	2.3	2.0	1.8	1.8	1.7	1.5	1.5	1.5		6.1	6.1	6.5	6.4	6.0	6.4	6.5	6.8	6.7	6.7	6.7	6.9	6.5	6.8	6.8
BMR00413_SGW_Nocticola sp.	25.2	7.7	5.0	8.6	7.2	7.0	7.0	7.2	7.3	7.2	7.2	6.8	6.8	6.8	6.7	6.9	6.9	6.9	6.8	6.8	6.8	6.8	6.8	6.8	7.0	6.8	7.0	6.7	6.4	6.4	6.6	5.9	5.6	5.7	5.7	5.9	5.4	5.4	5.9	6.1		1.5	1.9	1.9	1.1	1.5	5.0	5.4	5.2	5.2	5.2	4.5	4.0	4.7	4.7
BMR00412_HSTD_Nocticola sp.	24.8	7.9	5.0	8.5	7.6	7.4	7.4	7.7	7.6	7.6	7.6	7.3	7.3	7.3	6.7	6.8	6.8	6.8	7.1	7.1	7.0	7.0	7.0	7.0	7.4	7.0	7.0	6.8	6.7	6.7	6.2	5.8	5.5	5.9	5.9	5.8	5.3	5.3	5.6	6.1	1.5		0.8	0.6	0.8	0.9	6.2	6.5	6.4	6.4	6.4	5.8	5.3	6.2	6.2
BMR00167_HSTD_Nocticola sp.	25.1	8.3	5.5	8.4	7.8	7.6	7.6	7.9	7.8	7.8	7.8	7.4	7.4	7.4	7.1	7.3	7.3	7.3	7.6	7.6	7.4	7.4	7.4	7.4	7.9	7.4	7.4	7.0	7.1	7.1	6.7	6.2	5.9	6.4	6.4	6.2	5.8	5.8	6.1	6.5	1.9	0.8		0.8	1.3	1.4	6.7	7.0	6.8	6.8	6.8	6.3	5.8	6.7	6.7
BMR00169_CVCK_REG_Nocticola sp.	25.3	8.2	5.3	8.8	7.9	7.8	7.8	8.0	7.9	7.9	7.9	7.6	7.6	7.6	6.7	6.8	6.8	6.8	7.4	7.4	7.3	7.3	7.3	7.3	7.8	7.3	7.3	7.1	7.0	7.0	6.7	6.1	5.8	6.2	6.2	6.1	5.6	5.6	5.9	6.4	1.9	0.6	0.8		1.1	1.2	6.5	6.8	6.7	6.7	6.7	6.1	5.6	6.5	6.5
BMR00411_SGW_Nocticola	25.1	7.9	5.1	8.7	8.0	7.8	7.8	7.6	8.0	7.8	7.8	7.5	7.5	7.5	7.1	7.2	7.2	7.2	7.1	7.1	6.9	6.9	6.9	6.9	7.4	6.9	7.2	7.1	6.8	6.8	6.1	5.4	5.1	5.7	5.7	5.7	5.2	5.2	6.0	6.0	1.1	0.8	1.3	1.1		0.5	6.0	6.3	6.2	6.2	6.2	5.3	4.9	5.7	5.7
BMR00409_SGW_Nocticola	25.3	7.9	5.3	8.5	7.9	7.8	7.8	7.5	7.9	7.9	7.9	7.6	7.6	7.6	7.3	7.4	7.4	7.4	7.4	7.4	7.3	7.3	7.3	7.3	7.8	7.3	7.3	7.1	7.0	7.0	6.6	5.8	5.5	6.1	6.1	6.1	5.6	5.6	6.2	6.4	1.5	0.9	1.4	1.2	0.5		6.5	6.8	6.7	6.7	6.7	5.8	5.3	6.2	6.2
BMR00266_BS1E_Nocticola sp.	25.1	8.3	5.2	8.2	7.9	7.8	7.8	8.0	8.1	7.9	7.9	7.6	7.6	7.6	6.8	7.0	7.0	7.0	6.4	6.4	6.2	6.2	6.2	6.2	6.7	6.5	7.8	8.1	7.0	7.0	6.4	6.5	6.2	5.8	5.8	6.1	5.9	5.9	6.5	6.5	5.0	6.2	6.7	6.5	6.0	6.5		0.3	0.2	0.2	0.2	3.2	3.0	2.4	2.4
BMR00464_BS1E_Nocticola	25.1	8.6	5.5	8.5	8.2	8.1	8.1	8.4	8.4	8.2	8.2	7.9	7.9	7.9	7.1	7.3	7.3	7.3	6.4	6.4	6.2	6.2	6.2	6.2	6.7	6.5	8.1	8.4	7.3	7.3	6.7	6.8	6.5	6.1	6.1	6.4	6.2	6.2	6.8	6.8	5.4	6.5	7.0	6.8	6.3	6.8	0.3		0.2	0.2	0.2	3.5	3.3	2.7	2.7
BMR00470_BS1E_Nocticola	25.0	8.5	5.3	8.4	8.1	7.9	7.9	8.2	8.2	8.1	8.1	7.8	7.8	7.8	7.0	7.1	7.1	7.1	6.5	6.5	6.4	6.4	6.4	6.4	6.8	6.7	7.9	8.2	7.1	7.1	6.6	6.7	6.4	5.9	5.9	6.2	6.1	6.1	6.7	6.7	5.2	6.4	6.8	6.7	6.2	6.7	0.2	0.2		0.0	0.0	3.3	3.2	2.6	2.6
BMR00473_BS1E_Nocticola	25.0	8.5	5.3	8.4	8.1	7.9	7.9	8.2	8.2	8.1	8.1	7.8	7.8	7.8	7.0	7.1	7.1	7.1	6.5	6.5	6.4	6.4	6.4	6.4	6.8	6.7	7.9	8.2	7.1	7.1	6.6	6.7	6.4	5.9	5.9	6.2	6.1	6.1	6.7	6.7	5.2	6.4	6.8	6.7	6.2	6.7	0.2	0.2	0.0		0.0	3.3	3.2	2.6	2.6
BMR00263_BS1E_Nocticola sp.	25.0	8.5	5.3	8.4	8.1	7.9	7.9	8.2	8.2	8.1	8.1	7.8	7.8	7.8	7.0	7.1	7.1	7.1	6.5	6.5	6.4	6.4	6.4	6.4	6.8	6.7	7.9	8.2	7.1	7.1	6.6	6.7	6.4	5.9	5.9	6.2	6.1	6.1	6.7	6.7	5.2	6.4	6.8	6.7	6.2	6.7	0.2	0.2	0.0	0.0		3.3	3.2	2.6	2.6
BMR00460_SGW_Nocticola sp.	25.4	8.9	3.8	8.9	8.1	8.1	8.1	7.9	8.4	8.1	8.1	7.8	7.8	7.8	6.9	7.1	7.1	7.1	7.7	7.7	7.5	7.5	7.5	7.5	7.8	7.7	8.4	8.2	7.4	7.4	7.1	6.8	6.7	6.5	6.5	6.7	6.3	6.3	7.2	6.9	4.5	5.8	6.3	6.1	5.3	5.8	3.2	3.5	3.3	3.3	3.3		2.7	2.2	2.2
BMR00462_SGW_Nocticola sp.	25.0	8.8	5.8	8.7	8.4	8.4	8.4	8.2	8.7	8.4	8.4	8.1	8.1	8.1	5.9	6.1	6.1	6.1	7.3	7.3	7.1	7.1	7.1	7.1	7.6	7.3	7.7	7.2	6.8	6.8	6.6	6.6	6.3	6.3	6.3	6.5	6.1	6.1	6.8	6.5	4.0	5.3	5.8	5.6	4.9	5.3	3.0	3.3	3.2	3.2	3.2	2.7		0.9	0.9
BMR00174_SGW_Blattodea sp.	25.3	9.1	5.9	9.1	8.4	8.5	8.5	8.6	9.0	8.7	8.7	8.4	8.4	8.4	6.4	6.5	6.5	6.5	7.3	7.3	7.1	7.1	7.1	7.1	7.6	7.4	8.4	7.8	7.3	7.3	6.7	6.5	6.2	6.2	6.2	6.7	6.2	6.2	7.1	6.8	4.7	6.2	6.7	6.5	5.7	6.2	2.4	2.7	2.6	2.6	2.6	2.2	0.9		0.0
BMR00458_SGW_Nocticola sp.	25.3	9.1	5.9	9.1	8.4	8.5	8.5	8.6	9.0	8.7	8.7	8.4	8.4	8.4	6.4	6.5	6.5	6.5	7.3	7.3	7.1	7.1	7.1	7.1	7.6	7.4	8.4	7.8	7.3	7.3	6.7	6.5	6.2	6.2	6.2	6.7	6.2	6.2	7.1	6.8	4.7	6.2	6.7	6.5	5.7	6.2	2.4	2.7	2.6	2.6	2.6	2.2	0.9	0.0	

Appendix 13: Distance matrix of Coleoptera sequences/ lineages included in the analysis

COI divergence (%) of Coleoptera (regional comparisons)	C.o. O.G.	A.b. O.G	JV03	JV05	JV04	IV151	KU 519734	RT27	KU 519735	KU 519736	KU 519738	ML01	JV01	JV02	BMR 00472	JC14	JC17	BMR 00193	BMR 00581	Curculio nidae	KU 519731	BISEW0 540	KU 519728	BMR 00471	BMR 00523	KU 519722	KU 519729	KU 519732	MF03	KD03	KD05	KU 519718	LI44E 84259	ML02
HE961904_Ceratapion onopordi_OUTGROUP		24.0	59.3	58.0	58.1	60.6	63.0	63.1	59.3	59.8	59.3	65.2	60.4	59.7	58.5	58.5	58.7	59.8	64.0	63.6	64.6	63.3	65.4	62.8	62.2	63.2	63.0	64.5	63.4	62.8	62.7	62.8	62.8	62.7
HQ165206_Aglenus brunneus	24.0		59.4	60.1	59.4	59.3	60.9	60.5	60.1	60.2	60.4	63.2	62.5	60.1	58.8	59.3	59.1	59.8	64.9	62.1	64.8	63.3	65.2	62.5	62.0	61.9	61.7	64.1	62.8	64.9	64.9	64.8	64.9	64.9
JV03_RC15BS40051-20160608-BROCK4_Coleoptera_Carabidae	59.3	59.4		17.1	19.4	16.0	19.9	19.7	20.8	19.6	21.1	28.2	20.4	19.8	17.2	17.2	17.2	18.9	22.5	21.1	24.8	22.2	25.7	20.4	19.4	20.8	20.1	21.1	23.5	22.6	22.8	24.5	22.6	22.8
JV05_RC15BS4B0415-20160609-BROCK4_Coleoptera_Staphylinidae	58.0	60.1	17.1		17.2	17.6	23.1	22.6	18.4	18.7	18.4	28.2	24.1	22.0	19.0	18.7	18.5	21.4	22.3	20.1	25.2	22.0	26.0	20.5	21.5	22.0	22.2	23.3	24.0	22.3	22.2	23.6	22.3	22.3
JV04_RC15BS40051-20160608 BROCK4_Coleoptera_Staphylinidae	58.1	59.4	19.4	17.2		19.2	21.4	20.9	18.7	17.9	18.2	28.7	22.2	21.4	18.5	18.1	18.0	19.4	22.3	20.2	24.3	23.6	26.4	22.9	21.9	23.1	22.6	23.7	26.4	25.9	25.9	27.8	25.9	25.9
IV151_MEARC3814-20150807-ROBE_Coleoptera_Carabidae	60.6	59.3	16.0	17.6	19.2		20.4	20.0	22.2	21.9	20.4	30.2	20.8	20.5	16.1	16.0	15.8	19.8	20.7	19.0	23.6	22.5	26.0	20.5	20.3	20.8	19.5	20.8	25.0	23.3	23.4	24.5	23.3	23.4
KU519734_Pilbara_Ptiliidae	63.0	60.9	19.9	23.1	21.4	20.4		1.7	24.2	24.3	25.4	31.6	24.9	24.6	20.2	20.8	20.7	23.7	24.0	25.4	25.1	25.4	27.1	23.9	22.1	23.3	23.6	24.6	27.3	27.4	27.2	27.8	27.4	27.2
RT27_WAME34031_Mesa_K_Ptiliidae_Ptinella_Helix_CPT003	63.1	60.5	19.7	22.6	20.9	20.0	1.7		24.1	24.6	24.9	31.5	25.6	24.6	20.2	20.8	20.6	23.2	24.0	25.3	25.0	25.5	27.2	23.2	21.7	23.4	23.4	24.3	27.8	26.9	26.7	27.3	26.9	26.7
KU519735_Pilbara_Staphylinidae	59.3	60.1	20.8	18.4	18.7	22.2	24.2	24.1		4.3	8.7	30.7	23.6	22.8	22.3	23.3	23.1	23.1	24.3	22.9	25.7	21.7	26.7	21.1	21.6	23.6	24.2	25.1	24.8	24.9	24.8	24.9	24.9	24.8
KU519736_Pilbara_Staphylinidae	59.8	60.2	19.6	18.7	17.9	21.9	24.3	24.6	4.3		8.7	29.7	22.5	22.5	22.2	22.3	22.2	22.1	24.2	22.6	26.7	22.2	26.9	22.2	21.2	22.8	24.5	24.5	25.7	25.5	25.4	25.7	25.5	25.4
KU519738_Pilbara_Staphylinidae	59.3	60.4	21.1	18.4	18.2	20.4	25.4	24.9	8.7	8.7		29.7	22.6	22.3	21.9	21.7	21.6	21.6	23.1	22.9	26.0	22.3	25.8	22.2	21.0	24.2	23.4	24.6	25.9	24.6	24.8	24.9	24.6	24.8
ML01_MEBRC0025-20170526-ROBE_Coleoptera	65.2	63.2	28.2	28.2	28.7	30.2	31.6	31.5	30.7	29.7	29.7		28.4	29.3	29.4	29.5	29.3	33.3	34.3	33.3	36.4	30.6	35.2	31.6	31.0	33.9	33.3	33.0	36.1	33.1	33.1	35.2	33.1	33.1
JV01_GR14BS40032-20160608-BROCK4_Coleoptera_Carabidae	60.4	62.5	20.4	24.1	22.2	20.8	24.9	25.6	23.6	22.5	22.6	28.4		5.8	19.9	20.0	19.9	23.2	24.5	23.8	28.1	24.3	26.9	24.6	24.8	25.1	25.2	25.1	28.1	27.8	27.9	29.5	27.8	28.0
JV02_RC11BS3045-20160609-BROCK4_Coleoptera_Carabidae	59.7	60.1	19.8	22.0	21.4	20.5	24.6	24.6	22.8	22.5	22.3	29.3	5.8		19.6	20.1	20.0	22.9	24.4	24.2	26.8	23.6	26.4	23.6	23.5	24.3	23.5	23.3	27.2	28.1	28.2	28.1	28.1	28.2
BMR00472_VIV_Carabidae	58.5	58.8	17.2	19.0	18.5	16.1	20.2	20.2	22.3	22.2	21.9	29.4	19.9	19.6		3.0	2.9	19.9	22.5	22.2	24.9	22.5	26.1	21.4	20.4	21.3	21.0	22.6	26.2	26.0	25.8	25.5	26.0	25.8
JC14_DD14BS40014-20151125-BROCK4_Coleoptera Brockman	58.5	59.3	17.2	18.7	18.1	16.0	20.8	20.8	23.3	22.3	21.7	29.5	20.0	20.1	3.0		0.1	20.4	22.2	21.2	24.9	22.6	26.9	21.6	21.5	21.6	21.6	22.3	25.3	24.8	24.7	26.0	24.8	24.7
JC17_RC14BS40052-20151125-BROCK4_Coleoptera_Carabidae	58.7	59.1	17.2	18.5	18.0	15.8	20.7	20.6	23.1	22.2	21.6	29.3	19.9	20.0	2.9	0.1		20.3	22.0	21.0	24.8	22.6	26.9	21.4	21.3	21.4	21.4	22.3	25.3	24.7	24.6	25.8	24.7	24.6
BMR00193_DSM_Coleoptera sp.	59.8	59.8	18.9	21.4	19.4	19.8	23.7	23.2	23.1	22.1	21.6	33.3	23.2	22.9	19.9	20.4	20.3		20.3	22.6	25.5	23.7	25.4	22.6	21.5	22.6	21.3	22.6	24.3	24.4	24.2	24.9	24.4	24.2
BMR00581_BS1E_Aglenus?	64.0	64.9	22.5	22.3	22.3	20.7	24.0	24.0	24.3	24.2	23.1	34.3	24.5	24.4	22.5	22.2	22.0	20.3		22.3	22.5	23.9	24.3	22.3	21.5	22.3	22.2	23.7	23.5	23.3	23.4	23.9	23.3	23.4
Curculionidae_Pilbara	63.6	62.1	21.1	20.1	20.2	19.0	25.4	25.3	22.9	22.6	22.9	33.3	23.8	24.2	22.2	21.2	21.0	22.6	22.3		19.3	19.6	24.3	16.3	17.5	17.2	17.8	20.4	21.1	19.4	19.6	20.7	19.4	19.7
KU519731_Pilbara_Curculionidae	64.6	64.8	24.8	25.2	24.3	23.6	25.1	25.0	25.7	26.7	26.0	36.4	28.1	26.8	24.9	24.9	24.8	25.5	22.5	19.3		22.9	24.0	20.2	20.6	21.3	21.4	21.6	24.1	24.0	24.2	23.9	24.0	24.2
BIS EW0540_Curculionidae Genus2	63.3	63.3	22.2	22.0	23.6	22.5	25.4	25.5	21.7	22.2	22.3	30.6	24.3	23.6	22.5	22.6	22.6	23.7	23.9	19.6	22.9		18.8	20.1	20.0	21.3	21.9	21.1	23.5	22.8	23.1	24.2	22.8	23.1
KU519728_Pilbara_Curculionidae	65.4	65.2	25.7	26.0	26.4	26.0	27.1	27.2	26.7	26.9	25.8	35.2	26.9	26.4	26.1	26.9	26.9	25.4	24.3	24.3	24.0	18.8		22.8	22.7	23.1	23.4	24.3	25.2	24.3	24.2	24.0	24.3	24.2
BMR00471_VIV_Curculionidae	62.8	62.5	20.4	20.5	22.9	20.5	23.9	23.2	21.1	22.2	22.2	31.6	24.6	23.6	21.4	21.6	21.4	22.6	22.3	16.3	20.2	20.1	22.8		7.4	15.2	16.3	20.1	22.8	22.0	21.9	22.5	22.0	21.9
BMR00523_VIV_Curculionidae	62.2	62.0	19.4	21.5	21.9	20.3	22.1	21.7	21.6	21.2	21.0	31.0	24.8	23.5	20.4	21.5	21.3	21.5	21.5	17.5	20.6	20.0	22.7	7.4		14.4	14.4	19.1	22.7	22.8	23.0	23.3	22.8	23.0
KU519722_Pilbara_Curculionidae	63.2	61.9	20.8	22.0	23.1	20.8	23.3	23.4	23.6	22.8	24.2	33.9	25.1	24.3	21.3	21.6	21.4	22.6	22.3	17.2	21.3	21.3	23.1	15.2	14.4		12.6	19.6	22.2	21.7	21.6	22.3	21.7	21.6
KU519729_Pilbara_Curculionidae	63.0	61.7	20.1	22.2	22.6	19.5	23.6	23.4	24.2	24.5	23.4	33.3	25.2	23.5	21.0	21.6	21.4	21.3	22.2	17.8	21.4	21.9	23.4	16.3	14.4	12.6		19.1	22.3	21.4	21.3	21.9	21.4	21.3
KU519732_Pilbara_Curculionidae	64.5	64.1	21.1	23.3	23.7	20.8	24.6	24.3	25.1	24.5	24.6	33.0	25.1	23.3	22.6	22.3	22.3	22.6	23.7	20.4	21.6	21.1	24.3	20.1	19.1	19.6	19.1		20.2	19.0	19.1	19.1	19.0	19.1
MF03_RC12MEH022120151210-ROBE_Coleoptera_Curculionidae	63.4	62.8	23.5	24.0	26.4	25.0	27.3	27.8	24.8	25.7	25.9	36.1	28.1	27.2	26.2	25.3	25.3	24.3	23.5	21.1	24.1	23.5	25.2	22.8	22.7	22.2	22.3	20.2		13.1	13.0	14.4	13.1	13.0
KD03_GR15MEB0003.20160915.ROBE_Coleoptera_Curculionidae	62.8	64.9	22.6	22.3	25.9	23.3	27.4	26.9	24.9	25.5	24.6	33.1	27.8	28.1	26.0	24.8	24.7	24.4	23.3	19.4	24.0	22.8	24.3	22.0	22.8	21.7	21.4	19.0	13.1		0.1	3.3	0.0	0.1
KD05_GR15MEC0019.20160915.ROBE_Coleoptera_Curculionidae	62.7	64.9	22.8	22.2	25.9	23.4	27.2	26.7	24.8	25.4	24.8	33.1	27.9	28.2	25.8	24.7	24.6	24.2	23.4	19.6	24.2	23.1	24.2	21.9	23.0	21.6	21.3	19.1	13.0	0.1		3.2	0.1	0.0
KU519718_Pilbara_Curculionidae	62.8	64.8	24.5	23.6	27.8	24.5	27.8	27.3	24.9	25.7	24.9	35.2	29.5	28.1	25.5	26.0	25.8	24.9	23.9	20.7	23.9	24.2	24.0	22.5	23.3	22.3	21.9	19.1	14.4	3.3	3.2		3.3	3.2
LI44_E84259_ROBE_Coleoptera_Cryptorhynchinae	62.8	64.9	22.6	22.3	25.9	23.3	27.4	26.9	24.9	25.5	24.6	33.1	27.8	28.1	26.0	24.8	24.7	24.4	23.3	19.4	24.0	22.8	24.3	22.0	22.8	21.7	21.4	19.0	13.1	0.0	0.1	3.3		0.1
ML02_RC15MEC0084-20170527-ROBE_Coleoptera	62.7	64.9	22.8	22.3	25.9	23.4	27.2	26.7	24.8	25.4	24.8	33.1	28.0	28.2	25.8	24.7	24.6	24.2	23.4	19.7	24.2	23.1	24.2	21.9	23.0	21.6	21.3	19.1	13.0	0.1	0.0	3.2	0.1	

Appendix 14: Distance matrix of Hemiptera sequences/ lineages included in the analysis

COI divergence (%) of Hemiptera (regional comparisons)	O.G.	BMR 00486	BMR 00188	BMR 00190	BMR 00191	BMR 00267	BMR 00273	BMR 00406	BMR 00407	BMR 00757	BMR 00764	WAME 98572	WAME 98656	WAME 98671	BMR 00553	BMR 00206	BMR 00218	JY19	JY20	WAME 98539	WAME 98566	WAME 98594	WAME 98587	WAME 98657	WAME 98672	WAME 98675	WAME 98678	BMR 00260	BMR 00261	WAME 98593	BMR 00436	BMR 00487	BMR 00181	BMR 00183	BMR 00184	BMR 00189	BMR 00197	BMR 00200	BMR 00203	BMR 00208	BMR 00219	BMR 00221	BMR 00222	BMR 00226	BMR 00272	BMR 00404	BMR 00405	BMR 00408	BMR 00522	BMR 00524	BMR 00576	BMR 00636
Siphanta patruelis ww03906 (outgroup)		22.5	21.6	21.7	21.6	21.6	21.7	21.7	21.6	21.4	21.7	21.7	21.7	21.7	23.2	23.0	22.4	22.4	22.4	22.7	22.5	22.4	22.4	22.4	22.2	22.4	22.4	23.3	23.3	21.1	20.4	20.4	20.9	20.4	20.9	20.4	21.1	20.7	20.6	20.9	21.1	20.7	20.7	20.4	20.4	20.7	20.7	20.4	20.4	20.3	20.7	20.9
BMR00486_LN33774 Hemiptera HopeDowns	22.5		10.3	10.2	10.3	10.3	10.2	10.2	10.3	10.5	10.2	10.0	10.2	10.0	14.7	15.5	15.2	14.6	14.6	15.2	14.9	14.5	14.4	14.9	14.4	14.6	14.6	14.0	14.0	20.7	22.0	21.7	21.0	20.8	21.0	21.0	21.1	20.8	20.8	21.0	21.4	20.8	20.8	20.7	21.1	20.8	20.8	21.1	21.1	20.7	20.8	21.0
BMR00188 _BS3_Hemiptera sp.	21.6	10.3		1.1	0.0	0.0	1.1	1.1	0.0	0.2	1.1	0.3	1.1	0.3	16.3	15.8	16.4	15.5	15.5	16.0	15.5	15.9	15.3	15.3	15.7	15.5	15.8	13.7	13.7	19.5	20.9	20.8	21.3	21.4	21.3	21.0	21.4	21.1	21.4	21.3	21.9	21.1	21.1	21.3	21.1	21.1	21.1	21.1	21.1	20.7	21.1	21.3
BMR00190 _BS2_Meenoplidae sp.	21.7	10.2	1.1		1.1	1.1	0.0	0.0	1.1	1.2	0.0	1.1	0.0	1.1	16.3	16.0	16.6	15.7	15.7	16.1	15.7	15.6	15.5	15.5	15.5	15.7	15.7	13.7	13.7	19.6	20.6	20.5	21.0	21.1	21.0	20.7	21.1	20.8	21.1	21.0	21.4	20.8	20.8	21.0	20.8	20.8	20.8	20.8	20.8	20.4	20.8	21.0
BMR00191 _BS3_Meenoplidae sp.	21.6	10.3	0.0	1.1		0.0	1.1	1.1	0.0	0.2	1.1	0.3	1.1	0.3	16.3	15.8	16.4	15.5	15.5	16.0	15.5	15.9	15.3	15.3	15.7	15.5	15.8	13.7	13.7	19.5	20.9	20.8	21.3	21.4	21.3	21.0	21.4	21.1	21.4	21.3	21.9	21.1	21.1	21.3	21.1	21.1	21.1	21.1	21.1	20.7	21.1	21.3
BMR00267 _VIV_Meenoplidae sp.	21.6	10.3	0.0	1.1	0.0		1.1	1.1	0.0	0.2	1.1	0.3	1.1	0.3	16.3	15.8	16.4	15.5	15.5	16.0	15.5	15.9	15.3	15.3	15.7	15.5	15.8	13.7	13.7	19.5	20.9	20.8	21.3	21.4	21.3	21.0	21.4	21.1	21.4	21.3	21.9	21.1	21.1	21.3	21.1	21.1	21.1	21.1	21.1	20.7	21.1	21.3
BMR00273 _BS1E_Meenoplidae sp.	21.7	10.2	1.1	0.0	1.1	1.1		0.0	1.1	1.2	0.0	1.1	0.0	1.1	16.3	16.0	16.6	15.7	15.7	16.1	15.7	15.6	15.5	15.5	15.5	15.7	15.7	13.7	13.7	19.6	20.6	20.5	21.0	21.1	21.0	20.7	21.1	20.8	21.1	21.0	21.4	20.8	20.8	21.0	20.8	20.8	20.8	20.8	20.8	20.4	20.8	21.0
BMR00406 _BS2_Meenoplidae	21.7	10.2	1.1	0.0	1.1	1.1	0.0		1.1	1.2	0.0	1.1	0.0	1.1	16.3	16.0	16.6	15.7	15.7	16.1	15.7	15.6	15.5	15.5	15.5	15.7	15.7	13.7	13.7	19.6	20.6	20.5	21.0	21.1	21.0	20.7	21.1	20.8	21.1	21.0	21.4	20.8	20.8	21.0	20.8	20.8	20.8	20.8	20.8	20.4	20.8	21.0
BMR00407 _BS2_Meenoplidae sp.	21.6	10.3	0.0	1.1	0.0	0.0	1.1	1.1		0.2	1.1	0.3	1.1	0.3	16.3	15.8	16.4	15.5	15.5	16.0	15.5	15.9	15.3	15.3	15.7	15.5	15.8	13.7	13.7	19.5	20.9	20.8	21.3	21.4	21.3	21.0	21.4	21.1	21.4	21.3	21.9	21.1	21.1	21.3	21.1	21.1	21.1	21.1	21.1	20.7	21.1	21.3
BMR00757 _VIV_Meenoplidae?	21.4	10.5	0.2	1.2	0.2	0.2	1.2	1.2	0.2		1.2	0.5	1.2	0.5	16.1	16.0	16.3	15.7	15.7	16.1	15.7	16.1	15.5	15.5	15.8	15.7	16.0	13.5	13.5	19.5	20.9	20.8	21.3	21.4	21.3	21.0	21.4	21.1	21.4	21.3	21.9	21.1	21.1	21.3	21.1	21.1	21.1	21.1	21.1	20.7	21.1	21.3
BMR00764 _BS1W_Meenoplidae?	21.7	10.2	1.1	0.0	1.1	1.1	0.0	0.0	1.1	1.2		1.1	0.0	1.1	16.3	16.0	16.6	15.7	15.7	16.1	15.7	15.6	15.5	15.5	15.5	15.7	15.7	13.7	13.7	19.6	20.6	20.5	21.0	21.1	21.0	20.7	21.1	20.8	21.1	21.0	21.4	20.8	20.8	21.0	20.8	20.8	20.8	20.8	20.8	20.4	20.8	21.0
RT43_WAME98572_Phaconeura_WAM-PHAC002	21.7	10.0	0.3	1.1	0.3	0.3	1.1	1.1	0.3	0.5	1.1		1.0	0.0	16.1	15.7	16.3	14.9	14.9	15.4	14.9	15.5	14.8	14.8	15.1	14.9	15.2	13.5	13.5	19.2	20.8	20.7	21.1	21.3	21.1	20.8	21.3	21.0	21.3	21.1	21.7	21.0	21.0	21.1	21.0	21.0	21.0	21.0	21.0	20.5	21.0	21.1
RT53_WAME98656_Phaconeura_WAM-PHAC002	21.7	10.2	1.1	0.0	1.1	1.1	0.0	0.0	1.1	1.2	0.0	1.0		1.0	16.3	16.0	16.6	15.2	15.2	15.7	15.2	15.4	15.1	15.1	15.1	15.2	15.2	13.7	13.7	19.1	20.6	20.5	21.0	21.1	21.0	20.7	21.1	20.8	21.1	21.0	21.4	20.8	20.8	21.0	20.8	20.8	20.8	20.8	20.8	20.4	20.8	21.0
RT56_WAME98671_Phaconeura_WAM-PHAC002	21.7	10.0	0.3	1.1	0.3	0.3	1.1	1.1	0.3	0.5	1.1	0.0	1.0		16.1	15.7	16.3	14.9	14.9	15.4	14.9	15.5	14.8	14.8	15.1	14.9	15.2	13.5	13.5	19.2	20.8	20.7	21.1	21.3	21.1	20.8	21.3	21.0	21.3	21.1	21.7	21.0	21.0	21.1	21.0	21.0	21.0	21.0	21.0	20.5	21.0	21.1
BMR00553_LN35120 Hemiptera HopeDowns	23.2	14.7	16.3	16.3	16.3	16.3	16.3	16.3	16.3	16.1	16.3	16.1	16.3	16.1		13.0	12.7	11.8	11.8	12.6	12.1	12.0	11.6	12.6	11.6	11.8	11.8	13.2	13.2	20.9	21.2	21.2	20.3	20.3	20.3	20.0	20.5	20.2	20.5	20.3	20.9	20.2	20.2	20.3	19.8	20.2	20.2	19.8	19.8	19.7	20.2	20.3
BMR00206 _SGW_Meenoplidae sp.	23.0	15.5	15.8	16.0	15.8	15.8	16.0	16.0	15.8	16.0	16.0	15.7	16.0	15.7	13.0		3.5	2.1	2.1	1.5	2.1	2.3	2.3	1.4	2.3	2.1	2.1	10.6	10.6	22.0	22.8	22.8	22.2	21.7	22.2	22.2	22.3	22.0	21.7	22.2	22.2	22.0	22.0	21.6	22.0	22.0	22.0	22.0	22.0	21.7	22.0	22.2
BMR00218 _BS2_Meenoplidae? sp.	22.4	15.2	16.4	16.6	16.4	16.4	16.6	16.6	16.4	16.3	16.6	16.3	16.6	16.3	12.7	3.5		2.6	2.6	2.9	2.6	2.7	2.7	3.0	2.7	2.6	2.6	10.3	10.3	21.4	22.8	22.8	22.0	21.6	22.0	22.0	22.1	21.9	21.6	22.0	22.0	21.9	21.9	21.4	21.9	21.9	21.9	21.9	21.9	21.7	21.9	22.0
JY19_2139_Hemiptera_Meenoplidae	22.4	14.6	15.5	15.7	15.5	15.5	15.7	15.7	15.5	15.7	15.7	14.9	15.2	14.9	11.8	2.1	2.6		0.0	1.5	0.3	0.3	0.1	1.6	0.1	0.0	0.3	9.6	9.6	20.1	22.2	22.2	21.6	21.1	21.6	21.6	21.7	21.4	21.1	21.6	21.6	21.4	21.4	21.0	21.4	21.4	21.4	21.4	21.4	21.1	21.4	21.6
JY20_2356_Hemiptera_Meenoplidae	22.4	14.6	15.5	15.7	15.5	15.5	15.7	15.7	15.5	15.7	15.7	14.9	15.2	14.9	11.8	2.1	2.6	0.0		1.5	0.3	0.3	0.1	1.6	0.1	0.0	0.3	9.6	9.6	20.1	22.2	22.2	21.6	21.1	21.6	21.6	21.7	21.4	21.1	21.6	21.6	21.4	21.4	21.0	21.4	21.4	21.4	21.4	21.4	21.1	21.4	21.6
RT43_WAME98539_Phaconeura_WAM-PHAC001	22.7	15.2	16.0	16.1	16.0	16.0	16.1	16.1	16.0	16.1	16.1	15.4	15.7	15.4	12.6	1.5	2.9	1.5	1.5		1.5	1.6	1.6	1.0	1.6	1.5	1.5	10.2	10.2	21.0	22.8	22.8	22.2	21.7	22.2	22.2	22.3	22.0	21.7	22.2	22.2	22.0	22.0	21.6	22.0	22.0	22.0	22.0	22.0	21.7	22.0	22.2
RT43_WAME98566_Phaconeura_WAM-PHAC001	22.5	14.9	15.5	15.7	15.5	15.5	15.7	15.7	15.5	15.7	15.7	14.9	15.2	14.9	12.1	2.1	2.6	0.3	0.3	1.5		0.3	0.4	1.6	0.4	0.3	0.3	9.9	9.9	20.3	22.0	22.0	21.4	21.0	21.4	21.4	21.6	21.3	21.0	21.4	21.4	21.3	21.3	20.8	21.3	21.3	21.3	21.3	21.3	21.0	21.3	21.4
RT45_WAME98594_Phaconeura_WAM-PHAC001	22.4	14.5	15.9	15.6	15.9	15.9	15.6	15.6	15.9	16.1	15.6	15.5	15.4	15.5	12.0	2.3	2.7	0.3	0.3	1.6	0.3		0.5	1.7	0.2	0.3	0.0	10.3	10.3	20.4	21.2	21.3	20.8	20.3	20.8	20.8	20.9	20.8	20.3	20.8	20.8	20.8	20.8	20.1	20.6	20.8	20.8	20.6	20.6	20.3	20.8	20.8
RT46_WAME98587_Phaconeura_WAM-PHAC001	22.4	14.4	15.3	15.5	15.3	15.3	15.5	15.5	15.3	15.5	15.5	14.8	15.1	14.8	11.6	2.3	2.7	0.1	0.1	1.6	0.4	0.5		1.8	0.3	0.1	0.4	9.4	9.4	20.1	22.2	22.2	21.6	21.1	21.6	21.6	21.7	21.4	21.1	21.6	21.6	21.4	21.4	21.0	21.4	21.4	21.4	21.4	21.4	21.1	21.4	21.6
RT53_WAME98657_Phaconeura_WAM-PHAC001	22.4	14.9	15.3	15.5	15.3	15.3	15.5	15.5	15.3	15.5	15.5	14.8	15.1	14.8	12.6	1.4	3.0	1.6	1.6	1.0	1.6	1.7	1.8		1.8	1.6	1.6	10.0	10.0	20.5	22.5	22.5	21.6	21.1	21.6	21.6	21.7	21.4	21.1	21.6	21.6	21.4	21.4	21.0	21.4	21.4	21.4	21.4	21.4	21.1	21.4	21.6
RT56_WAME98672_Phaconeura_WAM-PHAC001	22.2	14.4	15.7	15.5	15.7	15.7	15.5	15.5	15.7	15.8	15.5	15.1	15.1	15.1	11.6	2.3	2.7	0.1	0.1	1.6	0.4	0.2	0.3	1.8		0.1	0.1	9.7	9.7	19.9	22.0	22.0	21.4	21.0	21.4	21.4	21.6	21.3	21.0	21.4	21.4	21.3	21.3	20.8	21.3	21.3	21.3	21.3	21.3	21.0	21.3	21.4
RT56_WAME98675_Phaconeura_WAM-PHAC001	22.4	14.6	15.5	15.7	15.5	15.5	15.7	15.7	15.5	15.7	15.7	14.9	15.2	14.9	11.8	2.1	2.6	0.0	0.0	1.5	0.3	0.3	0.1	1.6	0.1		0.3	9.6	9.6	20.1	22.2	22.2	21.6	21.1	21.6	21.6	21.7	21.4	21.1	21.6	21.6	21.4	21.4	21.0	21.4	21.4	21.4	21.4	21.4	21.1	21.4	21.6
RT56_WAME98678_Phaconeura_WAM-PHAC001	22.4	14.6	15.8	15.7	15.8	15.8	15.7	15.7	15.8	16.0	15.7	15.2	15.2	15.2	11.8	2.1	2.6	0.3	0.3	1.5	0.3	0.0	0.4	1.6	0.1	0.3		9.9	9.9	20.1	21.9	21.9	21.3	20.8	21.3	21.3	21.4	21.1	20.8	21.3	21.3	21.1	21.1	20.7	21.1	21.1	21.1	21.1	21.1	20.8	21.1	21.3
BMR00260 _BGCK_Hemiptera sp.	23.3	14.0	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.5	13.7	13.5	13.7	13.5	13.2	10.6	10.3	9.6	9.6	10.2	9.9	10.3	9.4	10.0	9.7	9.6	9.9		0.0	20.5	20.6	20.8	21.3	20.8	21.3	21.3	21.4	21.1	20.8	21.3	21.3	21.1	21.1	20.7	21.1	21.1	21.1	21.1	21.1	20.8	21.1	21.3
BMR00261 _BGCK_Meenoplidae sp.	23.3	14.0	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.5	13.7	13.5	13.7	13.5	13.2	10.6	10.3	9.6	9.6	10.2	9.9	10.3	9.4	10.0	9.7	9.6	9.9	0.0		20.5	20.6	20.8	21.3	20.8	21.3	21.3	21.4	21.1	20.8	21.3	21.3	21.1	21.1	20.7	21.1	21.1	21.1	21.1	21.1	20.8	21.1	21.3
RT46_WAME98593_Oliarus_WAM-CIXO001	21.1	20.7	19.5	19.6	19.5	19.5	19.6	19.6	19.5	19.5	19.6	19.2	19.1	19.2	20.9	22.0	21.4	20.1	20.1	21.0	20.3	20.4	20.1	20.5	19.9	20.1	20.1	20.5	20.5		11.3	11.1	10.0	9.9	10.0	9.6	10.2	9.9	10.2	10.0	10.8	9.9	9.9	10.0	9.4	9.9	9.9	9.4	9.4	9.7	9.9	10.0
BMR00436_LN36535 Hemiptera HopeDowns	20.4	22.0	20.9	20.6	20.9	20.9	20.6	20.6	20.9	20.9	20.6	20.8	20.6	20.8	21.2	22.8	22.8	22.2	22.2	22.8	22.0	21.2	22.2	22.5	22.0	22.2	21.9	20.6	20.6	11.3		0.0	3.7	4.3	3.7	4.2	3.9	3.9	4.5	3.7	5.1	3.9	3.9	4.3	4.0	3.9	3.9	4.0	4.0	3.9	3.9	3.7
BMR00487_LN33789 Hemiptera HopeDowns	20.4	21.7	20.8	20.5	20.8	20.8	20.5	20.5	20.8	20.8	20.5	20.7	20.5	20.7	21.2	22.8	22.8	22.2	22.2	22.8	22.0	21.3	22.2	22.5	22.0	22.2	21.9	20.8	20.8	11.1	0.0		3.8	4.3	3.8	4.3	4.0	4.0	4.6	3.8	5.2	4.0	4.0	4.4	4.1	4.0	4.0	4.1	4.1	4.0	4.0	3.8
BMR00181 _BS2_Meenoplidae sp.	20.9	21.0	21.3	21.0	21.3	21.3	21.0	21.0	21.3	21.3	21.0	21.1	21.0	21.1	20.3	22.2	22.0	21.6	21.6	22.2	21.4	20.8	21.6	21.6	21.4	21.6	21.3	21.3	21.3	10.0	3.7	3.8		0.8	0.0	1.1	0.2	0.2	0.8	0.0	1.5	0.2	0.2	0.6	0.9	0.2	0.2	0.9	0.9	0.8	0.2	0.0
BMR00183 _SGW_Meenoplidae sp.	20.4	20.8	21.4	21.1	21.4	21.4	21.1	21.1	21.4	21.4	21.1	21.3	21.1	21.3	20.3	21.7	21.6	21.1	21.1	21.7	21.0	20.3	21.1	21.1	21.0	21.1	20.8	20.8	20.8	9.9	4.3	4.3	0.8		0.8	1.5	0.9	0.9	0.3	0.8	1.1	0.9	0.9	0.2	1.4	0.9	0.9	1.4	1.4	1.2	0.9	0.8
BMR00184 _BS2_Meenoplidae sp.	20.9	21.0	21.3	21.0	21.3	21.3	21.0	21.0	21.3	21.3	21.0	21.1	21.0	21.1	20.3	22.2	22.0	21.6	21.6	22.2	21.4	20.8	21.6	21.6	21.4	21.6	21.3	21.3	21.3	10.0	3.7	3.8	0.0	0.8		1.1	0.2	0.2	0.8	0.0	1.5	0.2	0.2	0.6	0.9	0.2	0.2	0.9	0.9	0.8	0.2	0.0
BMR00189 _BS3_Meenoplidae sp.	20.4	21.0	21.0	20.7	21.0	21.0	20.7	20.7	21.0	21.0	20.7	20.8	20.7	20.8	20.0	22.2	22.0	21.6	21.6	22.2	21.4	20.8	21.6	21.6	21.4	21.6	21.3	21.3	21.3	9.6	4.2	4.3	1.1	1.5	1.1		1.2	1.2	1.5	1.1	2.1	1.2	1.2	1.4	0.2	1.2	1.2	0.2	0.2	0.9	1.2	1.1
BMR00197 _HSTD_Hemiptera sp.	21.1	21.1	21.4	21.1	21.4	21.4	21.1	21.1	21.4	21.4	21.1	21.3	21.1	21.3	20.5	22.3	22.1	21.7	21.7	22.3	21.6	20.9	21.7	21.7	21.6	21.7	21.4	21.4	21.4	10.2	3.9	4.0	0.2	0.9	0.2	1.2		0.3	0.9	0.2	1.7	0.3	0.3	0.8	1.1	0.3	0.3	1.1	1.1	0.9	0.3	0.2
BMR00200 _SGW_Meenoplidae? sp.	20.7	20.8	21.1	20.8	21.1	21.1	20.8	20.8	21.1	21.1	20.8	21.0	20.8	21.0	20.2	22.0	21.9	21.4	21.4	22.0	21.3	20.8	21.4	21.4	21.3	21.4	21.1	21.1	21.1	9.9	3.9	4.0	0.2	0.9	0.2	1.2	0.3		0.9	0.2	1.7	0.0	0.0	0.8	1.1	0.0	0.0	1.1	1.1	0.9	0.0	0.2
BMR00203 _BS2_Meenoplidae sp.	20.6	20.8	21.4	21.1	21.4	21.4	21.1	21.1	21.4	21.4	21.1	21.3	21.1	21.3	20.5	21.7	21.6	21.1	21.1	21.7	21.0	20.3	21.1	21.1	21.0	21.1	20.8	20.8	20.8	10.2	4.5	4.6	0.8	0.3	0.8	1.5	0.9	0.9		0.8	1.1	0.9	0.9	0.2	1.4	0.9	0.9	1.4	1.4	1.2	0.9	0.8
BMR00208 _BS2_Hemiptera sp.	20.9	21.0	21.3	21.0	21.3	21.3	21.0	21.0	21.3	21.3	21.0	21.1	21.0	21.1	20.3	22.2	22.0	21.6	21.6	22.2	21.4	20.8	21.6	21.6	21.4	21.6	21.3	21.3	21.3	10.0	3.7	3.8	0.0	0.8	0.0	1.1	0.2	0.2	0.8		1.5	0.2	0.2	0.6	0.9	0.2	0.2	0.9	0.9	0.8	0.2	0.0
BMR00219 _LNSG_Meenoplidae sp.	21.1	21.4	21.9	21.4	21.9	21.9	21.4	21.4	21.9	21.9	21.4	21.7	21.4	21.7	20.9	22.2	22.0	21.6	21.6	22.2	21.4	20.8	21.6	21.6	21.4	21.6	21.3	21.3	21.3	10.8	5.1	5.2	1.5	1.1	1.5	2.1	1.7	1.7	1.1	1.5		1.7	1.7	0.9	2.0	1.7	1.7	2.0	2.0	1.8	1.7	1.5
BMR00221 _HSTD_Hemiptera sp.	20.7	20.8	21.1	20.8	21.1	21.1	20.8	20.8	21.1	21.1	20.8	21.0	20.8	21.0	20.2	22.0	21.9	21.4	21.4	22.0	21.3	20.8	21.4	21.4	21.3	21.4	21.1	21.1	21.1	9.9	3.9	4.0	0.2	0.9	0.2	1.2	0.3	0.0	0.9	0.2	1.7		0.0	0.8	1.1	0.0	0.0	1.1	1.1	0.9	0.0	0.2
BMR00222 _SGW_Hemiptera sp.	20.7	20.8	21.1	20.8	21.1	21.1	20.8	20.8	21.1	21.1	20.8	21.0	20.8	21.0	20.2	22.0	21.9	21.4	21.4	22.0	21.3	20.8	21.4	21.4	21.3	21.4	21.1	21.1	21.1	9.9	3.9	4.0	0.2	0.9	0.2	1.2	0.3	0.0	0.9	0.2	1.7	0.0		0.8	1.1	0.0	0.0	1.1	1.1	0.9	0.0	0.2
BMR00226 _LNSG_Meenoplidae sp.	20.4	20.7	21.3	21.0	21.3	21.3	21.0	21.0	21.3	21.3	21.0	21.1	21.0	21.1	20.3	21.6	21.4	21.0	21.0	21.6	20.8	20.1	21.0	21.0	20.8	21.0	20.7	20.7	20.7	10.0	4.3	4.4	0.6	0.2	0.6	1.4	0.8	0.8	0.2	0.6	0.9	0.8	0.8		1.2	0.8	0.8	1.2	1.2	1.1	0.8	0.6
BMR00272 _VIV_Hemiptera sp.	20.4	21.1	21.1	20.8	21.1	21.1	20.8	20.8	21.1	21.1	20.8	21.0	20.8	21.0	19.8	22.0	21.9	21.4	21.4	22.0	21.3	20.6	21.4	21.4	21.3	21.4	21.1	21.1	21.1	9.4	4.0	4.1	0.9	1.4	0.9	0.2	1.1	1.1	1.4	0.9	2.0	1.1	1.1	1.2		1.1	1.1	0.0	0.0	0.8	1.1	0.9
BMR00404 _SGW_Meenoplidae?	20.7	20.8	21.1	20.8	21.1	21.1	20.8	20.8	21.1	21.1	20.8	21.0	20.8	21.0	20.2	22.0	21.9	21.4	21.4	22.0	21.3	20.8	21.4	21.4	21.3	21.4	21.1	21.1	21.1	9.9	3.9	4.0	0.2	0.9	0.2	1.2	0.3	0.0	0.9	0.2	1.7	0.0	0.0	0.8	1.1		0.0	1.1	1.1	0.9	0.0	0.2
BMR00405 _SGW_Meenoplidae?	20.7	20.8	21.1	20.8	21.1	21.1	20.8	20.8	21.1	21.1	20.8	21.0	20.8	21.0	20.2	22.0	21.9	21.4	21.4	22.0	21.3	20.8	21.4	21.4	21.3	21.4	21.1	21.1	21.1	9.9	3.9	4.0	0.2	0.9	0.2	1.2	0.3	0.0	0.9	0.2	1.7	0.0	0.0	0.8	1.1	0.0		1.1	1.1	0.9	0.0	0.2
BMR00408 _BS3_Meenoplidae sp.	20.4	21.1	21.1	20.8	21.1	21.1	20.8	20.8	21.1	21.1	20.8	21.0	20.8	21.0	19.8	22.0	21.9	21.4	21.4	22.0	21.3	20.6	21.4	21.4	21.3	21.4	21.1	21.1	21.1	9.4	4.0	4.1	0.9	1.4	0.9	0.2	1.1	1.1	1.4	0.9	2.0	1.1	1.1	1.2	0.0	1.1	1.1		0.0	0.8	1.1	0.9
BMR00522 _VIV_Meenoplidae	20.4	21.1	21.1	20.8	21.1	21.1	20.8	20.8	21.1	21.1	20.8	21.0	20.8	21.0	19.8	22.0	21.9	21.4	21.4	22.0	21.3	20.6	21.4	21.4	21.3	21.4	21.1	21.1	21.1	9.4	4.0	4.1	0.9	1.4	0.9	0.2	1.1	1.1	1.4	0.9	2.0	1.1	1.1	1.2	0.0	1.1	1.1	0.0		0.8	1.1	0.9
BMR00524 _BS1W_Meenoplidae	20.3	20.7	20.7	20.4	20.7	20.7	20.4	20.4	20.7	20.7	20.4	20.5	20.4	20.5	19.7	21.7	21.7	21.1	21.1	21.7	21.0	20.3	21.1	21.1	21.0	21.1	20.8	20.8	20.8	9.7	3.9	4.0	0.8	1.2	0.8	0.9	0.9	0.9	1.2	0.8	1.8	0.9	0.9	1.1	0.8	0.9	0.9	0.8	0.8		0.9	0.8
BMR00576 _SGW_Meenoplidae?	20.7	20.8	21.1	20.8	21.1	21.1	20.8	20.8	21.1	21.1	20.8	21.0	20.8	21.0	20.2	22.0	21.9	21.4	21.4	22.0	21.3	20.8	21.4	21.4	21.3	21.4	21.1	21.1	21.1	9.9	3.9	4.0	0.2	0.9	0.2	1.2	0.3	0.0	0.9	0.2	1.7	0.0	0.0	0.8	1.1	0.0	0.0	1.1	1.1	0.9		0.2
BMR00636 _BS2_Meenoplidae sp.	20.9	21.0	21.3	21.0	21.3	21.3	21.0	21.0	21.3	21.3	21.0	21.1	21.0	21.1	20.3	22.2	22.0	21.6	21.6	22.2	21.4	20.8	21.6	21.6	21.4	21.6	21.3	21.3	21.3	10.0	3.7	3.8	0.0	0.8	0.0	1.1	0.2	0.2	0.8	0.0	1.5	0.2	0.2	0.6	0.9	0.2	0.2	0.9	0.9	0.8	0.2	

Appendix 15: Distance matrix of Zygentoma (COI) sequences/ lineages included in the analysis

COI divergences (%) of Zygentoma (regional comparisons)	WAME 98594	WAME 98665	BMR0 0351	BMR0 0352	BMR0 0356	WAME 98679	BMR0 0350	BMR0 0355	BMR0 0108	BMR0 0282	BMR0 0281	WAME 98664	WAME 98659	WAME 98658	WAME 84272	WAME 98660	BMR0 0354	BMR0 0358	BMR0 0111	BMR0 0105	BMR0 0118	WAME 98688	WAME 98689	BMR0 0114	BMR0 0117	JC19
RT45_WAME98594_Phaconeura_WAM-PHAC001_OG		28.4	28.3	29.1	30.2	28.4	27.1	28.4	28.2	27.5	29.1	29.3	27.6	29.2	29.0	29.2	32.2	31.6	29.5	29.1	29.5	30.1	28.7	31.2	29.2	28.8
RT53_ROBE_WAME98665_Zygentoma?_2	28.4		20.2	20.4	20.9	21.1	19.7	21.4	21.6	22.8	22.5	22.3	21.7	21.1	21.9	21.6	22.5	23.3	21.4	21.6	21.4	22.3	21.8	23.6	20.9	20.1
BMR00351_WAF_Ateluridae sp.	28.3	20.2		1.7	1.5	14.0	14.3	15.0	20.7	19.6	21.1	22.3	20.1	20.3	20.8	21.0	21.9	21.5	22.6	22.2	22.3	20.8	20.8	22.6	21.7	21.1
BMR00352_WAJ_Zygentoma sp.	29.1	20.4	1.7		1.3	13.8	13.4	14.4	20.7	19.6	21.0	22.2	20.5	20.9	21.1	21.9	21.7	20.6	22.7	22.5	22.6	20.8	20.7	22.2	21.7	21.3
BMR00356_MTEE_Ateluridae sp.	30.2	20.9	1.5	1.3		13.7	13.9	14.5	21.6	20.1	21.8	23.3	21.3	21.4	21.9	21.8	22.8	21.1	23.4	22.9	23.1	20.8	20.2	23.1	22.5	22.1
RT56_PARA_WAME98679_Zygentoma?_2	28.4	21.1	14.0	13.8	13.7		11.6	12.9	20.5	19.8	19.3	20.7	20.5	19.8	20.6	21.1	23.6	23.0	20.9	21.0	21.3	21.1	20.2	20.7	21.1	20.7
BMR00350_WHill_Ateluridae sp.	27.1	19.7	14.3	13.4	13.9	11.6		1.7	17.1	18.8	17.6	20.0	19.5	18.8	18.8	19.1	23.8	21.4	20.2	20.5	20.3	20.2	19.5	21.7	20.0	20.9
BMR00355_WHill_Ateluridae sp.	28.4	21.4	15.0	14.4	14.5	12.9	1.7		17.3	19.1	18.6	20.9	20.1	19.6	19.3	20.0	24.6	22.6	22.4	22.8	22.6	21.2	20.8	23.6	21.2	22.5
BMR00108_HSTD_Nicoletiidae_Trinemura?	28.2	21.6	20.7	20.7	21.6	20.5	17.1	17.3		13.5	14.1	14.6	15.8	13.3	14.9	15.5	21.7	21.0	21.4	21.6	21.7	21.4	20.8	20.8	20.3	21.0
BMR00282_BS1E_Zygentoma sp.	27.5	22.8	19.6	19.6	20.1	19.8	18.8	19.1	13.5		14.1	15.2	16.1	16.1	16.3	16.1	22.6	20.2	20.6	20.7	20.8	20.2	20.8	22.5	21.9	22.5
BMR00281_VIV_Nicoletiidae_Trinemura?	29.1	22.5	21.1	21.0	21.8	19.3	17.6	18.6	14.1	14.1		13.1	13.7	15.6	15.5	15.5	22.5	22.4	22.0	22.2	22.3	20.8	20.5	21.7	20.9	21.3
RT53_ROBE_WAME98664_Zygentoma?_2	29.3	22.3	22.3	22.2	23.3	20.7	20.0	20.9	14.6	15.2	13.1		11.8	11.2	11.0	12.1	22.9	23.0	22.3	22.8	22.6	19.8	20.5	22.5	21.2	20.7
RT53_ROBE_WAME98659_Zygentoma?_2	27.6	21.7	20.1	20.5	21.3	20.5	19.5	20.1	15.8	16.1	13.7	11.8		11.3	10.5	11.1	21.3	21.9	22.0	22.2	22.2	19.5	20.5	20.7	21.1	20.4
RT53_ROBE_WAME98658_Zygentoma?_2	29.2	21.1	20.3	20.9	21.4	19.8	18.8	19.6	13.3	16.1	15.6	11.2	11.3		4.9	4.7	21.7	23.2	20.2	20.6	20.5	20.1	20.3	21.5	20.3	19.0
RT20_ROBE_WAME84272_Nicoletiidae	29.0	21.9	20.8	21.1	21.9	20.6	18.8	19.3	14.9	16.3	15.5	11.0	10.5	4.9		3.6	20.7	22.4	21.4	21.9	21.7	19.3	21.0	21.9	22.0	20.6
RT53_ROBE_WAME98660_Zygentoma?_2	29.2	21.6	21.0	21.9	21.8	21.1	19.1	20.0	15.5	16.1	15.5	12.1	11.1	4.7	3.6		21.3	22.6	20.8	21.1	21.0	19.1	19.7	21.7	22.7	21.4
BMR00354_WHill_Trinemura sp.	32.2	22.5	21.9	21.7	22.8	23.6	23.8	24.6	21.7	22.6	22.5	22.9	21.3	21.7	20.7	21.3		17.3	17.0	17.8	17.3	21.1	23.0	19.5	19.3	18.8
BMR00358_MTEE_Zygentoma sp.	31.6	23.3	21.5	20.6	21.1	23.0	21.4	22.6	21.0	20.2	22.4	23.0	21.9	23.2	22.4	22.6	17.3		20.2	20.1	20.2	18.3	19.2	19.4	21.1	22.0
BMR00111_BS2W_Nicoletiidae_Trinemura?	29.5	21.4	22.6	22.7	23.4	20.9	20.2	22.4	21.4	20.6	22.0	22.3	22.0	20.2	21.4	20.8	17.0	20.2		0.8	0.4	17.5	17.5	17.0	15.6	15.5
BMR00105_BS2W_Zygentoma sp.	29.1	21.6	22.2	22.5	22.9	21.0	20.5	22.8	21.6	20.7	22.2	22.8	22.2	20.6	21.9	21.1	17.8	20.1	0.8		0.5	17.3	17.3	17.6	15.6	16.0
BMR00118_BS2W_Nicoletiidae sp.	29.5	21.4	22.3	22.6	23.1	21.3	20.3	22.6	21.7	20.8	22.3	22.6	22.2	20.5	21.7	21.0	17.3	20.2	0.4	0.5		17.5	17.7	17.2	15.7	15.8
RT56_PARA_WAME98688_Zygentoma?_2	30.1	22.3	20.8	20.8	20.8	21.1	20.2	21.2	21.4	20.2	20.8	19.8	19.5	20.1	19.3	19.1	21.1	18.3	17.5	17.3	17.5		6.9	15.0	16.2	15.8
RT56_PARA_WAME98689_Zygentoma?_2	28.7	21.8	20.8	20.7	20.2	20.2	19.5	20.8	20.8	20.8	20.5	20.5	20.5	20.3	21.0	19.7	23.0	19.2	17.5	17.3	17.7	6.9		14.2	14.5	14.8
BMR00114_BS3X_Nicoletiinae sp.	31.2	23.6	22.6	22.2	23.1	20.7	21.7	23.6	20.8	22.5	21.7	22.5	20.7	21.5	21.9	21.7	19.5	19.4	17.0	17.6	17.2	15.0	14.2		13.0	13.2
BMR00117_BS3_Nicoletiinae sp.	29.2	20.9	21.7	21.7	22.5	21.1	20.0	21.2	20.3	21.9	20.9	21.2	21.1	20.3	22.0	22.7	19.3	21.1	15.6	15.6	15.7	16.2	14.5	13.0		4.2
JC19_BROCK4_Nicoletiidae `sp. Helix marra mamba`	28.8	20.1	21.1	21.3	22.1	20.7	20.9	22.5	21.0	22.5	21.3	20.7	20.4	19.0	20.6	21.4	18.8	22.0	15.5	16.0	15.8	15.8	14.8	13.2	4.2	

Appendix 16: Distance matrix of Zygentoma (12S) sequences/ lineages included in the analysis

12S divergences (%) of Zygentoma (regional comparisons)	O G	IV344	ML75	WAME 98619	JQ282164	JQ282165	FL5	IV334 M2ER	WAME 98686	WAME 98547	WAME 98687	WAME 98578	IV338	IV339	BMR 00285	BMR 00697	WAME 98580	WAME 98685	RT43	RT53	BMR 00840	BMR 00481	BMR 00699	BMR 00110	BMR 01222	MO21	IV229	MO09	WAME 98579	WAME 98680	WAME 98681	WAME 98596	JD17	BMR 00555	JD08	BMR 00357	BMR 00835	BMR 00836
CTXMTRRSSA Ctenolepisma longicaudata OUTGROUP		29.8	29.3	36.9	37.6	37.7	32.7	37.3	36.2	34.3	35.3	35.5	35.2	34.9	34.4	34.4	35.0	33.3	42.5	40.6	40.9	40.5	41.1	41.3	41.5	39.7	40.6	40.3	40.7	40.9	39.4	39.4	41.4	41.9	41.0	40.4	40.1	40.1
IV344_RC15MEB0171-20150115-SC-01_Thysanura	29.8		3.6	33.5	35.7	37.3	32.0	33.8	34.4	34.6	34.0	33.6	33.1	32.2	37.8	37.5	33.9	34.2	36.6	38.3	36.7	36.8	36.5	36.8	36.8	34.2	37.1	34.1	34.4	36.3	35.2	34.6	33.7	35.8	35.4	36.5	36.5	36.5
ML75_RC15MEC0029-20170712-T3-01_Thysanura	29.3	3.6		33.0	37.5	38.9	34.6	37.6	35.4	35.8	34.6	35.4	36.3	35.7	38.2	37.9	34.9	35.5	36.7	38.5	36.0	35.0	35.4	36.6	36.6	35.9	35.8	35.3	35.1	36.3	35.1	34.6	36.0	35.5	36.0	36.0	36.0	36.0
RT48_ROBE_WAME98619_Nicoletiidae_JIM_WAM-ZYGN001	36.9	33.5	33.0		39.3	40.2	38.1	41.9	40.9	39.2	40.3	37.7	39.9	39.8	41.1	40.8	40.0	40.3	40.9	40.8	37.0	38.7	37.3	36.8	37.4	38.4	38.6	37.4	35.2	35.3	34.7	34.5	35.5	35.8	36.1	35.4	34.8	34.8
JQ282164 Trinemura sp.1 WAMT82755	37.6	35.7	37.5	39.3		7.4	19.1	19.9	18.8	19.5	18.6	23.1	16.8	17.4	20.4	19.5	20.1	20.7	37.0	36.4	33.4	33.8	32.7	34.2	34.2	34.1	37.3	35.5	32.3	33.1	32.9	31.1	31.5	31.7	30.9	32.1	32.1	32.1
JQ282165 Trinemura sp.2 WAMT82742	37.7	37.3	38.9	40.2	7.4		18.5	20.9	18.6	20.2	18.3	23.2	16.5	17.1	21.1	19.3	20.8	22.0	37.7	38.0	33.8	33.3	33.4	33.7	33.7	34.8	38.3	35.9	34.2	34.7	34.5	32.4	31.6	31.8	31.3	31.6	31.3	31.3
FL5_ROBE_Trinemura `sp. Helix-TN014`	32.7	32.0	34.6	38.1	19.1	18.5		13.5	13.1	11.4	8.8	11.8	9.7	9.4	10.8	11.1	11.6	11.7	35.7	35.8	35.0	34.3	34.5	34.0	34.0	32.8	35.8	33.5	33.5	34.4	33.8	33.0	32.8	35.4	35.1	33.3	33.3	33.3
IV334_M2ERC0057T1-21_Thysanura	37.3	33.8	37.6	41.9	19.9	20.9	13.5		16.1	15.9	15.3	17.7	14.6	14.0	15.6	15.3	16.9	18.5	37.9	37.5	35.7	36.6	36.4	36.4	36.1	35.4	39.0	36.1	34.6	36.1	36.0	36.0	34.0	36.0	34.2	34.8	34.8	34.8
RT56_PARA_WAME98686_Trinemura_WAM-ZYGS003	36.2	34.4	35.4	40.9	18.8	18.6	13.1	16.1		10.1	11.5	15.3	13.4	13.1	13.1	12.5	11.2	12.0	36.2	37.0	36.3	36.6	35.8	36.3	36.1	36.6	37.5	36.0	35.3	35.6	35.3	35.1	35.5	34.9	35.0	34.1	33.5	33.5
RT43_PARA_WAME98547_Trinemura_WAM-ZYGS004	34.3	34.6	35.8	39.2	19.5	20.2	11.4	15.9	10.1		8.8	10.8	12.4	11.9	12.3	12.0	11.1	11.2	37.7	38.2	35.7	35.9	35.9	35.6	35.7	35.2	36.1	35.1	33.1	33.9	33.8	34.0	33.1	34.9	34.8	33.3	32.8	32.8
RT56_PARA_WAME98687_Trinemura_WAM-ZYGS005	35.3	34.0	34.6	40.3	18.6	18.3	8.8	15.3	11.5	8.8		11.8	10.7	10.7	11.7	11.4	9.9	12.3	35.8	35.5	35.0	35.1	34.8	34.0	34.3	34.0	35.5	34.0	32.7	33.3	33.2	32.8	33.1	35.5	35.9	33.9	33.6	33.6
RT43_PARA_WAME98578_Trinemura_WAM-ZYGS001	35.5	33.6	35.4	37.7	23.1	23.2	11.8	17.7	15.3	10.8	11.8		12.7	12.1	14.8	14.2	13.5	15.0	35.9	37.2	34.4	34.2	35.0	33.9	34.8	35.0	35.7	34.9	31.1	31.6	31.6	32.4	32.5	34.5	33.3	32.1	32.1	32.1
IV338_ROBE_Nicoletiinae sp. 'TN012'	35.2	33.1	36.3	39.9	16.8	16.5	9.7	14.6	13.4	12.4	10.7	12.7		2.0	13.1	12.5	13.4	15.3	36.5	35.3	36.6	36.5	36.8	36.9	36.9	35.3	38.9	36.6	34.8	36.3	36.2	35.1	33.8	36.3	35.1	34.7	34.7	34.7
IV339_ROBE_Nicoletiinae sp. 'TN012'	34.9	32.2	35.7	39.8	17.4	17.1	9.4	14.0	13.1	11.9	10.7	12.1	2.0		12.5	12.3	12.9	14.7	36.9	36.0	36.3	36.1	36.4	36.6	36.6	35.0	38.8	36.5	34.7	36.2	36.1	35.0	33.6	35.7	34.5	34.6	34.6	34.6
BMR00285_VIV_Nicoletiinae sp. Trinemura?	34.4	37.8	38.2	41.1	20.4	21.1	10.8	15.6	13.1	12.3	11.7	14.8	13.1	12.5		5.2	15.1	15.1	39.8	37.8	35.6	35.5	35.6	35.3	35.9	38.4	39.9	39.1	36.2	37.1	35.9	35.5	35.6	36.5	36.7	34.8	35.1	35.1
BMR00697_BS1C_Nicoletiinae sp.	34.4	37.5	37.9	40.8	19.5	19.3	11.1	15.3	12.5	12.0	11.4	14.2	12.5	12.3	5.2		14.3	14.5	39.8	38.4	35.8	35.5	35.3	35.0	35.6	36.2	37.7	36.9	36.5	36.8	36.2	36.3	35.3	35.6	35.6	34.8	34.5	34.5
RT46_PARA_WAME98580_Zygentoma	35.0	33.9	34.9	40.0	20.1	20.8	11.6	16.9	11.2	11.1	9.9	13.5	13.4	12.9	15.1	14.3		9.6	35.4	35.9	36.2	35.9	34.8	35.0	35.4	35.0	36.3	34.9	34.3	35.2	35.1	34.3	33.1	35.2	36.5	33.6	34.2	34.2
RT56_PARA_WAME98685_Trinemura_WAM-ZYGS002	33.3	34.2	35.5	40.3	20.7	22.0	11.7	18.5	12.0	11.2	12.3	15.0	15.3	14.7	15.1	14.5	9.6		36.4	36.4	35.7	35.4	34.9	35.2	35.5	33.6	36.1	34.6	33.9	35.0	34.4	32.9	34.3	34.3	36.0	34.0	34.5	34.5
RT43_PARA_WAME98556_Lepidospora_WAM-ZYGC001	42.5	36.6	36.7	40.9	37.0	37.7	35.7	37.9	36.2	37.7	35.8	35.9	36.5	36.9	39.8	39.8	35.4	36.4		9.7	32.3	33.8	32.1	32.3	32.7	33.0	35.3	34.2	33.2	34.3	33.7	33.4	33.9	33.9	34.4	34.4	34.4	34.4
RT53_ROBE_WAME98660_Lepidospora_HLX_TS007	40.6	38.3	38.5	40.8	36.4	38.0	35.8	37.5	37.0	38.2	35.5	37.2	35.3	36.0	37.8	38.4	35.9	36.4	9.7		30.6	31.6	30.7	30.1	30.6	33.2	34.5	33.6	30.0	31.4	31.8	30.5	32.5	32.4	32.8	31.0	31.3	31.3
BMR00840_BS1C_Atelurinae (Dodecastyla?) sp.	40.9	36.7	36.0	37.0	33.4	33.8	35.0	35.7	36.3	35.7	35.0	34.4	36.6	36.3	35.6	35.8	36.2	35.7	32.3	30.6		4.1	5.6	5.9	5.7	18.2	20.7	19.3	16.4	16.6	15.3	16.1	16.7	15.1	16.7	15.3	14.7	14.7
BMR00481_VIV_Atelurinae sp.	40.5	36.8	35.0	38.7	33.8	33.3	34.3	36.6	36.6	35.9	35.1	34.2	36.5	36.1	35.5	35.5	35.9	35.4	33.8	31.6	4.1		6.1	6.4	5.7	17.3	19.7	18.3	17.4	17.6	16.3	16.2	17.4	15.8	17.9	16.9	16.9	16.9
BMR00699_VIV_Atelurinae sp.	41.1	36.5	35.4	37.3	32.7	33.4	34.5	36.4	35.8	35.9	34.8	35.0	36.8	36.4	35.6	35.3	34.8	34.9	32.1	30.7	5.6	6.1		4.4	3.9	17.3	19.7	18.3	16.9	17.6	16.0	15.6	16.4	14.5	16.1	15.4	16.0	15.9
BMR00110_BS3_Atelurinae sp.	41.3	36.8	36.6	36.8	34.2	33.7	34.0	36.4	36.3	35.6	34.0	33.9	36.9	36.6	35.3	35.0	35.0	35.2	32.3	30.1	5.9	6.4	4.4		1.8	16.9	19.4	18.0	16.8	17.0	16.0	16.2	15.4	14.9	17.0	15.4	15.4	15.4
BMR01222_BS3_Zygentoma	41.5	36.8	36.6	37.4	34.2	33.7	34.0	36.1	36.1	35.7	34.3	34.8	36.9	36.6	35.9	35.6	35.4	35.5	32.7	30.6	5.7	5.7	3.9	1.8		17.5	19.8	18.6	17.2	17.4	16.7	16.9	16.1	15.3	17.5	15.8	15.8	15.8
MO21_GD16MEB0001-20170902-T1-08d_Thysanura	39.7	34.2	35.9	38.4	34.1	34.8	32.8	35.4	36.6	35.2	34.0	35.0	35.3	35.0	38.4	36.2	35.0	33.6	33.0	33.2	18.2	17.3	17.3	16.9	17.5		5.0	3.1	17.4	17.1	16.9	16.8	16.3	17.9	16.3	17.9	17.9	18.1
IV229_ROBE_Atelurinae `sp. Helix-TA009`	40.6	37.1	35.8	38.6	37.3	38.3	35.8	39.0	37.5	36.1	35.5	35.7	38.9	38.8	39.9	37.7	36.3	36.1	35.3	34.5	20.7	19.7	19.7	19.4	19.8	5.0		2.4	17.8	16.9	16.9	16.5	19.7	18.2	18.8	19.0	19.0	19.1
MO09_RC14MEB0101-20170902-T1-01_Thysanura	40.3	34.1	35.3	37.4	35.5	35.9	33.5	36.1	36.0	35.1	34.0	34.9	36.6	36.5	39.1	36.9	34.9	34.6	34.2	33.6	19.3	18.3	18.3	18.0	18.6	3.1	2.4		16.8	16.0	16.0	15.6	17.8	17.3	17.0	18.2	18.2	18.3
RT43_PARA_WAME98579_Dodecastyla_WAM_-ZYGA001	40.7	34.4	35.1	35.2	32.3	34.2	33.5	34.6	35.3	33.1	32.7	31.1	34.8	34.7	36.2	36.5	34.3	33.9	33.2	30.0	16.4	17.4	16.9	16.8	17.2	17.4	17.8	16.8		2.4	4.3	4.8	9.7	8.3	10.0	6.8	7.3	7.5
RT56_PARA_WAME98680_Dodecastyla_WAM-ZYGA001	40.9	36.3	36.3	35.3	33.1	34.7	34.4	36.1	35.6	33.9	33.3	31.6	36.3	36.2	37.1	36.8	35.2	35.0	34.3	31.4	16.6	17.6	17.6	17.0	17.4	17.1	16.9	16.0	2.4		4.6	5.6	10.0	8.9	10.2	7.0	7.0	7.2
RT56_PARA_WAME98681_Dodecastyla_WAM-ZYGA001	39.4	35.2	35.1	34.7	32.9	34.5	33.8	36.0	35.3	33.8	33.2	31.6	36.2	36.1	35.9	36.2	35.1	34.4	33.7	31.8	15.3	16.3	16.0	16.0	16.7	16.9	16.9	16.0	4.3	4.6		3.8	9.5	9.8	10.3	8.2	8.2	8.3
RT46_PARA_WAME98596_Dodecastyla_WAM-ZYGA	39.4	34.6	34.6	34.5	31.1	32.4	33.0	36.0	35.1	34.0	32.8	32.4	35.1	35.0	35.5	36.3	34.3	32.9	33.4	30.5	16.1	16.2	15.6	16.2	16.9	16.8	16.5	15.6	4.8	5.6	3.8		9.1	7.7	11.1	7.3	7.9	8.0
JD17_RC13KOOD021320151125-T4-5_Thysanura	41.4	33.7	36.0	35.5	31.5	31.6	32.8	34.0	35.5	33.1	33.1	32.5	33.8	33.6	35.6	35.3	33.1	34.3	33.9	32.5	16.7	17.4	16.4	15.4	16.1	16.3	19.7	17.8	9.7	10.0	9.5	9.1		7.7	7.7	7.1	7.1	7.1
BMR00555_LN39280_Stantec_Zygentoma_R_12S.ab1	41.9	35.8	35.5	35.8	31.7	31.8	35.4	36.0	34.9	34.9	35.5	34.5	36.3	35.7	36.5	35.6	35.2	34.3	33.9	32.4	15.1	15.8	14.5	14.9	15.3	17.9	18.2	17.3	8.3	8.9	9.8	7.7	7.7		7.1	6.7	6.7	6.7
JD08_YANDI_Thysanura	41.0	35.4	36.0	36.1	30.9	31.3	35.1	34.2	35.0	34.8	35.9	33.3	35.1	34.5	36.7	35.6	36.5	36.0	34.4	32.8	16.7	17.9	16.1	17.0	17.5	16.3	18.8	17.0	10.0	10.2	10.3	11.1	7.7	7.1		6.8	6.8	6.8
BMR00357_MTEE_Ateluridae sp.	40.4	36.5	36.0	35.4	32.1	31.6	33.3	34.8	34.1	33.3	33.9	32.1	34.7	34.6	34.8	34.8	33.6	34.0	34.4	31.0	15.3	16.9	15.4	15.4	15.8	17.9	19.0	18.2	6.8	7.0	8.2	7.3	7.1	6.7	6.8		0.6	0.7
BMR00835_WAJ_Zygentoma sp.	40.1	36.5	36.0	34.8	32.1	31.3	33.3	34.8	33.5	32.8	33.6	32.1	34.7	34.6	35.1	34.5	34.2	34.5	34.4	31.3	14.7	16.9	16.0	15.4	15.8	17.9	19.0	18.2	7.3	7.0	8.2	7.9	7.1	6.7	6.8	0.6		0.1
BMR00836_WAJ_Zygentoma sp.	40.1	36.5	36.0	34.8	32.1	31.3	33.3	34.8	33.5	32.8	33.6	32.1	34.7	34.6	35.1	34.5	34.2	34.5	34.4	31.3	14.7	16.9	15.9	15.4	15.8	18.1	19.1	18.3	7.5	7.2	8.3	8.0	7.1	6.7	6.8	0.7	0.1	

Appendix 17: Distance matrix of Amphipoda (Melitidae) sequences/ lineages included in the analysis (COI)

COI divergences (%) of Melitidae (regional comparisons)	OUT GROUP	BMR 01213	BMR 00515	BMR 00693	BMR 00510	BMR 00126	BMR 00080	BMR 00569	BMR 01225	BMR 00164	BMR 00747	BMR 00508	BMR 00136	BMR 00629	BMR 00494	BMR 00627	BMR 00145	BMR 01187	BMR 00170	BMR 01207	BMR 01190	BMR 00394	BMR 01227	BMR 00511	BMR 00398	BMR 00571	BMR 00632	BMR 00573	BMR 00125	BMR 00142	BMR 00157	BMR 00149	BMR 00634	BMR 00095	BMR 00513	BMR 01228	BMR 00079	BMR 00160	BMR 00128	BMR 00447	BMR 00178	BMR 00691	BMR 00076	BMR 00161	BMR 00749	BMR 00133	BMR 00454	BMR 00152	BMR 00452	BMR 00566	BMR 00633	BMR 00446	BMR 00457	BMR 00075	BMR 00506	BMR 00512	BMR 01186	BMR 00801	BMR 00288	BMR 00589	RT46	BMR 00646	BMR 00529	BMR 00369	BMR 00587	BMR 00367
Norcapensis mandibulis JQ608487_OUTGROUP		18.1	18.1	18.1	18.3	18.4	18.4	18.4	18.3	18.3	18.3	18.3	18.3	18.3	18.3	18.3	18.8	18.6	18.8	19.0	19.0	19.0	18.4	18.4	20.4	20.4	20.4	20.4	20.4	20.4	20.4	20.4	20.4	20.4	20.4	17.2	18.1	18.5	18.7	19.3	19.3	19.0	20.2	19.3	19.1	19.1	19.1	19.1	19.1	19.1	19.1	19.1	19.1	19.1	19.1	19.1	19.1	18.0	17.9	17.9	17.9	17.5	17.5	17.4	17.5	18.1
BMR01213_SGW_Nedsia sp.	18.1		0.0	0.0	0.4	0.4	0.4	0.4	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	3.0	2.7	2.5	5.6	5.6	5.6	4.7	4.7	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	5.6	7.3	6.6	6.2	7.9	7.7	7.9	9.2	8.1	7.9	7.9	7.9	7.9	7.9	7.9	7.8	7.9	7.9	7.9	7.9	7.9	7.9	11.9	11.8	11.8	15.2	15.7	15.7	15.6	15.4	15.6
BMR00515_SGW_Nedsia sp.	18.1	0.0		0.0	0.4	0.4	0.4	0.4	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	3.0	2.7	2.5	5.6	5.6	5.6	4.7	4.7	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	5.6	7.3	6.6	6.2	7.9	7.7	7.9	9.2	8.1	7.9	7.9	7.9	7.9	7.9	7.9	7.8	7.9	7.9	7.9	7.9	7.9	7.9	11.9	11.8	11.8	15.2	15.7	15.7	15.6	15.4	15.6
BMR00693_SGW_Nedsia sp.	18.1	0.0	0.0		0.4	0.4	0.4	0.4	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	3.0	2.7	2.5	5.6	5.6	5.6	4.7	4.7	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	5.6	7.3	6.6	6.2	7.9	7.7	7.9	9.2	8.1	7.9	7.9	7.9	7.9	7.9	7.9	7.8	7.9	7.9	7.9	7.9	7.9	7.9	11.9	11.8	11.8	15.2	15.7	15.7	15.6	15.4	15.6
BMR00510_SGW_Nedsia?	18.3	0.4	0.4	0.4		0.4	0.4	0.4	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	3.0	2.7	2.5	5.6	5.6	5.6	4.7	4.7	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	5.6	7.2	6.6	6.2	7.9	7.7	7.9	9.2	8.1	7.9	7.9	7.9	7.9	7.9	7.9	7.8	7.9	7.9	7.9	7.9	7.9	7.9	12.1	12.0	12.0	15.6	16.1	16.1	15.9	15.7	15.9
BMR00126_SGW_Nedsia sp.	18.4	0.4	0.4	0.4	0.4		0.0	0.0	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	3.0	2.7	2.5	5.6	5.6	5.6	4.7	4.7	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	5.6	7.3	6.6	6.0	7.9	7.7	7.9	9.2	8.1	7.9	7.9	7.9	7.9	7.9	7.9	7.8	7.9	7.9	7.9	7.9	7.9	7.9	12.1	12.0	12.0	15.6	16.1	16.1	15.9	15.7	15.9
BMR00080_SGW_Nedsia sp.	18.4	0.4	0.4	0.4	0.4	0.0		0.0	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	3.0	2.7	2.5	5.6	5.6	5.6	4.7	4.7	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	5.6	7.3	6.6	6.0	7.9	7.7	7.9	9.2	8.1	7.9	7.9	7.9	7.9	7.9	7.9	7.8	7.9	7.9	7.9	7.9	7.9	7.9	12.1	12.0	12.0	15.6	16.1	16.1	15.9	15.7	15.9
BMR00569_SGW_Nedsia sp.	18.4	0.4	0.4	0.4	0.4	0.0	0.0		0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	3.0	2.7	2.5	5.6	5.6	5.6	4.7	4.7	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	5.6	7.3	6.6	6.0	7.9	7.7	7.9	9.2	8.1	7.9	7.9	7.9	7.9	7.9	7.9	7.8	7.9	7.9	7.9	7.9	7.9	7.9	12.1	12.0	12.0	15.6	16.1	16.1	15.9	15.7	15.9
BMR01225_SGW_Nedsia sp.	18.3	0.2	0.2	0.2	0.2	0.2	0.2	0.2		0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.9	2.5	2.3	5.4	5.4	5.4	4.5	4.5	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	5.4	7.2	6.4	6.0	7.7	7.5	7.7	9.1	7.9	7.7	7.7	7.7	7.7	7.7	7.7	7.6	7.7	7.7	7.7	7.7	7.7	7.7	11.9	11.8	11.8	15.4	15.9	15.9	15.7	15.6	15.7
BMR00164_SGW_Nedsia sp.	18.3	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.0		0.0	0.0	0.0	0.0	0.0	0.0	2.9	2.5	2.3	5.4	5.4	5.4	4.5	4.5	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	5.4	7.2	6.4	6.0	7.7	7.5	7.7	9.1	7.9	7.7	7.7	7.7	7.7	7.7	7.7	7.6	7.7	7.7	7.7	7.7	7.7	7.7	11.9	11.8	11.8	15.4	15.9	15.9	15.7	15.6	15.7
BMR00747_SGW_Nedsia sp.	18.3	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.0	0.0		0.0	0.0	0.0	0.0	0.0	2.9	2.5	2.3	5.4	5.4	5.4	4.5	4.5	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	5.4	7.2	6.4	6.0	7.7	7.5	7.7	9.1	7.9	7.7	7.7	7.7	7.7	7.7	7.7	7.6	7.7	7.7	7.7	7.7	7.7	7.7	11.9	11.8	11.8	15.4	15.9	15.9	15.7	15.6	15.7
BMR00508_SGW_Nedsia sp.	18.3	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.0	0.0	0.0		0.0	0.0	0.0	0.0	2.9	2.5	2.3	5.4	5.4	5.4	4.5	4.5	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	5.4	7.2	6.4	6.0	7.7	7.5	7.7	9.1	7.9	7.7	7.7	7.7	7.7	7.7	7.7	7.6	7.7	7.7	7.7	7.7	7.7	7.7	11.9	11.8	11.8	15.4	15.9	15.9	15.7	15.6	15.7
BMR00136_SGW_Nedsia sp.	18.3	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.0	0.0	0.0	0.0		0.0	0.0	0.0	2.9	2.5	2.3	5.4	5.4	5.4	4.5	4.5	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	5.4	7.2	6.4	6.0	7.7	7.5	7.7	9.1	7.9	7.7	7.7	7.7	7.7	7.7	7.7	7.6	7.7	7.7	7.7	7.7	7.7	7.7	11.9	11.8	11.8	15.4	15.9	15.9	15.7	15.6	15.7
BMR00629_SGW_Nedsia sp.	18.3	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.0	0.0	0.0	0.0	0.0		0.0	0.0	2.9	2.5	2.3	5.4	5.4	5.4	4.5	4.5	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	5.4	7.2	6.4	6.0	7.7	7.5	7.7	9.1	7.9	7.7	7.7	7.7	7.7	7.7	7.7	7.6	7.7	7.7	7.7	7.7	7.7	7.7	11.9	11.8	11.8	15.4	15.9	15.9	15.7	15.6	15.7
BMR00494_SGW_Nedsia sp.	18.3	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.0	0.0	0.0	0.0	0.0	0.0		0.0	2.9	2.5	2.3	5.4	5.4	5.4	4.5	4.5	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	5.4	7.2	6.4	6.0	7.7	7.5	7.7	9.1	7.9	7.7	7.7	7.7	7.7	7.7	7.7	7.6	7.7	7.7	7.7	7.7	7.7	7.7	11.9	11.8	11.8	15.4	15.9	15.9	15.7	15.6	15.7
BMR00627_SGW_Nedsia sp.	18.3	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0		2.9	2.5	2.3	5.4	5.4	5.4	4.5	4.5	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	5.4	7.2	6.4	6.0	7.7	7.5	7.7	9.1	7.9	7.7	7.7	7.7	7.7	7.7	7.7	7.6	7.7	7.7	7.7	7.7	7.7	7.7	11.9	11.8	11.8	15.4	15.9	15.9	15.7	15.6	15.7
BMR00145_SGW_Nedsia? sp.	18.8	3.0	3.0	3.0	3.0	3.0	3.0	3.0	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.9		0.5	0.7	4.1	4.1	4.1	4.5	4.5	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.9	6.6	6.5	6.7	7.5	7.3	8.1	9.2	7.7	7.9	7.9	7.9	7.9	7.9	7.9	7.8	7.9	7.9	7.9	7.9	7.9	7.9	13.0	12.9	12.9	15.9	16.8	16.8	16.3	16.1	16.6
BMR01187_SGW_Nedsia?	18.6	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.5	2.5	2.5	2.5	2.5	2.5	2.5	2.5	0.5		0.2	4.3	4.3	4.3	4.1	4.1	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.6	6.1	6.1	6.3	7.2	7.0	7.7	8.9	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.4	7.5	7.5	7.5	7.5	7.5	7.5	12.6	12.5	12.5	15.4	16.3	16.3	15.7	15.6	16.1
BMR00170_SGW_Nedsia sp.	18.8	2.5	2.5	2.5	2.5	2.5	2.5	2.5	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	0.7	0.2		4.5	4.5	4.5	4.3	4.3	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.7	6.3	6.3	6.5	7.3	7.2	7.9	9.1	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.6	7.7	7.7	7.7	7.7	7.7	7.7	12.8	12.7	12.7	15.2	16.1	16.1	15.6	15.4	15.9
BMR01207_Caves Creek_Nedsia sp.	19.0	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	4.1	4.3	4.5		0.0	0.0	5.2	5.2	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.6	6.4	6.8	6.9	8.1	8.1	8.4	9.5	7.9	8.1	8.1	8.1	8.1	8.1	8.1	8.0	8.1	8.1	8.1	8.1	8.1	8.1	13.3	13.2	13.2	16.1	16.8	16.8	16.1	15.9	16.8
BMR01190_Caves Creek_Nedsia sp.	19.0	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	4.1	4.3	4.5	0.0		0.0	5.2	5.2	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.6	6.4	6.8	6.9	8.1	8.1	8.4	9.5	7.9	8.1	8.1	8.1	8.1	8.1	8.1	8.0	8.1	8.1	8.1	8.1	8.1	8.1	13.3	13.2	13.2	16.1	16.8	16.8	16.1	15.9	16.8
BMR00394_HSTD_Nedsia sp.	19.0	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	4.1	4.3	4.5	0.0	0.0		5.2	5.2	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.6	6.4	6.8	6.9	8.1	8.1	8.4	9.5	7.9	8.1	8.1	8.1	8.1	8.1	8.1	8.0	8.1	8.1	8.1	8.1	8.1	8.1	13.3	13.2	13.2	16.1	16.8	16.8	16.1	15.9	16.8
BMR01227_Caves Creek_Nedsia sp.	18.4	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.1	4.3	5.2	5.2	5.2		0.0	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.6	5.6	5.8	6.0	7.0	6.8	7.3	8.3	7.2	7.0	7.0	7.0	7.0	7.0	7.0	6.9	7.0	7.0	7.0	7.0	7.0	7.0	12.3	12.2	12.2	15.7	17.0	17.0	15.7	15.6	16.5
BMR00511_HSTD_Nedsia sp. "2/3 spines"	18.4	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.1	4.3	5.2	5.2	5.2	0.0		5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.6	5.6	5.8	6.0	7.0	6.8	7.3	8.3	7.2	7.0	7.0	7.0	7.0	7.0	7.0	6.9	7.0	7.0	7.0	7.0	7.0	7.0	12.3	12.2	12.2	15.7	17.0	17.0	15.7	15.6	16.5
BMR00398_HSTD_Nedsia sp.	20.4	6.1	6.1	6.1	6.3	6.3	6.3	6.3	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	5.7	5.2	5.4	6.4	6.4	6.4	5.4	5.4		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	6.6	6.1	7.1	6.8	7.3	7.5	7.7	8.7	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	13.7	13.6	13.6	15.9	17.4	17.4	16.3	16.1	16.3
BMR00571_HSTD_Nedsia sp. "2/3 spines"	20.4	6.1	6.1	6.1	6.3	6.3	6.3	6.3	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	5.7	5.2	5.4	6.4	6.4	6.4	5.4	5.4	0.0		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	6.6	6.1	7.1	6.8	7.3	7.5	7.7	8.7	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	13.7	13.6	13.6	15.9	17.4	17.4	16.3	16.1	16.3
BMR00632_HSTD_Nedsia sp.	20.4	6.1	6.1	6.1	6.3	6.3	6.3	6.3	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	5.7	5.2	5.4	6.4	6.4	6.4	5.4	5.4	0.0	0.0		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	6.6	6.1	7.1	6.8	7.3	7.5	7.7	8.7	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	13.7	13.6	13.6	15.9	17.4	17.4	16.3	16.1	16.3
BMR00573_HSTD_Nedsia sp.	20.4	6.1	6.1	6.1	6.3	6.3	6.3	6.3	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	5.7	5.2	5.4	6.4	6.4	6.4	5.4	5.4	0.0	0.0	0.0		0.0	0.0	0.0	0.0	0.0	0.0	0.0	6.6	6.1	7.1	6.8	7.3	7.5	7.7	8.7	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	13.7	13.6	13.6	15.9	17.4	17.4	16.3	16.1	16.3
BMR00125_HSTD_Nedsia sp. "2/3 spines"	20.4	6.1	6.1	6.1	6.3	6.3	6.3	6.3	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	5.7	5.2	5.4	6.4	6.4	6.4	5.4	5.4	0.0	0.0	0.0	0.0		0.0	0.0	0.0	0.0	0.0	0.0	6.6	6.1	7.1	6.8	7.3	7.5	7.7	8.7	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	13.7	13.6	13.6	15.9	17.4	17.4	16.3	16.1	16.3
BMR00142_HSTD_Nedsia sp.	20.4	6.1	6.1	6.1	6.3	6.3	6.3	6.3	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	5.7	5.2	5.4	6.4	6.4	6.4	5.4	5.4	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0	0.0	0.0	6.6	6.1	7.1	6.8	7.3	7.5	7.7	8.7	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	13.7	13.6	13.6	15.9	17.4	17.4	16.3	16.1	16.3
BMR00157_HSTD_Nedsia sp.	20.4	6.1	6.1	6.1	6.3	6.3	6.3	6.3	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	5.7	5.2	5.4	6.4	6.4	6.4	5.4	5.4	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0	0.0	6.6	6.1	7.1	6.8	7.3	7.5	7.7	8.7	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	13.7	13.6	13.6	15.9	17.4	17.4	16.3	16.1	16.3
BMR00149_HSTD_Nedsia sp.	20.4	6.1	6.1	6.1	6.3	6.3	6.3	6.3	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	5.7	5.2	5.4	6.4	6.4	6.4	5.4	5.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0	6.6	6.1	7.1	6.8	7.3	7.5	7.7	8.7	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	13.7	13.6	13.6	15.9	17.4	17.4	16.3	16.1	16.3
BMR00634_HSTD_Nedsia sp.	20.4	6.1	6.1	6.1	6.3	6.3	6.3	6.3	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	5.7	5.2	5.4	6.4	6.4	6.4	5.4	5.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	6.6	6.1	7.1	6.8	7.3	7.5	7.7	8.7	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	13.7	13.6	13.6	15.9	17.4	17.4	16.3	16.1	16.3
BMR00095_HSTD_Nedsia sp.	20.4	6.1	6.1	6.1	6.3	6.3	6.3	6.3	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	5.7	5.2	5.4	6.4	6.4	6.4	5.4	5.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	6.6	6.1	7.1	6.8	7.3	7.5	7.7	8.7	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	13.7	13.6	13.6	15.9	17.4	17.4	16.3	16.1	16.3
BMR00513_HSTD_Nedsia sp.	20.4	6.1	6.1	6.1	6.3	6.3	6.3	6.3	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	5.7	5.2	5.4	6.4	6.4	6.4	5.4	5.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		6.6	6.1	7.1	6.8	7.3	7.5	7.7	8.7	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	13.7	13.6	13.6	15.9	17.4	17.4	16.3	16.1	16.3
BMR01228_SGW_Nedsia sp.	17.2	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.9	5.6	5.7	6.6	6.6	6.6	5.6	5.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6		5.4	6.2	6.3	7.3	7.5	7.3	8.8	7.5	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	12.6	12.5	12.5	16.3	16.1	16.1	16.6	16.5	16.6
BMR00079_CVCK_REG_Nedsia sp.	18.1	7.3	7.3	7.3	7.2	7.3	7.3	7.3	7.2	7.2	7.2	7.2	7.2	7.2	7.2	7.2	6.6	6.1	6.3	6.4	6.4	6.4	5.6	5.6	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	5.4		6.3	6.1	6.6	6.8	6.6	7.7	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.2	6.3	6.3	6.3	6.3	6.3	6.3	11.9	11.8	11.8	16.3	16.5	16.5	16.3	16.1	17.0
BMR00160_HSTD_Nedsia sp.	18.5	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.5	6.1	6.3	6.8	6.8	6.8	5.8	5.8	7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.1	7.1	6.2	6.3		2.8	2.7	2.9	2.7	3.8	2.5	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	11.5	11.4	11.4	16.0	16.9	16.9	16.3	16.1	16.7
BMR00128_HSTD_Nedsia sp.	18.7	6.2	6.2	6.2	6.2	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.7	6.3	6.5	6.9	6.9	6.9	6.0	6.0	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.3	6.1	2.8		2.2	2.4	2.1	3.3	2.1	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	11.5	11.5	11.5	16.0	17.1	17.1	16.4	16.2	16.7
BMR00447_HSTD_Nedsia sp.	19.3	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.5	7.2	7.3	8.1	8.1	8.1	7.0	7.0	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	6.6	2.7	2.2		0.2	1.1	2.2	0.9	0.7	0.7	0.7	0.7	0.7	0.7	0.8	0.7	0.7	0.7	0.7	0.7	0.7	12.6	12.5	12.5	16.3	17.9	17.9	17.0	16.8	17.4
BMR00178_HSTD_Nedsia sp.	19.3	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.3	7.0	7.2	8.1	8.1	8.1	6.8	6.8	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	6.8	2.9	2.4	0.2		1.3	2.4	1.1	0.9	0.9	0.9	0.9	0.9	0.9	1.0	0.9	0.9	0.9	0.9	0.9	0.9	12.8	12.7	12.7	16.5	18.1	18.1	17.2	17.0	17.5
BMR00691_HSTD_Nedsia sp.	19.0	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	8.1	7.7	7.9	8.4	8.4	8.4	7.3	7.3	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.3	6.6	2.7	2.1	1.1	1.3		1.8	0.5	0.4	0.4	0.4	0.4	0.4	0.4	0.5	0.4	0.4	0.4	0.4	0.4	0.4	11.9	11.8	11.8	16.1	17.4	17.4	16.5	16.3	16.8
BMR00076_HSTD_Nedsia sp.	20.2	9.2	9.2	9.2	9.2	9.2	9.2	9.2	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.2	8.9	9.1	9.5	9.5	9.5	8.3	8.3	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.8	7.7	3.8	3.3	2.2	2.4	1.8		1.6	1.5	1.5	1.5	1.5	1.5	1.5	1.6	1.5	1.5	1.5	1.5	1.5	1.5	12.5	12.4	12.4	17.5	18.7	18.7	17.8	17.7	18.2
BMR00161_HSTD_Nedsia sp.	19.3	8.1	8.1	8.1	8.1	8.1	8.1	8.1	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.7	7.5	7.7	7.9	7.9	7.9	7.2	7.2	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.5	6.3	2.5	2.1	0.9	1.1	0.5	1.6		0.2	0.2	0.2	0.2	0.2	0.2	0.3	0.2	0.2	0.2	0.2	0.2	0.2	12.1	12.0	12.0	16.3	17.5	17.5	16.6	16.5	17.0
BMR00749_HSTD_Nedsia sp.	19.1	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.9	7.5	7.7	8.1	8.1	8.1	7.0	7.0	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	6.3	2.4	1.9	0.7	0.9	0.4	1.5	0.2		0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	11.9	11.8	11.8	16.3	17.5	17.5	16.6	16.5	17.0
BMR00133_HSTD_Nedsia sp.	19.1	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.9	7.5	7.7	8.1	8.1	8.1	7.0	7.0	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	6.3	2.4	1.9	0.7	0.9	0.4	1.5	0.2	0.0		0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	11.9	11.8	11.8	16.3	17.5	17.5	16.6	16.5	17.0
BMR00454_HSTD_Nedsia sp.	19.1	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.9	7.5	7.7	8.1	8.1	8.1	7.0	7.0	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	6.3	2.4	1.9	0.7	0.9	0.4	1.5	0.2	0.0	0.0		0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	11.9	11.8	11.8	16.3	17.5	17.5	16.6	16.5	17.0
BMR00152_HSTD_Nedsia sp.	19.1	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.9	7.5	7.7	8.1	8.1	8.1	7.0	7.0	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	6.3	2.4	1.9	0.7	0.9	0.4	1.5	0.2	0.0	0.0	0.0		0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	11.9	11.8	11.8	16.3	17.5	17.5	16.6	16.5	17.0
BMR00452_HSTD_Nedsia sp.	19.1	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.9	7.5	7.7	8.1	8.1	8.1	7.0	7.0	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	6.3	2.4	1.9	0.7	0.9	0.4	1.5	0.2	0.0	0.0	0.0	0.0		0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	11.9	11.8	11.8	16.3	17.5	17.5	16.6	16.5	17.0
BMR00566_HSTD_Nedsia?	19.1	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.9	7.5	7.7	8.1	8.1	8.1	7.0	7.0	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	6.3	2.4	1.9	0.7	0.9	0.4	1.5	0.2	0.0	0.0	0.0	0.0	0.0		0.1	0.0	0.0	0.0	0.0	0.0	0.0	11.9	11.8	11.8	16.3	17.5	17.5	16.6	16.5	17.0
BMR00633_HSTD_Nedsia sp.	19.1	7.8	7.8	7.8	7.8	7.8	7.8	7.8	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.8	7.4	7.6	8.0	8.0	8.0	6.9	6.9	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	6.2	2.4	1.9	0.8	1.0	0.5	1.6	0.3	0.1	0.1	0.1	0.1	0.1	0.1		0.1	0.1	0.1	0.1	0.1	0.1	11.8	11.7	11.7	16.2	17.4	17.4	16.6	16.4	16.9
BMR00446_HSTD_Nedsia sp. "2/3 spines"	19.1	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.9	7.5	7.7	8.1	8.1	8.1	7.0	7.0	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	6.3	2.4	1.9	0.7	0.9	0.4	1.5	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.1		0.0	0.0	0.0	0.0	0.0	11.9	11.8	11.8	16.3	17.5	17.5	16.6	16.5	17.0
BMR00457_HSTD_Nedsia sp. "2/3 spines"	19.1	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.9	7.5	7.7	8.1	8.1	8.1	7.0	7.0	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	6.3	2.4	1.9	0.7	0.9	0.4	1.5	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0		0.0	0.0	0.0	0.0	11.9	11.8	11.8	16.3	17.5	17.5	16.6	16.5	17.0
BMR00075_HSTD_Nedsia sp.	19.1	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.9	7.5	7.7	8.1	8.1	8.1	7.0	7.0	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	6.3	2.4	1.9	0.7	0.9	0.4	1.5	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0		0.0	0.0	0.0	11.9	11.8	11.8	16.3	17.5	17.5	16.6	16.5	17.0
BMR00506_HSTD_Nedsia sp.	19.1	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.9	7.5	7.7	8.1	8.1	8.1	7.0	7.0	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	6.3	2.4	1.9	0.7	0.9	0.4	1.5	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0		0.0	0.0	11.9	11.8	11.8	16.3	17.5	17.5	16.6	16.5	17.0
BMR00512_HSTD_Nedsia sp.	19.1	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.9	7.5	7.7	8.1	8.1	8.1	7.0	7.0	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	6.3	2.4	1.9	0.7	0.9	0.4	1.5	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0		0.0	11.9	11.8	11.8	16.3	17.5	17.5	16.6	16.5	17.0
BMR01186 _Caves Creek_Nedsia sp.	19.1	7.9	7.9	7.9	7.9	7.9	7.9	7.9	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.9	7.5	7.7	8.1	8.1	8.1	7.0	7.0	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	6.3	2.4	1.9	0.7	0.9	0.4	1.5	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0		11.9	11.8	11.8	16.3	17.5	17.5	16.6	16.5	17.0
BMR00801_BGCK_Nedsia sp "2/3 spines"	18.0	11.9	11.9	11.9	12.1	12.1	12.1	12.1	11.9	11.9	11.9	11.9	11.9	11.9	11.9	11.9	13.0	12.6	12.8	13.3	13.3	13.3	12.3	12.3	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	12.6	11.9	11.5	11.5	12.6	12.8	11.9	12.5	12.1	11.9	11.9	11.9	11.9	11.9	11.9	11.8	11.9	11.9	11.9	11.9	11.9	11.9		0.1	0.1	15.8	15.8	15.8	15.5	15.7	16.2
BMR00288_BGCK_Nedsia sp "2/3 spines"	17.9	11.8	11.8	11.8	12.0	12.0	12.0	12.0	11.8	11.8	11.8	11.8	11.8	11.8	11.8	11.8	12.9	12.5	12.7	13.2	13.2	13.2	12.2	12.2	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	12.5	11.8	11.4	11.5	12.5	12.7	11.8	12.4	12.0	11.8	11.8	11.8	11.8	11.8	11.8	11.7	11.8	11.8	11.8	11.8	11.8	11.8	0.1		0.0	15.7	15.7	15.7	15.4	15.6	16.1
BMR00589_BGCK_Nedsia sp "2/3 spines"	17.9	11.8	11.8	11.8	12.0	12.0	12.0	12.0	11.8	11.8	11.8	11.8	11.8	11.8	11.8	11.8	12.9	12.5	12.7	13.2	13.2	13.2	12.2	12.2	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	12.5	11.8	11.4	11.5	12.5	12.7	11.8	12.4	12.0	11.8	11.8	11.8	11.8	11.8	11.8	11.7	11.8	11.8	11.8	11.8	11.8	11.8	0.1	0.0		15.7	15.7	15.7	15.4	15.6	16.1
RT46_WAMC72443_Nedsia_WAM-AMPE003	17.9	15.2	15.2	15.2	15.6	15.6	15.6	15.6	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.4	15.9	15.4	15.2	16.1	16.1	16.1	15.7	15.7	15.9	15.9	15.9	15.9	15.9	15.9	15.9	15.9	15.9	15.9	15.9	16.3	16.3	16.0	16.0	16.3	16.5	16.1	17.5	16.3	16.3	16.3	16.3	16.3	16.3	16.3	16.2	16.3	16.3	16.3	16.3	16.3	16.3	15.8	15.7	15.7		6.1	6.1	1.6	1.8	1.6
BMR00646_BS1W_Nedsia sp "1 spine"	17.5	15.7	15.7	15.7	16.1	16.1	16.1	16.1	15.9	15.9	15.9	15.9	15.9	15.9	15.9	15.9	16.8	16.3	16.1	16.8	16.8	16.8	17.0	17.0	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.4	16.1	16.5	16.9	17.1	17.9	18.1	17.4	18.7	17.5	17.5	17.5	17.5	17.5	17.5	17.5	17.4	17.5	17.5	17.5	17.5	17.5	17.5	15.8	15.7	15.7	6.1		0.0	5.6	5.7	5.7
BMR00529_BS1W_Nedsia sp "1 spine"	17.5	15.7	15.7	15.7	16.1	16.1	16.1	16.1	15.9	15.9	15.9	15.9	15.9	15.9	15.9	15.9	16.8	16.3	16.1	16.8	16.8	16.8	17.0	17.0	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.4	16.1	16.5	16.9	17.1	17.9	18.1	17.4	18.7	17.5	17.5	17.5	17.5	17.5	17.5	17.5	17.4	17.5	17.5	17.5	17.5	17.5	17.5	15.8	15.7	15.7	6.1	0.0		5.6	5.7	5.7
BMR00369_BS1W_Nedsia sp "1 spine"	17.4	15.6	15.6	15.6	15.9	15.9	15.9	15.9	15.7	15.7	15.7	15.7	15.7	15.7	15.7	15.7	16.3	15.7	15.6	16.1	16.1	16.1	15.7	15.7	16.3	16.3	16.3	16.3	16.3	16.3	16.3	16.3	16.3	16.3	16.3	16.6	16.3	16.3	16.4	17.0	17.2	16.5	17.8	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.6	15.5	15.4	15.4	1.6	5.6	5.6		0.2	1.8
BMR00587_BS1W_Nedsia sp "1 spine"	17.5	15.4	15.4	15.4	15.7	15.7	15.7	15.7	15.6	15.6	15.6	15.6	15.6	15.6	15.6	15.6	16.1	15.6	15.4	15.9	15.9	15.9	15.6	15.6	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.5	16.1	16.1	16.2	16.8	17.0	16.3	17.7	16.5	16.5	16.5	16.5	16.5	16.5	16.5	16.4	16.5	16.5	16.5	16.5	16.5	16.5	15.7	15.6	15.6	1.8	5.7	5.7	0.2		2.0
BMR00367_BS1E_Nedsia sp "1 spine"	18.1	15.6	15.6	15.6	15.9	15.9	15.9	15.9	15.7	15.7	15.7	15.7	15.7	15.7	15.7	15.7	16.6	16.1	15.9	16.8	16.8	16.8	16.5	16.5	16.3	16.3	16.3	16.3	16.3	16.3	16.3	16.3	16.3	16.3	16.3	16.6	17.0	16.7	16.7	17.4	17.5	16.8	18.2	17.0	17.0	17.0	17.0	17.0	17.0	17.0	16.9	17.0	17.0	17.0	17.0	17.0	17.0	16.2	16.1	16.1	1.6	5.7	5.7	1.8	2.0	

Appendix 18: Distance matrix of Amphipoda (Melitidae) sequences/ lineages included in the analysis (concatenated COI and 16S)

Concatenate 16S and CO1 divergences (%) of Melitidae	BMR 00095	BMR 00571	BMR 00398	BMR 00511	BMR 01227	BMR 00178	BMR 00506	BMR 00512	BMR 00452	BMR 00152	BMR 00170	BMR 00569	BMR 00589	BMR 00801	BMR 00288	BMR 00529	BMR 00646	BMR 00367	BMR 00587	BMR 00369
BMR00095_HSTD_Nedsia sp.		0.0	0.0	3.6	3.6	4.8	4.8	4.8	4.8	4.8	3.7	4.4	10.5	10.6	10.6	15.0	14.9	15.4	13.8	13.9
BMR00571_HSTD_Nedsia sp. "2/3 spines"	0.0		0.0	3.6	3.6	4.8	4.8	4.8	4.8	4.8	3.7	4.4	10.5	10.6	10.6	15.0	14.9	15.4	13.8	13.9
BMR00398_HSTD_Nedsia sp.	0.0	0.0		3.6	3.6	4.8	4.8	4.8	4.8	4.8	3.7	4.4	10.5	10.6	10.6	15.0	14.9	15.4	13.8	13.9
BMR00511_HSTD_Nedsia sp. "2/3 spines"	3.6	3.6	3.6		0.0	4.6	4.8	4.8	4.8	4.8	3.1	3.4	9.7	9.7	9.7	14.9	14.8	15.7	13.7	13.8
BMR01227_Caves Creek_Nedsia sp.	3.6	3.6	3.6	0.0		4.6	4.8	4.8	4.8	4.8	3.1	3.4	9.7	9.7	9.7	14.9	14.8	15.7	13.7	13.8
BMR00178_HTSD_Nedsia sp.	4.8	4.8	4.8	4.6	4.6		0.7	0.7	0.7	0.7	4.7	5.1	10.1	10.2	10.1	15.6	15.5	16.4	14.5	14.6
BMR00506_HTSD_Nedsia sp.	4.8	4.8	4.8	4.8	4.8	0.7		0.0	0.0	0.0	5.2	5.5	9.6	9.6	9.6	15.4	15.3	16.3	14.4	14.5
BMR00512_HTSD_Nedsia sp.	4.8	4.8	4.8	4.8	4.8	0.7	0.0		0.0	0.0	5.2	5.5	9.6	9.6	9.6	15.4	15.3	16.3	14.4	14.5
BMR00452_HTSD_Nedsia sp.	4.8	4.8	4.8	4.8	4.8	0.7	0.0	0.0		0.0	5.2	5.5	9.6	9.6	9.6	15.4	15.3	16.3	14.4	14.5
BMR00152_HTSD_Nedsia sp.	4.8	4.8	4.8	4.8	4.8	0.7	0.0	0.0	0.0		5.2	5.5	9.6	9.6	9.6	15.4	15.3	16.3	14.4	14.5
BMR00170_SGW_Nedsia sp.	3.7	3.7	3.7	3.1	3.1	4.7	5.2	5.2	5.2	5.2		1.9	9.6	9.6	9.6	14.2	14.1	15.2	13.3	13.4
BMR00569_SGW_Nedsia sp.	4.4	4.4	4.4	3.4	3.4	5.1	5.5	5.5	5.5	5.5	1.9		9.1	9.2	9.2	14.4	14.3	15.5	13.6	13.7
BMR00589_BGCK_Nedsia sp. "2/3 spines"	10.5	10.5	10.5	9.7	9.7	10.1	9.6	9.6	9.6	9.6	9.6	9.1		0.0	0.0	15.0	14.9	16.3	14.2	14.2
BMR00801_BGCK_Nedsia sp. "2/3 spines"	10.6	10.6	10.6	9.7	9.7	10.2	9.6	9.6	9.6	9.6	9.6	9.2	0.0		0.0	15.1	14.9	16.4	14.3	14.2
BMR00288_BGCK_Nedsia sp. "2/3 spines"	10.6	10.6	10.6	9.7	9.7	10.1	9.6	9.6	9.6	9.6	9.6	9.2	0.0	0.0		15.0	14.9	16.3	14.3	14.2
BMR00529_BS1W_Nedsia sp. "1 spine"	15.0	15.0	15.0	14.9	14.9	15.6	15.4	15.4	15.4	15.4	14.2	14.4	15.0	15.1	15.0		0.1	6.0	5.6	5.5
BMR00646_BS1W_Nedsia sp. "1 spine"	14.9	14.9	14.9	14.8	14.8	15.5	15.3	15.3	15.3	15.3	14.1	14.3	14.9	14.9	14.9	0.1		5.9	5.5	5.4
BMR00367_BS1E_Nedsia sp. "1 spine"	15.4	15.4	15.4	15.7	15.7	16.4	16.3	16.3	16.3	16.3	15.2	15.5	16.3	16.4	16.3	6.0	5.9		3.5	3.4
BMR00587_BS1W_Nedsia sp. "1 spine"	13.8	13.8	13.8	13.7	13.7	14.5	14.4	14.4	14.4	14.4	13.3	13.6	14.2	14.3	14.3	5.6	5.5	3.5		0.1
BMR00369_BS1W_Nedsia sp. "1 spine"	13.9	13.9	13.9	13.8	13.8	14.6	14.5	14.5	14.5	14.5	13.4	13.7	14.2	14.2	14.2	5.5	5.4	3.4	0.1	

Appendix 19: Distance matrix of Amphipoda (Niphargidae and Bogidiellidae) sequences/ lineages included in the analysis

COI divergences (%) of Niphargidae and Bogidiellidae (regional comparisons)	O.G.	JF27 8086	IV128	BMR 00196	BMR 00204	BMR 00286	BMR 00370	BMR 00585	BMR 00802	BMR 00805	KE28	RT15	KE07	NH68	KE18	RT35	BMR 00150	BMR 00082	BMR 00134	BMR 00628	BMR 00081	BMR 00132	BMR 00154	BMR 00153	BMR 00162	BMR 00287	BMR 00525	BMR 00706
EU107636.1_Pygolabis paraburdoo_OUTGROUP		30.4	36.2	31.3	31.1	31.1	31.1	31.1	31.1	31.1	27.1	27.5	26.2	27.5	27.9	31.7	30.4	30.2	30.1	29.9	30.4	30.1	30.4	29.9	30.2	30.4	30.4	30.6
JF278086 Bogidiella albertmagni	30.4		33.5	24.4	24.3	24.3	24.3	24.3	24.3	24.3	22.4	21.3	22.5	20.8	20.6	22.5	22.2	22.5	22.6	22.5	22.5	22.0	22.2	22.8	22.3	22.6	22.5	22.3
IV128_DAVES-20150930-04_Niphargidae sp. Helix-AMN007	36.2	33.5		29.3	29.3	29.3	29.3	29.3	29.3	29.3	30.1	28.3	31.9	31.0	31.0	32.2	34.0	34.5	34.2	34.0	33.0	32.7	33.3	33.0	33.0	33.4	33.3	33.4
BMR00196_BGCK_Niphargidae?	31.3	24.4	29.3		0.2	0.2	0.2	0.2	0.2	0.2	24.8	23.3	25.2	24.3	24.3	26.1	23.1	22.8	23.1	23.1	23.4	22.9	23.3	23.1	23.4	23.4	23.4	23.1
BMR00204_BGCK_Niphargidae?	31.1	24.3	29.3	0.2		0.0	0.0	0.0	0.0	0.0	24.9	23.1	25.1	24.2	24.2	26.0	22.9	22.6	22.9	22.9	23.3	22.8	23.1	22.9	23.3	23.6	23.6	23.3
BMR00286_BGCK_Niphargidae?	31.1	24.3	29.3	0.2	0.0		0.0	0.0	0.0	0.0	24.9	23.1	25.1	24.2	24.2	26.0	22.9	22.6	22.9	22.9	23.3	22.8	23.1	22.9	23.3	23.6	23.6	23.3
BMR00370_BGCK_Amphipoda sp.	31.1	24.3	29.3	0.2	0.0	0.0		0.0	0.0	0.0	24.9	23.1	25.1	24.2	24.2	26.0	22.9	22.6	22.9	22.9	23.3	22.8	23.1	22.9	23.3	23.6	23.6	23.3
BMR00585_BGCK_Niphargidae sp.	31.1	24.3	29.3	0.2	0.0	0.0	0.0		0.0	0.0	24.9	23.1	25.1	24.2	24.2	26.0	22.9	22.6	22.9	22.9	23.3	22.8	23.1	22.9	23.3	23.6	23.6	23.3
BMR00802_BGCK_Niphargidae?	31.1	24.3	29.3	0.2	0.0	0.0	0.0	0.0		0.0	24.9	23.1	25.1	24.2	24.2	26.0	22.9	22.6	22.9	22.9	23.3	22.8	23.1	22.9	23.3	23.6	23.6	23.3
BMR00805_BGCK_Niphargidae?	31.1	24.3	29.3	0.2	0.0	0.0	0.0	0.0	0.0		24.9	23.1	25.1	24.2	24.2	26.0	22.9	22.6	22.9	22.9	23.3	22.8	23.1	22.9	23.3	23.6	23.6	23.3
KE28_32-20160910-02_Neoniphargidae sp. Helix-AMN003	27.1	22.4	30.1	24.8	24.9	24.9	24.9	24.9	24.9	24.9		6.3	15.6	15.9	18.4	20.5	18.8	18.5	18.5	18.5	19.0	18.7	18.5	18.7	18.8	17.8	17.7	17.5
RT15_WAMC71556_Bungaroo_Helix_AMN0003/007	27.5	21.3	28.3	23.3	23.1	23.1	23.1	23.1	23.1	23.1	6.3		15.2	15.5	16.9	20.6	18.5	18.5	18.7	18.5	18.7	18.4	18.5	18.5	18.5	17.8	17.7	17.6
KE07_200-20160910-01_Neoniphargidae sp. Helix-AMN008	26.2	22.5	31.9	25.2	25.1	25.1	25.1	25.1	25.1	25.1	15.6	15.2		12.2	18.9	20.8	19.8	19.6	19.6	19.3	19.8	19.3	19.5	19.1	19.6	19.3	19.2	19.0
NH68_JW024-20171213-06_Wesniphargus sp. Helix-AMN004	27.5	20.8	31.0	24.3	24.2	24.2	24.2	24.2	24.2	24.2	15.9	15.5	12.2		18.6	21.6	19.5	19.3	19.3	19.1	19.1	19.0	18.8	19.1	19.0	17.8	17.7	17.8
KE18_RR1-20160910-01_Neoniphargidae sp. Helix-AMN002	27.9	20.6	31.0	24.3	24.2	24.2	24.2	24.2	24.2	24.2	18.4	16.9	18.9	18.6		18.6	18.1	18.1	18.5	18.4	17.9	17.8	17.9	18.1	17.8	17.0	16.9	17.2
RT35_WAMC72400_Seven_Mile_Ck_Bogidiellidae	31.7	22.5	32.2	26.1	26.0	26.0	26.0	26.0	26.0	26.0	20.5	20.6	20.8	21.6	18.6		18.8	19.6	19.3	19.1	19.0	18.8	18.8	18.8	18.8	18.7	18.6	18.5
BMR00150_SGW_Bogidiellidae sp.	30.4	22.2	34.0	23.1	22.9	22.9	22.9	22.9	22.9	22.9	18.8	18.5	19.8	19.5	18.1	18.8		0.8	1.2	0.9	2.1	2.0	2.0	2.3	2.1	10.6	10.6	10.5
BMR00082_SGW_Bogidiellidae sp.	30.2	22.5	34.5	22.8	22.6	22.6	22.6	22.6	22.6	22.6	18.5	18.5	19.6	19.3	18.1	19.6	0.8		1.0	0.8	2.6	2.4	2.1	2.4	2.6	10.6	10.6	10.5
BMR00134_SGW_Bogidiellidae sp.	30.1	22.6	34.2	23.1	22.9	22.9	22.9	22.9	22.9	22.9	18.5	18.7	19.6	19.3	18.5	19.3	1.2	1.0		0.3	2.7	2.5	2.2	2.5	2.7	11.4	11.4	11.2
BMR00628_SGW_Bogidiellidae	29.9	22.5	34.0	23.1	22.9	22.9	22.9	22.9	22.9	22.9	18.5	18.5	19.3	19.1	18.4	19.1	0.9	0.8	0.3		2.4	2.3	2.0	2.3	2.4	11.1	11.1	10.9
BMR00081_HSTD_Bogidiellidae sp.	30.4	22.5	33.0	23.4	23.3	23.3	23.3	23.3	23.3	23.3	19.0	18.7	19.8	19.1	17.9	19.0	2.1	2.6	2.7	2.4		0.5	0.5	1.7	0.3	10.8	10.8	10.6
BMR00132_HSTD_Bogidiellidae sp.	30.1	22.0	32.7	22.9	22.8	22.8	22.8	22.8	22.8	22.8	18.7	18.4	19.3	19.0	17.8	18.8	2.0	2.4	2.5	2.3	0.5		0.6	1.5	0.5	10.5	10.5	10.3
BMR00154_HSTD_Bogidiellidae sp.	30.4	22.2	33.3	23.3	23.1	23.1	23.1	23.1	23.1	23.1	18.5	18.5	19.5	18.8	17.9	18.8	2.0	2.1	2.2	2.0	0.5	0.6		1.8	0.5	10.6	10.6	10.5
BMR00153_HSTD_Bogidiellidae sp.	29.9	22.8	33.0	23.1	22.9	22.9	22.9	22.9	22.9	22.9	18.7	18.5	19.1	19.1	18.1	18.8	2.3	2.4	2.5	2.3	1.7	1.5	1.8		1.7	11.1	11.1	10.9
BMR00162_HSTD_Bogidiellidae sp.	30.2	22.3	33.0	23.4	23.3	23.3	23.3	23.3	23.3	23.3	18.8	18.5	19.6	19.0	17.8	18.8	2.1	2.6	2.7	2.4	0.3	0.5	0.5	1.7		10.6	10.6	10.5
BMR00287_BS1W_Bogidiellidae sp.	30.4	22.6	33.4	23.4	23.6	23.6	23.6	23.6	23.6	23.6	17.8	17.8	19.3	17.8	17.0	18.7	10.6	10.6	11.4	11.1	10.8	10.5	10.6	11.1	10.6		0.0	1.1
BMR00525_BS1E_Amphipoda	30.4	22.5	33.3	23.4	23.6	23.6	23.6	23.6	23.6	23.6	17.7	17.7	19.2	17.7	16.9	18.6	10.6	10.6	11.4	11.1	10.8	10.5	10.6	11.1	10.6	0.0		1.1
BMR00706_BS1E_Amphipoda	30.6	22.3	33.4	23.1	23.3	23.3	23.3	23.3	23.3	23.3	17.5	17.6	19.0	17.8	17.2	18.5	10.5	10.5	11.2	10.9	10.6	10.3	10.5	10.9	10.5	1.1	1.1	

Appendix 20: Distance matrix of Amphipoda (*Pilbarus*) sequences/ lineages included in the analysis

COI divergences (%) of *Pilbarus* (regional comparisons)	O.G.	BMR 00509	BMR 00163	BMR 00135	BMR 00073	BMR 00083	BMR 00397	BMR 00127	BMR 00572	BMR 00175	DQ49 0125	BMR 00695	BMR 00507	BMR 00453	BMR 00455	BMR 00399	BMR 00096	BMR 00148	BMR 00131	BMR 00140	BMR 00143	BMR 00146	BMR 00151	BMR 00156	DQ25 6028	DQ25 6036	BMR 00396	BMR 00688	DQ25 6019	DQ49 0127	DQ25 6027	WAMC 72414	WAMC 72413	WAMC 72415
EU107636.1_Pygolabis paraburdoo_OUTGROUP		30.8	30.9	31.7	31.4	31.6	31.4	33.1	31.8	31.3	31.9	33.6	31.3	33.4	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.0	31.0	31.3	33.4	32.0	31.7	30.6	30.6	29.9	29.7
BMR00509_SGW_Pilbarus?	30.8		0.5	1.6	0.9	1.4	1.2	3.6	2.2	2.8	2.9	4.6	3.0	5.9	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.9	0.9	3.0	4.0	10.0	10.9	12.0	11.9	12.1	11.4
BMR00163_HSTD_Pilbarus sp.	30.9	0.5		1.4	1.0	1.5	1.3	3.7	2.3	2.9	3.0	4.7	3.1	6.0	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	0.7	1.0	1.0	3.1	4.0	10.0	10.7	12.2	12.0	12.0	11.2
BMR00135_SGE_Pilbarus sp.	31.7	1.6	1.4		1.5	2.3	1.8	4.4	3.0	3.5	3.5	5.2	3.7	6.5	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.6	1.6	3.7	4.9	10.5	11.7	12.8	12.6	12.7	12.0
BMR00073_CVCK_REG_Pilbarus sp.	31.4	0.9	1.0	1.5		1.2	0.6	3.3	1.9	2.0	1.8	4.3	2.3	5.4	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.6	0.6	2.2	4.0	9.6	10.8	11.9	11.7	12.1	11.3
BMR00083_SGW_Pilbarus?	31.6	1.4	1.5	2.3	1.2		1.1	3.1	2.2	2.0	3.3	4.5	1.8	4.8	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.3	1.3	1.9	4.4	10.2	11.6	12.6	12.4	12.7	11.9
BMR00397_CVCK_REG_Pilbarus?	31.4	1.2	1.3	1.8	0.6	1.1		3.2	1.7	1.0	2.6	4.2	1.0	3.0	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.9	0.9	1.1	4.1	10.0	11.4	13.2	13.0	12.9	12.1
BMR00127_SGW_Pilbarus sp.	33.1	3.6	3.7	4.4	3.3	3.1	3.2		4.1	3.8	4.7	5.7	3.7	6.7	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.5	3.5	3.8	5.9	11.9	13.0	13.9	13.9	14.9	13.9
BMR00572_SGW_Paramelitidae indet	31.8	2.2	2.3	3.0	1.9	2.2	1.7	4.1		1.7	3.2	4.4	1.7	4.5	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	2.0	2.0	1.7	5.2	10.8	12.2	13.4	13.2	13.4	12.7
BMR00175_HSTD_Paramelitidae; H07.ab1	31.3	2.8	2.9	3.5	2.0	2.0	1.0	3.8	1.7		2.4	4.2	3.7	5.5	2.2	2.2	2.2	2.2	2.2	2.2	2.2	2.2	2.2	2.2	2.5	2.5	4.3	3.8	9.8	11.0	14.3	14.3	13.0	13.5
DQ490125_Pilbarus sp. F TLF-2008 isolate wyloo	31.9	2.9	3.0	3.5	1.8	3.3	2.6	4.7	3.2	2.4		5.6	2.4	5.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.6	2.6	2.4	5.9	11.7	12.1	13.4	13.2	12.8	11.9
BMR00695_SGW_Pilbarus?	33.6	4.6	4.7	5.2	4.3	4.5	4.2	5.7	4.4	4.2	5.6		4.2	5.8	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.5	4.5	4.2	7.2	12.5	14.1	14.7	14.5	14.5	13.7
BMR00507_HSTD_PilbarusC05.ab1	31.3	3.0	3.1	3.7	2.3	1.8	1.0	3.7	1.7	3.7	2.4	4.2		7.0	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.7	2.7	3.1	3.8	9.8	11.0	14.5	14.4	12.9	13.8
BMR00453_HSTD_ParamelitidaeG12.ab1	33.4	5.9	6.0	6.5	5.4	4.8	3.0	6.7	4.5	5.5	5.3	5.8	7.0		5.3	5.3	5.3	5.3	5.3	5.3	5.3	5.3	5.3	5.3	5.4	5.4	7.2	6.6	11.0	11.9	16.3	16.8	14.5	16.1
BMR00455_HSTD_Pilbarus?	31.3	0.6	0.7	1.3	0.2	1.0	0.6	3.1	1.7	2.2	2.3	4.2	2.4	5.3		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.3	0.3	2.4	3.8	9.8	11.0	12.2	12.0	12.3	11.6
BMR00399_HSTD_Pilbarus sp.	31.3	0.6	0.7	1.3	0.2	1.0	0.6	3.1	1.7	2.2	2.3	4.2	2.4	5.3	0.0		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.3	0.3	2.4	3.8	9.8	11.0	12.2	12.0	12.3	11.6
BMR00096_HSTD_Pilbarus sp.	31.3	0.6	0.7	1.3	0.2	1.0	0.6	3.1	1.7	2.2	2.3	4.2	2.4	5.3	0.0	0.0		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.3	0.3	2.4	3.8	9.8	11.0	12.2	12.0	12.3	11.6
BMR00148_HSTD_Pilbarus sp.	31.3	0.6	0.7	1.3	0.2	1.0	0.6	3.1	1.7	2.2	2.3	4.2	2.4	5.3	0.0	0.0	0.0		0.0	0.0	0.0	0.0	0.0	0.0	0.3	0.3	2.4	3.8	9.8	11.0	12.2	12.0	12.3	11.6
BMR00131_HSTD_Pilbarus sp.	31.3	0.6	0.7	1.3	0.2	1.0	0.6	3.1	1.7	2.2	2.3	4.2	2.4	5.3	0.0	0.0	0.0	0.0		0.0	0.0	0.0	0.0	0.0	0.3	0.3	2.4	3.8	9.8	11.0	12.2	12.0	12.3	11.6
BMR00140_HSTD_Pilbarus sp.	31.3	0.6	0.7	1.3	0.2	1.0	0.6	3.1	1.7	2.2	2.3	4.2	2.4	5.3	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0	0.0	0.3	0.3	2.4	3.8	9.8	11.0	12.2	12.0	12.3	11.6
BMR00143_HSTD_Pilbarus sp.	31.3	0.6	0.7	1.3	0.2	1.0	0.6	3.1	1.7	2.2	2.3	4.2	2.4	5.3	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0	0.3	0.3	2.4	3.8	9.8	11.0	12.2	12.0	12.3	11.6
BMR00146_HSTD_Paramelitidae sp.	31.3	0.6	0.7	1.3	0.2	1.0	0.6	3.1	1.7	2.2	2.3	4.2	2.4	5.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.3	0.3	2.4	3.8	9.8	11.0	12.2	12.0	12.3	11.6
BMR00151_HSTD_Paramelitidae sp.	31.3	0.6	0.7	1.3	0.2	1.0	0.6	3.1	1.7	2.2	2.3	4.2	2.4	5.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.3	0.3	2.4	3.8	9.8	11.0	12.2	12.0	12.3	11.6
BMR00156_HSTD_Paramelitidae sp.	31.3	0.6	0.7	1.3	0.2	1.0	0.6	3.1	1.7	2.2	2.3	4.2	2.4	5.3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.3	0.3	2.4	3.8	9.8	11.0	12.2	12.0	12.3	11.6
DQ256028 Pilbarus sp. F TLF-2008 CVCK	31.0	0.9	1.0	1.6	0.6	1.3	0.9	3.5	2.0	2.5	2.6	4.5	2.7	5.4	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3		0.0	2.7	4.1	9.7	10.9	12.2	12.0	12.3	11.6
DQ256036 Pilbarus sp. F TLF-2008 CVCK	31.0	0.9	1.0	1.6	0.6	1.3	0.9	3.5	2.0	2.5	2.6	4.5	2.7	5.4	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.0		2.7	4.1	9.7	10.9	12.2	12.0	12.3	11.6
BMR00396_HSTD_PilbarusC01.ab1	31.3	3.0	3.1	3.7	2.2	1.9	1.1	3.8	1.7	4.3	2.4	4.2	3.1	7.2	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.7	2.7		3.8	9.8	11.0	14.5	14.6	13.2	13.8
BMR00688_SGW_Pilbarus?	33.4	4.0	4.0	4.9	4.0	4.4	4.1	5.9	5.2	3.8	5.9	7.2	3.8	6.6	3.8	3.8	3.8	3.8	3.8	3.8	3.8	3.8	3.8	3.8	4.1	4.1	3.8		13.1	14.3	15.0	15.0	15.1	14.3
DQ256019_Pilbarus sp. I TLF-2008	32.0	10.0	10.0	10.5	9.6	10.2	10.0	11.9	10.8	9.8	11.7	12.5	9.8	11.0	9.8	9.8	9.8	9.8	9.8	9.8	9.8	9.8	9.8	9.8	9.7	9.7	9.8	13.1		5.8	14.2	14.0	14.2	13.0
DQ490127_Pilbarus millsi	31.7	10.9	10.7	11.7	10.8	11.6	11.4	13.0	12.2	11.0	12.1	14.1	11.0	11.9	11.0	11.0	11.0	11.0	11.0	11.0	11.0	11.0	11.0	11.0	10.9	10.9	11.0	14.3	5.8		15.1	14.9	14.3	13.4
DQ256027_Pilbarus sp. H TLF-2008	30.6	12.0	12.2	12.8	11.9	12.6	13.2	13.9	13.4	14.3	13.4	14.7	14.5	16.3	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.2	14.5	15.0	14.2	15.1		0.2	8.3	8.2
RT35_WAMC72414_Turee_Ck_Pilbarus_sp_H	30.6	11.9	12.0	12.6	11.7	12.4	13.0	13.9	13.2	14.3	13.2	14.5	14.4	16.8	12.0	12.0	12.0	12.0	12.0	12.0	12.0	12.0	12.0	12.0	12.0	12.0	14.6	15.0	14.0	14.9	0.2		8.0	7.8
RT35_WAMC72413_Channar_Pilbarus_sp_G	29.9	12.1	12.0	12.7	12.1	12.7	12.9	14.9	13.4	13.0	12.8	14.5	12.9	14.5	12.3	12.3	12.3	12.3	12.3	12.3	12.3	12.3	12.3	12.3	12.3	12.3	13.2	15.1	14.2	14.3	8.3	8.0		2.4
RT35_WAMC72415_Seven_Mile_Ck_Pilbarus_sp_G	29.7	11.4	11.2	12.0	11.3	11.9	12.1	13.9	12.7	13.5	11.9	13.7	13.8	16.1	11.6	11.6	11.6	11.6	11.6	11.6	11.6	11.6	11.6	11.6	11.6	11.6	13.8	14.3	13.0	13.4	8.2	7.8	2.4	

Appendix 21: Distance matrix of Amphipoda (Paramelitidae) sequences/ lineages included in the analysis

COI divergences (%) of Paramelitidae (regional comparisons)	O.G.	LN35 145	BMR 00546	WAMC 72407	BMR 00155	BMR 00605	BMR 00165	BMR 00138	BMR 00123	BMR 00129	BMR 00448	BMR 00158	BMR 00159	BMR 00567	BMR 00694	BMR 00456	BMR 00692	BMR 00386	BMR 00387	BMR 00124	BMR 00097	BMR 00078	BMR 00139	BMR 00144	BMR 00514	BMR 00626	BMR 00635	BMR 00631	BMR 00575	BMR 00074	BMR 00141	BMR 00746	BMR 00077	BMR 00176	WAMC 72410	WAMC 72411	EF11 8245	WAMC 72438	NH54	BMR 00365	BMR 00526	BMR 00366	NH53	BMR 00586	BMR 00647	BMR 00705	EF55 8853	GK89	DQ83 8035	GK91
EU107636.1_Pygolabis paraburdoo_OUTGROUP		30.4	33.2	31.9	32.0	31.9	31.9	31.9	31.9	31.9	33.0	33.0	33.0	33.2	33.0	33.5	33.3	33.3	33.3	33.0	33.2	33.3	33.3	33.5	33.5	30.6	30.6	30.6	30.6	30.6	30.6	31.7	31.7	31.7	31.1	30.4	30.6	30.6	32.8	30.8	30.9	31.2	30.6	30.4	30.6	30.4	34.4	33.0	32.6	31.7
00488_LN35145 Amphipoda HopeDowns	30.4		21.9	20.4	22.8	22.6	22.6	22.6	22.6	22.6	21.3	21.3	21.3	21.7	21.6	21.9	21.9	21.7	21.9	21.7	22.7	21.4	21.4	21.4	21.6	18.4	18.2	18.2	18.2	18.2	18.2	19.3	19.3	19.3	20.7	22.0	19.0	18.5	21.7	21.1	21.2	21.3	21.5	21.5	21.7	21.9	22.2	21.4	19.9	18.8
BMR00546_DSM_Paramelitidae sp. B2NAM	33.2	21.9		18.8	24.0	23.9	23.9	23.9	23.9	23.9	19.3	19.3	19.3	19.5	19.3	19.7	19.5	19.1	19.3	19.0	20.1	18.7	19.1	18.7	18.8	18.7	18.5	18.5	18.5	18.5	18.5	19.1	19.1	19.1	19.1	19.9	20.2	19.6	22.9	21.1	21.2	21.6	21.8	21.5	21.9	22.0	23.5	22.1	21.4	21.0
RT35_WAMC72407_Turee_Ck_WAM_Yilgarus002	31.9	20.4	18.8		20.9	20.8	20.8	20.8	20.8	20.8	17.0	17.0	17.0	17.2	17.0	17.1	17.3	17.0	17.0	16.7	17.5	16.4	16.9	16.6	16.7	16.0	15.8	15.8	15.8	15.8	15.8	17.0	17.0	17.0	15.3	15.5	18.2	17.1	20.6	19.6	19.7	19.9	20.2	20.2	20.7	20.8	23.3	19.6	21.0	19.8
BMR00155_SGW_Maarrka sp.	32.0	22.8	24.0	20.9		0.2	0.2	0.2	0.2	0.2	20.0	20.0	20.0	20.3	20.3	19.9	19.6	19.3	19.4	19.6	20.5	19.3	19.6	19.3	19.4	20.9	20.8	20.8	20.8	20.8	20.8	21.9	21.9	21.9	21.8	21.4	21.2	17.8	18.4	20.9	21.0	21.7	20.9	21.2	21.2	21.4	23.1	20.5	22.5	21.5
BMR00605_HSTD_Maarrka sp.	31.9	22.6	23.9	20.8	0.2		0.0	0.0	0.0	0.0	19.9	19.9	19.9	20.2	20.2	19.8	19.5	19.1	19.3	19.5	20.4	19.1	19.5	19.1	19.3	20.8	20.7	20.7	20.7	20.7	20.7	21.7	21.7	21.7	21.7	21.3	21.1	17.6	18.4	20.8	20.9	21.6	20.8	21.1	21.1	21.3	22.9	20.4	22.3	21.4
BMR00165_HSTD_Maarrka sp.	31.9	22.6	23.9	20.8	0.2	0.0		0.0	0.0	0.0	19.9	19.9	19.9	20.2	20.2	19.8	19.5	19.1	19.3	19.5	20.4	19.1	19.5	19.1	19.3	20.8	20.7	20.7	20.7	20.7	20.7	21.7	21.7	21.7	21.7	21.3	21.1	17.6	18.4	20.8	20.9	21.6	20.8	21.1	21.1	21.3	22.9	20.4	22.3	21.4
BMR00138_HSTD_Maarrka sp.	31.9	22.6	23.9	20.8	0.2	0.0	0.0		0.0	0.0	19.9	19.9	19.9	20.2	20.2	19.8	19.5	19.1	19.3	19.5	20.4	19.1	19.5	19.1	19.3	20.8	20.7	20.7	20.7	20.7	20.7	21.7	21.7	21.7	21.7	21.3	21.1	17.6	18.4	20.8	20.9	21.6	20.8	21.1	21.1	21.3	22.9	20.4	22.3	21.4
BMR00123_HSTD_Maarrka sp.	31.9	22.6	23.9	20.8	0.2	0.0	0.0	0.0		0.0	19.9	19.9	19.9	20.2	20.2	19.8	19.5	19.1	19.3	19.5	20.4	19.1	19.5	19.1	19.3	20.8	20.7	20.7	20.7	20.7	20.7	21.7	21.7	21.7	21.7	21.3	21.1	17.6	18.4	20.8	20.9	21.6	20.8	21.1	21.1	21.3	22.9	20.4	22.3	21.4
BMR00129_HSTD_Maarrka sp.	31.9	22.6	23.9	20.8	0.2	0.0	0.0	0.0	0.0		19.9	19.9	19.9	20.2	20.2	19.8	19.5	19.1	19.3	19.5	20.4	19.1	19.5	19.1	19.3	20.8	20.7	20.7	20.7	20.7	20.7	21.7	21.7	21.7	21.7	21.3	21.1	17.6	18.4	20.8	20.9	21.6	20.8	21.1	21.1	21.3	22.9	20.4	22.3	21.4
BMR00448_SGW_Paramelitidae sp. B2NAM	33.0	21.3	19.3	17.0	20.0	19.9	19.9	19.9	19.9	19.9		0.0	0.0	2.6	2.4	3.3	3.2	2.9	3.0	3.2	4.1	3.3	3.2	2.7	2.6	17.3	17.5	17.5	17.5	17.5	17.5	17.8	17.8	17.8	16.3	16.7	18.3	16.4	19.7	18.7	18.6	18.7	20.5	19.4	18.8	19.0	22.0	20.4	21.1	19.9
BMR00158_HSTD_Paramelitidae sp. B2NAM?	33.0	21.3	19.3	17.0	20.0	19.9	19.9	19.9	19.9	19.9	0.0		0.0	2.6	2.4	3.3	3.2	2.9	3.0	3.2	4.1	3.3	3.2	2.7	2.6	17.3	17.5	17.5	17.5	17.5	17.5	17.8	17.8	17.8	16.3	16.7	18.3	16.4	19.7	18.7	18.6	18.7	20.5	19.4	18.8	19.0	22.0	20.4	21.1	19.9
BMR00159_HSTD_Paramelitidae sp.	33.0	21.3	19.3	17.0	20.0	19.9	19.9	19.9	19.9	19.9	0.0	0.0		2.6	2.4	3.3	3.2	2.9	3.0	3.2	4.1	3.3	3.2	2.7	2.6	17.3	17.5	17.5	17.5	17.5	17.5	17.8	17.8	17.8	16.3	16.7	18.3	16.4	19.7	18.7	18.6	18.7	20.5	19.4	18.8	19.0	22.0	20.4	21.1	19.9
BMR00567_CVCK_Pilbarus sp.	33.2	21.7	19.5	17.2	20.3	20.2	20.2	20.2	20.2	20.2	2.6	2.6	2.6		0.2	2.6	2.4	2.1	2.3	2.1	3.0	2.6	2.4	2.0	1.8	18.2	18.1	18.1	18.1	18.1	18.1	18.5	18.5	18.5	17.3	17.9	18.5	16.6	20.7	19.8	19.8	20.1	21.3	20.0	20.1	20.2	22.3	20.1	21.1	19.9
BMR00694_CVCK_Pilbarus sp.	33.0	21.6	19.3	17.0	20.3	20.2	20.2	20.2	20.2	20.2	2.4	2.4	2.4	0.2		2.4	2.3	2.0	2.1	2.0	2.8	2.4	2.3	1.8	1.7	18.1	17.9	17.9	17.9	17.9	17.9	18.4	18.4	18.4	17.2	17.8	18.3	16.4	20.6	19.6	19.7	19.9	21.1	19.9	19.9	20.1	22.2	20.1	21.1	19.9
BMR00456_HSTD_ParamelitidaeB12.ab1	33.5	21.9	19.7	17.1	19.9	19.8	19.8	19.8	19.8	19.8	3.3	3.3	3.3	2.6	2.4		1.2	0.9	1.0	1.2	1.7	1.3	1.2	1.0	0.9	18.4	18.3	18.3	18.3	18.3	18.3	18.7	18.7	18.7	16.4	17.2	18.5	16.5	20.1	19.7	19.7	19.6	21.2	20.1	20.1	20.3	22.4	20.3	20.4	19.5
BMR00692_HSTD_Paramelitidae sp. B2NAM	33.3	21.9	19.5	17.3	19.6	19.5	19.5	19.5	19.5	19.5	3.2	3.2	3.2	2.4	2.3	1.2		0.3	0.5	0.6	1.7	1.1	0.6	0.8	0.6	18.1	17.9	17.9	17.9	17.9	17.9	18.4	18.4	18.4	17.0	17.2	18.8	16.7	19.9	19.3	19.4	19.6	20.8	19.7	19.8	19.9	22.0	20.8	20.8	19.8
BMR00386_HSTD_Paramelitidae sp. B2NAM	33.3	21.7	19.1	17.0	19.3	19.1	19.1	19.1	19.1	19.1	2.9	2.9	2.9	2.1	2.0	0.9	0.3		0.2	0.3	1.6	0.8	0.6	0.5	0.3	17.9	17.8	17.8	17.8	17.8	17.8	18.2	18.2	18.2	16.8	17.2	18.6	16.4	19.7	19.0	19.1	19.5	20.5	19.4	19.5	19.6	21.9	20.5	20.7	19.6
BMR00387_HSTD_Paramelitidae sp. B2NAM	33.3	21.9	19.3	17.0	19.4	19.3	19.3	19.3	19.3	19.3	3.0	3.0	3.0	2.3	2.1	1.0	0.5	0.2		0.5	1.7	0.9	0.8	0.6	0.5	18.1	17.9	17.9	17.9	17.9	17.9	18.4	18.4	18.4	16.8	17.2	18.6	16.6	19.9	19.0	19.1	19.5	20.5	19.4	19.5	19.6	21.9	20.5	20.7	19.6
BMR00124_HSTD_Paramelitidae sp. B2NAM	33.0	21.7	19.0	16.7	19.6	19.5	19.5	19.5	19.5	19.5	3.2	3.2	3.2	2.1	2.0	1.2	0.6	0.3	0.5		1.2	1.1	0.9	0.8	0.6	17.9	17.8	17.8	17.8	17.8	17.8	18.2	18.2	18.2	16.8	17.2	18.6	16.4	20.1	18.7	18.8	19.1	20.5	19.1	19.5	19.6	21.9	20.4	20.8	19.8
BMR00097_HSTD_Paramelitidae sp.	33.2	22.7	20.1	17.5	20.5	20.4	20.4	20.4	20.4	20.4	4.1	4.1	4.1	3.0	2.8	1.7	1.7	1.6	1.7	1.2		2.3	2.2	1.7	1.6	18.4	18.3	18.3	18.3	18.3	18.3	19.0	19.0	19.0	17.0	17.5	19.5	17.1	20.9	19.9	19.9	20.1	21.5	20.2	20.5	20.7	22.3	20.7	21.5	20.7
BMR00078_HSTD_Paramelitidae sp. B2NAM	33.3	21.4	18.7	16.4	19.3	19.1	19.1	19.1	19.1	19.1	3.3	3.3	3.3	2.6	2.4	1.3	1.1	0.8	0.9	1.1	2.3		0.5	0.9	0.8	17.3	17.2	17.2	17.2	17.2	17.2	17.6	17.6	17.6	16.3	16.7	18.2	16.0	19.6	19.0	19.1	19.5	20.5	19.7	19.5	19.6	22.0	20.4	20.4	19.3
BMR00139_HSTD_Paramelitidae sp. B2NAM	33.3	21.4	19.1	16.9	19.6	19.5	19.5	19.5	19.5	19.5	3.2	3.2	3.2	2.4	2.3	1.2	0.6	0.6	0.8	0.9	2.2	0.5		0.8	0.6	17.6	17.5	17.5	17.5	17.5	17.5	17.9	17.9	17.9	16.8	16.9	18.3	16.3	19.6	19.3	19.4	19.8	20.8	19.7	19.8	19.9	22.0	20.5	20.4	19.3
BMR00144_HSTD_Pilbarus sp.	33.5	21.4	18.7	16.6	19.3	19.1	19.1	19.1	19.1	19.1	2.7	2.7	2.7	2.0	1.8	1.0	0.8	0.5	0.6	0.8	1.7	0.9	0.8		0.2	17.6	17.5	17.5	17.5	17.5	17.5	17.9	17.9	17.9	16.5	16.9	18.3	16.1	19.4	18.8	18.9	19.3	20.3	19.3	19.3	19.5	22.0	20.2	20.7	19.6
BMR00514_HSTD_Pilbarus sp.	33.5	21.6	18.8	16.7	19.4	19.3	19.3	19.3	19.3	19.3	2.6	2.6	2.6	1.8	1.7	0.9	0.6	0.3	0.5	0.6	1.6	0.8	0.6	0.2		17.6	17.5	17.5	17.5	17.5	17.5	17.9	17.9	17.9	16.7	17.0	18.5	16.3	19.6	19.0	19.1	19.5	20.5	19.4	19.5	19.6	21.9	20.4	20.5	19.5
BMR00626_BS3X_Paramelitidae sp. B2NAM	30.6	18.4	18.7	16.0	20.9	20.8	20.8	20.8	20.8	20.8	17.3	17.3	17.3	18.2	18.1	18.4	18.1	17.9	18.1	17.9	18.4	17.3	17.6	17.6	17.6		0.2	0.2	0.2	0.2	0.2	5.6	5.6	5.6	12.3	12.8	18.0	16.3	20.1	20.7	20.7	20.9	22.6	22.0	21.9	22.0	24.2	21.9	21.9	21.1
BMR00635_BS3X_Paramelitidae sp. B2NAM	30.6	18.2	18.5	15.8	20.8	20.7	20.7	20.7	20.7	20.7	17.5	17.5	17.5	18.1	17.9	18.3	17.9	17.8	17.9	17.8	18.3	17.2	17.5	17.5	17.5	0.2		0.0	0.0	0.0	0.0	5.5	5.5	5.5	12.1	12.6	17.9	16.1	19.9	20.8	20.9	21.0	22.4	21.9	22.0	22.2	24.3	21.7	21.7	21.0
BMR00631_BS3X_Paramelitidae sp. B2NAM	30.6	18.2	18.5	15.8	20.8	20.7	20.7	20.7	20.7	20.7	17.5	17.5	17.5	18.1	17.9	18.3	17.9	17.8	17.9	17.8	18.3	17.2	17.5	17.5	17.5	0.2	0.0		0.0	0.0	0.0	5.5	5.5	5.5	12.1	12.6	17.9	16.1	19.9	20.8	20.9	21.0	22.4	21.9	22.0	22.2	24.3	21.7	21.7	21.0
BMR00575_BS3X_Paramelitidae sp. B2NAM	30.6	18.2	18.5	15.8	20.8	20.7	20.7	20.7	20.7	20.7	17.5	17.5	17.5	18.1	17.9	18.3	17.9	17.8	17.9	17.8	18.3	17.2	17.5	17.5	17.5	0.2	0.0	0.0		0.0	0.0	5.5	5.5	5.5	12.1	12.6	17.9	16.1	19.9	20.8	20.9	21.0	22.4	21.9	22.0	22.2	24.3	21.7	21.7	21.0
BMR00074_BS3X_Paramelitidae sp. B2NAM	30.6	18.2	18.5	15.8	20.8	20.7	20.7	20.7	20.7	20.7	17.5	17.5	17.5	18.1	17.9	18.3	17.9	17.8	17.9	17.8	18.3	17.2	17.5	17.5	17.5	0.2	0.0	0.0	0.0		0.0	5.5	5.5	5.5	12.1	12.6	17.9	16.1	19.9	20.8	20.9	21.0	22.4	21.9	22.0	22.2	24.3	21.7	21.7	21.0
BMR00141_BS3X_Paramelitidae sp. B2NAM	30.6	18.2	18.5	15.8	20.8	20.7	20.7	20.7	20.7	20.7	17.5	17.5	17.5	18.1	17.9	18.3	17.9	17.8	17.9	17.8	18.3	17.2	17.5	17.5	17.5	0.2	0.0	0.0	0.0	0.0		5.5	5.5	5.5	12.1	12.6	17.9	16.1	19.9	20.8	20.9	21.0	22.4	21.9	22.0	22.2	24.3	21.7	21.7	21.0
BMR00746_BS3X_Paramelitidae sp. B2NAM	31.7	19.3	19.1	17.0	21.9	21.7	21.7	21.7	21.7	21.7	17.8	17.8	17.8	18.5	18.4	18.7	18.4	18.2	18.4	18.2	19.0	17.6	17.9	17.9	17.9	5.6	5.5	5.5	5.5	5.5	5.5		0.0	0.0	10.7	11.7	17.1	15.5	20.7	21.4	21.5	21.6	24.0	22.0	22.2	22.3	23.1	22.3	20.8	20.1
BMR00077_BS3X_Paramelitidae sp. B2NAM	31.7	19.3	19.1	17.0	21.9	21.7	21.7	21.7	21.7	21.7	17.8	17.8	17.8	18.5	18.4	18.7	18.4	18.2	18.4	18.2	19.0	17.6	17.9	17.9	17.9	5.6	5.5	5.5	5.5	5.5	5.5	0.0		0.0	10.7	11.7	17.1	15.5	20.7	21.4	21.5	21.6	24.0	22.0	22.2	22.3	23.1	22.3	20.8	20.1
BMR00176_BS3X_Paramelitidae sp. B2NAM	31.7	19.3	19.1	17.0	21.9	21.7	21.7	21.7	21.7	21.7	17.8	17.8	17.8	18.5	18.4	18.7	18.4	18.2	18.4	18.2	19.0	17.6	17.9	17.9	17.9	5.6	5.5	5.5	5.5	5.5	5.5	0.0	0.0		10.7	11.7	17.1	15.5	20.7	21.4	21.5	21.6	24.0	22.0	22.2	22.3	23.1	22.3	20.8	20.1
RT35_WAMC72410_Paraburdoo_Mine_WAM_Yilgarus001	31.1	20.7	19.1	15.3	21.8	21.7	21.7	21.7	21.7	21.7	16.3	16.3	16.3	17.3	17.2	16.4	17.0	16.8	16.8	16.8	17.0	16.3	16.8	16.5	16.7	12.3	12.1	12.1	12.1	12.1	12.1	10.7	10.7	10.7		3.0	18.1	15.6	18.1	21.0	21.1	21.3	22.4	21.0	21.4	21.5	22.7	20.7	21.8	21.1
RT35_WAMC72411_Seven_Mile_Ck_WAM_Yilgarus001	30.4	22.0	19.9	15.5	21.4	21.3	21.3	21.3	21.3	21.3	16.7	16.7	16.7	17.9	17.8	17.2	17.2	17.2	17.2	17.2	17.5	16.7	16.9	16.9	17.0	12.8	12.6	12.6	12.6	12.6	12.6	11.7	11.7	11.7	3.0		17.3	15.2	18.8	21.0	21.0	21.6	22.6	21.5	22.2	22.0	23.9	22.2	22.6	21.1
EF118245_Yilgarus sp. BES8834.3	30.6	19.0	20.2	18.2	21.2	21.1	21.1	21.1	21.1	21.1	18.3	18.3	18.3	18.5	18.3	18.5	18.8	18.6	18.6	18.6	19.5	18.2	18.3	18.3	18.5	18.0	17.9	17.9	17.9	17.9	17.9	17.1	17.1	17.1	18.1	17.3		11.1	19.5	19.6	19.6	19.9	20.8	19.8	20.6	20.8	24.2	19.7	19.4	19.0
RT46_WAMC72438_Yilgarus_WAM-AMPP003	30.6	18.5	19.6	17.1	17.8	17.6	17.6	17.6	17.6	17.6	16.4	16.4	16.4	16.6	16.4	16.5	16.7	16.4	16.6	16.4	17.1	16.0	16.3	16.1	16.3	16.3	16.1	16.1	16.1	16.1	16.1	15.5	15.5	15.5	15.6	15.2	11.1		18.2	18.5	18.6	19.0	19.9	18.8	19.3	19.5	22.9	17.7	17.9	16.5
NH54_25-20171213-02_ROBE_Paramelitidae	32.8	21.7	22.9	20.6	18.4	18.4	18.4	18.4	18.4	18.4	19.7	19.7	19.7	20.7	20.6	20.1	19.9	19.7	19.9	20.1	20.9	19.6	19.6	19.4	19.6	20.1	19.9	19.9	19.9	19.9	19.9	20.7	20.7	20.7	18.1	18.8	19.5	18.2		14.3	14.3	15.0	14.7	14.7	15.1	15.3	21.9	18.5	19.7	18.6
BMR00365_BGCK_Amphipoda sp.	30.8	21.1	21.1	19.6	20.9	20.8	20.8	20.8	20.8	20.8	18.7	18.7	18.7	19.8	19.6	19.7	19.3	19.0	19.0	18.7	19.9	19.0	19.3	18.8	19.0	20.7	20.8	20.8	20.8	20.8	20.8	21.4	21.4	21.4	21.0	21.0	19.6	18.5	14.3		0.1	0.4	3.9	2.1	1.7	1.8	23.3	21.6	22.3	21.3
BMR00526_BGCK_Paramelitidae sp.	30.9	21.2	21.2	19.7	21.0	20.9	20.9	20.9	20.9	20.9	18.6	18.6	18.6	19.8	19.7	19.7	19.4	19.1	19.1	18.8	19.9	19.1	19.4	18.9	19.1	20.7	20.9	20.9	20.9	20.9	20.9	21.5	21.5	21.5	21.1	21.0	19.6	18.6	14.3	0.1		0.3	4.0	2.0	1.6	1.7	23.3	21.7	22.4	21.4
BMR00366_BGCK_Amphipoda sp.	31.2	21.3	21.6	19.9	21.7	21.6	21.6	21.6	21.6	21.6	18.7	18.7	18.7	20.1	19.9	19.6	19.6	19.5	19.5	19.1	20.1	19.5	19.8	19.3	19.5	20.9	21.0	21.0	21.0	21.0	21.0	21.6	21.6	21.6	21.3	21.6	19.9	19.0	15.0	0.4	0.3		4.2	2.1	1.6	1.8	23.3	21.8	22.1	21.5
NH53_BC186-20171213-03_ROBE_Paramelitidae	30.6	21.5	21.8	20.2	20.9	20.8	20.8	20.8	20.8	20.8	20.5	20.5	20.5	21.3	21.1	21.2	20.8	20.5	20.5	20.5	21.5	20.5	20.8	20.3	20.5	22.6	22.4	22.4	22.4	22.4	22.4	24.0	24.0	24.0	22.4	22.6	20.8	19.9	14.7	3.9	4.0	4.2		3.5	3.7	3.5	24.0	22.4	23.4	21.8
BMR00586_BS1W_Paramelitidae sp.	30.4	21.5	21.5	20.2	21.2	21.1	21.1	21.1	21.1	21.1	19.4	19.4	19.4	20.0	19.9	20.1	19.7	19.4	19.4	19.1	20.2	19.7	19.7	19.3	19.4	22.0	21.9	21.9	21.9	21.9	21.9	22.0	22.0	22.0	21.0	21.5	19.8	18.8	14.7	2.1	2.0	2.1	3.5		1.7	1.8	24.1	22.3	22.6	21.5
BMR00647_BS1E_Paramelitidae	30.6	21.7	21.9	20.7	21.2	21.1	21.1	21.1	21.1	21.1	18.8	18.8	18.8	20.1	19.9	20.1	19.8	19.5	19.5	19.5	20.5	19.5	19.8	19.3	19.5	21.9	22.0	22.0	22.0	22.0	22.0	22.2	22.2	22.2	21.4	22.2	20.6	19.3	15.1	1.7	1.6	1.6	3.7	1.7		0.2	23.6	22.3	22.2	21.1
BMR00705_BS1E_Paramelitidae sp.	30.4	21.9	22.0	20.8	21.4	21.3	21.3	21.3	21.3	21.3	19.0	19.0	19.0	20.2	20.1	20.3	19.9	19.6	19.6	19.6	20.7	19.6	19.9	19.5	19.6	22.0	22.2	22.2	22.2	22.2	22.2	22.3	22.3	22.3	21.5	22.0	20.8	19.5	15.3	1.8	1.7	1.8	3.5	1.8	0.2		23.7	22.5	22.0	21.0
EF558853_Maarrka etheli	34.4	22.2	23.5	23.3	23.1	22.9	22.9	22.9	22.9	22.9	22.0	22.0	22.0	22.3	22.2	22.4	22.0	21.9	21.9	21.9	22.3	22.0	22.0	22.0	21.9	24.2	24.3	24.3	24.3	24.3	24.3	23.1	23.1	23.1	22.7	23.9	24.2	22.9	21.9	23.3	23.3	23.3	24.0	24.1	23.6	23.7		19.9	20.2	19.3
GK89_99YJWB03P1-1_YANDI_Maarrka	33.0	21.4	22.1	19.6	20.5	20.4	20.4	20.4	20.4	20.4	20.4	20.4	20.4	20.1	20.1	20.3	20.8	20.5	20.5	20.4	20.7	20.4	20.5	20.2	20.4	21.9	21.7	21.7	21.7	21.7	21.7	22.3	22.3	22.3	20.7	22.2	19.7	17.7	18.5	21.6	21.7	21.8	22.4	22.3	22.3	22.5	19.9		14.7	11.5
DQ838035_Maarrka weeliwollii	32.6	19.9	21.4	21.0	22.5	22.3	22.3	22.3	22.3	22.3	21.1	21.1	21.1	21.1	21.1	20.4	20.8	20.7	20.7	20.8	21.5	20.4	20.4	20.7	20.5	21.9	21.7	21.7	21.7	21.7	21.7	20.8	20.8	20.8	21.8	22.6	19.4	17.9	19.7	22.3	22.4	22.1	23.4	22.6	22.2	22.0	20.2	14.7		2.6
GK91_TS3DCP1-3_YANDI_Paramelitidae	31.7	18.8	21.0	19.8	21.5	21.4	21.4	21.4	21.4	21.4	19.9	19.9	19.9	19.9	19.9	19.5	19.8	19.6	19.6	19.8	20.7	19.3	19.3	19.6	19.5	21.1	21.0	21.0	21.0	21.0	21.0	20.1	20.1	20.1	21.1	21.1	19.0	16.5	18.6	21.3	21.4	21.5	21.8	21.5	21.1	21.0	19.3	11.5	2.6	

Appendix 22: Distance matrix of Bathynellacea (Bathynellidae) sequences/ lineages included in the analysis

COI divergences (%) of Bathynellidae (regional comparisons)	OUT GROUP	BMR 00711	BES 6932b	WAMC 74210	BES 7570a	BES 6932a	BES 6932c	BMR 00289	BMR 00710	BMR 00649	BMR 00590	BMR 00709	BMR 00530	BMR 00650	MF 074385	MF 074388	MF 074409	MF 074391	MF 074381	MK 135043	MK 135044	MK 135045
KR131708 Koonunga allambiensis OUTGROUP		26.3	27.5	27.7	27.7	27.7	27.7	25.5	25.3	24.7	25.0	25.0	25.0	25.0	26.7	25.9	28.5	28.3	28.3	26.9	18.7	25.5
BMR00711_BGCK_Bathynellidae sp.	26.3		23.7	23.9	23.9	23.9	23.9	23.8	22.9	22.5	22.8	22.8	22.9	22.9	23.8	24.0	22.7	26.4	24.7	22.0	24.5	23.6
BES6932b_Paraburdoo_HB17NLC006	27.5	23.7		0.5	0.5	0.5	0.5	25.8	25.1	25.4	24.9	25.1	25.1	25.1	25.1	24.0	27.5	26.7	25.6	24.9	16.4	23.6
RT56_WAMC74210_WAM-BATH001	27.7	23.9	0.5		0.0	0.0	0.0	25.9	25.2	25.6	25.1	25.3	25.2	25.2	24.5	23.7	27.1	26.0	25.6	24.5	15.7	23.2
BES7570a_Paraburdoo_HB15NLC001	27.7	23.9	0.5	0.0		0.0	0.0	25.9	25.2	25.6	25.1	25.3	25.2	25.2	25.1	24.2	27.5	26.7	26.0	25.1	17.3	23.8
BES6932a_Paraburdoo_HB17NLC006	27.7	23.9	0.5	0.0	0.0		0.0	25.9	25.2	25.6	25.1	25.3	25.2	25.2	25.1	24.2	27.5	26.7	26.0	25.1	17.3	23.8
BES6932c_Paraburdoo_HB17NLC006	27.7	23.9	0.5	0.0	0.0	0.0		25.9	25.2	25.6	25.1	25.3	25.2	25.2	25.1	24.2	27.5	26.7	26.0	25.1	17.3	23.8
BMR00289_BGCK_Bathynellidae sp.	25.5	23.8	25.8	25.9	25.9	25.9	25.9		11.4	11.1	11.4	11.4	11.4	11.1	22.0	22.4	22.7	25.9	25.6	26.3	22.7	26.1
BMR00710_BGCK_Bathynellidae sp.	25.3	22.9	25.1	25.2	25.2	25.2	25.2	11.4		0.9	0.6	0.6	0.8	0.8	20.7	19.8	21.8	23.3	22.7	22.7	18.2	24.9
BMR00649_BGCK_Bathynellidae sp.	24.7	22.5	25.4	25.6	25.6	25.6	25.6	11.1	0.9		0.3	0.3	0.8	0.8	21.3	20.9	22.0	23.8	23.4	24.0	20.6	25.4
BMR00590_BGCK_Bathynellidae sp.	25.0	22.8	24.9	25.1	25.1	25.1	25.1	11.4	0.6	0.3		0.0	0.5	0.5	20.9	20.0	21.6	23.1	22.7	23.1	18.2	24.7
BMR00709_BGCK_Bathynellidae sp.	25.0	22.8	25.1	25.3	25.3	25.3	25.3	11.4	0.6	0.3	0.0		0.5	0.5	21.1	20.6	22.2	23.6	23.1	23.8	19.6	25.2
BMR00530_BGCK_Bathynellidae sp.	25.0	22.9	25.1	25.2	25.2	25.2	25.2	11.4	0.8	0.8	0.5	0.5		0.3	20.7	19.8	21.8	23.3	22.5	23.1	17.3	24.7
BMR00650_BGCK_Bathynellidae sp.	25.0	22.9	25.1	25.2	25.2	25.2	25.2	11.1	0.8	0.8	0.5	0.5	0.3		21.1	19.8	21.4	23.3	22.5	23.6	18.2	25.1
Pilbaranella ethelensis MF074385	26.7	23.8	25.1	24.5	25.1	25.1	25.1	22.0	20.7	21.3	20.9	21.1	20.7	21.1		6.4	14.1	14.1	14.4	25.7	19.9	23.4
Pilbaranella ethelensis MF074388	25.9	24.0	24.0	23.7	24.2	24.2	24.2	22.4	19.8	20.9	20.0	20.6	19.8	19.8	6.4		15.2	14.8	15.1	26.9	18.8	21.8
Pilbaranella sp. C MF074409	28.5	22.7	27.5	27.1	27.5	27.5	27.5	22.7	21.8	22.0	21.6	22.2	21.8	21.4	14.1	15.2		13.9	14.4	27.4	17.7	22.1
Pilbaranella sp. A MF074391	28.3	26.4	26.7	26.0	26.7	26.7	26.7	25.9	23.3	23.8	23.1	23.6	23.3	23.3	14.1	14.8	13.9		13.4	26.4	17.7	21.3
Pilbaranella sp. B MF074381	28.3	24.7	25.6	25.6	26.0	26.0	26.0	25.6	22.7	23.4	22.7	23.1	22.5	22.5	14.4	15.1	14.4	13.4		26.1	16.2	23.4
Bathynellidae nr. Fortescuenella sp. MK135043	26.9	22.0	24.9	24.5	25.1	25.1	25.1	26.3	22.7	24.0	23.1	23.8	23.1	23.6	25.7	26.9	27.4	26.4	26.1		24.1	21.3
Fortescuenella serenitatis MK135044	18.7	24.5	16.4	15.7	17.3	17.3	17.3	22.7	18.2	20.6	18.2	19.6	17.3	18.2	19.9	18.8	17.7	17.7	16.2	24.1		2.3
Fortescuenella serenitatis MK135045	25.5	23.6	23.6	23.2	23.8	23.8	23.8	26.1	24.9	25.4	24.7	25.2	24.7	25.1	23.4	21.8	22.1	21.3	23.4	21.3	2.3	

Appendix 23: Distance matrix of Bathynellacea (Parabathynellidae) sequences/ lineages included in the analysis

COI divergences (%) of Parabathynellidae (regional comparisons)	O.G.	JN81 7405	JN81 7402	JN81 7408	JN81 7406	JN81 7407	KX02 2572	KX02 2566	JX28 6496	JX28 6485	JX28 6478	JX28 6491	JN81 7391	JN81 7390	BMR 00543	BMR 00542	BMR 00602	BMR 00645	BMR 00246	BMR 00418	BMR 00420	BMR 00480	BMR 00419	BMR 00541	JN81 7395	BMR 00372	BMR 00545
KR131708 Koonunga allambiensis OUTGROUP		25.3	28.1	27.6	27.6	27.3	28.5	27.6	25.2	26.8	26.1	26.4	27.3	26.3	25.3	26.6	26.4	26.6	27.8	27.7	28.0	27.7	27.5	27.7	28.9	25.0	25.6
Parabathynellidae sp. Lineage C JN817405	25.3		16.6	16.7	16.4	17.4	20.0	19.1	20.6	21.6	22.7	22.3	19.3	21.5	20.0	21.7	21.0	20.0	23.1	22.6	22.8	22.6	23.3	23.6	23.9	20.9	21.2
Billibathynella sp. 2B JN817402	28.1	16.6		17.4	16.2	15.5	19.3	19.1	19.7	18.3	19.7	19.3	17.7	20.8	18.1	21.7	21.2	18.4	21.9	21.4	21.2	21.4	21.2	22.1	22.9	19.9	18.2
Brevisomabathynella cunyuensis BES 13347 JN817408	27.6	16.7	17.4		9.5	9.7	18.9	17.9	19.5	20.9	21.3	21.3	19.2	21.3	18.4	22.4	21.9	16.3	20.6	21.0	20.7	21.0	18.4	18.5	24.8	22.4	21.7
Brevisomabathynella sp. 2 JN817406	27.6	16.4	16.2	9.5		11.3	18.8	18.0	20.0	20.2	21.1	21.1	20.6	22.9	18.3	22.8	22.1	18.6	22.7	22.6	22.8	22.6	20.0	20.2	23.6	21.0	19.6
Brevisomabathynella uramurdahensis A JN817407	27.3	17.4	15.5	9.7	11.3		18.5	18.9	20.0	20.0	20.9	20.9	18.4	22.6	21.3	21.9	21.4	18.6	22.4	23.1	22.8	23.1	20.3	20.2	23.2	22.3	21.7
Parabathynellidae sp. C2.A1 KX022572	28.5	20.0	19.3	18.9	18.8	18.5		12.3	21.1	21.8	22.0	22.2	20.2	21.4	19.5	23.3	23.1	22.8	26.8	26.7	26.4	26.7	25.0	25.6	23.4	21.4	20.4
Parabathynellidae sp. L2 KX022566	27.6	19.1	19.1	17.9	18.0	18.9	12.3		19.9	20.8	21.1	21.3	17.9	19.1	20.1	23.6	23.1	23.6	27.7	27.0	26.8	27.0	23.6	24.1	22.5	22.1	20.9
Parabathynellidae sp. 6I JX286496	25.2	20.6	19.7	19.5	20.0	20.0	21.1	19.9		16.7	17.2	17.0	23.7	20.6	20.4	22.5	22.3	22.2	24.6	24.3	24.1	24.3	22.7	23.0	27.7	20.7	20.2
Parabathynellidae sp. 4D JX286485	26.8	21.6	18.3	20.9	20.2	20.0	21.8	20.8	16.7		1.3	0.8	21.6	22.5	20.4	21.7	21.3	20.9	24.1	23.3	23.2	23.3	21.7	22.1	26.2	22.4	20.7
Parabathynellidae sp. 3G JX286478	26.1	22.7	19.7	21.3	21.1	20.9	22.0	21.1	17.2	1.3		0.8	21.6	22.7	21.0	21.3	21.3	21.2	24.5	23.6	23.5	23.6	22.0	22.5	26.0	22.4	20.9
Parabathynellidae sp. 4K JX286491	26.4	22.3	19.3	21.3	21.1	20.9	22.2	21.3	17.0	0.8	0.8		21.8	22.5	21.0	21.7	21.7	21.0	24.3	23.5	23.3	23.5	22.3	22.8	26.7	22.7	20.9
Atopobathynella hinzeae BES11166JN817391	27.3	19.3	17.7	19.2	20.6	18.4	20.2	17.9	23.7	21.6	21.6	21.8		17.0	22.4	24.5	24.7	21.9	26.8	26.1	25.9	26.1	21.7	22.6	21.3	20.3	19.8
Atopobathynella sp. 1 KMA-2012 JN817390	26.3	21.5	20.8	21.3	22.9	22.6	21.4	19.1	20.6	22.5	22.7	22.5	17.0		22.8	25.4	24.9	24.9	28.4	27.5	27.3	27.5	26.8	27.4	23.9	20.9	19.8
BMR00543_CVCK_nr Brevisomabathynella sp.	25.3	20.0	18.1	18.4	18.3	21.3	19.5	20.1	20.4	20.4	21.0	21.0	22.4	22.8		19.2	18.9	16.7	21.5	20.8	21.4	20.8	20.6	20.9	25.9	21.5	21.6
BMR00542_HSTD_nr Brevisomabathynella sp.	26.6	21.7	21.7	22.4	22.8	21.9	23.3	23.6	22.5	21.7	21.3	21.7	24.5	25.4	19.2		0.6	16.6	18.5	18.2	18.5	18.2	17.5	17.7	27.6	22.4	21.7
BMR00602_HSTD_nr Brevisomabathynella sp.	26.4	21.0	21.2	21.9	22.1	21.4	23.1	23.1	22.3	21.3	21.3	21.7	24.7	24.9	18.9	0.6		16.6	18.8	18.5	18.8	18.5	17.0	17.2	27.3	22.1	21.4
BMR00645_BS1E_Parabathynellidae	26.6	20.0	18.4	16.3	18.6	18.6	22.8	23.6	22.2	20.9	21.2	21.0	21.9	24.9	16.7	16.6	16.6		13.1	12.9	12.9	12.9	13.1	13.2	24.9	22.8	22.0
BMR00246_BS3_nr Brevisomabathynella sp.	27.8	23.1	21.9	20.6	22.7	22.4	26.8	27.7	24.6	24.1	24.5	24.3	26.8	28.4	21.5	18.5	18.8	13.1		0.3	1.1	0.3	14.3	14.5	30.9	24.9	23.5
BMR00418_BS3_nr Brevisomabathynella sp.	27.7	22.6	21.4	21.0	22.6	23.1	26.7	27.0	24.3	23.3	23.6	23.5	26.1	27.5	20.8	18.2	18.5	12.9	0.3		0.8	0.0	13.4	13.5	29.5	24.5	22.8
BMR00420_BS3_nr Brevisomabathynella sp.	28.0	22.8	21.2	20.7	22.8	22.8	26.4	26.8	24.1	23.2	23.5	23.3	25.9	27.3	21.4	18.5	18.8	12.9	1.1	0.8		0.8	13.5	13.6	29.3	24.5	22.8
BMR00480_BS3_nr Brevisomabathynella sp.	27.7	22.6	21.4	21.0	22.6	23.1	26.7	27.0	24.3	23.3	23.6	23.5	26.1	27.5	20.8	18.2	18.5	12.9	0.3	0.0	0.8		13.4	13.5	29.5	24.5	22.8
BMR00419_BS3_nr Brevisomabathynella sp.	27.5	23.3	21.2	18.4	20.0	20.3	25.0	23.6	22.7	21.7	22.0	22.3	21.7	26.8	20.6	17.5	17.0	13.1	14.3	13.4	13.5	13.4		0.2	28.3	23.4	22.8
BMR00541_BS3_nr Brevisomabathynella sp.	27.7	23.6	22.1	18.5	20.2	20.2	25.6	24.1	23.0	22.1	22.5	22.8	22.6	27.4	20.9	17.7	17.2	13.2	14.5	13.5	13.6	13.5	0.2		29.2	23.9	23.3
Kimberleybathynella sp. 1 KMA-2012 JN817395	28.9	23.9	22.9	24.8	23.6	23.2	23.4	22.5	27.7	26.2	26.0	26.7	21.3	23.9	25.9	27.6	27.3	24.9	30.9	29.5	29.3	29.5	28.3	29.2		20.6	20.7
BMR00372_CVCK_Atopobathynella sp.	25.0	20.9	19.9	22.4	21.0	22.3	21.4	22.1	20.7	22.4	22.4	22.7	20.3	20.9	21.5	22.4	22.1	22.8	24.9	24.5	24.5	24.5	23.4	23.9	20.6		3.7
BMR00545_CVCK_Atopobathynella sp.	25.6	21.2	18.2	21.7	19.6	21.7	20.4	20.9	20.2	20.7	20.9	20.9	19.8	19.8	21.6	21.7	21.4	22.0	23.5	22.8	22.8	22.8	22.8	23.3	20.7	3.7	

Appendix 24: Distance matrix of Isopoda (stygofauna) sequences/ lineages included in the analysis

COI divergences (%) of stygal Isopoda (regional comparisons)	O.G.	MF346645.1	BMR00675	BMR01162	EU107666	BMR01185	EU124873.1	AK7	EU107647.1	EU107579.1	EU107641.1	EU107664.1	EU124868.1	EU107636.1	RT56	EU107637.1	EU107639.1
OUTGROUPIV103_Daves-20150604-01_Amphipoda_RobeV		30.2	33.3	33.3	37.9	34.7	37.2	35.0	36.2	37.5	35.0	35.9	35.7	35.2	35.2	36.2	36.4
MF346645.1_Coxicerberus fukudai_Microcerberidea.gb	30.2		28.1	28.1	31.2	27.2	28.9	28.6	29.5	29.9	29.1	28.8	28.6	29.1	29.3	28.2	28.0
BMR00675_VIV_Isopoda (cf Pygolabis)	33.3	28.1		0.0	28.8	25.4	26.4	25.5	25.3	26.6	27.0	26.0	26.2	27.7	28.9	26.8	26.6
BMR01162_VIV_Isopoda (cf Pygolabis)	33.3	28.1	0.0		28.8	25.4	26.4	25.5	25.3	26.6	27.0	26.0	26.2	27.7	28.9	26.8	26.6
EU107666_Tainisopus sp.	37.9	31.2	28.8	28.8		24.8	25.0	25.5	28.1	26.4	24.4	26.0	26.2	26.4	26.4	25.7	24.4
BMR01185_Caves Creek_Pygolabis	34.7	27.2	25.4	25.4	24.8		19.7	18.5	20.4	17.9	18.2	19.3	19.5	21.1	21.0	19.5	18.2
EU124873.1_Pygolabis weeliwolli Pilbara_Finston et al. 2009.gb	37.2	28.9	26.4	26.4	25.0	19.7		17.3	19.5	16.4	15.8	15.1	15.3	17.5	16.9	16.8	17.5
AK7_PE112171_Pygolabis	35.0	28.6	25.5	25.5	25.5	18.5	17.3		16.4	13.3	15.5	13.5	13.7	17.1	16.1	18.4	16.9
EU107647.1_Pygolabis sp. 5 TLF-2007 Pilbara_Finston et al. 2009.gb	36.2	29.5	25.3	25.3	28.1	20.4	19.5	16.4		17.3	19.5	18.2	18.4	18.9	18.8	18.6	20.2
EU107579.1_Pygolabis humphreysi_Pilbara_Finston et al. 2009.gb	37.5	29.9	26.6	26.6	26.4	17.9	16.4	13.3	17.3		14.2	13.7	13.8	17.1	17.3	17.9	17.3
EU107641.1_Pygolabis sp. 7 TLF-2007 Pilbara_Finston et al. 2009.gb	35.0	29.1	27.0	27.0	24.4	18.2	15.8	15.5	19.5	14.2		13.3	13.5	17.5	17.3	18.4	18.8
EU107664.1_Pygolabis sp. 4 TLF-2007 Pilbara_Finston et al. 2009.gb	35.9	28.8	26.0	26.0	26.0	19.3	15.1	13.5	18.2	13.7	13.3		0.2	14.9	15.1	16.9	15.7
EU124868.1_Pygolabis sp. MC1_M3_16 Pilbara_Finston et al. 2009.gb	35.7	28.6	26.2	26.2	26.2	19.5	15.3	13.7	18.4	13.8	13.5	0.2		15.1	15.3	17.1	15.8
EU107636.1_Pygolabis paraburdoo Pilbara_Finston et al. 2009.gb	35.2	29.1	27.7	27.7	26.4	21.1	17.5	17.1	18.9	17.1	17.5	14.9	15.1		0.9	13.1	13.5
RT56_WAMC74183_Pygolabis_WAM-PYGO001	35.2	29.3	28.9	28.9	26.4	21.0	16.9	16.1	18.8	17.3	17.3	15.1	15.3	0.9		12.9	13.3
EU107637.1_Pygolabis gascoynensis Pilbara_Finston et al. 2009.gb	36.2	28.2	26.8	26.8	25.7	19.5	16.8	18.4	18.6	17.9	18.4	16.9	17.1	13.1	12.9		10.4
EU107639.1_Pygolabis eberhardi Pilbara_Finston et al. 2009.gb	36.4	28.0	26.6	26.6	24.4	18.2	17.5	16.9	20.2	17.3	18.8	15.7	15.8	13.5	13.3	10.4	

Appendix 25: Distance matrix of Oligochaeta (Enchytraeidae) sequences/ lineages included in the analysis

COI divergences (%) of Enchytraeidae (regional comparisons)	O.G.	BMR 01171	BMR 01183	KM2064 88	KM2064 77	BMR 00815	KM2065 16	JY06	BMR 01180	BMR 00809	BMR 00812	KM2064 79	RT56	JY08	JY09	JY07	JY11	KM2065 29	BMR 01169	JY10	BMR 00810	BMR 00813	BMR 01215	BMR 01200	WAMV 9278	WAMV 8924	KM2064 90	WAMV 8930	BMR 01177	BMR 01172	BMR 01175
KM206509_Naididae sp5._Ridley River_Brown et al. 2015_OUTGROUP		20.8	21.2	21.9	22.0	22.5	23.2	22.6	22.7	23.4	23.2	23.7	21.0	23.0	23.1	20.8	20.9	20.8	21.4	20.9	21.4	22.0	21.5	21.6	21.8	22.2	22.0	22.0	23.2	24.1	24.1
BMR01171_VIV_Oligochaeta	20.8		17.6	17.3	17.6	17.8	18.4	18.6	20.3	20.4	19.5	19.6	16.6	17.7	17.9	16.9	17.0	17.0	17.2	18.0	17.5	17.3	17.2	17.5	17.5	18.5	18.4	17.3	17.0	18.1	17.8
BMR01183_DSM_Enchytraeidae	21.2	17.6		15.7	16.6	17.0	17.5	17.3	17.9	18.2	17.9	16.9	16.0	16.9	16.7	16.4	16.4	14.9	16.7	16.7	16.3	16.9	15.5	16.3	16.6	17.0	17.3	16.1	15.3	16.6	16.4
KM206488_Echytraeidae sp12._ Fortescue_Brown et al 2015	21.9	17.3	15.7		12.4	14.3	14.5	18.9	18.6	19.6	19.8	16.8	15.4	14.2	14.1	16.7	16.4	17.1	16.3	15.5	16.0	16.6	16.3	16.3	15.7	15.9	17.0	15.4	15.5	16.3	16.4
KM206477_Echytraeidae sp13._McPhee Creek_Brown et al 2015	22.0	17.6	16.6	12.4		5.0	6.0	18.8	19.7	20.2	20.1	19.6	15.7	15.4	14.7	16.6	16.9	17.6	16.7	17.2	16.7	16.1	16.6	16.8	16.9	17.1	17.3	16.8	17.6	17.3	17.6
BMR00815_BGCK_Enchytraeidae sp.	22.5	17.8	17.0	14.3	5.0		4.0	18.9	19.4	20.2	19.8	19.9	16.6	16.0	15.5	16.7	17.2	17.5	16.6	17.8	16.7	17.5	16.1	17.4	17.2	17.2	18.1	17.3	18.5	17.9	18.1
KM206516_Echytraeidae sp11._Weelumurra Creek_Brown et al 2015	23.2	18.4	17.5	14.5	6.0	4.0		18.6	18.6	19.8	19.6	20.2	16.9	15.4	15.2	17.9	18.4	17.7	17.8	18.9	17.8	16.9	17.5	17.8	17.3	17.7	18.2	17.3	19.1	19.3	18.8
JY06_WAN_Dave Bore_Enchytraeidae `sp. Helix-OLE028`	22.6	18.6	17.3	18.9	18.8	18.9	18.6		7.5	8.2	8.2	16.6	15.9	17.4	17.3	16.9	17.3	16.2	16.9	17.6	15.4	16.5	16.1	16.4	16.2	16.4	17.8	16.1	16.5	18.0	17.7
BMR01180_BS3X_Oligochaeta	22.7	20.3	17.9	18.6	19.7	19.4	18.6	7.5		4.6	4.8	17.7	16.8	17.0	16.8	16.0	15.9	15.9	16.8	17.4	15.7	16.8	16.0	16.7	16.3	16.3	16.9	15.4	16.0	17.6	16.6
BMR00809_BS1E_Enchytraeidae sp.	23.4	20.4	18.2	19.6	20.2	20.2	19.8	8.2	4.6		1.4	19.3	16.1	17.9	17.5	17.3	17.3	15.5	17.5	17.3	16.1	16.6	16.4	16.9	16.7	16.7	18.5	16.6	17.3	18.5	17.6
BMR00812_BS1E_Oligochaeta sp.	23.2	19.5	17.9	19.8	20.1	19.8	19.6	8.2	4.8	1.4		19.1	15.8	17.2	16.7	16.7	17.0	15.2	17.8	17.0	16.3	16.6	16.4	16.6	16.4	16.4	18.4	16.9	17.0	18.2	17.3
KM206479_Echytraeidae sp10._North Shaw River_Brown et al 2015	23.7	19.6	16.9	16.8	19.6	19.9	20.2	16.6	17.7	19.3	19.1		13.8	14.1	14.3	14.8	15.0	12.5	14.3	12.4	13.0	13.8	13.0	13.2	13.9	13.9	13.9	13.3	13.2	15.1	14.0
RT56_WAMV8926_Enchytraeidae_WAM-ENCH003	21.0	16.6	16.0	15.4	15.7	16.6	16.9	15.9	16.8	16.1	15.8	13.8		8.7	9.6	7.9	8.2	8.4	9.1	8.9	8.2	8.1	8.8	8.9	9.5	9.9	12.7	10.8	10.3	10.6	10.8
JY08_WAN_Dave Bore_Enchytraeidae `sp. Helix-OLE030`	23.0	17.7	16.9	14.2	15.4	16.0	15.4	17.4	17.0	17.9	17.2	14.1	8.7		1.7	8.7	8.6	8.9	10.3	9.2	9.0	9.0	9.7	9.9	10.7	11.2	10.7	11.5	12.1	11.8	11.0
JY09_WAN_Dave Bore_Enchytraeidae `sp. Helix-OLE030`	23.1	17.9	16.7	14.1	14.7	15.5	15.2	17.3	16.8	17.5	16.7	14.3	9.6	1.7		9.0	8.8	9.1	10.3	9.2	8.8	9.0	9.1	9.3	10.2	10.6	10.5	11.7	11.7	11.4	10.6
JY07_WAN_Dave Bore_Enchytraeidae `sp. Helix-OLE026`	20.8	16.9	16.4	16.7	16.6	16.7	17.9	16.9	16.0	17.3	16.7	14.8	7.9	8.7	9.0		1.2	7.1	8.5	7.6	6.8	7.9	6.8	7.4	8.5	8.8	11.2	12.0	11.1	11.9	11.6
JY11_WAN_RR1_Enchytraeidae `sp. Helix-OLE026`	20.9	17.0	16.4	16.4	16.9	17.2	18.4	17.3	15.9	17.3	17.0	15.0	8.2	8.6	8.8	1.2		7.1	8.2	7.4	6.2	7.9	7.0	7.7	9.0	9.1	11.1	11.7	11.1	11.2	11.2
KM206529_Echytraeidae sp6._Brown et al 2015	20.8	17.0	14.9	17.1	17.6	17.5	17.7	16.2	15.9	15.5	15.2	12.5	8.4	8.9	9.1	7.1	7.1		7.1	6.5	5.9	6.5	5.5	6.9	8.1	8.6	11.9	10.1	9.9	11.2	10.6
BMR01169_SGW_Enchytraeidae	21.4	17.2	16.7	16.3	16.7	16.6	17.8	16.9	16.8	17.5	17.8	14.3	9.1	10.3	10.3	8.5	8.2	7.1		7.0	5.9	7.8	6.4	7.1	7.8	8.5	10.9	11.7	10.3	11.1	10.5
JY10_WAN_RR1_Enchytraeidae `sp. Helix-OLE029`	20.9	18.0	16.7	15.5	17.2	17.8	18.9	17.6	17.4	17.3	17.0	12.4	8.9	9.2	9.2	7.6	7.4	6.5	7.0		5.3	5.8	5.5	4.9	6.3	7.1	12.0	10.8	9.9	11.0	9.4
BMR00810_BGCK_Oligochaeta sp.	21.4	17.5	16.3	16.0	16.7	16.7	17.8	15.4	15.7	16.1	16.3	13.0	8.2	9.0	8.8	6.8	6.2	5.9	5.9	5.3		4.3	4.3	4.2	4.3	5.8	10.9	10.9	9.0	10.0	9.4
BMR00813_BS1W_Oligochaeta sp.	22.0	17.3	16.9	16.6	16.1	17.5	16.9	16.5	16.8	16.6	16.6	13.8	8.1	9.0	9.0	7.9	7.9	6.5	7.8	5.8	4.3		4.7	4.0	5.6	6.8	12.0	11.1	9.6	10.8	10.2
BMR01215_Caves Creek_Enchytraeidae	21.5	17.2	15.5	16.3	16.6	16.1	17.5	16.1	16.0	16.4	16.4	13.0	8.8	9.7	9.1	6.8	7.0	5.5	6.4	5.5	4.3	4.7		4.0	4.9	5.3	11.1	10.5	10.0	11.1	11.1
BMR01200_Lens G_Enchytraeidae	21.6	17.5	16.3	16.3	16.8	17.4	17.8	16.4	16.7	16.9	16.6	13.2	8.9	9.9	9.3	7.4	7.7	6.9	7.1	4.9	4.2	4.0	4.0		4.6	5.4	12.1	10.4	8.9	11.2	10.2
RT35_WAMV9278_Enchytraeidae_sp._E6_(2-4)	21.8	17.5	16.6	15.7	16.9	17.2	17.3	16.2	16.3	16.7	16.4	13.9	9.5	10.7	10.2	8.5	9.0	8.1	7.8	6.3	4.3	5.6	4.9	4.6		2.4	11.8	11.6	9.7	11.1	10.8
RT56_WAMV8924_Enchytraeidae_sp._E6_(2-4)	22.2	18.5	17.0	15.9	17.1	17.2	17.7	16.4	16.3	16.7	16.4	13.9	9.9	11.2	10.6	8.8	9.1	8.6	8.5	7.1	5.8	6.8	5.3	5.4	2.4		12.1	11.7	9.9	11.1	11.1
KM206490_Echytraeidae sp8._Upper Fortescue_Brown et al 2015	22.0	18.4	17.3	17.0	17.3	18.1	18.2	17.8	16.9	18.5	18.4	13.9	12.7	10.7	10.5	11.2	11.1	11.9	10.9	12.0	10.9	12.0	11.1	12.1	11.8	12.1		10.6	9.6	11.4	10.9
RT56_WAMV8930_Enchytraeidae_WAM-ENCH002	22.0	17.3	16.1	15.4	16.8	17.3	17.3	16.1	15.4	16.6	16.9	13.3	10.8	11.5	11.7	12.0	11.7	10.1	11.7	10.8	10.9	11.1	10.5	10.4	11.6	11.7	10.6		8.4	8.8	8.2
BMR01177_BS3_Oligochaeta	23.2	17.0	15.3	15.5	17.6	18.5	19.1	16.5	16.0	17.3	17.0	13.2	10.3	12.1	11.7	11.1	11.1	9.9	10.3	9.9	9.0	9.6	10.0	8.9	9.7	9.9	9.6	8.4		5.6	5.6
BMR01172_Caves Creek_Oligochaeta	24.1	18.1	16.6	16.3	17.3	17.9	19.3	18.0	17.6	18.5	18.2	15.1	10.6	11.8	11.4	11.9	11.2	11.2	11.1	11.0	10.0	10.8	11.1	11.2	11.1	11.1	11.4	8.8	5.6		2.1
BMR01175_Caves Creek_Oligochaeta	24.1	17.8	16.4	16.4	17.6	18.1	18.8	17.7	16.6	17.6	17.3	14.0	10.8	11.0	10.6	11.6	11.2	10.6	10.5	9.4	9.4	10.2	11.1	10.2	10.8	11.1	10.9	8.2	5.6	2.1	

Appendix 26: Distance matrix of Oligochaeta (Phreodrilidae) sequences/ lineages included in the analysis

COI divergences (%) of Phreodrilidae (regional comparisons)	OG	BMR 00744	KM2065 21	BMR 00808	BMR 01191	KM2065 11	KM2065 24	KM2065 22	BMR 01173	KM2065 23	KM2064 98	BMR 00814	BMR 01161	JY21	BMR 01188	KM2065 28	BMR 00811	BMR 00624	BMR 00684	WAMV 8910	BMR 00817	BMR 01196
Orobdella ketagalan_OUTGROUP		25.4	27.1	27.7	27.2	27.8	26.2	27.4	28.1	27.5	26.3	26.2	26.6	25.6	25.9	26.7	25.9	26.0	26.3	27.2	27.4	28.5
BMR00744_BGCK_Oligochaeta sp.	25.4		16.0	21.7	21.9	21.0	20.7	19.3	20.4	15.6	18.5	17.5	17.2	16.4	17.5	17.0	18.1	17.9	18.2	19.8	20.7	19.9
KM206521_Phreodrilidae sp.16_Eel Creek_Brown et al. 2015	27.1	16.0		19.6	19.6	19.2	18.6	18.6	22.7	15.5	17.0	16.9	17.0	16.9	16.9	16.3	17.0	17.6	17.9	19.2	21.7	19.9
BMR00808_BGCK_Phreodrilidae sp.	27.7	21.7	19.6		17.9	19.8	18.4	19.3	22.3	21.9	20.7	20.4	20.7	20.8	20.8	21.5	20.7	21.0	21.0	18.2	19.9	19.3
BMR01191_SGW_Oligochaeta	27.2	21.9	19.6	17.9		18.2	18.0	19.3	24.2	21.4	20.5	20.2	20.7	19.9	21.0	21.1	20.7	20.7	21.0	17.5	17.2	16.3
KM206511_Phreodrilidae sp.5_Ridley River_Brown et al. 2015	27.8	21.0	19.2	19.8	18.2		19.7	18.9	22.6	20.8	19.7	20.2	20.7	20.8	20.5	20.7	20.5	19.7	20.1	17.0	19.0	18.5
KM206524_Phreodrilidae sp.8_North Shaw River_Brown et al. 2015	26.2	20.7	18.6	18.4	18.0	19.7		18.3	22.2	19.0	19.4	18.8	18.8	18.8	18.6	18.3	19.7	19.1	19.5	18.7	20.0	18.3
KM206522_Phreodrilidae sp.9_Eel Creek_Brown et al. 2015	27.4	19.3	18.6	19.3	19.3	18.9	18.3		23.2	18.6	18.3	17.7	18.0	18.0	17.8	18.3	18.2	18.5	18.5	18.9	19.0	18.3
BMR01173_Caves Creek_Oligochaeta	28.1	20.4	22.7	22.3	24.2	22.6	22.2	23.2		22.8	24.4	23.2	23.3	23.0	23.6	23.3	23.2	23.6	23.3	21.5	22.9	23.0
KM206523_Phreodrilidae sp.13_Black Range Creek_Brown et al. 2015	27.5	15.6	15.5	21.9	21.4	20.8	19.0	18.6	22.8		10.9	9.2	9.5	9.6	9.5	9.9	9.8	9.2	9.6	19.9	20.9	21.1
KM206498_Phreodrilidae sp.11_Fortescue_Brown et al. 2015	26.3	18.5	17.0	20.7	20.5	19.7	19.4	18.3	24.4	10.9		8.2	8.1	7.6	8.5	8.7	9.4	8.0	8.1	20.7	21.0	21.7
BMR00814_BS1E_Phreodrilidae sp.	26.2	17.5	16.9	20.4	20.2	20.2	18.8	17.7	23.2	9.2	8.2		2.0	2.7	3.0	2.7	3.2	3.1	3.2	21.0	21.0	21.6
BMR01161_BS3X_Oligochaeta	26.6	17.2	17.0	20.7	20.7	20.7	18.8	18.0	23.3	9.5	8.1	2.0		2.4	2.4	2.1	3.8	3.3	3.3	21.4	21.4	21.9
JY21_WAN_RC14WAD0346_Phreodrilidae `sp. Helix-OLP12`	25.6	16.4	16.9	20.8	19.9	20.8	18.8	18.0	23.0	9.6	7.6	2.7	2.4		2.7	2.3	4.7	4.0	4.1	20.4	20.8	21.6
BMR01188_BS3_Phreodrilidae?	25.9	17.5	16.9	20.8	21.0	20.5	18.6	17.8	23.6	9.5	8.5	3.0	2.4	2.7		2.6	4.7	4.0	4.1	20.8	21.0	21.6
KM206528_Phreodrilidae sp.12_Fortescue_Brown et al. 2015	26.7	17.0	16.3	21.5	21.1	20.7	18.3	18.3	23.3	9.9	8.7	2.7	2.1	2.3	2.6		3.9	3.3	3.1	20.2	20.6	21.7
BMR00811_BS1W_Phreodrilidae sp.	25.9	18.1	17.0	20.7	20.7	20.5	19.7	18.2	23.2	9.8	9.4	3.2	3.8	4.7	4.7	3.9		2.2	2.3	21.0	21.6	22.3
BMR00624_BS1E_Oligochaeta sp.	26.0	17.9	17.6	21.0	20.7	19.7	19.1	18.5	23.6	9.2	8.0	3.1	3.3	4.0	4.0	3.3	2.2		0.5	21.0	21.7	22.3
BMR00684_BS1W_Oligochaeta sp.	26.3	18.2	17.9	21.0	21.0	20.1	19.5	18.5	23.3	9.6	8.1	3.2	3.3	4.1	4.1	3.1	2.3	0.5		21.1	21.6	22.5
RT46_WAMV8910_Phreodrilidae_WAM-PHRE001	27.2	19.8	19.2	18.2	17.5	17.0	18.7	18.9	21.5	19.9	20.7	21.0	21.4	20.4	20.8	20.2	21.0	21.0	21.1		15.7	15.7
BMR00817_BS1E_Oligochaeta sp.	27.4	20.7	21.7	19.9	17.2	19.0	20.0	19.0	22.9	20.9	21.0	21.0	21.4	20.8	21.0	20.6	21.6	21.7	21.6	15.7		12.8
BMR01196_Caves Creek_Phreodrilidae	28.5	19.9	19.9	19.3	16.3	18.5	18.3	18.3	23.0	21.1	21.7	21.6	21.9	21.6	21.6	21.7	22.3	22.3	22.5	15.7	12.8	

Appendix 27: Distance matrix of Oligochaeta (Naididae) sequences/ lineages included in the analysis

COI divergences (%) of Naididae (regional comparisons)	O.G.	WAMV 9284	JY22	KM 206493	KM 206509	BMR 01212	WAMV 8916
KM206479_Echytraeidae sp10._North Shaw River_Brown et al 2015_OUTGROUP		19.0	20.3	21.4	23.7	22.0	22.3
RT35_WAMV9284_Naididae_Pristina	19.0		18.1	18.9	18.4	18.3	19.4
JY22_WAN_RC15WAC0384_Pristina longiseta	20.3	18.1		18.5	18.2	17.6	17.6
KM206493_Naididae sp3._Upper Fortescue_Brown et al. 2015	21.4	18.9	18.5		20.2	20.3	19.3
KM206509_Naididae sp5._Ridley River_Brown et al. 2015	23.7	18.4	18.2	20.2		20.2	17.0
BMR01212_Caves Creek_Oligochaeta	22.0	18.3	17.6	20.3	20.2		14.9
RT46_WAMV8916_Naididae_WAM-NAID002	22.3	19.4	17.6	19.3	17.0	14.9	

APPENDIX D: Molecular Systematics Analysis Report - Addendum

Biologic Environmental Survey Pty Ltd
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East Perth
WA 6004
AUSTRALIA

Tuesday, 15 March 2022

RE: Addendum to Greater Brockman Subterranean Fauna Survey Molecular Systematics Analysis

Biologic (2020) details molecular systematics analyses (DNA barcoding) of 600 subterranean fauna (stygofauna and troglofauna) specimens collected from Rio Tinto’s Greater Brockman Project (the Study Area). This addendum to that report adds 169 newly collected and sequenced stygofauna and troglofauna specimens. These new specimens were collected during targeted surveys in October 2020, February 2021, and August 2021. In addition to these, three parabathynellids and one Coleoptera from the original baseline surveys (2019-2020) were also included for sequencing and analysis.

DNA extraction, amplification and sequencing followed the methods described in Biologic (2020). Phylogenetic analyses for this addendum included the original comparative set of sequences from that report, as well as any other sequences produced since Biologic (2020) analyses were conducted. For each taxonomic group, the selected sequences were aligned using the MAFFT (Multiple Alignment using Fast Fourier Transform) algorithm (Katoh *et al.*, 2002). Trees were constructed on resulting alignments using the RaxML (Stamatakis, 2014) plugin in GENEIOUS Prime, using 1,000 bootstrap replicates and the GTR+G substitution model.

Of the 173 samples included in this addendum, 158 specimens successfully amplified, while 15 failed to produce a high quality, on target sequence (Table 1). Specimen details are outlined in Appendix A.

Table 1: Summary of taxonomic groups and sequencing success.

Taxa	High Quality Sequence	Failed amplification, low quality, or contamination	TOTAL
Arachnida: Araneae	2	1	3
Arachnida: Palpigradi	3		3
Arachnida: Scorpiones	1		1
Clitellata: Enchytraeida: Enchytraeidae	16	1	17
Clitellata: Haplotaxida: Phreodrilidae	14	1	15
Diplopoda: Polydesmida	1		1
Diplopoda: Polyxenida	1		1
Entognatha: Diplura	9		9
Insecta: Coleoptera: Carabidae	2		2
Insecta: Zygentoma: Nicoletiidae	5	1	6
Malacostraca: Copepoda: Hexanauplia	2	2	4
Malacostraca: Amphipoda: Bogidiellidae	1		1
Malacostraca: Amphipoda: Eriopisidae	2		2
Malacostraca: Amphipoda: Paramelitidae	42	1	43
Malacostraca: Isopoda: Microcerberidae	1		1
Malacostraca: Syncarida: Bathynellidae	3		3
Malacostraca: Syncarida: Parabathynellidae	42	7	49
Pauropoda	6	1	7
Symphyla: Cephalostigmata: Scutigerellidae	5		5
TOTAL	**158**	**15**	**173**

Arachnida: Araneae

Two spiders were successfully sequenced (Table 1). One specimen matched a previously detected OTU from Biologic (2020), Gnaphosidae `sp. Biologic-ARAN006` (Figure 1). The other specimen formed a new OTU, *Prethopalpus* `sp. Biologic-ARAN023, 13% divergent from *Prethopalpus* `sp. ARAN002. Intra- and interspecific genetic distances are provided in Appendix B.

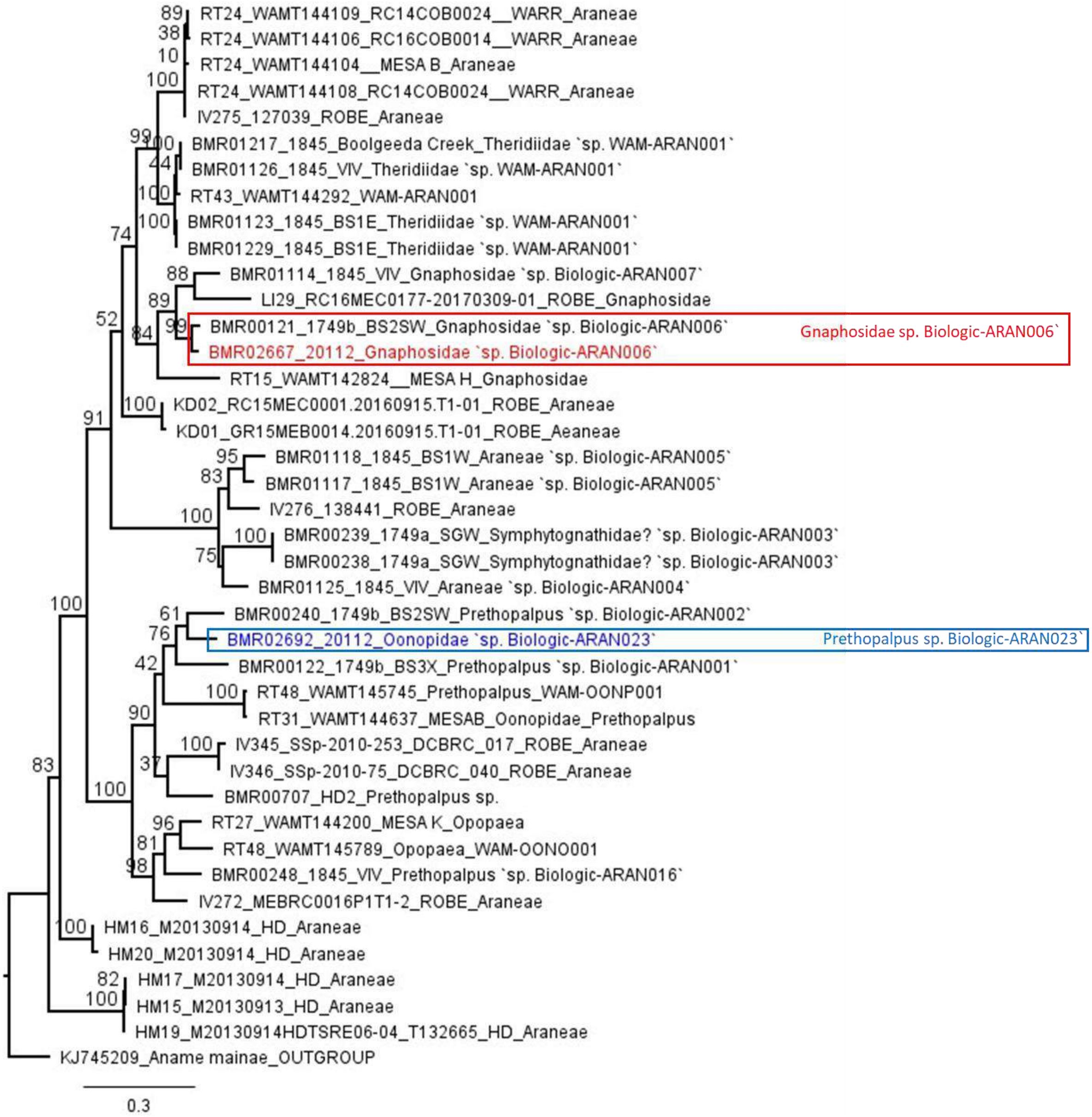


Figure 1: Phylogenetic tree of Araneae. Newly added sequences are denoted with 20112 after the BMR number.

Arachnida: Palpigradi

Three specimens of Palpigradi formed three singleton OTUs (Figure 2) and did not match any previously collected OTUs. Palpigradi `sp. Biologic-PALP031` and `PALP032` are 17.9% different at the COI locus. Palpigradi `sp. Biologic-PALP033` is most closely related to Palpigradi `sp. Biologic-PALP005` (26.6% COI). Intra- and interspecific genetic distances are provided in Appendix B.

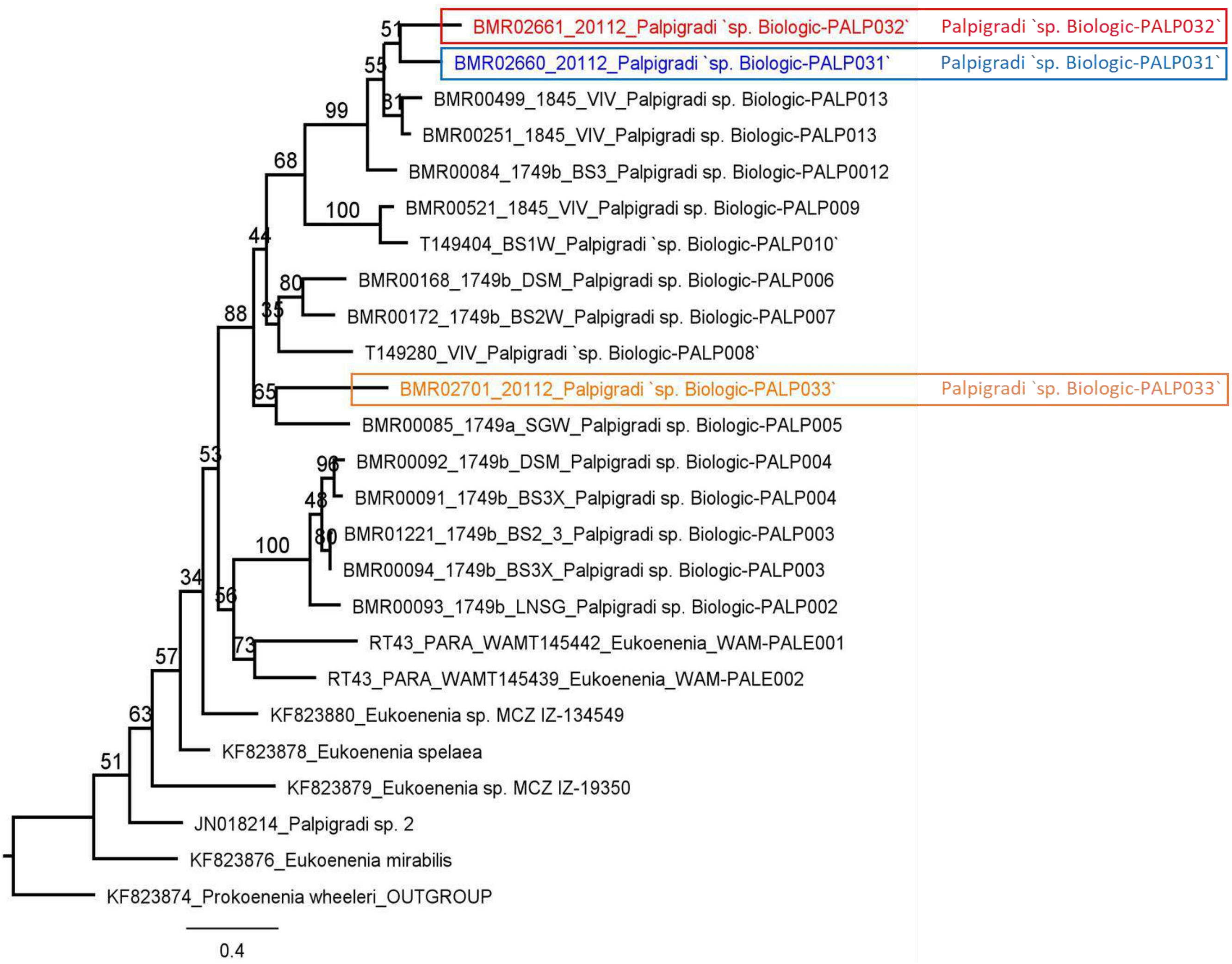


Figure 2: Phylogenetic tree of Palpigradi. Newly added sequences are denoted with 20112 after the BMR number.

Arachnida: Scorpiones

A single scorpion specimen was collected from the recent survey and successfully sequenced. The specimen failed to match any available sequences, but BLAST analysis placed it within the bothriurid scorpion family, and was closest to *Cercophonius*, the only Australian bothriurid genus (16.5% COI difference; Figure 3). The OTU was named Scorpiones `sp. Biologic-SCOR002`. Intra- and interspecific genetic distances are provided in Appendix B.

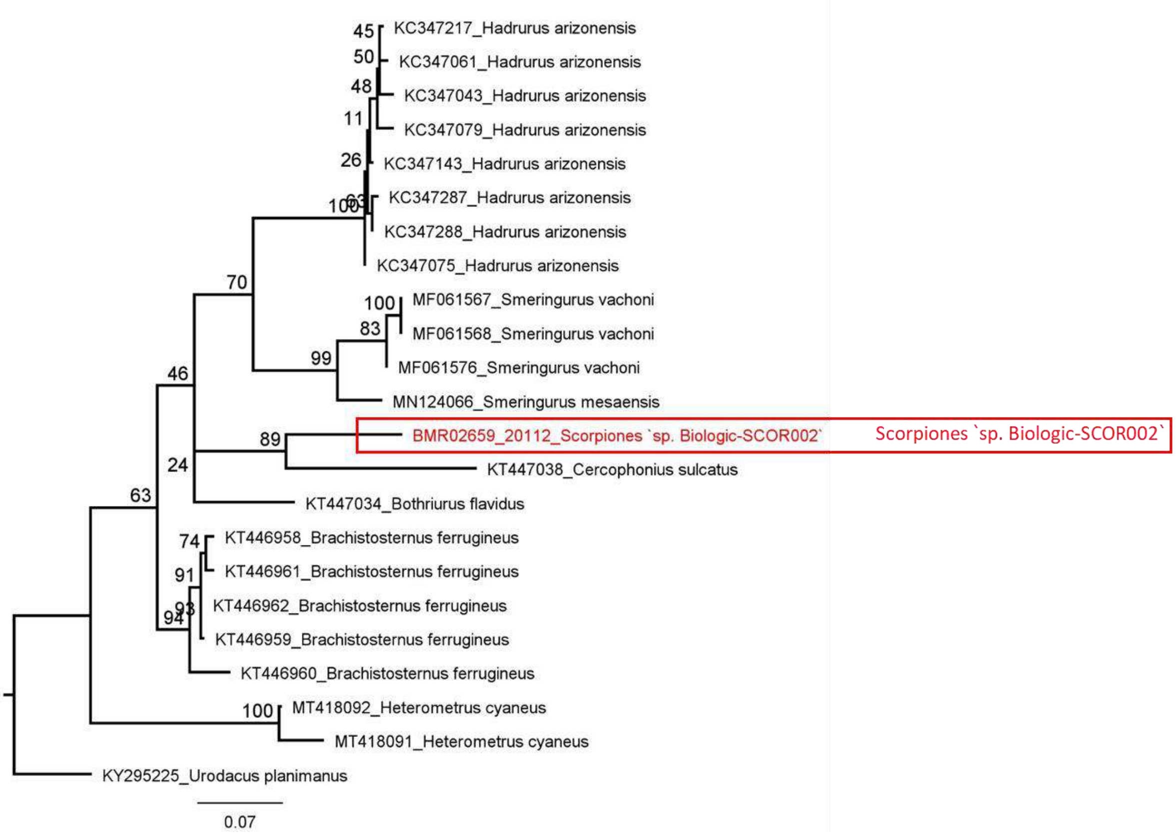


Figure 3: Phylogenetic tree of Scorpiones. Newly added sequences are denoted with 20112 after the BMR number.

Clitellata: Enchytraeida: Enchytraeidae

Nine of the 16 newly sequenced specimens matched five OTUs previously sequenced in Biologic (2020) (Figure 4). The remaining seven sequences formed four new OTUs currently only known from the Study Area.

Surveys of the neighbouring Angelo River and Rhodes Ridge regions have yielded three sequences that are 0.9-6.1% divergent from the single, previously sequenced Enchytraeidae `sp. Biologic-OLIG017` specimen (Appendix B) from Greater Brockman. Based on intraspecific divergences observed within Pilbara enchytraeids, we consider these sequences to belong to the same OTU, which dramatically extends the distribution of this OTU. Intra- and interspecific genetic distances are provided in Appendix B. In addition to previous external matches (Biologic, 2020), Enchytraeidae `sp. Biologic-OLIG004` has been found to also align with sequences from the Rhodes Ridge and Angelo River area. Similarly, Enchytraeidae `sp. E11` and `sp. Biologic-OLIG006` have now also been found at Angelo River. The enchytraeid phylogeny showed two specimens nested within Enchytraeidae `sp. Biologic-OLIG006` with very low bootstrap support. Thee two specimens (KM206490 Enchytraeidae `sp. 8` and WAMV8930 Enchytraeidae `sp. WAM-ENH002`) are on longer branches and more divergent (7.5-11.4%) than specimens identified as within Enchytraeidae `sp. Biologic-OLIG006` (2.1-7.3%). These may all represent a single taxon, but for now we consider Enchytraeidae `sp. Biologic-OLIG006` as separate from Enchytraeidae `sp. 8` and Enchytraeidae `sp. WAM-ENH002`, awaiting more phylogenetic resolution. Enchytraeidae `sp. Biologic-OLIG016` has been found to match two sequences from the Goldfields, greatly extending this OTU’s range (300+ km).

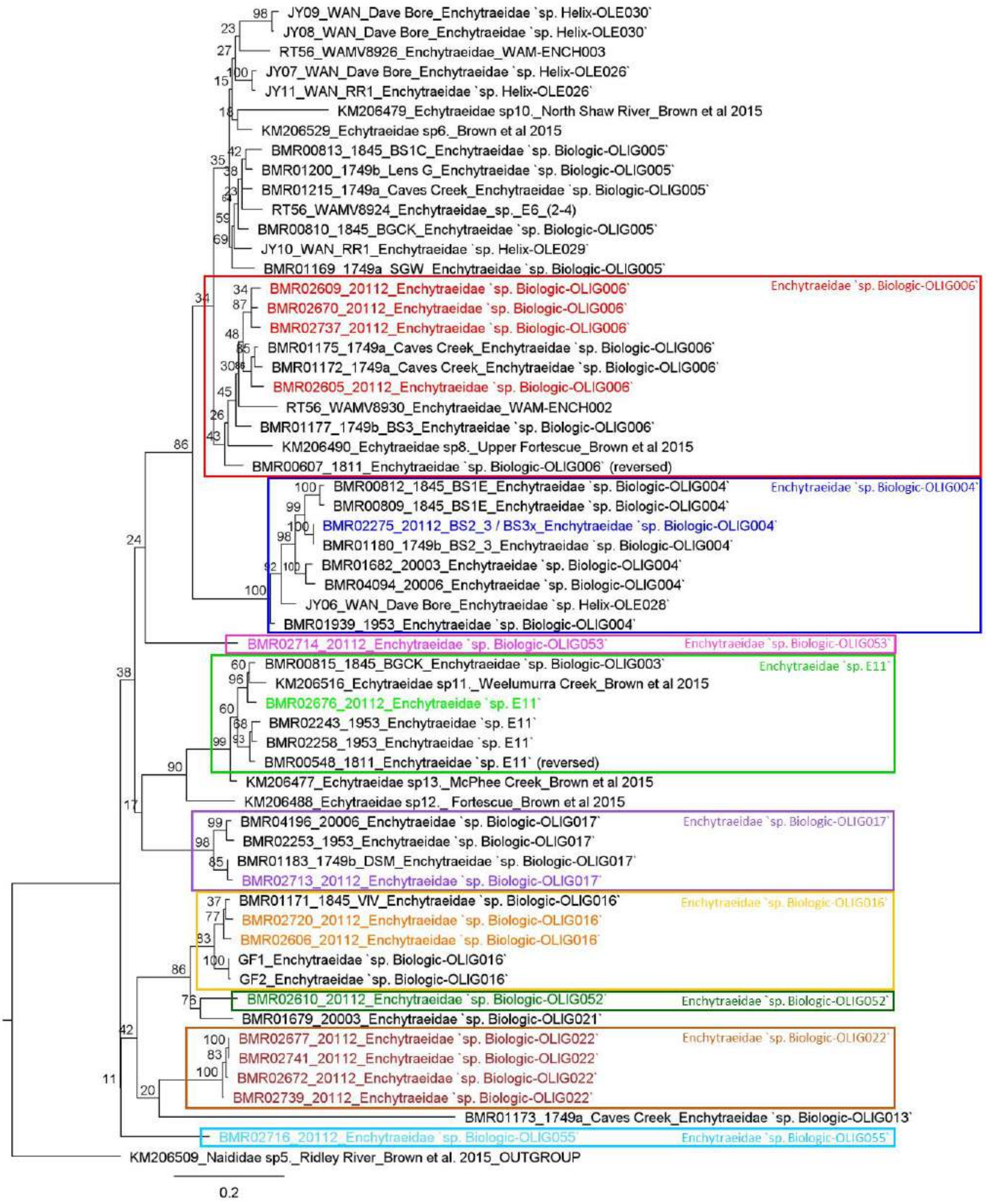


Figure 4: Phylogenetic tree of Enchytraeidae. Newly added sequences are denoted with 20112 after the BMR number.

Clitellata: Haplotaxida: Phreodrilidae

Twelve of the 14 phreodrilid sequences added to this analysis matched Phreodrilidae `sp. P12`, an OTU originally delimited in Brown *et al.* (2015) and detected in the Study Area in Biologic (2020) (Figure 5). Another specimen matched Phreodrilidae `sp. Biologic-OLIG011`, originally delimited in Biologic (2020). The final specimen formed its own OTU, *Antarctodrilus* `sp. Biologic-OLIG054`. Intra- and interspecific genetic distances are provided in Appendix B.

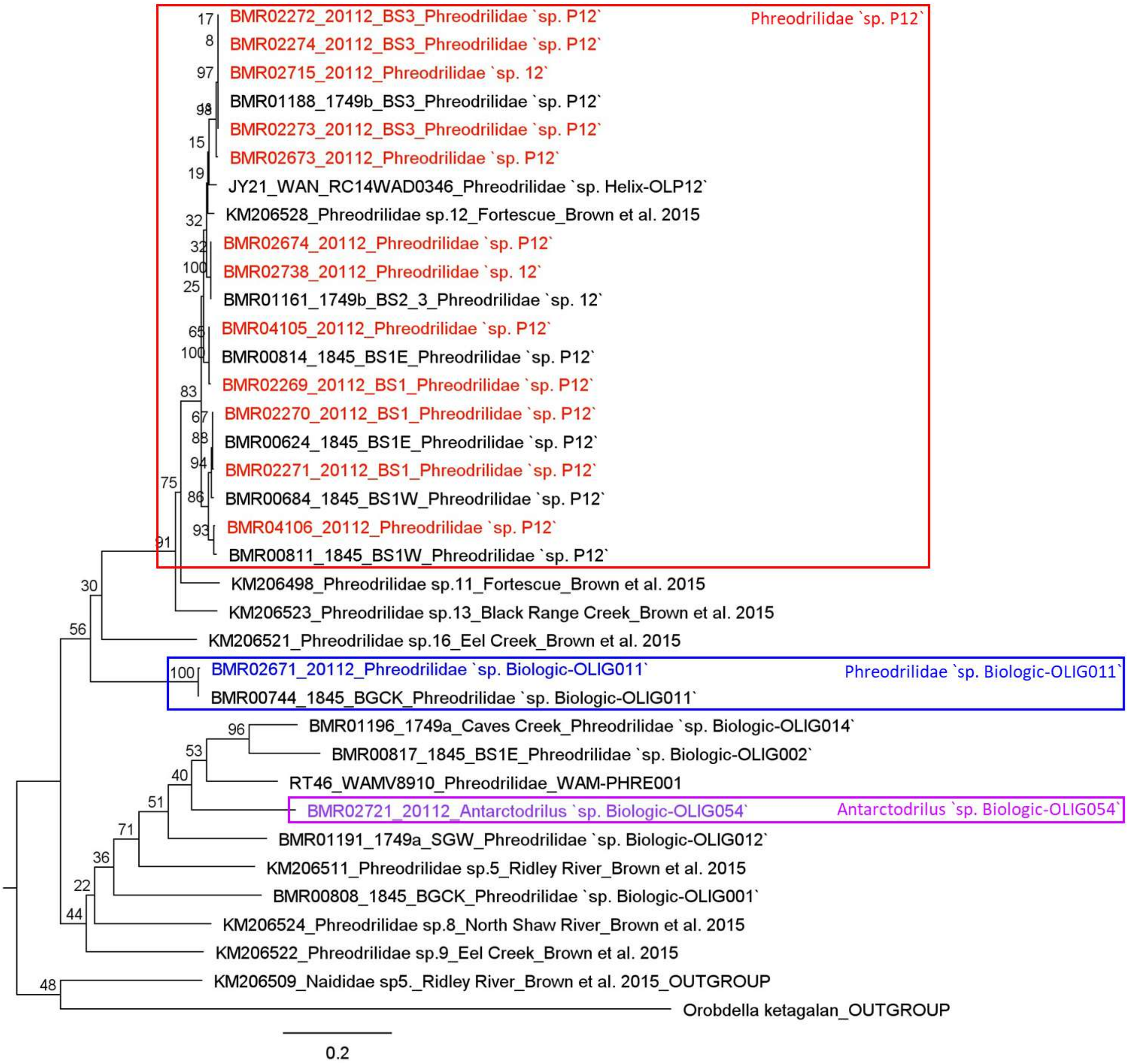


Figure 5: Phylogenetic tree of Phreodrilidae. Newly added sequences are denoted with 20112 after the BMR number.

Diplopoda: Polydesmida

A single specimen of Polydesmida was sequenced at COI, which did not match any available data (Figure 6). Polydesmida `sp. Biologic-POLD002` was most closely related to a Haplodesmidae specimen from the Robe Valley (IV379: 15.9% COI difference). Intra- and interspecific genetic distances are provided in Appendix B.

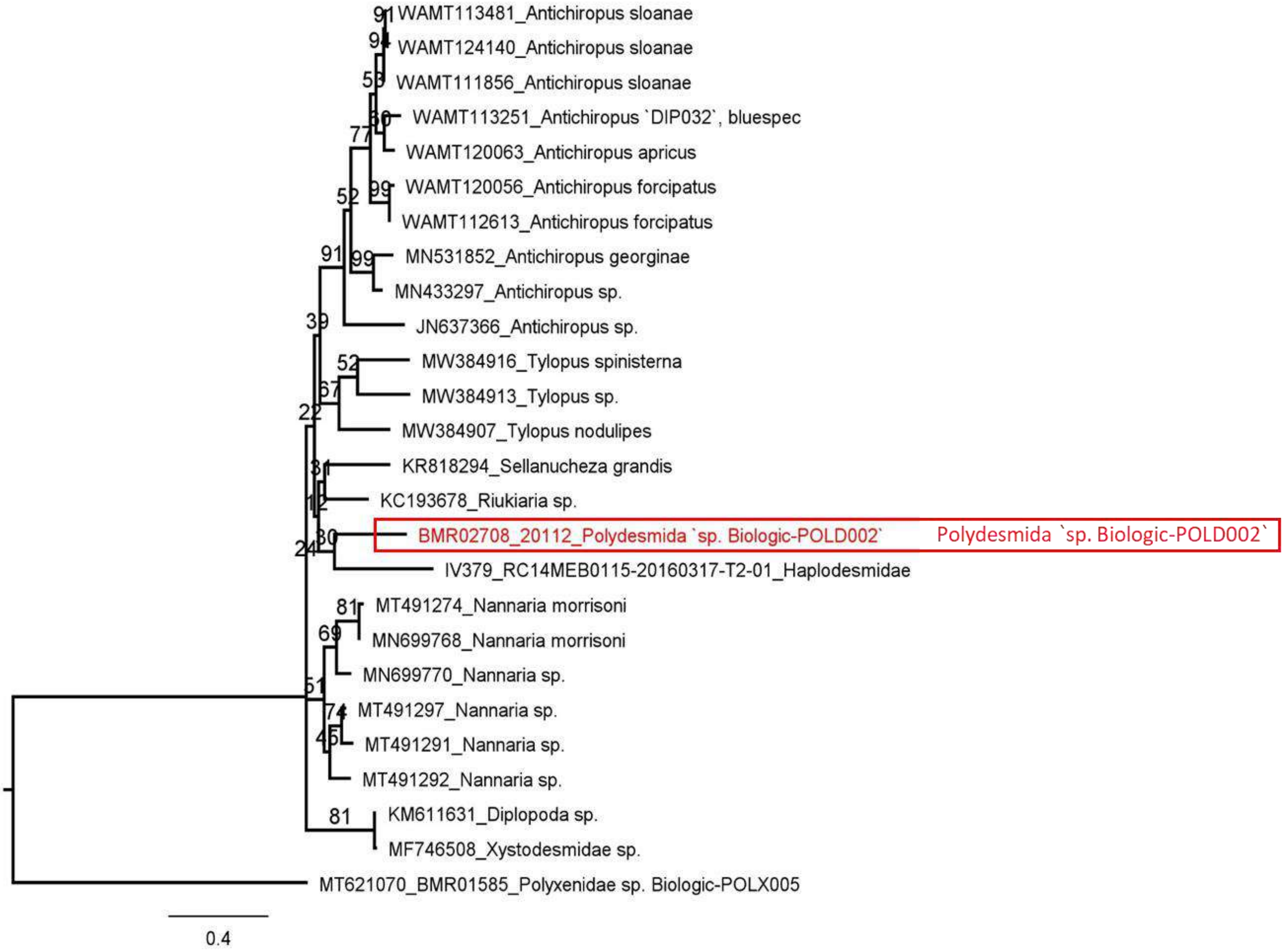


Figure 6: Phylogenetic tree of Polydesmida. Newly added sequences are denoted with 20112 after the BMR number.

Diplopoda: Polyxenida

A single specimen of Polyxenida was added to the analysis (Figure 7). This specimen did not match any existing OTU from the area, forming a unique OTU; and was named Lophoproctidae `sp. Biologic-POLX006`. This specimen matched a specimen from Bungaroo Valley, ca. 38 km SSE of Pannawonica, and two specimens from Angelo River, ca. 110 km west of Newman. This OTU has a linear distance of 100+ km.

In Biologic (2020), Polyxenida `sp. Biologic-POLX003` included BMR00477. Subsequent analysis and the addition of more samples suggests that this specimen belongs to another OTU; Polyxenida `sp. Biologic-POLX005` (See the dotted box in Figure 7). This OTU is distributed regionally, occurring at West Angelas, Angelo River and Rhodes Ridge, and has a linear distance of ~205 km. Intra- and interspecific genetic distances are provided in Appendix B.

Figure 7: Phylogenetic tree of Polyxenida. Newly added sequences are denoted with 20112 after the BMR number.

Entognatha: Diplura

The nine successfully sequenced Diplura specimens formed 6 OTUs (Figure 8), all of which were not sampled in Biologic (2020). One of these OTUs, Japygidae `sp. Biologic-DIPL028`, also matched a previously sequenced specimen from Greater Brockman, JC18_BROCK4_Japygidae `sp. Helix marra mamba`. Intra- and interspecific genetic distances are provided in Appendix B.

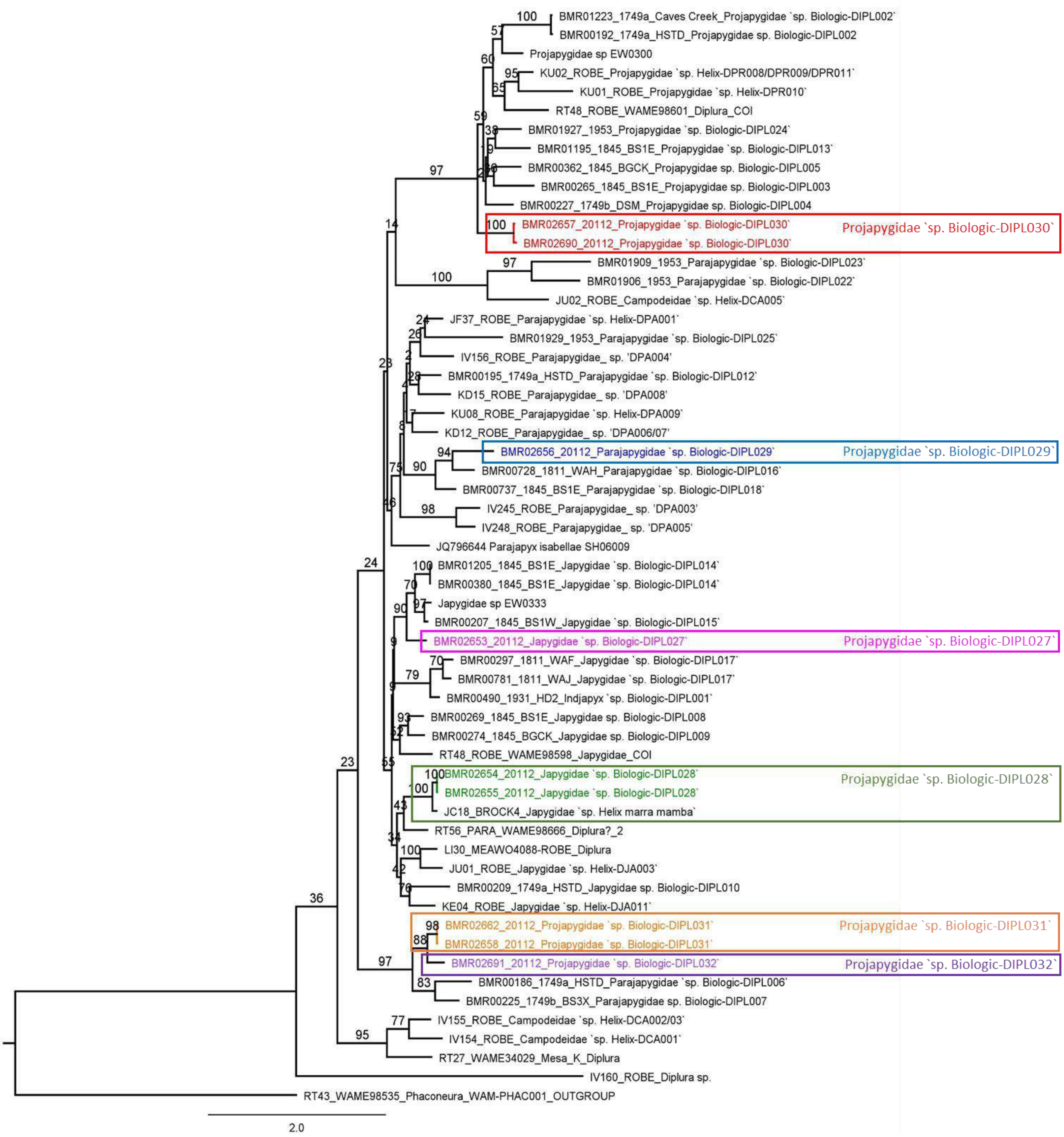


Figure 8: Phylogenetic tree of Diplura. Newly added sequences are denoted with 20112 after the BMR number.

Hexanauplia

The two Hexanauplia specimens successfully sequenced formed two new OTUs, which did not match any available sequences (Figure 9). These OTUs were named Calanoida `sp. Biologic-CALA002` and *Diacyclops* `sp. Biologic-CYCL029`, and were >14% and 24% divergent from all other sequences in the analysis, respectively. Intra- and interspecific genetic distances are provided in Appendix B.

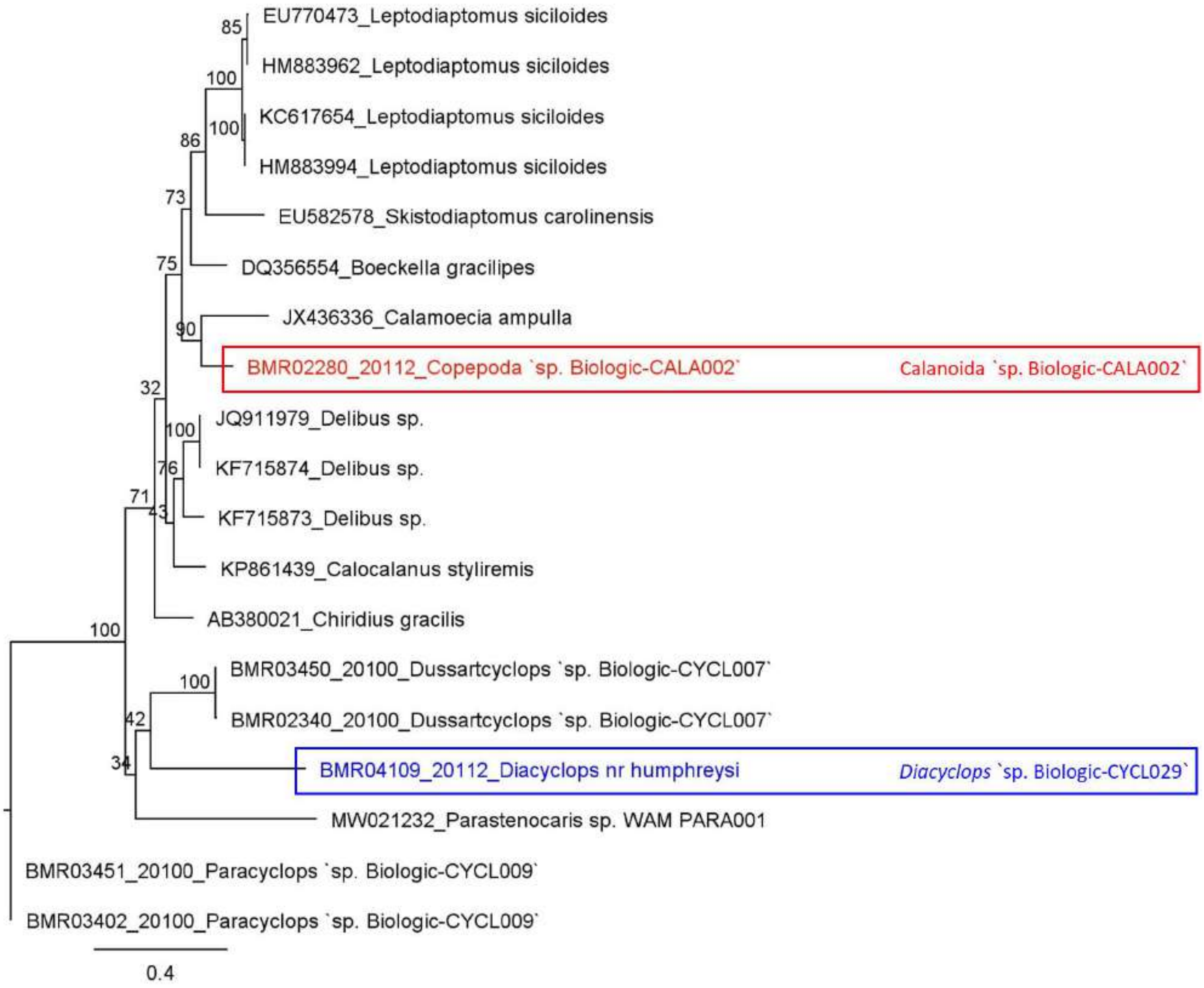


Figure 9: Phylogenetic tree of Hexanauplia. Newly added sequences are denoted with 20112 after the BMR number.

Insecta: Coleoptera: Carabidae

One of the Coleoptera specimens sequenced in this addendum matched the previously sequenced OTU, Carabidae `sp. Biologic-COLE001` (Figure 10). The other (BMR00378), sampled during the original baseline surveys, matched the widely distributed *Ptinella* `sp. Helix-CPT003, which has been sampled from Mesa K, Angelo River, and Rhodes Ridge. Intra- and interspecific genetic distances are provided in Appendix B.

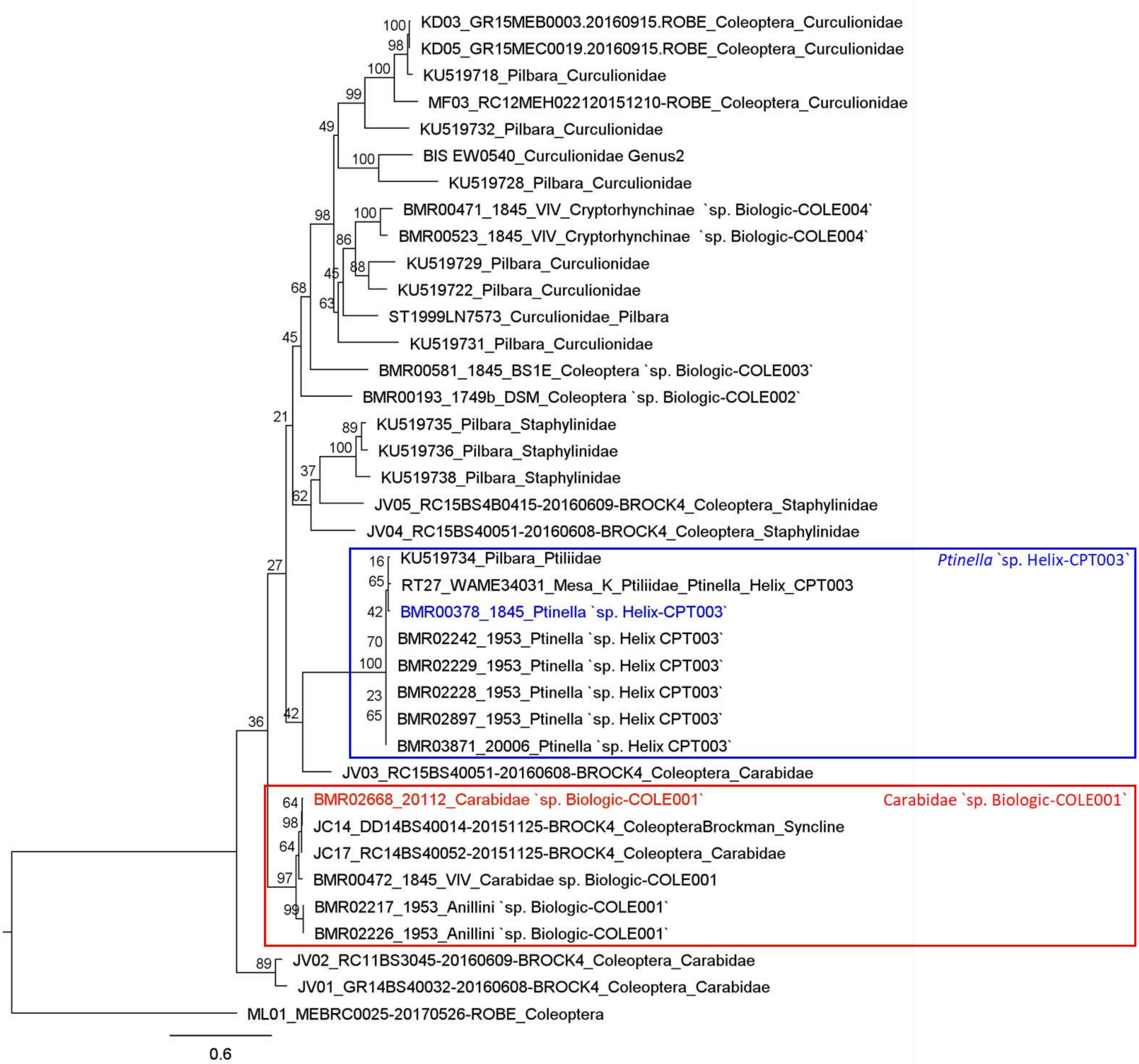


Figure 10: Phylogenetic tree of Coleoptera. Newly added sequences are denoted with 20112 after the BMR number.

Insecta: Zygentoma: Nicoletiidae

Five Zygentoma specimens were successfully sequenced, four of which formed new, singleton OTUs (Figure 11). The fifth grouped with Nicoletiinae `sp. Biologic-ZYGE006`. Intra- and interspecific genetic distances are provided in Appendix B.

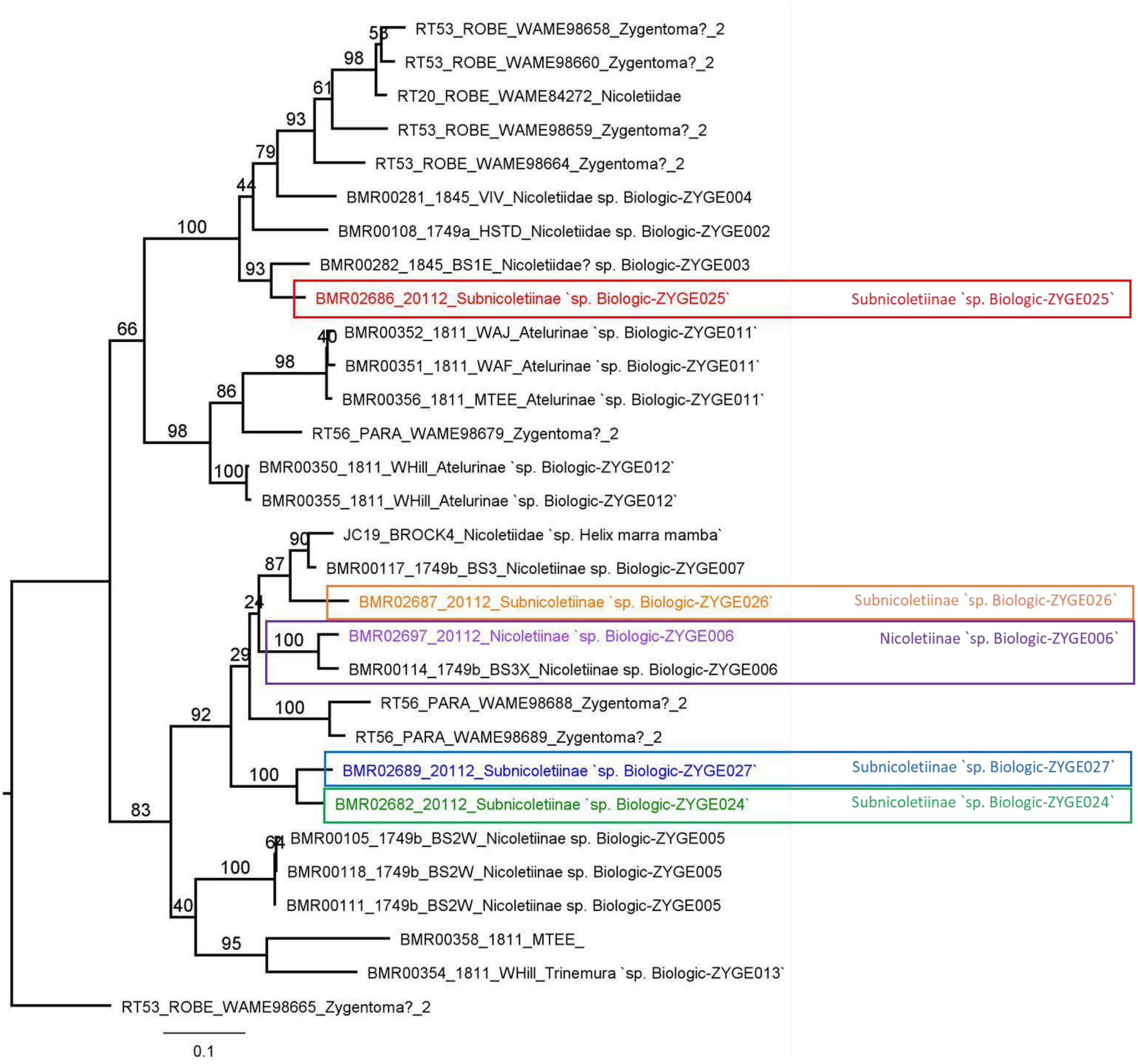


Figure 11: Phylogenetic tree of Zygentoma. Newly added sequences are denoted with 20112 after the BMR number.

Malacostraca: Amphipoda: Bogidiellidae

One bogidiellid specimen was successfully sequenced, matching a previously sequenced OTU from the Study Area (Biologic, 2020). This OTU appears to be closely related to Bogidiellidae `sp. WAM-AMPB003` from Greater Paraburdoo (Cullen & Harvey, 2018), with 7.3 – 7.8% COI divergence. It is possible that `Biologic-AMPH011` and `WAM-AMPB003` form a single OTU, but bootstrap support between these clades is low and more data would be needed to ascertain any potential relatedness. Intra- and interspecific genetic distances are provided in Appendix B.

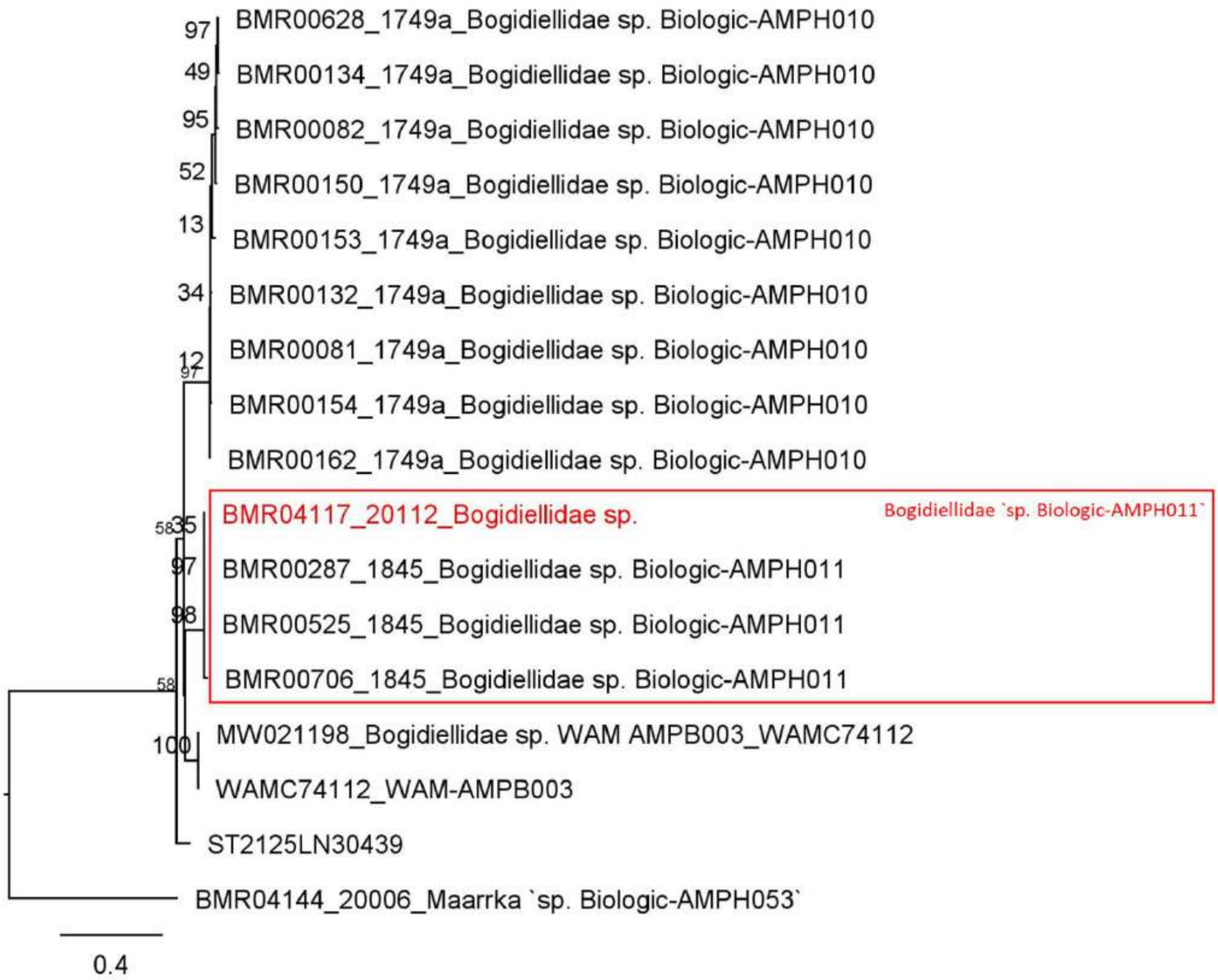


Figure 12: Phylogenetic tree of Bogidiellidae. Newly added sequences are denoted with 20112 after the BMR number.

Malacostraca: Amphipoda: Eriopisidae

Two eriopisid specimens from were successfully sequenced, with one matching a previously sequenced OTU, *Nedsia* `sp. WAM-AMPE003`. This OTU includes specimens previously sequenced from the Study Area (Biologic, 2020) and a sequence from Greater Paraburdoo (Cullen & Harvey, 2018). A recently published paper has described the specimen matching sequence OK170024 as *Nedsia nanutarra* King & Cooper 2021 and so we apply that name to this lineage ({King, 2021 #6779}).

Although this clade is relatively closely related to *Nedsia* `sp. A5`, `sp. WAM-AMPE001`, and `WAM-AMPE002` (6.3 - 8.0%), these OTUs have been found to be distinct (King *et al.*, 2021). Genetic differences at which OTUs in this group are delineated appear to be low compared to other groups. The second specimen sequenced from the Study Area, *Nedsia* `sp. Biologic-AMPH052`, is therefore not considered to form an OTU with its closest genetic matches (Eriopisidae `sp. H-AME022: 6.9%; NH104: 6.5%) and instead forms a singleton OTU.

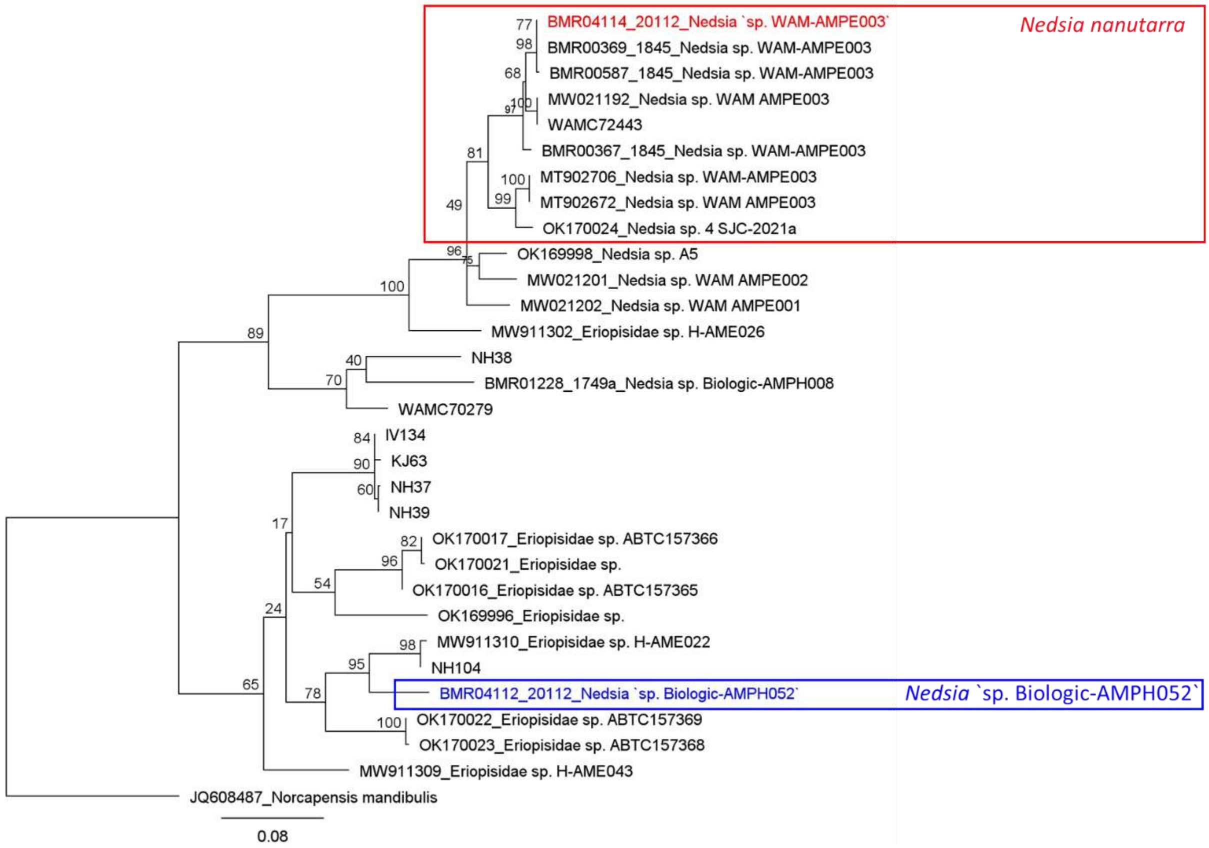


Figure 13: Phylogenetic tree of Eriopisidae. Newly added sequences are denoted with 20112 after the BMR number.

Malacostraca: Amphipoda: Paramelitidae

Thirty-nine of the 42 new paramelitid sequences matched two OTUs originally delimited in Biologic (2020), Paramelitidae `sp. Biologic-AMPH015` and Paramelitidae `sp. Helix-AMP037` (Figure 14). Two new OTUs were also detected, Paramelitidae `sp. Biologic-AMPH047` and Paramelitidae `sp. Biologic-AMPH048`, which did not match regional sequences. Intra- and interspecific genetic distances are provided in Appendix B.

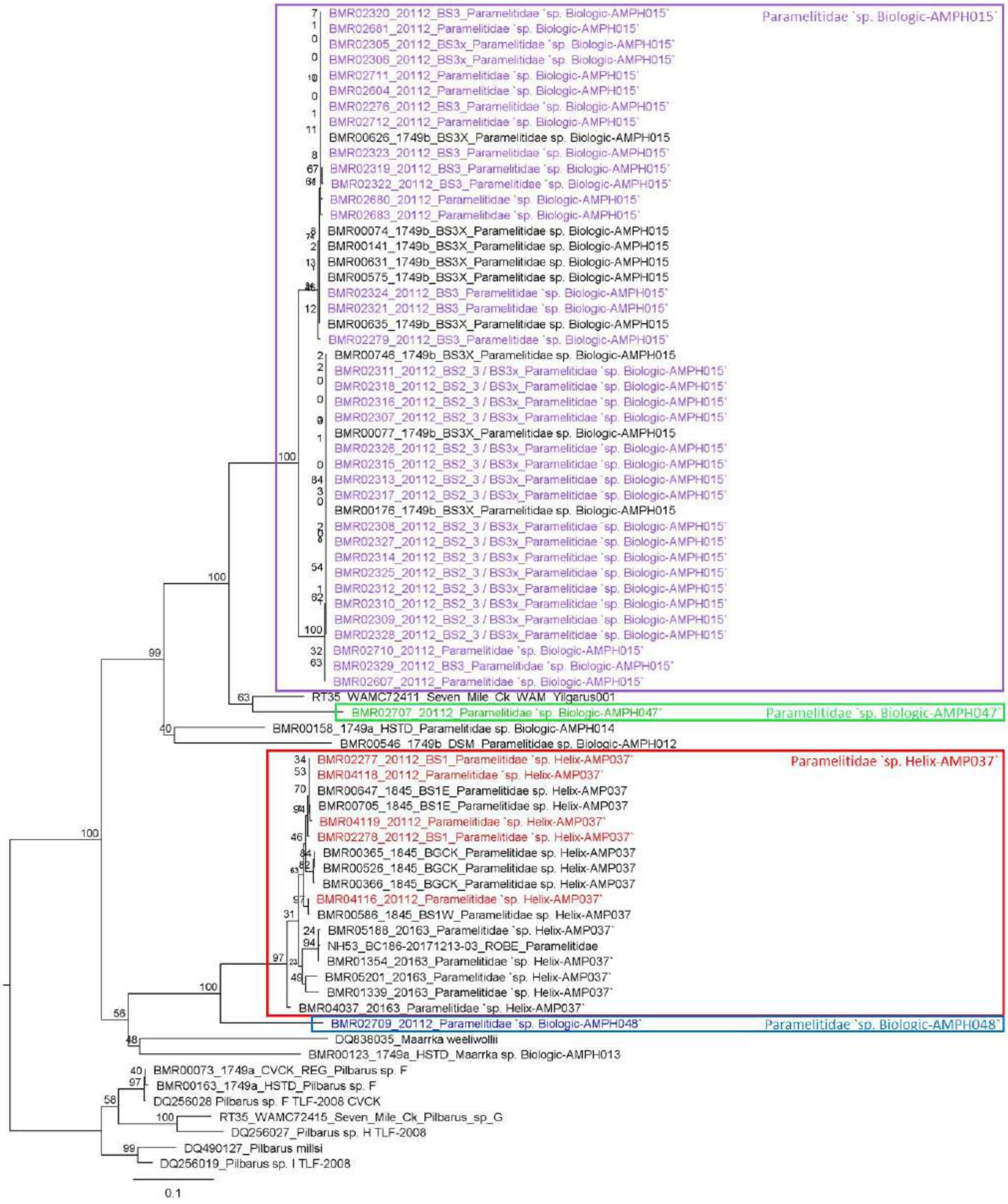


Figure 14: Phylogenetic tree of Paramelitidae. Newly added sequences are denoted with 20112 after the BMR number.

Malacostraca: Isopoda: Microcerberidae

The single specimen of Microcerberidae successfully amplified and was found to be ~15% divergent from another Pilbara microceberid, Microcerberidae sp. H-ISM002 (Figure 15). Microcerberidae sp. H-ISM002 was collected from Bungaroo Creek. Unfortunately, there are sequences from only one other microcerberid species on GenBank, *Coxicerberus fukudai* from Korea and Japan, making it difficult to comment on the systematic position of the microcerberid collected in this study. This new OTU was named Microcerberidae `sp. Biologic-ISOP026`. Intra- and interspecific genetic distances are provided in Appendix B.

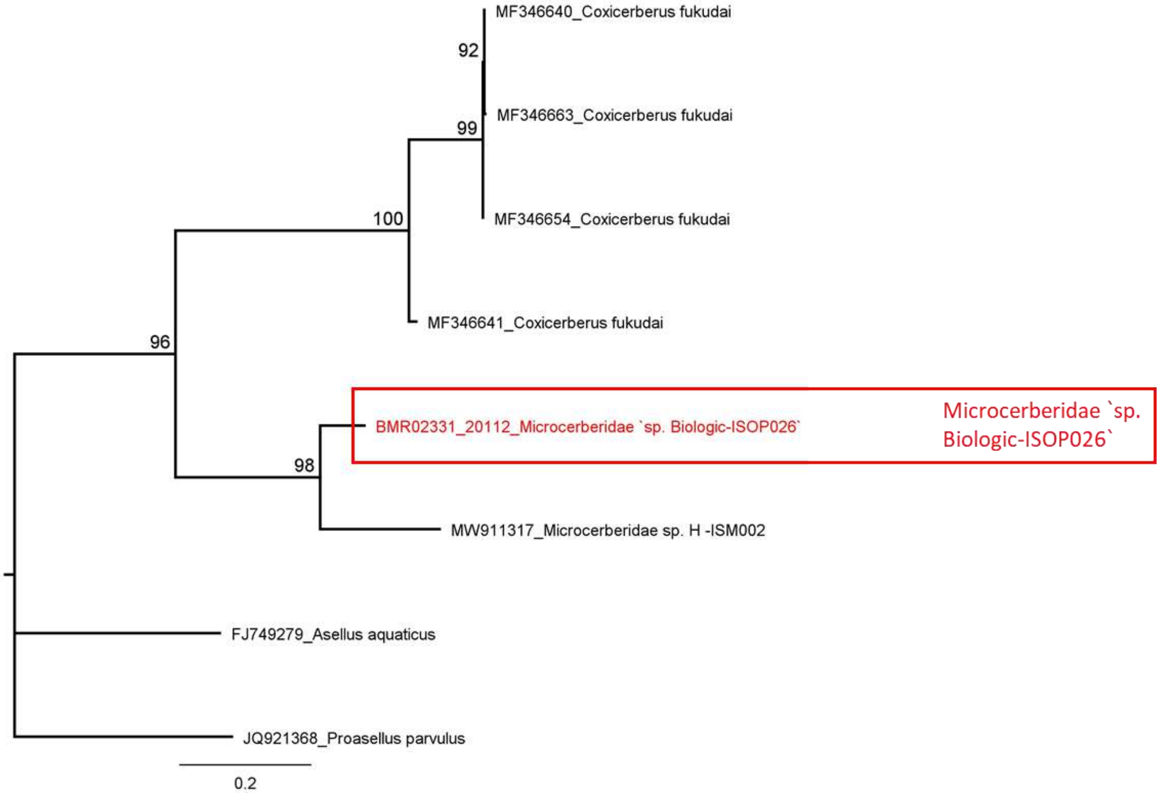


Figure 15: Phylogenetic tree of Microcerberidae. Newly added sequences are denoted with 20112 after the BMR number.

Malacostraca: Syncarida: Bathynellidae

Three bathynellid specimens matched existing OTUs; Bathynellidae `sp. Biologic-BATH002` and Bathynellidae `sp. Biologic-BATH003` (Figure 16). Intra- and interspecific genetic distances are provided in Appendix B.

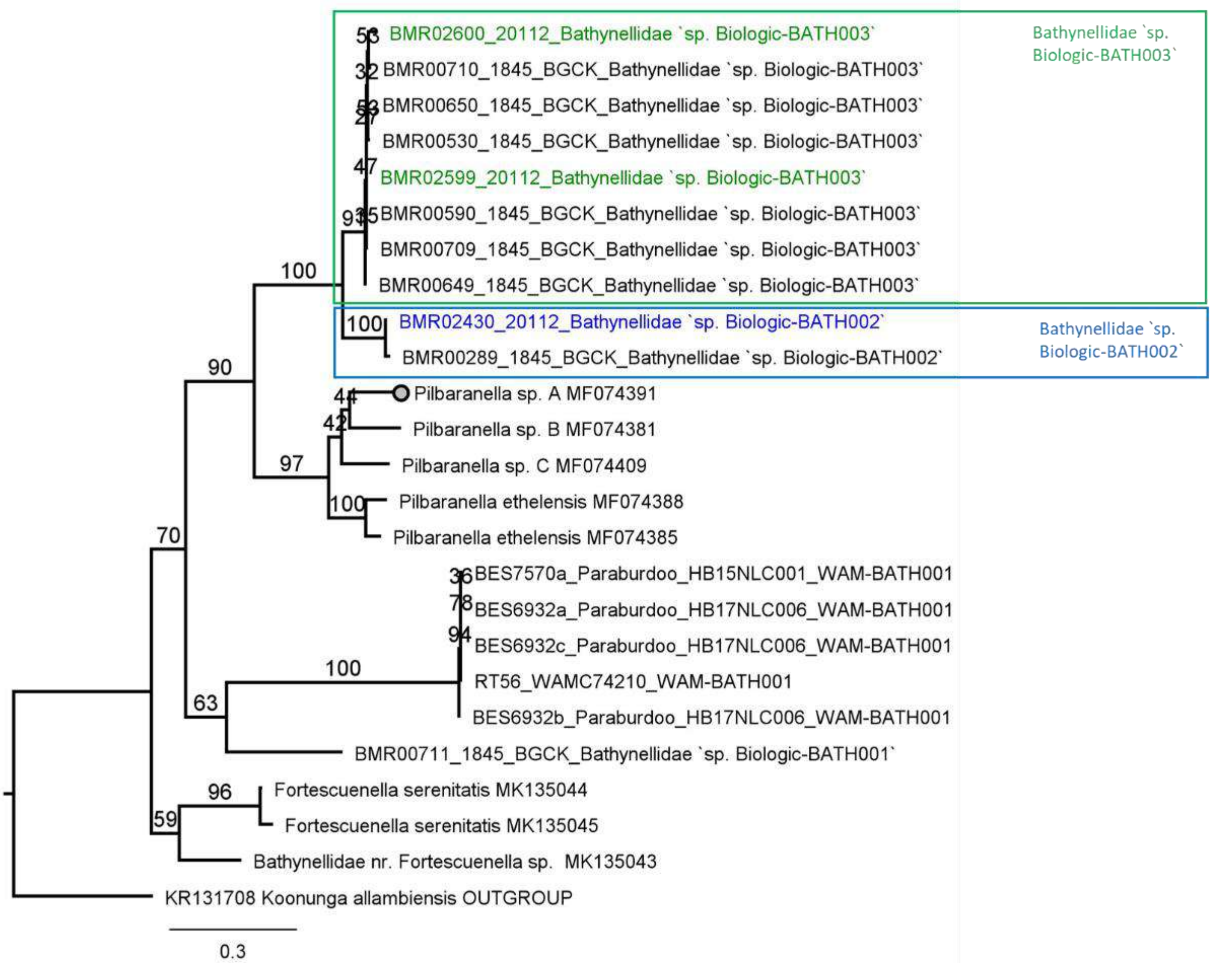


Figure 16: Phylogenetic tree of Bathynellidae. Newly added sequences are denoted with 20112 after the BMR number.

Malacostraca: Syncarida: Parabathynellidae

Of the 42 successfully sequenced parabathynellids, 24 matched three previously sequenced and delimited OTUs, Parabathynellidae `sp. Biologic-PBAT003`, Parabathynellidae `sp. Biologic-PBAT004`, and Parabathynellidae `sp. Biologic-PBAT005` (Figure 17). Fifteen specimens collected during the targeted surveys formed three new OTUs, Parabathynellidae `sp. Biologic-PBAT012`, *Atopobathynella* `sp. Biologic-PBAT013`, and Parabathynellidae `sp. Biologic-PBAT022`. The three specimens from the original survey that were included in this analysis matched one of these new OTUs, *Atopobathynella* `sp. Biologic-PBAT013`, and formed a new OTU, *Atopobathynella* `sp. Biologic-PBAT014`. Intra- and interspecific genetic distances are provided in Appendix B.

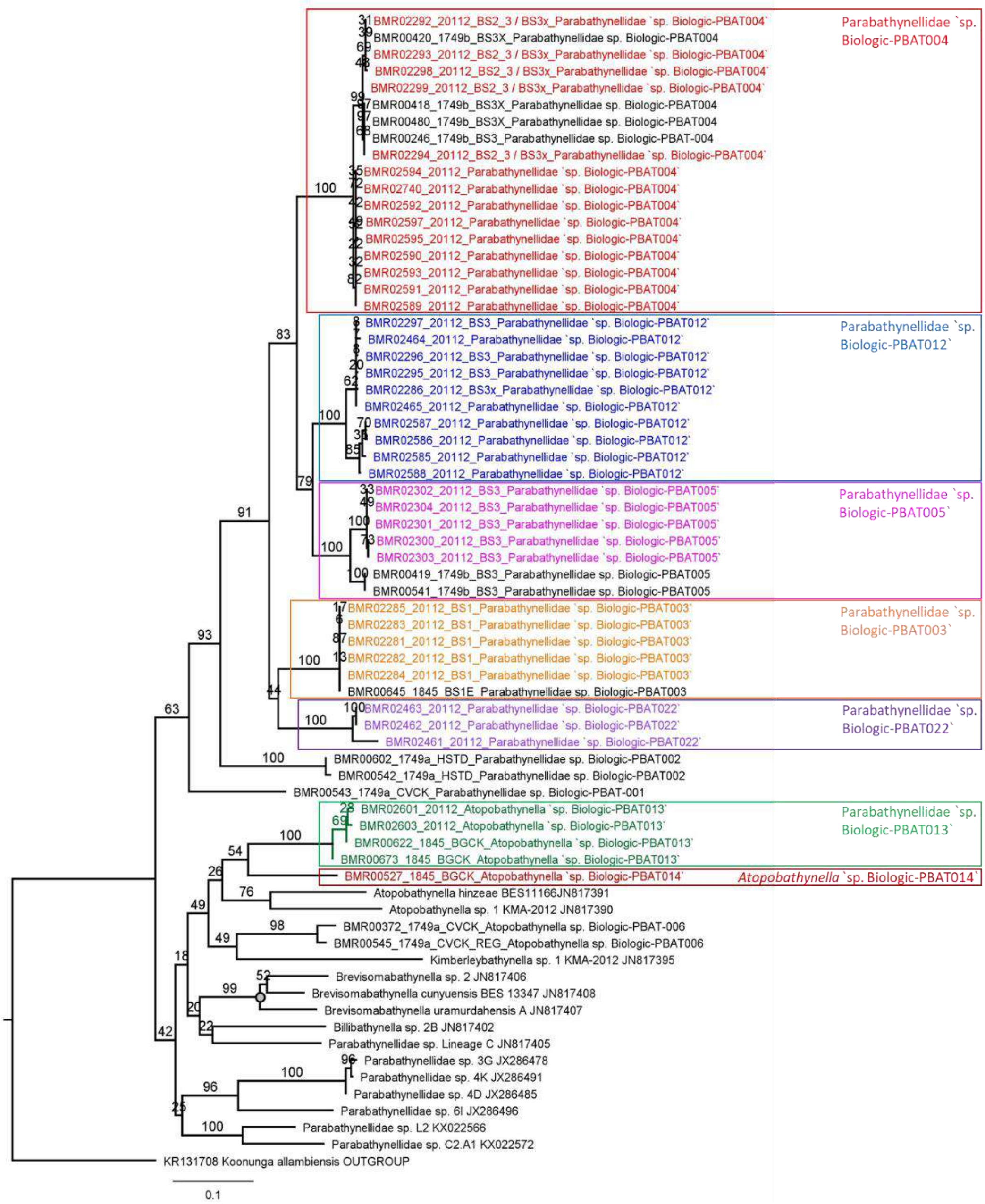


Figure 17: Phylogenetic tree of Parabathynellidae. Newly added sequences are denoted with 20112 after the BMR number.

Pauropoda

There were six successfully sequenced Pauropod specimens. One of these specimens matched the previously sequenced Pauropoda `sp. Biologic-PAUR008`. The remaining five specimens formed singleton OTUs (Figure 18).

In addition to analysing newly sequenced specimens, OTUs delimited in Biologic (2020) were BLASTed to discover new matches, with sequences that were not available at the time of that analysis. Two OTUs matched newly available sequences from GenBank, Pauropoda `sp. Biologic-PAUR004` and Pauropoda `sp. Biologic-PAUR009` (denoted with dashed boxes in Figure 18). Both of these GenBank specimens were collected from Rocklea Station, ~45 km NNE of Paraburdoo. This means that the linear distances for Pauropoda `sp. Biologic-PAUR004` is now 45.5 km, and 45.0 km for Pauropoda `sp. Biologic-PAUR009`.

In addition to these new matches, three of the specimens delimited in Biologic (2020) matched non-pauropod sequences. Pauropoda `sp. Biologic-PAUR001` (BMR00252) BLASTed within 8-10% of sequences of Cecidomyiidae, a family of Diptera (flies), and a subsequenct phylogenetic analysis found BMR00252 was nested within this family. Pauropoda `sp. Biologic-PAUR002` (BMR00421) BLASTed with 12-13% of Chironomidae specimens, another family of Diptera. Both of these specimens likely represent contamination and the OTUs Pauropoda `sp. Biologic-PAUR001` and Pauropoda `sp. Biologic-PAUR002`have been removed from the analyses.

Pauropoda `sp. Biologic-PAUR003` (BMR00255) was found to have an identical sequence to a Palpigradi specimen (BMR00251, Palpigradi `sp. Biologic-PALP-13`). This would extend the linear distance of Palpigradi `sp. Biologic-PALP-13` from 7.5 km to 15.4 km, and from being restricted to Vivash, to also including BS1. This is an unusual distribution for a palpigrade, especially with no genetic distance between sequences in such distant locations. In addition, misidentifying a Palpigradi and a Pauropoda is unlikely. We conclude that the specimen BMR00255 has been contaminated, and as such the OTU Pauropoda `sp. Biologic-PAUR003` has been removed from the analyses. Intra- and interspecific genetic distances are provided in Appendix B.

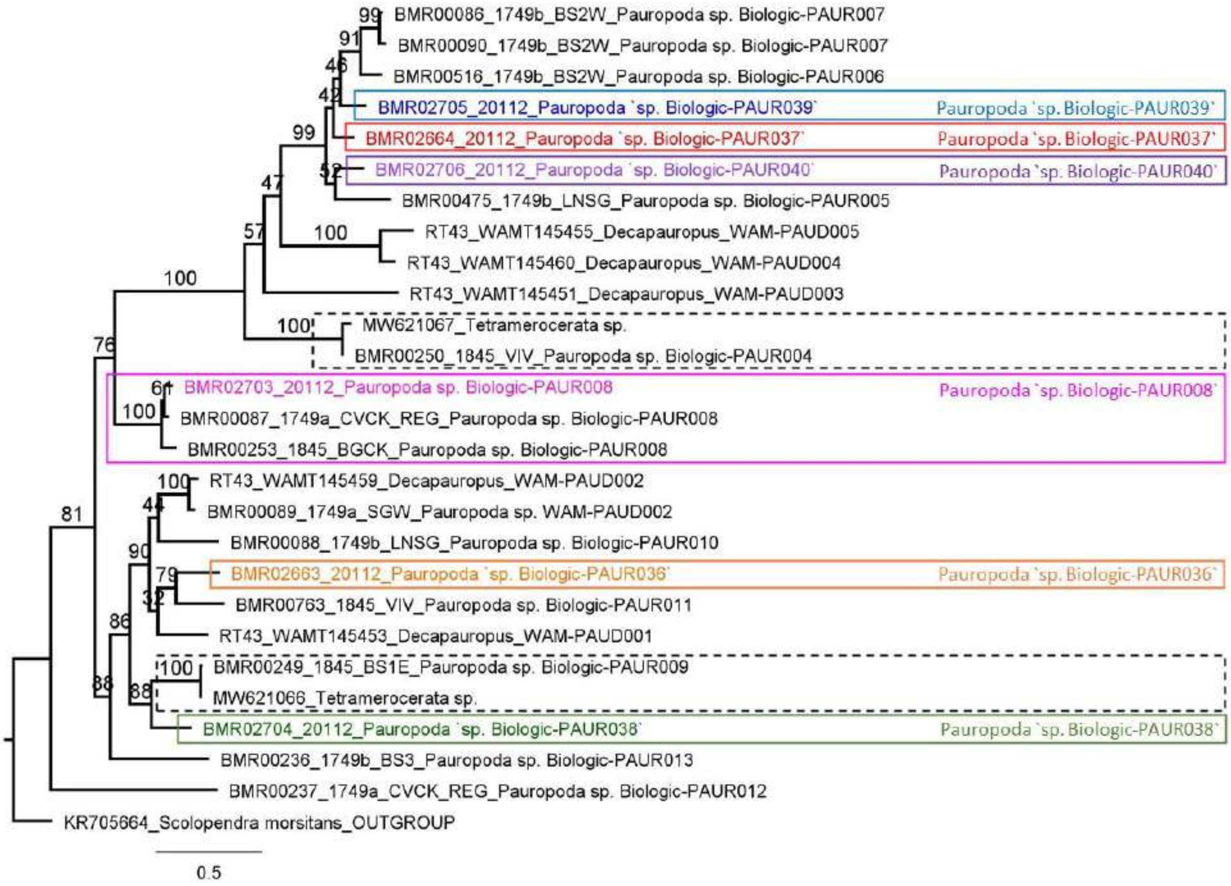


Figure 18: Phylogenetic tree of Pauropoda. Newly added sequences are denoted with 20112 after the BMR number. The dashed boxes represent newly discovered matches to OTUs delimited in Biologic (2020).

Symphyla: Cephalostigmata: Scutigerellidae

Five Symphyla specimens were successfully sequenced. Two of these specimens matched the previously delimited *Hanseniella* `sp. Biologic-SYMP003` (Figure 19). The remaining three specimens all formed unique, singleton OTUs. Intra- and interspecific genetic distances are provided in Appendix B.

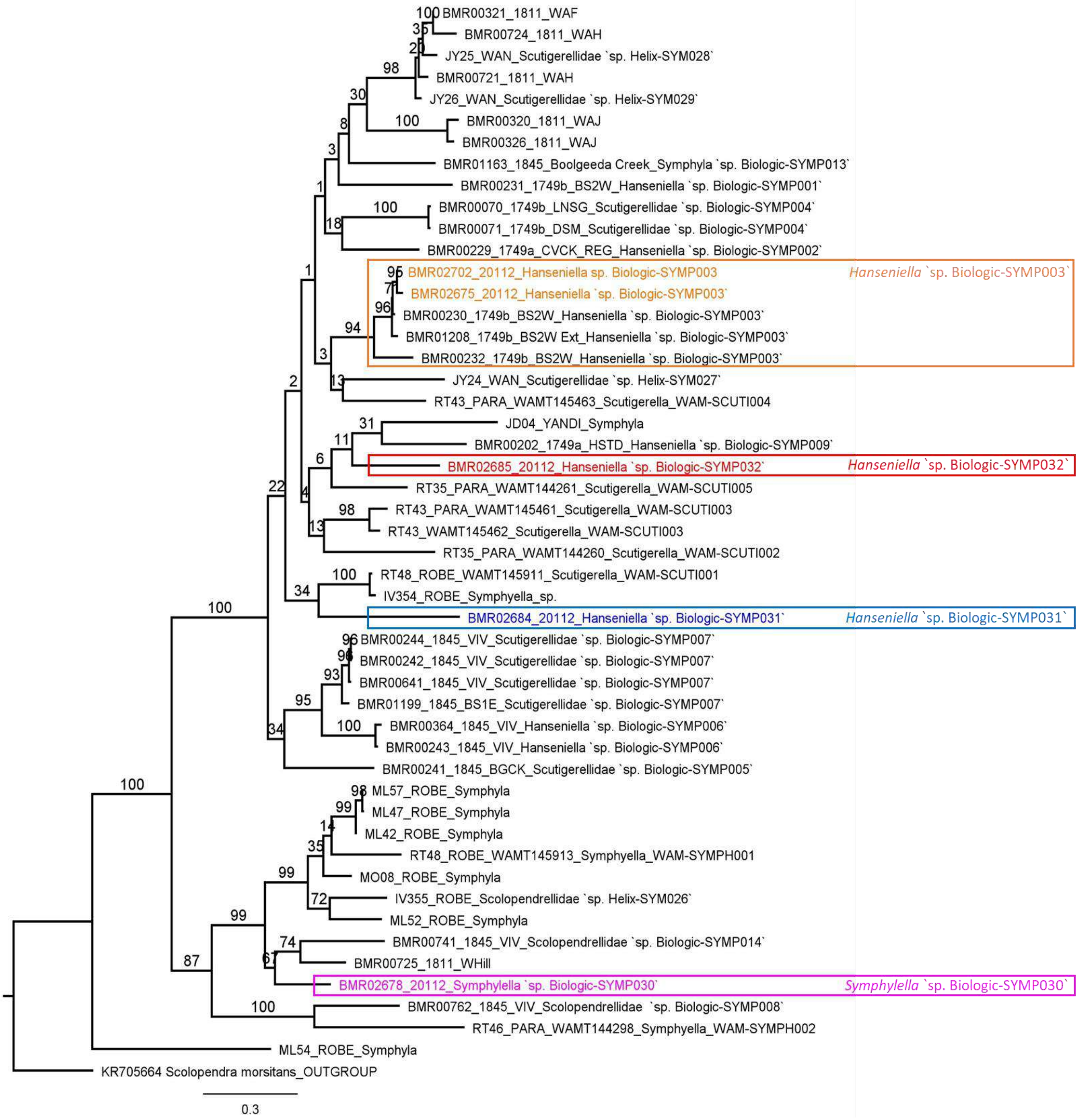


Figure 19: Phylogenetic tree of Scutigerellidae. Newly added sequences are denoted with 20112 after the BMR number.

Summary

In total, 62 OTUs were delimited from 158 specimens.

- Arachnida: Araneae – Two OTUs, one matching a previously sequenced OTU from the Study Area, the other new to the Study Area. All restricted to the Study Area.
- Arachnida: Palpigradi – Three OTUs, all new and restricted to the Study Area.
- Arachnida: Scopiones – One OTU, new and restricted to the Study Area.
- Clitellata: Enchytraeida – Enchytraeidae: Nine OTUs, five matching a previously sequenced OTUs from the Study Area, of which three are restricted to the Study Area. Two of the five matching a previously sequenced OTUs from the Study Area match sequences outside the Study Area. Four OTUs are new and restricted to the Study Area.
- Clitellata: Haplotaxida – Phreodrilidae: Three OTUs, two matching previously sequenced OTUs from the Study Area, of which one is restricted to the Study Area and the other matches sequences outside the Study Area. The final OTU in new and restricted to the Study Area.
- Diplopoda – Two OTUs, one new and restricted to the Study Area, the other new to the Study Area and matching sequences outside the Study Area. Also, one re-delimitation of a previously sequenced OTU.
- Entognatha: Diplura – Six OTUs, five new and restricted to the Study Area. The final OTU matches a preciously sequenced specimen but is restricted to the Study Area.
- Hexanauplia – Two OTUs, both new and restricted to the Study Area.
- Insecta: Coleoptera: Carabidae – Two OTUs, one matching a previously sequenced OTU restricted to the Study Area, and another matching a widespread OTU.
- Insecta: Zygentoma: Nicoletiidae – Five OTUs, four new and restricted to the Study Area, with the final matching a previously sequenced OTU and restricted to the Study Area.
- Malacostraca: Amphipoda: Bogidiellidae – One OTU, matching a previously sequenced OTU restricted to the Study Area.
- Malacostraca: Amphipoda: Eriopisidae – Two OTUs, one new and restricted to Study Area, one matching previously sequenced OTU that is not restricted to the Study Area.
- Malacostraca: Amphipoda: Paramelitidae – Four OTUs, two matching previously sequenced OTUs, and two new. All are restricted to the Study Area.
- Malacostraca: Isopoda: Microcerberidae: One OTU, new and restricted to the Study Area.
- Malacostraca: Syncarida: Bathynellidae – Two OTUs, both matching previously sequenced OTUs which are restricted to the Study Area.
- Malacostraca: Syncarida: Parabathynellidae – Seven OTUs, three matching previously sequenced OTUs. The remaining four are newly sequenced OTUs. All OTUs are restricted to the Study Area.
- Pauropoda – Six OTUs, five newly sequenced OTUs, with the final OTU matching a previously sequenced OTU. All OTUs are restricted to the Study Area. Two OTUs sequenced previously

detected new matches to specimens outside of the Study Area. Three previously sequenced OTUs have been identified as contamination.

- Symphyla: Cephalostigmata: Scutigerellidae – Four OTUs, three new and one matching a previously sequenced OTU. All OTUs are restricted to the Study Area.

References

Biologic. (2020). *Greater Brockman Subterranean Fauna Survey Molecular Systematics Analysis*. Unpublished report prepared for RTIO. Biologic Environmental Survey, East perth, WA.

Brown, L., Finston, T., Humphreys, G., Eberhard, S., & Pinder, A. (2015). Groundwater oligochaetes show complex genetic patterns of distribution in the Pilbara region of Western Australia. *Invertebrate Systematics, 29*(5), 405-420.

Cullen, K., & Harvey, M. (2018). *Molecular Systematics of Subfauna from Greater Paraburdoo – Final Report*. Unpublished report prepared for Rio Tinto Iron Ore.

Katoh, K., Misawa, K., Kuma, K., & Miyata, T. (2002). MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. *Nucleic Acids Research, 30*(14), 3059-3066.

King, R., Fagan-Jeffries, E., Bradford, T., Stringer, D., Finston, T., Halse, S., . . . Cooper, S. (2021). Cryptic Diversity Down Under: defining species in the subterranean amphipod genus Nedsia Barnard and Williams (Hadzioidea: Eriopisidae) from the Pilbara, Western Australia. *Invertebrate Systematics*.

Stamatakis, A. (2014). RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics, 30*(9), 1312-1313.

Appendix A: Specimen details

BMR	Unique ID code	Site	Latitude	Longitude	Lowest_ID_Legacy	OTU_Name	Reaction_State
Arachnida: Araneae							
BMR02693	8154	RC17BS1E0302	-22.522	117.161	Araneae sp.		FAIL; PCR
BMR02692	10520	RC06BS3M023	-22.537	117.423	Oonopidae sp.	Oonopidae `sp. Biologic-ARAN023`	PASS
BMR02667	8248	RC11BS3201	-22.519	117.427	Prodidominae sp.	Gnaphosidae `sp. Biologic-ARAN006`	PASS
Arachnida: Palpigradi							
BMR02660	10769	RC06BS3M023	-22.537	117.423	Palpigradi sp.	Palpigradi `sp. Biologic-PALP031`	PASS
BMR02661	10869	RC19BS3X0365	-22.476	117.464	Palpigradi sp.	Palpigradi `sp. Biologic-PALP032`	PASS
BMR02701	11144	GBODSMKARA02	-22.488	117.463	Palpigradi sp.	Palpigradi `sp. Biologic-PALP033`	PASS
Arachnida: Scopiones							
BMR02659	11137	RC06BS3M019	-22.532	117.426	Scorpiones sp.	Scorpiones `sp. Biologic-SCOR002`	PASS
Clitellata: Enchytraeida: Enchytraeidae							
BMR02275	8150	RC11BS3210	-22.517	117.428	Enchytraidae sp.	Enchytraeidae `sp. Biologic-OLIG004`	PASS
BMR02605	11197	GR19BS3X0048	-22.509	117.436	Enchytraeidae sp.	Enchytraeidae `sp. Biologic-OLIG006`	PASS
BMR02606	11107	GBODSMKARA05	-22.490	117.496	Enchytraeidae sp.	Enchytraeidae `sp. Biologic-OLIG016`	PASS
BMR02608	11159	RC19BS3X0292	-22.488	117.453	Enchytraeidae sp.		FAIL; PCR
BMR02609	11195	RC19BS3X0245	-22.477	117.458	Enchytraeidae sp.	Enchytraeidae `sp. Biologic-OLIG006`	PASS
BMR02610	8028	RC06BS1B005	-22.518	117.231	Enchytraeidae sp.	Enchytraeidae `sp. Biologic-OLIG052`	PASS
BMR02670	10577	RC19BS3X0297	-22.495	117.444	Enchytraeidae sp.	Enchytraeidae `sp. Biologic-OLIG006`	PASS
BMR02672	10939	GBOBS3xKARA03	-22.494	117.446	Enchytraeidae sp.	Enchytraeidae `sp. Biologic-OLIG022`	PASS
BMR02676	10568	GBOBS3KARA01	-22.563	117.408	Enchytraeidae sp.	Enchytraeidae `sp. E11`	PASS
BMR02677	10822	GBODSMKARA02	-22.488	117.463	Enchytraeidae sp.	Enchytraeidae `sp. Biologic-OLIG022`	PASS
BMR02713	10923	BS1_KARA07	-22.569	117.209	Enchytraeidae sp.	Enchytraeidae `sp. Biologic-OLIG017`	PASS
BMR02714	8331	BS1_KARA06	-22.574	117.195	Enchytraeidae sp.	Enchytraeidae `sp. Biologic-OLIG053`	PASS
BMR02716	10944	BS1_Kara02	-22.575	117.190	Enchytraeidae sp.	Enchytraeidae `sp. Biologic-OLIG055`	PASS
BMR02720	11119	RC19BS3X0327	-22.504	117.442	Enchytraeidae sp.	Enchytraeidae `sp. Biologic-OLIG016`	PASS
BMR02737	11178	GBODSMKARA01	-22.491	117.473	Enchytraeidae sp.	Enchytraeidae `sp. Biologic-OLIG006`	PASS
BMR02739	10583	GBOBS3xKARA02	-22.490	117.451	Enchytraeidae sp.	Enchytraeidae `sp. Biologic-OLIG022`	PASS
BMR02741	10758	GBODSMKARA03	-22.486	117.458	Enchytraeidae sp.	Enchytraeidae `sp. Biologic-OLIG022`	PASS
Clitellata: Haplotaxida: Phreodrilidae							
BMR02269	8269	MB19BS1E0005	-22.511	117.212	Phreodrilidae sp.	Phreodrilidae `sp. P12`	PASS
BMR02270	9406	RC17BS1E0304	-22.524	117.161	Phreodrilidae sp.	Phreodrilidae `sp. P12`	PASS
BMR02271	9053	RC17BS1E0304	-22.524	117.161	Phreodrilidae sp.	Phreodrilidae `sp. P12`	PASS
BMR02272	8315	MB19BS30005	-22.569	117.397	Phreodrilidae sp.	Phreodrilidae `sp. P12`	PASS
BMR02273	9007	MB19BS30005	-22.569	117.397	Phreodrilidae sp.	Phreodrilidae `sp. P12`	PASS
BMR02274	8991	MB19BS30005	-22.569	117.397	Phreodrilidae sp.	Phreodrilidae `sp. P12`	PASS
BMR02671	8428	BS1_KARA06	-22.574	117.195	Phreodrilidae sp.	Phreodrilidae `sp. Biologic-OLIG011`	PASS
BMR02673	11257	RC19BS3X0337	-22.531	117.426	Phreodrilidae sp.	Phreodrilidae `sp. P12`	PASS
BMR02674	9914	RC19BS3X0354	-22.482	117.458	Phreodrilidae sp.	Phreodrilidae `sp. P12`	PASS
BMR02694	9971	GR19BS3X0047	-22.529	117.425	Antarctodrilus sp.		FAIL; PCR
BMR02715	8033	MB19BS30003	-22.573	117.391	Phreodrilidae sp.	Phreodrilidae `sp. 12`	PASS
BMR02721	10628	BS1_Kara02	-22.575	117.190	Antarctodrilus sp.	Antarctodrilus `sp. Biologic-OLIG054`	PASS
BMR02738	10266	RC16BSSM0098	-22.476	117.472	Phreodrilidae sp.	Phreodrilidae `sp. 12`	PASS
BMR04105	12053	MB19BS1E0005	-22.511	117.212	Phreodrilidae sp.	Phreodrilidae `sp. P12`	PASS
BMR04106	12066	MB19BS1E0015	-22.518	117.191	Phreodrilidae sp.	Phreodrilidae `sp. P12`	PASS
Diplopoda							
BMR02669	10815	GBODSMKARA05	-22.490	117.496	Diplopoda sp.	Polyxenida `sp. Biologic-POLX006`	PASS
BMR02708	10073	RC19BS3X0354	-22.482	117.458	Diplopoda sp.	Polydesmida `sp. Biologic-POLD002`	PASS
Entognatha: Diplura							

BMR02653	9213	MB19BS30002	-22.575	117.388	Japygidae sp.	Japygidae `sp. Biologic-DIPL027`	PASS
BMR02654	10326	RC11BS3209	-22.517	117.429	Japygidae sp.	Japygidae `sp. Biologic-DIPL028`	PASS
BMR02655	10633	RC19BS3X0364	-22.477	117.465	Japygidae sp.	Japygidae `sp. Biologic-DIPL028`	PASS
BMR02656	10871	GBODSMKARA01	-22.491	117.473	Parajapygidae sp.	Parajapygidae `sp. Biologic-DIPL029`	PASS
BMR02657	11160	GBODSMKARA04	-22.490	117.496	Projapygidae sp.	Projapygidae `sp. Biologic-DIPL030`	PASS
BMR02658	10191	RC19BS3X0354	-22.482	117.458	Projapygidae sp.	Projapygidae `sp. Biologic-DIPL031`	PASS
BMR02662	11101	RC19BS3X0366	-22.481	117.453	Projapygidae sp.	Projapygidae `sp. Biologic-DIPL031`	PASS
BMR02690	11057	GBODSMKARA01	-22.491	117.473	Projapygidae sp.	Projapygidae `sp. Biologic-DIPL030`	PASS
BMR02691	10752	RC06BS3M023	-22.537	117.423	Projapygidae sp.	Projapygidae `sp. Biologic-DIPL032`	PASS
Hexanauplia							
BMR02280	9103	MB19BS3X0003	-22.520	117.426	Hexanauplia sp.	Copepoda `sp. Biologic-CALA002`	PASS
BMR04109	10832	RC20BS10636	-22.514	117.225	Diacyclops nr humphreysi	Diacyclops `sp. Biologic-CYCL029`	PASS
BMR04110	11585	PZ06BS4B004	-22.550	117.218	Diacyclops nr humphreysi		FAIL; bad seq
BMR04111	10918	MB20BS1W0009	-22.532	117.113	Diacyclops nr humphreysi		FAIL; bad seq
Insecta: Coleoptera: Carabidae							
BMR02668	8370	GR19BS3X0042	-22.496	117.444	Anillini sp.	Carabidae `sp. Biologic-COLE001`	PASS
Insecta: Zygentoma: Nicoletiidae							
BMR02682	10884	GBODSMKARA01	-22.491	117.473	Subnicoletiinae sp.	Subnicoletiinae `sp. Biologic-ZYGE024`	PASS
BMR02686	10564	RC06BS3M020	-22.532	117.425	Subnicoletiinae sp.	Subnicoletiinae `sp. Biologic-ZYGE025`	PASS
BMR02687	9904	BS1_Kara02	-22.575	117.190	Subnicoletiinae sp.	Subnicoletiinae `sp. Biologic-ZYGE026`	PASS
BMR02688	10514	RC06BS3M020	-22.532	117.425	Atelurinae sp.		FAIL; bad seq
BMR02689	10204	GBODSMKARA04	-22.490	117.496	Subnicoletiinae sp.	Subnicoletiinae `sp. Biologic-ZYGE027`	PASS
BMR02697	10763	RC06BS3M023	-22.537	117.423	Subnicoletiinae sp.	Nicoletiinae `sp. Biologic-ZYGE006	PASS
Malacostraca: Amphipoda: Bogidiellidae							
BMR04117	12364	MB20BS1W0009	-22.532	117.113	Bogidiellidae sp.	Bogidiellidae `sp. Biologic-AMPH011`	PASS
Malacostraca: Amphipoda: Eriopisidae							
BMR04112	12360	MB20BS1W0009	-22.532	117.113	Melitidae sp.	Nedsia `sp. Biologic-AMPH052`	PASS
BMR04114	12361	MB20BS1W0009	-22.532	117.113	Nedsia sp.	Nedsia nanutarra	PASS
Malacostraca: Amphipoda: Paramelitidae							
BMR02276	8378	MB19BS30008	-22.561	117.406	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02277	9145	RC17BS1E0133	-22.516	117.205	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Helix-AMP037`	PASS
BMR02278	8364	RC17BS1E0308	-22.522	117.167	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Helix-AMP037`	PASS
BMR02279	8134	RC17BS30052	-22.562	117.399	Paramelitidae indet.	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02305	8155	MB19BS3X0002	-22.532	117.428	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02306	8201	MB19BS3X0002	-22.532	117.428	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02307	10267	RC11BS3007	-22.491	117.446	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02308	10381	RC11BS3007	-22.491	117.446	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02309	10382	RC11BS3007	-22.491	117.446	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02310	10383	RC11BS3007	-22.491	117.446	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02311	10384	RC11BS3007	-22.491	117.446	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02312	10385	RC11BS3007	-22.491	117.446	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02313	10386	RC11BS3007	-22.491	117.446	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02314	10387	RC11BS3007	-22.491	117.446	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02315	10388	RC11BS3007	-22.491	117.446	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02316	10389	RC11BS3007	-22.491	117.446	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02317	10390	RC11BS3007	-22.491	117.446	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02318	10391	RC11BS3007	-22.491	117.446	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02319	10149	MB19BS3X0001	-22.539	117.424	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02320	10392	MB19BS3X0001	-22.539	117.424	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02321	10393	MB19BS3X0001	-22.539	117.424	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02322	10394	MB19BS3X0001	-22.539	117.424	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Biologic-AMPH015`	PASS

BMR02323	10395	MB19BS3X0001	-22.539	117.424	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02324	10396	MB19BS3X0001	-22.539	117.424	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02325	8443	RC11BS3018	-22.498	117.441	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02326	10441	RC11BS3018	-22.498	117.441	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02327	10442	RC11BS3018	-22.498	117.441	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02328	10443	RC11BS3018	-22.498	117.441	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02329	10444	MB19BS3X0007	-22.489	117.453	Paramelitidae sp U3 plum setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02604	11154b	RC06BS3M024	-22.536	117.422	Paramelitidae sp. indet.	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02607	10004b	RC19BS3X0354	-22.482	117.458	Paramelitidae sp. indet.	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02680	10691	MB19BS3X0001	-22.539	117.424	Paramelitidae sp. U3 plum. setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02681	11133	RC19BS3X0338	-22.530	117.426	Paramelitidae sp. U3 plum. setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02683	11072	RC19BS3X0337	-22.531	117.426	Paramelitidae sp. U3 plum. setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02707	8095	MB19BS30003	-22.573	117.391	Paramelitidae sp. U3 plum. setae	Paramelitidae `sp. Biologic-AMPH047`	PASS
BMR02709	8061	RC19BS3X0295	-22.486	117.451	Paramelitidae sp. U3 plum. setae	Paramelitidae `sp. Biologic-AMPH048`	PASS
BMR02710	10004a	RC19BS3X0354	-22.482	117.458	Paramelitidae sp. U3 plum. setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02711	11154a	RC06BS3M024	-22.536	117.422	Paramelitidae sp. U3 plum. setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR02712	10207	RC19BS3X0335	-22.532	117.428	Paramelitidae sp. U3 plum. setae	Paramelitidae `sp. Biologic-AMPH015`	PASS
BMR04115	12362	MB20BS1W0009	-22.532	117.113	Paramelitidae sp.		FAIL; bad seq
BMR04116	12363	MB20BS1W0009	-22.532	117.113	Paramelitidae sp.	Paramelitidae `sp. Helix-AMP037`	PASS
BMR04118	12365	MB19BS1E0003	-22.516	117.205	Paramelitidae sp.	Paramelitidae `sp. Helix-AMP037`	PASS
BMR04119	12366	MB19BS1E0003	-22.516	117.205	Paramelitidae sp.	Paramelitidae `sp. Helix-AMP037`	PASS
Malacostraca: Isopoda: Microcerberidae							
BMR02331	8450	MB19BS3X0002	-22.532	117.428	Microcerberidae sp.	Microcerberidae `sp. Biologic-ISOP026`	PASS
Malacostraca: Syncarida: Bathynellidae							
BMR02430	10749	PZ06BS4B006	-22.566	117.224	Bathynellidae sp. indet.	Bathynellidae `sp. Biologic-BATH002`	PASS
BMR02599	10765a	BS1_Kara02	-22.575	117.190	Bathynellidae sp. indet.	Bathynellidae `sp. Biologic-BATH003`	PASS
BMR02600	10765b	BS1_Kara02	-22.575	117.190	Bathynellidae sp. indet.	Bathynellidae `sp. Biologic-BATH003`	PASS
Malacostraca: Syncarida: Parabathynellidae							
BMR00527	7410	BS4-KC08	-22.575	117.186	Atopobathynella sp.	Atopobathynella `sp. Biologic-PBAT014`	PASS
BMR00622	6814	BS4-KC02	-22.575	117.189	Atopobathynella sp.	Atopobathynella `sp. Biologic-PBAT013`	PASS
BMR00673	5503	BS4-KC01	-22.576	117.190	Atopobathynella sp.	Atopobathynella `sp. Biologic-PBAT013`	PASS
BMR02281	9110a	RC17BS1E0304	-22.524	117.161	Parabathynellidae nr. Brevisoma b.	Parabathynellidae `sp. Biologic-PBAT003`	PASS
BMR02282	9110b	RC17BS1E0304	-22.524	117.161	Parabathynellidae nr. Brevisoma b.	Parabathynellidae `sp. Biologic-PBAT003`	PASS
BMR02283	9110c	RC17BS1E0304	-22.524	117.161	Parabathynellidae nr. Brevisoma b.	Parabathynellidae `sp. Biologic-PBAT003`	PASS
BMR02284	9110d	RC17BS1E0304	-22.524	117.161	Parabathynellidae nr. Brevisoma b.	Parabathynellidae `sp. Biologic-PBAT003`	PASS
BMR02285	9110e	RC17BS1E0304	-22.524	117.161	Parabathynellidae nr. Brevisoma b.	Parabathynellidae `sp. Biologic-PBAT003`	PASS
BMR02286	8093	MB19BS3X0002	-22.532	117.428	Parabathynellidae nr. Brevisoma b.	Parabathynellidae `sp. Biologic-PBAT012`	PASS
BMR02292	10261a	RC11BS3007	-22.491	117.446	Parabathynellidae nr. Brevisoma b.	Parabathynellidae `sp. Biologic-PBAT004`	PASS
BMR02293	10261b	RC11BS3007	-22.491	117.446	Parabathynellidae nr. Brevisoma b.	Parabathynellidae `sp. Biologic-PBAT004`	PASS
BMR02294	10261c	RC11BS3007	-22.491	117.446	Parabathynellidae nr. Brevisoma b.	Parabathynellidae `sp. Biologic-PBAT004`	PASS
BMR02295	8362a	MB19BS3X0001	-22.539	117.424	Parabathynellidae nr. Brevisoma b.	Parabathynellidae `sp. Biologic-PBAT012`	PASS
BMR02296	8362b	MB19BS3X0001	-22.539	117.424	Parabathynellidae nr. Brevisoma b.	Parabathynellidae `sp. Biologic-PBAT012`	PASS
BMR02297	8362c	MB19BS3X0001	-22.539	117.424	Parabathynellidae nr. Brevisoma b.	Parabathynellidae `sp. Biologic-PBAT012`	PASS
BMR02298	8275a	GR19BS3X0042	-22.496	117.444	Parabathynellidae nr. Brevisoma b.	Parabathynellidae `sp. Biologic-PBAT004`	PASS
BMR02299	8275b	GR19BS3X0042	-22.496	117.444	Parabathynellidae nr. Brevisoma b.	Parabathynellidae `sp. Biologic-PBAT004`	PASS
BMR02300	8393a	RC17BS30052	-22.562	117.399	Parabathynellidae nr. Brevisoma b.	Parabathynellidae `sp. Biologic-PBAT005`	PASS
BMR02301	8393b	RC17BS30052	-22.562	117.399	Parabathynellidae nr. Brevisoma b.	Parabathynellidae `sp. Biologic-PBAT005`	PASS
BMR02302	8393c	RC17BS30052	-22.562	117.399	Parabathynellidae nr. Brevisoma b.	Parabathynellidae `sp. Biologic-PBAT005`	PASS
BMR02303	8393d	RC17BS30052	-22.562	117.399	Parabathynellidae nr. Brevisoma b.	Parabathynellidae `sp. Biologic-PBAT005`	PASS
BMR02304	8393e	RC17BS30052	-22.562	117.399	Parabathynellidae nr. Brevisoma b.	Parabathynellidae `sp. Biologic-PBAT005`	PASS
BMR02288	10325b	MB19BS3X0007	-22.489	117.453	Parabathynellidae nr. Brevisoma b.		FAIL; bad seq

BMR02289	10325c	MB19BS3X0007	-22.489	117.453	Parabathynellidae nr. Brevisoma b.		FAIL; bad seq
BMR02290	10325d	MB19BS3X0007	-22.489	117.453	Parabathynellidae nr. Brevisoma b.		FAIL; bad seq
BMR02287	10325a	MB19BS3X0007	-22.489	117.453	Parabathynellidae nr. Brevisoma b.		FAIL; contamination
BMR02291	10325e	MB19BS3X0007	-22.489	117.453	Parabathynellidae nr. Brevisoma b.		FAIL; contamination
BMR02330	10082	MB19BS3X0009	-22.483	117.459	Parabathynellidae nr. Brevisoma b.		FAIL; contamination
BMR02461	10698a	PZ06BS4B006	-22.566	117.224	Parabathynellidae nr. Brevisomabathynella sp. indet.	Parabathynellidae `sp. Biologic-PBAT022`	PASS
BMR02462	10698b	PZ06BS4B006	-22.566	117.224	Parabathynellidae nr. Brevisomabathynella sp. indet.	Parabathynellidae `sp. Biologic-PBAT022`	PASS
BMR02463	10698c	PZ06BS4B006	-22.566	117.224	Parabathynellidae nr. Brevisomabathynella sp. indet.	Parabathynellidae `sp. Biologic-PBAT022`	PASS
BMR02464	11198	MB19BS3X0002	-22.532	117.428	Parabathynellidae nr. Brevisomabathynella sp. indet.	Parabathynellidae `sp. Biologic-PBAT012`	PASS
BMR02465	10747	RC19BS3X0337	-22.531	117.426	Parabathynellidae nr. Brevisomabathynella sp. indet.	Parabathynellidae `sp. Biologic-PBAT012`	PASS
BMR02585	10271a	GR19BS3X0047	-22.529	117.425	Parabathynellidae nr. Brevisomabathynella sp. indet.	Parabathynellidae `sp. Biologic-PBAT012`	PASS
BMR02586	10271b	GR19BS3X0047	-22.529	117.425	Parabathynellidae nr. Brevisomabathynella sp. indet.	Parabathynellidae `sp. Biologic-PBAT012`	PASS
BMR02587	10271c	GR19BS3X0047	-22.529	117.425	Parabathynellidae nr. Brevisomabathynella sp. indet.	Parabathynellidae `sp. Biologic-PBAT012`	PASS
BMR02588	10271d	GR19BS3X0047	-22.529	117.425	Parabathynellidae nr. Brevisomabathynella sp. indet.	Parabathynellidae `sp. Biologic-PBAT012`	PASS
BMR02589	11104	RC19BS3X0366	-22.481	117.453	Parabathynellidae nr. Brevisomabathynella sp. indet.	Parabathynellidae `sp. Biologic-PBAT004`	PASS
BMR02590	11184a	MB19BS3X0007	-22.489	117.453	Parabathynellidae nr. Brevisomabathynella sp. indet.	Parabathynellidae `sp. Biologic-PBAT004`	PASS
BMR02591	11184b	MB19BS3X0007	-22.489	117.453	Parabathynellidae nr. Brevisomabathynella sp. indet.	Parabathynellidae `sp. Biologic-PBAT004`	PASS
BMR02592	11184c	MB19BS3X0007	-22.489	117.453	Parabathynellidae nr. Brevisomabathynella sp. indet.	Parabathynellidae `sp. Biologic-PBAT004`	PASS
BMR02593	10016a	RC19BS3X0354	-22.482	117.458	Parabathynellidae nr. Brevisomabathynella sp. indet.	Parabathynellidae `sp. Biologic-PBAT004`	PASS
BMR02594	10016b	RC19BS3X0354	-22.482	117.458	Parabathynellidae nr. Brevisomabathynella sp. indet.	Parabathynellidae `sp. Biologic-PBAT004`	PASS
BMR02595	10016c	RC19BS3X0354	-22.482	117.458	Parabathynellidae nr. Brevisomabathynella sp. indet.	Parabathynellidae `sp. Biologic-PBAT004`	PASS
BMR02597	10016e	RC19BS3X0354	-22.482	117.458	Parabathynellidae nr. Brevisomabathynella sp. indet.	Parabathynellidae `sp. Biologic-PBAT004`	PASS
BMR02601	10765c	BS1_Kara02	-22.575	117.190	Atopobathynella sp. indet.	Atopobathynella `sp. Biologic-PBAT013`	PASS
BMR02602	10765d	BS1_Kara02	-22.575	117.190	Atopobathynella sp. indet.		FAIL; PCR
BMR02603	10765e	BS1_Kara02	-22.575	117.190	Atopobathynella sp. indet.	Atopobathynella `sp. Biologic-PBAT013`	PASS
BMR02740	10325f	MB19BS3X0007	-22.489	117.453	Parabathynellidae nr. Brevisomabathynella sp. indet.	Parabathynellidae `sp. Biologic-PBAT004`	PASS
Pauropoda							
BMR02663	10753	GBODSMKARA02	-22.488	117.463	Pauropoda sp.	Pauropoda `sp. Biologic-PAUR036`	PASS
BMR02664	10994	RC19BS3X0207	-22.459	117.476	Pauropoda sp.	Pauropoda `sp. Biologic-PAUR037`	PASS
BMR02665	11074	RC11BS3010	-22.498	117.447	Pauropoda sp.		FAIL; PCR
BMR02703	10570	GBODSMKARA05	-22.490	117.496	Pauropoda sp.	Pauropoda sp. Biologic-PAUR008	PASS
BMR02704	10522	RC06BS3M023	-22.537	117.423	Pauropoda sp.	Pauropoda `sp. Biologic-PAUR038`	PASS
BMR02705	10209	RC11BS3225	-22.515	117.429	Pauropoda sp. indet.	Pauropoda `sp. Biologic-PAUR039`	PASS
BMR02706	8372	RC11BS3200	-22.519	117.428	Pauropoda sp. indet.	Pauropoda `sp. Biologic-PAUR040`	PASS
Symphyla: Cephalostigmata: Scutigerellidae							
BMR02675	11210	RC19BS3X0245	-22.477	117.458	Hanseniella sp.	Hanseniella `sp. Biologic-SYMP003`	PASS
BMR02678	10625	GBOBS3xKARA02	-22.490	117.451	Symphylella sp.	Symphylella `sp. Biologic-SYMP030`	PASS
BMR02684	11176	RC19BS3X0336	-22.531	117.427	Hanseniella sp.	Hanseniella `sp. Biologic-SYMP031`	PASS
BMR02685	10089	GBOBS3xKARA01	-22.488	117.453	Hanseniella sp.	Hanseniella `sp. Biologic-SYMP032`	PASS
BMR02702	11253	RC11BS3010	-22.498	117.447	Hanseniella sp.	Hanseniella sp. Biologic-SYMP003	PASS

Appendix B: Pairwise Genetic Distances for each taxon.

Arachnida: Araneae

COI Pairwise Distances (%)	BMR00121	BMR02667	BMR01114	LI29	RT15	BMR01123	BMR01229	RT43	BMR01126	BMR01217	IV275	KD01	KD02	HM15	HM17	HM19	HM16	HM20	KJ745209	BMR00122	BMR00240	BMR02692	BMR00707	IV345	IV346	BMR00248	IV272	RT27	RT48	BMR00238	BMR00239	BMR01117	BMR01118	IV276	BMR01125	RT31	RT48
BMR00121_1749b_BS2SW_Gnaphosidae `sp. Biologic-ARAN006`		3.3	12.8	16.6	16.0	16.9	16.9	16.7	17.0	17.0	16.4	17.5	17.6	22.0	22.0	24.1	20.4	20.8	21.7	21.7	22.3	21.4	22.0	22.2	22.2	22.3	23.6	21.0	24.0	24.9	24.9	22.3	23.3	23.7	21.3	25.0	25.2
BMR02667_20112_Gnaphosidae `sp. Biologic-ARAN006`	3.3		13.2	16.5	16.1	16.3	16.3	16.1	16.5	16.5	18.3	18.1	17.4	22.4	22.2	23.4	20.7	21.1	21.1	23.3	23.3	22.7	23.6	23.2	22.7	23.1	24.2	21.1	23.1	25.3	25.3	20.9	22.0	23.9	20.5	25.2	25.3
BMR01114_1845_VIV_Gnaphosidae `sp. Biologic-ARAN007`	12.8	13.2		14.3	17.0	17.5	17.5	17.3	17.3	17.3	16.4	18.7	18.5	21.3	21.3	20.3	22.0	22.5	21.3	23.1	21.7	25.3	22.5	24.6	24.6	23.9	23.6	22.9	24.9	24.2	24.2	23.9	24.2	24.2	24.2	26.8	26.4
LI29_RC16MEC0177-20170309-01_ROBE_Gnaphosidae	16.6	16.5	14.3		18.1	18.1	18.1	17.9	18.4	18.4	19.5	19.5	19.5	22.0	21.9	21.2	22.8	22.9	25.1	24.9	23.9	26.7	24.9	24.4	23.4	24.6	23.7	23.7	24.0	26.1	26.1	24.0	22.6	24.6	26.0	28.0	27.8
RT15_WAMT142824__MESA H_Gnaphosidae	16.0	16.1	17.0	18.1		18.5	18.5	18.2	18.2	18.2	19.0	19.1	19.3	20.4	20.4	21.7	20.4	20.4	24.2	21.3	22.0	23.1	22.6	23.2	22.5	23.6	25.4	23.3	25.8	23.6	23.6	21.3	21.1	21.8	22.9	26.4	26.1
BMR01123_1845_BS1E_Theridiidae `sp. WAM-ARAN001`	16.9	16.3	17.5	18.1	18.5		0.0	1.4	1.8	1.8	10.2	15.2	15.2	23.7	23.6	23.6	19.8	19.8	23.6	23.3	23.1	25.6	23.4	24.6	23.9	23.3	23.4	24.1	26.3	22.9	22.9	23.4	23.6	24.4	22.0	27.3	27.3
BMR01229_1845_BS1E_Theridiidae `sp. WAM-ARAN001`	16.9	16.3	17.5	18.1	18.5	0.0		1.4	1.8	1.8	10.2	15.2	15.2	23.7	23.6	23.6	19.8	19.8	23.6	23.3	23.1	25.6	23.4	24.6	23.9	23.3	23.4	24.1	26.3	22.9	22.9	23.4	23.6	24.4	22.0	27.3	27.3
RT43_WAMT144292_WAM-ARAN001	16.7	16.1	17.3	17.9	18.2	1.4	1.4		2.0	2.0	10.2	15.4	15.4	23.2	23.3	22.9	20.2	20.5	23.6	23.4	22.9	25.6	22.6	24.6	23.9	23.4	23.9	24.2	26.6	23.3	23.3	23.4	23.7	24.1	22.0	27.0	27.0
BMR01126_1845_VIV_Theridiidae `sp. WAM-ARAN001`	17.0	16.5	17.3	18.4	18.2	1.8	1.8	2.0		0.0	10.3	15.4	15.4	23.7	23.7	23.6	20.1	20.1	23.9	23.3	23.1	25.8	22.9	24.6	23.9	23.6	23.9	24.5	26.3	22.8	22.8	23.6	24.6	24.4	22.3	27.9	27.9
BMR01217_1845_Boolgeeda Creek_Theridiidae `sp. WAM-ARAN001`	17.0	16.5	17.3	18.4	18.2	1.8	1.8	2.0	0.0		10.3	15.4	15.4	23.7	23.7	23.6	20.1	20.1	23.9	23.3	23.1	25.8	22.9	24.6	23.9	23.6	23.9	24.5	26.3	22.8	22.8	23.6	24.6	24.4	22.3	27.9	27.9
IV275_127039_ROBE_Araneae	16.4	18.3	16.4	19.5	19.0	10.2	10.2	10.2	10.3	10.3		16.6	16.6	22.4	22.0	22.4	20.2	20.7	23.6	23.4	24.0	25.8	21.9	24.4	24.4	23.1	24.8	24.1	26.1	23.7	23.7	24.2	25.4	23.6	22.8	28.2	27.9
KD01_GR15MEB0014.20160915.T1-01_ROBE_Aeaneae	17.5	18.1	18.7	19.5	19.1	15.2	15.2	15.4	15.4	15.4	16.6		0.9	23.6	23.3	22.0	18.5	19.3	22.5	22.5	24.3	24.9	21.9	22.2	22.5	22.2	22.3	22.0	24.3	24.2	24.2	23.6	23.3	24.2	23.1	26.4	26.3
KD02_RC15MEC0001.20160915.T1-01_ROBE_Araneae	17.6	17.4	18.5	19.5	19.3	15.2	15.2	15.4	15.4	15.4	16.6	0.9		23.7	23.4	21.7	18.4	18.8	21.9	22.6	24.6	25.1	21.9	22.5	22.7	22.5	21.9	21.4	23.7	23.6	23.6	22.9	22.9	23.9	22.5	26.2	26.1
HM15_M20130913_HD_Araneae	22.0	22.4	21.3	22.0	20.4	23.7	23.7	23.2	23.7	23.7	22.4	23.6	23.7		0.3	0.5	18.3	18.6	20.2	23.4	23.2	26.4	22.9	22.1	21.9	22.6	22.8	21.1	24.8	24.8	24.8	24.4	24.2	23.2	25.3	26.7	26.6
HM16_M20130914_HD_Araneae	20.4	20.7	22.0	22.8	20.4	19.8	19.8	20.2	20.1	20.1	20.2	18.5	18.4	18.3	18.2	16.9		1.5	19.0	21.3	21.4	24.9	22.9	23.2	22.9	22.3	21.6	21.7	23.7	23.9	23.9	24.6	24.0	24.4	23.6	27.6	27.6
HM20_M20130914_HD_Araneae	20.8	21.1	22.5	22.9	20.4	19.8	19.8	20.5	20.1	20.1	20.7	19.3	18.8	18.6	18.5	16.9	1.5		19.3	22.0	21.9	24.2	23.6	22.7	22.5	22.9	21.3	21.7	24.2	23.7	23.7	25.1	24.9	24.7	24.8	27.4	27.5
KJ745209_Aname mainae_OUTGROUP	21.7	21.1	21.3	25.1	24.2	23.6	23.6	23.6	23.9	23.9	23.6	22.5	21.9	20.2	19.9	18.1	19.0	19.3		24.6	22.3	25.6	22.2	21.7	22.0	22.2	22.0	23.3	26.1	26.0	26.0	24.9	25.8	26.5	25.7	27.3	26.7
BMR00122_1749b_BS3X_Prethopalpus `sp. Biologic-ARAN001`	21.7	23.3	23.1	24.9	21.3	23.3	23.3	23.4	23.3	23.3	23.4	22.5	22.6	23.4	22.8	23.9	21.3	22.0	24.6		16.6	15.2	17.8	19.9	18.9	22.8	20.7	20.9	23.7	26.1	26.1	26.3	26.7	28.2	27.5	23.8	24.0
BMR00240_1749b_BS2SW_Prethopalpus `sp. Biologic-ARAN002`	22.3	23.3	21.7	23.9	22.0	23.1	23.1	22.9	23.1	23.1	24.0	24.3	24.6	23.2	22.8	23.6	21.4	21.9	22.3	16.6		13.0	18.2	17.7	17.0	19.0	19.0	19.5	20.7	28.7	28.7	27.2	26.9	27.7	26.4	23.2	23.0
BMR02692_20112_Oonopidae `sp. Biologic-ARAN023`	21.4	22.7	25.3	26.7	23.1	25.6	25.6	25.6	25.8	25.8	25.8	24.9	25.1	26.4	25.6	25.5	24.9	24.2	25.6	15.2	13.0		19.2	15.6	15.8	19.8	19.6	18.9	21.4	25.3	25.3	24.7	24.2	26.3	24.4	19.8	20.7
BMR00707_HD2_Prethopalpus sp.	22.0	23.6	22.5	24.9	22.6	23.4	23.4	22.6	22.9	22.9	21.9	21.9	21.9	22.9	22.6	22.7	22.9	23.6	22.2	17.8	18.2	19.2		15.8	15.6	18.8	18.2	18.5	19.9	25.5	25.5	24.9	24.9	26.5	25.8	21.2	21.8
IV345_SSp-2010-253_DCBRC_017_ROBE_Araneae	22.2	23.2	24.6	24.4	23.2	24.6	24.6	24.6	24.6	24.6	24.4	22.2	22.5	22.1	21.3	21.7	23.2	22.7	21.7	19.9	17.7	15.6	15.8		1.4	20.1	18.2	19.4	22.0	24.6	24.6	24.4	24.6	26.9	23.4	23.0	23.6
IV346_SSp-2010-75_DCBRC_040_ROBE_Araneae	22.2	22.7	24.6	23.4	22.5	23.9	23.9	23.9	23.9	23.9	24.4	22.5	22.7	21.9	21.0	21.5	22.9	22.5	22.0	18.9	17.0	15.8	15.6	1.4		20.1	17.5	19.4	21.5	24.4	24.4	23.4	24.1	26.6	22.9	22.3	22.7
BMR00248_1845_VIV_Prethopalpus `sp. Biologic-ARAN016`	22.3	23.1	23.9	24.6	23.6	23.3	23.3	23.4	23.6	23.6	23.1	22.2	22.5	22.6	22.0	21.7	22.3	22.9	22.2	22.8	19.0	19.8	18.8	20.1	20.1		14.3	14.6	14.9	26.6	26.6	26.4	25.4	27.2	26.4	25.0	24.5
IV272_MEBRC0016P1T1-2_ROBE_Araneae	23.6	24.2	23.6	23.7	25.4	23.4	23.4	23.9	23.9	23.9	24.8	22.3	21.9	22.8	22.2	22.4	21.6	21.3	22.0	20.7	19.0	19.6	18.2	18.2	17.5	14.3		14.2	16.4	25.2	25.2	24.9	25.8	25.9	25.5	24.4	24.3
RT27_WAMT144200_MESA K_Opopaea	21.0	21.1	22.9	23.7	23.3	24.1	24.1	24.2	24.5	24.5	24.1	22.0	21.4	21.1	20.9	21.5	21.7	21.7	23.3	20.9	19.5	18.9	18.5	19.4	19.4	14.6	14.2		12.2	27.2	27.2	25.9	26.6	27.5	26.1	23.5	23.3
RT48_WAMT145789_Opopaea_WAM-OONO001	24.0	23.1	24.9	24.0	25.8	26.3	26.3	26.6	26.3	26.3	26.1	24.3	23.7	24.8	24.2	24.3	23.7	24.2	26.1	23.7	20.7	21.4	19.9	22.0	21.5	14.9	16.4	12.2		29.9	29.9	28.3	27.7	29.6	28.0	25.0	24.9
BMR00238_1749a_SGW_Symphytognathidae? `sp. Biologic-ARAN003	24.9	25.3	24.2	26.1	23.6	22.9	22.9	23.3	22.8	22.8	23.7	24.2	23.6	24.8	24.3	23.2	23.9	23.7	26.0	26.1	28.7	25.3	25.5	24.6	24.4	26.6	25.2	27.2	29.9		0.0	15.0	16.3	14.7	13.8	29.1	29.1
BMR00239_1749a_SGW_Symphytognathidae? `sp. Biologic-ARAN003	24.9	25.3	24.2	26.1	23.6	22.9	22.9	23.3	22.8	22.8	23.7	24.2	23.6	24.8	24.3	23.2	23.9	23.7	26.0	26.1	28.7	25.3	25.5	24.6	24.4	26.6	25.2	27.2	29.9	0.0		15.0	16.3	14.7	13.8	29.1	29.1
BMR01117_1845_BS1W_Araneae `sp. Biologic-ARAN005`	22.3	20.9	23.9	24.0	21.3	23.4	23.4	23.4	23.6	23.6	24.2	23.6	22.9	24.4	24.2	23.9	24.6	25.1	24.9	26.3	27.2	24.7	24.9	24.4	23.4	26.4	24.9	25.9	28.3	15.0	15.0		6.8	11.8	12.3	26.4	26.6
BMR01118_1845_BS1W_Araneae `sp. Biologic-ARAN005`	23.3	22.0	24.2	22.6	21.1	23.6	23.6	23.7	24.6	24.6	25.4	23.3	22.9	24.2	24.2	23.6	24.0	24.9	25.8	26.7	26.9	24.2	24.9	24.6	24.1	25.4	25.8	26.6	27.7	16.3	16.3	6.8		12.8	13.2	28.2	28.1
IV276_138441_ROBE_Araneae	23.7	23.9	24.2	24.6	21.8	24.4	24.4	24.1	24.4	24.4	23.6	24.2	23.9	23.2	23.6	24.8	24.4	24.7	26.5	28.2	27.7	26.3	26.5	26.9	26.6	27.2	25.9	27.5	29.6	14.7	14.7	11.8	12.8		13.3	28.9	29.4
BMR01125_1845_VIV_Araneae `sp. Biologic-ARAN004`	21.3	20.5	24.2	26.0	22.9	22.0	22.0	22.0	22.3	22.3	22.8	23.1	22.5	25.3	24.8	23.4	23.6	24.8	25.7	27.5	26.4	24.4	25.8	23.4	22.9	26.4	25.5	26.1	28.0	13.8	13.8	12.3	13.2	13.3		29.3	29.3
RT31_WAMT144637_MESAB_Oonopidae_Prethopalpus	25.0	25.2	26.8	28.0	26.4	27.3	27.3	27.0	27.9	27.9	28.2	26.4	26.2	26.7	27.0	27.4	27.6	27.4	27.3	23.8	23.2	19.8	21.2	23.0	22.3	25.0	24.4	23.5	25.0	29.1	29.1	26.4	28.2	28.9	29.3		1.5
RT48_WAMT145745_Prethopalpus_WAM-OONP001	25.2	25.3	26.4	27.8	26.1	27.3	27.3	27.0	27.9	27.9	27.9	26.3	26.1	26.6	26.4	26.5	27.6	27.5	26.7	24.0	23.0	20.7	21.8	23.6	22.7	24.5	24.3	23.3	24.9	29.1	29.1	26.6	28.1	29.4	29.3	1.5	

Arachnida: Palpigradi

COI Pairwise Distances (%)	BMR00521	T149404	BMR00251	BMR00499	BMR00084	BMR02660	BMR02661	BMR00172	BMR00168	T149280	BMR00085	WAMT145442	WAMT145439	KF823880	KF823878	JN018214	KF823876	BMR00091	BMR00092	BMR00094	BMR01221	BMR00093	KF823879	BMR02701	KF823874
BMR00521_1845_VIV_Palpigradi sp. Biologic-PALP009		10.1	22.3	24.3	21.4	24.4	23.5	24.6	24.6	24.7	27.9	30.2	27.0	27.4	26.6	26.4	28.4	30.2	31.3	30.7	30.7	31.0	28.1	29.0	26.5
T149404_BS1W_Palpigradi `sp. Biologic-PALP010`	10.1		22.3	22.6	22.9	23.1	23.2	24.9	26.1	24.6	29.8	31.0	27.8	28.3	26.5	26.0	27.2	32.2	32.5	31.8	31.8	31.6	28.7	31.3	25.2
BMR00251_1845_VIV_Palpigradi sp. Biologic-PALP013	22.3	22.3		7.2	13.3	15.0	16.8	23.4	24.9	22.6	29.3	30.5	29.9	27.8	30.3	27.3	30.3	35.1	35.7	34.5	34.7	34.4	30.4	32.8	25.8
BMR00499_1845_VIV_Palpigradi sp. Biologic-PALP013	24.3	22.6	7.2		14.8	15.9	18.3	23.8	25.6	23.8	30.2	32.1	30.2	28.9	30.3	27.8	29.5	34.8	35.7	35.1	35.1	34.7	31.0	33.3	26.5
BMR00084_1749b_BS3_Palpigradi sp. Biologic-PALP0012	21.4	22.9	13.3	14.8		15.9	18.0	22.9	24.3	21.2	28.4	29.9	29.0	27.2	30.1	29.2	30.0	33.1	34.0	33.3	33.4	33.3	28.2	31.0	26.1
BMR02660_20112_Palpigradi `sp. Biologic-PALP031`	24.4	23.1	15.0	15.9	15.9		17.9	25.6	27.0	22.7	29.9	32.7	30.7	30.1	31.0	28.7	30.0	35.1	36.6	35.7	35.7	35.3	30.4	33.5	27.8
BMR02661_20112_Palpigradi `sp. Biologic-PALP032`	23.5	23.2	16.8	18.3	18.0	17.9		25.2	26.0	23.8	30.2	33.0	31.9	27.2	30.1	27.8	31.2	33.7	34.2	33.3	33.1	34.4	30.8	32.6	27.4
BMR00172_1749b_BS2W_Palpigradi sp. Biologic-PALP007	24.6	24.9	23.4	23.8	22.9	25.6	25.2		15.7	19.4	24.1	26.4	26.6	22.5	24.8	27.0	31.0	28.2	29.6	28.4	28.4	28.7	30.2	27.1	28.0
BMR00168_1749b_DSM_Palpigradi sp. Biologic-PALP006	24.6	26.1	24.9	25.6	24.3	27.0	26.0	15.7		22.3	22.4	29.3	26.7	24.5	23.5	27.8	32.9	30.2	30.7	29.5	29.5	28.4	30.8	25.3	30.1
T149280_VIV_Palpigradi `sp. Biologic-PALP008`	24.7	24.6	22.6	23.8	21.2	22.7	23.8	19.4	22.3		25.2	28.2	26.7	24.5	27.2	28.4	29.8	30.4	30.7	29.3	29.6	29.3	29.3	28.2	26.6
BMR00085_1749a_SGW_Palpigradi sp. Biologic-PALP005	27.9	29.8	29.3	30.2	28.4	29.9	30.2	24.1	22.4	25.2		28.1	26.4	25.4	25.8	29.9	32.7	27.2	28.4	27.0	27.0	29.5	31.4	26.6	32.4
RT43_PARA_WAMT145442_Eukoenenia_WAM-PALE001	30.2	31.0	30.5	32.1	29.9	32.7	33.0	26.4	29.3	28.2	28.1		24.3	27.4	26.6	27.4	32.0	27.3	28.6	26.4	26.3	26.9	29.9	32.8	31.8
RT43_PARA_WAMT145439_Eukoenenia_WAM-PALE002	27.0	27.8	29.9	30.2	29.0	30.7	31.9	26.6	26.7	26.7	26.4	24.3		24.6	24.0	25.8	31.2	27.0	27.6	24.6	24.6	28.1	30.8	27.9	31.8
KF823880_Eukoenenia sp. MCZ IZ-134549	27.4	28.3	27.8	28.9	27.2	30.1	27.2	22.5	24.5	24.5	25.4	27.4	24.6		19.0	24.5	28.4	23.9	23.7	25.5	25.4	24.9	27.0	26.6	26.9
KF823878_Eukoenenia spelaea	26.6	26.5	30.3	30.3	30.1	31.0	30.1	24.8	23.5	27.2	25.8	26.6	24.0	19.0		21.1	25.2	24.6	25.5	23.5	23.4	23.9	26.2	27.1	28.7
JN018214_Palpigradi sp. 2	26.4	26.0	27.3	27.8	29.2	28.7	27.8	27.0	27.8	28.4	29.9	27.4	25.8	24.5	21.1		25.5	31.1	30.8	29.0	29.0	27.9	28.2	31.7	26.6
KF823876_Eukoenenia mirabilis	28.4	27.2	30.3	29.5	30.0	30.0	31.2	31.0	32.9	29.8	32.7	32.0	31.2	28.4	25.2	25.5		33.9	33.5	32.4	32.4	31.0	28.5	34.8	26.9
BMR00091_1749b_BS3X_Palpigradi sp. Biologic-PALP004	30.2	32.2	35.1	34.8	33.1	35.1	33.7	28.2	30.2	30.4	27.2	27.3	27.0	23.9	24.6	31.1	33.9		6.9	10.2	10.2	16.1	31.0	28.4	36.5
BMR00092_1749b_DSM_Palpigradi sp. Biologic-PALP004	31.3	32.5	35.7	35.7	34.0	36.6	34.2	29.6	30.7	30.7	28.4	28.6	27.6	23.7	25.5	30.8	33.5	6.9		10.8	11.1	16.7	31.1	29.5	36.4
BMR00094_1749b_BS3X_Palpigradi sp. Biologic-PALP003	30.7	31.8	34.5	35.1	33.3	35.7	33.3	28.4	29.5	29.3	27.0	26.4	24.6	25.5	23.5	29.0	32.4	10.2	10.8		0.6	15.3	31.6	28.2	36.4
BMR01221_1749b_BS2_3_Palpigradi sp. Biologic-PALP003	30.7	31.8	34.7	35.1	33.4	35.7	33.1	28.4	29.5	29.6	27.0	26.3	24.6	25.4	23.4	29.0	32.4	10.2	11.1	0.6		15.6	31.4	28.4	36.4
BMR00093_1749b_LNSG_Palpigradi sp. Biologic-PALP002	31.0	31.6	34.4	34.7	33.3	35.3	34.4	28.7	28.4	29.3	29.5	26.9	28.1	24.9	23.9	27.9	31.0	16.1	16.7	15.3	15.6		31.3	30.2	35.5
KF823879_Eukoenenia sp. MCZ IZ-19350	28.1	28.7	30.4	31.0	28.2	30.4	30.8	30.2	30.8	29.3	31.4	29.9	30.8	27.0	26.2	28.2	28.5	31.0	31.1	31.6	31.4	31.3		33.7	29.7
BMR02701_20112_Palpigradi `sp. Biologic-PALP033`	29.0	31.3	32.8	33.3	31.0	33.5	32.6	27.1	25.3	28.2	26.6	32.8	27.9	26.6	27.1	31.7	34.8	28.4	29.5	28.2	28.4	30.2	33.7		35.9
KF823874_Prokoenenia wheeleri_OUTGROUP	26.5	25.2	25.8	26.5	26.1	27.8	27.4	28.0	30.1	26.6	32.4	31.8	31.8	26.9	28.7	26.6	26.9	36.5	36.4	36.4	36.4	35.5	29.7	35.9	

Arachnida: Scopiones

COI Pairwise Distances (%)	BMR02659	MF061567	MF061568	MF061576	MN124066	KC347043	KC347061	KC347217	KC347075	KC347143	KC347287	KC347288	KC347079	KT447034	KT446958	KT446959	KT446962	KT446961	KT446960	KY295225	MT418091	MT418092	KT447038
BMR02659_20112_Scorpiones `sp. Biologic-SCOR002`		14.8	14.8	15.0	15.2	15.2	15.0	15.4	15.2	15.4	15.6	15.4	15.2	14.1	15.2	14.8	14.5	14.8	14.1	17.0	15.0	15.0	16.5
MF061567_Smeringurus vachoni	14.8		0.0	1.3	7.7	13.0	13.0	12.8	12.8	13.0	13.9	13.4	11.7	14.3	14.5	14.1	13.9	14.5	14.8	14.5	18.5	18.3	16.5
MF061568_Smeringurus vachoni	14.8	0.0		1.3	7.7	13.0	13.0	12.8	12.8	13.0	13.9	13.4	11.7	14.3	14.5	14.1	13.9	14.5	14.8	14.5	18.5	18.3	16.5
MF061576_Smeringurus vachoni	15.0	1.3	1.3		7.0	13.0	13.0	12.8	12.3	12.6	13.4	13.0	11.7	13.7	14.1	13.7	13.4	14.1	14.8	14.1	17.6	17.8	16.7
MN124066_Smeringurus mesaensis	15.2	7.7	7.7	7.0		13.2	12.3	12.6	11.9	12.1	12.6	12.1	12.3	14.1	13.4	13.9	13.7	14.5	14.1	15.9	17.4	17.6	17.2
KC347043_Hadrurus arizonensis	15.2	13.0	13.0	13.0	13.2		1.8	1.3	2.0	2.2	2.6	2.6	2.2	14.5	12.8	12.6	12.3	13.2	13.4	14.1	17.6	18.1	19.8
KC347061_Hadrurus arizonensis	15.0	13.0	13.0	13.0	12.3	1.8		0.9	2.0	1.8	2.2	2.2	2.2	14.1	13.7	13.4	13.2	14.1	13.0	14.5	16.7	17.8	19.2
KC347217_Hadrurus arizonensis	15.4	12.8	12.8	12.8	12.6	1.3	0.9		1.5	1.3	1.8	1.8	1.8	14.5	13.0	12.8	12.6	13.4	12.8	14.3	17.2	18.3	19.4
KC347075_Hadrurus arizonensis	15.2	12.8	12.8	12.3	11.9	2.0	2.0	1.5		0.7	1.1	0.7	2.0	13.4	13.0	12.8	12.6	13.4	12.8	14.3	17.2	17.8	19.4
KC347143_Hadrurus arizonensis	15.4	13.0	13.0	12.6	12.1	2.2	1.8	1.3	0.7		0.9	0.9	2.2	14.1	13.2	13.0	12.8	13.7	13.0	14.5	16.7	17.8	19.4
KC347287_Hadrurus arizonensis	15.6	13.9	13.9	13.4	12.6	2.6	2.2	1.8	1.1	0.9		0.4	2.6	14.5	14.1	13.9	13.7	14.5	13.4	15.4	17.4	18.5	19.4
KC347288_Hadrurus arizonensis	15.4	13.4	13.4	13.0	12.1	2.6	2.2	1.8	0.7	0.9	0.4		2.6	14.1	13.7	13.4	13.2	14.1	13.0	15.0	17.4	18.5	19.6
KC347079_Hadrurus arizonensis	15.2	11.7	11.7	11.7	12.3	2.2	2.2	1.8	2.0	2.2	2.6	2.6		13.7	13.0	12.8	12.6	13.4	12.8	14.3	17.8	18.5	18.9
KT447034_Bothriurus flavidus	14.1	14.3	14.3	13.7	14.1	14.5	14.1	14.5	13.4	14.1	14.5	14.1	13.7		11.0	11.5	11.2	11.5	12.1	16.3	16.3	15.2	15.0
KT446958_Brachistosternus ferrugineus	15.2	14.5	14.5	14.1	13.4	12.8	13.7	13.0	13.0	13.2	14.1	13.7	13.0	11.0		1.3	1.1	1.3	4.8	13.0	15.4	14.3	15.6
KT446959_Brachistosternus ferrugineus	14.8	14.1	14.1	13.7	13.9	12.6	13.4	12.8	12.8	13.0	13.9	13.4	12.8	11.5	1.3		0.2	1.3	4.4	12.3	15.2	14.8	15.6
KT446962_Brachistosternus ferrugineus	14.5	13.9	13.9	13.4	13.7	12.3	13.2	12.6	12.6	12.8	13.7	13.2	12.6	11.2	1.1	0.2		1.1	4.2	12.1	15.0	14.5	15.4
KT446961_Brachistosternus ferrugineus	14.8	14.5	14.5	14.1	14.5	13.2	14.1	13.4	13.4	13.7	14.5	14.1	13.4	11.5	1.3	1.3	1.1		4.8	12.6	15.9	15.0	15.4
KT446960_Brachistosternus ferrugineus	14.1	14.8	14.8	14.8	14.1	13.4	13.0	12.8	12.8	13.0	13.4	13.0	12.8	12.1	4.8	4.4	4.2	4.8		12.8	15.2	14.5	16.5
KY295225_Urodacus planimanus	17.0	14.5	14.5	14.1	15.9	14.1	14.5	14.3	14.3	14.5	15.4	15.0	14.3	16.3	13.0	12.3	12.1	12.6	12.8		14.8	15.6	18.0
MT418091_Heterometrus cyaneus	15.0	18.5	18.5	17.6	17.4	17.6	16.7	17.2	17.2	16.7	17.4	17.4	17.8	16.3	15.4	15.2	15.0	15.9	15.2	14.8		3.7	20.0
MT418092_Heterometrus cyaneus	15.0	18.3	18.3	17.8	17.6	18.1	17.8	18.3	17.8	17.8	18.5	18.5	18.5	15.2	14.3	14.8	14.5	15.0	14.5	15.6	3.7		19.2
KT447038_Cercophonius sulcatus	16.5	16.5	16.5	16.7	17.2	19.8	19.2	19.4	19.4	19.4	19.4	19.6	18.9	15.0	15.6	15.6	15.4	15.4	16.5	18.0	20.0	19.2	

Clitellata: Enchytraeida: Enchytraeidae

COI pairwise distances (%)	BMR01173	KM206509	BMR02739	BMR02672	BMR02677	BMR02741	BMR02714	JY06	BMR01939	BMR01682	BMR04094	BMR01180	BMR02275	BMR00809	BMR00812	KM206479	JY08	JY09	RT56	JY07	JY11	BMR01169	KM206529	RT56	JY10	BMR00813	BMR00810	BMR01200	BMR01215	KM206490	RT56	BMR00607	BMR01177	BMR02737	BMR02609	BMR02670	BMR02605	BMR01172	BMR01175	BMR01403	BMR01399	BMR02606	BMR01171	BMR02720	BMR01679	BMR02610	BMR02716	BMR01183	BMR02713	BMR02253	BMR04196	KM206488	BMR02243	BMR00548	BMR02258	BMR02676	KM206516	BMR00815	KM206477
BMR01173_1749a_Caves Creek_Enchytraeidae `sp. Biologic-OLIG013`		26.3	22.9	22.9	22.6	22.6	23.6	22.2	22.3	23.2	24.2	22.0	22.0	23.5	24.1	24.0	22.3	22.4	22.7	22.0	22.7	22.3	21.7	22.9	22.3	22.1	21.4	21.3	20.9	23.3	21.7	22.4	22.6	21.7	21.2	21.4	21.8	22.9	22.3	22.6	23.0	22.1	22.7	21.7	23.9	24.4	24.1	22.7	22.7	22.6	22.7	21.1	23.5	23.5	24.2	23.0	23.2	22.4	22.3
KM206509_Naididae sp5._Ridley River_Brown et al. 2015_OUTGROUP	26.3		19.7	19.9	19.6	19.6	21.9	22.6	22.5	22.8	23.5	22.7	22.8	23.4	23.2	23.8	23.0	23.1	21.1	20.8	20.9	21.4	21.2	22.3	20.9	22.0	21.4	21.5	21.5	22.2	22.2	23.4	23.2	24.1	24.4	24.3	23.4	24.1	24.1	20.6	21.4	20.6	20.8	20.5	20.5	20.9	22.3	21.2	21.5	21.9	21.7	22.0	22.6	22.9	22.9	23.2	23.4	22.5	22.2
BMR02739_20112_Enchytraeidae `sp. Biologic-OLIG022`	22.9	19.7		1.2	1.5	1.5	18.7	19.9	19.0	20.8	19.8	20.0	20.1	21.4	21.3	20.4	16.8	16.3	16.4	17.6	18.1	16.9	17.9	19.2	18.0	18.1	17.6	17.9	17.8	17.6	18.5	18.4	18.1	19.0	17.8	18.5	17.5	17.9	18.1	18.4	18.3	17.0	17.3	16.9	17.3	18.2	17.2	17.9	17.5	17.3	17.2	17.9	16.6	16.9	16.7	18.2	18.1	17.3	16.3
BMR02672_20112_Enchytraeidae `sp. Biologic-OLIG022`	22.9	19.9	1.2		0.9	0.9	19.0	19.9	18.7	21.7	20.7	20.3	20.4	21.7	21.9	20.3	17.3	16.7	16.4	18.1	18.1	16.9	17.9	19.0	18.0	18.4	17.6	18.0	17.8	18.1	18.7	18.7	18.5	19.3	18.4	19.0	17.9	18.1	18.5	18.8	19.2	17.5	17.8	17.3	17.2	18.4	17.9	17.9	17.8	17.6	17.5	17.2	17.3	17.5	17.5	18.7	18.5	17.5	16.1
BMR02677_20112_Enchytraeidae `sp. Biologic-OLIG022`	22.6	19.6	1.5	0.9		0.0	18.4	20.1	19.0	21.3	20.4	20.3	20.4	21.4	21.3	20.1	16.6	16.1	15.7	17.8	18.2	16.7	17.8	19.0	17.3	17.9	17.6	17.4	17.6	18.2	18.7	18.7	18.7	19.0	18.4	19.0	17.8	17.9	18.4	18.7	18.7	17.6	17.9	17.5	17.9	18.4	17.9	18.5	18.4	18.2	18.1	17.6	17.2	17.5	17.3	18.8	18.7	17.6	16.6
BMR02741_20112_Enchytraeidae `sp. Biologic-OLIG022`	22.6	19.6	1.5	0.9	0.0		18.4	20.1	19.0	21.3	20.4	20.3	20.4	21.4	21.3	20.1	16.6	16.1	15.7	17.8	18.2	16.7	17.8	19.0	17.3	17.9	17.6	17.4	17.6	18.2	18.7	18.7	18.7	19.0	18.4	19.0	17.8	17.9	18.4	18.7	18.7	17.6	17.9	17.5	17.9	18.4	17.9	18.5	18.4	18.2	18.1	17.6	17.2	17.5	17.3	18.8	18.7	17.6	16.6
BMR02714_20112_Enchytraeidae `sp. Biologic-OLIG053`	23.6	21.9	18.7	19.0	18.4	18.4		18.5	18.4	19.6	19.8	19.8	19.9	19.9	19.6	18.3	17.1	16.7	16.0	18.5	18.7	18.5	17.2	17.8	17.5	16.9	17.9	17.0	18.1	17.3	16.3	17.3	17.2	16.7	17.2	17.5	17.0	17.6	17.3	18.1	17.4	17.3	17.8	17.0	17.9	18.5	16.6	16.1	16.1	17.3	16.7	17.0	18.4	18.5	18.5	17.9	17.6	18.4	17.3
JY06_WAN_Dave Bore_Enchytraeidae `sp. Helix-OLE028`	22.2	22.6	19.9	19.9	20.1	20.1	18.5		5.3	7.3	7.6	7.5	7.6	8.2	8.2	16.6	17.4	17.3	15.9	16.9	17.3	16.9	16.2	16.4	17.6	16.5	15.4	16.3	16.1	17.8	16.1	16.9	16.5	16.1	16.4	17.0	16.2	18.0	17.7	18.8	21.3	18.8	18.6	18.8	19.3	18.6	19.3	17.3	17.5	18.6	18.5	18.9	19.6	19.7	19.7	19.6	18.6	18.9	18.8
BMR01939_1953_Enchytraeidae `sp. Biologic-OLIG004`	22.3	22.5	19.0	18.7	19.0	19.0	18.4	5.3		7.5	7.5	7.1	7.1	8.2	8.4	15.4	16.3	15.5	14.3	15.2	15.1	15.4	13.8	13.7	15.4	14.9	13.8	13.8	13.7	15.5	14.0	14.3	14.6	13.8	14.0	14.3	15.1	15.5	15.5	19.6	22.0	19.2	19.3	19.6	20.4	19.2	18.5	15.8	16.3	17.3	17.5	17.6	18.8	18.5	18.2	18.7	18.4	17.6	17.5
BMR01682_20003_Enchytraeidae `sp. Biologic-OLIG004`	23.2	22.8	20.8	21.7	21.3	21.3	19.6	7.3	7.5		2.7	5.7	5.8	7.0	6.8	17.7	15.9	15.5	16.0	15.2	15.5	17.3	15.5	16.3	16.8	16.0	15.4	16.3	15.8	16.1	14.9	16.4	15.8	15.2	15.5	16.1	15.7	17.2	16.6	20.8	22.0	19.8	19.6	19.9	20.2	19.0	18.1	18.2	18.1	18.2	18.2	19.0	17.9	18.4	18.2	19.0	18.2	18.2	18.4
BMR04094_20006_Enchytraeidae `sp. Biologic-OLIG004`	24.2	23.5	19.8	20.7	20.4	20.4	19.8	7.6	7.5	2.7		6.0	6.1	7.3	7.1	17.5	16.6	16.6	16.0	16.1	16.4	17.2	16.1	16.7	16.8	16.6	16.1	16.8	16.6	16.4	15.1	16.9	16.0	15.4	15.4	16.1	16.4	17.2	16.9	20.7	21.6	20.4	20.1	20.4	19.9	18.8	17.8	18.8	18.7	18.1	18.7	18.7	18.1	18.8	18.7	19.3	19.2	18.8	18.8
BMR01180_1749b_BS2_3_Enchytraeidae `sp. Biologic-OLIG004`	22.0	22.7	20.0	20.3	20.3	20.3	19.8	7.5	7.1	5.7	6.0		0.1	4.6	4.8	17.7	17.0	16.8	16.8	16.0	15.9	16.8	15.9	16.3	17.4	16.8	15.7	16.6	16.0	17.0	15.4	15.6	16.0	15.0	15.1	15.3	15.9	17.6	16.6	21.1	22.8	20.4	20.3	20.3	20.7	19.7	18.2	17.9	17.7	18.6	18.5	18.6	19.2	19.1	19.4	20.1	18.6	19.4	19.7
BMR02275_20112_BS2_3 / BS3x_Enchytraeidae `sp. Biologic-OLIG004`	22.0	22.8	20.1	20.4	20.4	20.4	19.9	7.6	7.1	5.8	6.1	0.1		4.7	4.9	17.7	17.1	16.9	16.9	16.0	15.8	16.7	15.8	16.4	17.3	16.7	15.7	16.5	16.0	17.0	15.5	15.7	16.1	15.1	15.2	15.4	16.0	17.6	16.7	21.1	22.9	20.5	20.4	20.4	20.7	19.6	18.1	17.8	17.6	18.5	18.4	18.7	19.3	19.2	19.5	20.2	18.7	19.5	19.8
BMR00809_1845_BS1E_Enchytraeidae `sp. Biologic-OLIG004`	23.5	23.4	21.4	21.7	21.4	21.4	19.9	8.2	8.2	7.0	7.3	4.6	4.7		1.4	19.3	17.9	17.5	16.1	17.3	17.3	17.5	15.5	16.7	17.3	16.6	16.1	16.8	16.4	18.5	16.6	16.9	17.3	16.7	17.2	17.2	16.4	18.5	17.6	21.4	23.1	20.2	20.4	21.3	21.9	20.4	19.6	18.2	18.1	20.4	20.4	19.6	20.1	20.1	19.6	21.0	19.8	20.2	20.2
BMR00812_1845_BS1E_Enchytraeidae `sp. Biologic-OLIG004`	24.1	23.2	21.3	21.9	21.3	21.3	19.6	8.2	8.4	6.8	7.1	4.8	4.9	1.4		19.1	17.3	16.7	15.8	16.7	17.0	17.8	15.2	16.4	17.0	16.6	16.3	16.5	16.4	18.4	16.9	16.7	17.0	17.0	17.2	17.5	16.3	18.2	17.3	20.8	22.5	19.3	19.5	20.4	21.1	19.5	19.2	17.9	17.8	19.8	20.1	19.8	19.9	19.9	19.8	20.5	19.6	19.8	20.1
KM206479_Echytraeidae sp10._North Shaw River_Brown et al 2015	24.0	23.8	20.4	20.3	20.1	20.1	18.3	16.6	15.4	17.7	17.5	17.7	17.7	19.3	19.1		14.2	14.3	13.8	14.8	15.0	14.3	12.5	14.0	12.4	13.8	13.0	13.2	13.0	14.0	13.3	14.5	13.2	12.9	13.3	13.5	14.0	15.1	14.0	20.3	21.1	20.4	19.6	19.6	21.5	20.4	20.1	16.9	16.7	18.5	18.7	16.9	19.8	20.4	19.9	20.4	20.3	19.9	19.6
JY08_WAN_Dave Bore_Enchytraeidae `sp. Helix-OLE030`	22.3	23.0	16.8	17.3	16.6	16.6	17.1	17.4	16.3	15.9	16.6	17.0	17.1	17.9	17.3	14.2		1.8	8.7	8.7	8.6	10.3	8.9	11.2	9.2	9.0	9.0	9.7	9.7	10.7	11.5	11.2	12.1	11.5	10.9	11.3	10.7	11.8	11.0	18.3	18.8	17.9	17.7	16.8	19.7	18.8	18.8	17.0	16.5	17.7	16.5	14.2	15.4	15.6	16.0	16.2	15.4	16.0	15.4
JY09_WAN_Dave Bore_Enchytraeidae `sp. Helix-OLE030`	22.4	23.1	16.3	16.7	16.1	16.1	16.7	17.3	15.5	15.5	16.6	16.8	16.9	17.5	16.7	14.3	1.8		9.6	9.0	8.8	10.3	9.1	10.6	9.2	9.0	8.8	9.2	9.1	10.5	11.7	10.3	11.7	11.4	11.1	11.6	10.9	11.4	10.6	18.5	18.5	17.5	17.9	17.3	19.8	18.7	18.4	16.7	16.3	17.8	16.6	14.1	15.1	15.8	15.7	16.0	15.2	15.5	14.7
RT56_WAMV8926_Enchytraeidae_WAM-ENCH003	22.7	21.1	16.4	16.4	15.7	15.7	16.0	15.9	14.3	16.0	16.0	16.8	16.9	16.1	15.8	13.8	8.7	9.6		7.9	8.2	9.1	8.2	10.2	8.9	8.1	8.2	8.7	8.8	12.9	11.1	10.2	10.3	11.4	10.3	10.9	10.0	10.6	10.8	16.1	17.0	16.4	16.6	15.8	19.5	18.4	18.1	16.0	16.1	16.9	16.9	15.7	16.3	16.0	16.6	16.9	17.2	16.6	16.0
JY07_WAN_Dave Bore_Enchytraeidae `sp. Helix-OLE026`	22.0	20.8	17.6	18.1	17.8	17.8	18.5	16.9	15.2	15.2	16.1	16.0	16.0	17.3	16.7	14.8	8.7	9.0	7.9		1.2	8.5	7.1	8.8	7.6	7.9	6.8	7.2	6.8	11.3	12.0	10.9	11.1	11.6	11.3	12.0	10.9	11.9	11.6	17.0	18.3	16.4	16.9	16.3	19.3	18.5	18.2	16.4	15.7	17.3	17.0	16.7	16.4	16.7	17.2	17.0	17.9	16.7	16.6
JY11_WAN_RR1_Enchytraeidae `sp. Helix-OLE026`	22.7	20.9	18.1	18.1	18.2	18.2	18.7	17.3	15.1	15.5	16.4	15.9	15.8	17.3	17.0	15.0	8.6	8.8	8.2	1.2		8.2	7.1	9.1	7.4	7.9	6.2	7.5	7.0	11.1	11.7	11.3	11.1	11.6	11.4	11.9	10.9	11.3	11.3	17.5	18.7	16.6	17.0	16.4	19.2	18.4	18.7	16.4	15.7	17.6	17.0	16.4	17.0	17.0	17.8	17.5	18.4	17.2	16.9
BMR01169_1749a_SGW_Enchytraeidae `sp. Biologic-OLIG005`	22.3	21.4	16.9	16.9	16.7	16.7	18.5	16.9	15.4	17.3	17.2	16.8	16.7	17.5	17.8	14.3	10.3	10.3	9.1	8.5	8.2		7.1	8.5	7.0	7.8	5.9	6.9	6.4	10.9	11.7	10.0	10.3	9.9	10.2	10.2	10.8	11.1	10.5	17.5	19.2	16.9	17.2	17.0	18.1	17.0	19.2	16.7	16.6	16.7	17.2	16.3	16.9	17.2	17.3	17.2	17.8	16.6	16.7
KM206529_Echytraeidae sp6._Brown et al 2015	21.7	21.2	17.9	17.9	17.8	17.8	17.2	16.2	13.8	15.5	16.1	15.9	15.8	15.5	15.2	12.5	8.9	9.1	8.2	7.1	7.1	7.1		8.5	6.5	6.5	5.9	6.8	5.5	11.9	10.0	9.6	9.9	10.0	10.2	10.5	10.0	11.3	10.6	18.4	20.0	16.9	17.0	16.7	19.6	18.2	18.4	14.9	14.4	16.1	15.8	17.2	17.9	17.6	18.4	17.5	17.8	17.5	17.6
RT56_WAMV8924_Enchytraeidae_sp._E6_(2-4)	22.9	22.3	19.2	19.0	19.0	19.0	17.8	16.4	13.7	16.3	16.7	16.3	16.4	16.7	16.4	14.0	11.2	10.6	10.2	8.8	9.1	8.5	8.5		7.1	6.8	5.8	5.2	5.3	12.3	12.0	9.3	9.9	10.6	9.9	10.9	10.8	11.1	11.1	19.6	21.8	17.8	18.5	18.5	20.4	18.5	19.0	17.0	16.6	17.6	16.6	16.3	17.6	18.4	18.1	17.8	18.1	17.2	17.5
JY10_WAN_RR1_Enchytraeidae `sp. Helix-OLE029`	22.3	20.9	18.0	18.0	17.3	17.3	17.5	17.6	15.4	16.8	16.8	17.4	17.3	17.3	17.0	12.4	9.2	9.2	8.9	7.6	7.4	7.0	6.5	7.1		5.8	5.3	4.8	5.5	12.0	10.8	9.4	9.9	10.8	10.5	11.3	9.9	11.0	9.4	18.6	20.2	18.0	18.0	17.8	20.2	17.8	18.3	16.7	16.2	17.0	17.2	15.5	17.0	17.6	18.1	18.3	18.9	17.8	17.2
BMR00813_1845_BS1C_Enchytraeidae `sp. Biologic-OLIG005`	22.1	22.0	18.1	18.4	17.9	17.9	16.9	16.5	14.9	16.0	16.6	16.8	16.7	16.6	16.6	13.8	9.0	9.0	8.1	7.9	7.9	7.8	6.5	6.8	5.8		4.3	3.9	4.7	12.0	11.1	10.0	9.6	10.5	9.9	10.2	9.9	10.8	10.2	17.6	18.7	16.3	17.3	16.7	20.1	17.9	17.9	16.9	16.1	18.1	17.6	16.6	16.3	16.6	17.0	17.6	16.9	17.5	16.1
BMR00810_1845_BGCK_Enchytraeidae `sp. Biologic-OLIG005`	21.4	21.4	17.6	17.6	17.6	17.6	17.9	15.4	13.8	15.4	16.1	15.7	15.7	16.1	16.3	13.0	9.0	8.8	8.2	6.8	6.2	5.9	5.9	5.8	5.3	4.3		4.0	4.3	10.9	10.9	8.8	9.0	9.9	9.4	9.7	9.1	10.0	9.4	17.9	20.0	16.7	17.5	16.7	19.2	17.9	18.5	16.3	15.8	17.3	16.7	16.0	16.9	17.3	17.3	17.9	17.8	16.7	16.7
BMR01200_1749b_Lens G_Enchytraeidae `sp. Biologic-OLIG005`	21.3	21.5	17.9	18.0	17.4	17.4	17.0	16.3	13.8	16.3	16.8	16.6	16.5	16.8	16.5	13.2	9.7	9.2	8.7	7.2	7.5	6.9	6.8	5.2	4.8	3.9	4.0		3.9	11.9	10.3	9.5	8.7	9.8	9.7	10.1	9.8	11.0	10.1	17.4	18.6	16.6	17.4	16.8	19.7	18.0	17.7	16.2	15.7	17.1	17.4	16.2	16.5	17.6	17.0	17.7	17.7	17.3	16.6
BMR01215_1749a_Caves Creek_Enchytraeidae `sp. Biologic-OLIG005`	20.9	21.5	17.8	17.8	17.6	17.6	18.1	16.1	13.7	15.8	16.6	16.0	16.0	16.4	16.4	13.0	9.7	9.1	8.8	6.8	7.0	6.4	5.5	5.3	5.5	4.7	4.3	3.9		11.1	10.5	9.7	10.0	10.8	10.8	11.1	10.5	11.1	11.1	17.9	19.4	16.7	17.2	16.9	20.2	17.8	18.8	15.5	15.1	17.0	16.6	16.3	16.4	17.0	16.6	17.3	17.5	16.1	16.6
KM206490_Echytraeidae sp8._Upper Fortescue_Brown et al 2015	23.3	22.2	17.6	18.1	18.2	18.2	17.3	17.8	15.5	16.1	16.4	17.0	17.0	18.5	18.4	14.0	10.7	10.5	12.9	11.3	11.1	10.9	11.9	12.3	12.0	12.0	10.9	11.9	11.1		10.8	9.9	9.6	10.2	10.9	10.9	10.9	11.4	10.9	18.5	19.6	18.5	18.4	17.8	19.5	18.7	17.6	17.3	17.2	17.8	17.6	17.3	16.7	17.6	17.3	18.1	18.5	18.1	17.6
RT56_WAMV8930_Enchytraeidae_WAM-ENCH002	21.7	22.2	18.5	18.7	18.7	18.7	16.3	16.1	14.0	14.9	15.1	15.4	15.5	16.6	16.9	13.3	11.5	11.7	11.1	12.0	11.7	11.7	10.0	12.0	10.8	11.1	10.9	10.3	10.5	10.8		9.4	8.4	7.5	8.7	8.2	8.5	8.8	8.2	17.8	18.3	17.8	17.3	17.3	19.8	17.6	17.5	16.1	16.3	17.0	17.0	15.7	17.5	17.3	17.5	17.8	17.6	17.3	17.2
BMR00607_1811_Enchytraeidae `sp. Biologic-OLIG006`	22.4	23.4	18.4	18.7	18.7	18.7	17.3	16.9	14.3	16.4	16.9	15.6	15.7	16.9	16.7	14.5	11.2	10.3	10.2	10.9	11.3	10.0	9.6	9.3	9.4	10.0	8.8	9.5	9.7	9.9	9.4		7.0	7.3	7.3	7.3	6.7	7.1	6.5	18.4	19.6	17.5	18.2	17.8	20.1	19.0	17.2	16.0	16.1	16.1	16.1	16.7	17.6	17.5	17.9	17.9	17.8	17.6	16.9
BMR01177_1749b_BS3_Enchytraeidae `sp. Biologic-OLIG006`	22.6	23.2	18.1	18.5	18.7	18.7	17.2	16.5	14.6	15.8	16.0	16.0	16.1	17.3	17.0	13.2	12.1	11.7	10.3	11.1	11.1	10.3	9.9	9.9	9.9	9.6	9.0	8.7	10.0	9.6	8.4	7.0		5.9	5.2	5.6	6.5	5.6	5.6	17.5	18.7	16.6	17.0	16.7	19.2	17.8	17.0	15.4	15.5	16.3	16.3	15.5	18.5	18.5	18.7	19.2	19.2	18.5	17.6
BMR02737_20112_Enchytraeidae `sp. Biologic-OLIG006`	21.7	24.1	19.0	19.3	19.0	19.0	16.7	16.1	13.8	15.2	15.4	15.0	15.1	16.7	17.0	12.9	11.5	11.4	11.4	11.6	11.6	9.9	10.0	10.6	10.8	10.5	9.9	9.8	10.8	10.2	7.5	7.3	5.9		3.3	2.9	5.9	5.5	5.2	18.1	20.3	18.1	18.1	17.3	19.0	17.6	17.8	15.5	15.7	17.2	16.9	16.9	18.1	18.2	17.8	17.9	18.2	17.9	17.5
BMR02609_20112_Enchytraeidae `sp. Biologic-OLIG006`	21.2	24.4	17.8	18.4	18.4	18.4	17.2	16.4	14.0	15.5	15.4	15.1	15.2	17.2	17.2	13.3	10.9	11.1	10.3	11.3	11.4	10.2	10.2	9.9	10.5	9.9	9.4	9.7	10.8	10.9	8.7	7.3	5.2	3.3		2.7	5.9	5.5	4.9	17.9	19.4	17.9	18.4	17.3	18.5	17.8	17.8	15.8	15.7	17.2	16.7	15.7	17.8	17.3	17.6	17.0	17.6	17.3	16.1
BMR02670_20112_Enchytraeidae `sp. Biologic-OLIG006`	21.4	24.3	18.5	19.0	19.0	19.0	17.5	17.0	14.3	16.1	16.1	15.3	15.4	17.2	17.5	13.5	11.3	11.6	10.9	12.0	11.9	10.2	10.5	10.9	11.3	10.2	9.7	10.1	11.1	10.9	8.2	7.3	5.6	2.9	2.7		5.9	5.3	4.9	18.4	20.3	18.1	18.7	17.6	18.8	18.2	18.1	16.1	16.3	17.5	17.3	16.3	17.6	17.2	17.6	17.3	17.3	17.3	16.9
BMR02605_20112_Enchytraeidae `sp. Biologic-OLIG006`	21.8	23.4	17.5	17.9	17.8	17.8	17.0	16.2	15.1	15.7	16.4	15.9	16.0	16.4	16.3	14.0	10.7	10.9	10.0	10.9	10.9	10.8	10.0	10.8	9.9	9.9	9.1	9.8	10.5	10.9	8.5	6.7	6.5	5.9	5.9	5.9		4.1	3.2	17.9	19.2	16.6	17.2	16.3	19.3	18.2	17.6	16.3	16.4	17.2	17.3	15.8	18.1	17.9	18.4	18.7	18.7	17.6	17.6
BMR01172_1749a_Caves Creek_Enchytraeidae `sp. Biologic-OLIG006`	22.9	24.1	17.9	18.1	17.9	17.9	17.6	18.0	15.5	17.2	17.2	17.6	17.6	18.5	18.2	15.1	11.8	11.4	10.6	11.9	11.3	11.1	11.3	11.1	11.0	10.8	10.0	11.0	11.1	11.4	8.8	7.1	5.6	5.5	5.5	5.3	4.1		2.1	18.8	20.0	17.5	18.1	17.2	19.8	18.4	18.1	16.6	16.7	17.6	16.9	16.3	18.5	18.4	18.8	18.4	19.3	17.9	17.3
BMR01175_1749a_Caves Creek_Enchytraeidae `sp. Biologic-OLIG006`	22.3	24.1	18.1	18.5	18.4	18.4	17.3	17.7	15.5	16.6	16.9	16.6	16.7	17.6	17.3	14.0	11.0	10.6	10.8	11.6	11.3	10.5	10.6	11.1	9.4	10.2	9.4	10.1	11.1	10.9	8.2	6.5	5.6	5.2	4.9	4.9	3.2	2.1		18.7	19.6	17.3	17.8	16.9	19.0	18.2	18.1	16.4	16.6	17.2	17.3	16.4	18.4	18.2	18.7	18.2	18.8	18.1	17.6
GF1_Enchytraeidae `sp. Biologic-OLIG016`	22.6	20.6	18.4	18.8	18.7	18.7	18.1	18.8	19.6	20.8	20.7	21.1	21.1	21.4	20.8	20.3	18.3	18.5	16.1	17.0	17.5	17.5	18.4	19.6	18.6	17.6	17.9	17.4	17.9	18.5	17.8	18.4	17.5	18.1	17.9	18.4	17.9	18.8	18.7		0.2	5.0	4.6	4.6	10.0	11.3	17.5	18.5	18.7	19.8	19.3	18.2	19.5	18.4	18.2	19.9	19.6	19.3	18.1
GF2_Enchytraeidae `sp. Biologic-OLIG016`	23.0	21.4	18.3	19.2	18.7	18.7	17.4	21.3	22.0	22.0	21.6	22.8	22.9	23.1	22.5	21.1	18.8	18.5	17.0	18.3	18.7	19.2	20.0	21.8	20.2	18.7	20.0	18.6	19.4	19.6	18.3	19.6	18.7	20.3	19.4	20.3	19.2	20.0	19.6	0.2		5.3	4.8	5.5	11.7	11.2	17.8	20.0	19.6	20.9	20.5	18.9	20.0	19.6	18.9	21.2	20.7	20.3	18.3
BMR02606_20112_Enchytraeidae `sp. Biologic-OLIG016`	22.1	20.6	17.0	17.5	17.6	17.6	17.3	18.8	19.2	19.8	20.4	20.4	20.5	20.2	19.3	20.4	17.9	17.5	16.4	16.4	16.6	16.9	16.9	17.8	18.0	16.3	16.7	16.6	16.7	18.5	17.8	17.5	16.6	18.1	17.9	18.1	16.6	17.5	17.3	5.0	5.3		2.1	2.6	11.1	11.1	16.7	18.1	17.9	19.3	18.8	17.5	19.0	18.2	18.5	19.2	19.2	18.2	17.8
BMR01171_1845_VIV_Enchytraeidae `sp. Biologic-OLIG016`	22.7	20.8	17.3	17.8	17.9	17.9	17.8	18.6	19.3	19.6	20.1	20.3	20.4	20.4	19.5	19.6	17.7	17.9	16.6	16.9	17.0	17.2	17.0	18.5	18.0	17.3	17.5	17.4	17.2	18.4	17.3	18.2	17.0	18.1	18.4	18.7	17.2	18.1	17.8	4.6	4.8	2.1		2.0	10.5	10.2	17.5	17.6	17.3	18.8	18.4	17.3	18.4	17.6	17.6	18.8	18.4	17.8	17.6
BMR02720_20112_Enchytraeidae `sp. Biologic-OLIG016`	21.7	20.5	16.9	17.3	17.5	17.5	17.0	18.8	19.6	19.9	20.4	20.3	20.4	21.3	20.4	19.6	16.8	17.3	15.8	16.3	16.4	17.0	16.7	18.5	17.8	16.7	16.7	16.8	16.9	17.8	17.3	17.8	16.7	17.3	17.3	17.6	16.3	17.2	16.9	4.6	5.5	2.6	2.0		10.5	10.8	17.5	17.5	17.3	18.5	18.1	17.5	18.2	17.2	17.8	18.4	18.1	17.6	17.3
BMR01679_20003_Enchytraeidae `sp. Biologic-OLIG021`	23.9	20.5	17.3	17.2	17.9	17.9	17.9	19.3	20.4	20.2	19.9	20.7	20.7	21.9	21.1	21.5	19.7	19.8	19.5	19.3	19.2	18.1	19.6	20.4	20.2	20.1	19.2	19.7	20.2	19.5	19.8	20.1	19.2	19.0	18.5	18.8	19.3	19.8	19.0	10.0	11.7	11.1	10.5	10.5		9.7	17.5	16.4	16.6	17.0	16.7	17.2	19.3	19.2	18.7	19.8	20.2	19.6	18.8
BMR02610_20112_Enchytraeidae `sp. Biologic-OLIG052`	24.4	20.9	18.2	18.4	18.4	18.4	18.5	18.6	19.2	19.0	18.8	19.7	19.6	20.4	19.5	20.4	18.8	18.7	18.4	18.5	18.4	17.0	18.2	18.5	17.8	17.9	17.9	18.0	17.8	18.7	17.6	19.0	17.8	17.6	17.8	18.2	18.2	18.4	18.2	11.3	11.2	11.1	10.2	10.8	9.7		18.1	17.9	18.1	18.4	18.5	17.9	18.1	17.8	17.6	17.3	17.9	17.2	17.3
BMR02716_20112_Enchytraeidae `sp. Biologic-OLIG055`	24.1	22.3	17.2	17.9	17.9	17.9	16.6	19.3	18.5	18.1	17.8	18.2	18.1	19.6	19.2	20.1	18.8	18.4	18.1	18.2	18.7	19.2	18.4	19.0	18.3	17.9	18.5	17.7	18.8	17.6	17.5	17.2	17.0	17.8	17.8	18.1	17.6	18.1	18.1	17.5	17.8	16.7	17.5	17.5	17.5	18.1		17.5	17.3	17.3	18.1	17.5	16.9	18.1	17.8	18.4	17.6	17.9	17.0
BMR01183_1749b_DSM_Enchytraeidae `sp. Biologic-OLIG017`	22.7	21.2	17.9	17.9	18.5	18.5	16.1	17.3	15.8	18.2	18.8	17.9	17.8	18.2	17.9	16.9	17.0	16.7	16.0	16.4	16.4	16.7	14.9	17.0	16.7	16.9	16.3	16.2	15.5	17.3	16.1	16.0	15.4	15.5	15.8	16.1	16.3	16.6	16.4	18.5	20.0	18.1	17.6	17.5	16.4	17.9	17.5		0.9	5.5	5.0	15.7	17.8	17.9	17.6	17.3	17.5	17.0	16.6
BMR02713_20112_Enchytraeidae `sp. Biologic-OLIG017`	22.7	21.5	17.5	17.8	18.4	18.4	16.1	17.5	16.3	18.1	18.7	17.7	17.6	18.1	17.8	16.7	16.5	16.3	16.1	15.7	15.7	16.6	14.4	16.6	16.2	16.1	15.8	15.7	15.1	17.2	16.3	16.1	15.5	15.7	15.7	16.3	16.4	16.7	16.6	18.7	19.6	17.9	17.3	17.3	16.6	18.1	17.3	0.9		6.1	5.6	15.5	17.6	17.8	17.5	17.2	17.3	17.2	16.4
BMR02253_1953_Enchytraeidae `sp. Biologic-OLIG017`	22.6	21.9	17.3	17.6	18.2	18.2	17.3	18.6	17.3	18.2	18.1	18.6	18.5	20.4	19.8	18.5	17.7	17.8	16.9	17.3	17.6	16.7	16.1	17.6	17.0	18.1	17.3	17.1	17.0	17.8	17.0	16.1	16.3	17.2	17.2	17.5	17.2	17.6	17.2	19.8	20.9	19.3	18.8	18.5	17.0	18.4	17.3	5.5	6.1		2.0	16.1	18.5	18.1	18.7	17.8	18.1	17.0	17.0
BMR04196_20006_Enchytraeidae `sp. Biologic-OLIG017`	22.7	21.7	17.2	17.5	18.1	18.1	16.7	18.5	17.5	18.2	18.7	18.5	18.4	20.4	20.1	18.7	16.5	16.6	16.9	17.0	17.0	17.2	15.8	16.6	17.2	17.6	16.7	17.4	16.6	17.6	17.0	16.1	16.3	16.9	16.7	17.3	17.3	16.9	17.3	19.3	20.5	18.8	18.4	18.1	16.7	18.5	18.1	5.0	5.6	2.0		15.8	18.5	18.1	18.7	17.8	17.8	17.0	17.0
KM206488_Echytraeidae sp12._ Fortescue_Brown et al 2015	21.1	22.0	17.9	17.2	17.6	17.6	17.0	18.9	17.6	19.0	18.7	18.6	18.7	19.6	19.8	16.9	14.2	14.1	15.7	16.7	16.4	16.3	17.2	16.3	15.5	16.6	16.0	16.2	16.3	17.3	15.7	16.7	15.5	16.9	15.7	16.3	15.8	16.3	16.4	18.2	18.9	17.5	17.3	17.5	17.2	17.9	17.5	15.7	15.5	16.1	15.8		13.5	14.1	14.3	15.2	14.7	14.3	12.6
BMR02243_1953_Enchytraeidae `sp. E11`	23.5	22.6	16.6	17.3	17.2	17.2	18.4	19.6	18.8	17.9	18.1	19.2	19.3	20.1	19.9	19.8	15.4	15.1	16.3	16.4	17.0	16.9	17.9	17.6	17.0	16.3	16.9	16.5	16.4	16.7	17.5	17.6	18.5	18.1	17.8	17.6	18.1	18.5	18.4	19.5	20.0	19.0	18.4	18.2	19.3	18.1	16.9	17.8	17.6	18.5	18.5	13.5		2.7	2.4	6.4	6.4	6.1	5.8
BMR00548_1811_Enchytraeidae `sp. E11` (reversed)	23.5	22.9	16.9	17.5	17.5	17.5	18.5	19.7	18.5	18.4	18.8	19.1	19.2	20.1	19.9	20.4	15.6	15.8	16.0	16.7	17.0	17.2	17.6	18.4	17.6	16.6	17.3	17.6	17.0	17.6	17.3	17.5	18.5	18.2	17.3	17.2	17.9	18.4	18.2	18.4	19.6	18.2	17.6	17.2	19.2	17.8	18.1	17.9	17.8	18.1	18.1	14.1	2.7		2.0	5.2	6.1	5.8	5.2
BMR02258_1953_Enchytraeidae `sp. E11`	24.2	22.9	16.7	17.5	17.3	17.3	18.5	19.7	18.2	18.2	18.7	19.4	19.5	19.6	19.8	19.9	16.0	15.7	16.6	17.2	17.8	17.3	18.4	18.1	18.1	17.0	17.3	17.0	16.6	17.3	17.5	17.9	18.7	17.8	17.6	17.6	18.4	18.8	18.7	18.2	18.9	18.5	17.6	17.8	18.7	17.6	17.8	17.6	17.5	18.7	18.7	14.3	2.4	2.0		6.2	6.5	6.2	5.3
BMR02676_20112_Enchytraeidae `sp. E11`	23.0	23.2	18.2	18.7	18.8	18.8	17.9	19.6	18.7	19.0	19.3	20.1	20.2	21.0	20.5	20.4	16.2	16.0	16.9	17.0	17.5	17.2	17.5	17.8	18.3	17.6	17.9	17.7	17.3	18.1	17.8	17.9	19.2	17.9	17.0	17.3	18.7	18.4	18.2	19.9	21.2	19.2	18.8	18.4	19.8	17.3	18.4	17.3	17.2	17.8	17.8	15.2	6.4	5.2	6.2		4.7	2.9	5.3
KM206516_Echytraeidae sp11._Weelumurra Creek_Brown et al 2015	23.2	23.4	18.1	18.5	18.7	18.7	17.6	18.6	18.4	18.2	19.2	18.6	18.7	19.8	19.6	20.3	15.4	15.2	17.2	17.9	18.4	17.8	17.8	18.1	18.9	16.9	17.8	17.7	17.5	18.5	17.6	17.8	19.2	18.2	17.6	17.3	18.7	19.3	18.8	19.6	20.7	19.2	18.4	18.1	20.2	17.9	17.6	17.5	17.3	18.1	17.8	14.7	6.4	6.1	6.5	4.7		4.0	6.1
BMR00815_1845_BGCK_Enchytraeidae `sp. Biologic-OLIG003`	22.4	22.5	17.3	17.5	17.6	17.6	18.4	18.9	17.6	18.2	18.8	19.4	19.5	20.2	19.8	19.9	16.0	15.5	16.6	16.7	17.2	16.6	17.5	17.2	17.8	17.5	16.7	17.3	16.1	18.1	17.3	17.6	18.5	17.9	17.3	17.3	17.6	17.9	18.1	19.3	20.3	18.2	17.8	17.6	19.6	17.2	17.9	17.0	17.2	17.0	17.0	14.3	6.1	5.8	6.2	2.9	4.0		5.0
KM206477_Echytraeidae sp13._McPhee Creek_Brown et al 2015	22.3	22.2	16.3	16.1	16.6	16.6	17.3	18.8	17.5	18.4	18.8	19.7	19.8	20.2	20.1	19.6	15.4	14.7	16.0	16.6	16.9	16.7	17.6	17.5	17.2	16.1	16.7	16.6	16.6	17.6	17.2	16.9	17.6	17.5	16.1	16.9	17.6	17.3	17.6	18.1	18.3	17.8	17.6	17.3	18.8	17.3	17.0	16.6	16.4	17.0	17.0	12.6	5.8	5.2	5.3	5.3	6.1	5.0	

Clitellata: Haplotaxida: Phreodrilidae

COI pairwise differences (%)	BMR04105	BMR00624	BMR02270	BMR02271	BMR00684	BMR00811	BMR00814	BMR02269	BMR01161	BMR02674	BMR02738	KM206528	JY21	BMR01188	BMR02272	BMR02273	BMR02274	BMR02715	BMR02673	BMR04106	KM206498	KM206523	BMR00744	BMR02671	BMR00808	BMR00817	BMR01196	BMR02721	RT46	BMR01191	KM206511	KM206524	KM206522	KM206509	O. ketagalan	KM206521
BMR04105_20112_Phreodrilidae `sp. P12`		3.1	3.0	3.2	3.2	3.2	0.0	0.2	2.0	2.0	2.0	2.7	2.7	3.0	3.0	3.0	3.0	3.0	2.9	2.89	8.2	9.2	17.5	17.6	20.4	21.0	21.6	21.6	21.0	20.2	20.2	18.8	17.7	21.2	26.2	16.9
BMR00624_1845_BS1E_Phreodrilidae `sp. P12`	3.1		0.1	0.2	0.5	2.2	3.1	3.3	3.3	3.3	3.3	3.3	4.0	4.0	4.0	4.0	4.0	4.0	3.5	1.9	8.0	9.2	17.9	18.1	21.1	21.7	22.3	21.8	21.1	20.7	19.7	19.1	18.5	21.2	26.0	17.6
BMR02270_20112_BS1_Phreodrilidae `sp. P12`	3.0	0.1		0.2	0.5	2.1	3.0	3.2	3.2	3.2	3.2	3.2	4.0	4.0	4.0	4.0	4.0	4.0	3.5	1.82	7.9	9.2	17.9	18.1	21.0	21.7	22.2	21.7	21.0	20.7	19.6	19.1	18.5	21.2	26.0	17.5
BMR02271_20112_BS1_Phreodrilidae `sp. P12`	3.2	0.2	0.2		0.6	2.3	3.2	3.3	3.3	3.3	3.3	3.4	4.1	4.1	4.1	4.1	4.1	4.1	3.7	1.98	8.1	9.3	18.1	18.2	20.8	21.9	22.0	21.6	20.8	20.5	19.8	19.2	18.5	21.4	26.2	17.6
BMR00684_1845_BS1W_Phreodrilidae `sp. P12`	3.2	0.5	0.5	0.6		2.3	3.2	3.3	3.3	3.3	3.3	3.1	4.1	4.1	4.1	4.1	4.1	4.1	3.7	1.98	8.1	9.7	18.2	18.4	21.0	21.6	22.5	21.9	21.1	21.0	20.1	19.6	18.5	21.4	26.3	17.9
BMR00811_1845_BS1W_Phreodrilidae `sp. P12`	3.2	2.2	2.1	2.3	2.3		3.2	3.3	3.8	3.8	3.8	3.9	4.7	4.7	4.7	4.7	4.7	4.7	4.6	0.61	9.4	9.8	18.1	18.2	20.7	21.6	22.3	22.6	21.0	20.7	20.5	19.7	18.2	21.4	25.9	17.0
BMR00814_1845_BS1E_Phreodrilidae `sp. P12`	0.0	3.1	3.0	3.2	3.2	3.2		0.2	2.0	2.0	2.0	2.7	2.7	3.0	3.0	3.0	3.0	3.0	2.9	2.89	8.2	9.2	17.5	17.6	20.4	21.0	21.6	21.6	21.0	20.2	20.2	18.8	17.7	21.2	26.2	16.9
BMR02269_20112_BS1_Phreodrilidae `sp. P12`	0.2	3.3	3.2	3.3	3.3	3.3	0.2		2.1	2.1	2.1	2.9	2.9	3.2	3.2	3.2	3.2	3.2	3.1	3.04	8.4	9.3	17.6	17.8	20.4	21.0	21.6	21.6	21.0	20.2	20.2	18.8	17.7	21.2	26.3	17.0
BMR01161_1749b_BS2_3_Phreodrilidae `sp. 12`	2.0	3.3	3.2	3.3	3.3	3.8	2.0	2.1		0.0	0.0	2.1	2.4	2.4	2.4	2.4	2.4	2.4	2.6	3.5	8.1	9.5	17.2	17.3	20.7	21.4	21.9	21.7	21.4	20.7	20.7	18.8	18.0	21.5	26.6	17.0
BMR02674_20112_Phreodrilidae `sp. P12`	2.0	3.3	3.2	3.3	3.3	3.8	2.0	2.1	0.0		0.0	2.1	2.4	2.4	2.4	2.4	2.4	2.4	2.6	3.5	8.1	9.5	17.2	17.3	20.7	21.4	21.9	21.7	21.4	20.7	20.7	18.8	18.0	21.5	26.6	17.0
BMR02738_20112_Phreodrilidae `sp. 12`	2.0	3.3	3.2	3.3	3.3	3.8	2.0	2.1	0.0	0.0		2.1	2.4	2.4	2.4	2.4	2.4	2.4	2.6	3.5	8.1	9.5	17.2	17.3	20.7	21.4	21.9	21.7	21.4	20.7	20.7	18.8	18.0	21.5	26.6	17.0
KM206528_Phreodrilidae sp.12_Fortescue_Brown et al. 2015	2.7	3.3	3.2	3.4	3.1	3.9	2.7	2.9	2.1	2.1	2.1		2.3	2.6	2.6	2.6	2.6	2.6	1.4	3.7	8.7	10.0	17.0	17.2	21.5	20.6	21.7	21.4	20.3	21.1	20.7	18.3	18.3	21.3	26.7	16.4
JY21_WAN_RC14WAD0346_Phreodrilidae `sp. Helix-OLP12`	2.7	4.0	4.0	4.1	4.1	4.7	2.7	2.9	2.4	2.4	2.4	2.3		2.7	2.7	2.7	2.7	2.7	2.9	4.41	7.6	9.7	16.4	16.6	20.8	20.8	21.6	21.1	20.4	19.9	20.8	18.8	18.0	21.2	25.6	16.9
BMR01188_1749b_BS3_Phreodrilidae `sp. P12`	3.0	4.0	4.0	4.1	4.1	4.7	3.0	3.2	2.4	2.4	2.4	2.6	2.7		0.0	0.0	0.0	0.0	0.4	4.41	8.5	9.5	17.5	17.6	20.8	21.0	21.6	21.7	20.8	21.0	20.5	18.6	17.9	21.4	25.9	16.9
BMR02272_20112_BS3_Phreodrilidae `sp. P12`	3.0	4.0	4.0	4.1	4.1	4.7	3.0	3.2	2.4	2.4	2.4	2.6	2.7	0.0		0.0	0.0	0.0	0.4	4.41	8.5	9.5	17.5	17.6	20.8	21.0	21.6	21.7	20.8	21.0	20.5	18.6	17.9	21.4	25.9	16.9
BMR02273_20112_BS3_Phreodrilidae `sp. P12`	3.0	4.0	4.0	4.1	4.1	4.7	3.0	3.2	2.4	2.4	2.4	2.6	2.7	0.0	0.0		0.0	0.0	0.4	4.41	8.5	9.5	17.5	17.6	20.8	21.0	21.6	21.7	20.8	21.0	20.5	18.6	17.9	21.4	25.9	16.9
BMR02274_20112_BS3_Phreodrilidae `sp. P12`	3.0	4.0	4.0	4.1	4.1	4.7	3.0	3.2	2.4	2.4	2.4	2.6	2.7	0.0	0.0	0.0		0.0	0.4	4.41	8.5	9.5	17.5	17.6	20.8	21.0	21.6	21.7	20.8	21.0	20.5	18.6	17.9	21.4	25.9	16.9
BMR02715_20112_Phreodrilidae `sp. 12`	3.0	4.0	4.0	4.1	4.1	4.7	3.0	3.2	2.4	2.4	2.4	2.6	2.7	0.0	0.0	0.0	0.0		0.4	4.41	8.5	9.5	17.5	17.6	20.8	21.0	21.6	21.7	20.8	21.0	20.5	18.6	17.9	21.4	25.9	16.9
BMR02673_20112_Phreodrilidae `sp. P12`	2.9	3.5	3.5	3.7	3.7	4.6	2.9	3.1	2.6	2.6	2.6	1.4	2.9	0.4	0.4	0.4	0.4	0.4		4.41	9.0	9.1	18.7	18.9	22.3	21.8	22.0	22.0	21.2	22.9	20.3	18.9	17.9	21.4	25.8	16.7
BMR04106_20112_Phreodrilidae `sp. P12`	2.9	1.9	1.8	2.0	2.0	0.6	2.9	3.0	3.5	3.5	3.5	3.7	4.4	4.4	4.4	4.4	4.4	4.4	4.4		9.1	9.7	17.8	17.9	20.7	21.9	22.6	23.0	21.3	20.7	20.5	19.7	18.0	21.4	25.7	17.0
KM206498_Phreodrilidae sp.11_Fortescue_Brown et al. 2015	8.2	8.0	7.9	8.1	8.1	9.4	8.2	8.4	8.1	8.1	8.1	8.7	7.6	8.5	8.5	8.5	8.5	8.5	9.0	9.12		10.9	18.5	18.4	20.7	21.0	21.7	21.9	21.1	20.5	20.1	19.6	18.3	22.0	26.8	17.0
KM206523_Phreodrilidae sp.13_Black Range Creek_Brown et al. 2015	9.2	9.2	9.2	9.3	9.7	9.8	9.2	9.3	9.5	9.5	9.5	10.0	9.7	9.5	9.5	9.5	9.5	9.5	9.1	9.65	10.9		15.6	15.8	21.9	20.9	21.1	21.1	19.9	21.4	20.9	19.0	18.7	23.1	27.5	15.6
BMR00744_1845_BGCK_Phreodrilidae `sp. Biologic-OLIG011`	17.5	17.9	17.9	18.1	18.2	18.1	17.5	17.6	17.2	17.2	17.2	17.0	16.4	17.5	17.5	17.5	17.5	17.5	18.7	17.8	18.5	15.6		0.2	21.7	20.7	19.9	20.4	19.8	21.9	21.0	20.7	19.3	20.8	25.4	16.0
BMR02671_20112_Phreodrilidae `sp. Biologic-OLIG011`	17.6	18.1	18.1	18.2	18.4	18.2	17.6	17.8	17.3	17.3	17.3	17.2	16.6	17.6	17.6	17.6	17.6	17.6	18.9	17.9	18.4	15.8	0.2		21.6	20.5	19.8	20.5	19.6	21.7	20.8	20.8	19.5	20.9	25.6	16.1
BMR00808_1845_BGCK_Phreodrilidae `sp. Biologic-OLIG001`	20.4	21.1	21.0	20.8	21.0	20.7	20.4	20.4	20.7	20.7	20.7	21.5	20.8	20.8	20.8	20.8	20.8	20.8	22.3	20.7	20.7	21.9	21.7	21.6		19.9	19.3	19.6	18.2	17.9	19.8	18.4	19.3	24.6	27.7	19.6
BMR00817_1845_BS1E_Phreodrilidae `sp. Biologic-OLIG002`	21.0	21.7	21.7	21.9	21.6	21.6	21.0	21.0	21.4	21.4	21.4	20.6	20.8	21.0	21.0	21.0	21.0	21.0	21.8	21.9	21.0	20.9	20.7	20.5	19.9		12.8	17.3	15.7	17.2	19.0	20.0	19.0	23.4	27.4	21.7
BMR01196_1749a_Caves Creek_Phreodrilidae `sp. Biologic-OLIG014`	21.6	22.3	22.2	22.0	22.5	22.3	21.6	21.6	21.9	21.9	21.9	21.7	21.6	21.6	21.6	21.6	21.6	21.6	22.0	22.6	21.7	21.1	19.9	19.8	19.3	12.8		16.3	15.7	16.3	18.5	18.3	18.3	25.0	28.5	19.9
BMR02721_20112_Antarctodrilus `sp. Biologic-OLIG054`	21.6	21.8	21.7	21.6	21.9	22.6	21.6	21.6	21.7	21.7	21.7	21.4	21.1	21.7	21.7	21.7	21.7	21.7	22.0	23	21.9	21.1	20.4	20.5	19.6	17.3	16.3		15.4	17.2	19.0	19.9	19.0	24.0	30.1	19.2
RT46_WAMV8910_Phreodrilidae_WAM-PHRE001	21.0	21.1	21.0	20.8	21.1	21.0	21.0	21.0	21.4	21.4	21.4	20.3	20.4	20.8	20.8	20.8	20.8	20.8	21.2	21.3	21.1	19.9	19.8	19.6	18.2	15.7	15.7	15.4		17.5	17.3	18.9	19.0	24.0	27.7	19.3
BMR01191_1749a_SGW_Phreodrilidae `sp. Biologic-OLIG012`	20.2	20.7	20.7	20.5	21.0	20.7	20.2	20.2	20.7	20.7	20.7	21.1	19.9	21.0	21.0	21.0	21.0	21.0	22.9	20.7	20.5	21.4	21.9	21.7	17.9	17.2	16.3	17.2	17.5		18.2	18.0	19.3	22.5	27.3	19.6
KM206511_Phreodrilidae sp.5_Ridley River_Brown et al. 2015	20.2	19.7	19.6	19.8	20.1	20.5	20.2	20.2	20.7	20.7	20.7	20.7	20.8	20.5	20.5	20.5	20.5	20.5	20.3	20.5	20.1	20.9	21.0	20.8	19.8	19.0	18.5	19.0	17.3	18.2		19.9	19.0	22.6	28.3	19.3
KM206524_Phreodrilidae sp.8_North Shaw River_Brown et al. 2015	18.8	19.1	19.1	19.2	19.6	19.7	18.8	18.8	18.8	18.8	18.8	18.3	18.8	18.6	18.6	18.6	18.6	18.6	18.9	19.7	19.6	19.0	20.7	20.8	18.4	20.0	18.3	19.9	18.9	18.0	19.9		18.3	21.3	26.5	18.8
KM206522_Phreodrilidae sp.9_Eel Creek_Brown et al. 2015	17.7	18.5	18.5	18.5	18.5	18.2	17.7	17.7	18.0	18.0	18.0	18.3	18.0	17.9	17.9	17.9	17.9	17.9	17.9	18	18.3	18.7	19.3	19.5	19.3	19.0	18.3	19.0	19.0	19.3	19.0	18.3		23.0	27.4	18.7
KM206509_Naididae sp5._Ridley River_Brown et al. 2015_OUTGROUP	21.2	21.2	21.2	21.4	21.4	21.4	21.2	21.2	21.5	21.5	21.5	21.3	21.2	21.4	21.4	21.4	21.4	21.4	21.4	21.4	22.0	23.1	20.8	20.9	24.6	23.4	25.0	24.0	24.0	22.5	22.6	21.3	23.0		26.9	22.2
Orobdella ketagalan_OUTGROUP	26.2	26.0	26.0	26.2	26.3	25.9	26.2	26.3	26.6	26.6	26.6	26.7	25.6	25.9	25.9	25.9	25.9	25.9	25.8	25.7	26.8	27.5	25.4	25.6	27.7	27.4	28.5	30.1	27.7	27.3	28.3	26.5	27.4	26.9		27.3
KM206521_Phreodrilidae sp.16_Eel Creek_Brown et al. 2015	16.9	17.6	17.5	17.6	17.9	17.0	16.9	17.0	17.0	17.0	17.0	16.4	16.9	16.9	16.9	16.9	16.9	16.9	16.7	17	17.0	15.6	16.0	16.1	19.6	21.7	19.9	19.2	19.3	19.6	19.3	18.8	18.7	22.2	27.3	

Diplopoda: Polydesmida

COI Pairwise Distances (%)	BMR02708	KC193678	MN699768	MT491274	MN699770	MT491291	MT491297	MT491292	KM611631	MF746508	KR818294	JN637366	MN433297	MN531852	WAMT111856	WAMT113481	WAMT124140	WAMT120063	WAMT113251	WAMT112613	WAMT120056	MW384907	MW384913	MW384916	IV379	MT621070
BMR02708_20112_Polydesmida `sp. Biologic-POLD002`		14.2	12.6	13.0	13.7	13.0	12.3	13.0	15.6	15.9	15.6	16.1	16.0	15.2	15.1	15.3	15.3	15.3	14.8	15.7	15.7	16.2	16.2	16.0	15.9	24.0
KC193678_Riukiaria sp.	14.2		12.9	13.3	12.2	12.3	12.0	11.5	12.7	13.0	11.8	15.8	13.8	15.6	13.0	13.2	13.2	14.1	13.6	13.6	13.6	14.0	15.8	15.8	14.0	20.7
MN699768_Nannaria morrisoni	12.6	12.9		1.0	6.4	8.8	8.8	9.5	11.9	12.2	15.8	15.3	14.3	14.8	14.1	14.3	14.3	13.8	13.8	15.5	16.0	13.4	13.8	15.5	16.2	22.9
MT491274_Nannaria morrisoni	13.0	13.3	1.0		6.5	9.3	8.8	10.0	13.0	13.3	15.3	15.0	15.5	16.5	13.8	14.0	14.0	13.8	14.2	15.3	16.3	14.3	13.3	16.3	16.5	23.6
MN699770_Nannaria sp.	13.7	12.2	6.4	6.5		9.0	8.5	8.5	12.7	13.0	14.7	16.1	14.2	15.2	13.9	14.2	14.2	13.7	14.1	14.9	14.9	13.4	13.4	15.2	14.2	22.7
MT491291_Nannaria sp.	13.0	12.3	8.8	9.3	9.0		3.3	7.8	12.0	12.3	13.0	14.8	13.8	13.5	13.8	14.0	14.0	13.0	13.2	15.8	15.8	13.5	13.3	14.0	15.0	24.3
MT491297_Nannaria sp.	12.3	12.0	8.8	8.8	8.5	3.3		6.8	12.0	12.3	13.0	14.8	14.0	13.5	13.3	13.5	13.5	12.3	13.2	15.5	16.0	12.3	13.3	13.3	15.0	23.6
MT491292_Nannaria sp.	13.0	11.5	9.5	10.0	8.5	7.8	6.8		11.8	12.0	13.0	13.8	12.8	13.0	14.0	14.3	14.3	14.3	14.0	13.8	14.3	13.0	12.8	13.0	14.8	24.1
KM611631_Diplopoda sp.	15.6	12.7	11.9	13.0	12.7	12.0	12.0	11.8		0.6	16.5	15.8	13.1	13.1	13.9	14.1	14.1	13.2	14.7	15.7	15.9	15.8	14.9	14.3	15.1	22.5
MF746508_Xystodesmidae sp.	15.9	13.0	12.2	13.3	13.0	12.3	12.3	12.0	0.6		16.6	16.1	13.2	13.4	14.0	14.2	14.2	13.3	14.9	15.8	16.0	15.9	15.0	14.6	15.2	22.3
KR818294_Sellanucheza grandis	15.6	11.8	15.8	15.3	14.7	13.0	13.0	13.0	16.5	16.6		16.0	15.1	14.4	12.6	12.8	12.8	14.4	15.2	13.6	13.6	14.0	15.1	15.3	16.2	23.6
JN637366_Antichiropus sp.	16.1	15.8	15.3	15.0	16.1	14.8	14.8	13.8	15.8	16.1	16.0		13.1	13.9	11.4	11.4	11.4	11.8	11.7	10.9	11.8	16.4	15.1	13.8	16.8	24.3
MN433297_Antichiropus sp.	16.0	13.8	14.3	15.5	14.2	13.8	14.0	12.8	13.1	13.2	15.1	13.1		5.8	7.8	8.3	8.3	10.1	10.3	10.3	10.5	13.6	14.7	12.4	15.8	22.9
MN531852_Antichiropus georginae	15.2	15.6	14.8	16.5	15.2	13.5	13.5	13.0	13.1	13.4	14.4	13.9	5.8		10.7	10.7	10.7	10.7	11.9	11.8	11.5	13.1	16.2	13.3	16.7	25.1
WAMT111856_Antichiropus sloanae	15.1	13.0	14.1	13.8	13.9	13.8	13.3	14.0	13.9	14.0	12.6	11.4	7.8	10.7		0.4	0.4	5.3	7.3	6.9	6.9	12.8	14.8	12.1	16.2	22.4
WAMT113481_Antichiropus sloanae	15.3	13.2	14.3	14.0	14.2	14.0	13.5	14.3	14.1	14.2	12.8	11.4	8.3	10.7	0.4		0.0	5.3	7.7	7.3	7.3	13.0	14.6	12.1	16.4	22.7
WAMT124140_Antichiropus sloanae	15.3	13.2	14.3	14.0	14.2	14.0	13.5	14.3	14.1	14.2	12.8	11.4	8.3	10.7	0.4	0.0		5.3	7.7	7.3	7.3	13.0	14.6	12.1	16.4	22.7
WAMT120063_Antichiropus apricus	15.3	14.1	13.8	13.8	13.7	13.0	12.3	14.3	13.2	13.3	14.4	11.8	10.1	10.7	5.3	5.3	5.3		5.7	8.4	9.3	13.7	14.8	14.1	14.9	23.6
WAMT113251_Antichiropus `DIP032`, bluespec	14.8	13.6	13.8	14.2	14.1	13.2	13.2	14.0	14.7	14.9	15.2	11.7	10.3	11.9	7.3	7.7	7.7	5.7		8.2	9.1	14.7	15.2	14.1	15.7	22.2
WAMT112613_Antichiropus forcipatus	15.7	13.6	15.5	15.3	14.9	15.8	15.5	13.8	15.7	15.8	13.6	10.9	10.3	11.8	6.9	7.3	7.3	8.4	8.2		1.3	13.9	14.8	13.4	15.5	23.3
WAMT120056_Antichiropus forcipatus	15.7	13.6	16.0	16.3	14.9	15.8	16.0	14.3	15.9	16.0	13.6	11.8	10.5	11.5	6.9	7.3	7.3	9.3	9.1	1.3		13.2	15.7	13.2	15.7	23.7
MW384907_Tylopus nodulipes	16.2	14.0	13.4	14.3	13.4	13.5	12.3	13.0	15.8	15.9	14.0	16.4	13.6	13.1	12.8	13.0	13.0	13.7	14.7	13.9	13.2		12.4	13.8	17.8	22.7
MW384913_Tylopus sp.	16.2	15.8	13.8	13.3	13.4	13.3	13.3	12.8	14.9	15.0	15.1	15.1	14.7	16.2	14.8	14.6	14.6	14.8	15.2	14.8	15.7	12.4		11.6	18.7	23.6
MW384916_Tylopus spinisterna	16.0	15.8	15.5	16.3	15.2	14.0	13.3	13.0	14.3	14.6	15.3	13.8	12.4	13.3	12.1	12.1	12.1	14.1	14.1	13.4	13.2	13.8	11.6		17.6	23.3
IV379_RC14MEB0115-20160317-T2-01_Haplodesmidae	15.9	14.0	16.2	16.5	14.2	15.0	15.0	14.8	15.1	15.2	16.2	16.8	15.8	16.7	16.2	16.4	16.4	14.9	15.7	15.5	15.7	17.8	18.7	17.6		22.5
MT621070_BMR01585_Polyxenidae sp. Biologic-POLX005	24.0	20.7	22.9	23.6	22.7	24.3	23.6	24.1	22.5	22.3	23.6	24.3	22.9	25.1	22.4	22.7	22.7	23.6	22.2	23.3	23.7	22.7	23.6	23.3	22.5	

Diplopoda: Polyxenida

COI Pairwise Distances (%)	MG279506	MF592725	BMR00233	BMR00669	BMR01869	BMR00416	BMR00612	BMR01866	BMR01870	P6	S46	S55	P32	P62	S22	S23	P4	P11	P12	P15	BMR00234	BMR00235	P34	BMR01872	BMR00476	BMR00415	BMR00262	P33	P3	BMR00312	BMR00552	BMR00315	BMR00316	BMR01863	BMR01873	BMR01876	P1	P52	P50	S12	S31	S45	BMR00492	BMR00317	BMR00668	BMR00477	MT621070	MW621058	MG204535	BMR02669	P53	BMR01871	BMR01881	MF592721	KY820868	MH932612
MG279506 Monographis queenslandicus		16.5	16.0	16.0	16.0	16.1	16.0	15.8	15.8	15.5	15.8	16.5	16.1	15.5	15.2	16.9	17.6	17.7	15.9	16.3	14.8	14.6	15.2	14.5	14.6	15.0	14.8	14.8	14.8	15.5	15.6	15.6	15.3	16.0	15.6	15.6	15.3	15.9	15.4	17.4	16.6	16.5	15.0	16.0	15.8	15.3	15.3	15.6	15.1	14.3	13.9	14.1	14.1	18.0	22.3	21.3
MF592725 Alloproctoides sp. VV-2017	16.5		18.6	18.6	18.6	18.8	18.6	18.6	18.6	19.7	18.6	18.9	19.0	19.0	19.0	18.2	19.3	19.3	18.4	18.6	16.9	16.9	17.4	17.1	17.1	17.3	17.8	17.8	17.1	18.0	18.2	18.6	18.0	18.0	17.5	17.3	18.0	17.9	18.5	18.5	18.5	17.6	18.2	16.9	17.1	17.3	17.3	17.6	15.7	17.8	17.3	17.8	17.8	17.5	19.2	20.3
BMR00233_1749b_DSM_Polxenida sp. Biologic-POLX002	16.0	18.6		0.0	0.0	0.2	0.2	0.3	0.3	2.6	1.2	1.6	2.0	1.8	1.9	4.0	8.6	7.6	4.2	4.4	11.9	11.3	11.1	10.8	10.3	11.4	10.6	10.8	11.4	10.8	10.9	11.1	10.8	10.9	10.9	11.7	11.2	11.0	11.4	11.6	10.8	11.5	10.0	11.4	11.3	11.6	11.9	10.7	16.7	17.9	17.7	18.4	18.4	20.3	25.3	22.8
BMR00669_1811_Polxenida `sp. Biologic-POLX002`	16.0	18.6	0.0		0.0	0.2	0.2	0.3	0.3	2.6	1.2	1.6	2.0	1.8	1.9	4.0	8.6	7.6	4.2	4.4	11.9	11.3	11.1	10.8	10.3	11.4	10.6	10.8	11.4	10.8	10.9	11.1	10.8	10.9	10.9	11.7	11.2	11.0	11.4	11.6	10.8	11.5	10.0	11.4	11.3	11.6	11.9	10.7	16.7	17.9	17.7	18.4	18.4	20.3	25.3	22.8
BMR01869_1953_Lophoproctidae `sp. Biologic-POLX002`	16.0	18.6	0.0	0.0		0.2	0.2	0.3	0.3	2.6	1.2	1.6	2.0	1.8	1.9	4.0	8.6	7.6	4.2	4.4	11.9	11.3	11.1	10.8	10.3	11.4	10.6	10.8	11.4	10.8	10.9	11.1	10.8	10.9	10.9	11.7	11.2	11.0	11.4	11.6	10.8	11.5	10.0	11.4	11.3	11.6	11.9	10.7	16.7	17.9	17.7	18.4	18.4	20.3	25.3	22.8
BMR00416_1749b_DSM_Polxenida sp. Biologic-POLX002	16.1	18.8	0.2	0.2	0.2		0.3	0.5	0.5	2.8	1.4	1.8	2.0	2.0	2.0	4.1	8.7	7.7	4.3	4.5	12.0	11.4	11.2	10.6	10.5	11.3	10.8	10.9	11.3	10.9	11.1	10.9	10.9	11.1	11.1	11.9	11.4	11.2	11.5	11.8	10.9	11.5	10.2	11.6	11.4	11.7	12.0	10.7	16.9	18.1	17.9	18.5	18.5	20.5	25.5	23.0
BMR00612_1811_Polxenida `sp. Biologic-POLX002`	16.0	18.6	0.2	0.2	0.2	0.3		0.5	0.5	2.8	1.4	1.8	2.1	2.0	1.9	4.1	8.7	7.7	4.3	4.5	12.0	11.4	11.2	10.9	10.5	11.6	10.8	10.9	11.6	10.9	11.1	11.3	10.9	11.1	11.1	11.9	11.4	11.2	11.5	11.8	10.9	11.6	10.2	11.6	11.4	11.7	12.0	10.9	16.7	17.9	17.7	18.4	18.4	20.3	25.3	22.8
BMR01866_1953_Lophoproctidae `sp. Biologic-POLX002`	15.8	18.6	0.3	0.3	0.3	0.5	0.5		0.0	2.9	1.5	1.9	2.1	2.1	2.2	4.3	8.8	7.7	4.5	4.7	11.7	11.4	11.4	10.9	10.5	11.3	10.8	11.1	11.3	10.9	11.1	11.3	10.9	11.1	11.1	11.9	11.4	11.2	11.5	11.6	10.8	11.5	10.3	11.6	11.4	11.7	12.0	10.9	16.7	17.9	17.7	18.4	18.4	20.3	25.5	22.8
BMR01870_1953_Lophoproctidae `sp. Biologic-POLX002`	15.8	18.6	0.3	0.3	0.3	0.5	0.5	0.0		2.9	1.5	1.9	2.1	2.1	2.2	4.3	8.8	7.7	4.5	4.7	11.7	11.4	11.4	10.9	10.5	11.3	10.8	11.1	11.3	10.9	11.1	11.3	10.9	11.1	11.1	11.9	11.4	11.2	11.5	11.6	10.8	11.5	10.3	11.6	11.4	11.7	12.0	10.9	16.7	17.9	17.7	18.4	18.4	20.3	25.5	22.8
P6_RC08SILVPIT1-3_Polyxenida	15.5	19.7	2.6	2.6	2.6	2.8	2.8	2.9	2.9		3.3	3.3	3.5	3.5	3.8	5.5	9.7	8.6	5.6	6.0	13.1	12.1	11.9	11.8	11.2	12.5	11.4	12.1	12.3	11.6	11.8	11.6	11.6	11.8	12.0	12.5	11.5	12.1	11.9	11.1	11.0	11.1	10.9	12.5	12.3	12.9	12.9	12.8	16.2	17.5	17.2	17.3	17.3	20.8	19.5	22.4
S46_RHWRC0303P2T2-3_Polyxenida_Hmstd-Namm-Silv	15.8	18.6	1.2	1.2	1.2	1.4	1.4	1.5	1.5	3.3		2.6	2.9	1.1	1.2	4.2	8.8	7.5	4.5	4.7	10.9	10.8	10.6	10.6	9.7	10.9	10.0	10.3	11.0	10.2	10.3	10.5	10.2	10.2	10.2	10.9	10.7	10.5	10.8	11.1	10.3	10.6	10.0	11.7	11.6	11.9	12.2	11.3	16.1	17.6	17.4	18.1	18.1	20.0	24.7	22.3
S55_RC08NAM389P2T3-2_Polyxenida_Hmstd-Namm-Silv	16.5	18.9	1.6	1.6	1.6	1.8	1.8	1.9	1.9	3.3	2.6		1.9	2.9	3.1	3.9	9.1	7.8	3.9	4.3	12.3	11.7	11.7	11.4	10.8	11.9	11.1	11.4	12.1	11.4	11.6	11.4	11.4	11.6	11.2	12.2	12.0	11.9	12.1	11.5	10.5	11.9	10.6	11.9	11.9	12.3	12.5	11.7	17.2	18.2	17.9	18.7	18.7	20.2	25.0	23.0
P32_RC05TCB476P1T2-4_T98386_Polyxenida	16.1	19.0	2.0	2.0	2.0	2.0	2.1	2.1	2.1	3.5	2.9	1.9		3.2	3.5	4.4	9.3	8.0	4.7	5.1	12.3	11.4	11.5	11.1	10.6	11.4	11.1	11.5	11.4	11.3	11.4	11.1	11.3	11.1	11.3	12.1	11.6	11.8	11.9	12.0	11.2	11.8	11.1	12.1	12.1	12.4	12.8	12.1	16.6	18.3	18.1	18.8	18.8	20.2	21.9	23.3
P62_CGBRC0285P1T2-2A_T102623A_Polyxenida	15.5	19.0	1.8	1.8	1.8	2.0	2.0	2.1	2.1	3.5	1.1	2.9	3.2		1.7	4.4	9.3	7.7	4.5	4.7	11.6	11.1	11.1	10.9	9.9	11.6	10.4	11.3	11.4	10.8	10.9	10.9	10.8	10.8	10.9	11.6	11.1	11.2	11.4	11.6	10.8	10.8	10.4	11.8	11.6	11.9	12.3	12.4	16.1	17.9	17.9	18.4	18.4	20.9	21.3	22.3
S22_CGBRC0278P2T1-2_Polyxenida_Hmstd-Namm-Silv	15.2	19.0	1.9	1.9	1.9	2.0	1.9	2.2	2.2	3.8	1.2	3.1	3.5	1.7		5.0	9.9	8.4	5.1	5.5	11.4	11.2	11.3	11.0	10.1	11.5	10.5	11.2	11.5	10.9	11.0	11.0	10.9	10.9	11.0	11.7	11.3	11.3	11.5	11.5	10.9	11.4	10.7	12.3	12.2	12.3	13.0	12.4	16.3	17.9	17.9	18.4	18.4	20.2	21.2	22.8
S23_RC09SV023P2T1-3_Polyxenida_Hmstd-Namm-Silv	16.9	18.2	4.0	4.0	4.0	4.1	4.1	4.3	4.3	5.5	4.2	3.9	4.4	4.4	5.0		7.3	5.1	2.2	2.8	12.0	11.1	11.4	10.9	10.5	11.6	10.6	11.3	11.8	11.4	11.6	11.9	11.7	11.9	11.3	12.5	12.1	11.9	12.5	11.8	10.9	12.2	10.8	12.2	12.2	12.5	12.5	12.2	17.0	17.0	16.9	17.5	17.5	19.0	25.6	23.1
P4_RC08SILV0795PIT1-3_Polyxenida	17.6	19.3	8.6	8.6	8.6	8.7	8.7	8.8	8.8	9.7	8.8	9.1	9.3	9.3	9.9	7.3		7.4	8.6	9.0	11.0	10.2	10.2	9.9	9.8	10.4	9.8	9.8	10.7	10.2	10.4	10.8	10.5	10.8	10.4	11.1	11.1	10.9	11.4	12.5	12.0	13.0	11.3	12.5	12.5	12.5	12.8	13.0	18.1	19.2	18.8	19.5	19.5	19.7	27.0	24.2
P11_RC08SILV0795PIT3-3_Polyxenida	17.7	19.3	7.6	7.6	7.6	7.7	7.7	7.7	7.7	8.6	7.5	7.8	8.0	7.7	8.4	5.1	7.4		6.5	7.0	11.2	10.3	10.8	10.1	9.5	10.8	9.8	10.6	11.0	10.5	10.6	10.9	10.6	10.8	10.3	11.2	11.1	10.8	11.1	12.4	11.5	12.6	11.5	12.0	12.0	12.0	12.3	12.2	17.9	18.8	18.5	19.1	19.1	19.9	26.8	23.5
P12_RC07S10B259P1T3-1_Polyxenida	15.9	18.4	4.2	4.2	4.2	4.3	4.3	4.5	4.5	5.6	4.5	3.9	4.7	4.5	5.1	2.2	8.6	6.5		1.9	12.6	11.1	11.6	11.3	10.8	11.8	11.1	11.6	11.7	11.5	11.6	12.0	11.8	12.0	11.8	12.6	11.8	11.8	12.3	12.0	11.2	12.2	10.8	12.1	12.1	12.5	12.5	12.9	16.4	17.3	17.3	17.8	17.8	19.3	21.0	22.9
P15_RC07S10B102P1T1-1_Polyxenida	16.3	18.6	4.4	4.4	4.4	4.5	4.5	4.7	4.7	6.0	4.7	4.3	5.1	4.7	5.5	2.8	9.0	7.0	1.9		13.2	11.3	11.7	11.5	11.0	12.0	11.3	11.8	11.9	11.3	11.5	12.2	12.0	12.2	12.0	12.8	12.0	12.0	12.3	12.2	11.2	11.9	11.2	12.2	12.2	12.7	12.5	13.3	16.7	17.8	17.9	18.3	18.3	19.9	21.4	23.3
BMR00234_1749b_BS3X_Polxenida sp. Biologic-POLX003`	14.8	16.9	11.9	11.9	11.9	12.0	12.0	11.7	11.7	13.1	10.9	12.3	12.3	11.6	11.4	12.0	11.0	11.2	12.6	13.2		3.7	3.8	3.3	3.2	3.2	3.5	3.7	3.3	5.2	5.2	5.5	5.0	6.1	5.9	5.6	5.8	5.6	5.9	9.7	8.8	10.5	9.0	9.4	9.3	8.7	9.7	9.2	16.3	18.1	17.8	18.4	18.4	17.8	25.2	22.5
BMR00235_1749b_BS2W_Polxenida `sp. Biologic-POLX003`	14.6	16.9	11.3	11.3	11.3	11.4	11.4	11.4	11.4	12.1	10.8	11.7	11.4	11.1	11.2	11.1	10.2	10.3	11.1	11.3	3.7		2.6	2.1	1.7	2.3	2.6	2.9	2.3	4.4	4.6	5.2	4.7	5.5	5.3	5.3	5.5	5.1	5.3	9.7	8.9	10.8	8.5	8.5	8.4	7.8	8.8	8.3	16.1	17.2	16.8	17.5	17.5	18.8	25.2	22.8
P34_RC05TCB667P1T2-1_T98389_Polyxenida	15.2	17.4	11.1	11.1	11.1	11.2	11.2	11.4	11.4	11.9	10.6	11.7	11.5	11.1	11.3	11.4	10.2	10.8	11.6	11.7	3.8	2.6		2.7	3.1	3.4	3.2	2.7	3.3	4.8	4.8	5.2	4.9	5.5	5.4	5.4	5.5	5.3	5.7	9.8	8.9	10.5	8.9	8.9	8.8	8.5	9.1	8.3	16.7	18.0	17.7	17.9	17.9	18.5	25.4	23.8
BMR01872_1953_Lophoproctidae `sp. Biologic-POLX003`	14.5	17.1	10.8	10.8	10.8	10.6	10.9	10.9	10.9	11.8	10.6	11.4	11.1	10.9	11.0	10.9	9.9	10.1	11.3	11.5	3.3	2.1	2.7		2.3	2.3	2.6	3.2	2.2	4.6	4.6	4.6	4.7	5.2	5.0	5.0	5.3	5.1	5.4	9.5	8.5	10.1	8.5	8.5	8.4	7.8	8.8	8.1	16.9	17.0	16.6	17.3	17.3	18.4	25.3	22.8
BMR00476_1749b_BS2SW_Polxenida `sp. Biologic-POLX003`	14.6	17.1	10.3	10.3	10.3	10.5	10.5	10.5	10.5	11.2	9.7	10.8	10.6	9.9	10.1	10.5	9.8	9.5	10.8	11.0	3.2	1.7	3.1	2.3		2.7	2.1	3.4	2.8	4.6	4.7	4.9	4.6	5.6	5.5	5.5	5.3	4.9	5.3	9.0	8.2	10.1	8.7	7.9	7.8	7.1	8.2	7.6	16.3	17.3	17.0	17.6	17.6	17.8	25.2	22.8
BMR00415_1749a_SGW_Polxenida `sp. Biologic-POLX003`	15.0	17.3	11.4	11.4	11.4	11.3	11.6	11.3	11.3	12.5	10.9	11.9	11.4	11.6	11.5	11.6	10.4	10.8	11.8	12.0	3.2	2.3	3.4	2.3	2.7		3.0	3.6	0.3	4.6	4.6	4.6	4.4	5.5	5.3	5.3	5.2	5.3	5.6	9.2	8.3	10.1	9.0	9.7	9.6	9.0	10.0	9.8	16.6	18.1	17.6	18.4	18.4	18.2	25.8	23.6
BMR00262_1845_BS1C_Polxenida `sp. Biologic-POLX003`	14.8	17.8	10.6	10.6	10.6	10.8	10.8	10.8	10.8	11.4	10.0	11.1	11.1	10.4	10.5	10.6	9.8	9.8	11.1	11.3	3.5	2.6	3.2	2.6	2.1	3.0		3.7	3.1	4.4	4.4	4.6	4.3	5.3	5.2	5.2	5.0	5.1	5.4	9.0	8.0	9.9	8.5	8.4	8.2	7.6	8.8	8.3	16.4	17.6	17.1	17.9	17.9	18.0	25.2	23.0
P33_WD05TCB006P1T2-2_T98384_Polyxenida	14.8	17.8	10.8	10.8	10.8	10.9	10.9	11.1	11.1	12.1	10.3	11.4	11.5	11.3	11.2	11.3	9.8	10.6	11.6	11.8	3.7	2.9	2.7	3.2	3.4	3.6	3.7		3.4	4.3	4.3	5.3	4.8	5.6	5.1	5.5	5.2	4.9	5.1	9.5	8.8	10.2	9.7	9.4	9.2	8.5	9.6	9.6	16.1	17.3	17.3	17.1	17.1	18.4	21.4	23.1
P3_RC08SILV0796PIT1-2_Polyxenida	14.8	17.1	11.4	11.4	11.4	11.3	11.6	11.3	11.3	12.3	11.0	12.1	11.4	11.4	11.5	11.8	10.7	11.0	11.7	11.9	3.3	2.3	3.3	2.2	2.8	0.3	3.1	3.4		4.7	4.7	4.7	4.6	5.7	5.4	5.5	5.0	5.2	5.6	9.0	8.3	9.8	9.2	9.7	9.5	8.9	10.0	9.8	16.0	18.1	17.5	18.4	18.4	18.0	23.2	23.8
BMR00312_1811_Polxenida `sp. Biologic-POLX003`	15.5	18.0	10.8	10.8	10.8	10.9	10.9	10.9	10.9	11.6	10.2	11.4	11.3	10.8	10.9	11.4	10.2	10.5	11.5	11.3	5.2	4.4	4.8	4.6	4.6	4.6	4.4	4.3	4.7		0.3	2.0	1.7	1.8	2.0	2.0	2.3	1.9	2.8	8.9	7.9	9.9	8.2	8.7	8.5	8.5	9.0	8.7	16.4	18.1	17.8	18.4	18.4	18.2	25.0	22.8
BMR00552_1811_Polxenida `sp. Biologic-POLX003`	15.6	18.2	10.9	10.9	10.9	11.1	11.1	11.1	11.1	11.8	10.3	11.6	11.4	10.9	11.0	11.6	10.4	10.6	11.6	11.5	5.2	4.6	4.8	4.6	4.7	4.6	4.4	4.3	4.7	0.3		2.0	1.7	1.8	2.0	2.0	2.3	1.6	2.7	9.0	8.0	9.7	8.4	8.8	8.7	8.7	9.1	8.9	16.6	18.2	17.9	18.5	18.5	18.2	25.0	23.0
BMR00315_1811_Polxenida `sp. Biologic-POLX003`	15.6	18.6	11.1	11.1	11.1	10.9	11.3	11.3	11.3	11.6	10.5	11.4	11.1	10.9	11.0	11.9	10.8	10.9	12.0	12.2	5.5	5.2	5.2	4.6	4.9	4.6	4.6	5.3	4.7	2.0	2.0		1.5	2.1	2.3	2.0	2.5	2.7	4.1	8.5	7.6	10.1	8.1	9.0	8.8	8.8	9.3	8.7	16.9	19.0	18.8	19.3	19.3	18.2	26.1	23.0
BMR00316_1811_Polxenida `sp. Biologic-POLX003`	15.3	18.0	10.8	10.8	10.8	10.9	10.9	10.9	10.9	11.6	10.2	11.4	11.3	10.8	10.9	11.7	10.5	10.6	11.8	12.0	5.0	4.7	4.9	4.7	4.6	4.4	4.3	4.8	4.6	1.7	1.7	1.5		2.0	2.1	1.8	1.8	2.4	3.5	8.4	7.4	10.1	8.1	8.7	8.5	8.5	9.0	8.5	16.1	18.5	18.3	18.8	18.8	17.8	25.6	22.6
BMR01863_1953_Lophoproctidae `sp. Biologic-POLX003`	16.0	18.0	10.9	10.9	10.9	11.1	11.1	11.1	11.1	11.8	10.2	11.6	11.1	10.8	10.9	11.9	10.8	10.8	12.0	12.2	6.1	5.5	5.5	5.2	5.6	5.5	5.3	5.6	5.7	1.8	1.8	2.1	2.0		1.1	1.2	2.6	2.4	4.0	9.0	8.0	10.2	8.4	8.8	8.8	8.8	9.3	8.5	16.9	18.7	18.4	19.0	19.0	18.0	25.9	22.5
BMR01873_1953_Lophoproctidae `sp. Biologic-POLX003`	15.6	17.5	10.9	10.9	10.9	11.1	11.1	11.1	11.1	12.0	10.2	11.2	11.3	10.9	11.0	11.3	10.4	10.3	11.8	12.0	5.9	5.3	5.4	5.0	5.5	5.3	5.2	5.1	5.4	2.0	2.0	2.3	2.1	1.1		1.4	2.6	2.2	3.8	8.9	7.9	10.1	8.4	8.5	8.5	8.5	9.0	8.5	16.3	18.4	17.9	18.7	18.7	17.5	25.8	22.0
BMR01876_1953_Lophoproctidae `sp. Biologic-POLX003`	15.6	17.3	11.7	11.7	11.7	11.9	11.9	11.9	11.9	12.5	10.9	12.2	12.1	11.6	11.7	12.5	11.1	11.2	12.6	12.8	5.6	5.3	5.4	5.0	5.5	5.3	5.2	5.5	5.5	2.0	2.0	2.0	1.8	1.2	1.4		2.8	2.5	4.1	9.3	8.3	10.1	8.7	8.8	9.0	9.0	9.4	8.9	16.4	18.5	18.3	18.8	18.8	17.8	26.1	22.2
P1_DD08SILV09PIT1-1_Polyxenida	15.3	18.0	11.2	11.2	11.2	11.4	11.4	11.4	11.4	11.5	10.7	12.0	11.6	11.1	11.3	12.1	11.1	11.1	11.8	12.0	5.8	5.5	5.5	5.3	5.3	5.2	5.0	5.2	5.0	2.3	2.3	2.5	1.8	2.6	2.6	2.8		2.4	3.6	8.4	7.6	9.3	8.2	8.8	8.7	8.7	9.1	8.7	15.9	18.8	18.4	19.2	19.2	17.8	22.9	22.3
P52_RC03WR096P1T1-3B_Polyxenida	15.9	17.9	11.0	11.0	11.0	11.2	11.2	11.2	11.2	12.1	10.5	11.9	11.8	11.2	11.3	11.9	10.9	10.8	11.8	12.0	5.6	5.1	5.3	5.1	4.9	5.3	5.1	4.9	5.2	1.9	1.6	2.7	2.4	2.4	2.2	2.5	2.4		3.0	8.7	7.9	9.6	8.8	8.3	8.2	8.2	8.6	8.4	15.6	18.4	18.2	18.7	18.7	17.7	22.1	22.6
P50_MEGDC0057AP1T1-3C_T99566C_Polyxenida	15.4	18.5	11.4	11.4	11.4	11.5	11.5	11.5	11.5	11.9	10.8	12.1	11.9	11.4	11.5	12.5	11.4	11.1	12.3	12.3	5.9	5.3	5.7	5.4	5.3	5.6	5.4	5.1	5.6	2.8	2.7	4.1	3.5	4.0	3.8	4.1	3.6	3.0		8.7	8.0	9.7	9.1	9.3	9.1	9.1	9.4	9.5	15.9	17.8	17.3	18.1	18.1	18.3	21.7	22.9
S12_CGBRC0293P2T2-2_Polyxenida_Hmstd-Namm-Silv	17.4	18.5	11.6	11.6	11.6	11.8	11.8	11.6	11.6	11.1	11.1	11.5	12.0	11.6	11.5	11.8	12.5	12.4	12.0	12.2	9.7	9.7	9.8	9.5	9.0	9.2	9.0	9.5	9.0	8.9	9.0	8.5	8.4	9.0	8.9	9.3	8.4	8.7	8.7		0.9	6.2	8.5	9.3	9.3	9.3	10.0	9.7	16.8	20.0	20.0	19.9	19.9	17.7	26.2	23.3
S31_CGBRC0285P2T2-2_Polyxenida_Hmstd-Namm-Silv	16.6	18.5	10.8	10.8	10.8	10.9	10.9	10.8	10.8	11.0	10.3	10.5	11.2	10.8	10.9	10.9	12.0	11.5	11.2	11.2	8.8	8.9	8.9	8.5	8.2	8.3	8.0	8.8	8.3	7.9	8.0	7.6	7.4	8.0	7.9	8.3	7.6	7.9	8.0	0.9		5.6	8.0	8.8	8.8	8.8	9.5	9.3	16.4	19.6	19.6	20.0	20.0	17.3	25.2	22.2
S45_RHWRC0250P2T3-3_Polyxenida_Hmstd-Namm-Silv	16.5	17.6	11.5	11.5	11.5	11.5	11.6	11.5	11.5	11.1	10.6	11.9	11.8	10.8	11.4	12.2	13.0	12.6	12.2	11.9	10.5	10.8	10.5	10.1	10.1	10.1	9.9	10.2	9.8	9.9	9.7	10.1	10.1	10.2	10.1	10.1	9.3	9.6	9.7	6.2	5.6		9.7	10.1	9.9	9.9	10.7	11.5	16.5	20.0	19.4	20.5	20.5	20.2	24.9	22.5
BMR00492_1931_BHT_Lophoproctidae `sp. Biologic-POLX001	15.0	18.2	10.0	10.0	10.0	10.2	10.2	10.3	10.3	10.9	10.0	10.6	11.1	10.4	10.7	10.8	11.3	11.5	10.8	11.2	9.0	8.5	8.9	8.5	8.7	9.0	8.5	9.7	9.2	8.2	8.4	8.1	8.1	8.4	8.4	8.7	8.2	8.8	9.1	8.5	8.0	9.7		8.8	8.7	8.8	9.3	8.9	16.1	18.2	17.7	18.5	18.5	18.0	25.3	22.3
BMR00317_1811_Polxenida `sp. Biologic-POLX005`	16.0	16.9	11.4	11.4	11.4	11.6	11.6	11.6	11.6	12.5	11.7	11.9	12.1	11.8	12.3	12.2	12.5	12.0	12.1	12.2	9.4	8.5	8.9	8.5	7.9	9.7	8.4	9.4	9.7	8.7	8.8	9.0	8.7	8.8	8.5	8.8	8.8	8.3	9.3	9.3	8.8	10.1	8.8		0.2	1.1	1.2	1.5	15.7	18.1	17.6	18.4	18.4	16.9	25.3	22.6
BMR00668_1811_Polxenida `sp. Biologic-POLX005`	15.8	17.1	11.3	11.3	11.3	11.4	11.4	11.4	11.4	12.3	11.6	11.9	12.1	11.6	12.2	12.2	12.5	12.0	12.1	12.2	9.3	8.4	8.8	8.4	7.8	9.6	8.2	9.2	9.5	8.5	8.7	8.8	8.5	8.8	8.5	9.0	8.7	8.2	9.1	9.3	8.8	9.9	8.7	0.2		0.9	1.1	1.3	15.8	18.1	17.6	18.4	18.4	17.1	25.2	22.8
BMR00477_1749b_LNSG_Polxenida `sp. Biologic-POLX005`	15.3	17.3	11.6	11.6	11.6	11.7	11.7	11.7	11.7	12.9	11.9	12.3	12.4	11.9	12.3	12.5	12.5	12.0	12.5	12.7	8.7	7.8	8.5	7.8	7.1	9.0	7.6	8.5	8.9	8.5	8.7	8.8	8.5	8.8	8.5	9.0	8.7	8.2	9.1	9.3	8.8	9.9	8.8	1.1	0.9		1.5	1.5	15.5	17.6	17.1	17.9	17.9	16.9	25.3	22.2
MT621070_BMR01585_Polyxenidae sp. Biologic-POLX005	15.3	17.3	11.9	11.9	11.9	12.0	12.0	12.0	12.0	12.9	12.2	12.5	12.8	12.3	13.0	12.5	12.8	12.3	12.5	12.5	9.7	8.8	9.1	8.8	8.2	10.0	8.8	9.6	10.0	9.0	9.1	9.3	9.0	9.3	9.0	9.4	9.1	8.6	9.4	10.0	9.5	10.7	9.3	1.2	1.1	1.5		2.2	15.7	17.9	17.3	18.2	18.2	16.9	25.5	22.8
MW621058	15.6	17.6	10.7	10.7	10.7	10.7	10.9	10.9	10.9	12.8	11.3	11.7	12.1	12.4	12.4	12.2	13.0	12.2	12.9	13.3	9.2	8.3	8.3	8.1	7.6	9.8	8.3	9.6	9.8	8.7	8.9	8.7	8.5	8.5	8.5	8.9	8.7	8.4	9.5	9.7	9.3	11.5	8.9	1.5	1.3	1.5	2.2		14.8	17.4	17.4	18.3	18.3	17.3	19.1	22.4
MG204535 L. queenslandicus CH_AV_LQ1	15.1	15.7	16.7	16.7	16.7	16.9	16.7	16.7	16.7	16.2	16.1	17.2	16.6	16.1	16.3	17.0	18.1	17.9	16.4	16.7	16.3	16.1	16.7	16.9	16.3	16.6	16.4	16.1	16.0	16.4	16.6	16.9	16.1	16.9	16.3	16.4	15.9	15.6	15.9	16.8	16.4	16.5	16.1	15.7	15.8	15.5	15.7	14.8		16.1	15.6	16.7	16.7	19.2	21.3	21.9
BMR02669_20112_Polyxenida `sp. Biologic-POLX006`	14.3	17.8	17.9	17.9	17.9	18.1	17.9	17.9	17.9	17.5	17.6	18.2	18.3	17.9	17.9	17.0	19.2	18.8	17.3	17.8	18.1	17.2	18.0	17.0	17.3	18.1	17.6	17.3	18.1	18.1	18.2	19.0	18.5	18.7	18.4	18.5	18.8	18.4	17.8	20.0	19.6	20.0	18.2	18.1	18.1	17.6	17.9	17.4	16.1		0.6	1.2	1.2	19.8	25.8	24.3
P53_BC051P1T1-2_Polyxenida_NoRaw	13.9	17.3	17.7	17.7	17.7	17.9	17.7	17.7	17.7	17.2	17.4	17.9	18.1	17.9	17.9	16.9	18.8	18.5	17.3	17.9	17.8	16.8	17.7	16.6	17.0	17.6	17.1	17.3	17.5	17.8	17.9	18.8	18.3	18.4	17.9	18.3	18.4	18.2	17.3	20.0	19.6	19.4	17.7	17.6	17.6	17.1	17.3	17.4	15.6	0.6		0.6	0.6	19.4	23.1	24.3
BMR01871_1953_Lophoproctidae `sp. Biologic-POLX006`	14.1	17.8	18.4	18.4	18.4	18.5	18.4	18.4	18.4	17.3	18.1	18.7	18.8	18.4	18.4	17.5	19.5	19.1	17.8	18.3	18.4	17.5	17.9	17.3	17.6	18.4	17.9	17.1	18.4	18.4	18.5	19.3	18.8	19.0	18.7	18.8	19.2	18.7	18.1	19.9	20.0	20.5	18.5	18.4	18.4	17.9	18.2	18.3	16.7	1.2	0.6		0.0	19.8	26.4	24.9
BMR01881_1953_Lophoproctidae `sp. Biologic-POLX006`	14.1	17.8	18.4	18.4	18.4	18.5	18.4	18.4	18.4	17.3	18.1	18.7	18.8	18.4	18.4	17.5	19.5	19.1	17.8	18.3	18.4	17.5	17.9	17.3	17.6	18.4	17.9	17.1	18.4	18.4	18.5	19.3	18.8	19.0	18.7	18.8	19.2	18.7	18.1	19.9	20.0	20.5	18.5	18.4	18.4	17.9	18.2	18.3	16.7	1.2	0.6	0.0		19.8	26.4	24.9
MF592721 Propolyxenus forsteri	18.0	17.5	20.3	20.3	20.3	20.5	20.3	20.3	20.3	20.8	20.0	20.2	20.2	20.9	20.2	19.0	19.7	19.9	19.3	19.9	17.8	18.8	18.5	18.4	17.8	18.2	18.0	18.4	18.0	18.2	18.2	18.2	17.8	18.0	17.5	17.8	17.8	17.7	18.3	17.7	17.3	20.2	18.0	16.9	17.1	16.9	16.9	17.3	19.2	19.8	19.4	19.8	19.8		21.1	22.6
KY820868 Phryssonotus sp. WA	22.3	19.2	25.3	25.3	25.3	25.5	25.3	25.5	25.5	19.5	24.7	25.0	21.9	21.3	21.2	25.6	27.0	26.8	21.0	21.4	25.2	25.2	25.4	25.3	25.2	25.8	25.2	21.4	23.2	25.0	25.0	26.1	25.6	25.9	25.8	26.1	22.9	22.1	21.7	26.2	25.2	24.9	25.3	25.3	25.2	25.3	25.5	19.1	21.3	25.8	23.1	26.4	26.4	21.1		29.9
MH932612 Antichiropus sp. DIP174_OUTGROUP	21.3	20.3	22.8	22.8	22.8	23.0	22.8	22.8	22.8	22.4	22.3	23.0	23.3	22.3	22.8	23.1	24.2	23.5	22.9	23.3	22.5	22.8	23.8	22.8	22.8	23.6	23.0	23.1	23.8	22.8	23.0	23.0	22.6	22.5	22.0	22.2	22.3	22.6	22.9	23.3	22.2	22.5	22.3	22.6	22.8	22.2	22.8	22.4	21.9	24.3	24.3	24.9	24.9	22.6	29.9	

Entognatha: Diplura

COI Pairwise Distances (%)	EW0333	BMR00207	BMR01205	BMR00380	BMR02653	WAME98666	JC18	BMR02654	BMR02655	RT48	BMR00269	BMR00274	KE04	BMR00297	BMR00781	BMR00490	BMR00209	LI30	JU01	JQ796644	IV156	JF37	KD12	KU08	KD15	BMR00195	BMR00728	BMR00737	BMR02656	IV245	IV248	BMR01929	EW0300	BMR01195	BMR01927	BMR00227	BMR00362	BMR00265	KU02	WAME98601	BMR01223	BMR00192	BMR02657	BMR02690	WAME34029	IV154	IV155	BMR00186	BMR00225	BMR02658	BMR02662	BMR02691	KU01	JU02	BMR01906	BMR01909	WAME98535	IV160
Japygidae sp EW0333		4.2	8.8	8.8	12.2	14.3	13.5	13.4	13.4	16.3	14.7	14.9	16.0	17.3	17.0	16.0	16.7	16.0	17.0	18.4	21.1	18.2	17.8	17.9	18.7	19.6	21.5	20.4	24.0	22.9	21.6	22.2	23.7	25.5	25.1	25.4	25.5	25.1	26.6	23.6	25.8	25.8	23.6	23.9	24.6	26.1	25.1	24.5	22.5	22.6	22.3	23.1	33.1	27.5	27.1	28.3	29.2	28.5
BMR00207_1845_BS1W_Japygidae `sp. Biologic-DIPL015`	4.2		8.3	8.3	11.5	13.4	14.1	13.6	13.6	15.5	13.8	14.6	14.6	17.0	16.5	15.3	15.8	15.6	16.4	17.0	20.2	16.5	17.0	15.8	17.6	17.9	21.3	20.6	23.4	21.7	20.8	22.2	23.4	23.8	23.7	24.4	24.6	25.5	25.8	21.9	26.0	26.3	23.4	24.0	24.2	24.4	24.8	23.8	21.4	22.0	22.0	22.6	32.9	27.7	27.6	27.9	27.9	29.0
BMR01205_1845_BS1E_Japygidae `sp. Biologic-DIPL014`	8.8	8.3		0.0	10.6	14.3	17.3	17.2	17.2	16.9	14.4	15.0	15.5	16.0	15.8	15.8	16.3	17.3	16.6	18.1	21.6	20.1	19.6	18.7	19.8	19.9	19.9	21.6	23.3	22.5	21.9	22.8	24.8	24.5	24.5	25.8	25.4	25.2	26.3	24.5	25.9	25.8	24.8	24.9	23.9	27.2	26.2	22.9	22.0	21.7	21.4	22.5	32.7	26.8	25.5	28.0	27.7	28.3
BMR00380_1845_BS1E_Japygidae `sp. Biologic-DIPL014`	8.8	8.3	0.0		10.6	14.3	17.3	17.2	17.2	16.9	14.4	15.0	15.5	16.0	15.8	15.8	16.3	17.3	16.6	18.1	21.6	20.1	19.6	18.7	19.8	19.9	19.9	21.6	23.3	22.5	21.9	22.8	24.8	24.5	24.5	25.8	25.4	25.2	26.3	24.5	25.9	25.8	24.8	24.9	23.9	27.2	26.2	22.9	22.0	21.7	21.4	22.5	32.7	26.8	25.5	28.0	27.7	28.3
BMR02653_20112_Japygidae `sp. Biologic-DIPL027`	12.2	11.5	10.6	10.6		14.3	16.0	14.8	14.8	15.7	14.3	13.8	15.4	15.0	15.2	15.2	16.7	16.4	16.6	18.2	19.1	16.4	17.0	18.7	18.2	17.9	20.3	21.0	24.8	23.1	21.4	21.3	24.0	24.0	23.7	26.1	24.6	25.7	26.1	23.9	25.0	24.8	25.4	25.8	24.1	27.1	26.2	23.3	22.9	22.2	21.9	23.4	32.1	25.6	26.0	27.2	28.6	30.0
RT56_PARA_WAME98666_Diplura?_2	14.3	13.4	14.3	14.3	14.3		13.8	16.1	16.1	15.0	14.6	14.6	14.6	16.0	16.6	16.0	16.1	16.1	16.1	18.2	19.8	17.9	17.9	19.9	18.8	20.1	22.2	19.8	23.4	21.1	20.8	23.7	23.1	23.6	22.0	22.5	25.1	25.7	25.8	22.3	25.0	25.1	22.9	23.3	23.7	25.7	24.8	24.3	21.6	21.7	21.9	22.5	32.2	23.9	29.5	27.7	26.7	30.8
JC18_BROCK4_Japygidae `sp. Helix marra mamba`	13.5	14.1	17.3	17.3	16.0	13.8		4.4	4.6	18.4	14.1	14.4	15.5	18.2	17.8	17.6	18.4	16.1	18.5	21.3	21.3	18.7	18.2	20.5	19.3	20.5	22.8	20.1	24.0	22.6	23.7	21.7	24.0	24.0	24.0	24.2	26.7	26.1	27.5	23.3	25.8	25.4	23.3	23.4	24.9	26.6	25.8	25.1	22.6	23.9	24.0	23.4	33.3	25.6	28.4	27.8	28.6	31.1
BMR02654_20112_Japygidae `sp. Biologic-DIPL028`	13.4	13.6	17.2	17.2	14.8	16.1	4.4		0.2	18.7	15.0	14.8	16.3	20.5	20.3	18.5	17.0	15.9	18.7	22.5	23.3	21.8	19.8	23.3	20.7	21.8	24.9	22.9	25.1	25.1	23.8	23.3	22.9	23.1	24.4	23.6	25.1	25.1	26.0	22.5	26.3	26.0	22.5	22.2	27.5	25.6	25.9	26.2	23.8	24.7	24.9	24.7	33.3	28.3	28.6	29.1	26.9	33.3
BMR02655_20112_Japygidae `sp. Biologic-DIPL028`	13.4	13.6	17.2	17.2	14.8	16.1	4.6	0.2		18.7	14.8	15.0	16.3	20.3	20.0	18.3	17.0	15.9	18.7	22.5	23.3	21.8	19.8	23.3	20.9	21.6	24.9	22.9	24.9	25.1	23.8	23.3	23.1	23.3	24.2	23.8	25.3	24.9	26.2	22.2	26.1	25.8	22.5	22.0	27.3	25.8	26.1	26.0	24.0	24.7	24.9	24.7	33.0	28.3	28.6	29.1	26.9	33.3
RT48_ROBE_WAME98598_Japygidae_COI	16.3	15.5	16.9	16.9	15.7	15.0	18.4	18.7	18.7		13.7	13.8	16.9	16.4	16.3	17.2	17.5	17.0	17.0	16.9	17.2	16.4	17.9	16.7	17.9	17.9	21.0	19.0	21.3	22.8	20.7	22.6	25.2	25.1	23.9	25.4	25.2	25.5	25.5	24.5	25.0	24.9	27.1	26.7	25.0	25.5	25.4	25.5	22.9	23.4	23.7	24.8	32.2	25.6	27.8	29.0	28.1	29.0
BMR00269_1845_BS1E_Japygidae sp. Biologic-DIPL008	14.7	13.8	14.4	14.4	14.3	14.6	14.1	15.0	14.8	13.7		9.6	15.4	16.9	16.6	15.5	18.1	16.0	16.3	17.8	18.8	18.5	17.8	18.8	19.8	17.3	21.3	20.2	23.1	22.0	21.4	24.0	24.8	24.0	23.9	23.7	24.3	24.5	27.2	22.8	25.6	25.4	24.6	24.5	24.6	25.1	23.2	25.5	22.2	23.3	23.1	23.7	33.0	25.5	27.7	28.7	28.3	29.8
BMR00274_1845_BGCK_Japygidae sp. Biologic-DIPL009	14.9	14.6	15.0	15.0	13.8	14.6	14.4	14.8	15.0	13.8	9.6		15.5	15.0	16.0	14.9	16.6	16.1	16.0	17.2	19.1	18.4	19.1	18.8	18.7	18.8	19.4	21.0	21.7	23.4	21.0	23.3	24.3	24.0	24.0	25.4	24.9	24.6	26.7	23.9	25.5	25.1	24.9	24.6	24.6	26.3	23.5	25.2	22.3	24.2	24.0	24.0	33.1	26.1	26.1	25.7	29.5	29.3
KE04_ROBE_Japygidae `sp. Helix-DJA011`	16.0	14.6	15.5	15.5	15.4	14.6	15.5	16.3	16.3	16.9	15.4	15.5		16.4	17.3	17.5	15.2	15.0	15.8	18.7	20.5	18.2	20.5	20.5	18.7	18.8	21.2	21.0	22.0	23.4	22.9	21.4	26.0	23.6	24.2	26.4	27.5	27.4	27.7	24.6	25.8	25.8	24.6	25.1	22.3	25.4	26.2	24.5	22.8	24.3	24.3	24.9	33.0	27.1	26.6	27.5	27.1	29.5
BMR00297_1811_WAF_Japygidae `sp. Biologic-DIPL017`	17.3	17.0	16.0	16.0	15.0	16.0	18.2	20.5	20.3	16.4	16.9	15.0	16.4		6.4	9.0	18.2	17.9	17.3	17.8	20.8	20.8	20.2	18.2	19.8	21.1	22.1	22.3	24.3	23.1	21.9	22.9	25.2	23.7	20.7	26.7	26.4	25.8	26.9	25.8	25.6	25.1	25.8	26.0	24.4	25.5	24.8	24.3	23.1	22.3	22.2	22.9	30.4	24.0	27.1	27.5	29.0	29.0
BMR00781_1811_WAJ_Japygidae `sp. Biologic-DIPL017`	17.0	16.5	15.8	15.8	15.2	16.6	17.8	20.3	20.0	16.3	16.6	16.0	17.3	6.4		9.0	20.1	18.5	17.3	17.9	20.1	19.9	20.2	19.0	20.5	21.9	23.8	23.4	25.7	22.6	22.8	24.0	24.3	23.1	20.4	26.3	26.3	25.4	27.8	24.8	25.5	24.9	25.5	25.7	23.9	26.4	25.4	24.6	24.9	22.6	22.8	23.6	30.6	24.7	26.1	28.3	28.4	30.8
BMR00490_1931_HD2_Indjapyx `sp. Biologic-DIPL001`	16.0	15.3	15.8	15.8	15.2	16.0	17.6	18.5	18.3	17.2	15.5	14.9	17.5	9.0	9.0		18.5	18.4	16.7	17.5	19.9	20.5	20.2	20.4	19.6	20.7	23.3	22.2	24.8	23.6	21.3	23.1	24.2	24.5	23.1	24.6	25.2	24.2	26.7	24.2	24.4	24.3	25.8	25.8	26.8	26.7	24.2	24.6	23.9	22.9	23.1	23.6	31.3	23.6	27.4	27.7	29.5	28.7
BMR00209_1749a_HSTD_Japygidae sp. Biologic-DIPL010	16.7	15.8	16.3	16.3	16.7	16.1	18.4	17.0	17.0	17.5	18.1	16.6	15.2	18.2	20.1	18.5		17.5	17.8	19.3	22.0	20.4	21.4	21.1	20.1	19.8	21.7	22.6	22.6	24.3	22.2	23.7	26.3	26.0	26.7	26.7	26.9	28.9	27.1	26.3	26.5	26.4	26.9	26.9	24.6	26.1	26.1	24.9	24.0	25.2	25.4	23.7	34.3	28.8	28.4	28.3	31.0	29.7
LI30_MEAWO4088-ROBE_Diplura	16.0	15.6	17.3	17.3	16.4	16.1	16.1	15.9	15.9	17.0	16.0	16.1	15.0	17.9	18.5	18.4	17.5		10.9	18.8	19.8	18.1	18.8	19.8	19.8	18.7	23.1	20.7	22.2	21.9	22.6	22.0	24.6	24.9	27.8	25.5	27.7	26.4	28.4	24.8	26.1	26.1	24.5	25.1	25.0	27.4	27.5	25.5	22.9	23.4	23.3	24.9	34.0	26.6	27.4	28.9	29.3	28.8
JU01_ROBE_Japygidae `sp. Helix-DJA003`	17.0	16.4	16.6	16.6	16.6	16.1	18.5	18.7	18.7	17.0	16.3	16.0	15.8	17.3	17.3	16.7	17.8	10.9		18.2	21.1	19.3	19.5	18.8	19.9	20.1	21.3	21.6	22.6	22.3	22.5	23.3	24.8	25.2	26.1	25.5	26.9	27.2	27.5	25.2	26.8	26.4	25.5	25.2	24.9	27.2	25.9	25.8	23.1	23.1	22.9	24.8	31.9	24.8	27.8	27.7	29.6	29.0
JQ796644 Parajapyx isabellae SH06009	18.4	17.0	18.1	18.1	18.2	18.2	21.3	22.5	22.5	16.9	17.8	17.2	18.7	17.8	17.9	17.5	19.3	18.8	18.2		18.8	17.3	17.2	17.9	19.3	18.5	20.1	19.8	21.6	21.3	21.9	22.5	24.9	24.3	25.4	24.9	24.2	25.7	25.4	24.0	24.5	24.6	23.1	23.6	24.1	26.7	25.1	24.0	20.7	23.7	23.4	24.5	32.5	24.7	27.1	26.1	29.2	28.2
IV156_ROBE_Parajapygidae_ sp. DPA004	21.1	20.2	21.6	21.6	19.1	19.8	21.3	23.3	23.3	17.2	18.8	19.1	20.5	20.8	20.1	19.9	22.0	19.8	21.1	18.8		14.0	16.6	16.0	16.4	15.7	18.7	19.9	22.0	21.3	20.1	20.8	26.6	25.7	26.1	25.8	27.7	27.8	27.1	26.6	26.4	26.6	27.2	27.5	27.2	27.2	26.1	26.4	26.6	25.2	25.4	26.1	35.4	25.6	26.7	27.4	30.5	30.5
JF37_ROBE_Parajapygidae `sp. Helix-DPA001`	18.2	16.5	20.1	20.1	16.4	17.9	18.7	21.8	21.8	16.4	18.5	18.4	18.2	20.8	19.9	20.5	20.4	18.1	19.3	17.3	14.0		15.7	15.0	15.0	14.6	17.2	17.6	19.5	18.5	19.8	18.8	24.5	24.3	26.0	25.4	27.5	26.0	26.9	25.5	25.5	25.4	26.1	26.6	25.4	26.9	25.8	25.7	24.8	24.0	23.6	24.8	34.0	26.1	27.1	28.3	29.0	29.2
KD12_ROBE_Parajapygidae_ sp. DPA006/07	17.8	17.0	19.6	19.6	17.0	17.9	18.2	19.8	19.8	17.9	17.8	19.1	20.5	20.2	20.2	20.2	21.4	18.8	19.5	17.2	16.6	15.7		14.7	15.4	15.2	19.6	16.9	20.5	19.1	19.3	21.3	25.5	25.8	25.5	24.9	26.3	24.9	26.6	24.6	26.5	26.1	25.4	25.4	26.0	27.8	26.9	26.4	23.9	23.7	24.0	24.8	33.4	24.5	28.0	28.0	28.7	29.8
KU08_ROBE_Parajapygidae `sp. Helix-DPA009`	17.9	15.8	18.7	18.7	18.7	19.9	20.5	23.3	23.3	16.7	18.8	18.8	20.5	18.2	19.0	20.4	21.1	19.8	18.8	17.9	16.0	15.0	14.7		16.4	14.0	18.3	18.7	20.2	20.2	20.1	22.0	26.7	25.7	24.9	26.1	26.3	26.7	25.7	26.4	26.1	26.3	26.6	26.4	24.4	26.6	25.0	26.0	23.3	23.9	23.6	23.9	33.4	26.0	26.0	29.5	29.9	30.1
KD15_ROBE_Parajapygidae_ sp. DPA008	18.7	17.6	19.8	19.8	18.2	18.8	19.3	20.7	20.9	17.9	19.8	18.7	18.7	19.8	20.5	19.6	20.1	19.8	19.9	19.3	16.4	15.0	15.4	16.4		13.5	18.7	18.8	21.3	20.8	19.8	20.2	25.1	27.1	25.7	26.3	26.9	25.8	25.8	25.4	25.5	25.8	27.5	27.5	25.0	26.9	26.4	25.4	23.6	22.8	23.3	24.5	32.5	26.0	28.4	26.6	29.2	28.3
BMR00195_1749a_HSTD_Parajapygidae `sp. Biologic-DIPL012`	19.6	17.9	19.9	19.9	17.9	20.1	20.5	21.8	21.6	17.9	17.3	18.8	18.8	21.1	21.9	20.7	19.8	18.7	20.1	18.5	15.7	14.6	15.2	14.0	13.5		18.7	16.9	19.6	20.7	19.0	20.8	26.3	25.8	24.6	25.5	26.6	26.1	27.5	24.6	24.7	24.9	25.7	25.5	25.0	26.4	25.8	23.6	23.7	22.9	23.3	23.9	34.2	26.4	26.9	28.1	30.2	29.5
BMR00728_1811_WAH_Parajapygidae `sp. Biologic-DIPL016`	21.5	21.3	19.9	19.9	20.3	22.2	22.8	24.9	24.9	21.0	21.3	19.4	21.2	22.1	23.8	23.3	21.7	23.1	21.3	20.1	18.7	17.2	19.6	18.3	18.7	18.7		14.9	14.7	22.6	22.0	21.9	26.2	27.1	28.2	28.1	27.1	28.9	26.3	27.7	24.7	25.0	26.6	26.6	27.2	29.0	27.2	25.8	25.4	25.9	25.2	24.6	34.7	29.6	26.8	28.0	30.8	28.7
BMR00737_1845_BS1E_Parajapygidae `sp. Biologic-DIPL018`	20.4	20.6	21.6	21.6	21.0	19.8	20.1	22.9	22.9	19.0	20.2	21.0	21.0	22.3	23.4	22.2	22.6	20.7	21.6	19.8	19.9	17.6	16.9	18.7	18.8	16.9	14.9		16.9	21.1	22.0	21.9	27.5	26.4	27.7	27.1	26.7	28.3	28.1	26.7	25.6	25.8	27.5	27.1	27.5	29.6	28.8	27.5	25.4	25.7	26.3	26.3	34.8	26.0	27.8	28.3	32.4	29.0
BMR02656_20112_Parajapygidae `sp. Biologic-DIPL029`	24.0	23.4	23.3	23.3	24.8	23.4	24.0	25.1	24.9	21.3	23.1	21.7	22.0	24.3	25.7	24.8	22.6	22.2	22.6	21.6	22.0	19.5	20.5	20.2	21.3	19.6	14.7	16.9		23.6	22.9	23.7	27.8	29.0	30.2	29.0	27.4	28.4	29.2	29.0	27.1	26.9	29.5	29.5	26.5	29.0	30.1	27.1	26.3	26.6	26.7	24.9	37.5	28.8	26.3	28.7	34.3	30.1
IV245_ROBE_Parajapygidae_ sp. DPA003	22.9	21.7	22.5	22.5	23.1	21.1	22.6	25.1	25.1	22.8	22.0	23.4	23.4	23.1	22.6	23.6	24.3	21.9	22.3	21.3	21.3	18.5	19.1	20.2	20.8	20.7	22.6	21.1	23.6		12.3	22.0	28.6	25.5	27.1	27.2	28.4	28.9	31.0	26.7	27.3	27.2	26.4	27.2	24.7	28.1	27.2	26.3	26.3	25.1	25.1	25.2	36.6	23.4	27.8	27.4	31.5	31.0
IV248_ROBE_Parajapygidae_ sp. DPA005	21.6	20.8	21.9	21.9	21.4	20.8	23.7	23.8	23.8	20.7	21.4	21.0	22.9	21.9	22.8	21.3	22.2	22.6	22.5	21.9	20.1	19.8	19.3	20.1	19.8	19.0	22.0	22.0	22.9	12.3		22.9	28.0	26.1	26.7	26.3	26.9	26.6	30.4	28.0	25.8	26.0	27.1	28.0	25.7	27.7	26.6	25.5	26.0	24.3	24.3	24.3	37.3	22.8	25.8	26.4	32.1	29.7
BMR01929_1953_Parajapygidae `sp. Biologic-DIPL025`	22.2	22.2	22.8	22.8	21.3	23.7	21.7	23.3	23.3	22.6	24.0	23.3	21.4	22.9	24.0	23.1	23.7	22.0	23.3	22.5	20.8	18.8	21.3	22.0	20.2	20.8	21.9	21.9	23.7	22.0	22.9		30.1	27.7	29.9	32.1	30.9	28.9	31.3	29.8	29.1	29.6	29.3	30.1	28.6	30.1	28.5	26.6	27.5	26.4	26.1	27.2	37.8	25.8	27.5	26.9	35.1	31.0
Projapygidae sp EW0300	23.7	23.4	24.8	24.8	24.0	23.1	24.0	22.9	23.1	25.2	24.8	24.3	26.0	25.2	24.3	24.2	26.3	24.6	24.8	24.9	26.6	24.5	25.5	26.7	25.1	26.3	26.2	27.5	27.8	28.6	28.0	30.1		17.8	16.7	16.3	16.6	16.9	16.9	16.9	17.1	17.0	18.1	17.9	27.2	27.8	29.0	27.2	27.4	27.7	27.7	25.8	24.7	26.9	30.7	31.9	28.3	32.5
BMR01195_1845_BS1E_Projapygidae `sp. Biologic-DIPL013`	25.5	23.8	24.5	24.5	24.0	23.6	24.0	23.1	23.3	25.1	24.0	24.0	23.6	23.7	23.1	24.5	26.0	24.9	25.2	24.3	25.7	24.3	25.8	25.7	27.1	25.8	27.1	26.4	29.0	25.5	26.1	27.7	17.8		14.0	16.1	17.2	18.5	18.2	16.4	19.1	18.7	17.8	18.5	27.0	28.9	29.0	28.3	26.9	27.2	27.4	27.4	24.1	28.0	31.9	32.2	27.8	34.1
BMR01927_1953_Projapygidae `sp. Biologic-DIPL024`	25.1	23.7	24.5	24.5	23.7	22.0	24.0	24.4	24.2	23.9	23.9	24.0	24.2	20.7	20.4	23.1	26.7	27.8	26.1	25.4	26.1	26.0	25.5	24.9	25.7	24.6	28.2	27.7	30.2	27.1	26.7	29.9	16.7	14.0		15.7	14.9	17.2	16.3	18.5	18.3	18.1	17.2	16.9	25.7	28.9	30.0	27.1	26.1	25.1	25.1	24.2	23.5	25.3	31.6	30.7	29.6	34.9
BMR00227_1749b_DSM_Projapygidae sp. Biologic-DIPL004	25.4	24.4	25.8	25.8	26.1	22.5	24.2	23.6	23.8	25.4	23.7	25.4	26.4	26.7	26.3	24.6	26.7	25.5	25.5	24.9	25.8	25.4	24.9	26.1	26.3	25.5	28.1	27.1	29.0	27.2	26.3	32.1	16.3	16.1	15.7		13.7	16.4	17.6	19.6	19.8	19.5	17.8	18.1	28.3	28.6	28.7	27.2	26.9	27.4	27.4	26.7	24.4	26.1	28.7	30.1	28.7	34.3
BMR00362_1845_BGCK_Projapygidae sp. Biologic-DIPL005	25.5	24.6	25.4	25.4	24.6	25.1	26.7	25.1	25.3	25.2	24.3	24.9	27.5	26.4	26.3	25.2	26.9	27.7	26.9	24.2	27.7	27.5	26.3	26.3	26.9	26.6	27.1	26.7	27.4	28.4	26.9	30.9	16.6	17.2	14.9	13.7		16.6	15.4	17.8	18.8	18.5	17.3	17.9	27.3	29.5	29.6	27.1	28.0	27.1	26.6	26.1	24.7	27.4	29.2	30.9	32.5	32.9
BMR00265_1845_BS1E_Projapygidae sp. Biologic-DIPL003	25.1	25.5	25.2	25.2	25.7	25.7	26.1	25.1	24.9	25.5	24.5	24.6	27.4	25.8	25.4	24.2	28.9	26.4	27.2	25.7	27.8	26.0	24.9	26.7	25.8	26.1	28.9	28.3	28.4	28.9	26.6	28.9	16.9	18.5	17.2	16.4	16.6		18.4	18.7	20.6	20.5	19.5	19.8	28.2	30.7	29.1	26.9	27.4	26.1	26.0	27.1	25.3	28.0	30.4	29.9	30.1	33.3
KU02_ROBE_Projapygidae `sp. Helix-DPR008/DPR009/DPR011`	26.6	25.8	26.3	26.3	26.1	25.8	27.5	26.0	26.2	25.5	27.2	26.7	27.7	26.9	27.8	26.7	27.1	28.4	27.5	25.4	27.1	26.9	26.6	25.7	25.8	27.5	26.3	28.1	29.2	31.0	30.4	31.3	16.9	18.2	16.3	17.6	15.4	18.4		17.8	17.9	17.9	20.4	20.2	28.8	29.0	29.3	28.4	27.7	28.1	28.1	28.0	20.6	29.1	31.2	31.8	31.3	33.1
RT48_ROBE_WAME98601_Diplura_COI	23.6	21.9	24.5	24.5	23.9	22.3	23.3	22.5	22.2	24.5	22.8	23.9	24.6	25.8	24.8	24.2	26.3	24.8	25.2	24.0	26.6	25.5	24.6	26.4	25.4	24.6	27.7	26.7	29.0	26.7	28.0	29.8	16.9	16.4	18.5	19.6	17.8	18.7	17.8		20.7	20.5	20.1	20.4	27.3	29.3	29.8	30.1	27.4	28.4	28.6	27.4	24.4	28.2	33.1	30.4	30.4	32.3
BMR01223_1749a_Caves Creek_Projapygidae `sp. Biologic-DIPL002	25.8	26.0	25.9	25.9	25.0	25.0	25.8	26.3	26.1	25.0	25.6	25.5	25.8	25.6	25.5	24.4	26.5	26.1	26.8	24.5	26.4	25.5	26.5	26.1	25.5	24.7	24.7	25.6	27.1	27.3	25.8	29.1	17.1	19.1	18.3	19.8	18.8	20.6	17.9	20.7		1.1	18.8	18.6	28.1	29.6	29.6	28.0	26.8	25.9	25.9	25.6	26.9	26.9	30.3	30.9	29.6	31.8
BMR00192_1749a_HSTD_Projapygidae sp. Biologic-DIPL002	25.8	26.3	25.8	25.8	24.8	25.1	25.4	26.0	25.8	24.9	25.4	25.1	25.8	25.1	24.9	24.3	26.4	26.1	26.4	24.6	26.6	25.4	26.1	26.3	25.8	24.9	25.0	25.8	26.9	27.2	26.0	29.6	17.0	18.7	18.1	19.5	18.5	20.5	17.9	20.5	1.1		18.8	18.7	28.2	29.8	29.5	27.7	26.9	25.5	25.5	25.2	26.1	26.8	29.9	31.5	29.3	32.0
BMR02657_20112_Projapygidae `sp. Biologic-DIPL030`	23.6	23.4	24.8	24.8	25.4	22.9	23.3	22.5	22.5	27.1	24.6	24.9	24.6	25.8	25.5	25.8	26.9	24.5	25.5	23.1	27.2	26.1	25.4	26.6	27.5	25.7	26.6	27.5	29.5	26.4	27.1	29.3	18.1	17.8	17.2	17.8	17.3	19.5	20.4	20.1	18.8	18.8		2.3	25.4	27.2	28.5	25.4	26.6	26.6	26.3	26.7	28.3	28.3	30.4	31.3	29.9	32.6
BMR02690_20112_Projapygidae `sp. Biologic-DIPL030`	23.9	24.0	24.9	24.9	25.8	23.3	23.4	22.2	22.0	26.7	24.5	24.6	25.1	26.0	25.7	25.8	26.9	25.1	25.2	23.6	27.5	26.6	25.4	26.4	27.5	25.5	26.6	27.1	29.5	27.2	28.0	30.1	17.9	18.5	16.9	18.1	17.9	19.8	20.2	20.4	18.6	18.7	2.3		25.0	28.6	29.3	25.7	27.7	27.4	27.1	27.2	27.9	28.2	30.7	31.9	29.8	33.1
RT27_WAME34029_Mesa_K_Diplura	24.6	24.2	23.9	23.9	24.1	23.7	24.9	27.5	27.3	25.0	24.6	24.6	22.3	24.4	23.9	26.8	24.6	25.0	24.9	24.1	27.2	25.4	26.0	24.4	25.0	25.0	27.2	27.5	26.5	24.7	25.7	28.6	27.2	27.0	25.7	28.3	27.3	28.2	28.8	27.3	28.1	28.2	25.4	25.0		19.1	20.6	23.2	24.7	25.0	25.0	25.2	33.7	24.1	27.0	28.8	31.9	29.3
IV154_ROBE_Campodeidae `sp. Helix-DCA001`	26.1	24.4	27.2	27.2	27.1	25.7	26.6	25.6	25.8	25.5	25.1	26.3	25.4	25.5	26.4	26.7	26.1	27.4	27.2	26.7	27.2	26.9	27.8	26.6	26.9	26.4	29.0	29.6	29.0	28.1	27.7	30.1	27.8	28.9	28.9	28.6	29.5	30.7	29.0	29.3	29.6	29.8	27.2	28.6	19.1		14.7	26.7	27.2	26.6	27.1	25.2	35.4	28.0	28.0	30.1	31.8	32.8
IV155_ROBE_Campodeidae `sp. Helix-DCA002/03`	25.1	24.8	26.2	26.2	26.2	24.8	25.8	25.9	26.1	25.4	23.2	23.5	26.2	24.8	25.4	24.2	26.1	27.5	25.9	25.1	26.1	25.8	26.9	25.0	26.4	25.8	27.2	28.8	30.1	27.2	26.6	28.5	29.0	29.0	30.0	28.7	29.6	29.1	29.3	29.8	29.6	29.5	28.5	29.3	20.6	14.7		26.2	25.9	25.6	25.8	25.9	34.8	26.8	27.7	29.8	31.2	30.8
BMR00186_1749a_HSTD_Parajapygidae `sp. Biologic-DIPL006`	24.5	23.8	22.9	22.9	23.3	24.3	25.1	26.2	26.0	25.5	25.5	25.2	24.5	24.3	24.6	24.6	24.9	25.5	25.8	24.0	26.4	25.7	26.4	26.0	25.4	23.6	25.8	27.5	27.1	26.3	25.5	26.6	27.2	28.3	27.1	27.2	27.1	26.9	28.4	30.1	28.0	27.7	25.4	25.7	23.2	26.7	26.2		16.3	17.9	17.6	18.2	35.4	26.8	28.6	29.5	30.4	31.6
BMR00225_1749b_BS3X_Parajapygidae sp. Biologic-DIPL007	22.5	21.4	22.0	22.0	22.9	21.6	22.6	23.8	24.0	22.9	22.2	22.3	22.8	23.1	24.9	23.9	24.0	22.9	23.1	20.7	26.6	24.8	23.9	23.3	23.6	23.7	25.4	25.4	26.3	26.3	26.0	27.5	27.4	26.9	26.1	26.9	28.0	27.4	27.7	27.4	26.8	26.9	26.6	27.7	24.7	27.2	25.9	16.3		17.3	17.6	17.0	34.8	27.1	30.2	29.8	28.6	30.0
BMR02658_20112_Projapygidae `sp. Biologic-DIPL031`	22.6	22.0	21.7	21.7	22.2	21.7	23.9	24.7	24.7	23.4	23.3	24.2	24.3	22.3	22.6	22.9	25.2	23.4	23.1	23.7	25.2	24.0	23.7	23.9	22.8	22.9	25.9	25.7	26.6	25.1	24.3	26.4	27.7	27.2	25.1	27.4	27.1	26.1	28.1	28.4	25.9	25.5	26.6	27.4	25.0	26.6	25.6	17.9	17.3		0.9	9.6	35.1	26.1	28.7	29.3	28.4	30.6
BMR02662_20112_Projapygidae `sp. Biologic-DIPL031`	22.3	22.0	21.4	21.4	21.9	21.9	24.0	24.9	24.9	23.7	23.1	24.0	24.3	22.2	22.8	23.1	25.4	23.3	22.9	23.4	25.4	23.6	24.0	23.6	23.3	23.3	25.2	26.3	26.7	25.1	24.3	26.1	27.7	27.4	25.1	27.4	26.6	26.0	28.1	28.6	25.9	25.5	26.3	27.1	25.0	27.1	25.8	17.6	17.6	0.9		10.2	34.9	25.8	28.7	29.6	28.4	30.3
BMR02691_20112_Projapygidae `sp. Biologic-DIPL032`	23.1	22.6	22.5	22.5	23.4	22.5	23.4	24.7	24.7	24.8	23.7	24.0	24.9	22.9	23.6	23.6	23.7	24.9	24.8	24.5	26.1	24.8	24.8	23.9	24.5	23.9	24.6	26.3	24.9	25.2	24.3	27.2	25.8	27.4	24.2	26.7	26.1	27.1	28.0	27.4	25.6	25.2	26.7	27.2	25.2	25.2	25.9	18.2	17.0	9.6	10.2		34.8	25.2	26.1	29.2	30.4	31.8
KU01_ROBE_Projapygidae `sp. Helix-DPR010`	33.1	32.9	32.7	32.7	32.1	32.2	33.3	33.3	33.0	32.2	33.0	33.1	33.0	30.4	30.6	31.3	34.3	34.0	31.9	32.5	35.4	34.0	33.4	33.4	32.5	34.2	34.7	34.8	37.5	36.6	37.3	37.8	24.7	24.1	23.5	24.4	24.7	25.3	20.6	24.4	26.9	26.1	28.3	27.9	33.7	35.4	34.8	35.4	34.8	35.1	34.9	34.8		32.7	36.7	38.3	37.2	40.5
JU02_ROBE_Campodeidae `sp. Helix-DCA005`	27.5	27.7	26.8	26.8	25.6	23.9	25.6	28.3	28.3	25.6	25.5	26.1	27.1	24.0	24.7	23.6	28.8	26.6	24.8	24.7	25.6	26.1	24.5	26.0	26.0	26.4	29.6	26.0	28.8	23.4	22.8	25.8	26.9	28.0	25.3	26.1	27.4	28.0	29.1	28.2	26.9	26.8	28.3	28.2	24.1	28.0	26.8	26.8	27.1	26.1	25.8	25.2	32.7		23.1	23.7	35.2	32.9
BMR01906_1953_Parajapygidae `sp. Biologic-DIPL022`	27.1	27.6	25.5	25.5	26.0	29.5	28.4	28.6	28.6	27.8	27.7	26.1	26.6	27.1	26.1	27.4	28.4	27.4	27.8	27.1	26.7	27.1	28.0	26.0	28.4	26.9	26.8	27.8	26.3	27.8	25.8	27.5	30.7	31.9	31.6	28.7	29.2	30.4	31.2	33.1	30.3	29.9	30.4	30.7	27.0	28.0	27.7	28.6	30.2	28.7	28.7	26.1	36.7	23.1		19.8	36.0	34.8
BMR01909_1953_Parajapygidae `sp. Biologic-DIPL023`	28.3	27.9	28.0	28.0	27.2	27.7	27.8	29.1	29.1	29.0	28.7	25.7	27.5	27.5	28.3	27.7	28.3	28.9	27.7	26.1	27.4	28.3	28.0	29.5	26.6	28.1	28.0	28.3	28.7	27.4	26.4	26.9	31.9	32.2	30.7	30.1	30.9	29.9	31.8	30.4	30.9	31.5	31.3	31.9	28.8	30.1	29.8	29.5	29.8	29.3	29.6	29.2	38.3	23.7	19.8		37.2	33.9
RT43_WAME98535_Phaconeura_WAM-PHAC001_OUTGROUP	29.2	27.9	27.7	27.7	28.6	26.7	28.6	26.9	26.9	28.1	28.3	29.5	27.1	29.0	28.4	29.5	31.0	29.3	29.6	29.2	30.5	29.0	28.7	29.9	29.2	30.2	30.8	32.4	34.3	31.5	32.1	35.1	28.3	27.8	29.6	28.7	32.5	30.1	31.3	30.4	29.6	29.3	29.9	29.8	31.9	31.8	31.2	30.4	28.6	28.4	28.4	30.4	37.2	35.2	36.0	37.2		36.1
IV160_ROBE_Diplura sp.	28.5	29.0	28.3	28.3	30.0	30.8	31.1	33.3	33.3	29.0	29.8	29.3	29.5	29.0	30.8	28.7	29.7	28.8	29.0	28.2	30.5	29.2	29.8	30.1	28.3	29.5	28.7	29.0	30.1	31.0	29.7	31.0	32.5	34.1	34.9	34.3	32.9	33.3	33.1	32.3	31.8	32.0	32.6	33.1	29.3	32.8	30.8	31.6	30.0	30.6	30.3	31.8	40.5	32.9	34.8	33.9	36.1	

Hexanauplia

COI Pairwise Distances (%)	BMR04109	AB380021	BMR02280	DQ356554	JQ911979	KF715874	KF715873	KP861439	EU770473	HM883962	HM883994	KC617654	JX436336	EU582578	BMR02340	BMR03450	BMR03402	BMR03451	MW021232
BMR04109_20112_Diacyclops nr humphreysi		25.0	26.3	25.1	24.0	24.1	23.1	23.7	25.3	24.8	25.7	25.7	25.2	24.6	23.7	23.5	26.8	26.8	28.8
AB380021_Chiridius gracilis	25.0		16.3	15.1	13.6	14.0	14.7	13.3	17.4	17.5	17.5	17.5	19.7	18.8	20.1	19.9	23.1	23.1	24.1
BMR02280_20112_Copepoda `sp. Biologic-CALA002`	26.3	16.3		15.6	14.6	14.6	15.2	16.1	16.3	16.3	16.0	16.0	16.0	16.0	20.4	20.2	25.1	25.1	25.7
DQ356554_Boeckella gracilipes	25.1	15.1	15.6		14.1	14.4	14.3	13.5	14.9	15.1	14.8	14.8	18.4	16.8	21.5	21.4	25.0	25.0	24.2
JQ911979_Delibus sp.	24.0	13.6	14.6	14.1		0.0	7.8	10.7	16.5	16.7	16.7	16.7	18.2	18.3	20.6	20.4	22.5	22.3	25.0
KF715874_Delibus sp.	24.1	14.0	14.6	14.4	0.0		7.9	11.0	17.3	17.5	17.3	17.3	18.6	18.7	21.4	21.2	23.0	22.9	25.1
KF715873_Delibus sp.	23.1	14.7	15.2	14.3	7.8	7.9		11.9	16.7	16.6	16.7	16.7	19.4	18.3	20.3	20.1	22.9	22.7	25.0
KP861439_Calocalanus styliremis	23.7	13.3	16.1	13.5	10.7	11.0	11.9		16.0	15.8	15.8	15.8	17.5	18.4	20.6	20.4	22.0	21.8	23.5
EU770473_Leptodiaptomus siciloides	25.3	17.4	16.3	14.9	16.5	17.3	16.7	16.0		0.5	2.3	2.3	19.8	16.0	22.1	21.9	25.4	25.4	26.1
HM883962_Leptodiaptomus siciloides	24.8	17.5	16.3	15.1	16.7	17.5	16.6	15.8	0.5		2.1	2.1	20.0	16.1	22.0	21.9	25.7	25.7	26.1
HM883994_Leptodiaptomus siciloides	25.7	17.5	16.0	14.8	16.7	17.3	16.7	15.8	2.3	2.1		0.0	18.7	16.0	21.1	21.0	25.7	25.7	25.9
KC617654_Leptodiaptomus siciloides	25.7	17.5	16.0	14.8	16.7	17.3	16.7	15.8	2.3	2.1	0.0		18.7	16.0	21.1	21.0	25.7	25.7	25.9
JX436336_Calamoecia ampulla	25.2	19.7	16.0	18.4	18.2	18.6	19.4	17.5	19.8	20.0	18.7	18.7		19.4	23.4	23.2	24.6	24.6	25.7
EU582578_Skistodiaptomus carolinensis	24.6	18.8	16.0	16.8	18.3	18.7	18.3	18.4	16.0	16.1	16.0	16.0	19.4		22.2	22.1	26.2	26.2	24.2
BMR02340_20100_Dussartcyclops `sp. Biologic-CYCL007`	23.7	20.1	20.4	21.5	20.6	21.4	20.3	20.6	22.1	22.0	21.1	21.1	23.4	22.2		0.2	24.5	24.5	26.6
BMR03450_20100_Dussartcyclops `sp. Biologic-CYCL007`	23.5	19.9	20.2	21.4	20.4	21.2	20.1	20.4	21.9	21.9	21.0	21.0	23.2	22.1	0.2		24.3	24.3	26.4
BMR03402_20100_Paracyclops `sp. Biologic-CYCL009`	26.8	23.1	25.1	25.0	22.5	23.0	22.9	22.0	25.4	25.7	25.7	25.7	24.6	26.2	24.5	24.3		0.2	28.2
BMR03451_20100_Paracyclops `sp. Biologic-CYCL009`	26.8	23.1	25.1	25.0	22.3	22.9	22.7	21.8	25.4	25.7	25.7	25.7	24.6	26.2	24.5	24.3	0.2		28.1
MW021232_Parastenocaris sp. WAM PARA001	28.8	24.1	25.7	24.2	25.0	25.1	25.0	23.5	26.1	26.1	25.9	25.9	25.7	24.2	26.6	26.4	28.2	28.1	

Insecta: Coleoptera: Carabidae

COI Pariwise Distances (%)	JV05	JV03	JV02	JV01	ML01	KU519738	KU519736	KU519735	JV04	BMR02217	BMR02226	JC17	JC14	BMR02668	BMR00472	BMR00581	BMR00193	MF03	KU519718	KD05	KD03	KU519732	KU519731	KU519729	KU519722	BMR00523	BMR00471	ST1999LN7573	KU519728	BIS EW0540	RT27	KU519734	BMR00378	BMR02228	BMR02897	BMR03871	BMR02229	BMR02242
JV05_RC15BS4B0415-20160609-BROCK4_Coleoptera_Staphylinidae		17.8	22.5	25.1	29.2	18.4	18.7	18.4	17.9	19.4	19.5	19.3	19.5	19.6	19.0	22.3	21.4	24.6	23.6	23.1	23.3	23.3	25.2	22.2	22.0	21.1	20.5	21.0	26.0	23.0	22.6	23.1	23.1	23.7	23.7	23.7	23.6	23.6
JV03_RC15BS40051-20160608-BROCK4_Coleoptera_Carabidae	17.8		20.3	21.3	29.2	21.1	19.6	20.8	20.2	19.8	19.8	17.9	17.9	18.1	17.2	22.5	19.0	24.1	24.5	23.7	23.6	21.1	24.8	20.1	20.8	19.0	20.4	22.0	25.7	23.1	19.7	19.9	20.4	20.1	20.1	20.1	20.2	20.2
JV02_RC11BS3045-20160609-BROCK4_Coleoptera_Carabidae	22.5	20.3		6.0	29.9	22.4	22.5	22.8	21.9	21.9	21.7	20.4	20.6	20.4	19.6	24.4	22.9	27.8	28.1	28.8	28.8	23.3	26.9	23.5	24.3	23.2	23.6	24.8	26.4	24.1	24.6	24.6	24.9	25.4	25.4	25.4	25.4	25.4
JV01_GR14BS40032-20160608-BROCK4_Coleoptera_Carabidae	25.1	21.3	6.0		29.5	22.6	22.5	23.6	23.1	22.3	22.1	20.7	20.8	20.8	19.9	24.5	23.2	28.8	29.5	29.0	29.0	25.1	28.1	25.2	25.1	24.5	24.6	24.8	26.9	25.4	25.7	24.9	25.8	25.5	25.5	25.5	25.7	25.7
ML01_MEBRC0025-20170526-ROBE_Coleoptera	29.2	29.2	29.9	29.5		29.7	29.7	30.7	29.8	30.3	30.0	30.4	30.6	30.6	29.4	34.3	33.3	36.9	35.2	34.3	34.3	33.0	36.5	33.3	33.9	30.7	31.6	34.6	35.2	31.8	31.5	31.6	32.1	31.3	31.3	31.3	31.5	31.5
KU519738_Pilbara_Staphylinidae	18.4	21.1	22.4	22.6	29.7		8.7	8.7	18.2	22.7	22.8	21.6	21.7	21.6	21.9	23.1	21.6	25.9	24.9	24.8	24.6	24.6	26.0	23.4	24.2	20.7	22.2	22.9	25.8	22.3	24.9	25.4	25.4	25.1	25.1	25.1	25.2	25.2
KU519736_Pilbara_Staphylinidae	18.7	19.6	22.5	22.5	29.7	8.7		4.3	17.9	23.5	23.6	22.2	22.3	22.2	22.2	24.2	22.1	25.7	25.7	25.4	25.5	24.5	26.8	24.5	22.8	20.8	22.2	22.6	26.9	22.2	24.6	24.3	24.6	24.3	24.3	24.3	24.5	24.5
KU519735_Pilbara_Staphylinidae	18.4	20.8	22.8	23.6	30.7	8.7	4.3		18.7	23.8	23.9	23.1	23.3	23.1	22.3	24.3	23.1	24.8	24.9	24.8	24.9	25.1	25.7	24.2	23.6	21.3	21.1	22.9	26.8	21.7	24.1	24.2	24.3	24.3	24.3	24.3	24.3	24.3
JV04_RC15BS40051-20160608-BROCK4_Coleoptera_Staphylinidae	17.9	20.2	21.9	23.1	29.8	18.2	17.9	18.7		20.6	20.2	18.7	18.8	19.0	18.5	22.3	19.4	27.0	27.8	26.9	27.1	23.7	24.3	22.6	23.1	21.6	23.0	21.4	26.4	24.3	20.9	21.4	21.4	21.6	21.6	21.6	21.5	21.5
BMR02217_1953_Anillini `sp. Biologic-COLE001`	19.4	19.8	21.9	22.3	30.3	22.7	23.5	23.8	20.6		0.2	6.1	6.3	6.5	6.3	22.1	20.3	25.9	26.3	25.7	25.8	23.4	26.0	23.2	23.5	21.5	22.1	23.4	27.8	23.4	22.1	22.3	22.7	21.5	21.5	21.5	21.5	21.5
BMR02226_1953_Anillini `sp. Biologic-COLE001`	19.5	19.8	21.7	22.1	30.0	22.8	23.6	23.9	20.2	0.2		6.3	6.5	6.8	6.5	22.4	20.3	25.9	26.1	25.5	25.7	23.1	25.8	22.8	23.4	21.6	22.2	23.3	27.5	23.0	21.9	22.1	22.5	21.3	21.3	21.3	21.3	21.3
JC17_RC14BS40052-20151125-BROCK4_Coleoptera_Carabidae	19.3	17.9	20.4	20.7	30.4	21.6	22.2	23.1	18.7	6.1	6.3		0.2	0.5	2.9	22.0	20.3	25.9	25.8	25.5	25.7	22.3	24.8	21.4	21.4	21.0	21.4	21.9	26.9	23.6	20.6	20.7	21.1	21.3	21.3	21.3	21.5	21.5
JC14_DD14BS40014-20151125-BROCK4_ColeopteraBrockman_Syncline	19.5	17.9	20.6	20.8	30.6	21.7	22.3	23.3	18.8	6.3	6.5	0.2		0.3	3.0	22.2	20.4	25.9	26.0	25.7	25.8	22.3	24.9	21.6	21.6	21.1	21.6	22.0	26.9	23.6	20.8	20.8	21.3	21.5	21.5	21.5	21.6	21.6
BMR02668_20112_Carabidae `sp. Biologic-COLE001`	19.6	18.1	20.4	20.8	30.6	21.6	22.2	23.1	19.0	6.5	6.8	0.5	0.3		3.0	22.0	20.6	25.9	26.1	25.8	26.0	22.5	25.1	21.7	21.7	21.3	21.7	22.2	27.1	23.7	20.8	20.8	21.3	21.5	21.5	21.5	21.6	21.6
BMR00472_1845_VIV_Carabidae sp. Biologic-COLE001	19.0	17.2	19.6	19.9	29.4	21.9	22.2	22.3	18.5	6.3	6.5	2.9	3.0	3.0		22.5	19.9	26.2	25.5	25.8	26.0	22.6	24.9	21.0	21.3	20.1	21.4	22.2	26.1	22.5	20.2	20.2	20.7	20.5	20.5	20.5	20.7	20.7
BMR00581_1845_BS1E_Coleoptera `sp. Biologic-COLE003`	22.3	22.5	24.4	24.5	34.3	23.1	24.2	24.3	22.3	22.1	22.4	22.0	22.2	22.0	22.5		20.3	23.5	23.9	23.4	23.3	23.7	22.5	22.2	22.3	21.1	22.3	22.3	24.3	23.9	24.0	24.0	24.6	24.3	24.3	24.3	24.2	24.2
BMR00193_1749b_DSM_Coleoptera `sp. Biologic-COLE002`	21.4	19.0	22.9	23.2	33.3	21.6	22.1	23.1	19.4	20.3	20.3	20.3	20.4	20.6	19.9	20.3		24.3	24.9	24.2	24.4	22.6	25.5	21.3	22.6	21.1	22.6	22.6	25.4	23.7	23.2	23.7	23.7	23.7	23.7	23.7	23.9	23.9
MF03_RC12MEH02212015121O-ROBE_Coleoptera_Curculionidae	24.6	24.1	27.8	28.8	36.9	25.9	25.7	24.8	27.0	25.9	25.9	25.9	25.9	25.9	26.2	23.5	24.3		14.4	13.3	13.4	20.2	24.1	22.3	22.2	22.3	22.8	21.6	25.2	24.1	27.8	27.4	28.0	28.1	28.1	28.1	28.0	28.0
KU519718_Pilbara_Curculionidae	23.6	24.5	28.1	29.5	35.2	24.9	25.7	24.9	27.8	26.3	26.1	25.8	26.0	26.1	25.5	23.9	24.9	14.4		3.2	3.3	19.2	23.9	21.9	22.3	23.0	22.5	20.7	24.0	24.2	27.3	27.8	27.7	27.5	27.5	27.5	27.5	27.5
KD05_GR15MEC0019.20160915.ROBE_Coleoptera_Curculionidae	23.1	23.7	28.8	29.0	34.3	24.8	25.4	24.8	26.9	25.7	25.5	25.5	25.7	25.8	25.8	23.4	24.2	13.3	3.2		0.2	19.2	24.2	21.3	21.6	22.6	21.9	20.4	24.2	24.0	26.7	27.2	27.4	27.2	27.2	27.2	27.2	27.2
KD03_GR15MEB0003.20160915.ROBE_Coleoptera_Curculionidae	23.3	23.6	28.8	29.0	34.3	24.6	25.5	24.9	27.1	25.8	25.7	25.7	25.8	26.0	26.0	23.3	24.4	13.4	3.3	0.2		19.0	24.0	21.4	21.7	22.5	22.0	20.3	24.3	23.9	26.9	27.4	27.5	27.3	27.3	27.3	27.3	27.3
KU519732_Pilbara_Curculionidae	23.3	21.1	23.3	25.1	33.0	24.6	24.5	25.1	23.7	23.4	23.1	22.3	22.3	22.5	22.6	23.7	22.6	20.2	19.2	19.2	19.0		21.6	19.2	19.6	18.7	20.1	20.4	24.3	21.1	24.3	24.6	25.1	25.1	25.1	25.1	25.2	25.2
KU519731_Pilbara_Curculionidae	25.2	24.8	26.9	28.1	36.5	26.0	26.8	25.7	24.3	26.0	25.8	24.8	24.9	25.1	24.9	22.5	25.5	24.1	23.9	24.2	24.0	21.6		21.4	21.3	20.2	20.2	19.3	24.0	23.0	25.0	25.1	24.8	25.5	25.5	25.5	25.4	25.4
KU519729_Pilbara_Curculionidae	22.2	20.1	23.5	25.2	33.3	23.4	24.5	24.2	22.6	23.2	22.8	21.4	21.6	21.7	21.0	22.2	21.3	22.3	21.9	21.3	21.4	19.2	21.4		12.6	14.0	16.3	17.8	23.4	21.9	23.4	23.6	23.6	23.4	23.4	23.4	23.4	23.4
KU519722_Pilbara_Curculionidae	22.0	20.8	24.3	25.1	33.9	24.2	22.8	23.6	23.1	23.5	23.4	21.4	21.6	21.7	21.3	22.3	22.6	22.2	22.3	21.6	21.7	19.6	21.3	12.6		14.0	15.2	17.2	23.1	21.3	23.4	23.3	23.3	23.6	23.6	23.6	23.7	23.7
BMR00523_1845_VIV_Cryptorhynchinae `sp. Biologic-COLE004`	21.1	19.0	23.2	24.5	30.7	20.7	20.8	21.3	21.6	21.5	21.6	21.0	21.1	21.3	20.1	21.1	21.1	22.3	23.0	22.6	22.5	18.7	20.2	14.0	14.0		7.0	17.2	22.3	19.6	21.4	21.7	22.2	22.1	22.1	22.1	21.9	21.9
BMR00471_1845_VIV_Cryptorhynchinae `sp. Biologic-COLE004`	20.5	20.4	23.6	24.6	31.6	22.2	22.2	21.1	23.0	22.1	22.2	21.4	21.6	21.7	21.4	22.3	22.6	22.8	22.5	21.9	22.0	20.1	20.2	16.3	15.2	7.0		16.3	22.8	20.1	23.2	23.9	24.3	24.3	24.3	24.3	24.2	24.2
ST1999LN7573_Curculionidae_Pilbara	21.0	22.0	24.8	24.8	34.6	22.9	22.6	22.9	21.4	23.4	23.3	21.9	22.0	22.2	22.2	22.3	22.6	21.6	20.7	20.4	20.3	20.4	19.3	17.8	17.2	17.2	16.3		24.3	20.8	25.3	25.4	25.7	25.8	25.8	25.8	25.8	25.8
KU519728_Pilbara_Curculionidae	26.0	25.7	26.4	26.9	35.2	25.8	26.9	26.8	26.4	27.8	27.5	26.9	26.9	27.1	26.1	24.3	25.4	25.2	24.0	24.2	24.3	24.3	24.0	23.4	23.1	22.3	22.8	24.3		18.8	27.2	27.1	27.4	27.6	27.6	27.6	27.6	27.6
BIS EW0540_Curculionidae Genus2	23.0	23.1	24.1	25.4	31.8	22.3	22.2	21.7	24.3	23.4	23.0	23.6	23.6	23.7	22.5	23.9	23.7	24.1	24.2	24.0	23.9	21.1	23.0	21.9	21.3	19.6	20.1	20.8	18.8		25.5	25.4	25.7	25.8	25.8	25.8	25.8	25.8
RT27_WAME34031_Mesa_K_Ptiliidae_Ptinella_Helix_CPT003	22.6	19.7	24.6	25.7	31.5	24.9	24.6	24.1	20.9	22.1	21.9	20.6	20.8	20.8	20.2	24.0	23.2	27.8	27.3	26.7	26.9	24.3	25.0	23.4	23.4	21.4	23.2	25.3	27.2	25.5		1.7	1.8	3.3	3.3	3.3	3.2	3.2
KU519734_Pilbara_Ptiliidae	23.1	19.9	24.6	24.9	31.6	25.4	24.3	24.2	21.4	22.3	22.1	20.7	20.8	20.8	20.2	24.0	23.7	27.4	27.8	27.2	27.4	24.6	25.1	23.6	23.3	21.7	23.9	25.4	27.1	25.4	1.7		1.4	2.9	2.9	2.9	2.7	2.7
BMR00378_1845_Ptinella `sp. Helix-CPT003`	23.1	20.4	24.9	25.8	32.1	25.4	24.6	24.3	21.4	22.7	22.5	21.1	21.3	21.3	20.7	24.6	23.7	28.0	27.7	27.4	27.5	25.1	24.8	23.6	23.3	22.2	24.3	25.7	27.4	25.7	1.8	1.4		3.0	3.0	3.0	2.9	2.9
BMR02228_1953_Ptinella `sp. Helix CPT003`	23.7	20.1	25.4	25.5	31.3	25.1	24.3	24.3	21.6	21.5	21.3	21.3	21.5	21.5	20.5	24.3	23.7	28.1	27.5	27.2	27.3	25.1	25.5	23.4	23.6	22.1	24.3	25.8	27.6	25.8	3.3	2.9	3.0		0.0	0.0	0.2	0.2
BMR02897_1953_Ptinella `sp. Helix CPT003`	23.7	20.1	25.4	25.5	31.3	25.1	24.3	24.3	21.6	21.5	21.3	21.3	21.5	21.5	20.5	24.3	23.7	28.1	27.5	27.2	27.3	25.1	25.5	23.4	23.6	22.1	24.3	25.8	27.6	25.8	3.3	2.9	3.0	0.0		0.0	0.2	0.2
BMR03871_20006_Ptinella `sp. Helix CPT003`	23.7	20.1	25.4	25.5	31.3	25.1	24.3	24.3	21.6	21.5	21.3	21.3	21.5	21.5	20.5	24.3	23.7	28.1	27.5	27.2	27.3	25.1	25.5	23.4	23.6	22.1	24.3	25.8	27.6	25.8	3.3	2.9	3.0	0.0	0.0		0.2	0.2
BMR02229_1953_Ptinella `sp. Helix CPT003`	23.6	20.2	25.4	25.7	31.5	25.2	24.5	24.3	21.5	21.5	21.3	21.5	21.6	21.6	20.7	24.2	23.9	28.0	27.5	27.2	27.3	25.2	25.4	23.4	23.7	21.9	24.2	25.8	27.6	25.8	3.2	2.7	2.9	0.2	0.2	0.2		0.0
BMR02242_1953_Ptinella `sp. Helix CPT003`	23.6	20.2	25.4	25.7	31.5	25.2	24.5	24.3	21.5	21.5	21.3	21.5	21.6	21.6	20.7	24.2	23.9	28.0	27.5	27.2	27.3	25.2	25.4	23.4	23.7	21.9	24.2	25.8	27.6	25.8	3.2	2.7	2.9	0.2	0.2	0.2	0.0	

Insecta: Zygentoma: Nicoletiidae

COI Pairwise Distances (%)	JC19	BMR00117	BMR02687	BMR02697	BMR00114	WAME98688	WAME98689	BMR02682	BMR02689	BMR00354	BMR00105	BMR00111	BMR00118	BMR00358	WAME84272	WAME98660	WAME98658	WAME98659	WAME98664	BMR00281	BMR02686	BMR00282	BMR00108	WAME98679	BMR00350	BMR00355	BMR00351	BMR00352	BMR00356	WAME98665
JC19_BROCK4_Nicoletiidae `sp. Helix marra mamba`		4.2	12.3	13.2	13.2	15.8	14.8	15.5	15.0	18.8	16.0	15.5	15.8	22.0	20.6	21.4	19.0	20.4	20.7	21.3	23.3	22.5	21.0	20.7	20.9	22.5	21.1	21.3	22.1	20.1
BMR00117_1749b_BS3_Nicoletiinae sp. Biologic-ZYGE007	4.2		9.7	12.6	13.0	16.2	14.5	13.9	13.9	19.3	15.6	15.6	15.7	21.1	22.0	22.7	20.3	21.1	21.2	20.9	21.6	21.9	20.3	21.1	20.0	21.2	21.7	21.7	22.5	20.9
BMR02687_20112_Subnicoletiinae `sp. Biologic-ZYGE026`	12.3	9.7		14.8	15.2	16.5	14.8	15.2	17.6	21.6	17.0	17.2	17.2	21.8	22.0	22.0	21.8	21.6	22.7	24.2	21.6	22.5	21.6	23.8	22.7	24.0	21.6	22.5	22.6	21.6
BMR02697_20112_Nicoletiinae `sp. Biologic-ZYGE006	13.2	12.6	14.8		5.2	15.0	14.3	15.8	15.2	19.6	17.0	16.5	16.6	19.8	20.7	21.0	20.9	21.3	22.9	21.7	23.3	23.4	21.4	21.0	20.9	22.6	21.6	21.3	21.6	24.0
BMR00114_1749b_BS3X_Nicoletiinae sp. Biologic-ZYGE006	13.2	13.0	15.2	5.2		15.0	14.2	15.5	14.7	19.5	17.6	17.0	17.2	19.4	21.9	21.7	21.5	20.7	22.5	21.7	23.6	22.5	20.8	20.7	21.7	23.6	22.6	22.2	23.1	23.6
RT56_PARA_WAME98688_Zygentoma?_2	15.8	16.2	16.5	15.0	15.0		6.9	16.9	16.4	21.1	17.3	17.5	17.5	18.3	19.3	19.1	20.1	19.5	19.8	20.8	22.5	20.2	21.4	21.1	20.2	21.2	20.8	20.8	20.8	22.3
RT56_PARA_WAME98689_Zygentoma?_2	14.8	14.5	14.8	14.3	14.2	6.9		15.9	15.7	23.0	17.3	17.5	17.7	19.2	21.0	19.7	20.3	20.5	20.5	20.5	22.5	20.8	20.8	20.2	19.5	20.8	20.8	20.7	20.2	21.8
BMR02682_20112_Subnicoletiinae `sp. Biologic-ZYGE024`	15.5	13.9	15.2	15.8	15.5	16.9	15.9		7.5	20.3	17.5	17.9	17.7	21.6	21.9	20.4	20.6	21.0	22.0	22.0	23.4	22.0	20.8	21.6	20.3	21.6	20.4	20.9	21.6	22.0
BMR02689_20112_Subnicoletiinae `sp. Biologic-ZYGE027`	15.0	13.9	17.6	15.2	14.7	16.4	15.7	7.5		19.6	17.2	17.7	17.6	20.7	22.0	21.0	21.1	21.1	22.3	21.9	23.6	22.8	21.1	21.9	20.0	21.4	21.1	21.7	22.4	21.3
BMR00354_1811_WHill_Trinemura `sp. Biologic-ZYGE013`	18.8	19.3	21.6	19.6	19.5	21.1	23.0	20.3	19.6		17.8	17.0	17.3	17.3	20.7	21.3	21.7	21.3	22.9	22.5	25.1	22.6	21.7	23.6	23.8	24.6	21.9	21.7	22.8	22.5
BMR00105_1749b_BS2W_Nicoletiinae sp. Biologic-ZYGE005	16.0	15.6	17.0	17.0	17.6	17.3	17.3	17.5	17.2	17.8		0.8	0.5	20.1	21.9	21.1	20.6	22.2	22.8	22.2	24.2	20.7	21.6	21.0	20.5	22.8	22.2	22.5	22.9	21.6
BMR00111_1749b_BS2W_Nicoletiinae sp. Biologic-ZYGE005	15.5	15.6	17.2	16.5	17.0	17.5	17.5	17.9	17.7	17.0	0.8		0.4	20.2	21.4	20.8	20.2	22.0	22.3	22.0	24.4	20.6	21.4	20.9	20.2	22.4	22.6	22.7	23.4	21.4
BMR00118_1749b_BS2W_Nicoletiinae sp. Biologic-ZYGE005	15.8	15.7	17.2	16.6	17.2	17.5	17.7	17.7	17.6	17.3	0.5	0.4		20.2	21.7	21.0	20.5	22.2	22.6	22.3	24.4	20.8	21.7	21.3	20.3	22.6	22.3	22.6	23.1	21.4
BMR00358_1811_MTEE_	22.0	21.1	21.8	19.8	19.4	18.3	19.2	21.6	20.7	17.3	20.1	20.2	20.2		22.4	22.6	23.2	21.9	23.0	22.4	22.7	20.2	21.0	23.0	21.4	22.6	21.5	20.6	21.1	23.3
RT20_ROBE_WAME84272_Nicoletiidae	20.6	22.0	22.0	20.7	21.9	19.3	21.0	21.9	22.0	20.7	21.9	21.4	21.7	22.4		3.6	4.9	10.5	11.0	15.5	15.9	16.3	14.9	20.6	18.8	19.3	20.8	21.1	21.9	21.9
RT53_ROBE_WAME98660_Zygentoma?_2	21.4	22.7	22.0	21.0	21.7	19.1	19.7	20.4	21.0	21.3	21.1	20.8	21.0	22.6	3.6		4.7	11.1	12.1	15.5	16.5	16.1	15.5	21.1	19.1	20.0	21.0	21.9	21.8	21.6
RT53_ROBE_WAME98658_Zygentoma?_2	19.0	20.3	21.8	20.9	21.5	20.1	20.3	20.6	21.1	21.7	20.6	20.2	20.5	23.2	4.9	4.7		11.3	11.2	15.6	16.1	16.1	13.3	19.8	18.8	19.6	20.3	20.9	21.4	21.1
RT53_ROBE_WAME98659_Zygentoma?_2	20.4	21.1	21.6	21.3	20.7	19.5	20.5	21.0	21.1	21.3	22.2	22.0	22.2	21.9	10.5	11.1	11.3		11.8	13.7	15.2	16.1	15.8	20.5	19.5	20.1	20.1	20.5	21.3	21.7
RT53_ROBE_WAME98664_Zygentoma?_2	20.7	21.2	22.7	22.9	22.5	19.8	20.5	22.0	22.3	22.9	22.8	22.3	22.6	23.0	11.0	12.1	11.2	11.8		13.1	14.1	15.2	14.6	20.7	20.0	20.9	22.3	22.2	23.3	22.3
BMR00281_1845_VIV_Nicoletiidae sp. Biologic-ZYGE004	21.3	20.9	24.2	21.7	21.7	20.8	20.5	22.0	21.9	22.5	22.2	22.0	22.3	22.4	15.5	15.5	15.6	13.7	13.1		12.1	14.1	14.1	19.3	17.6	18.6	21.1	21.0	21.8	22.5
BMR02686_20112_Subnicoletiinae `sp. Biologic-ZYGE025`	23.3	21.6	21.6	23.3	23.6	22.5	22.5	23.4	23.6	25.1	24.2	24.4	24.4	22.7	15.9	16.5	16.1	15.2	14.1	12.1		8.6	13.7	20.7	19.6	19.8	19.4	19.2	18.8	22.9
BMR00282_1845_BS1E_Nicoletiidae? sp. Biologic-ZYGE003	22.5	21.9	22.5	23.4	22.5	20.2	20.8	22.0	22.8	22.6	20.7	20.6	20.8	20.2	16.3	16.1	16.1	16.1	15.2	14.1	8.6		13.5	19.8	18.8	19.1	19.6	19.6	20.1	22.8
BMR00108_1749a_HSTD_Nicoletiidae sp. Biologic-ZYGE002	21.0	20.3	21.6	21.4	20.8	21.4	20.8	20.8	21.1	21.7	21.6	21.4	21.7	21.0	14.9	15.5	13.3	15.8	14.6	14.1	13.7	13.5		20.5	17.1	17.3	20.7	20.7	21.6	21.6
RT56_PARA_WAME98679_Zygentoma?_2	20.7	21.1	23.8	21.0	20.7	21.1	20.2	21.6	21.9	23.6	21.0	20.9	21.3	23.0	20.6	21.1	19.8	20.5	20.7	19.3	20.7	19.8	20.5		11.6	12.9	14.0	13.8	13.7	21.1
BMR00350_1811_WHill_Atelurinae `sp. Biologic-ZYGE012`	20.9	20.0	22.7	20.9	21.7	20.2	19.5	20.3	20.0	23.8	20.5	20.2	20.3	21.4	18.8	19.1	18.8	19.5	20.0	17.6	19.6	18.8	17.1	11.6		1.7	14.3	13.4	13.9	19.7
BMR00355_1811_WHill_Atelurinae `sp. Biologic-ZYGE012`	22.5	21.2	24.0	22.6	23.6	21.2	20.8	21.6	21.4	24.6	22.8	22.4	22.6	22.6	19.3	20.0	19.6	20.1	20.9	18.6	19.8	19.1	17.3	12.9	1.7		15.0	14.4	14.5	21.4
BMR00351_1811_WAF_Atelurinae `sp. Biologic-ZYGE011`	21.1	21.7	21.6	21.6	22.6	20.8	20.8	20.4	21.1	21.9	22.2	22.6	22.3	21.5	20.8	21.0	20.3	20.1	22.3	21.1	19.4	19.6	20.7	14.0	14.3	15.0		1.7	1.5	20.2
BMR00352_1811_WAJ_Atelurinae `sp. Biologic-ZYGE011`	21.3	21.7	22.5	21.3	22.2	20.8	20.7	20.9	21.7	21.7	22.5	22.7	22.6	20.6	21.1	21.9	20.9	20.5	22.2	21.0	19.2	19.6	20.7	13.8	13.4	14.4	1.7		1.3	20.4
BMR00356_1811_MTEE_Atelurinae `sp. Biologic-ZYGE011`	22.1	22.5	22.6	21.6	23.1	20.8	20.2	21.6	22.4	22.8	22.9	23.4	23.1	21.1	21.9	21.8	21.4	21.3	23.3	21.8	18.8	20.1	21.6	13.7	13.9	14.5	1.5	1.3		20.9
RT53_ROBE_WAME98665_Zygentoma?_2	20.1	20.9	21.6	24.0	23.6	22.3	21.8	22.0	21.3	22.5	21.6	21.4	21.4	23.3	21.9	21.6	21.1	21.7	22.3	22.5	22.9	22.8	21.6	21.1	19.7	21.4	20.2	20.4	20.9	

Malacostraca: Amphipoda: Bogidiellidae

COI Pairwise Distances (%)	BMR00081	BMR00132	BMR00154	BMR00162	BMR00153	BMR00082	BMR00150	BMR00134	BMR00628	BMR00287	BMR00525	BMR04117	BMR00706	MW021198	WAMC74112	ST2125LN30439	BMR04144
BMR00081_1749a_Bogidiellidae sp. Biologic-AMPH010		0.5	0.5	0.3	1.7	2.6	2.1	2.7	2.4	10.8	10.8	10.8	10.6	9.6	9.6	9.6	25.2
BMR00132_1749a_Bogidiellidae sp. Biologic-AMPH010	0.5		0.6	0.5	1.5	2.4	2.0	2.6	2.3	10.5	10.5	10.5	10.3	9.3	9.3	9.2	24.9
BMR00154_1749a_Bogidiellidae sp. Biologic-AMPH010	0.5	0.6		0.5	1.8	2.1	2.0	2.2	2.0	10.6	10.6	10.6	10.5	9.5	9.5	9.5	24.9
BMR00162_1749a_Bogidiellidae sp. Biologic-AMPH010	0.3	0.5	0.5		1.7	2.6	2.1	2.7	2.4	10.6	10.6	10.6	10.5	9.5	9.5	9.5	25.0
BMR00153_1749a_Bogidiellidae sp. Biologic-AMPH010	1.7	1.5	1.8	1.7		2.4	2.3	2.6	2.3	11.1	11.1	11.1	10.9	9.5	9.5	9.5	25.0
BMR00082_1749a_Bogidiellidae sp. Biologic-AMPH010	2.6	2.4	2.1	2.6	2.4		0.8	1.0	0.8	10.6	10.6	10.6	10.5	9.6	9.6	10.4	25.2
BMR00150_1749a_Bogidiellidae sp. Biologic-AMPH010	2.1	2.0	2.0	2.1	2.3	0.8		1.2	0.9	10.6	10.6	10.6	10.5	9.8	9.8	10.2	25.2
BMR00134_1749a_Bogidiellidae sp. Biologic-AMPH010	2.7	2.6	2.2	2.7	2.6	1.0	1.2		0.3	11.4	11.4	11.4	11.2	9.3	9.3	10.3	25.2
BMR00628_1749a_Bogidiellidae sp. Biologic-AMPH010	2.4	2.3	2.0	2.4	2.3	0.8	0.9	0.3		11.1	11.1	11.1	10.9	9.3	9.3	10.1	25.0
BMR00287_1845_Bogidiellidae sp. Biologic-AMPH011	10.8	10.5	10.6	10.6	11.1	10.6	10.6	11.4	11.1		0.0	0.0	1.1	7.3	7.3	9.2	24.9
BMR00525_1845_Bogidiellidae sp. Biologic-AMPH011	10.8	10.5	10.6	10.6	11.1	10.6	10.6	11.4	11.1	0.0		0.0	1.1	7.3	7.3	9.2	24.9
BMR04117_20112_Bogidiellidae sp.	10.8	10.5	10.6	10.6	11.1	10.6	10.6	11.4	11.1	0.0	0.0		1.1	7.3	7.3	9.2	24.9
BMR00706_1845_Bogidiellidae sp. Biologic-AMPH011	10.6	10.3	10.5	10.5	10.9	10.5	10.5	11.2	10.9	1.1	1.1	1.1		7.8	7.8	9.0	24.6
MW021198_Bogidiellidae sp. WAM AMPB003_WAMC74112	9.6	9.3	9.5	9.5	9.5	9.6	9.8	9.3	9.3	7.3	7.3	7.3	7.8		0.0	7.9	25.0
WAMC74112_WAM-AMPB003	9.6	9.3	9.5	9.5	9.5	9.6	9.8	9.3	9.3	7.3	7.3	7.3	7.8	0.0		7.9	25.0
ST2125LN30439	9.6	9.2	9.5	9.5	9.5	10.4	10.2	10.3	10.1	9.2	9.2	9.2	9.0	7.9	7.9		23.3
BMR04144_20006_Maarrka `sp. Biologic-AMPH053`	25.2	24.9	24.9	25.0	25.0	25.2	25.2	25.2	25.0	24.9	24.9	24.9	24.6	25.0	25.0	23.3	

Malacostraca: Amphipoda: Eriopisidae

COI Pariwise Distances (%)	BMR00367	MW021192	WAMC72443	BMR00369	BMR00587	BMR04114	MT902672	MT902706	OK170024	MW021201	OK169998	MW021202	MW911302	BMR01228	WAMC70279	NH38	BMR04112	MW911310	NH104	OK170022	OK170023	OK169996	OK170016	OK170017	OK170021	IV134	NH37	NH39	KJ63	MW911309	JQ608487	BMR07289
BMR00367_1845_Nedsia sp. WAM-AMPE003		1.6	1.6	1.7	1.9	1.9	5.7	5.7	6.1	6.3	6.8	6.5	9.7	16.9	15.2	16.2	16.3	15.7	15.7	15.0	14.9	15.0	17.6	17.6	17.6	17.8	18.2	18.2	18.2	16.4	18.2	28.3
MW021192_Nedsia sp. WAM AMPE003	1.6		0.0	1.8	2.0	2.0	6.3	6.3	6.3	6.7	7.0	6.5	9.4	16.6	15.4	16.2	16.0	16.2	16.2	15.2	15.1	14.8	16.9	16.9	16.9	18.1	18.4	18.4	18.4	16.3	18.1	28.8
WAMC72443	1.6	0.0		1.8	2.0	2.0	6.3	6.3	6.3	6.7	7.0	6.5	9.4	16.6	15.4	16.2	16.0	16.2	16.2	15.2	15.1	14.8	16.9	16.9	16.9	18.1	18.4	18.4	18.4	16.3	18.1	28.8
BMR00369_1845_Nedsia sp. WAM-AMPE003	1.7	1.8	1.8		0.2	0.2	5.7	5.7	5.5	6.7	6.6	7.0	9.0	17.2	14.7	15.3	16.3	15.6	15.9	14.8	14.7	14.0	16.5	16.5	16.5	17.5	17.8	17.8	17.7	15.6	17.6	28.8
BMR00587_1845_Nedsia sp. WAM-AMPE003	1.9	2.0	2.0	0.2		0.3	5.9	5.9	5.7	6.8	6.8	7.1	9.1	17.0	14.5	15.1	16.2	15.4	15.8	15.0	14.9	14.2	16.3	16.3	16.3	17.3	17.6	17.6	17.5	15.5	17.8	28.6
BMR04114_20112_Nedsia `sp. WAM-AMPE003`	1.9	2.0	2.0	0.2	0.3		5.8	5.8	5.5	6.8	6.6	7.1	9.1	17.3	14.8	15.4	16.4	15.7	16.0	14.8	14.7	14.0	16.5	16.5	16.5	17.6	17.9	17.9	17.7	15.8	17.8	28.9
MT902672_Nedsia sp. WAM AMPE003	5.7	6.3	6.3	5.7	5.9	5.8		0.0	2.3	6.9	6.6	6.9	10.0	16.6	14.6	15.5	16.3	15.0	15.0	15.7	15.5	15.9	17.3	17.3	17.3	16.3	16.6	16.6	16.9	16.1	17.7	28.9
MT902706_Nedsia sp. WAM-AMPE003	5.7	6.3	6.3	5.7	5.9	5.8	0.0		2.3	6.9	6.6	6.9	10.0	16.6	14.6	15.5	16.3	15.0	15.0	15.7	15.5	15.9	17.3	17.3	17.3	16.3	16.6	16.6	16.9	16.1	17.7	28.9
OK170024_Nedsia sp. 4 SJC-2021a	6.1	6.3	6.3	5.5	5.7	5.5	2.3	2.3		7.0	7.2	8.0	11.4	17.3	14.4	16.3	16.9	16.5	16.5	16.3	16.1	16.5	16.9	16.9	17.1	16.1	16.1	16.1	16.1	16.3	15.6	28.5
MW021201_Nedsia sp. WAM AMPE002	6.3	6.7	6.7	6.7	6.8	6.8	6.9	6.9	7.0		4.5	6.4	10.5	16.7	15.3	15.6	16.6	16.1	16.1	16.7	16.6	17.1	17.3	17.8	17.8	17.0	17.3	17.3	17.0	17.2	17.5	29.7
OK169998_Nedsia sp. A5	6.8	7.0	7.0	6.6	6.8	6.6	6.6	6.6	7.2	4.5		6.0	11.3	17.7	15.1	16.8	18.7	17.2	17.2	16.8	16.6	17.2	17.5	17.9	17.9	17.9	18.3	18.3	17.9	18.3	16.2	30.2
MW021202_Nedsia sp. WAM AMPE001	6.5	6.5	6.5	7.0	7.1	7.1	6.9	6.9	8.0	6.4	6.0		9.3	16.7	15.1	15.4	15.5	15.8	15.8	16.5	16.1	16.9	17.8	17.3	17.3	17.9	18.3	18.3	18.5	16.6	17.0	28.8
MW911302_Eriopisidae sp. H-AME026	9.7	9.4	9.4	9.0	9.1	9.1	10.0	10.0	11.4	10.5	11.3	9.3		16.1	14.0	13.9	16.0	14.8	14.8	15.9	15.7	15.6	17.8	17.6	17.6	16.1	16.4	16.4	16.5	17.2	18.7	29.9
BMR01228_1749a_Nedsia sp. Biologic-AMPH008	16.9	16.6	16.6	17.2	17.0	17.3	16.6	16.6	17.3	16.7	17.7	16.7	16.1		8.8	10.3	16.0	15.5	15.3	16.5	16.4	15.6	15.2	15.6	15.6	16.3	16.4	16.3	16.4	15.6	16.1	31.7
WAMC70279	15.2	15.4	15.4	14.7	14.5	14.8	14.6	14.6	14.4	15.3	15.1	15.1	14.0	8.8		9.4	16.0	14.7	14.5	14.8	14.4	13.5	14.2	14.6	14.6	14.2	14.4	14.2	14.6	14.7	16.9	31.9
NH38	16.2	16.2	16.2	15.3	15.1	15.4	15.5	15.5	16.3	15.6	16.8	15.4	13.9	10.3	9.4		16.2	15.3	15.4	15.7	15.5	13.5	16.1	16.5	16.7	14.8	14.7	14.5	15.0	15.5	16.5	32.4
BMR04112_20112_Nedsia `sp. Biologic-AMPH052`	16.3	16.0	16.0	16.3	16.2	16.4	16.3	16.3	16.9	16.6	18.7	15.5	16.0	16.0	16.0	16.2		6.9	6.5	9.7	9.8	10.6	10.6	10.6	10.4	10.7	10.7	10.7	10.7	11.2	15.5	29.6
MW911310_Eriopisidae sp. H-AME022	15.7	16.2	16.2	15.6	15.4	15.7	15.0	15.0	16.5	16.1	17.2	15.8	14.8	15.5	14.7	15.3	6.9		0.5	9.3	9.6	10.8	12.1	12.1	11.8	10.6	10.9	10.9	11.1	12.2	16.4	32.2
NH104	15.7	16.2	16.2	15.9	15.8	16.0	15.0	15.0	16.5	16.1	17.2	15.8	14.8	15.3	14.5	15.4	6.5	0.5		8.7	8.9	10.2	11.4	11.4	11.2	10.1	10.5	10.5	10.6	12.0	16.7	31.7
OK170022_Eriopisidae sp. ABTC157369	15.0	15.2	15.2	14.8	15.0	14.8	15.7	15.7	16.3	16.7	16.8	16.5	15.9	16.5	14.8	15.7	9.7	9.3	8.7		0.4	8.7	11.0	11.0	10.8	11.2	11.4	11.2	11.2	11.4	15.9	31.2
OK170023_Eriopisidae sp. ABTC157368	14.9	15.1	15.1	14.7	14.9	14.7	15.5	15.5	16.1	16.6	16.6	16.1	15.7	16.4	14.4	15.5	9.8	9.6	8.9	0.4		8.9	11.3	11.0	10.8	11.5	11.7	11.5	11.5	11.3	16.1	31.0
OK169996_Eriopisidae sp.	15.0	14.8	14.8	14.0	14.2	14.0	15.9	15.9	16.5	17.1	17.2	16.9	15.6	15.6	13.5	13.5	10.6	10.8	10.2	8.7	8.9		8.7	8.9	8.9	10.6	11.2	11.0	10.6	11.8	16.3	32.6
OK170016_Eriopisidae sp. ABTC157365	17.6	16.9	16.9	16.5	16.3	16.5	17.3	17.3	16.9	17.3	17.5	17.8	17.8	15.2	14.2	16.1	10.6	12.1	11.4	11.0	11.3	8.7		1.5	1.7	9.1	9.3	9.5	9.1	11.2	15.0	31.7
OK170017_Eriopisidae sp. ABTC157366	17.6	16.9	16.9	16.5	16.3	16.5	17.3	17.3	16.9	17.8	17.9	17.3	17.6	15.6	14.6	16.5	10.6	12.1	11.4	11.0	11.0	8.9	1.5		0.2	9.7	9.9	10.2	9.7	12.3	15.0	31.3
OK170021_Eriopisidae sp.	17.6	16.9	16.9	16.5	16.3	16.5	17.3	17.3	17.1	17.8	17.9	17.3	17.6	15.6	14.6	16.7	10.4	11.8	11.2	10.8	10.8	8.9	1.7	0.2		9.5	9.7	9.9	9.5	12.1	15.0	31.3
IV134	17.8	18.1	18.1	17.5	17.3	17.6	16.3	16.3	16.1	17.0	17.9	17.9	16.1	16.3	14.2	14.8	10.7	10.6	10.1	11.2	11.5	10.6	9.1	9.7	9.5		0.5	0.3	0.5	10.3	16.2	30.4
NH37	18.2	18.4	18.4	17.8	17.6	17.9	16.6	16.6	16.1	17.3	18.3	18.3	16.4	16.4	14.4	14.7	10.7	10.9	10.5	11.4	11.7	11.2	9.3	9.9	9.7	0.5		0.2	1.0	10.2	16.1	30.4
NH39	18.2	18.4	18.4	17.8	17.6	17.9	16.6	16.6	16.1	17.3	18.3	18.3	16.4	16.3	14.2	14.5	10.7	10.9	10.5	11.2	11.5	11.0	9.5	10.2	9.9	0.3	0.2		0.8	10.3	15.9	30.2
KJ63	18.2	18.4	18.4	17.7	17.5	17.7	16.9	16.9	16.1	17.0	17.9	18.5	16.5	16.4	14.6	15.0	10.7	11.1	10.6	11.2	11.5	10.6	9.1	9.7	9.5	0.5	1.0	0.8		10.7	16.4	31.0
MW911309_Eriopisidae sp. H-AME043	16.4	16.3	16.3	15.6	15.5	15.8	16.1	16.1	16.3	17.2	18.3	16.6	17.2	15.6	14.7	15.5	11.2	12.2	12.0	11.4	11.3	11.8	11.2	12.3	12.1	10.3	10.2	10.3	10.7		16.1	29.1
JQ608487_Norcapensis mandibulis	18.2	18.1	18.1	17.6	17.8	17.8	17.7	17.7	15.6	17.5	16.2	17.0	18.7	16.1	16.9	16.5	15.5	16.4	16.7	15.9	16.1	16.3	15.0	15.0	15.0	16.2	16.1	15.9	16.4	16.1		29.7
BMR07289_20006_Maarrka weeliwollii	28.3	28.8	28.8	28.8	28.6	28.9	28.9	28.9	28.5	29.7	30.2	28.8	29.9	31.7	31.9	32.4	29.6	32.2	31.7	31.2	31.0	32.6	31.7	31.3	31.3	30.4	30.4	30.2	31.0	29.1	29.7	

Malacostraca: Amphipoda: Paramelitidae. OTUs with many specimens from the original report that were not sampled here have been trimmed down to a single specimen to improve clarity of this table.

COI Pairwise Distances (%)	BMR00073	DQ256028	BMR00163	DQ256019	DQ490127	DQ256027	RT35	DQ838035	BMR00074	BMR00141	BMR00575	BMR00631	BMR00635	BMR02321	BMR02324	BMR00626	BMR02276	BMR02305	BMR02306	BMR02320	BMR02323	BMR02604	BMR02681	BMR02711	BMR02712	BMR02319	BMR02680	BMR02683	BMR02322	BMR02279	BMR00077	BMR00176	BMR00746	BMR02307	BMR02308	BMR02309	BMR02310	BMR02311	BMR02312	BMR02314	BMR02315	BMR02316	BMR02318	BMR02325	BMR02326	BMR02327	BMR02328	BMR02313	BMR02317	BMR02329	BMR02607	BMR02710	RT35	BMR02707	BMR00158	BMR00546	BMR00365	BMR00526	BMR00366	BMR00586	BMR04116	BMR00647	BMR02277	BMR04118	BMR00705	BMR04119	BMR02278	BMR01354	NH53	BMR05188	BMR04037	BMR05201	BMR01339	BMR02709	BMR00123
BMR00073_1749a_CVCK_REG_Pilbarus sp. F		0.6	1.0	14.3	10.8	11.9	11.3	20.3	23.5	23.5	23.5	23.5	23.5	23.5	23.5	23.7	23.7	23.7	23.7	23.7	23.7	23.7	23.7	23.7	23.6	23.8	23.5	23.8	23.8	23.5	22.8	22.8	22.8	22.8	22.8	22.8	22.8	22.8	22.8	22.8	22.8	22.8	22.8	22.8	22.8	22.8	22.8	22.9	22.9	22.6	22.6	22.6	22.9	22.9	22.6	23.1	24.0	24.1	24.3	24.0	24.0	24.6	24.6	24.6	24.5	24.6	24.3	24.4	23.9	25.3	26.3	24.1	25.6	22.8	22.5
DQ256028 Pilbarus sp. F TLF-2008 CVCK	0.6		1.0	14.2	10.9	12.2	11.6	21.4	24.3	24.3	24.3	24.3	24.3	24.3	24.3	24.5	24.5	24.5	24.5	24.5	24.5	24.5	24.5	24.5	24.4	24.6	24.3	24.6	24.5	24.3	23.9	23.9	23.9	23.9	23.9	23.9	23.9	23.9	23.9	23.9	23.9	23.9	23.9	23.9	23.9	23.9	23.8	23.9	23.9	23.7	23.7	23.7	23.3	23.0	23.0	23.9	23.3	23.3	23.4	23.6	23.6	24.2	24.2	24.2	24.0	24.2	23.9	24.0	23.6	24.9	25.8	23.7	25.3	22.6	23.1
BMR00163_1749a_HSTD_Pilbarus sp. F	1.0	1.0		14.5	10.7	12.2	11.3	21.2	24.8	24.8	24.8	24.8	24.8	24.8	24.8	24.9	24.9	24.9	24.9	24.9	24.9	24.9	24.9	24.9	24.9	25.0	24.8	25.1	24.9	24.8	23.7	23.7	23.7	23.7	23.7	23.7	23.7	23.7	23.7	23.7	23.7	23.7	23.7	23.7	23.7	23.7	23.6	23.8	23.8	23.6	23.6	23.6	23.1	22.7	22.5	23.7	24.1	24.2	24.3	24.2	24.2	24.9	24.9	24.9	24.7	24.9	24.5	24.7	24.3	25.8	26.7	24.2	26.2	22.8	23.1
DQ256019_Pilbarus sp. I TLF-2008	14.3	14.2	14.5		5.8	18.6	17.4	26.9	27.7	27.7	27.7	27.7	27.7	27.7	27.7	27.8	27.8	27.8	27.8	27.8	27.8	27.8	27.8	27.8	27.8	28.0	27.7	28.0	28.0	27.5	26.9	26.9	26.9	26.9	26.9	26.9	26.9	26.9	26.9	26.9	26.9	26.9	26.9	26.9	26.9	26.9	26.9	26.9	26.9	27.0	27.0	27.0	27.7	26.9	26.1	27.4	27.8	27.9	28.1	28.8	28.6	28.6	28.6	28.6	28.8	28.9	28.3	29.4	25.0	31.3	30.6	28.3	30.0	26.4	26.7
DQ490127_Pilbarus millsi	10.8	10.9	10.7	5.8		15.1	13.4	22.8	24.5	24.5	24.5	24.5	24.5	24.5	24.5	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.8	24.5	24.8	24.8	24.3	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.6	23.6	23.6	23.8	22.8	22.8	24.0	24.1	24.2	24.5	24.3	24.3	24.6	24.6	24.6	24.8	25.0	24.3	25.5	25.5	26.1	24.9	23.8	25.1	22.8	23.6
DQ256027_Pilbarus sp. H TLF-2008	11.9	12.2	12.2	18.6	15.1		8.2	22.0	23.9	23.9	23.9	23.9	23.9	23.9	23.9	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.2	23.9	24.2	24.0	23.9	23.9	23.9	23.9	23.9	23.9	23.9	23.9	23.9	23.9	23.9	23.9	23.9	23.9	23.9	23.9	23.9	23.8	23.9	23.9	23.7	23.7	23.7	23.1	24.2	23.3	24.6	26.0	26.1	26.1	26.1	26.0	26.8	26.8	26.8	26.6	26.8	26.4	26.1	25.5	26.7	25.8	25.5	26.0	23.7	22.3
RT35_WAMC72415_Seven_Mile_Ck_Pilbarus_sp_G	11.3	11.6	11.3	17.4	13.4	8.2		22.8	22.3	22.3	22.3	22.3	22.3	22.3	22.3	22.5	22.5	22.5	22.5	22.5	22.5	22.5	22.5	22.5	22.5	22.6	22.3	22.6	22.8	22.2	22.5	22.5	22.5	22.5	22.5	22.5	22.5	22.5	22.5	22.5	22.5	22.5	22.5	22.5	22.5	22.5	22.4	22.6	22.6	22.5	22.5	22.5	21.9	21.7	21.3	23.1	25.2	25.2	25.0	25.4	25.2	26.0	26.0	26.0	26.1	26.3	25.7	26.6	26.1	26.9	26.4	25.8	26.4	23.6	22.5
DQ838035_Maarrka weeliwollii	20.3	21.4	21.2	26.9	22.8	22.0	22.8		21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.7	21.7	22.0	21.7	21.7	20.8	20.8	20.8	20.8	20.8	20.8	20.8	20.8	20.8	20.8	20.8	20.8	20.8	20.8	20.8	20.8	20.4	20.9	20.9	21.0	21.0	21.0	22.6	22.6	21.1	21.4	22.3	22.4	22.1	22.5	22.5	22.2	22.2	22.2	22.0	22.2	22.3	23.1	23.4	23.1	22.3	22.0	22.0	22.2	22.3
BMR00074_1749b_BS3X_Paramelitidae sp. Biologic-AMPH015	23.5	24.3	24.8	27.7	24.5	23.9	22.3	21.7		0.0	0.0	0.0	0.0	0.0	0.0	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.3	0.3	0.3	0.3	0.5	0.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.6	5.3	5.3	5.3	12.6	14.4	17.5	18.5	20.8	20.9	21.0	21.7	21.6	22.0	22.0	22.0	22.2	22.3	21.7	21.9	22.4	21.4	21.8	21.1	21.4	23.3	20.7
BMR00141_1749b_BS3X_Paramelitidae sp. Biologic-AMPH015	23.5	24.3	24.8	27.7	24.5	23.9	22.3	21.7	0.0		0.0	0.0	0.0	0.0	0.0	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.3	0.3	0.3	0.3	0.5	0.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.6	5.3	5.3	5.3	12.6	14.4	17.5	18.5	20.8	20.9	21.0	21.7	21.6	22.0	22.0	22.0	22.2	22.3	21.7	21.9	22.4	21.4	21.8	21.1	21.4	23.3	20.7
BMR00575_1749b_BS3X_Paramelitidae sp. Biologic-AMPH015	23.5	24.3	24.8	27.7	24.5	23.9	22.3	21.7	0.0	0.0		0.0	0.0	0.0	0.0	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.3	0.3	0.3	0.3	0.5	0.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.6	5.3	5.3	5.3	12.6	14.4	17.5	18.5	20.8	20.9	21.0	21.7	21.6	22.0	22.0	22.0	22.2	22.3	21.7	21.9	22.4	21.4	21.8	21.1	21.4	23.3	20.7
BMR00631_1749b_BS3X_Paramelitidae sp. Biologic-AMPH015	23.5	24.3	24.8	27.7	24.5	23.9	22.3	21.7	0.0	0.0	0.0		0.0	0.0	0.0	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.3	0.3	0.3	0.3	0.5	0.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.6	5.3	5.3	5.3	12.6	14.4	17.5	18.5	20.8	20.9	21.0	21.7	21.6	22.0	22.0	22.0	22.2	22.3	21.7	21.9	22.4	21.4	21.8	21.1	21.4	23.3	20.7
BMR00635_1749b_BS3X_Paramelitidae sp. Biologic-AMPH015	23.5	24.3	24.8	27.7	24.5	23.9	22.3	21.7	0.0	0.0	0.0	0.0		0.0	0.0	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.3	0.3	0.3	0.3	0.5	0.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.6	5.3	5.3	5.3	12.6	14.4	17.5	18.5	20.8	20.9	21.0	21.7	21.6	22.0	22.0	22.0	22.2	22.3	21.7	21.9	22.4	21.4	21.8	21.1	21.4	23.3	20.7
BMR02321_20112_BS3_Paramelitidae `sp. Biologic-AMPH015`	23.5	24.3	24.8	27.7	24.5	23.9	22.3	21.7	0.0	0.0	0.0	0.0	0.0		0.0	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.3	0.3	0.3	0.3	0.5	0.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.6	5.3	5.3	5.3	12.6	14.4	17.5	18.5	20.8	20.9	21.0	21.7	21.6	22.0	22.0	22.0	22.2	22.3	21.7	21.9	22.4	21.4	21.8	21.1	21.4	23.3	20.7
BMR02324_20112_BS3_Paramelitidae `sp. Biologic-AMPH015`	23.5	24.3	24.8	27.7	24.5	23.9	22.3	21.7	0.0	0.0	0.0	0.0	0.0	0.0		0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.3	0.3	0.3	0.3	0.5	0.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.6	5.3	5.3	5.3	12.6	14.4	17.5	18.5	20.8	20.9	21.0	21.7	21.6	22.0	22.0	22.0	22.2	22.3	21.7	21.9	22.4	21.4	21.8	21.1	21.4	23.3	20.7
BMR00626_1749b_BS3X_Paramelitidae sp. Biologic-AMPH015	23.7	24.5	24.9	27.8	24.6	24.0	22.5	21.9	0.2	0.2	0.2	0.2	0.2	0.2	0.2		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.2	0.2	0.2	0.3	0.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.8	5.7	5.7	5.5	5.5	5.5	12.8	14.6	17.3	18.7	20.7	20.7	20.9	21.9	21.7	21.9	21.9	21.9	22.0	22.2	21.6	22.0	22.6	21.4	21.8	21.3	21.4	23.4	20.8
BMR02276_20112_BS3_Paramelitidae `sp. Biologic-AMPH015`	23.7	24.5	24.9	27.8	24.6	24.0	22.5	21.9	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.0		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.2	0.2	0.2	0.3	0.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.8	5.7	5.7	5.5	5.5	5.5	12.8	14.6	17.3	18.7	20.7	20.7	20.9	21.9	21.7	21.9	21.9	21.9	22.0	22.2	21.6	22.0	22.6	21.4	21.8	21.3	21.4	23.4	20.8
BMR02305_20112_BS3x_Paramelitidae `sp. Biologic-AMPH015`	23.7	24.5	24.9	27.8	24.6	24.0	22.5	21.9	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.0	0.0		0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.2	0.2	0.2	0.3	0.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.8	5.7	5.7	5.5	5.5	5.5	12.8	14.6	17.3	18.7	20.7	20.7	20.9	21.9	21.7	21.9	21.9	21.9	22.0	22.2	21.6	22.0	22.6	21.4	21.8	21.3	21.4	23.4	20.8
BMR02306_20112_BS3x_Paramelitidae `sp. Biologic-AMPH015`	23.7	24.5	24.9	27.8	24.6	24.0	22.5	21.9	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.0	0.0	0.0		0.0	0.0	0.0	0.0	0.0	0.1	0.2	0.2	0.2	0.3	0.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.8	5.7	5.7	5.5	5.5	5.5	12.8	14.6	17.3	18.7	20.7	20.7	20.9	21.9	21.7	21.9	21.9	21.9	22.0	22.2	21.6	22.0	22.6	21.4	21.8	21.3	21.4	23.4	20.8
BMR02320_20112_BS3_Paramelitidae `sp. Biologic-AMPH015`	23.7	24.5	24.9	27.8	24.6	24.0	22.5	21.9	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.0	0.0	0.0	0.0		0.0	0.0	0.0	0.0	0.1	0.2	0.2	0.2	0.3	0.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.8	5.7	5.7	5.5	5.5	5.5	12.8	14.6	17.3	18.7	20.7	20.7	20.9	21.9	21.7	21.9	21.9	21.9	22.0	22.2	21.6	22.0	22.6	21.4	21.8	21.3	21.4	23.4	20.8
BMR02323_20112_BS3_Paramelitidae `sp. Biologic-AMPH015`	23.7	24.5	24.9	27.8	24.6	24.0	22.5	21.9	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0	0.1	0.2	0.2	0.2	0.3	0.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.8	5.7	5.7	5.5	5.5	5.5	12.8	14.6	17.3	18.7	20.7	20.7	20.9	21.9	21.7	21.9	21.9	21.9	22.0	22.2	21.6	22.0	22.6	21.4	21.8	21.3	21.4	23.4	20.8
BMR02604_20112_Paramelitidae `sp. Biologic-AMPH015`	23.7	24.5	24.9	27.8	24.6	24.0	22.5	21.9	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.1	0.2	0.2	0.2	0.3	0.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.8	5.7	5.7	5.5	5.5	5.5	12.8	14.6	17.3	18.7	20.7	20.7	20.9	21.9	21.7	21.9	21.9	21.9	22.0	22.2	21.6	22.0	22.6	21.4	21.8	21.3	21.4	23.4	20.8
BMR02681_20112_Paramelitidae `sp. Biologic-AMPH015`	23.7	24.5	24.9	27.8	24.6	24.0	22.5	21.9	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.1	0.2	0.2	0.2	0.3	0.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.8	5.7	5.7	5.5	5.5	5.5	12.8	14.6	17.3	18.7	20.7	20.7	20.9	21.9	21.7	21.9	21.9	21.9	22.0	22.2	21.6	22.0	22.6	21.4	21.8	21.3	21.4	23.4	20.8
BMR02711_20112_Paramelitidae `sp. Biologic-AMPH015`	23.7	24.5	24.9	27.8	24.6	24.0	22.5	21.9	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.1	0.2	0.2	0.2	0.3	0.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.8	5.7	5.7	5.5	5.5	5.5	12.8	14.6	17.3	18.7	20.7	20.7	20.9	21.9	21.7	21.9	21.9	21.9	22.0	22.2	21.6	22.0	22.6	21.4	21.8	21.3	21.4	23.4	20.8
BMR02712_20112_Paramelitidae `sp. Biologic-AMPH015`	23.6	24.4	24.9	27.8	24.6	24.0	22.5	21.9	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1		0.3	0.3	0.3	0.4	0.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.9	5.8	5.8	5.6	5.6	5.6	12.9	14.6	17.4	18.7	20.8	20.9	21.0	22.0	21.9	22.0	22.0	22.0	22.2	22.3	21.7	22.2	22.6	21.5	22.0	21.4	21.5	23.4	20.8
BMR02319_20112_BS3_Paramelitidae `sp. Biologic-AMPH015`	23.8	24.6	25.0	28.0	24.8	24.2	22.6	21.7	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.3		0.3	0.3	0.2	0.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.9	5.8	5.8	5.6	5.6	5.6	12.9	14.4	17.2	18.5	20.8	20.9	21.0	22.0	21.9	22.0	22.0	22.0	22.2	22.3	21.7	22.2	22.7	21.4	21.8	21.4	21.4	23.3	20.8
BMR02680_20112_Paramelitidae `sp. Biologic-AMPH015`	23.5	24.3	24.8	27.7	24.5	23.9	22.3	21.7	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.3	0.3		0.3	0.5	0.8	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.6	5.3	5.3	5.3	12.9	14.4	17.5	18.8	20.5	20.6	20.7	21.7	21.6	21.7	21.7	21.7	21.9	22.0	21.4	21.9	22.4	21.2	21.6	21.1	21.2	23.6	20.7
BMR02683_20112_Paramelitidae `sp. Biologic-AMPH015`	23.8	24.6	25.1	28.0	24.8	24.2	22.6	22.0	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.3	0.3	0.3		0.5	0.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.9	5.8	5.8	5.6	5.6	5.6	12.9	14.7	17.5	18.8	20.8	20.9	21.0	22.0	21.9	22.0	22.0	22.0	22.2	22.3	21.7	22.2	22.7	21.6	22.0	21.4	21.6	23.6	21.0
BMR02322_20112_BS3_Paramelitidae `sp. Biologic-AMPH015`	23.8	24.5	24.9	28.0	24.8	24.0	22.8	21.7	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.4	0.2	0.5	0.5		0.9	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.9	5.8	5.8	5.6	5.6	5.6	12.8	14.3	17.2	18.5	20.8	20.9	21.0	22.0	21.9	22.0	22.0	22.0	22.2	22.3	21.7	22.3	22.9	21.6	21.8	21.6	21.6	23.1	20.8
BMR02279_20112_BS3_Paramelitidae `sp. Biologic-AMPH015`	23.5	24.3	24.8	27.5	24.3	23.9	22.2	21.7	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.7	0.8	0.8	0.8	0.9		5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.8	5.7	5.7	5.5	5.5	5.5	12.6	14.3	17.3	18.5	20.7	20.7	20.9	21.6	21.4	21.9	21.9	21.9	22.0	22.2	21.6	21.7	22.3	21.2	21.6	21.0	21.2	23.4	20.7
BMR00077_1749b_BS3X_Paramelitidae sp. Biologic-AMPH015	22.8	23.9	23.7	26.9	23.4	23.9	22.5	20.8	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.7	5.8	5.5	5.8	5.8	5.6		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.2	0.2	0.2	11.7	14.3	17.8	19.2	21.4	21.5	21.6	21.9	21.7	22.2	22.2	22.2	22.3	22.5	21.9	23.6	24.0	24.2	24.0	22.2	23.6	22.6	21.7
BMR00176_1749b_BS3X_Paramelitidae sp. Biologic-AMPH015	22.8	23.9	23.7	26.9	23.4	23.9	22.5	20.8	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.7	5.8	5.5	5.8	5.8	5.6	0.0		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.2	0.2	0.2	11.7	14.3	17.8	19.2	21.4	21.5	21.6	21.9	21.7	22.2	22.2	22.2	22.3	22.5	21.9	23.6	24.0	24.2	24.0	22.2	23.6	22.6	21.7
BMR00746_1749b_BS3X_Paramelitidae sp. Biologic-AMPH015	22.8	23.9	23.7	26.9	23.4	23.9	22.5	20.8	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.7	5.8	5.5	5.8	5.8	5.6	0.0	0.0		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.2	0.2	0.2	11.7	14.3	17.8	19.2	21.4	21.5	21.6	21.9	21.7	22.2	22.2	22.2	22.3	22.5	21.9	23.6	24.0	24.2	24.0	22.2	23.6	22.6	21.7
BMR02307_20112_BS2_3 / BS3x_Paramelitidae `sp. Biologic-AMPH015`	22.8	23.9	23.7	26.9	23.4	23.9	22.5	20.8	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.7	5.8	5.5	5.8	5.8	5.6	0.0	0.0	0.0		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.2	0.2	0.2	11.7	14.3	17.8	19.2	21.4	21.5	21.6	21.9	21.7	22.2	22.2	22.2	22.3	22.5	21.9	23.6	24.0	24.2	24.0	22.2	23.6	22.6	21.7
BMR02308_20112_BS2_3 / BS3x_Paramelitidae `sp. Biologic-AMPH015`	22.8	23.9	23.7	26.9	23.4	23.9	22.5	20.8	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.7	5.8	5.5	5.8	5.8	5.6	0.0	0.0	0.0	0.0		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.2	0.2	0.2	11.7	14.3	17.8	19.2	21.4	21.5	21.6	21.9	21.7	22.2	22.2	22.2	22.3	22.5	21.9	23.6	24.0	24.2	24.0	22.2	23.6	22.6	21.7
BMR02309_20112_BS2_3 / BS3x_Paramelitidae `sp. Biologic-AMPH015`	22.8	23.9	23.7	26.9	23.4	23.9	22.5	20.8	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.7	5.8	5.5	5.8	5.8	5.6	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.2	0.2	0.2	11.7	14.3	17.8	19.2	21.4	21.5	21.6	21.9	21.7	22.2	22.2	22.2	22.3	22.5	21.9	23.6	24.0	24.2	24.0	22.2	23.6	22.6	21.7
BMR02310_20112_BS2_3 / BS3x_Paramelitidae `sp. Biologic-AMPH015`	22.8	23.9	23.7	26.9	23.4	23.9	22.5	20.8	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.7	5.8	5.5	5.8	5.8	5.6	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.2	0.2	0.2	11.7	14.3	17.8	19.2	21.4	21.5	21.6	21.9	21.7	22.2	22.2	22.2	22.3	22.5	21.9	23.6	24.0	24.2	24.0	22.2	23.6	22.6	21.7
BMR02311_20112_BS2_3 / BS3x_Paramelitidae `sp. Biologic-AMPH015`	22.8	23.9	23.7	26.9	23.4	23.9	22.5	20.8	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.7	5.8	5.5	5.8	5.8	5.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.2	0.2	0.2	11.7	14.3	17.8	19.2	21.4	21.5	21.6	21.9	21.7	22.2	22.2	22.2	22.3	22.5	21.9	23.6	24.0	24.2	24.0	22.2	23.6	22.6	21.7
BMR02312_20112_BS2_3 / BS3x_Paramelitidae `sp. Biologic-AMPH015`	22.8	23.9	23.7	26.9	23.4	23.9	22.5	20.8	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.7	5.8	5.5	5.8	5.8	5.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.2	0.2	0.2	11.7	14.3	17.8	19.2	21.4	21.5	21.6	21.9	21.7	22.2	22.2	22.2	22.3	22.5	21.9	23.6	24.0	24.2	24.0	22.2	23.6	22.6	21.7
BMR02314_20112_BS2_3 / BS3x_Paramelitidae `sp. Biologic-AMPH015`	22.8	23.9	23.7	26.9	23.4	23.9	22.5	20.8	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.7	5.8	5.5	5.8	5.8	5.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.2	0.2	0.2	11.7	14.3	17.8	19.2	21.4	21.5	21.6	21.9	21.7	22.2	22.2	22.2	22.3	22.5	21.9	23.6	24.0	24.2	24.0	22.2	23.6	22.6	21.7
BMR02315_20112_BS2_3 / BS3x_Paramelitidae `sp. Biologic-AMPH015`	22.8	23.9	23.7	26.9	23.4	23.9	22.5	20.8	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.7	5.8	5.5	5.8	5.8	5.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.2	0.2	0.2	11.7	14.3	17.8	19.2	21.4	21.5	21.6	21.9	21.7	22.2	22.2	22.2	22.3	22.5	21.9	23.6	24.0	24.2	24.0	22.2	23.6	22.6	21.7
BMR02316_20112_BS2_3 / BS3x_Paramelitidae `sp. Biologic-AMPH015`	22.8	23.9	23.7	26.9	23.4	23.9	22.5	20.8	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.7	5.8	5.5	5.8	5.8	5.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.2	0.2	0.2	11.7	14.3	17.8	19.2	21.4	21.5	21.6	21.9	21.7	22.2	22.2	22.2	22.3	22.5	21.9	23.6	24.0	24.2	24.0	22.2	23.6	22.6	21.7
BMR02318_20112_BS2_3 / BS3x_Paramelitidae `sp. Biologic-AMPH015`	22.8	23.9	23.7	26.9	23.4	23.9	22.5	20.8	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.7	5.8	5.5	5.8	5.8	5.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0	0.0	0.1	0.1	0.2	0.2	0.2	11.7	14.3	17.8	19.2	21.4	21.5	21.6	21.9	21.7	22.2	22.2	22.2	22.3	22.5	21.9	23.6	24.0	24.2	24.0	22.2	23.6	22.6	21.7
BMR02325_20112_BS2_3 / BS3x_Paramelitidae `sp. Biologic-AMPH015`	22.8	23.9	23.7	26.9	23.4	23.9	22.5	20.8	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.7	5.8	5.5	5.8	5.8	5.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.0	0.1	0.1	0.2	0.2	0.2	11.7	14.3	17.8	19.2	21.4	21.5	21.6	21.9	21.7	22.2	22.2	22.2	22.3	22.5	21.9	23.6	24.0	24.2	24.0	22.2	23.6	22.6	21.7
BMR02326_20112_BS2_3 / BS3x_Paramelitidae `sp. Biologic-AMPH015`	22.8	23.9	23.7	26.9	23.4	23.9	22.5	20.8	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.7	5.8	5.5	5.8	5.8	5.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.0	0.1	0.1	0.2	0.2	0.2	11.7	14.3	17.8	19.2	21.4	21.5	21.6	21.9	21.7	22.2	22.2	22.2	22.3	22.5	21.9	23.6	24.0	24.2	24.0	22.2	23.6	22.6	21.7
BMR02327_20112_BS2_3 / BS3x_Paramelitidae `sp. Biologic-AMPH015`	22.8	23.9	23.7	26.9	23.4	23.9	22.5	20.8	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.7	5.8	5.5	5.8	5.8	5.6	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.0	0.1	0.1	0.2	0.2	0.2	11.7	14.3	17.8	19.2	21.4	21.5	21.6	21.9	21.7	22.2	22.2	22.2	22.3	22.5	21.9	23.6	24.0	24.2	24.0	22.2	23.6	22.6	21.7
BMR02328_20112_BS2_3 / BS3x_Paramelitidae `sp. Biologic-AMPH015`	22.8	23.8	23.6	26.9	23.4	23.8	22.4	20.4	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.9	5.9	5.6	5.9	5.9	5.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0		0.1	0.1	0.2	0.2	0.2	11.7	14.2	17.7	19.4	21.6	21.7	21.6	21.9	21.8	22.2	22.2	22.2	22.4	22.6	21.9	23.6	24.1	24.2	24.0	22.4	23.6	22.9	21.9
BMR02313_20112_BS2_3 / BS3x_Paramelitidae `sp. Biologic-AMPH015`	22.9	23.9	23.8	26.9	23.4	23.9	22.6	20.9	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.8	5.8	5.6	5.8	5.8	5.7	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1		0.1	0.2	0.2	0.2	11.8	14.4	17.9	19.2	21.5	21.6	21.7	22.0	21.8	22.3	22.3	22.3	22.4	22.6	22.0	23.6	24.0	24.3	24.1	22.3	23.7	22.7	21.8
BMR02317_20112_BS2_3 / BS3x_Paramelitidae `sp. Biologic-AMPH015`	22.9	23.9	23.8	26.9	23.4	23.9	22.6	20.9	5.6	5.6	5.6	5.6	5.6	5.6	5.6	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.8	5.8	5.6	5.8	5.8	5.7	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1		0.2	0.2	0.2	11.8	14.4	17.9	19.2	21.5	21.6	21.7	22.0	21.8	22.3	22.3	22.3	22.4	22.6	22.0	23.6	24.0	24.3	24.1	22.3	23.7	22.7	21.8
BMR02329_20112_BS3_Paramelitidae `sp. Biologic-AMPH015`	22.6	23.7	23.6	27.0	23.6	23.7	22.5	21.0	5.3	5.3	5.3	5.3	5.3	5.3	5.3	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.3	5.6	5.6	5.5	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2		0.0	0.0	11.6	14.3	17.6	19.3	21.3	21.4	21.5	21.9	21.7	22.2	22.2	22.2	22.3	22.5	21.9	23.6	24.0	24.2	24.0	22.2	23.4	22.8	21.6
BMR02607_20112_Paramelitidae `sp. Biologic-AMPH015`	22.6	23.7	23.6	27.0	23.6	23.7	22.5	21.0	5.3	5.3	5.3	5.3	5.3	5.3	5.3	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.3	5.6	5.6	5.5	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.0		0.0	11.6	14.3	17.6	19.3	21.3	21.4	21.5	21.9	21.7	22.2	22.2	22.2	22.3	22.5	21.9	23.6	24.0	24.2	24.0	22.2	23.4	22.8	21.6
BMR02710_20112_Paramelitidae `sp. Biologic-AMPH015`	22.6	23.7	23.6	27.0	23.6	23.7	22.5	21.0	5.3	5.3	5.3	5.3	5.3	5.3	5.3	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.5	5.6	5.6	5.3	5.6	5.6	5.5	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.2	0.0	0.0		11.6	14.3	17.6	19.3	21.3	21.4	21.5	21.9	21.7	22.2	22.2	22.2	22.3	22.5	21.9	23.6	24.0	24.2	24.0	22.2	23.4	22.8	21.6
RT35_WAMC72411_Seven_Mile_Ck_WAM_Yilgarus001	22.9	23.3	23.1	27.7	23.8	23.1	21.9	22.6	12.6	12.6	12.6	12.6	12.6	12.6	12.6	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.9	12.9	12.9	12.9	12.8	12.6	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.8	11.8	11.6	11.6	11.6		12.6	16.7	19.9	21.0	21.1	21.6	21.4	21.3	22.2	22.2	22.2	22.0	22.2	21.9	23.0	22.9	24.7	24.9	22.2	23.6	22.2	21.3
BMR02707_20112_Paramelitidae `sp. Biologic-AMPH047`	22.9	23.0	22.7	26.9	22.8	24.2	21.7	22.6	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.6	14.6	14.6	14.6	14.6	14.6	14.6	14.6	14.6	14.6	14.4	14.4	14.7	14.3	14.3	14.3	14.3	14.3	14.3	14.3	14.3	14.3	14.3	14.3	14.3	14.3	14.3	14.3	14.3	14.3	14.3	14.2	14.4	14.4	14.3	14.3	14.3	12.6		17.2	19.3	20.8	20.9	21.2	20.8	20.8	21.3	21.3	21.3	21.4	21.6	21.0	21.4	21.6	20.7	20.9	21.1	20.5	20.8	22.2
BMR00158_1749a_HSTD_Paramelitidae sp. Biologic-AMPH014	22.6	23.0	22.5	26.1	22.8	23.3	21.3	21.1	17.5	17.5	17.5	17.5	17.5	17.5	17.5	17.3	17.3	17.3	17.3	17.3	17.3	17.3	17.3	17.3	17.4	17.2	17.5	17.5	17.2	17.3	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.7	17.9	17.9	17.6	17.6	17.6	16.7	17.2		19.3	18.7	18.6	18.7	19.3	19.5	18.8	18.8	18.8	19.0	19.2	18.8	20.4	20.5	20.9	20.3	20.1	20.7	20.2	19.9
BMR00546_1749b_DSM_Paramelitidae sp. Biologic-AMPH012	23.1	23.9	23.7	27.4	24.0	24.6	23.1	21.4	18.5	18.5	18.5	18.5	18.5	18.5	18.5	18.7	18.7	18.7	18.7	18.7	18.7	18.7	18.7	18.7	18.7	18.5	18.8	18.8	18.5	18.5	19.2	19.2	19.2	19.2	19.2	19.2	19.2	19.2	19.2	19.2	19.2	19.2	19.2	19.2	19.2	19.2	19.4	19.2	19.2	19.3	19.3	19.3	19.9	19.3	19.3		21.1	21.2	21.6	21.4	21.3	21.9	21.9	21.9	22.0	21.9	21.9	21.6	21.8	20.8	22.3	21.7	21.2	23.4	23.9
BMR00365_1845_BGCK_Paramelitidae sp. Helix-AMP037	24.0	23.3	24.1	27.8	24.1	26.0	25.2	22.3	20.8	20.8	20.8	20.8	20.8	20.8	20.8	20.7	20.7	20.7	20.7	20.7	20.7	20.7	20.7	20.7	20.8	20.8	20.5	20.8	20.8	20.7	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.6	21.5	21.5	21.3	21.3	21.3	21.0	20.8	18.7	21.1		0.1	0.4	2.0	1.8	1.7	1.7	1.7	1.8	2.0	1.7	4.0	3.9	3.5	3.7	3.7	3.5	16.0	20.8
BMR00526_1845_BGCK_Paramelitidae sp. Helix-AMP037	24.1	23.3	24.2	27.9	24.2	26.1	25.2	22.4	20.9	20.9	20.9	20.9	20.9	20.9	20.9	20.7	20.7	20.7	20.7	20.7	20.7	20.7	20.7	20.7	20.9	20.9	20.6	20.9	20.9	20.7	21.5	21.5	21.5	21.5	21.5	21.5	21.5	21.5	21.5	21.5	21.5	21.5	21.5	21.5	21.5	21.5	21.7	21.6	21.6	21.4	21.4	21.4	21.1	20.9	18.6	21.2	0.1		0.3	1.9	1.8	1.6	1.6	1.6	1.8	1.9	1.6	4.0	4.0	3.6	3.8	3.7	3.6	16.0	20.9
BMR00366_1845_BGCK_Paramelitidae sp. Helix-AMP037	24.3	23.4	24.3	28.1	24.5	26.1	25.0	22.1	21.0	21.0	21.0	21.0	21.0	21.0	21.0	20.9	20.9	20.9	20.9	20.9	20.9	20.9	20.9	20.9	21.0	21.0	20.7	21.0	21.0	20.9	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.7	21.7	21.5	21.5	21.5	21.6	21.2	18.7	21.6	0.4	0.3		2.0	1.8	1.6	1.6	1.6	1.8	2.0	1.6	4.3	4.2	4.0	4.2	4.1	4.0	16.4	21.6
BMR00586_1845_BS1W_Paramelitidae sp. Helix-AMP037	24.0	23.6	24.2	28.8	24.3	26.1	25.4	22.5	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	22.0	22.0	21.7	22.0	22.0	21.6	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	22.0	22.0	21.9	21.9	21.9	21.4	20.8	19.3	21.4	2.0	1.9	2.0		0.2	1.5	1.5	1.5	1.7	1.8	1.5	3.5	3.4	3.5	3.5	3.8	4.4	16.1	21.0
BMR04116_20112_Paramelitidae `sp. Helix-AMP037`	24.0	23.6	24.2	28.6	24.3	26.0	25.2	22.5	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.9	21.9	21.6	21.9	21.9	21.4	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.8	21.8	21.8	21.7	21.7	21.7	21.3	20.8	19.5	21.3	1.8	1.8	1.8	0.2		1.4	1.4	1.4	1.5	1.7	1.4	3.3	3.2	3.3	3.7	3.7	4.2	16.3	21.0
BMR00647_1845_BS1E_Paramelitidae sp. Helix-AMP037	24.6	24.2	24.9	28.6	24.6	26.8	26.0	22.2	22.0	22.0	22.0	22.0	22.0	22.0	22.0	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	22.0	22.0	21.7	22.0	22.0	21.9	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.3	22.3	22.2	22.2	22.2	22.2	21.3	18.8	21.9	1.7	1.6	1.6	1.5	1.4		0.0	0.0	0.2	0.3	0.3	3.8	3.7	3.5	3.3	3.5	4.0	16.9	21.1
BMR02277_20112_BS1_Paramelitidae `sp. Helix-AMP037`	24.6	24.2	24.9	28.6	24.6	26.8	26.0	22.2	22.0	22.0	22.0	22.0	22.0	22.0	22.0	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	22.0	22.0	21.7	22.0	22.0	21.9	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.3	22.3	22.2	22.2	22.2	22.2	21.3	18.8	21.9	1.7	1.6	1.6	1.5	1.4	0.0		0.0	0.2	0.3	0.3	3.8	3.7	3.5	3.3	3.5	4.0	16.9	21.1
BMR04118_20112_Paramelitidae `sp. Helix-AMP037`	24.6	24.2	24.9	28.6	24.6	26.8	26.0	22.2	22.0	22.0	22.0	22.0	22.0	22.0	22.0	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	22.0	22.0	21.7	22.0	22.0	21.9	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.3	22.3	22.2	22.2	22.2	22.2	21.3	18.8	21.9	1.7	1.6	1.6	1.5	1.4	0.0	0.0		0.2	0.3	0.3	3.8	3.7	3.5	3.3	3.5	4.0	16.9	21.1
BMR00705_1845_BS1E_Paramelitidae sp. Helix-AMP037	24.5	24.0	24.7	28.8	24.8	26.6	26.1	22.0	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.0	22.0	22.0	22.0	22.0	22.0	22.0	22.0	22.0	22.2	22.2	21.9	22.2	22.2	22.0	22.3	22.3	22.3	22.3	22.3	22.3	22.3	22.3	22.3	22.3	22.3	22.3	22.3	22.3	22.3	22.3	22.4	22.4	22.4	22.3	22.3	22.3	22.0	21.4	19.0	22.0	1.8	1.8	1.8	1.7	1.5	0.2	0.2	0.2		0.2	0.5	3.7	3.6	3.5	3.3	3.7	4.0	17.0	21.3
BMR04119_20112_Paramelitidae `sp. Helix-AMP037`	24.6	24.2	24.9	28.9	25.0	26.8	26.3	22.2	22.3	22.3	22.3	22.3	22.3	22.3	22.3	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.3	22.3	22.0	22.3	22.3	22.2	22.5	22.5	22.5	22.5	22.5	22.5	22.5	22.5	22.5	22.5	22.5	22.5	22.5	22.5	22.5	22.5	22.6	22.6	22.6	22.5	22.5	22.5	22.2	21.6	19.2	21.9	2.0	1.9	2.0	1.8	1.7	0.3	0.3	0.3	0.2		0.6	3.8	3.7	3.7	3.5	3.8	4.2	16.9	21.1
BMR02278_20112_BS1_Paramelitidae `sp. Helix-AMP037`	24.3	23.9	24.5	28.3	24.3	26.4	25.7	22.3	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.6	21.7	21.7	21.4	21.7	21.7	21.6	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	21.9	22.0	22.0	21.9	21.9	21.9	21.9	21.0	18.8	21.9	1.7	1.6	1.6	1.5	1.4	0.3	0.3	0.3	0.5	0.6		3.8	3.7	3.5	3.3	3.5	4.0	16.6	21.1
BMR01354_20163_Paramelitidae `sp. Helix-AMP037`	24.4	24.0	24.7	29.4	25.5	26.1	26.6	23.1	21.9	21.9	21.9	21.9	21.9	21.9	21.9	22.0	22.0	22.0	22.0	22.0	22.0	22.0	22.0	22.0	22.2	22.2	21.9	22.2	22.3	21.7	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.0	21.4	20.4	21.6	4.0	4.0	4.3	3.5	3.3	3.8	3.8	3.8	3.7	3.8	3.8		0.2	0.2	3.7	4.0	3.7	16.4	21.0
NH53_BC186-20171213-03_ROBE_Paramelitidae	23.9	23.6	24.3	25.0	25.5	25.5	26.1	23.4	22.4	22.4	22.4	22.4	22.4	22.4	22.4	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.7	22.4	22.7	22.9	22.3	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.1	24.0	24.0	24.0	24.0	24.0	22.9	21.6	20.5	21.8	3.9	4.0	4.2	3.4	3.2	3.7	3.7	3.7	3.6	3.7	3.7	0.2		0.2	3.8	3.7	3.8	16.0	20.8
BMR05188_20163_Paramelitidae `sp. Helix-AMP037`	25.3	24.9	25.8	31.3	26.1	26.7	26.9	23.1	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.5	21.4	21.2	21.6	21.6	21.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.3	24.3	24.2	24.2	24.2	24.7	20.7	20.9	20.8	3.5	3.6	4.0	3.5	3.3	3.5	3.5	3.5	3.5	3.7	3.5	0.2	0.2		4.0	3.5	4.0	17.0	23.1
BMR04037_20163_Paramelitidae `sp. Helix-AMP037`	26.3	25.8	26.7	30.6	24.9	25.8	26.4	22.3	21.8	21.8	21.8	21.8	21.8	21.8	21.8	21.8	21.8	21.8	21.8	21.8	21.8	21.8	21.8	21.8	22.0	21.8	21.6	22.0	21.8	21.6	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.0	24.1	24.1	24.0	24.0	24.0	24.9	20.9	20.3	22.3	3.7	3.8	4.2	3.5	3.7	3.3	3.3	3.3	3.3	3.5	3.3	3.7	3.8	4.0		4.2	4.2	18.1	22.9
BMR05201_20163_Paramelitidae `sp. Helix-AMP037`	24.1	23.7	24.2	28.3	23.8	25.5	25.8	22.0	21.1	21.1	21.1	21.1	21.1	21.1	21.1	21.3	21.3	21.3	21.3	21.3	21.3	21.3	21.3	21.3	21.4	21.4	21.1	21.4	21.6	21.0	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.2	22.4	22.3	22.3	22.2	22.2	22.2	22.2	21.1	20.1	21.7	3.7	3.7	4.1	3.8	3.7	3.5	3.5	3.5	3.7	3.8	3.5	4.0	3.7	3.5	4.2		3.5	16.4	20.2
BMR01339_20163_Paramelitidae `sp. Helix-AMP037`	25.6	25.3	26.2	30.0	25.1	26.0	26.4	22.0	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.5	21.4	21.2	21.6	21.6	21.2	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.6	23.7	23.7	23.4	23.4	23.4	23.6	20.5	20.7	21.2	3.5	3.6	4.0	4.4	4.2	4.0	4.0	4.0	4.0	4.2	4.0	3.7	3.8	4.0	4.2	3.5		17.0	21.8
BMR02709_20112_Paramelitidae `sp. Biologic-AMPH048`	22.8	22.6	22.8	26.4	22.8	23.7	23.6	22.2	23.3	23.3	23.3	23.3	23.3	23.3	23.3	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.3	23.6	23.6	23.1	23.4	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.6	22.9	22.7	22.7	22.8	22.8	22.8	22.2	20.8	20.2	23.4	16.0	16.0	16.4	16.1	16.3	16.9	16.9	16.9	17.0	16.9	16.6	16.4	16.0	17.0	18.1	16.4	17.0		21.1
BMR00123_1749a_HSTD_Maarrka sp. Biologic-AMPH013	22.5	23.1	23.1	26.7	23.6	22.3	22.5	22.3	20.7	20.7	20.7	20.7	20.7	20.7	20.7	20.8	20.8	20.8	20.8	20.8	20.8	20.8	20.8	20.8	20.8	20.8	20.7	21.0	20.8	20.7	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.7	21.9	21.8	21.8	21.6	21.6	21.6	21.3	22.2	19.9	23.9	20.8	20.9	21.6	21.0	21.0	21.1	21.1	21.1	21.3	21.1	21.1	21.0	20.8	23.1	22.9	20.2	21.8	21.1	

Malacostraca: Isopoda: Microcerberidae

COI Pairwise Distances (%)	BMR02331	MW911317	MF346640	MF346654	MF346663	MF346641	FJ749279	JQ921368
BMR02331_20112_Microcerberidae `sp. Biologic-ISOP026`		14.7	21.9	21.8	21.8	21.9	23.2	24.0
MW911317_Microcerberidae sp. H -ISM002	14.7		24.6	24.5	24.6	23.2	23.4	24.9
MF346640_Coxicerberus fukudai	21.9	24.6		0.2	0.2	9.5	25.5	25.2
MF346654_Coxicerberus fukudai	21.8	24.5	0.2		0.4	9.4	25.4	25.0
MF346663_Coxicerberus fukudai	21.8	24.6	0.2	0.4		9.5	25.4	25.0
MF346641_Coxicerberus fukudai	21.9	23.2	9.5	9.4	9.5		25.7	22.5
FJ749279_Asellus aquaticus	23.2	23.4	25.5	25.4	25.4	25.7		21.7
JQ921368_Proasellus parvulus	24.0	24.9	25.2	25.0	25.0	22.5	21.7	

Malacostraca: Syncarida: Bathynellidae

COI Pairwise Distances (%)	MK135043	MK135044	MK135045	MF074385	MF074388	MF074409	MF074391	MF074381	BMR00289	BMR02430	BMR00530	BMR00650	BMR00590	BMR00709	BMR00649	BMR00710	BMR02599	BMR02600	BMR00711	BES6932a	BES6932c	BES7570a	WAMC74210	BES6932b	KR131708
Bathynellidae nr. Fortescuenella sp. MK135043		14.8	17.4	22.0	23.2	23.8	22.7	22.4	26.3	26.2	23.1	23.6	23.1	23.8	24.0	22.7	22.0	22.4	22.0	25.1	25.1	25.1	24.5	24.9	26.9
Fortescuenella serenitatis MK135044	14.8		2.3	19.9	18.8	17.7	17.7	16.2	22.7	20.9	17.3	18.2	18.2	19.6	20.6	18.2	20.3	20.3	24.5	17.3	17.3	17.3	15.7	16.4	18.8
Fortescuenella serenitatis MK135045	17.4	2.3		23.4	21.8	22.1	21.3	23.4	26.1	25.7	24.7	25.1	24.7	25.2	25.4	24.9	23.9	24.3	23.6	23.8	23.8	23.8	23.2	23.6	25.5
Pilbaranella ethelensis MF074385	22.0	19.9	23.4		6.4	14.1	14.1	14.4	22.0	22.4	20.7	21.1	20.9	21.1	21.3	20.7	20.5	20.2	23.8	25.1	25.1	25.1	24.5	25.1	26.7
Pilbaranella ethelensis MF074388	23.2	18.8	21.8	6.4		15.2	14.8	15.1	22.4	22.1	19.8	19.8	20.0	20.6	20.9	19.8	19.8	19.5	24.0	24.2	24.2	24.2	23.7	24.0	25.9
Pilbaranella sp. C MF074409	23.8	17.7	22.1	14.1	15.2		13.9	14.4	22.7	22.6	21.8	21.4	21.6	22.2	22.0	21.8	20.2	20.3	22.7	27.5	27.5	27.5	27.1	27.5	28.5
Pilbaranella sp. A MF074391	22.7	17.7	21.3	14.1	14.8	13.9		13.4	25.9	26.0	23.3	23.3	23.1	23.6	23.8	23.3	21.8	22.0	26.4	26.7	26.7	26.7	26.0	26.7	28.3
Pilbaranella sp. B MF074381	22.4	16.2	23.4	14.4	15.1	14.4	13.4		25.6	25.2	22.5	22.5	22.7	23.1	23.4	22.7	21.5	21.5	24.7	26.0	26.0	26.0	25.6	25.6	28.3
BMR00289_1845_BGCK_Bathynellidae `sp. Biologic-BATH002`	26.3	22.7	26.1	22.0	22.4	22.7	25.9	25.6		0.7	11.4	11.1	11.4	11.4	11.1	11.4	12.1	12.7	23.8	25.9	25.9	25.9	25.9	25.8	25.5
BMR02430_20112_Bathynellidae `sp. Biologic-BATH002`	26.2	20.9	25.7	22.4	22.1	22.6	26.0	25.2	0.7		11.1	10.6	11.1	11.4	11.2	11.1	11.1	11.8	25.0	26.4	26.4	26.4	26.4	26.4	26.7
BMR00530_1845_BGCK_Bathynellidae `sp. Biologic-BATH003`	23.1	17.3	24.7	20.7	19.8	21.8	23.3	22.5	11.4	11.1		0.3	0.5	0.5	0.8	0.8	0.4	2.1	22.9	25.2	25.2	25.2	25.2	25.1	25.0
BMR00650_1845_BGCK_Bathynellidae `sp. Biologic-BATH003`	23.6	18.2	25.1	21.1	19.8	21.4	23.3	22.5	11.1	10.6	0.3		0.5	0.5	0.8	0.8	0.4	2.1	22.9	25.2	25.2	25.2	25.2	25.1	25.0
BMR00590_1845_BGCK_Bathynellidae `sp. Biologic-BATH003`	23.1	18.2	24.7	20.9	20.0	21.6	23.1	22.7	11.4	11.1	0.5	0.5		0.0	0.3	0.6	0.0	1.7	22.8	25.1	25.1	25.1	25.1	24.9	25.0
BMR00709_1845_BGCK_Bathynellidae `sp. Biologic-BATH003`	23.8	19.6	25.2	21.1	20.6	22.2	23.6	23.1	11.4	11.4	0.5	0.5	0.0		0.3	0.6	0.0	1.7	22.8	25.3	25.3	25.3	25.3	25.1	25.0
BMR00649_1845_BGCK_Bathynellidae `sp. Biologic-BATH003`	24.0	20.6	25.4	21.3	20.9	22.0	23.8	23.4	11.1	11.2	0.8	0.8	0.3	0.3		0.9	0.2	1.9	22.5	25.6	25.6	25.6	25.6	25.4	24.7
BMR00710_1845_BGCK_Bathynellidae `sp. Biologic-BATH003`	22.7	18.2	24.9	20.7	19.8	21.8	23.3	22.7	11.4	11.1	0.8	0.8	0.6	0.6	0.9		0.4	1.7	22.9	25.2	25.2	25.2	25.2	25.1	25.3
BMR02599_20112_Bathynellidae `sp. Biologic-BATH003`	22.0	20.3	23.9	20.5	19.8	20.2	21.8	21.5	12.1	11.1	0.4	0.4	0.0	0.0	0.2	0.4		1.7	23.8	26.5	26.5	26.5	25.9	26.5	26.7
BMR02600_20112_Bathynellidae `sp. Biologic-BATH003`	22.4	20.3	24.3	20.2	19.5	20.3	22.0	21.5	12.7	11.8	2.1	2.1	1.7	1.7	1.9	1.7	1.7		24.0	26.7	26.7	26.7	26.1	26.7	26.9
BMR00711_1845_BGCK_Bathynellidae `sp. Biologic-BATH001`	22.0	24.5	23.6	23.8	24.0	22.7	26.4	24.7	23.8	25.0	22.9	22.9	22.8	22.8	22.5	22.9	23.8	24.0		23.9	23.9	23.9	23.9	23.7	26.3
BES6932a_Paraburdoo_HB17NLC006_WAM-BATH001	25.1	17.3	23.8	25.1	24.2	27.5	26.7	26.0	25.9	26.4	25.2	25.2	25.1	25.3	25.6	25.2	26.5	26.7	23.9		0.0	0.0	0.0	0.5	27.7
BES6932c_Paraburdoo_HB17NLC006_WAM-BATH001	25.1	17.3	23.8	25.1	24.2	27.5	26.7	26.0	25.9	26.4	25.2	25.2	25.1	25.3	25.6	25.2	26.5	26.7	23.9	0.0		0.0	0.0	0.5	27.7
BES7570a_Paraburdoo_HB15NLC001_WAM-BATH001	25.1	17.3	23.8	25.1	24.2	27.5	26.7	26.0	25.9	26.4	25.2	25.2	25.1	25.3	25.6	25.2	26.5	26.7	23.9	0.0	0.0		0.0	0.5	27.7
RT56_WAMC74210_WAM-BATH001	24.5	15.7	23.2	24.5	23.7	27.1	26.0	25.6	25.9	26.4	25.2	25.2	25.1	25.3	25.6	25.2	25.9	26.1	23.9	0.0	0.0	0.0		0.5	27.7
BES6932b_Paraburdoo_HB17NLC006_WAM-BATH001	24.9	16.4	23.6	25.1	24.0	27.5	26.7	25.6	25.8	26.4	25.1	25.1	24.9	25.1	25.4	25.1	26.5	26.7	23.7	0.5	0.5	0.5	0.5		27.5
KR131708 Koonunga allambiensis OUTGROUP	26.9	18.8	25.5	26.7	25.9	28.5	28.3	28.3	25.5	26.7	25.0	25.0	25.0	25.0	24.7	25.3	26.7	26.9	26.3	27.7	27.7	27.7	27.7	27.5	

Malacostraca: Syncarida: Parabathynellidae.

COI Pairwise Distances (%)	JN817391	BMR00622	BMR02603	BMR02601	BMR00673	JN817390	KX022572	KX022566	JN817402	JN817408	JN817406	JN817407	JN817405	BMR00246	BMR00418	BMR00480	BMR00420	BMR02292	BMR02293	BMR02298	BMR02294	BMR02299	BMR02589	BMR02590	BMR02591	BMR02593	BMR02592	BMR02594	BMR02740	BMR02597	BMR02595	BMR02286	BMR02295	BMR02296	BMR02297	BMR02464	BMR02465	BMR02585	BMR02586	BMR02587	BMR02588	BMR02300	BMR02303	BMR02301	BMR02302	BMR02304	BMR02281	BMR02282	BMR02283	BMR02284	BMR02285	BMR00419	BMR00541	BMR00645	BMR02461	BMR02462	BMR02463	BMR00542	BMR00602	BMR00543	JX286478	JX286491	JX286485	JX286496	BMR00372	BMR00545	BMR00527	JN817395	KR131708
Atopobathynella hinzeae BES11166JN817391		15.6	15.4	15.2	15.9	17.0	20.2	17.9	17.7	19.2	20.6	18.4	19.3	26.8	26.1	26.1	25.9	23.4	23.4	23.6	23.6	23.4	26.2	25.8	25.9	25.9	25.9	25.9	25.9	25.8	26.1	21.2	21.5	21.5	21.5	21.1	21.3	21.8	22.0	21.8	21.8	20.7	20.7	20.9	20.9	20.9	20.3	20.3	20.3	20.3	20.3	21.7	22.4	21.9	26.3	24.2	24.2	24.5	24.7	22.4	21.6	21.8	21.6	23.7	20.3	19.8	22.2	21.3	27.3
BMR00622_1845_BGCK_Atopobathynella `sp. Biologic-PBAT013`	15.6		0.3	0.5	1.6	18.8	21.2	18.5	18.5	19.2	19.5	19.5	19.8	26.4	26.0	26.0	26.0	24.4	24.4	24.6	24.4	24.3	25.7	25.7	25.7	25.7	25.8	25.8	25.8	25.7	26.2	22.6	23.0	23.0	22.8	22.6	23.0	23.4	23.6	23.4	23.4	22.1	22.1	22.1	22.1	22.1	21.6	21.6	21.6	21.6	21.6	23.3	23.6	22.7	25.1	23.6	23.6	23.8	22.9	20.9	21.3	21.3	20.4	22.4	19.8	20.0	16.4	21.4	26.2
BMR02603_20112_Atopobathynella `sp. Biologic-PBAT013`	15.4	0.3		1.1	2.0	18.8	20.4	18.0	18.2	19.2	18.9	19.3	19.4	26.7	26.3	26.3	25.8	24.4	24.4	24.6	24.4	24.3	25.9	25.7	25.7	25.7	25.8	25.8	25.8	25.7	26.2	22.6	23.0	23.0	22.8	21.6	22.2	22.4	22.6	22.4	22.8	22.1	22.1	22.1	22.1	22.1	21.6	21.6	21.6	21.6	21.6	23.8	24.0	23.3	25.1	23.6	23.6	23.5	22.7	21.8	22.0	22.0	21.2	22.6	20.0	20.2	17.6	21.3	26.4
BMR02601_20112_Atopobathynella `sp. Biologic-PBAT013`	15.2	0.5	1.1		1.8	18.6	20.6	18.2	18.1	19.0	19.1	19.1	19.6	26.9	26.5	26.5	26.0	24.4	24.4	24.6	24.4	24.3	25.9	25.7	25.7	25.7	25.8	25.8	25.8	25.7	26.2	22.5	22.8	22.8	22.6	21.3	21.9	21.8	22.1	22.1	22.6	22.0	22.0	22.0	22.0	22.0	21.5	21.5	21.5	21.5	21.5	23.8	24.0	23.3	24.9	23.3	23.3	24.2	23.3	21.8	21.8	21.8	21.0	22.8	20.2	20.4	17.6	21.1	26.4
BMR00673_1845_BGCK_Atopobathynella `sp. Biologic-PBAT013`	15.9	1.6	2.0	1.8		18.3	21.5	18.5	18.1	19.7	19.7	19.3	19.8	26.6	25.8	25.8	25.8	24.1	24.1	24.3	24.1	23.9	25.5	25.5	25.5	25.5	25.6	25.6	25.6	25.5	25.8	22.0	22.3	22.3	22.1	22.0	22.3	22.5	22.6	22.5	22.5	21.8	21.8	21.8	21.8	21.8	21.8	21.8	21.8	21.8	21.8	22.7	22.9	23.1	24.4	22.9	22.9	23.8	22.9	20.5	22.1	22.1	21.3	21.9	19.2	19.4	16.8	21.2	25.7
Atopobathynella sp. 1 KMA-2012 JN817390	17.0	18.8	18.8	18.6	18.3		21.4	19.1	20.8	21.3	22.9	22.6	21.5	28.4	27.5	27.5	27.3	26.7	26.7	26.5	26.9	26.7	27.1	27.0	26.8	26.8	27.3	27.3	27.3	27.0	27.0	24.7	25.1	25.1	25.1	24.9	25.1	25.6	25.8	25.6	25.6	26.0	26.0	26.2	26.2	26.2	24.4	24.4	24.4	24.4	24.4	26.8	27.2	24.9	26.6	25.4	25.4	25.4	24.9	22.8	22.7	22.5	22.5	20.7	20.9	19.8	20.7	23.9	26.3
Parabathynellidae sp. C2.A1 KX022572	20.2	21.2	20.4	20.6	21.5	21.4		12.3	19.3	18.9	18.8	18.5	20.0	26.8	26.7	26.7	26.4	24.3	24.3	24.1	24.5	24.3	26.5	25.9	26.2	26.2	26.4	26.4	26.4	25.9	26.2	23.6	23.8	23.8	23.8	23.2	23.2	24.2	24.4	24.2	24.2	22.7	22.7	22.9	22.9	22.9	22.0	22.0	22.0	22.0	22.0	25.0	25.3	22.8	24.3	22.8	22.8	23.3	23.1	19.5	22.0	22.2	21.8	21.1	21.4	20.4	22.2	23.4	28.5
Parabathynellidae sp. L2 KX022566	17.9	18.5	18.0	18.2	18.5	19.1	12.3		19.1	17.9	18.0	18.9	19.1	27.7	27.0	27.0	26.8	24.9	24.9	24.7	25.0	24.9	26.8	26.5	26.5	26.5	27.0	27.0	27.0	26.5	27.3	23.3	23.5	23.5	23.5	22.9	23.1	23.6	23.8	23.6	23.6	22.4	22.4	22.6	22.6	22.6	22.0	22.0	22.0	22.0	22.0	23.6	23.9	23.6	26.0	24.6	24.6	23.6	23.1	20.1	21.1	21.3	20.8	19.9	22.1	20.9	21.8	22.5	27.6
Billibathynella sp. 2B JN817402	17.7	18.5	18.2	18.1	18.1	20.8	19.3	19.1		17.4	16.2	15.5	16.6	21.9	21.4	21.4	21.2	19.5	19.5	19.7	19.7	19.5	20.7	20.6	20.5	20.5	20.7	20.7	20.7	20.6	21.0	19.1	19.5	19.3	19.5	18.9	19.3	19.3	19.4	19.3	19.3	19.5	19.5	19.5	19.5	19.5	17.9	17.9	17.9	17.9	17.9	21.2	21.9	18.4	22.4	20.3	20.3	21.7	21.2	18.1	19.7	19.3	18.3	19.7	19.9	18.2	20.3	22.9	28.1
Brevisomabathynella cunyuensis BES 13347 JN817408	19.2	19.2	19.2	19.0	19.7	21.3	18.9	17.9	17.4		9.5	9.7	16.7	20.6	21.0	21.0	20.7	20.4	20.4	20.6	20.6	20.4	20.7	20.4	20.5	20.5	21.0	21.0	21.0	20.4	21.2	20.6	21.0	20.6	20.8	20.6	21.0	22.6	22.9	22.6	22.6	18.3	18.3	18.1	18.1	18.1	16.1	16.1	16.1	16.1	16.1	18.4	18.3	16.3	19.8	19.1	19.1	22.4	21.9	18.4	21.3	21.3	20.9	19.5	22.4	21.7	18.4	24.8	27.6
Brevisomabathynella sp. 2 JN817406	20.6	19.5	18.9	19.1	19.7	22.9	18.8	18.0	16.2	9.5		11.3	16.4	22.7	22.6	22.6	22.8	22.6	22.6	22.7	22.4	22.6	22.4	22.0	22.2	22.2	22.6	22.6	22.6	22.0	22.8	21.0	21.4	21.4	21.2	20.8	21.1	21.8	22.0	21.8	21.8	20.3	20.3	20.2	20.2	20.2	19.5	19.5	19.5	19.5	19.5	20.0	20.0	18.6	21.9	20.0	20.0	22.8	22.1	18.3	21.1	21.1	20.2	20.0	21.0	19.6	19.2	23.6	27.6
Brevisomabathynella uramurdahensis A JN817407	18.4	19.5	19.3	19.1	19.3	22.6	18.5	18.9	15.5	9.7	11.3		17.4	22.4	23.1	23.1	22.8	21.9	21.9	22.1	22.1	21.9	21.9	21.6	21.7	21.7	21.9	21.9	21.9	21.6	22.1	19.7	20.0	19.8	19.8	19.4	19.8	21.3	21.5	21.3	21.3	19.5	19.5	19.3	19.3	19.3	18.8	18.8	18.8	18.8	18.8	20.3	20.0	18.6	21.2	19.6	19.6	21.9	21.4	21.3	20.9	20.9	20.0	20.0	22.3	21.7	17.6	23.2	27.3
Parabathynellidae sp. Lineage C JN817405	19.3	19.8	19.4	19.6	19.8	21.5	20.0	19.1	16.6	16.7	16.4	17.4		23.1	22.6	22.6	22.8	20.9	20.9	21.0	20.7	20.9	22.9	22.5	22.7	22.7	23.1	23.1	23.1	22.5	23.3	20.5	20.7	20.7	20.5	20.1	20.4	20.9	21.1	20.9	20.9	20.9	20.9	20.7	20.7	20.7	19.5	19.5	19.5	19.5	19.5	23.3	23.3	20.0	22.4	20.0	20.0	21.7	21.0	20.0	22.7	22.3	21.6	20.7	20.9	21.2	21.8	23.9	25.3
BMR00246_1749b_BS3_Parabathynellidae sp. Biologic-PBAT-004	26.8	26.4	26.7	26.9	26.6	28.4	26.8	27.7	21.9	20.6	22.7	22.4	23.1		0.3	0.3	1.1	0.9	0.9	0.9	0.4	0.6	2.4	2.1	2.1	2.1	2.1	2.1	2.1	2.3	2.4	13.3	13.7	13.5	13.3	14.3	14.8	14.9	14.3	14.9	14.1	14.5	14.5	14.2	14.2	14.2	12.5	12.5	12.5	12.5	12.5	14.3	14.3	13.1	17.9	16.4	16.4	18.5	18.8	21.5	24.5	24.3	24.1	24.6	24.9	23.5	25.7	30.9	27.8
BMR00418_1749b_BS3X_Parabathynellidae sp. Biologic-PBAT004	26.1	26.0	26.3	26.5	25.8	27.5	26.7	27.0	21.4	21.0	22.6	23.1	22.6	0.3		0.0	0.8	0.4	0.4	0.7	0.0	0.2	1.9	1.6	1.6	1.6	1.8	1.8	1.8	1.8	2.1	12.6	13.0	12.8	12.6	13.5	14.0	13.9	13.4	13.9	13.2	13.7	13.7	13.4	13.4	13.4	12.8	12.8	12.8	12.8	12.8	13.4	13.3	12.9	17.4	16.3	16.3	18.2	18.5	20.8	23.6	23.5	23.3	24.3	24.5	22.8	24.9	29.5	27.7
BMR00480_1749b_BS3X_Parabathynellidae sp. Biologic-PBAT004	26.1	26.0	26.3	26.5	25.8	27.5	26.7	27.0	21.4	21.0	22.6	23.1	22.6	0.3	0.0		0.8	0.4	0.4	0.7	0.0	0.2	1.9	1.6	1.6	1.6	1.8	1.8	1.8	1.8	2.1	12.6	13.0	12.8	12.6	13.5	14.0	13.9	13.4	13.9	13.2	13.7	13.7	13.4	13.4	13.4	12.8	12.8	12.8	12.8	12.8	13.4	13.3	12.9	17.4	16.3	16.3	18.2	18.5	20.8	23.6	23.5	23.3	24.3	24.5	22.8	24.9	29.5	27.7
BMR00420_1749b_BS3X_Parabathynellidae sp. Biologic-PBAT004	25.9	26.0	25.8	26.0	25.8	27.3	26.4	26.8	21.2	20.7	22.8	22.8	22.8	1.1	0.8	0.8		0.0	0.0	0.2	0.4	0.2	1.9	1.6	1.6	1.6	1.8	1.8	1.8	1.8	2.1	12.6	13.0	12.8	12.6	13.1	13.6	13.5	12.9	13.5	13.2	13.7	13.7	13.4	13.4	13.4	12.8	12.8	12.8	12.8	12.8	13.5	13.5	12.9	17.4	16.7	16.7	18.5	18.8	21.4	23.5	23.3	23.2	24.1	24.5	22.8	25.1	29.3	28.0
BMR02292_20112_BS2_3 / BS3x_Parabathynellidae `sp. Biologic-PBAT004`	23.4	24.4	24.4	24.4	24.1	26.7	24.3	24.9	19.5	20.4	22.6	21.9	20.9	0.9	0.4	0.4	0.0		0.0	0.2	0.3	0.2	1.9	1.6	1.6	1.6	1.8	1.8	1.8	1.8	2.1	11.1	11.5	11.3	11.1	11.1	11.5	11.8	11.6	11.8	11.8	12.5	12.5	12.3	12.3	12.3	12.8	12.8	12.8	12.8	12.8	13.0	12.9	12.8	17.4	16.7	16.7	18.9	19.4	20.6	23.2	23.0	22.8	25.0	25.7	24.4	28.3	27.0	29.5
BMR02293_20112_BS2_3 / BS3x_Parabathynellidae `sp. Biologic-PBAT004`	23.4	24.4	24.4	24.4	24.1	26.7	24.3	24.9	19.5	20.4	22.6	21.9	20.9	0.9	0.4	0.4	0.0	0.0		0.2	0.3	0.2	1.9	1.6	1.6	1.6	1.8	1.8	1.8	1.8	2.1	11.1	11.5	11.3	11.1	11.1	11.5	11.8	11.6	11.8	11.8	12.5	12.5	12.3	12.3	12.3	12.8	12.8	12.8	12.8	12.8	13.0	12.9	12.8	17.4	16.7	16.7	18.9	19.4	20.6	23.2	23.0	22.8	25.0	25.7	24.4	28.3	27.0	29.5
BMR02298_20112_BS2_3 / BS3x_Parabathynellidae `sp. Biologic-PBAT004`	23.6	24.6	24.6	24.6	24.3	26.5	24.1	24.7	19.7	20.6	22.7	22.1	21.0	0.9	0.7	0.7	0.2	0.2	0.2		0.5	0.3	2.1	1.8	1.8	1.8	2.0	2.0	2.0	2.0	2.3	11.3	11.6	11.5	11.3	11.3	11.6	12.0	11.8	12.0	12.0	12.6	12.6	12.5	12.5	12.5	12.8	12.8	12.8	12.8	12.8	13.2	13.2	12.8	17.6	17.0	17.0	18.7	19.2	20.8	23.5	23.2	23.0	25.2	25.9	24.7	28.3	27.0	29.7
BMR02294_20112_BS2_3 / BS3x_Parabathynellidae `sp. Biologic-PBAT004`	23.6	24.4	24.4	24.4	24.1	26.9	24.5	25.0	19.7	20.6	22.4	22.1	20.7	0.4	0.0	0.0	0.4	0.3	0.3	0.5		0.2	1.9	1.6	1.6	1.6	1.8	1.8	1.8	1.8	2.1	11.1	11.5	11.3	11.1	11.1	11.5	11.8	11.6	11.8	11.8	12.5	12.5	12.3	12.3	12.3	12.8	12.8	12.8	12.8	12.8	13.0	12.9	12.8	17.4	16.3	16.3	18.9	19.4	20.2	23.5	23.2	23.0	25.0	25.9	24.7	28.0	27.2	29.2
BMR02299_20112_BS2_3 / BS3x_Parabathynellidae `sp. Biologic-PBAT004`	23.4	24.3	24.3	24.3	23.9	26.7	24.3	24.9	19.5	20.4	22.6	21.9	20.9	0.6	0.2	0.2	0.2	0.2	0.2	0.3	0.2		1.7	1.3	1.4	1.4	1.5	1.5	1.5	1.6	1.9	11.0	11.3	11.1	11.0	11.0	11.3	11.6	11.5	11.6	11.6	12.3	12.3	12.1	12.1	12.1	12.6	12.6	12.6	12.6	12.6	12.8	12.7	12.6	17.6	16.5	16.5	18.7	19.2	20.4	23.2	23.0	22.8	24.8	25.7	24.4	28.0	27.0	29.5
BMR02589_20112_Parabathynellidae `sp. Biologic-PBAT004`	26.2	25.7	25.9	25.9	25.5	27.1	26.5	26.8	20.7	20.7	22.4	21.9	22.9	2.4	1.9	1.9	1.9	1.9	1.9	2.1	1.9	1.7		0.3	0.3	0.3	0.3	0.3	0.3	0.5	0.5	12.0	12.5	12.2	12.0	12.0	12.5	12.0	11.8	12.0	12.0	12.9	12.9	12.7	12.7	12.7	12.2	12.2	12.2	12.2	12.2	12.5	12.5	12.2	17.1	15.9	15.9	18.9	18.9	20.9	24.2	24.0	23.7	24.9	25.3	24.1	28.0	29.3	30.0
BMR02590_20112_Parabathynellidae `sp. Biologic-PBAT004`	25.8	25.7	25.7	25.7	25.5	27.0	25.9	26.5	20.6	20.4	22.0	21.6	22.5	2.1	1.6	1.6	1.6	1.6	1.6	1.8	1.6	1.3	0.3		0.0	0.0	0.0	0.0	0.0	0.2	0.2	11.9	12.3	12.1	11.9	11.9	12.3	11.9	11.6	11.9	11.9	12.8	12.8	12.5	12.5	12.5	12.3	12.3	12.3	12.3	12.3	12.3	12.2	12.3	17.0	15.9	15.9	18.6	18.6	20.5	23.5	23.3	23.0	24.6	25.2	23.9	28.0	29.3	29.7
BMR02591_20112_Parabathynellidae `sp. Biologic-PBAT004`	25.9	25.7	25.7	25.7	25.5	26.8	26.2	26.5	20.5	20.5	22.2	21.7	22.7	2.1	1.6	1.6	1.6	1.6	1.6	1.8	1.6	1.4	0.3	0.0		0.0	0.0	0.0	0.0	0.2	0.2	11.7	12.2	12.0	11.7	11.7	12.2	11.7	11.5	11.7	11.7	12.6	12.6	12.4	12.4	12.4	12.0	12.0	12.0	12.0	12.0	12.2	12.2	12.0	16.8	15.6	15.6	18.6	18.6	20.6	23.9	23.7	23.4	24.6	25.2	23.9	28.0	29.2	29.7
BMR02593_20112_Parabathynellidae `sp. Biologic-PBAT004`	25.9	25.7	25.7	25.7	25.5	26.8	26.2	26.5	20.5	20.5	22.2	21.7	22.7	2.1	1.6	1.6	1.6	1.6	1.6	1.8	1.6	1.4	0.3	0.0	0.0		0.0	0.0	0.0	0.2	0.2	11.7	12.2	12.0	11.7	11.7	12.2	11.7	11.5	11.7	11.7	12.6	12.6	12.4	12.4	12.4	12.0	12.0	12.0	12.0	12.0	12.2	12.2	12.0	16.8	15.6	15.6	18.6	18.6	20.6	23.9	23.7	23.4	24.6	25.2	23.9	28.0	29.2	29.7
BMR02592_20112_Parabathynellidae `sp. Biologic-PBAT004`	25.9	25.8	25.8	25.8	25.6	27.3	26.4	27.0	20.7	21.0	22.6	21.9	23.1	2.1	1.8	1.8	1.8	1.8	1.8	2.0	1.8	1.5	0.3	0.0	0.0	0.0		0.0	0.0	0.2	0.2	12.1	12.6	12.3	12.1	12.1	12.6	12.1	11.9	12.1	12.1	13.0	13.0	12.8	12.8	12.8	12.3	12.3	12.3	12.3	12.3	12.6	12.2	12.3	17.2	16.1	16.1	18.7	18.7	20.4	23.6	23.3	23.1	25.1	25.0	23.8	28.0	29.3	29.7
BMR02594_20112_Parabathynellidae `sp. Biologic-PBAT004`	25.9	25.8	25.8	25.8	25.6	27.3	26.4	27.0	20.7	21.0	22.6	21.9	23.1	2.1	1.8	1.8	1.8	1.8	1.8	2.0	1.8	1.5	0.3	0.0	0.0	0.0	0.0		0.0	0.2	0.2	12.1	12.6	12.3	12.1	12.1	12.6	12.1	11.9	12.1	12.1	13.0	13.0	12.8	12.8	12.8	12.3	12.3	12.3	12.3	12.3	12.6	12.2	12.3	17.2	16.1	16.1	18.7	18.7	20.4	23.6	23.3	23.1	25.1	25.0	23.8	28.0	29.3	29.7
BMR02740_20112_Parabathynellidae `sp. Biologic-PBAT004`	25.9	25.8	25.8	25.8	25.6	27.3	26.4	27.0	20.7	21.0	22.6	21.9	23.1	2.1	1.8	1.8	1.8	1.8	1.8	2.0	1.8	1.5	0.3	0.0	0.0	0.0	0.0	0.0		0.2	0.2	12.1	12.6	12.3	12.1	12.1	12.6	12.1	11.9	12.1	12.1	13.0	13.0	12.8	12.8	12.8	12.3	12.3	12.3	12.3	12.3	12.6	12.2	12.3	17.2	16.1	16.1	18.7	18.7	20.4	23.6	23.3	23.1	25.1	25.0	23.8	28.0	29.3	29.7
BMR02597_20112_Parabathynellidae `sp. Biologic-PBAT004`	25.8	25.7	25.7	25.7	25.5	27.0	25.9	26.5	20.6	20.4	22.0	21.6	22.5	2.3	1.8	1.8	1.8	1.8	1.8	2.0	1.8	1.6	0.5	0.2	0.2	0.2	0.2	0.2	0.2		0.2	11.9	12.3	12.1	11.9	11.9	12.3	11.9	11.6	11.9	11.9	13.0	13.0	12.8	12.8	12.8	12.3	12.3	12.3	12.3	12.3	12.5	12.5	12.3	17.0	15.9	15.9	18.6	18.6	20.5	23.5	23.3	23.0	24.4	24.9	23.7	28.0	29.3	30.0
BMR02595_20112_Parabathynellidae `sp. Biologic-PBAT004`	26.1	26.2	26.2	26.2	25.8	27.0	26.2	27.3	21.0	21.2	22.8	22.1	23.3	2.4	2.1	2.1	2.1	2.1	2.1	2.3	2.1	1.9	0.5	0.2	0.2	0.2	0.2	0.2	0.2	0.2		11.8	12.3	12.1	11.8	11.8	12.3	11.8	11.6	11.8	11.8	13.0	13.0	12.8	12.8	12.8	11.6	11.6	11.6	11.6	11.6	12.5	12.2	11.6	16.7	15.5	15.5	18.6	18.6	20.8	23.2	23.0	23.2	25.1	25.2	23.4	28.5	29.5	28.7
BMR02286_20112_BS3x_Parabathynellidae `sp. Biologic-PBAT012`	21.2	22.6	22.6	22.5	22.0	24.7	23.6	23.3	19.1	20.6	21.0	19.7	20.5	13.3	12.6	12.6	12.6	11.1	11.1	11.3	11.1	11.0	12.0	11.9	11.7	11.7	12.1	12.1	12.1	11.9	11.8		0.3	0.3	0.3	0.3	0.3	3.0	3.1	3.0	3.0	8.9	8.9	8.7	8.7	8.7	12.8	12.8	12.8	12.8	12.8	10.1	10.4	12.8	15.0	14.3	14.3	17.6	17.0	20.0	23.2	23.0	22.4	24.1	24.7	24.0	28.0	25.3	29.2
BMR02295_20112_BS3_Parabathynellidae `sp. Biologic-PBAT012`	21.5	23.0	23.0	22.8	22.3	25.1	23.8	23.5	19.5	21.0	21.4	20.0	20.7	13.7	13.0	13.0	13.0	11.5	11.5	11.6	11.5	11.3	12.5	12.3	12.2	12.2	12.6	12.6	12.6	12.3	12.3	0.3		0.3	0.3	0.3	0.3	3.0	3.1	3.0	3.0	9.2	9.2	9.0	9.0	9.0	13.1	13.1	13.1	13.1	13.1	10.6	10.9	13.2	15.4	14.8	14.8	18.1	17.4	19.8	23.7	23.5	22.8	24.3	24.9	24.2	28.3	25.3	29.5
BMR02296_20112_BS3_Parabathynellidae `sp. Biologic-PBAT012`	21.5	23.0	23.0	22.8	22.3	25.1	23.8	23.5	19.3	20.6	21.4	19.8	20.7	13.5	12.8	12.8	12.8	11.3	11.3	11.5	11.3	11.1	12.2	12.1	12.0	12.0	12.3	12.3	12.3	12.1	12.1	0.3	0.3		0.3	0.3	0.3	3.0	3.1	3.0	3.0	9.2	9.2	9.0	9.0	9.0	13.0	13.0	13.0	13.0	13.0	10.6	10.9	13.0	15.2	14.5	14.5	18.1	17.4	20.0	23.7	23.5	22.8	24.3	24.7	24.0	28.0	25.4	29.2
BMR02297_20112_BS3_Parabathynellidae `sp. Biologic-PBAT012`	21.5	22.8	22.8	22.6	22.1	25.1	23.8	23.5	19.5	20.8	21.2	19.8	20.5	13.3	12.6	12.6	12.6	11.1	11.1	11.3	11.1	11.0	12.0	11.9	11.7	11.7	12.1	12.1	12.1	11.9	11.8	0.3	0.3	0.3		0.3	0.3	3.0	3.1	3.0	3.0	8.9	8.9	8.7	8.7	8.7	13.1	13.1	13.1	13.1	13.1	10.1	10.4	13.2	15.2	14.5	14.5	17.8	17.2	20.3	23.7	23.5	22.8	24.1	24.7	24.0	28.0	25.4	29.2
BMR02464_20112_Parabathynellidae `sp. Biologic-PBAT012`	21.1	22.6	21.6	21.3	22.0	24.9	23.2	22.9	18.9	20.6	20.8	19.4	20.1	14.3	13.5	13.5	13.1	11.1	11.1	11.3	11.1	11.0	12.0	11.9	11.7	11.7	12.1	12.1	12.1	11.9	11.8	0.3	0.3	0.3	0.3		0.6	3.0	2.9	2.7	3.4	8.9	8.9	8.7	8.7	8.7	12.8	12.8	12.8	12.8	12.8	11.3	11.6	14.0	15.4	14.8	14.8	18.1	17.5	20.7	24.1	23.9	23.2	24.1	24.6	24.0	27.9	25.1	29.1
BMR02465_20112_Parabathynellidae `sp. Biologic-PBAT012`	21.3	23.0	22.2	21.9	22.3	25.1	23.2	23.1	19.3	21.0	21.1	19.8	20.4	14.8	14.0	14.0	13.6	11.5	11.5	11.6	11.5	11.3	12.5	12.3	12.2	12.2	12.6	12.6	12.6	12.3	12.3	0.3	0.3	0.3	0.3	0.6		3.2	3.4	3.1	3.1	9.2	9.2	9.0	9.0	9.0	13.1	13.1	13.1	13.1	13.1	11.7	12.0	14.0	15.4	14.8	14.8	18.2	17.5	20.8	23.9	23.7	23.1	24.5	24.6	24.0	28.0	25.3	29.2
BMR02585_20112_Parabathynellidae `sp. Biologic-PBAT012`	21.8	23.4	22.4	21.8	22.5	25.6	24.2	23.6	19.3	22.6	21.8	21.3	20.9	14.9	13.9	13.9	13.5	11.8	11.8	12.0	11.8	11.6	12.0	11.9	11.7	11.7	12.1	12.1	12.1	11.9	11.8	3.0	3.0	3.0	3.0	3.0	3.2		0.3	0.8	0.5	10.2	10.2	10.0	10.0	10.0	13.8	13.8	13.8	13.8	13.8	11.6	11.9	15.3	15.4	14.3	14.3	19.3	18.6	21.8	24.3	24.1	23.5	25.2	25.5	24.4	28.6	26.4	30.5
BMR02586_20112_Parabathynellidae `sp. Biologic-PBAT012`	22.0	23.6	22.6	22.1	22.6	25.8	24.4	23.8	19.4	22.9	22.0	21.5	21.1	14.3	13.4	13.4	12.9	11.6	11.6	11.8	11.6	11.5	11.8	11.6	11.5	11.5	11.9	11.9	11.9	11.6	11.6	3.1	3.1	3.1	3.1	2.9	3.4	0.3		0.2	0.8	10.3	10.3	10.2	10.2	10.2	13.6	13.6	13.6	13.6	13.6	11.5	11.8	14.8	15.6	14.5	14.5	19.2	18.6	21.8	24.3	24.1	23.5	25.2	25.5	24.4	28.6	26.5	30.5
BMR02587_20112_Parabathynellidae `sp. Biologic-PBAT012`	21.8	23.4	22.4	22.1	22.5	25.6	24.2	23.6	19.3	22.6	21.8	21.3	20.9	14.9	13.9	13.9	13.5	11.8	11.8	12.0	11.8	11.6	12.0	11.9	11.7	11.7	12.1	12.1	12.1	11.9	11.8	3.0	3.0	3.0	3.0	2.7	3.1	0.8	0.2		0.6	10.2	10.2	10.0	10.0	10.0	13.8	13.8	13.8	13.8	13.8	11.6	11.9	15.3	15.4	14.3	14.3	19.3	18.6	21.8	24.5	24.3	23.7	25.2	25.5	24.4	28.6	26.4	30.5
BMR02588_20112_Parabathynellidae `sp. Biologic-PBAT012`	21.8	23.4	22.8	22.6	22.5	25.6	24.2	23.6	19.3	22.6	21.8	21.3	20.9	14.1	13.2	13.2	13.2	11.8	11.8	12.0	11.8	11.6	12.0	11.9	11.7	11.7	12.1	12.1	12.1	11.9	11.8	3.0	3.0	3.0	3.0	3.4	3.1	0.5	0.8	0.6		10.2	10.2	10.0	10.0	10.0	13.8	13.8	13.8	13.8	13.8	10.9	11.2	14.2	15.4	14.3	14.3	18.2	17.5	20.8	23.5	23.3	22.7	24.7	24.4	23.4	27.7	26.4	29.4
BMR02300_20112_BS3_Parabathynellidae `sp. Biologic-PBAT005`	20.7	22.1	22.1	22.0	21.8	26.0	22.7	22.4	19.5	18.3	20.3	19.5	20.9	14.5	13.7	13.7	13.7	12.5	12.5	12.6	12.5	12.3	12.9	12.8	12.6	12.6	13.0	13.0	13.0	13.0	13.0	8.9	9.2	9.2	8.9	8.9	9.2	10.2	10.3	10.2	10.2		0.0	0.2	0.2	0.2	13.6	13.6	13.6	13.6	13.6	4.4	4.5	13.7	17.6	15.6	15.6	18.5	18.3	20.3	22.6	22.4	22.1	22.6	25.8	24.4	26.2	25.6	29.5
BMR02303_20112_BS3_Parabathynellidae `sp. Biologic-PBAT005`	20.7	22.1	22.1	22.0	21.8	26.0	22.7	22.4	19.5	18.3	20.3	19.5	20.9	14.5	13.7	13.7	13.7	12.5	12.5	12.6	12.5	12.3	12.9	12.8	12.6	12.6	13.0	13.0	13.0	13.0	13.0	8.9	9.2	9.2	8.9	8.9	9.2	10.2	10.3	10.2	10.2	0.0		0.2	0.2	0.2	13.6	13.6	13.6	13.6	13.6	4.4	4.5	13.7	17.6	15.6	15.6	18.5	18.3	20.3	22.6	22.4	22.1	22.6	25.8	24.4	26.2	25.6	29.5
BMR02301_20112_BS3_Parabathynellidae `sp. Biologic-PBAT005`	20.9	22.1	22.1	22.0	21.8	26.2	22.9	22.6	19.5	18.1	20.2	19.3	20.7	14.2	13.4	13.4	13.4	12.3	12.3	12.5	12.3	12.1	12.7	12.5	12.4	12.4	12.8	12.8	12.8	12.8	12.8	8.7	9.0	9.0	8.7	8.7	9.0	10.0	10.2	10.0	10.0	0.2	0.2		0.0	0.0	13.4	13.4	13.4	13.4	13.4	4.2	4.3	13.4	17.4	15.4	15.4	18.3	18.1	20.0	22.4	22.1	21.9	22.8	25.6	24.2	26.2	25.6	29.2
BMR02302_20112_BS3_Parabathynellidae `sp. Biologic-PBAT005`	20.9	22.1	22.1	22.0	21.8	26.2	22.9	22.6	19.5	18.1	20.2	19.3	20.7	14.2	13.4	13.4	13.4	12.3	12.3	12.5	12.3	12.1	12.7	12.5	12.4	12.4	12.8	12.8	12.8	12.8	12.8	8.7	9.0	9.0	8.7	8.7	9.0	10.0	10.2	10.0	10.0	0.2	0.2	0.0		0.0	13.4	13.4	13.4	13.4	13.4	4.2	4.3	13.4	17.4	15.4	15.4	18.3	18.1	20.0	22.4	22.1	21.9	22.8	25.6	24.2	26.2	25.6	29.2
BMR02304_20112_BS3_Parabathynellidae `sp. Biologic-PBAT005`	20.9	22.1	22.1	22.0	21.8	26.2	22.9	22.6	19.5	18.1	20.2	19.3	20.7	14.2	13.4	13.4	13.4	12.3	12.3	12.5	12.3	12.1	12.7	12.5	12.4	12.4	12.8	12.8	12.8	12.8	12.8	8.7	9.0	9.0	8.7	8.7	9.0	10.0	10.2	10.0	10.0	0.2	0.2	0.0	0.0		13.4	13.4	13.4	13.4	13.4	4.2	4.3	13.4	17.4	15.4	15.4	18.3	18.1	20.0	22.4	22.1	21.9	22.8	25.6	24.2	26.2	25.6	29.2
BMR02281_20112_BS1_Parabathynellidae `sp. Biologic-PBAT003`	20.3	21.6	21.6	21.5	21.8	24.4	22.0	22.0	17.9	16.1	19.5	18.8	19.5	12.5	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.6	12.2	12.3	12.0	12.0	12.3	12.3	12.3	12.3	11.6	12.8	13.1	13.0	13.1	12.8	13.1	13.8	13.6	13.8	13.8	13.6	13.6	13.4	13.4	13.4		0.0	0.0	0.0	0.0	13.7	13.6	0.0	15.2	13.2	13.2	18.1	18.1	16.6	21.5	21.3	21.1	23.0	24.2	22.9	26.9	24.4	28.5
BMR02282_20112_BS1_Parabathynellidae `sp. Biologic-PBAT003`	20.3	21.6	21.6	21.5	21.8	24.4	22.0	22.0	17.9	16.1	19.5	18.8	19.5	12.5	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.6	12.2	12.3	12.0	12.0	12.3	12.3	12.3	12.3	11.6	12.8	13.1	13.0	13.1	12.8	13.1	13.8	13.6	13.8	13.8	13.6	13.6	13.4	13.4	13.4	0.0		0.0	0.0	0.0	13.7	13.6	0.0	15.2	13.2	13.2	18.1	18.1	16.6	21.5	21.3	21.1	23.0	24.2	22.9	26.9	24.4	28.5
BMR02283_20112_BS1_Parabathynellidae `sp. Biologic-PBAT003`	20.3	21.6	21.6	21.5	21.8	24.4	22.0	22.0	17.9	16.1	19.5	18.8	19.5	12.5	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.6	12.2	12.3	12.0	12.0	12.3	12.3	12.3	12.3	11.6	12.8	13.1	13.0	13.1	12.8	13.1	13.8	13.6	13.8	13.8	13.6	13.6	13.4	13.4	13.4	0.0	0.0		0.0	0.0	13.7	13.6	0.0	15.2	13.2	13.2	18.1	18.1	16.6	21.5	21.3	21.1	23.0	24.2	22.9	26.9	24.4	28.5
BMR02284_20112_BS1_Parabathynellidae `sp. Biologic-PBAT003`	20.3	21.6	21.6	21.5	21.8	24.4	22.0	22.0	17.9	16.1	19.5	18.8	19.5	12.5	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.6	12.2	12.3	12.0	12.0	12.3	12.3	12.3	12.3	11.6	12.8	13.1	13.0	13.1	12.8	13.1	13.8	13.6	13.8	13.8	13.6	13.6	13.4	13.4	13.4	0.0	0.0	0.0		0.0	13.7	13.6	0.0	15.2	13.2	13.2	18.1	18.1	16.6	21.5	21.3	21.1	23.0	24.2	22.9	26.9	24.4	28.5
BMR02285_20112_BS1_Parabathynellidae `sp. Biologic-PBAT003`	20.3	21.6	21.6	21.5	21.8	24.4	22.0	22.0	17.9	16.1	19.5	18.8	19.5	12.5	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.6	12.2	12.3	12.0	12.0	12.3	12.3	12.3	12.3	11.6	12.8	13.1	13.0	13.1	12.8	13.1	13.8	13.6	13.8	13.8	13.6	13.6	13.4	13.4	13.4	0.0	0.0	0.0	0.0		13.7	13.6	0.0	15.2	13.2	13.2	18.1	18.1	16.6	21.5	21.3	21.1	23.0	24.2	22.9	26.9	24.4	28.5
BMR00419_1749b_BS3_Parabathynellidae sp. Biologic-PBAT005	21.7	23.3	23.8	23.8	22.7	26.8	25.0	23.6	21.2	18.4	20.0	20.3	23.3	14.3	13.4	13.4	13.5	13.0	13.0	13.2	13.0	12.8	12.5	12.3	12.2	12.2	12.6	12.6	12.6	12.5	12.5	10.1	10.6	10.6	10.1	11.3	11.7	11.6	11.5	11.6	10.9	4.4	4.4	4.2	4.2	4.2	13.7	13.7	13.7	13.7	13.7		0.0	13.1	17.6	15.6	15.6	17.5	17.0	20.6	22.0	22.3	21.7	22.7	23.4	22.8	23.9	28.3	27.5
BMR00541_1749b_BS3_Parabathynellidae sp. Biologic-PBAT005	22.4	23.6	24.0	24.0	22.9	27.2	25.3	23.9	21.9	18.3	20.0	20.0	23.3	14.3	13.3	13.3	13.5	12.9	12.9	13.2	12.9	12.7	12.5	12.2	12.2	12.2	12.2	12.2	12.2	12.5	12.2	10.4	10.9	10.9	10.4	11.6	12.0	11.9	11.8	11.9	11.2	4.5	4.5	4.3	4.3	4.3	13.6	13.6	13.6	13.6	13.6	0.0		13.0	18.1	16.1	16.1	17.5	17.1	20.7	22.3	22.7	22.0	22.8	23.8	23.1	23.9	29.2	27.5
BMR00645_1845_BS1E_Parabathynellidae sp. Biologic-PBAT003	21.9	22.7	23.3	23.3	23.1	24.9	22.8	23.6	18.4	16.3	18.6	18.6	20.0	13.1	12.9	12.9	12.9	12.8	12.8	12.8	12.8	12.6	12.2	12.3	12.0	12.0	12.3	12.3	12.3	12.3	11.6	12.8	13.2	13.0	13.2	14.0	14.0	15.3	14.8	15.3	14.2	13.7	13.7	13.4	13.4	13.4	0.0	0.0	0.0	0.0	0.0	13.1	13.0		15.2	13.2	13.2	16.6	16.6	16.7	21.2	21.0	20.9	22.2	22.8	22.0	24.7	24.9	26.6
BMR02461_20112_Parabathynellidae `sp. Biologic-PBAT022`	26.3	25.1	25.1	24.9	24.4	26.6	24.3	26.0	22.4	19.8	21.9	21.2	22.4	17.9	17.4	17.4	17.4	17.4	17.4	17.6	17.4	17.6	17.1	17.0	16.8	16.8	17.2	17.2	17.2	17.0	16.7	15.0	15.4	15.2	15.2	15.4	15.4	15.4	15.6	15.4	15.4	17.6	17.6	17.4	17.4	17.4	15.2	15.2	15.2	15.2	15.2	17.6	18.1	15.2		3.7	3.7	19.6	19.2	19.7	22.0	21.8	21.6	23.8	24.9	23.8	25.2	29.0	29.0
BMR02462_20112_Parabathynellidae `sp. Biologic-PBAT022`	24.2	23.6	23.6	23.3	22.9	25.4	22.8	24.6	20.3	19.1	20.0	19.6	20.0	16.4	16.3	16.3	16.7	16.7	16.7	17.0	16.3	16.5	15.9	15.9	15.6	15.6	16.1	16.1	16.1	15.9	15.5	14.3	14.8	14.5	14.5	14.8	14.8	14.3	14.5	14.3	14.3	15.6	15.6	15.4	15.4	15.4	13.2	13.2	13.2	13.2	13.2	15.6	16.1	13.2	3.7		0.0	18.7	18.3	18.0	21.1	20.9	20.9	22.2	23.6	22.9	24.8	27.1	28.5
BMR02463_20112_Parabathynellidae `sp. Biologic-PBAT022`	24.2	23.6	23.6	23.3	22.9	25.4	22.8	24.6	20.3	19.1	20.0	19.6	20.0	16.4	16.3	16.3	16.7	16.7	16.7	17.0	16.3	16.5	15.9	15.9	15.6	15.6	16.1	16.1	16.1	15.9	15.5	14.3	14.8	14.5	14.5	14.8	14.8	14.3	14.5	14.3	14.3	15.6	15.6	15.4	15.4	15.4	13.2	13.2	13.2	13.2	13.2	15.6	16.1	13.2	3.7	0.0		18.7	18.3	18.0	21.1	20.9	20.9	22.2	23.6	22.9	24.8	27.1	28.5
BMR00542_1749a_HSTD_Parabathynellidae sp. Biologic-PBAT002	24.5	23.8	23.5	24.2	23.8	25.4	23.3	23.6	21.7	22.4	22.8	21.9	21.7	18.5	18.2	18.2	18.5	18.9	18.9	18.7	18.9	18.7	18.9	18.6	18.6	18.6	18.7	18.7	18.7	18.6	18.6	17.6	18.1	18.1	17.8	18.1	18.2	19.3	19.2	19.3	18.2	18.5	18.5	18.3	18.3	18.3	18.1	18.1	18.1	18.1	18.1	17.5	17.5	16.6	19.6	18.7	18.7		0.6	19.2	21.3	21.7	21.7	22.5	22.4	21.7	23.3	27.6	26.6
BMR00602_1749a_HSTD_Parabathynellidae sp. Biologic-PBAT002	24.7	22.9	22.7	23.3	22.9	24.9	23.1	23.1	21.2	21.9	22.1	21.4	21.0	18.8	18.5	18.5	18.8	19.4	19.4	19.2	19.4	19.2	18.9	18.6	18.6	18.6	18.7	18.7	18.7	18.6	18.6	17.0	17.4	17.4	17.2	17.5	17.5	18.6	18.6	18.6	17.5	18.3	18.3	18.1	18.1	18.1	18.1	18.1	18.1	18.1	18.1	17.0	17.1	16.6	19.2	18.3	18.3	0.6		18.9	21.3	21.7	21.3	22.3	22.1	21.4	23.3	27.3	26.4
BMR00543_1749a_CVCK_Parabathynellidae sp. Biologic-PBAT-001	22.4	20.9	21.8	21.8	20.5	22.8	19.5	20.1	18.1	18.4	18.3	21.3	20.0	21.5	20.8	20.8	21.4	20.6	20.6	20.8	20.2	20.4	20.9	20.5	20.6	20.6	20.4	20.4	20.4	20.5	20.8	20.0	19.8	20.0	20.3	20.7	20.8	21.8	21.8	21.8	20.8	20.3	20.3	20.0	20.0	20.0	16.6	16.6	16.6	16.6	16.6	20.6	20.7	16.7	19.7	18.0	18.0	19.2	18.9		21.0	21.0	20.4	20.4	21.5	21.6	22.3	25.9	25.3
Parabathynellidae sp. 3G JX286478	21.6	21.3	22.0	21.8	22.1	22.7	22.0	21.1	19.7	21.3	21.1	20.9	22.7	24.5	23.6	23.6	23.5	23.2	23.2	23.5	23.5	23.2	24.2	23.5	23.9	23.9	23.6	23.6	23.6	23.5	23.2	23.2	23.7	23.7	23.7	24.1	23.9	24.3	24.3	24.5	23.5	22.6	22.6	22.4	22.4	22.4	21.5	21.5	21.5	21.5	21.5	22.0	22.3	21.2	22.0	21.1	21.1	21.3	21.3	21.0		0.8	1.3	17.2	22.4	20.9	19.7	26.0	26.1
Parabathynellidae sp. 4K JX286491	21.8	21.3	22.0	21.8	22.1	22.5	22.2	21.3	19.3	21.3	21.1	20.9	22.3	24.3	23.5	23.5	23.3	23.0	23.0	23.2	23.2	23.0	24.0	23.3	23.7	23.7	23.3	23.3	23.3	23.3	23.0	23.0	23.5	23.5	23.5	23.9	23.7	24.1	24.1	24.3	23.3	22.4	22.4	22.1	22.1	22.1	21.3	21.3	21.3	21.3	21.3	22.3	22.7	21.0	21.8	20.9	20.9	21.7	21.7	21.0	0.8		0.8	17.0	22.7	20.9	20.4	26.7	26.4
Parabathynellidae sp. 4D JX286485	21.6	20.4	21.2	21.0	21.3	22.5	21.8	20.8	18.3	20.9	20.2	20.0	21.6	24.1	23.3	23.3	23.2	22.8	22.8	23.0	23.0	22.8	23.7	23.0	23.4	23.4	23.1	23.1	23.1	23.0	23.2	22.4	22.8	22.8	22.8	23.2	23.1	23.5	23.5	23.7	22.7	22.1	22.1	21.9	21.9	21.9	21.1	21.1	21.1	21.1	21.1	21.7	22.0	20.9	21.6	20.9	20.9	21.7	21.3	20.4	1.3	0.8		16.7	22.4	20.7	20.4	26.2	26.8
Parabathynellidae sp. 6I JX286496	23.7	22.4	22.6	22.8	21.9	20.7	21.1	19.9	19.7	19.5	20.0	20.0	20.7	24.6	24.3	24.3	24.1	25.0	25.0	25.2	25.0	24.8	24.9	24.6	24.6	24.6	25.1	25.1	25.1	24.4	25.1	24.1	24.3	24.3	24.1	24.1	24.5	25.2	25.2	25.2	24.7	22.6	22.6	22.8	22.8	22.8	23.0	23.0	23.0	23.0	23.0	22.7	22.8	22.2	23.8	22.2	22.2	22.5	22.3	20.4	17.2	17.0	16.7		20.7	20.2	18.1	27.7	25.2
BMR00372_1749a_CVCK_Atopobathynella sp. Biologic-PBAT-006	20.3	19.8	20.0	20.2	19.2	20.9	21.4	22.1	19.9	22.4	21.0	22.3	20.9	24.9	24.5	24.5	24.5	25.7	25.7	25.9	25.9	25.7	25.3	25.2	25.2	25.2	25.0	25.0	25.0	24.9	25.2	24.7	24.9	24.7	24.7	24.6	24.6	25.5	25.5	25.5	24.4	25.8	25.8	25.6	25.6	25.6	24.2	24.2	24.2	24.2	24.2	23.4	23.8	22.8	24.9	23.6	23.6	22.4	22.1	21.5	22.4	22.7	22.4	20.7		3.7	19.4	20.6	25.0
BMR00545_1749a_CVCK_REG_Atopobathynella sp. Biologic-PBAT006	19.8	20.0	20.2	20.4	19.4	19.8	20.4	20.9	18.2	21.7	19.6	21.7	21.2	23.5	22.8	22.8	22.8	24.4	24.4	24.7	24.7	24.4	24.1	23.9	23.9	23.9	23.8	23.8	23.8	23.7	23.4	24.0	24.2	24.0	24.0	24.0	24.0	24.4	24.4	24.4	23.4	24.4	24.4	24.2	24.2	24.2	22.9	22.9	22.9	22.9	22.9	22.8	23.1	22.0	23.8	22.9	22.9	21.7	21.4	21.6	20.9	20.9	20.7	20.2	3.7		18.2	20.7	25.6
BMR00527_1845_BGCK_Atopobathynella `sp. Biologic-PBAT014`	22.2	16.4	17.6	17.6	16.8	20.7	22.2	21.8	20.3	18.4	19.2	17.6	21.8	25.7	24.9	24.9	25.1	28.3	28.3	28.3	28.0	28.0	28.0	28.0	28.0	28.0	28.0	28.0	28.0	28.0	28.5	28.0	28.3	28.0	28.0	27.9	28.0	28.6	28.6	28.6	27.7	26.2	26.2	26.2	26.2	26.2	26.9	26.9	26.9	26.9	26.9	23.9	23.9	24.7	25.2	24.8	24.8	23.3	23.3	22.3	19.7	20.4	20.4	18.1	19.4	18.2		26.4	25.9
Kimberleybathynella sp. 1 KMA-2012 JN817395	21.3	21.4	21.3	21.1	21.2	23.9	23.4	22.5	22.9	24.8	23.6	23.2	23.9	30.9	29.5	29.5	29.3	27.0	27.0	27.0	27.2	27.0	29.3	29.3	29.2	29.2	29.3	29.3	29.3	29.3	29.5	25.3	25.3	25.4	25.4	25.1	25.3	26.4	26.5	26.4	26.4	25.6	25.6	25.6	25.6	25.6	24.4	24.4	24.4	24.4	24.4	28.3	29.2	24.9	29.0	27.1	27.1	27.6	27.3	25.9	26.0	26.7	26.2	27.7	20.6	20.7	26.4		28.9
KR131708 Koonunga allambiensis OUTGROUP	27.3	26.2	26.4	26.4	25.7	26.3	28.5	27.6	28.1	27.6	27.6	27.3	25.3	27.8	27.7	27.7	28.0	29.5	29.5	29.7	29.2	29.5	30.0	29.7	29.7	29.7	29.7	29.7	29.7	30.0	28.7	29.2	29.5	29.2	29.2	29.1	29.2	30.5	30.5	30.5	29.4	29.5	29.5	29.2	29.2	29.2	28.5	28.5	28.5	28.5	28.5	27.5	27.5	26.6	29.0	28.5	28.5	26.6	26.4	25.3	26.1	26.4	26.8	25.2	25.0	25.6	25.9	28.9	

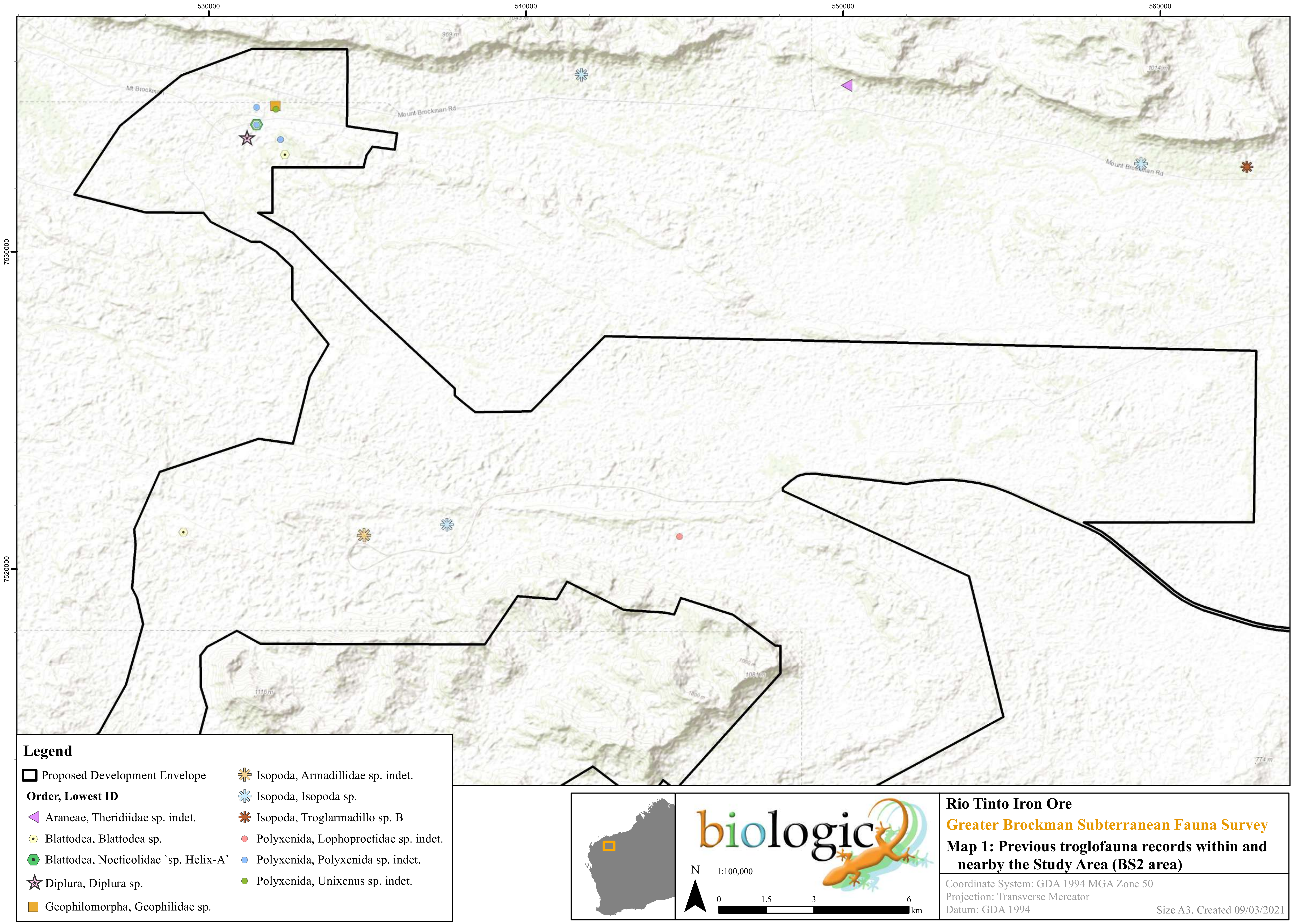
Pauropoda

COI Pairwise Distances (%)	BMR02705	BMR02664	BMR02706	BMR00516	BMR00086	BMR00090	BMR00475	WAMT145460	WAMT145455	BMR00250	MW621067	WAMT145451	BMR02703	BMR00087	BMR00253	BMR00089	WAMT145459	WAMT145453	BMR00088	BMR00763	BMR02663	BMR00249	MW621066	BMR02704	BMR00236	KR705664	BMR00237
BMR02705_20112_Pauropoda `sp. Biologic-PAUR039`		12.6	15.6	15.2	16.1	15.7	19.6	22.0	24.7	26.7	29.3	25.6	30.0	29.5	30.0	31.9	33.7	34.4	33.3	33.0	32.2	31.9	32.0	33.7	34.6	33.9	35.0
BMR02664_20112_Pauropoda `sp. Biologic-PAUR037`	12.6		13.7	15.4	14.8	14.9	20.2	23.6	25.1	24.7	27.7	28.2	29.5	30.2	30.4	32.6	33.5	34.6	34.1	33.7	31.1	31.7	32.2	33.9	34.6	33.3	36.3
BMR02706_20112_Pauropoda `sp. Biologic-PAUR040`	15.6	13.7		18.5	18.4	17.8	17.5	23.9	26.4	25.2	27.0	26.6	27.7	27.4	27.2	33.4	33.9	33.6	35.3	34.3	31.9	31.6	31.6	33.1	33.9	31.4	34.0
BMR00516_1749b_BS2W_Pauropoda sp. Biologic-PAUR006	15.2	15.4	18.5		11.1	12.2	19.6	23.1	25.1	24.2	24.8	25.4	30.5	30.1	30.2	33.7	33.1	35.4	33.4	33.3	31.9	31.9	31.8	33.1	34.7	32.6	34.2
BMR00086_1749b_BS2W_Pauropoda sp. Biologic-PAUR007	16.1	14.8	18.4	11.1		3.0	18.3	24.5	25.5	25.8	27.1	26.6	31.0	29.9	30.4	35.0	34.2	34.8	34.0	34.3	34.5	32.7	32.6	33.6	33.4	33.0	35.0
BMR00090_1749b_BS2W_Pauropoda sp. Biologic-PAUR007	15.7	14.9	17.8	12.2	3.0		18.9	25.3	25.1	26.2	27.6	26.0	30.3	29.4	30.1	33.9	33.8	34.4	33.8	33.9	33.8	32.1	32.0	33.3	33.1	32.9	35.6
BMR00475_1749b_LNSG_Pauropoda sp. Biologic-PAUR005	19.6	20.2	17.5	19.6	18.3	18.9		29.1	28.9	31.9	31.9	28.2	30.9	30.0	30.5	33.6	34.1	34.6	35.2	35.5	33.8	34.2	34.2	35.8	33.9	30.7	35.8
RT43_WAMT145460_Decapauropus_WAM-PAUD004	22.0	23.6	23.9	23.1	24.5	25.3	29.1		12.4	27.1	28.0	28.4	30.9	30.1	31.8	33.4	34.1	34.9	35.1	32.5	33.7	34.0	33.9	34.5	33.6	32.3	36.3
RT43_WAMT145455_Decapauropus_WAM-PAUD005	24.7	25.1	26.4	25.1	25.5	25.1	28.9	12.4		27.4	28.1	27.0	29.8	29.2	31.0	34.3	34.1	33.5	33.7	32.5	34.5	32.5	32.3	33.9	34.1	31.6	35.3
BMR00250_1845_VIV_Pauropoda sp. Biologic-PAUR004	26.7	24.7	25.2	24.2	25.8	26.2	31.9	27.1	27.4		2.8	28.4	30.1	29.6	29.3	33.4	32.8	33.0	33.3	33.9	33.4	31.6	31.3	32.2	33.5	30.1	33.6
MW621067_Tetramerocerata sp.	29.3	27.7	27.0	24.8	27.1	27.6	31.9	28.0	28.1	2.8		30.0	32.0	31.0	31.5	35.7	34.7	36.0	35.7	35.8	34.8	33.2	32.9	33.5	35.1	31.4	36.5
RT43_WAMT145451_Decapauropus_WAM-PAUD003	25.6	28.2	26.6	25.4	26.6	26.0	28.2	28.4	27.0	28.4	30.0		28.7	28.4	28.7	32.2	31.9	32.2	33.0	34.3	32.2	31.0	30.9	31.8	33.7	32.3	33.4
BMR02703_20112_Pauropoda sp. Biologic-PAUR008	30.0	29.5	27.7	30.5	31.0	30.3	30.9	30.9	29.8	30.1	32.0	28.7		3.8	7.4	24.2	25.1	24.9	25.8	26.1	25.2	23.1	23.3	24.2	28.2	25.1	29.5
BMR00087_1749a_CVCK_REG_Pauropoda sp. Biologic-PAUR008	29.5	30.2	27.4	30.1	29.9	29.4	30.0	30.1	29.2	29.6	31.0	28.4	3.8		6.2	22.9	23.4	24.9	25.1	26.0	25.1	22.2	22.4	22.9	26.9	24.5	29.3
BMR00253_1845_BGCK_Pauropoda sp. Biologic-PAUR008	30.0	30.4	27.2	30.2	30.4	30.1	30.5	31.8	31.0	29.3	31.5	28.7	7.4	6.2		24.8	24.8	24.9	25.5	25.7	24.9	22.8	23.0	24.0	27.4	24.7	28.4
BMR00089_1749a_SGW_Pauropoda sp. WAM-PAUD002	31.9	32.6	33.4	33.7	35.0	33.9	33.6	33.4	34.3	33.4	35.7	32.2	24.2	22.9	24.8		5.0	19.0	19.1	20.4	20.7	20.1	19.9	21.0	25.7	25.4	30.1
RT43_WAMT145459_Decapauropus_WAM-PAUD002	33.7	33.5	33.9	33.1	34.2	33.8	34.1	34.1	34.1	32.8	34.7	31.9	25.1	23.4	24.8	5.0		17.4	19.1	20.7	20.5	20.5	20.4	21.1	26.1	25.9	29.6
RT43_WAMT145453_Decapauropus_WAM-PAUD001	34.4	34.6	33.6	35.4	34.8	34.4	34.6	34.9	33.5	33.0	36.0	32.2	24.9	24.9	24.9	19.0	17.4		20.2	20.8	22.2	23.4	23.6	21.1	27.4	28.9	30.4
BMR00088_1749b_LNSG_Pauropoda sp. Biologic-PAUR010	33.3	34.1	35.3	33.4	34.0	33.8	35.2	35.1	33.7	33.3	35.7	33.0	25.8	25.1	25.5	19.1	19.1	20.2		22.6	20.5	23.4	23.4	22.9	25.5	28.5	30.7
BMR00763_1845_VIV_Pauropoda sp. Biologic-PAUR011	33.0	33.7	34.3	33.3	34.3	33.9	35.5	32.5	32.5	33.9	35.8	34.3	26.1	26.0	25.7	20.4	20.7	20.8	22.6		18.8	23.3	23.3	24.5	26.0	28.3	31.8
BMR02663_20112_Pauropoda `sp. Biologic-PAUR036`	32.2	31.1	31.9	31.9	34.5	33.8	33.8	33.7	34.5	33.4	34.8	32.2	25.2	25.1	24.9	20.7	20.5	22.2	20.5	18.8		22.2	22.1	22.2	25.8	26.5	32.5
BMR00249_1845_BS1E_Pauropoda sp. Biologic-PAUR009	31.9	31.7	31.6	31.9	32.7	32.1	34.2	34.0	32.5	31.6	33.2	31.0	23.1	22.2	22.8	20.1	20.5	23.4	23.4	23.3	22.2		1.0	17.3	25.1	27.9	30.7
MW621066_Tetramerocerata sp.	32.0	32.2	31.6	31.8	32.6	32.0	34.2	33.9	32.3	31.3	32.9	30.9	23.3	22.4	23.0	19.9	20.4	23.6	23.4	23.3	22.1	1.0		17.4	25.1	27.7	30.6
BMR02704_20112_Pauropoda `sp. Biologic-PAUR038`	33.7	33.9	33.1	33.1	33.6	33.3	35.8	34.5	33.9	32.2	33.5	31.8	24.2	22.9	24.0	21.0	21.1	21.1	22.9	24.5	22.2	17.3	17.4		27.4	28.0	29.5
BMR00236_1749b_BS3_Pauropoda sp. Biologic-PAUR013	34.6	34.6	33.9	34.7	33.4	33.1	33.9	33.6	34.1	33.5	35.1	33.7	28.2	26.9	27.4	25.7	26.1	27.4	25.5	26.0	25.8	25.1	25.1	27.4		26.6	29.9
KR705664_Scolopendra morsitans_OUTGROUP	33.9	33.3	31.4	32.6	33.0	32.9	30.7	32.3	31.6	30.1	31.4	32.3	25.1	24.5	24.7	25.4	25.9	28.9	28.5	28.3	26.5	27.9	27.7	28.0	26.6		29.8
BMR00237_1749a_CVCK_REG_Pauropoda sp. Biologic-PAUR012	35.0	36.3	34.0	34.2	35.0	35.6	35.8	36.3	35.3	33.6	36.5	33.4	29.5	29.3	28.4	30.1	29.6	30.4	30.7	31.8	32.5	30.7	30.6	29.5	29.9	29.8	

Symphyla: Cephalostigmata: Scutigerellidae

COI Pairwise Distances (%)	BMR02678	BMR00725	BMR00741	WAMT145913	MO08	ML57	ML47	ML42	ML52	IV355	BMR00762	WAMT144298	BMR00231	BMR00242	BMR00244	BMR00641	BMR01199	BMR00243	BMR00364	BMR00241	WAMT145462	WAMT145461	BMR00229	BMR01208	BMR00230	BMR02675	BMR02702	BMR00232	WAMT145463	BMR00071	BMR00070	JY25	BMR00321	JY26	BMR00721	BMR00724	BMR00326	BMR00320	JY24	WAMT144260	BMR01163	BMR02685	WAMT144261	WAMT145911	IV354	BMR00202	JD04	BMR02684	ML54	KR705664
BMR02678_20112_Symphylella `sp. Biologic-SYMP030`		14.3	16.1	16.7	16.3	14.8	15.0	15.3	16.8	16.7	22.7	26.0	22.9	24.2	24.2	24.0	23.6	23.8	24.8	22.9	22.0	22.9	24.7	21.8	22.2	21.1	21.8	22.7	22.5	23.1	25.4	24.7	24.2	23.8	23.3	25.2	23.8	24.9	25.6	25.3	22.8	20.8	24.9	23.6	24.4	23.3	23.4	25.3	25.9	24.4
BMR00725_1811_WHill	14.3		13.5	17.5	15.6	14.9	14.8	14.8	15.8	17.2	23.4	23.1	26.3	25.4	25.4	25.4	24.3	25.1	26.4	24.6	24.2	26.0	26.3	24.6	24.6	24.2	24.8	23.4	26.9	24.6	25.9	26.1	25.8	25.8	26.0	30.9	26.9	27.4	26.7	26.1	27.6	23.0	25.7	24.3	24.5	24.8	24.1	26.3	25.8	26.6
BMR00741_1845_VIV_Scolopendrellidae `sp. Biologic-SYMP014`	16.1	13.5		19.8	17.6	18.1	18.1	17.9	19.4	18.9	22.5	26.1	26.7	25.2	25.2	25.4	24.9	25.7	27.8	24.0	25.2	26.3	25.8	25.2	25.7	25.8	25.7	24.0	26.0	25.7	28.5	24.6	24.5	23.1	24.0	29.8	25.5	25.7	27.6	27.8	26.2	26.1	27.4	24.3	24.8	26.9	27.3	25.2	27.4	27.1
RT48_ROBE_WAMT145913_Symphyella_WAM-SYMPH001	16.7	17.5	19.8		12.2	11.8	11.8	11.3	14.1	14.2	23.4	25.6	27.4	25.8	25.8	25.8	25.1	25.8	26.4	25.7	25.7	25.8	27.1	23.7	23.7	23.7	23.6	25.2	25.4	26.4	27.6	26.7	26.4	26.4	26.3	30.1	28.0	28.1	29.0	26.3	28.3	26.9	27.5	25.7	25.8	26.9	28.7	26.6	25.2	24.6
MO08_ROBE_Symphyla	16.3	15.6	17.6	12.2		8.6	8.2	7.9	10.9	12.1	21.9	25.3	24.4	24.2	24.2	24.4	23.7	23.5	24.2	23.9	24.7	25.5	26.0	23.5	23.7	22.9	23.4	23.9	25.0	25.4	26.8	24.7	24.7	25.4	24.9	27.5	27.5	28.7	27.5	26.2	25.4	24.7	25.5	24.7	25.3	24.5	26.2	27.7	26.2	23.8
ML57_ROBE_Symphyla	14.8	14.9	18.1	11.8	8.6		0.3	1.3	12.5	13.3	22.6	25.2	26.0	25.2	25.2	25.7	24.4	25.5	26.1	24.7	25.3	26.5	26.7	24.7	24.9	24.7	25.2	24.7	25.5	25.0	25.9	25.4	25.0	25.7	24.5	28.8	27.4	28.2	27.4	25.5	27.0	25.9	27.3	25.0	25.5	25.2	27.3	27.9	26.4	23.8
ML47_ROBE_Symphyla	15.0	14.8	18.1	11.8	8.2	0.3		1.3	12.3	13.3	22.4	25.0	25.7	25.0	25.0	25.5	24.2	25.4	25.9	24.4	25.0	26.2	26.5	24.7	24.7	24.5	25.0	24.5	25.2	24.7	25.7	25.0	24.7	25.4	24.2	28.6	27.0	27.8	27.2	25.3	26.9	25.5	27.1	24.7	25.2	25.0	27.0	27.9	26.2	23.8
ML42_ROBE_Symphyla	15.3	14.8	17.9	11.3	7.9	1.3	1.3		12.3	13.1	22.1	24.7	25.2	24.9	24.9	25.4	24.0	25.4	25.9	24.4	24.8	26.0	26.4	23.9	24.0	23.9	24.4	24.0	25.3	24.5	25.5	25.4	25.0	25.7	24.4	28.6	27.2	28.2	26.9	25.3	26.9	26.0	27.0	25.0	25.5	25.9	27.2	27.0	26.5	23.6
ML52_ROBE_Symphyla	16.8	15.8	19.4	14.1	10.9	12.5	12.3	12.3		11.7	22.4	25.0	24.7	25.2	25.2	25.4	25.0	24.2	25.6	23.9	26.2	26.5	26.7	24.9	24.7	24.9	24.5	25.2	26.6	27.4	27.4	27.4	26.7	26.9	26.7	29.0	27.9	27.6	25.9	24.5	27.2	26.2	26.3	25.3	25.5	24.5	26.6	28.7	26.0	27.2
IV355_ROBE_Scolopendrellidae `sp. Helix-SYM026`	16.7	17.2	18.9	14.2	12.1	13.3	13.3	13.1	11.7		19.4	23.0	23.4	23.0	23.0	23.0	21.4	22.1	22.2	22.3	24.5	25.1	24.3	22.9	22.7	21.8	23.0	22.1	23.3	23.6	23.2	24.7	25.2	24.5	25.0	29.4	25.8	27.5	24.3	24.6	24.2	24.4	23.7	22.1	22.4	23.4	24.6	25.8	23.6	25.1
BMR00762_1845_VIV_Scolopendrellidae `sp. Biologic-SYMP008`	22.7	23.4	22.5	23.4	21.9	22.6	22.4	22.1	22.4	19.4		20.4	24.0	25.1	25.1	24.8	24.2	24.6	25.7	25.7	24.0	25.1	24.6	24.5	24.2	24.0	24.3	23.1	25.8	25.1	25.9	26.4	24.3	24.3	24.8	27.0	25.2	26.6	27.4	25.4	26.5	26.2	24.6	23.8	24.3	24.9	26.8	26.4	27.9	27.2
RT46_PARA_WAMT144298_Symphyella_WAM-SYMPH002	26.0	23.1	26.1	25.6	25.3	25.2	25.0	24.7	25.0	23.0	20.4		24.0	26.3	26.3	26.7	25.4	26.0	27.2	26.4	24.9	25.1	25.1	26.3	25.5	25.4	25.7	26.1	25.6	26.9	27.2	27.2	26.4	26.4	27.8	30.4	26.6	27.2	27.8	24.7	26.4	26.5	25.0	24.6	24.4	26.1	27.7	28.3	26.2	26.5
BMR00231_1749b_BS2W_Hanseniella `sp. Biologic-SYMP001`	22.9	26.3	26.7	27.4	24.4	26.0	25.7	25.2	24.7	23.4	24.0	24.0		19.5	19.5	19.5	18.8	19.5	19.9	18.1	18.5	19.0	17.8	17.8	17.9	17.6	17.9	19.5	19.0	19.9	19.2	19.0	19.0	18.1	18.5	21.8	17.6	18.0	19.4	19.6	17.4	19.0	16.4	18.4	18.2	19.0	18.4	20.2	27.9	26.3
BMR00242_1845_VIV_Scutigerellidae `sp. Biologic-SYMP007`	24.2	25.4	25.2	25.8	24.2	25.2	25.0	24.9	25.2	23.0	25.1	26.3	19.5		0.2	0.8	3.3	12.2	12.4	15.8	16.3	16.7	16.3	16.7	16.3	16.6	16.7	17.6	18.1	18.4	17.7	18.4	17.9	17.9	17.8	20.7	18.1	19.1	19.2	17.6	18.8	20.7	18.2	17.1	17.6	19.0	21.6	20.2	28.9	26.0
BMR00244_1845_VIV_Scutigerellidae `sp. Biologic-SYMP007`	24.2	25.4	25.2	25.8	24.2	25.2	25.0	24.9	25.2	23.0	25.1	26.3	19.5	0.2		0.9	3.5	12.0	12.4	15.7	16.3	16.7	16.4	16.7	16.3	16.6	16.7	17.6	17.9	18.4	17.7	18.4	17.9	17.9	17.8	20.7	18.1	19.1	19.1	17.6	18.8	20.6	18.2	16.9	17.5	18.8	21.6	20.4	28.9	26.2
BMR00641_1845_VIV_Scutigerellidae `sp. Biologic-SYMP007`	24.0	25.4	25.4	25.8	24.4	25.7	25.5	25.4	25.4	23.0	24.8	26.7	19.5	0.8	0.9		3.2	12.0	12.3	15.7	16.6	17.0	16.1	16.6	16.4	16.7	16.9	17.6	18.2	18.5	17.7	18.7	17.9	17.8	17.8	20.5	18.5	19.0	19.7	17.9	19.2	20.9	18.1	17.2	17.8	19.0	21.6	20.4	28.8	25.9
BMR01199_1845_BS1E_Scutigerellidae `sp. Biologic-SYMP007`	23.6	24.3	24.9	25.1	23.7	24.4	24.2	24.0	25.0	21.4	24.2	25.4	18.8	3.3	3.5	3.2		11.9	11.7	15.4	16.3	16.7	16.1	16.6	16.3	16.4	16.7	17.6	17.6	17.2	15.8	18.2	17.8	17.2	17.5	20.7	18.1	18.5	19.8	17.9	18.3	21.1	17.6	17.2	17.3	18.1	21.2	20.1	27.8	25.1
BMR00243_1845_VIV_Hanseniella `sp. Biologic-SYMP006`	23.8	25.1	25.7	25.8	23.5	25.5	25.4	25.4	24.2	22.1	24.6	26.0	19.5	12.2	12.0	12.0	11.9		2.1	16.1	17.0	16.9	19.1	16.9	16.9	16.9	17.2	17.2	19.5	19.0	18.4	19.0	18.8	19.1	19.1	22.2	19.1	20.2	19.4	18.7	17.9	20.5	16.1	18.9	18.8	19.1	19.9	20.5	27.6	25.4
BMR00364_1845_VIV_Hanseniella `sp. Biologic-SYMP006`	24.8	26.4	27.8	26.4	24.2	26.1	25.9	25.9	25.6	22.2	25.7	27.2	19.9	12.4	12.4	12.3	11.7	2.1		17.4	17.8	18.3	20.2	17.3	17.1	16.9	17.4	17.4	19.9	19.4	18.5	20.1	20.0	20.8	19.8	22.9	19.4	20.4	21.1	19.5	18.1	20.9	16.7	19.9	19.6	19.0	20.0	20.8	27.9	26.2
BMR00241_1845_BGCK_Scutigerellidae `sp. Biologic-SYMP005`	22.9	24.6	24.0	25.7	23.9	24.7	24.4	24.4	23.9	22.3	25.7	26.4	18.1	15.8	15.7	15.7	15.4	16.1	17.4		17.8	18.2	19.3	18.7	18.2	18.4	19.0	18.7	19.9	18.1	17.9	20.1	19.0	18.7	19.0	23.5	17.9	19.0	19.1	18.8	18.6	19.4	19.3	17.1	17.5	17.5	21.2	19.9	27.4	25.3
RT43_WAMT145462_Scutigerella_WAM-SCUTI003	22.0	24.2	25.2	25.7	24.7	25.3	25.0	24.8	26.2	24.5	24.0	24.9	18.5	16.3	16.3	16.6	16.3	17.0	17.8	17.8		5.3	16.9	16.1	16.0	16.4	16.7	17.3	16.7	16.9	17.5	18.2	17.3	17.0	17.3	20.8	19.5	20.0	19.4	16.7	18.5	19.4	16.4	17.2	17.0	17.5	20.3	19.3	26.5	26.6
RT43_PARA_WAMT145461_Scutigerella_WAM-SCUTI003	22.9	26.0	26.3	25.8	25.5	26.5	26.2	26.0	26.5	25.1	25.1	25.1	19.0	16.7	16.7	17.0	16.7	16.9	18.3	18.2	5.3		18.1	15.5	15.2	15.7	16.0	17.9	17.1	17.6	17.3	18.8	18.7	17.6	17.8	22.1	19.3	19.8	20.2	16.7	17.6	20.2	16.1	18.1	18.0	19.5	19.9	21.1	27.4	27.1
BMR00229_1749a_CVCK_REG_Hanseniella `sp. Biologic-SYMP002`	24.7	26.3	25.8	27.1	26.0	26.7	26.5	26.4	26.7	24.3	24.6	25.1	17.8	16.3	16.4	16.1	16.1	19.1	20.2	19.3	16.9	18.1		16.0	15.8	17.0	17.0	15.5	16.9	16.4	16.2	17.3	16.9	16.6	17.2	19.9	18.8	19.5	18.8	20.4	18.6	20.4	18.4	20.0	19.6	18.5	19.9	20.2	28.6	27.2
BMR01208_1749b_BS2W Ext_Hanseniella `sp. Biologic-SYMP003`	21.8	24.6	25.2	23.7	23.5	24.7	24.7	23.9	24.9	22.9	24.5	26.3	17.8	16.7	16.7	16.6	16.6	16.9	17.3	18.7	16.1	15.5	16.0		1.7	3.2	2.6	9.0	16.0	17.0	16.0	17.8	17.8	18.1	17.9	19.9	17.8	19.0	17.2	17.3	17.4	18.3	16.0	17.5	18.1	19.6	18.5	20.1	26.8	24.7
BMR00230_1749b_BS2W_Hanseniella `sp. Biologic-SYMP003`	22.2	24.6	25.7	23.7	23.7	24.9	24.7	24.0	24.7	22.7	24.2	25.5	17.9	16.3	16.3	16.4	16.3	16.9	17.1	18.2	16.0	15.2	15.8	1.7		2.3	1.7	8.5	16.4	16.6	15.6	17.8	17.6	18.1	17.9	19.9	17.8	19.0	16.9	17.3	16.8	18.5	15.8	17.7	18.2	19.3	18.4	20.4	26.3	25.0
BMR02675_20112_Hanseniella `sp. Biologic-SYMP003`	21.1	24.2	25.8	23.7	22.9	24.7	24.5	23.9	24.9	21.8	24.0	25.4	17.6	16.6	16.6	16.7	16.4	16.9	16.9	18.4	16.4	15.7	17.0	3.2	2.3		1.5	9.4	16.1	16.9	15.6	18.4	18.4	18.7	18.2	20.9	18.4	19.5	18.0	17.2	17.1	17.6	15.8	17.2	17.8	19.0	18.5	21.0	25.4	24.4
BMR02702_20112_Hanseniella sp. Biologic-SYMP003	21.8	24.8	25.7	23.6	23.4	25.2	25.0	24.4	24.5	23.0	24.3	25.7	17.9	16.7	16.7	16.9	16.7	17.2	17.4	19.0	16.7	16.0	17.0	2.6	1.7	1.5		9.6	16.6	17.5	16.2	18.2	18.2	18.2	18.1	20.1	18.1	19.1	17.4	17.3	17.6	18.2	15.8	17.7	18.2	19.5	18.5	20.8	26.1	25.0
BMR00232_1749b_BS2W_Hanseniella `sp. Biologic-SYMP003`	22.7	23.4	24.0	25.2	23.9	24.7	24.5	24.0	25.2	22.1	23.1	26.1	19.5	17.6	17.6	17.6	17.6	17.2	17.4	18.7	17.3	17.9	15.5	9.0	8.5	9.4	9.6		17.5	17.2	16.2	18.7	18.2	18.4	18.4	20.9	17.8	19.0	16.6	19.0	17.4	19.5	18.1	16.9	17.6	19.8	18.5	20.5	24.7	25.1
RT43_PARA_WAMT145463_Scutigerella_WAM-SCUTI004	22.5	26.9	26.0	25.4	25.0	25.5	25.2	25.3	26.6	23.3	25.8	25.6	19.0	18.1	17.9	18.2	17.6	19.5	19.9	19.9	16.7	17.1	16.9	16.0	16.4	16.1	16.6	17.5		19.3	18.1	18.4	18.2	19.0	19.0	22.6	18.4	20.3	18.5	19.1	18.6	18.0	18.5	17.2	17.0	17.9	20.1	21.1	28.5	25.4
BMR00071_1749b_DSM_Scutigerellidae `sp. Biologic-SYMP004`	23.1	24.6	25.7	26.4	25.4	25.0	24.7	24.5	27.4	23.6	25.1	26.9	19.9	18.4	18.4	18.5	17.2	19.0	19.4	18.1	16.9	17.6	16.4	17.0	16.6	16.9	17.5	17.2	19.3		0.6	17.6	17.8	17.8	17.0	21.2	19.3	19.8	17.5	20.2	18.5	19.3	17.2	18.6	19.0	19.8	19.7	19.3	26.9	28.9
BMR00070_1749b_LNSG_Scutigerellidae `sp. Biologic-SYMP004`	25.4	25.9	28.5	27.6	26.8	25.9	25.7	25.5	27.4	23.2	25.9	27.2	19.2	17.7	17.7	17.7	15.8	18.4	18.5	17.9	17.5	17.3	16.2	16.0	15.6	15.6	16.2	16.2	18.1	0.6		17.3	18.4	17.9	16.2	21.4	18.8	19.4	16.5	18.8	17.7	19.3	16.9	18.6	18.8	19.6	18.9	20.3	24.9	29.1
JY25_WAN_Scutigerellidae `sp. Helix-SYM028`	24.7	26.1	24.6	26.7	24.7	25.4	25.0	25.4	27.4	24.7	26.4	27.2	19.0	18.4	18.4	18.7	18.2	19.0	20.1	20.1	18.2	18.8	17.3	17.8	17.8	18.4	18.2	18.7	18.4	17.6	17.3		5.0	5.0	5.3	9.0	17.3	18.1	17.8	20.5	17.7	19.7	18.5	17.5	17.9	18.8	21.0	20.2	27.8	27.2
BMR00321_1811_WAF	24.2	25.8	24.5	26.4	24.7	25.0	24.7	25.0	26.7	25.2	24.3	26.4	19.0	17.9	17.9	17.9	17.8	18.8	20.0	19.0	17.3	18.7	16.9	17.8	17.6	18.4	18.2	18.2	18.2	17.8	18.4	5.0		4.6	5.0	5.2	17.0	17.6	17.4	19.9	17.2	18.3	18.8	17.2	17.8	18.2	20.7	19.3	26.9	26.2
JY26_WAN_Scutigerellidae `sp. Helix-SYM029`	23.8	25.8	23.1	26.4	25.4	25.7	25.4	25.7	26.9	24.5	24.3	26.4	18.1	17.9	17.9	17.8	17.2	19.1	20.8	18.7	17.0	17.6	16.6	18.1	18.1	18.7	18.2	18.4	19.0	17.8	17.9	5.0	4.6		3.6	9.0	16.6	16.9	17.1	19.0	16.5	18.2	17.8	16.4	16.9	17.6	20.8	19.8	27.6	26.5
BMR00721_1811_WAH	23.3	26.0	24.0	26.3	24.9	24.5	24.2	24.4	26.7	25.0	24.8	27.8	18.5	17.8	17.8	17.8	17.5	19.1	19.8	19.0	17.3	17.8	17.2	17.9	17.9	18.2	18.1	18.4	19.0	17.0	16.2	5.3	5.0	3.6		8.6	16.9	17.3	17.5	19.5	16.9	18.6	18.4	16.4	17.2	18.8	20.7	20.4	27.8	26.5
BMR00724_1811_WAH	25.2	30.9	29.8	30.1	27.5	28.8	28.6	28.6	29.0	29.4	27.0	30.4	21.8	20.7	20.7	20.5	20.7	22.2	22.9	23.5	20.8	22.1	19.9	19.9	19.9	20.9	20.1	20.9	22.6	21.2	21.4	9.0	5.2	9.0	8.6		21.6	22.0	19.8	23.7	20.8	21.7	21.7	20.8	21.9	22.6	22.7	23.4	31.2	30.4
BMR00326_1811_WAJ	23.8	26.9	25.5	28.0	27.5	27.4	27.0	27.2	27.9	25.8	25.2	26.6	17.6	18.1	18.1	18.5	18.1	19.1	19.4	17.9	19.5	19.3	18.8	17.8	17.8	18.4	18.1	17.8	18.4	19.3	18.8	17.3	17.0	16.6	16.9	21.6		4.1	17.1	19.3	17.1	19.2	19.6	17.8	18.2	19.1	20.3	21.7	28.6	27.1
BMR00320_1811_WAJ	24.9	27.4	25.7	28.1	28.7	28.2	27.8	28.2	27.6	27.5	26.6	27.2	18.0	19.1	19.1	19.0	18.5	20.2	20.4	19.0	20.0	19.8	19.5	19.0	19.0	19.5	19.1	19.0	20.3	19.8	19.4	18.1	17.6	16.9	17.3	22.0	4.1		18.2	20.2	18.9	20.2	21.2	18.8	19.5	19.8	20.8	22.3	27.9	27.9
JY24_WAN_Scutigerellidae `sp. Helix-SYM027`	25.6	26.7	27.6	29.0	27.5	27.4	27.2	26.9	25.9	24.3	27.4	27.8	19.4	19.2	19.1	19.7	19.8	19.4	21.1	19.1	19.4	20.2	18.8	17.2	16.9	18.0	17.4	16.6	18.5	17.5	16.5	17.8	17.4	17.1	17.5	19.8	17.1	18.2		18.0	19.0	21.2	20.6	19.3	19.8	19.5	19.5	22.0	26.9	28.6
RT35_PARA_WAMT144260_Scutigerella_WAM-SCUTI002	25.3	26.1	27.8	26.3	26.2	25.5	25.3	25.3	24.5	24.6	25.4	24.7	19.6	17.6	17.6	17.9	17.9	18.7	19.5	18.8	16.7	16.7	20.4	17.3	17.3	17.2	17.3	19.0	19.1	20.2	18.8	20.5	19.9	19.0	19.5	23.7	19.3	20.2	18.0		18.9	19.7	19.5	18.3	18.2	18.8	21.0	21.4	27.7	26.2
BMR01163_1845_Boolgeeda Creek_Symphyla `sp. Biologic-SYMP013`	22.8	27.6	26.2	28.3	25.4	27.0	26.9	26.9	27.2	24.2	26.5	26.4	17.4	18.8	18.8	19.2	18.3	17.9	18.1	18.6	18.5	17.6	18.6	17.4	16.8	17.1	17.6	17.4	18.6	18.5	17.7	17.7	17.2	16.5	16.9	20.8	17.1	18.9	19.0	18.9		20.5	17.4	17.7	18.2	19.2	18.0	19.8	28.6	27.2
BMR02685_20112_Hanseniella `sp. Biologic-SYMP032`	20.8	23.0	26.1	26.9	24.7	25.9	25.5	26.0	26.2	24.4	26.2	26.5	19.0	20.7	20.6	20.9	21.1	20.5	20.9	19.4	19.4	20.2	20.4	18.3	18.5	17.6	18.2	19.5	18.0	19.3	19.3	19.7	18.3	18.2	18.6	21.7	19.2	20.2	21.2	19.7	20.5		15.9	19.0	18.7	18.3	19.6	19.9	27.7	25.4
RT35_PARA_WAMT144261_Scutigerella_WAM-SCUTI005	24.9	25.7	27.4	27.5	25.5	27.3	27.1	27.0	26.3	23.7	24.6	25.0	16.4	18.2	18.2	18.1	17.6	16.1	16.7	19.3	16.4	16.1	18.4	16.0	15.8	15.8	15.8	18.1	18.5	17.2	16.9	18.5	18.8	17.8	18.4	21.7	19.6	21.2	20.6	19.5	17.4	15.9		19.2	18.9	18.2	18.9	20.5	27.7	27.1
RT48_ROBE_WAMT145911_Scutigerella_WAM-SCUTI001	23.6	24.3	24.3	25.7	24.7	25.0	24.7	25.0	25.3	22.1	23.8	24.6	18.4	17.1	16.9	17.2	17.2	18.9	19.9	17.1	17.2	18.1	20.0	17.5	17.7	17.2	17.7	16.9	17.2	18.6	18.6	17.5	17.2	16.4	16.4	20.8	17.8	18.8	19.3	18.3	17.7	19.0	19.2		1.7	19.0	18.5	18.4	27.2	26.6
IV354_ROBE_Symphyella_sp.	24.4	24.5	24.8	25.8	25.3	25.5	25.2	25.5	25.5	22.4	24.3	24.4	18.2	17.6	17.5	17.8	17.3	18.8	19.6	17.5	17.0	18.0	19.6	18.1	18.2	17.8	18.2	17.6	17.0	19.0	18.8	17.9	17.8	16.9	17.2	21.9	18.2	19.5	19.8	18.2	18.2	18.7	18.9	1.7		18.8	19.3	18.8	27.4	27.2
BMR00202_1749a_HSTD_Hanseniella `sp. Biologic-SYMP009`	23.3	24.8	26.9	26.9	24.5	25.2	25.0	25.9	24.5	23.4	24.9	26.1	19.0	19.0	18.8	19.0	18.1	19.1	19.0	17.5	17.5	19.5	18.5	19.6	19.3	19.0	19.5	19.8	17.9	19.8	19.6	18.8	18.2	17.6	18.8	22.6	19.1	19.8	19.5	18.8	19.2	18.3	18.2	19.0	18.8		18.9	21.7	27.3	25.3
JD04_YANDI_Symphyla	23.4	24.1	27.3	28.7	26.2	27.3	27.0	27.2	26.6	24.6	26.8	27.7	18.4	21.6	21.6	21.6	21.2	19.9	20.0	21.2	20.3	19.9	19.9	18.5	18.4	18.5	18.5	18.5	20.1	19.7	18.9	21.0	20.7	20.8	20.7	22.7	20.3	20.8	19.5	21.0	18.0	19.6	18.9	18.5	19.3	18.9		21.6	30.2	28.5
BMR02684_20112_Hanseniella `sp. Biologic-SYMP031`	25.3	26.3	25.2	26.6	27.7	27.9	27.9	27.0	28.7	25.8	26.4	28.3	20.2	20.2	20.4	20.4	20.1	20.5	20.8	19.9	19.3	21.1	20.2	20.1	20.4	21.0	20.8	20.5	21.1	19.3	20.3	20.2	19.3	19.8	20.4	23.4	21.7	22.3	22.0	21.4	19.8	19.9	20.5	18.4	18.8	21.7	21.6		29.6	27.5
ML54_ROBE_Symphyla	25.9	25.8	27.4	25.2	26.2	26.4	26.2	26.5	26.0	23.6	27.9	26.2	27.9	28.9	28.9	28.8	27.8	27.6	27.9	27.4	26.5	27.4	28.6	26.8	26.3	25.4	26.1	24.7	28.5	26.9	24.9	27.8	26.9	27.6	27.8	31.2	28.6	27.9	26.9	27.7	28.6	27.7	27.7	27.2	27.4	27.3	30.2	29.6		23.6
KR705664 Scolopendra morsitans_OUTGROUP	24.4	26.6	27.1	24.6	23.8	23.8	23.8	23.6	27.2	25.1	27.2	26.5	26.3	26.0	26.2	25.9	25.1	25.4	26.2	25.3	26.6	27.1	27.2	24.7	25.0	24.4	25.0	25.1	25.4	28.9	29.1	27.2	26.2	26.5	26.5	30.4	27.1	27.9	28.6	26.2	27.2	25.4	27.1	26.6	27.2	25.3	28.5	27.5	23.6	

APPENDIX E: Previous subterranean fauna records nearby and within the Study Area



biologic

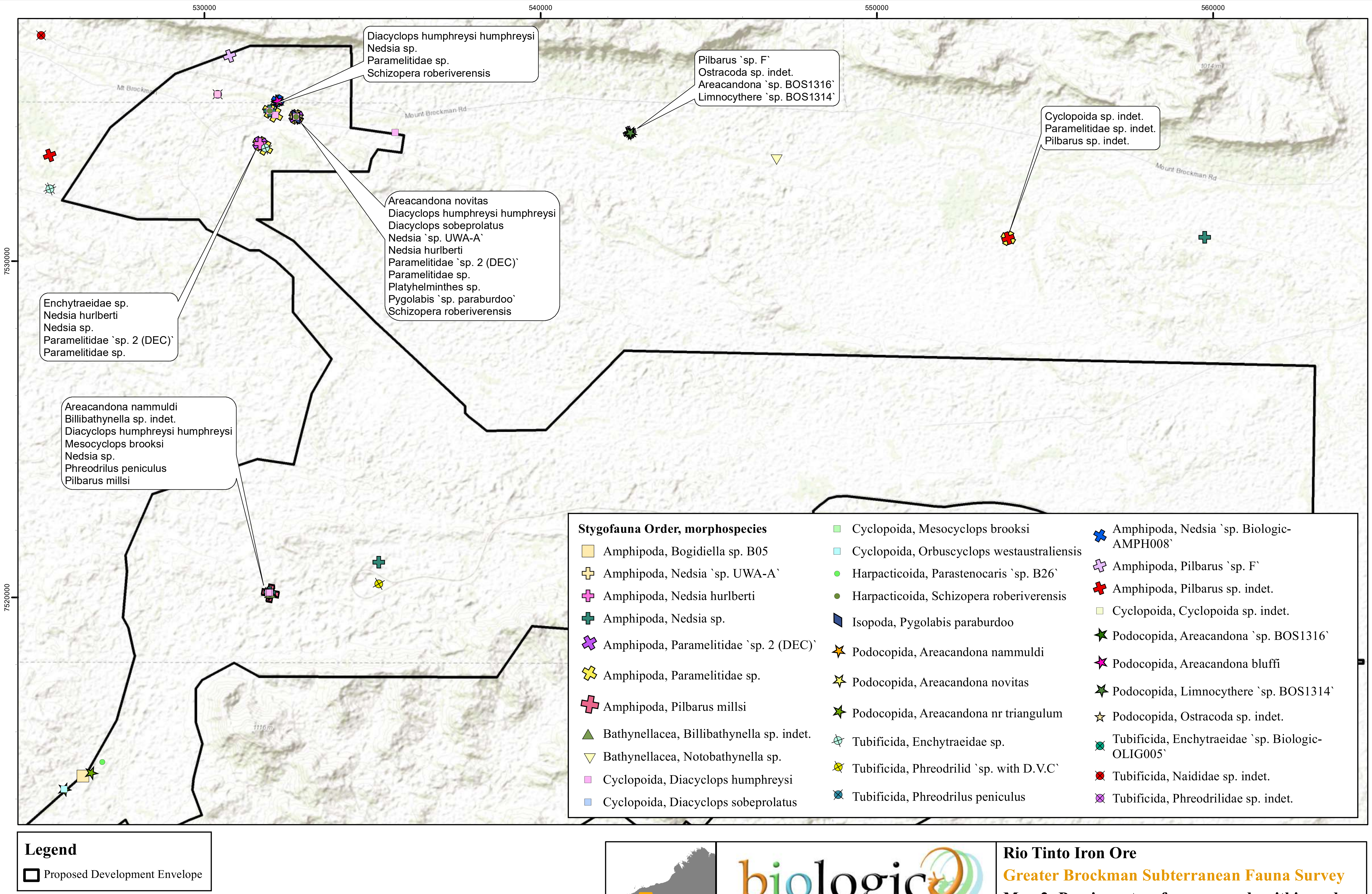
Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Map 1: Previous troglofauna records within and nearby the Study Area (BS2 area)

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

Size A3. Created 09/03/2021



biologic

N

1:100,000

0 1.5 3 6 km

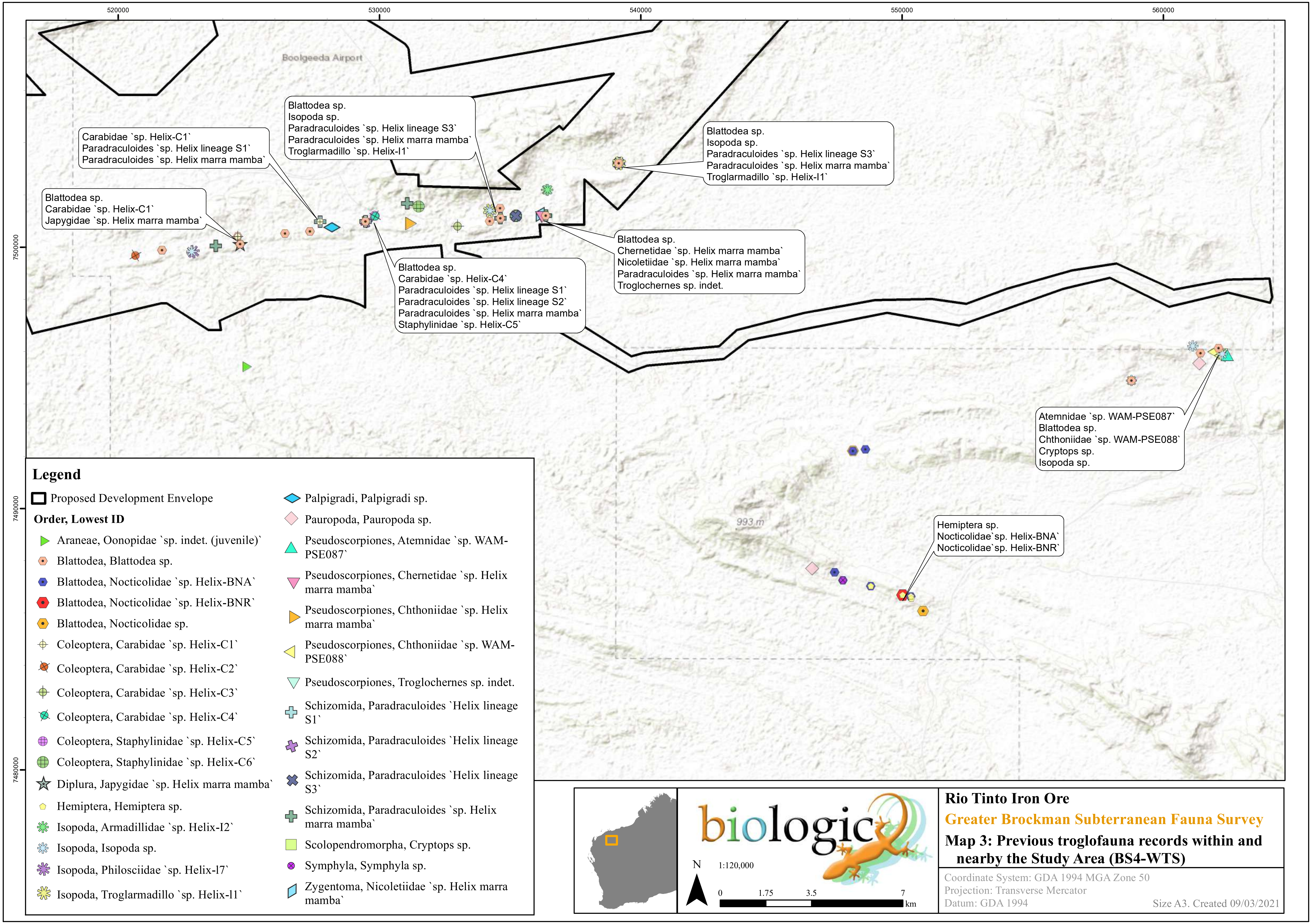
Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Map 2: Previous stygofauna records within and nearby the Study Area (BS2 area)

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

Size A3. Created 09/03/2021



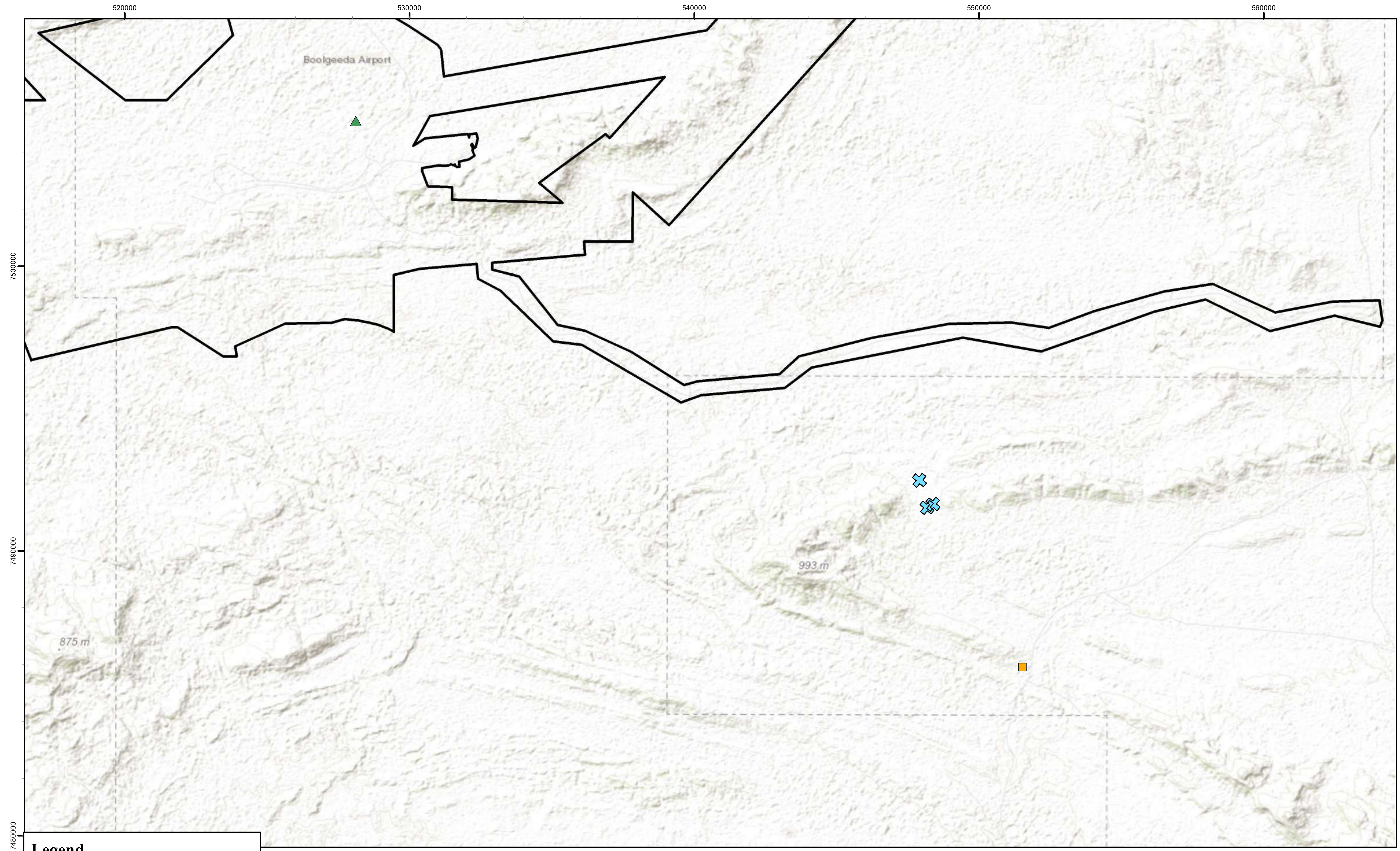
Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Map 3: Previous troglofauna records within and nearby the Study Area (BS4-WTS)

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

Size A3. Created 09/03/2021

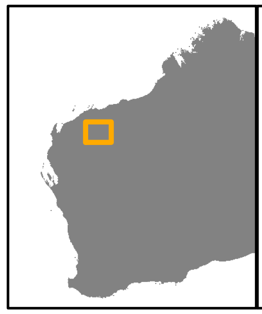


Legend

- ☐ Proposed Development Envelope

Stygofauna Order, morphospecies

- ✖ Amphipoda, Paramelitidae `sp. B22`
- ▲ Bathynellacea, Bathynellacea sp.
- ■ Cyclopoida, Diacyclops sp.



N

1:120,000

0 1.75 3.5 7 km

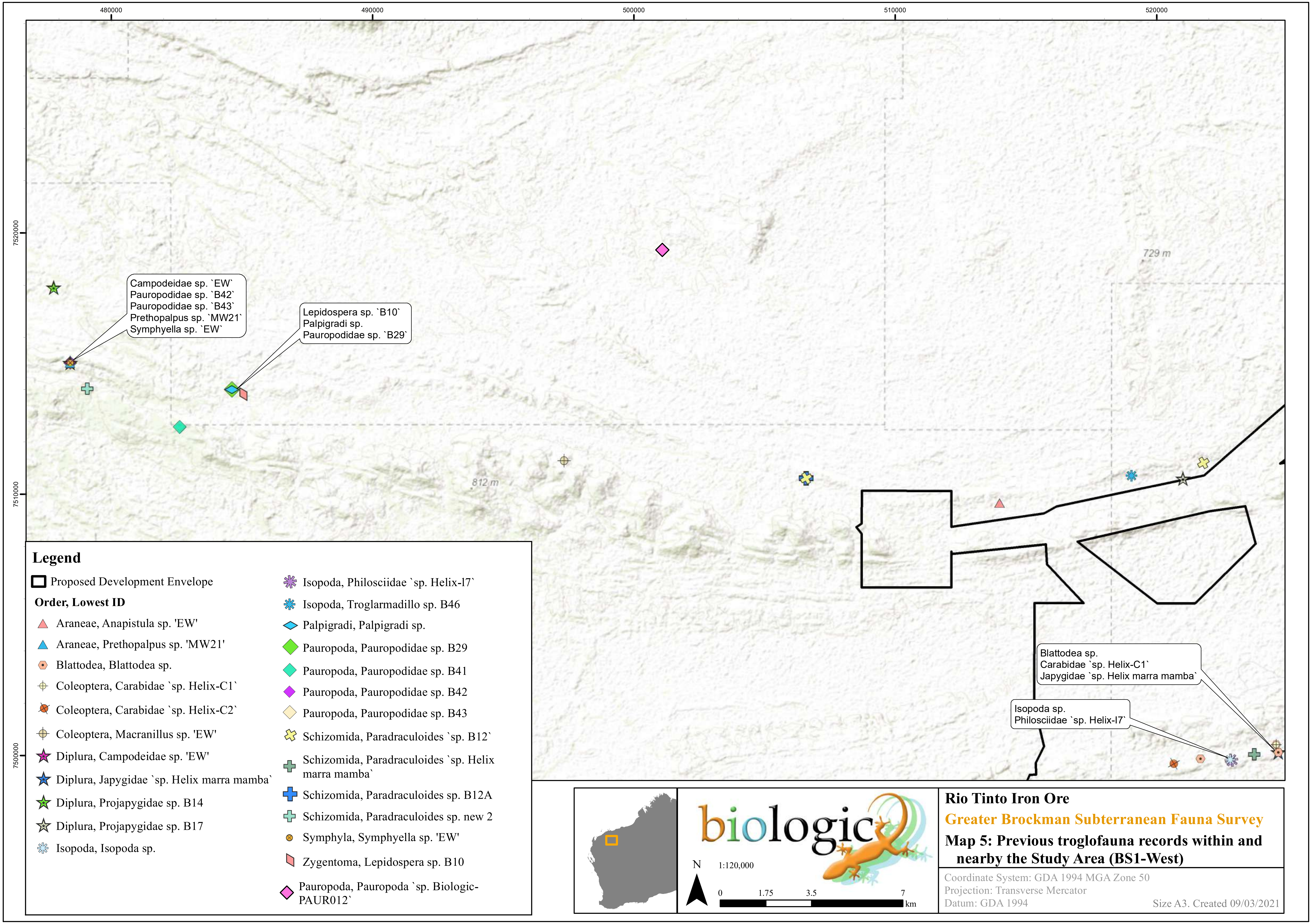
Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Map 4: Previous stygofauna records within and nearby the Study Area (BS4-WTS)

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

Size A3. Created 09/03/2021



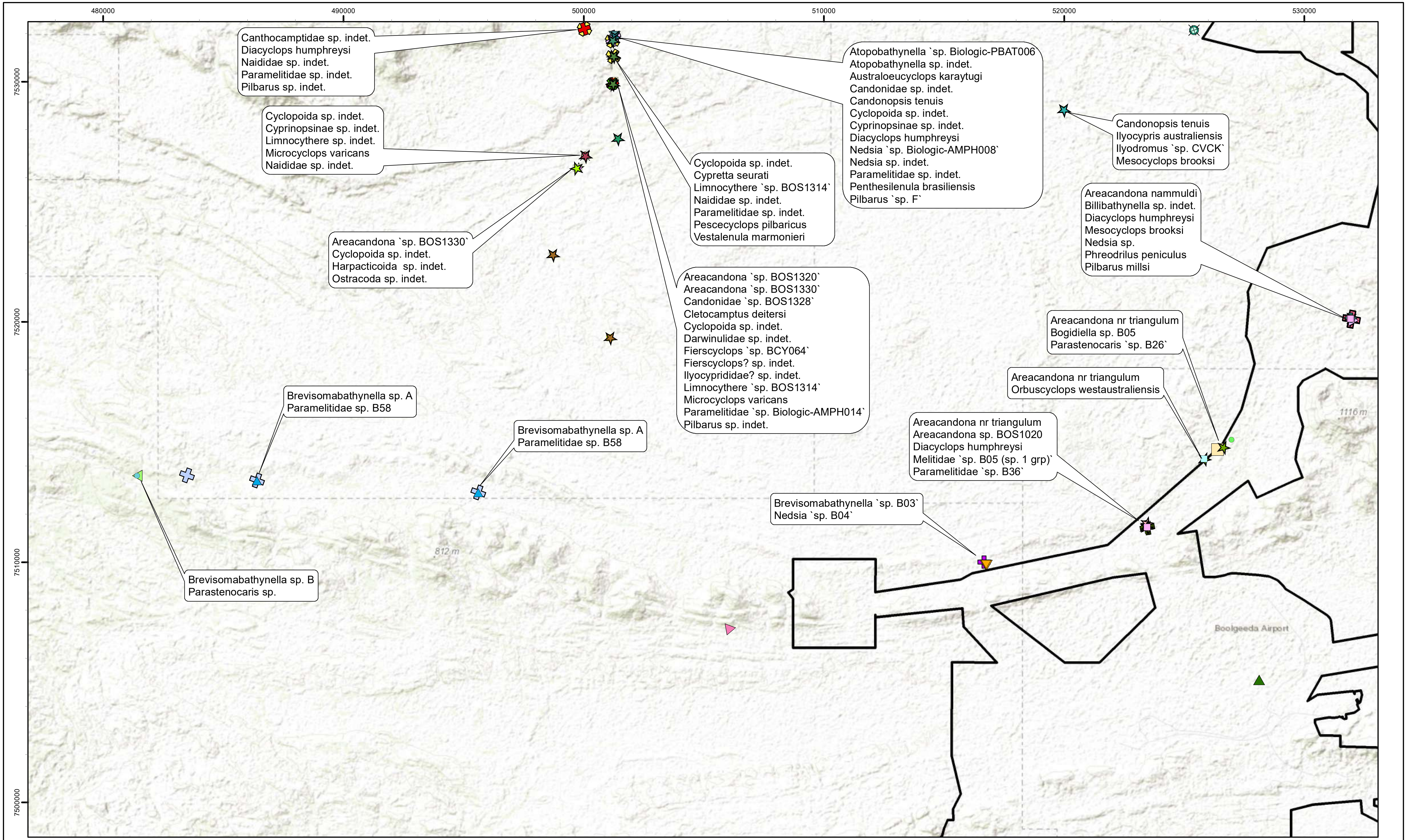
biologic

Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

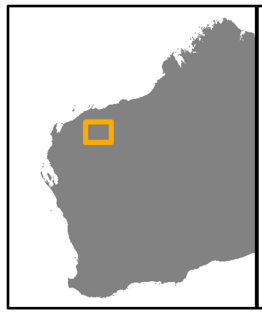
Map 5: Previous troglofauna records within and nearby the Study Area (BS1-West)

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994
Size A3. Created 09/03/2021



Legend

□ Proposed Development Envelope



biologic

N

1:140,000

0 2 4 8 km

Rio Tinto Iron Ore

Greater Brockman Subterranean Fauna Survey

Map 6: Previous stygofauna records within and nearby the Study Area (BS1-West)

Coordinate System: GDA 1994 MGA Zone 50
Projection: Transverse Mercator
Datum: GDA 1994

Size A3. Created 09/03/2021

Legend

Order, Lowest ID

- ▲ Araneae, Anapistula sp. 'EW'
- ▶ Araneae, Oonopidae `sp. indet. (juvenile)`
- ▲ Araneae, Prethopalpus sp. 'MW21'
- ◀ Araneae, Theridiidae sp. indet.
- ⬢ Blattodea, Blattodea sp.
- ⬢ Blattodea, Nocticolidae `sp. Helix-A`
- ⬢ Blattodea, Nocticolidae `sp. Helix-BNA`
- ⬢ Blattodea, Nocticolidae `sp. Helix-BNR`
- ⬢ Blattodea, Nocticolidae sp.
- ⊕ Coleoptera, Carabidae `sp. Helix-C1`
- ⊕ Coleoptera, Carabidae `sp. Helix-C2`
- ⊕ Coleoptera, Carabidae `sp. Helix-C3`
- ⊕ Coleoptera, Carabidae `sp. Helix-C4`
- ⊕ Coleoptera, Macranillus sp. 'EW'
- ⊕ Coleoptera, Staphylinidae `sp. Helix-C5`
- ⊕ Coleoptera, Staphylinidae `sp. Helix-C6`
- ☆ Diplura, Campodeidae sp. 'EW'
- ☆ Diplura, Diplura sp.
- ☆ Diplura, Japygidae `sp. Helix marra mamba`
- ☆ Diplura, Projapygidae sp. B14
- ☆ Diplura, Projapygidae sp. B17
- ■ Geophilomorpha, Geophilidae sp.
- ⬟ Hemiptera, Hemiptera sp.
- ✳ Isopoda, Armadillidae `sp. Helix-I2`
- ✳ Isopoda, Armadillidae sp. indet.
- ✳ Isopoda, Hanoniscus `sp. B10`
- ✳ Isopoda, Isopoda sp.
- ✳ Isopoda, Philosciidae `sp. Helix-I7`
- ✳ Isopoda, Troglarmadillo `sp. Helix-I1`
- ✳ Isopoda, Troglarmadillo sp. B
- ✳ Isopoda, Troglarmadillo sp. B46
- ◆ Palpigradi, Palpigradi sp.
- ◆ Pauropoda, Pauropoda sp.
- ◆ Pauropoda, Pauropodidae sp. B29
- ◆ Pauropoda, Pauropodidae sp. B41
- ◆ Pauropoda, Pauropodidae sp. B42
- ◆ Pauropoda, Pauropodidae sp. B43
- ● Polyxenida, Lophoproctidae sp. indet.
- ● Polyxenida, Polyxenida sp. indet.
- ● Polyxenida, Unixenus sp. indet.
- ▽ Pseudoscorpiones, Atemnidae `sp. WAM-PSE087`
- ▽ Pseudoscorpiones, Chernetidae `sp. Helix marra mamba`
- ▽ Pseudoscorpiones, Chthoniidae `sp. Helix marra mamba`
- ▽ Pseudoscorpiones, Chthoniidae `sp. WAM-PSE088`
- ▽ Pseudoscorpiones, Troglochernes sp. indet.
- ✚ Schizomida, Hubbardiidae `sp. indet. (juvenile)`
- ✚ Schizomida, Paradraculoides `Helix lineage S1`
- ✚ Schizomida, Paradraculoides `Helix lineage S2`
- ✚ Schizomida, Paradraculoides `Helix lineage S3`
- ✚ Schizomida, Paradraculoides `sp. B11`
- ✚ Schizomida, Paradraculoides `sp. B12`
- ✚ Schizomida, Paradraculoides `sp. Helix marra mamba`
- ✖ Schizomida, Paradraculoides `sp. Helix-D`
- ✚ Schizomida, Paradraculoides sp. B12A
- ✚ Schizomida, Paradraculoides sp. new 2
- ✚ Schizomida, Schizomida sp.
- ■ Scolopendromorpha, Cryptops sp.
- ⊗ Symphyla, Symphyella sp. 'EW'
- ⊗ Symphyla, Symphyla sp.
- ▰ Zygentoma, Lepidospera sp. B10
- ▰ Zygentoma, Nicoletiidae `sp. Helix marra mamba`
- ▲ Araneae, Symphytognathidae? `sp. Biologic-ARAN003`
- ⬢ Blattodea, Nocticola `sp. Biologic-BLAT009`
- ⬢ Blattodea, Nocticola `sp. Biologic-BLAT010`
- ⬢ Blattodea, Nocticola `sp. Biologic-BLAT011`
- ▶ Cephalostigmata, Hanseniella `sp. Biologic-SYMP002`
- ▶ Cephalostigmata, Hanseniella `sp. Biologic-SYMP009`
- ▶ Cephalostigmata, Symphyla sp. indet.
- ⊕ Coleoptera, Carabidae `sp. SGW`
- ★ Diplura, Japygidae `sp. Biologic-DIPL010`
- ★ Diplura, Japygidae sp. indet.
- ★ Diplura, Parajapygidae `sp. Biologic-DIPL006`
- ★ Diplura, Parajapygidae `sp. Biologic-DIPL012`
- ★ Diplura, Projapygidae `sp. Biologic-DIPL002`
- ★ Diplura, Projapygidae sp. indet.
- ⬟ Hemiptera, Meenoplidae `sp. Biologic-HEMI001`
- ⬟ Hemiptera, Phaconeura `sp. WAM-PHAC001`
- ✳ Isopoda, Armadillidae `sp. Biologic-ISOP009`
- ✳ Isopoda, Philosciidae `sp. Biologic-ISOP001`
- ◆ Palpigradi, Palpigradi `sp. Biologic-PALP005`
- ◆ Pauropoda, Pauropoda `sp. Biologic-PAUR008`
- ◆ Pauropoda, Pauropoda `sp. Biologic-PAUR012`
- ◆ Pauropoda, Pauropoda sp. indet.
- ◆ Pauropoda, Pauropoda `sp. WAM-PAUD002`
- ● Polyxenida, Polyxenida `sp. Biologic-POLX003`
- ▲ Pseudoscorpiones, Olpiidae? `sp. Biologic-PSEU002`
- ✚ Schizomida, Draculoides `sp. Biologic-SCHI012`
- ✚ Schizomida, Draculoides `sp. Biologic-SCHI013`
- ✚ Schizomida, Draculoides `sp. Biologic-SCHI014`
- ✚ Schizomida, Draculoides `sp. Biologic-SCHI015`
- ✖ Schizomida, Draculoides `sp. Biologic-SCHI016`
- ✖ Schizomida, Draculoides `sp. Biologic-SCHI018`
- ■ Scolopendromorpha, Scolopendromorpha `sp. Biologic-CHIL004`
- ▰ Zygentoma, Atelurinae sp. indet.
- ▰ Zygentoma, Nicoletiidae? `sp. Biologic-ZYGE003`

Rio Tinto Iron Ore
Greater Brockman Subterranean Fauna Survey
Previous troglofauna records within and nearby the Study Area

Legend

Stygofauna Order, morphospecies

■ Amphipoda, Bogidiella sp. B05
■ Amphipoda, Bogidiellidae sp. 1
✖ Amphipoda, Maarrka etheli
✚ Amphipoda, Melitidae `B05 (sp. 1 grp)`
✚ Amphipoda, Nedsia `sp. B04`
✚ Amphipoda, Nedsia `sp. UWA-A`
✚ Amphipoda, Nedsia hurlberti
✚ Amphipoda, Nedsia sp.
✖ Amphipoda, Paramelitidae `sp. 2 (DEC)`
✖ Amphipoda, Paramelitidae `sp. 6 (DEC)`
✖ Amphipoda, Paramelitidae `sp. B22`
✚ Amphipoda, Paramelitidae `sp. B36`
✖ Amphipoda, Paramelitidae sp.
✚ Amphipoda, Paramelitidae sp. B58
✚ Amphipoda, Pilbarus millsi
▲ Bathynellacea, Bathynellacea sp.
▲ Bathynellacea, Billibathynella sp. indet.
▲ Bathynellacea, Brevisomabathynella sp. A
▲ Bathynellacea, Brevisomabathynella sp. B
▲ Bathynellacea, Brevisomabathynella sp. B03
▲ Bathynellacea, Brevisomabathynella sp. C
▽ Bathynellacea, Notobathynella sp.
■ Cyclopoida, Cyclopoida sp. indet
■ Cyclopoida, Diacyclops humphreysi
■ Cyclopoida, Diacyclops sobeprolatus
■ Cyclopoida, Diacyclops sp.
■ Cyclopoida, Mesocyclops brooksi
■ Cyclopoida, Orbuscyclops westaustraliensis
■ Cyclopoida, Pescecyclops pilbaricus
● Harpacticoida, Harpacticoida sp. indet
● Harpacticoida, Parastenocaris `sp. B26`
● Harpacticoida, Parastenocaris jane
● Harpacticoida, Parastenocaris sp.
● Harpacticoida, Schizopera roberiverensis
▰ Isopoda, Pygolabis paraburdoo
▰ Isopoda, Pygolabis sp. indet
★ Podocopida, Areacandona arteria
★ Podocopida, Areacandona bluffi
★ Podocopida, Areacandona nammuldi
★ Podocopida, Areacandona novitas
★ Podocopida, Areacandona nr triangulum
☆ Podocopida, Areacandona sp. BOS1020
☆ Podocopida, Humphreyscandona woutersi
★ Podocopida, Ilyodromus sp. 2
☆ Podocopida, Ostracoda sp. indet.
⬠ Polychaeta, Namanereis sp. indet.
⊗ Tubificida, Enchytraeidae sp.
⊗ Tubificida, Phreodrilid `sp. with D.V.C`
⊗ Tubificida, Phreodrilidae `sp. with S.V.C`
⊗ Tubificida, Phreodrilus peniculus
■ Amphipoda, Amphipoda sp. indet.
■ Amphipoda, Bogidiellidae `sp. Biologic-AMPH010`
■ Amphipoda, Maarrka `sp. Biologic-AMPH013`
✖ Amphipoda, Maarrka sp. indet.
✖ Amphipoda, Nedsia `sp. Biologic-AMPH008`
✖ Amphipoda, Paramelitidae `sp. Biologic-AMPH014`
✚ Amphipoda, Pilbarus `sp. F`
✚ Amphipoda, Pilbarus sp. indet.
▼ Bathynellacea, Atopobathynella `sp. Biologic-PBAT006`
▼ Bathynellacea, Atopobathynella sp. indet.
▼ Bathynellacea, Parabathynellidae `sp. Biologic-PBAT001`
▼ Bathynellacea, Parabathynellidae `sp. Biologic-PBAT002`
◀ Copepoda, Copepoda sp. indet.
■ Cyclopoida, Australoeucyclops karaytugi
■ Cyclopoida, Fierscyclops `sp. BCY064`
■ Cyclopoida, Fierscyclops? sp. indet.
■ Cyclopoida, Microcyclops varicans
■ Cyclopoida, Thermocyclops aberrans
● Harpacticoida, Canthocamptidae sp. indet.
● Harpacticoida, Cletocamptus deitersi
● Harpacticoida, Megastygonitocrella `sp. SGW`
● Harpacticoida, Parastenocaris `sp. BHA263`
● Harpacticoida, Stygonitocrella `sp. SGW`
▰ Isopoda, Pygolabis `sp. Biologic-ISOP010`
★ Phyllodocida, Namanereis `sp. CVCK`
★ Podocopida, Areacandona `sp. BOS1316`
★ Podocopida, Areacandona `sp. BOS1320`
★ Podocopida, Areacandona `sp. BOS1322`
★ Podocopida, Areacandona `sp. BOS1323`
★ Podocopida, Areacandona `sp. BOS1326`
★ Podocopida, Areacandona `sp. BOS1330`
★ Podocopida, Areacandona bluffi
★ Podocopida, Areacandona sp. indet.
★ Podocopida, Candonidae `sp. BOS1328`
★ Podocopida, Candonidae sp. indet.
★ Podocopida, Candonopsis tenuis
★ Podocopida, Cypretta `sp. BOS1324`
★ Podocopida, Cypretta `sp. BOS861`
★ Podocopida, Cypretta seurati
★ Podocopida, Cypretta sp. indet.
★ Podocopida, Cyprinopsinae sp. indet.
★ Podocopida, Darwinulidae sp. indet.
★ Podocopida, Humphreyscandona `sp. BOS1327`
★ Podocopida, Ilyocyprididae? sp. indet.
★ Podocopida, Ilyocypris australiensis
★ Podocopida, Ilyodromus `sp. CVCK`
★ Podocopida, Limnocythere `sp. BOS1314`
★ Podocopida, Limnocythere sp. indet.
★ Podocopida, Penthesilenula brasiliensis
★ Podocopida, Vestalenula marmonieri
⊗ Tubificida, Enchytraeidae `sp. Biologic-OLIG005`
⊗ Tubificida, Enchytraeidae `sp. Biologic-OLIG013`
⊗ Tubificida, Enchytraeidae `sp. Biologic-OLIG018`
⊗ Tubificida, Naididae `sp. Biologic-OLIG015`
⊗ Tubificida, Naididae sp. indet.
⊗ Tubificida, Phreodrilidae `sp. Biologic-OLIG012`
⊗ Tubificida, Phreodrilidae `sp. Biologic-OLIG014`
⊗ Tubificida, Phreodrilidae sp. indet.

biologic

Rio Tinto Iron Ore
Greater Brockman Subterranean Fauna Survey
Previous stygofauna records within and nearby the Study Area

APPENDIX F: Database search data

Note: The above appendix has been provided to the client in Excel Spreadsheet format.

File name: “GBO_SUBF_Appendices B, E and F.xlsx”.

APPENDIX G: Water physicochemical measurements observed during the current survey

Note: The above appendix has been provided to the client in Excel Spreadsheet format.

File name: “GBO_SUBF_Appendices B, E and F.xlsx”.

APPENDIX H: Combined (current and previous surveys) troglofauna results to date

Taxon	Data source	Taxonomic certainty	BS1	BS2	BS3	BS4	Total	Distribution comments, Linear Range (LR)	Taxonomic, ecological comments	Subterranean status, SRE status
Araneae										
Anapistula sp. 'EW'	Third party	Med, Morpho	x				**2**	Occurs beyond Dev Envelope	Typically SRE when troglobitic	Troglobitic, Potential SRE
Araneae `sp. Biologic-ARAN004`	Biologic	High, DNA				x	**1**	Singleton/ single site	Typically SRE when troglobitic	Potential troglobite, Potential SRE
Araneae `sp. Biologic-ARAN005`	Biologic	High, DNA	x				**2**	Multiple sites, LR 1.7 km	Typically SRE when troglobitic	Potential troglobite, Potential SRE
Gnaphosidae `sp. Biologic-ARAN006`	Biologic	High, DNA		x	x		**2**	Occurs beyond Dev Envelope	Typically SRE when troglobitic	Potential troglobite, Potential SRE
Gnaphosidae `sp. Biologic-ARAN007`	Biologic	High, DNA				x	**1**	Occurs beyond Dev Envelope	Typically SRE when troglobitic	Potential troglobite, Potential SRE
Prethopalpus `sp. Biologic-ARAN001`	Biologic	High, DNA			x		**1**	Singleton/ single site	Typically SRE when troglobitic	Troglobitic, Potential SRE
Prethopalpus `sp. Biologic-ARAN002`	Biologic	High, DNA		x			**1**	Singleton/ single site	Typically SRE when troglobitic	Troglobitic, Potential SRE
Prethopalpus `sp. Biologic-ARAN016`	Biologic	High, DNA				x	**1**	Occurs beyond Dev Envelope	Typically SRE when troglobitic	Troglobitic, Potential SRE
Prethopalpus `sp. Biologic-ARAN023`	Biologic	High, DNA			x		**1**	Singleton/ single site	Typically SRE when troglobitic	Troglobitic, Potential SRE
Prethopalpus sp. 'MW21'	Third party	Med, Morpho					**1**	Occurs beyond Dev Envelope	Typically SRE when troglobitic	Troglobitic, Potential SRE
Theridiidae `sp. WAM-ARAN001`	Biologic	High, DNA	x				**5**	Widespread regionally, Paraburdoo	Can be SRE when troglobitic, widespread epigean	Not troglobite, Widespread
Palpigradi										
Palpigradi `sp. Biologic-PALP002`	Biologic	High, DNA		x			**1**	Singleton/ single site	Typically troglobitic SRE, almost never epigean	Potential troglobite, Potential SRE
Palpigradi `sp. Biologic-PALP003`	Biologic	High, DNA			x		**2**	Multiple sites, LR 0.2 km	Typically troglobitic SRE, almost never epigean	Potential troglobite, Potential SRE
Palpigradi `sp. Biologic-PALP004`	Biologic	High, DNA			x		**2**	Multiple sites, LR 3.3 km	Typically troglobitic SRE, almost never epigean	Potential troglobite, Potential SRE
Palpigradi `sp. Biologic-PALP006`	Biologic	High, DNA			x		**1**	Singleton/ single site	Typically troglobitic SRE, almost never epigean	Potential troglobite, Potential SRE
Palpigradi `sp. Biologic-PALP007`	Biologic	High, DNA		x			**1**	Singleton/ single site	Typically troglobitic SRE, almost never epigean	Potential troglobite, Potential SRE
Palpigradi `sp. Biologic-PALP008`	Biologic	High, DNA				x	**1**	Singleton/ single site	Typically troglobitic SRE, almost never epigean	Potential troglobite, Potential SRE
Palpigradi `sp. Biologic-PALP009`	Biologic	High, DNA				x	**1**	Occurs beyond Dev Envelope	Typically troglobitic SRE, almost never epigean	Potential troglobite, Potential SRE
Palpigradi `sp. Biologic-PALP010`	Biologic	High, DNA	x				**1**	Singleton/ single site	Typically troglobitic SRE, almost never epigean	Potential troglobite, Potential SRE
Palpigradi `sp. Biologic-PALP012`	Biologic	High, DNA			x		**1**	Singleton/ single site	Typically troglobitic SRE, almost never epigean	Potential troglobite, Potential SRE
Palpigradi `sp. Biologic-PALP013`	Biologic	High, DNA				x	**6**	Occurs beyond Dev Envelope	Typically troglobitic SRE, almost never epigean	Potential troglobite, Potential SRE
Palpigradi `sp. Biologic-PALP031`	Biologic	High, DNA			x		**1**	Singleton/ single site	Typically troglobitic SRE, almost never epigean	Potential troglobite, Potential SRE
Palpigradi `sp. Biologic-PALP032`	Biologic	High, DNA			x		**1**	Singleton/ single site	Typically troglobitic SRE, almost never epigean	Potential troglobite, Potential SRE
Palpigradi `sp. Biologic-PALP033`	Biologic	High, DNA			x		**1**	Singleton/ single site	Typically troglobitic SRE, almost never epigean	Potential troglobite, Potential SRE
Pseudoscorpiones										
Chthoniidae `sp. Biologic-PSEU004`	Biologic	High, DNA	x				**4**	Multiple sites, LR 0.5 km	Typically SRE when troglobitic	Troglobitic, Potential SRE

Taxon	Data source	Taxonomic certainty	BS1	BS2	BS3	BS4	Total	Distribution comments, Linear Range (LR)	Taxonomic, ecological comments	Subterranean status, SRE status
Chthoniidae `sp. Biologic-PSEU005`	Biologic	High, DNA				x	**1**	Occurs beyond Dev Envelope	Typically SRE when troglobitic	Troglobitic, Potential SRE
Chthoniidae `sp. Biologic-PSEU006`	Biologic	High, DNA	x				**3**	Multiple sites, LR 1.0 km	Typically SRE when troglobitic	Troglobitic, Potential SRE
Chthoniidae `sp. Biologic-PSEU007`	Biologic	High, DNA			x		**1**	Singleton/ single site	Typically SRE when troglobitic	Troglobitic, Potential SRE
Chthoniidae `sp. Biologic-PSEU008`	Biologic	High, DNA				x	**1**	Occurs beyond Dev Envelope	Typically SRE when troglobitic	Troglobitic, Potential SRE
Chthoniidae `sp. Biologic-PSEU009`	Biologic	High, DNA				x	**2**	Occurs beyond Dev Envelope	Typically SRE when troglobitic	Troglobitic, Potential SRE
Indolpium `sp. Biologic-PSEU003`	Biologic	High, DNA	x				**1**	Singleton/ single site	Typically SRE when troglobitic	Potential troglobite, Potential SRE
Atemnidae `sp. WAM-PSE087`	Previous survey	High, DNA					**1**	Occurs beyond Dev Envelope	Typically SRE when troglobitic	Potential troglobite, Potential SRE
Chernetidae `sp. Helix marra mamba`	Previous survey	High, DNA			x		**1**	Singleton/ single site	Typically SRE when troglobitic	Potential troglobite, Potential SRE
Chthoniidae `sp. Helix marra mamba`	Previous survey	High, DNA				x	**1**	Singleton/ single site	Typically SRE when troglobitic	Troglobitic, Potential SRE
Chthoniidae `sp. WAM-PSE088`	Previous survey	High, DNA					**2**	Occurs beyond Dev Envelope	Typically SRE when troglobitic	Troglobitic, Potential SRE
Troglochernes sp. indet.	Previous survey	Med, Morpho, Spatial info			x		**1**	Singleton/ single site	Typically SRE when troglobitic	Potential troglobite, Potential SRE
Schizomida										
Draculoides `sp. Biologic-SCHI010`	Biologic	High, DNA				x	**1**	Occurs beyond Dev Envelope	Typically troglobitic SRE, almost never epigean	Troglobitic, Potential SRE
Draculoides `sp. Biologic-SCHI011`	Biologic	High, DNA				x	**2**	Occurs beyond Dev Envelope	Typically troglobitic SRE, almost never epigean	Troglobitic, Potential SRE
Draculoides `sp. Biologic-SCHI017`	Biologic	High, DNA	x				**4**	Multiple sites, LR 2.0 km	Typically troglobitic SRE, almost never epigean	Troglobitic, Potential SRE
Draculoides `sp. Biologic-SCHI019`	Biologic	High, DNA	x				**11**	Multiple sites, LR 15.7 km	Typically troglobitic SRE, almost never epigean	Troglobitic, Potential SRE
Paradraculoides `Helix lineage S1`	Previous survey	High, DNA				x	**4**	Defunct OTU, synonym P. `sp. Helix Marra Mamba`	Typically troglobitic SRE, almost never epigean	Troglobite, Potential SRE
Paradraculoides `Helix lineage S2`	Previous survey	High, DNA				x	**1**	Defunct OTU, synonym P. `sp. Helix Marra Mamba`	Typically troglobitic SRE, almost never epigean	Troglobite, Potential SRE
Paradraculoides `Helix lineage S3`	Previous survey	High, DNA			x		**2**	Defunct OTU, synonym P. `sp. Helix Marra Mamba`	Typically troglobitic SRE, almost never epigean	Troglobite, Potential SRE
Paradraculoides `sp. B12`	Third party	Med, Morpho	x				**2**	Multiple sites beyond Dev Envelope, LR 15.0 km. Morpho only, no DNA.	Typically troglobitic SRE, almost never epigean	Troglobitic, Potential SRE
Paradraculoides `sp. Helix marra mamba`	Previous survey	High, DNA			x	x	**11**	Multiple sites, LR 15.7 km	Typically troglobitic SRE, almost never epigean	Troglobitic, Potential SRE
Paradraculoides sp. B12A	Third party	High, DNA					**1**	Occurs beyond Dev Envelope	Typically troglobitic SRE, almost never epigean	Troglobitic, Potential SRE
Paradraculoides sp. new 2	Third party	High, DNA					**1**	Occurs beyond Dev Envelope	Typically troglobitic SRE, almost never epigean	Troglobitic, Potential SRE
Scorpiones										
Scorpiones `sp. Biologic-SCOR002`	Biologic	High, DNA			x		**1**	Singleton/ single site	Typically SRE when troglobitic	Troglobitic, Potential SRE
Isopoda										
Armadillidae `sp. Biologic-ISOP002`	Biologic	High, DNA	x				**2**	Singleton/ single site	Typically SRE when troglobitic	Potential troglobite, Potential SRE
Armadillidae `sp. Biologic-ISOP004`	Biologic	High, DNA				x	**1**	Occurs beyond Dev Envelope	Typically SRE when troglobitic	Potential troglobite, Potential SRE

Taxon	Data source	Taxonomic certainty	BS1	BS2	BS3	BS4	Total	Distribution comments, Linear Range (LR)	Taxonomic, ecological comments	Subterranean status, SRE status
Armadillidae `sp. Biologic-ISOP008`	Biologic	High, DNA				x	**1**	Occurs beyond Dev Envelope	Typically SRE when troglobitic	Potential troglobite, Potential SRE
Buddelundia? `sp. Biologic-ISOP005`	Biologic	High, DNA			x		**1**	Singleton/ single site	Typically SRE when troglobitic	Uncertain troglobite, Potential SRE
Buddelundia? `sp. Biologic-ISOP006`	Biologic	High, DNA			x		**1**	Singleton/ single site	Typically SRE when troglobitic	Uncertain troglobite, Potential SRE
Isopoda `sp. Biologic-ISOP007`	Biologic	High, DNA			x		**1**	Singleton/ single site	Typically SRE when troglobitic	Potential troglobite, Potential SRE
Philosciidae `sp. Biologic-ISOP001`	Biologic	High, DNA		x			**1**	DNA match: `sp. Helix-I7`and with specimen from SGCCK. Multiple sites/ disjunct habitats, LR 41 km	Typically SRE when troglobitic	Not troglobite, unlikely SRE
Armadillidae `sp. Helix-I1`	Previous survey	High, DNA			x		**3**	Singleton/ single site	Typically SRE when troglobitic	Potential troglobite, Potential SRE
Armadillidae `sp. Helix-I2`	Previous survey	High, DNA			x		**1**	Singleton/ single site	Typically SRE when troglobitic	Potential troglobite, Potential SRE
Philosciidae `sp. Helix-I7`	Previous survey	High, DNA				x	**1**	Synonym: Philosciidae `sp. Biologic-ISOP001`. Defunct OTU	Can be SRE when troglobitic, epigean	Not troglobite, unlikely SRE
Troglarmadillo `sp. Helix-I1`	Previous survey	High, DNA			x		**2**	Multiple sites, LR 5.3 km	Typically SRE when troglobitic	Potential troglobite, Potential SRE
Troglarmadillo sp. B46	Third party	High, Morpho	x				**1**	Occurs beyond Dev Envelope	Typically SRE when troglobitic	Potential troglobite, Potential SRE
Geophilomorpha										
Geophilomorpha `sp. Biologic-CHIL002`	Biologic	High, DNA	x				**1**	Singleton/ single site	Typically SRE when troglobitic, often SRE when epigean	Potential troglobite, Potential SRE
Geophilomorpha `sp. Biologic-CHIL007`	Biologic	High, DNA	x				**4**	Singleton/ single site	Typically SRE when troglobitic, often SRE when epigean	Potential troglobite, Potential SRE
Scolopendromorpha										
Cormocephalus `sp. A`	Biologic	High, DNA		x			**1**	Occurs beyond Dev Envelope. DNA match with regional sequence from Trinity Bore and Mesa B. LR 100+ km	Typically SRE when troglobitic, some SREs when epigean	Not troglobite, Widespread
Scolopendromorpha `sp. Biologic-CHIL005`	Biologic	High, DNA				x	**1**	Singleton/ single site	Typically SRE when troglobitic, some SREs when epigean	Uncertain troglobite, Potential SRE
Scolopendromorpha `sp. Biologic-CHIL006`	Biologic	High, DNA				x	**3**	Collected from hyporheic samples only, LR 0.8 km	Typically SRE when troglobitic, some SREs when epigean	Not troglobite, Potential SRE
Scolopendromorpha `sp. BS1`	Biologic	Med, Morpho, Spatial info	x				**1**	Singleton/ single site	Typically SRE when troglobitic, some SREs when epigean	Potential troglobite, Potential SRE
Cryptops sp. indet.	Previous survey	Med, Morpho, Spatial info					**2**	Occurs beyond Dev Envelope	Typically SRE when troglobitic, some SREs when epigean	Uncertain troglobite, Potential SRE
Symphyla										
Hanseniella `sp. Biologic-SYMP001`	Biologic	High, DNA		x			**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Hanseniella `sp. Biologic-SYMP003`	Biologic	High, DNA		x	x		**5**	Multiple sites, LR 16.4 km	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Hanseniella `sp. Biologic-SYMP006`	Biologic	High, DNA				x	**2**	Occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Hanseniella `sp. Biologic-SYMP031`	Biologic	High, DNA			x		**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Hanseniella `sp. Biologic-SYMP032`	Biologic	High, DNA			x		**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Scolopendrellidae `sp. Biologic-SYMP008`	Biologic	High, DNA				x	**1**	Occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Scolopendrellidae `sp. Biologic-SYMP014`	Biologic	High, DNA				x	**1**	Occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE

Taxon	Data source	Taxonomic certainty	BS1	BS2	BS3	BS4	Total	Distribution comments, Linear Range (LR)	Taxonomic, ecological comments	Subterranean status, SRE status
Scutigerellidae `sp. Biologic-SYMP004`	Biologic	High, DNA		x	x		**2**	Multiple sites, LR 2.9 km	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Scutigerellidae `sp. Biologic-SYMP005`	Biologic	High, DNA				x	**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Scutigerellidae `sp. Biologic-SYMP007`	Biologic	High, DNA	x			x	**4**	Multiple sites/ disjunct habitats, LR 12.0 km	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Symphyla `sp. Biologic-SYMP013`	Biologic	High, DNA				x	**4**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Symphylella `sp. Biologic-SYMP030`	Biologic	High, DNA			x		**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Symphylella `sp. BS4`	Biologic	Med, Morpho, Spatial info				x	**2**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Symphylella `sp. BS1`	Biologic	Med, Morpho, Spatial info	x				**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Symphyella sp. 'EW'	Third party	Med, Morpho					**1**	Occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Scolopendrellopsis `sp. BS1`	Biologic	High, DNA	x				**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Pauropoda										
Pauropoda `sp. Biologic-PAUR004`	Biologic	High, DNA				x	**1**	Occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Not troglobite, uncertain SRE
Pauropoda `sp. Biologic-PAUR005`	Biologic	High, DNA		x			**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Pauropoda `sp. Biologic-PAUR006`	Biologic	High, DNA		x			**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Pauropoda `sp. Biologic-PAUR007`	Biologic	High, DNA		x			**2**	Multiple sites, LR 1.2 km	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Pauropoda `sp. Biologic-PAUR008`	Biologic	High, DNA				x	**1**	External DNA match with specimen from SGCCK. Multiple sites/ disjunct habitats, LR 52.6 km	Can be SRE when troglobitic, some potential soil fauna	Not troglobite, uncertain SRE
Pauropoda `sp. Biologic-PAUR009`	Biologic	High, DNA	x				**1**	External DNA match with sequences from Rocklea Station (GenBank)	Can be SRE when troglobitic, some potential soil fauna	Not troglobite, uncertain SRE
Pauropoda `sp. Biologic-PAUR010`	Biologic	High, DNA		x			**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Pauropoda `sp. Biologic-PAUR011`	Biologic	High, DNA				x	**1**	Occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Pauropoda `sp. Biologic-PAUR013`	Biologic	High, DNA			x		**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Pauropoda `sp. Biologic-PAUR036`	Biologic	High, DNA			x		**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Pauropoda `sp. Biologic-PAUR037`	Biologic	High, DNA			x		**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Pauropoda `sp. Biologic-PAUR038`	Biologic	High, DNA			x		**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Pauropoda `sp. Biologic-PAUR039`	Biologic	High, DNA			x		**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Pauropoda `sp. Biologic-PAUR040`	Biologic	High, DNA			x		**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Pauropodidae sp. B29	Third party	Med, Morpho					**1**	Occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Pauropodidae sp. B41	Third party	Med, Morpho					**1**	Occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE

Taxon	Data source	Taxonomic certainty	BS1	BS2	BS3	BS4	Total	Distribution comments, Linear Range (LR)	Taxonomic, ecological comments	Subterranean status, SRE status
Pauropodidae sp. B42	Third party	Med, Morpho					**2**	Occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Pauropodidae sp. B43	Third party	Med, Morpho					**1**	Occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Polydesmida										
Polydesmida `sp. Biologic-POLD002`	Biologic	High, DNA			x		**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Troglobitic, Potential SRE
Polyxenida										
Polyxenida `sp. Biologic-POLX002`	Biologic	High, DNA			x		**2**	External DNA match with specimens from Robe Headwaters, Turee Syncline and Western Turner Syncline (Biota 2009, Biota 2013, Biota 2014). LR 100+ km	Typically widespread trogloxene	Not troglobite, widespread
Polyxenida `sp. Biologic-POLX003`	Biologic	High, DNA	x	x	x		**4**	External DNA match with specimens from Paraburdoo, Turee Syncline and Mesa G. LR 100+ km	Typically widespread trogloxene	Not troglobite, widespread
Polyxenida `sp. Biologic-POLX005`	Biologic	High, DNA		x			**1**	External DNA match with specimens from West Angelas, Angelo River and Rhodes Ridge. LR 100+ km	Typically widespread trogloxene	Not troglobite, widespread
Lophoproctidae `sp. Biologic-POLX006`	Biologic	High, DNA			x		**1**	External DNA match with specimens from Angelo River. LR 100+ km	Typically widespread trogloxene	Not troglobite, widespread
Diplura										
Japygidae `sp. Biologic-DIPL008`	Biologic	High, DNA	x				**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Japygidae `sp. Biologic-DIPL009`	Biologic	High, DNA				x	**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Japygidae `sp. Biologic-DIPL014`	Biologic	High, DNA	x				**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Japygidae `sp. Biologic-DIPL015`	Biologic	High, DNA	x				**1**	Multiple sites, disjunct habitats. LR 20 km (synonym Japygidae sp. B37)	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Japygidae `sp. Biologic-DIPL027`	Biologic	High, DNA			x		**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Japygidae `sp. Biologic-DIPL028`	Biologic	High, DNA			x		**1**	External DNA match with a Helix sequence from BS4. LR 27.1 km.	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Parajapygidae `sp. Biologic-DIPL007`	Biologic	High, DNA			x		**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Parajapygidae `sp. Biologic-DIPL018`	Biologic	High, DNA	x				**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Parajapygidae `sp. Biologic-DIPL029`	Biologic	High, DNA			x		**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Projapygidae `sp. Biologic-DIPL003`	Biologic	High, DNA	x				**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Projapygidae `sp. Biologic-DIPL004`	Biologic	High, DNA			x		**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Projapygidae `sp. Biologic-DIPL005`	Biologic	High, DNA				x	**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Projapygidae `sp. Biologic-DIPL013`	Biologic	High, DNA	x				**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Projapygidae `sp. Biologic-DIPL030`	Biologic	High, DNA			x		**2**	Multiple sites, LR 2.4 km	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Projapygidae `sp. Biologic-DIPL031`	Biologic	High, DNA			x		**2**	Multiple sites, LR 0.6 km	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Projapygidae `sp. Biologic-DIPL032`	Biologic	High, DNA			x		**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE

Taxon	Data source	Taxonomic certainty	BS1	BS2	BS3	BS4	Total	Distribution comments, Linear Range (LR)	Taxonomic, ecological comments	Subterranean status, SRE status
Campodeidae sp. 'EW'	Third party	Med, Morpho					**1**	Occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Japygidae `sp. Helix marra mamba`	Previous survey	High, DNA				x	**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Projapygidae sp. B14	Third party	Med, Morpho					**1**	Occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Projapygidae sp. B17	Third party	Med, Morpho	x				**1**	Occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Blattodea										
Nocticola `sp. Biologic-BLAT005`	Biologic	High, DNA	x				**4**	Multiple sites, LR 1.6 km	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Nocticola `sp. Biologic-BLAT006`	Biologic	High, DNA	x				**5**	Multiple sites, LR 2.0 km	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Nocticola `sp. Biologic-BLAT007`	Biologic	High, DNA	x	x	x	x	**12**	Multiple sites/ disjunct habitats, LR 44.0 km. Occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Not troglobite, unlikely SRE
Nocticola `sp. Biologic-BLAT008`	Biologic	High, DNA		x	x		**10**	Multiple sites/ disjunct habitats, LR 18.6 km	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Nocticola `sp. Biologic-BLAT010`	Biologic	High, DNA	x				**9**	External DNA match with specimen from SGCCK. Multiple sites/ disjunct habitats, LR 33.2 km	Can be SRE when troglobitic, some potential soil fauna	Not troglobite, unlikely SRE
Nocticola `sp. Biologic-BLAT012`	Biologic	High, DNA				x	**1**	Occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Nocticolidae `sp. Helix-BNA`	Previous survey	High, DNA					**25**	Occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Nocticolidae `sp. Helix-BNR`	Previous survey	High, DNA					**1**	Occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Coleoptera										
Carabidae `sp. Biologic-COLE001`	Biologic	High, DNA			x		**1**	DNA match: Carabidae `sp. Helix-C1`. LR 40.7 km. Occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Not troglobite, unlikely SRE
Coleoptera `sp. Biologic-COLE002`	Biologic	High, DNA			x		**3**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Coleoptera `sp. Biologic-COLE003`	Biologic	High, DNA	x				**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Cryptorhynchinae `sp. Biologic-COLE004`	Biologic	High, DNA				x	**2**	Occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Ptinella? `sp. BS1`	Biologic	Med, Morpho, Spatial info	x				**4**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Staphylinidae? `sp. BS1`	Biologic	Med, Morpho, Spatial info	x				**3**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Carabidae `sp. Helix-C1`	Previous survey	High, DNA				x	**3**	Synonym: Carabidae `sp. Biologic-COLE001`. Defunct OTU	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, unlikely SRE
Carabidae `sp. Helix-C2`	Previous survey	High, DNA				x	**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Carabidae `sp. Helix-C3`	Previous survey	High, DNA			x		**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Carabidae `sp. Helix-C4`	Previous survey	High, DNA				x	**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Macranillus sp. 'EW'	Third party	Med, Morpho					**1**	Occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Staphylinidae `sp. Helix-C5`	Previous survey	High, DNA				x	**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE
Staphylinidae `sp. Helix-C6`	Previous survey	High, DNA				x	**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, Potential SRE

Taxon	**Data source**	**Taxonomic certainty**	**BS1**	**BS2**	**BS3**	**BS4**	**Total**	**Distribution comments, Linear Range (LR)**	**Taxonomic, ecological comments**	**Subterranean status, SRE status**
Hemiptera										
Meenoplidae `sp. Biologic-HEMI001`	Biologic	High, DNA	x	x	x	x	**12**	External DNA match with specimen from SGCCK. Multiple sites/ disjunct habitats, LR 48.2 km. Occurs beyond Dev Envelope	Typically widespread trogloxene	Not troglobite, unlikely SRE
Meenoplidae `sp. Biologic-HEMI004`	Biologic	High, DNA				x	**2**	Collected from hyporheic samples only, LR 0.1 km	Typically widespread trogloxene	Not troglobite, unlikely SRE
Phaconeura `sp. WAM-PHAC001`	Biologic	High, DNA		x			**1**	External DNA match withy specimens from Paraburdoo (Cullen & Harvey, 2018)	Typically widespread trogloxene	Not troglobite, Widespread
Phaconeura `sp. WAM-PHAC002`	Biologic	High, DNA	x	x	x	x	**9**	External DNA match withy specimens from Paraburdoo (Cullen & Harvey, 2018)	Typically widespread trogloxene	Not troglobite, Widespread
Zygentoma										
Atelurinae `sp. Biologic-ZYGE008`	Biologic	High, DNA	x		x	x	**6**	Multiple sites/ disjunct habitats, LR 35.7 km. Occurs beyond Dev Envelope.	Typically widespread trogloxene	Not troglobite, unlikely SRE
Nicoletiidae `sp. Biologic-ZYGE002`	Biologic	High, DNA					**1**	Occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Nicoletiidae `sp. Biologic-ZYGE004`	Biologic	High, DNA	x				**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Nicoletiinae `sp. Biologic-ZYGE005`	Biologic	High, DNA		x			**3**	Multiple sites, LR 2.4 km	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Nicoletiinae `sp. Biologic-ZYGE006`	Biologic	High, DNA			x		**2**	Multiple sites, LR 2.3 km	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Nicoletiinae `sp. Biologic-ZYGE007`	Biologic	High, DNA			x		**1**	DNA match: Nicoletiinae `sp. Helix Marra Mamba`. 2 pits LR 4.5 km	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Nicoletiinae `sp. Biologic-ZYGE015`	Biologic	High, DNA	x				**2**	Multiple sites/ disjunct habitats, LR 17.5 km. Occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Uncertain troglobite, unlikely SRE
Lepidospera sp. B10	Third party	High, Morpho					**1**	Occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Nicoletiidae `sp. Helix marra mamba`	Previous survey	High, DNA				x	**1**	Synonym: Nicoletiinae `sp. Biologic-ZYGE007`. Defunct OTU.	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Subnicoletiinae `sp. Biologic-ZYGE024`	Biologic	High, DNA			x		**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Subnicoletiinae `sp. Biologic-ZYGE025`	Biologic	High, DNA			x		**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Subnicoletiinae `sp. Biologic-ZYGE026`	Biologic	High, DNA				x	**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Subnicoletiinae `sp. Biologic-ZYGE027`	Biologic	High, DNA			x		**1**	Singleton/ single site	Can be SRE when troglobitic, some potential soil fauna	Potential troglobite, Potential SRE
Total species			**39**	**21**	**58**	**48**	**164**			
INDETERMINATE TAXA (Species ID unconfirmed)										
Araneae sp. indet.	Biologic	Low, indet	x			x	**13**	n/a - indet. could be multiple sp.	Typically SRE when troglobitic	Unknown
Armadillidae sp. indet.	Biologic & Previous survey	Low, indet	x	x		x	**6**	n/a - indet. could be multiple sp.	Typically SRE when troglobitic	Unknown
Atelurinae sp. indet.	Biologic	Low, indet	x		x		**19**	n/a - indet. could be multiple sp.	Typically widespread trogloxene	Unknown
Blattidae sp. indet.	Biologic	Low, indet		x	x	x	**1**	n/a - indet. could be multiple sp. Also occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Unknown
Blattodea sp. indet.	Previous survey	Low, indet		x		x	**45**	n/a - indet. could be multiple sp. Also occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Unknown
Chilopoda sp. indet.	Biologic	Low, indet	x				**1**	singleton indet. - could represent other known species	Can be SRE when troglobitic, some potential SRE soil fauna	Unknown

Taxon	**Data source**	**Taxonomic certainty**	**BS1**	**BS2**	**BS3**	**BS4**	**Total**	**Distribution comments, Linear Range (LR)**	**Taxonomic, ecological comments**	**Subterranean status, SRE status**
Chthoniidae sp. indet.	Biologic	Low, indet	x				**1**	singleton indet. - could represent other known species	Typically SRE when troglobitic	Unknown
Diplopoda sp. indet.	Biologic	Low, indet			x		**8**	n/a - indet. could be multiple sp.	Can be SRE when troglobitic, some potential soil fauna	Unknown
Geophilidae sp. indet.	Previous survey	Low, indet					**1**	n/a - indet. could be multiple sp.	Typically SRE when troglobitic	Unknown
Geophilida sp. indet.	Biologic	Low, indet	x				**3**	singleton indet. - could represent other known species	Can be SRE when troglobitic, some potential SRE soil fauna	Unknown
Geophilomorpha sp. indet.	Biologic	Low, indet	x				**3**	singleton indet. - could represent other known species	Can be SRE when troglobitic, some potential SRE soil fauna	Unknown
Hanseniella sp. indet.	Biologic	Low, indet	x		x	x	**15**	singleton indet. - could represent other known species	Can be SRE when troglobitic, some potential SRE soil fauna	Unknown
Hemiptera sp. indet.	Previous survey	Low, indet					**16**	Occurs beyond Dev Envelope	Typically widespread trogloxene	Unknown
Hemiptera sp. indet.	Biologic	Low, indet	x	x	x	x	**47**	n/a - indet. could be multiple sp.	Typically widespread trogloxene	Unknown
Isopoda sp. indet.	Biologic & Previous survey	Low, indet		x	x	x	**25**	n/a - indet. could be multiple sp.	Can be SRE when troglobitic, some potential SRE soil fauna	Unknown
Japygidae sp. indet.	Biologic	Low, indet	x			x	**4**	n/a - indet. could be multiple sp.	Can be SRE when troglobitic, some potential soil fauna	Unknown
Lophoproctidae sp. indet.	Biologic & Previous survey	Low, indet		x			**9**	n/a - indet. could be multiple sp.	Typically widespread trogloxene	Unknown
Meenoplidae sp. indet.	Biologic	Low, indet	x	x	x	x	**53**	n/a - indet. could be multiple sp.	Typically widespread trogloxene	Unknown
Nicoletiinae sp. indet.	Biologic	Low, indet	x	x		x	**20**	n/a - indet. could be multiple sp.	Can be SRE when troglobitic, some potential soil fauna	Unknown
Nocticola sp. indet.	Biologic	Low, indet	x	x	x	x	**106**	n/a - indet. could be multiple sp.	Can be SRE when troglobitic, some potential soil fauna	Unknown
Nocticolidae sp. indet.	Previous survey	Low, indet					**3**	Occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Unknown
Oonopidae `sp. (juvenile)`	Previous survey	Low, indet					**1**	Occurs beyond Dev Envelope	Typically SRE when troglobitic	Unknown
Oonopidae sp. indet.	Biologic	Low, indet			x		**1**	singleton indet. - could represent other known species	Typically SRE when troglobitic	Unknown
Palpigradi sp. indet.	Biologic	Low, indet			x	x	**39**	n/a - indet. could be multiple sp.	Typically troglobitic SRE, almost never epigean	Likely Troglobitic
Parajapygidae sp. indet.	Biologic	Low, indet	x		x		**2**	n/a - indet. could be multiple sp.	Can be SRE when troglobitic, some potential soil fauna	Unknown
Pauropoda sp. indet.	Previous survey	Low, indet					**2**	Occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Unknown
Pauropoda sp. indet.	Biologic	Low, indet	x		x	x	**86**	n/a - indet. could be multiple sp.	Can be SRE when troglobitic, some potential soil fauna	Unknown
Philosciidae sp. indet.	Biologic	Low, indet		x			**2**	singleton indet. - could represent other known species	Can be SRE when troglobitic, epigean	Unknown
Polyxenida sp. indet.	Biologic	Low, indet	x	x	x	x	**13**	n/a - indet. could be multiple sp.	Typically widespread trogloxene	Unknown
Projapygidae sp. indet.	Biologic	Low, indet	x		x	x	**22**	n/a - indet. could be multiple sp.	Can be SRE when troglobitic, some potential soil fauna	Unknown
Pseudoscorpiones sp. indet.	Biologic	Low, indet	x		x		**3**	n/a - indet. could be multiple sp.	Typically SRE when troglobitic	Unknown
Schizomida sp. indet.	Biologic	Low, indet	x				**19**	n/a - indet. could be multiple sp.	Typically troglobitic SRE, almost never epigean	Likely Troglobitic

Taxon	Data source	Taxonomic certainty	BS1	BS2	BS3	BS4	Total	Distribution comments, Linear Range (LR)	Taxonomic, ecological comments	Subterranean status, SRE status
Subnicoletiinae sp. indet.	Biologic	Low, indet			x	x	**10**	n/a - indet. could be multiple sp.	Can be SRE when troglobitic, some potential soil fauna	Unknown
Symphyla sp. indet.	Previous survey	Low, indet					**1**	Occurs beyond Dev Envelope	Can be SRE when troglobitic, some potential soil fauna	Unknown
Symphyla sp. indet.	Biologic	Low, indet	x	x	x	x	**34**	n/a - indet. could be multiple sp.	Can be SRE when troglobitic, some potential soil fauna	Unknown

APPENDIX I: Combined (current and previous surveys) stygofauna results to date

Taxon	Data source	Taxonomic certainty	BS1	BS2	BS3	BS4	Total	Distribution comments, Linear Range (LR)	Taxonomic, ecological comments	Subterranean status, SRE status
Amphipoda										
Amphipoda `sp. Biologic-AMPH009`	Biologic	High, DNA				x	**56**	Locally restricted, LR 0.9 km	Unique OTU, near *Niphargus*, possibly SRE or widespread	Potential stygobite, Potential SRE
Bogidiella `sp. B05`	Previous survey	Med, Morpho		x			**1**	Locally restricted	Third-party OTU, unable to align to current specimens	Potential stygobite, Potential SRE
Bogidiellidae `sp. Biologic-AMPH011`	Biologic	High, DNA	x				**3**	Likely locally widespread, LR 11.8 km	Unique OTU, group can be SRE or widespread	Potential stygobite, Potential SRE
Nedsia `sp. Biologic-AMPH003`	Biologic	High, DNA				x	**125**	Single site only	Unique OTU, group can be SRE or widespread	Potential stygobite, Potential SRE
Nedsia `sp. Biologic-AMPH052`	Biologic	High, DNA	x				**1**	Regionally widespread, LR 100+ km	Unique OTU, known to be widespread	Uncertain stygobite, Widespread
Nedsia `sp. WAM-AMPE003`	Biologic	High, DNA	x				**5**	Regionally widespread, LR 100+ km	Unique OTU, known to be widespread	Uncertain stygobite, Widespread
Nedsia `sp. B04`	3rd Party & Previous survey	Med, Morpho	x				**7**	Regionally widespread, LR 81 km	Previous survey OTU, unable to align to current specimens	Uncertain stygobite, Locally widespread
Melitidae `sp. B05 (sp. 1 group)`	3rd Party & Previous survey	Med, Morpho	x				**1**	Locally widespread, LR 74 km	Unique OTU, group can be SRE or widespread	Uncertain stygobite, Locally widespread
Paramelitidae `sp. Biologic-AMPH012`	Biologic	High, DNA			x		**1**	Singleton/ single site	Unique OTU, group can be SRE or widespread	Potential stygobite, Potential SRE
Paramelitidae `sp. Biologic-AMPH015`	Biologic	High, DNA			x		**44**	Locally restricted, LR 11 km	Unique OTU, group can be SRE or widespread	Potential stygobite, Potential SRE
Paramelitidae `sp. Helix-AMP037`	Biologic	High, DNA	x			x	**9**	Regionally widespread, LR 100+ km	Unique OTU, known to be widespread	Uncertain stygobite, Widespread
Paramelitidae `sp. Biologic-AMPH047`	Biologic	High, DNA			x		**1**	Singleton/ single site	Unique OTU, group can be SRE or widespread	Potential stygobite, Potential SRE
Paramelitidae `sp. Biologic-AMPH048`	Biologic	High, DNA			x		**1**	Singleton/ single site	Unique OTU, group can be SRE or widespread	Potential stygobite, Potential SRE
Paramelitidae `sp. B22`	Previous survey	Med, Morpho					**15**	Occurs beyond Dev Envelope	Third-party OTU, unable to align to current specimens	Potential stygobite, Potential SRE
Paramelitidae `sp. B36`	3rd Party & Previous survey	Med, Morpho	x				**5**	Regionally widespread, LR 80 km	Third-party OTU, unable to align to current specimens	Uncertain stygobite, uncertain SRE
Paramelitidae `sp. B58`	3rd Party	Med, Morpho					**5**	Occurs beyond Dev Envelope	Third-party OTU, unable to align to current specimens	Potential stygobite, Potential SRE
Pilbarus millsi	Previous survey	High, Morpho		x			**1**	Regionally widespread	Previous survey OTU, unable to align to current specimens	Uncertain stygobite, Widespread
Bathynellacea										
Atopobathynella `sp. BGCK`	Biologic	Med, Morpho, Spatial info				x	**1**	Singleton/ single site	Unique OTU, group is always stygobitic, rarely widespread	Stygobite, Potential SRE
Atopobathynella `sp. Biologic-PBAT013`	Biologic	High, DNA (unique lineage)				x	**15**	Locally restricted (0.13 km)	Unique OTU, group is always stygobitic, rarely widespread	Stygobite, Potential SRE
Atopobathynella `sp. Biologic-PBAT014`	Biologic	High, DNA (unique lineage)				x	**1**	Singleton/ single site	Unique OTU, group is always stygobitic, rarely widespread	Stygobite, Potential SRE
Bathynellidae `sp. Biologic-BATH001`	Biologic	High, DNA				x	**1**	Singleton/ single site	Unique OTU, group is always stygobitic, rarely widespread	Stygobite, Potential SRE
Bathynellidae `sp. Biologic-BATH002`	Biologic	High, DNA				x	**2**	Locally restricted (4 km)	Unique OTU, group is always stygobitic, rarely widespread	Stygobite, Potential SRE
Bathynellidae `sp. Biologic-BATH003`	Biologic	High, DNA				x	**8**	Locally restricted (0.4 km)	Unique OTU, group is always stygobitic, rarely widespread	Stygobite, Potential SRE
Billibathynella sp. indet.	Previous survey	Low, Morpho		x			**1**	Uncertain	Previous OTU, group is always stygobitic, rarely widespread	Stygobite, Potential SRE
Brevisomabathynella `sp. A`	3rd Party	High, Morpho					**3**	Occurs beyond Dev Envelope. LR 10 km	Third-party OTU, group is always stygobitic, rarely widespread	Stygobite, Potential SRE

Taxon	Data source	Taxonomic certainty	BS1	BS2	BS3	BS4	Total	Distribution comments, Linear Range (LR)	Taxonomic, ecological comments	Subterranean status, SRE status
Brevisomabathynella `sp. B`	3rd Party	High, Morpho					**1**	Occurs beyond Dev Envelope	Third-party OTU, group is always stygobitic, rarely widespread	Stygobite, Potential SRE
Brevisomabathynella `sp. B03`	3rd Party & Previous survey	High, Morpho	x				**3**	Singleton/ single site	Third-party OTU, group is always stygobitic, rarely widespread	Stygobite, Potential SRE
Brevisomabathynella `sp. C`	3rd Party	High, Morpho					**1**	Occurs beyond Dev Envelope	Third-party OTU, group is always stygobitic, rarely widespread	Stygobite, Potential SRE
Parabathynellidae `sp. Biologic-PBAT003`	Biologic	High, DNA	x				**6**	Singleton/ single site	Unique OTU, group is always stygobitic, rarely widespread	Stygobite, Potential SRE
Parabathynellidae `sp. Biologic-PBAT004`	Biologic	High, DNA			x		**22**	Locally restricted, 2 km	Unique OTU, group is always stygobitic, rarely widespread	Stygobite, Potential SRE
Parabathynellidae `sp. Biologic-PBAT005`	Biologic	High, DNA			x		**7**	Locally restricted, 0.8 km	Unique OTU, group is always stygobitic, rarely widespread	Stygobite, Potential SRE
Parabathynellidae `sp. Biologic-PBAT012`	Biologic	High, DNA			x		**10**	Locally restricted, 1 km	Unique OTU, group is always stygobitic, rarely widespread	Stygobite, Potential SRE
Parabathynellidae `sp. Biologic-PBAT022`	Biologic	High, DNA				x	**3**	Singleton/ single site	Unique OTU, group is always stygobitic, rarely widespread	Stygobite, Potential SRE
Calanoida										
Calanoida `sp. Biologic-CALA002`	Biologic	High, DNA			x		**1**	Singleton/ single site	Unique OTU, group often widespread	Uncertain stygobite, uncertain SRE
Cyclopoida										
Anzcyclops? `sp. BS3`	Biologic	Med, Morpho, Spatial info			x		**2**	Locally restricted (4.5 km)	Unique OTU, group often widespread	Potential stygobite, uncertain SRE
Diacyclops humphreysi (humphreysi)	Biologic, Previous, & 3rd party	High, Morpho				x	**40**	Regionally widespread, LR 700 km	Named species, known to be widespread	Not stygobite, Widespread
Diacyclops `sp. Biologic-CYCL029`	Biologic	High, DNA	x				**1**	Singleton/ single site	Unique OTU, group often widespread	Uncertain stygobite, uncertain SRE
Mesocyclops brooksi	Biologic & Previous survey	High, Morpho		x			**1**	Regionally widespread, LR 600 km	Named species, known to be widespread	Not stygobite, Widespread
Mesocyclops notius	Biologic	High, Morpho					**1**	Occurs beyond Dev Envelope	Named species, known to be widespread	Not stygobite, Widespread
Microcyclops varicans	Biologic	High, Morpho				x	**3**	Regionally widespread (1000+ km)	Named species, known to be widespread	Not stygobite, Widespread
Orbuscyclops westaustraliensis	Previous survey	High, Morpho		x			**3**	Regionally widespread	Named species, known to be widespread	Not stygobite, Widespread
Thermocyclops aberrans	Biologic	High, Morpho		x			**2**	Occurs beyond Dev Envelope	Named species, known to be widespread	Not stygobite, Widespread
Thermocyclops cf. *aberrans*	Biologic	Med, Morpho				x	**9**	Singleton/ single site	Unique OTU, group often widespread	Uncertain stygobite, uncertain SRE
Harpacticoida										
Parastenocaris `sp. B26`	Previous survey	High, Morpho		x			**6**	Regionally widespread	Unique OTU, group can be SRE or widespread	Uncertain stygobite, uncertain SRE
Isopoda										
Microcerberidae `sp. Biologic-ISOP026	Biologic	Med, Morpho, Spatial info			x		**1**	Singleton/ single site	Unique OTU, uncertain distribution	Potential stygobite, Potential SRE
Isopoda `sp. Biologic-ISOP011`	Biologic	High, DNA				x	**35**	Occurs beyond Dev Envelope	Unique OTU, uncertain distribution	Potential stygobite, Potential SRE
Podocopida										
Areacandona nammuldi	Previous survey	High, Morpho		x			**28**	Confirmed SRE, in approved impact area.	Named species, Confirmed SRE	Stygobite, Confirmed SRE
Areacandona nr triangulum	3rd Party & Previous survey	High, Morpho	x	x			**7**	Locally restricted, LR 4.6 km	Unique OTU from previous survey, Potential SRE	Stygobite, Potential SRE

Taxon	Data source	Taxonomic certainty	BS1	BS2	BS3	BS4	Total	Distribution comments, Linear Range (LR)	Taxonomic, ecological comments	Subterranean status, SRE status
Areacandona sp. BOS1020	3rd Party & Previous survey	High, Morpho	x				**2**	Locally restricted, LR 0.15 km	Unique OTU, group can be SRE or widespread	Stygobite, Potential SRE
Candonopsis tenuis	Biologic	High, Morpho				x	**20**	Regionally widespread, LR 360+ km	Named species, known to be widespread	Not stygobite, Widespread
Cypretta seurati	Biologic	High, Morpho	x				**2**	Regionally widespread, LR 600+ km	Named species, known to be widespread	Not stygobite, Widespread
Limnocythere `sp. BOS1314`	Biologic	High, Morpho				x	**12**	Locally widespread, LR 41.8 km	Unique OTU, group can be SRE or widespread	Uncertain stygobite, uncertain SRE
Trombidiformes										
Pezidae `sp. BGCK`	Biologic	Med, Morpho, Spatial info				x	**3**	Singleton/ single site	Uncertain OTU, unique as precaution, group widespread	Uncertain stygobite, uncertain SRE
Pezidae `sp. BS3X`	Biologic	Med, Morpho, Spatial info			x		**1**	Singleton/ single site	Uncertain OTU, unique as precaution, group widespread	Uncertain stygobite, uncertain SRE
Tubificida										
Enchytraeidae `sp. E6`			x			x	**3**	External match with sequences from Rhodes Ridge and McPhee Creek (Biologic internal database). Regionally widespread, LR 300+ km.	Unique OTU, group often widespread	Not stygobite, Widespread
Enchytraeidae `sp. E11`					x	x	**2**	External match with sequences from Weelamurra Creek and McPhee Creek (Brown et al., 2015), and West Angelas (Biologic 2020). Regionally widespread, LR 300+ km.	Unique OTU, group often widespread	Not stygobite, Widespread
Enchytraeidae `sp. Biologic-OLIG004`	Biologic	High, DNA	x		x		**9**	External match with sequences from Rhodes Ridge and Angelo River (Biologic internal database). Regionally widespread, LR 200+ km.	Unique OTU, group often widespread	Not stygobite, Widespread
Enchytraeidae `sp. Biologic-OLIG006`	Biologic	High, DNA	x		x	x	**6**	External match with sequences from West Angelas (Biologic, unpublished data). Regionally widespread, LR 160+ km	Unique OTU, group often widespread	Not stygobite, Widespread
Enchytraeidae `sp. Biologic-OLIG016`	Biologic	High, DNA			x	x	**15**	Occurs beyond Dev Envelope. Locally widespread (46 km)	Unique OTU, group often widespread	Not stygobite, uncertain SRE
Enchytraeidae `sp. Biologic-OLIG017`	Biologic	High, DNA			x	x	**2**	DNA match with regional sequence from Angelo River. LR 160+ km	Unique OTU, group often widespread	Not stygobite, Widespread
Enchytraeidae `sp. Biologic-OLIG018`	Biologic	High, DNA			x		**5**	Locally widespread, LR 48.6 km	Unique OTU, group often widespread	Not stygobite, uncertain SRE
Enchytraeidae `sp. Biologic-OLIG022`	Biologic	High, DNA			x		**11**	External DNA match with sequences from McPhee Creek (Biologic 2020). Regionally widespread, LR 300+ km	Unique OTU, group often widespread	Not stygobite, Widespread
Enchytraeidae `sp. Biologic-OLIG052`	Biologic	High, DNA	x				**1**	Singleton/ single site	Unique OTU, group often widespread	Not stygobite, unlikely SRE
Enchytraeidae `sp. Biologic-OLIG053`	Biologic	High, DNA				x	**1**	Singleton/ single site	Unique OTU, group often widespread	Not stygobite, unlikely SRE
Enchytraeidae `sp. Biologic-OLIG055`	Biologic	High, DNA					**1**	Singleton/ single site	Unique OTU, group often widespread	Not stygobite, unlikely SRE
Antarctodrilus `sp. Biologic-OLIG054`	Biologic	High, DNA				x	**1**	Singleton/ single site	Unique OTU, group often widespread	Not stygobite, unlikely SRE
Phreodrilid with dissimilar ventral chaetae	Previous survey	Low, Morpho		x			**3**	Defunct OTU	Previous survey OTU, unable to align to current specimens	Defunct OTU, synonym
Phreodrilidae `sp. 12`	Biologic	High, DNA	x		x		**25**	Regionally widespread, LR 300+ km	Unique OTU, known to be widespread	Not stygobite, Widespread
Phreodrilidae `sp. Biologic-OLIG001`	Biologic	High, DNA				x	**1**	Singleton/ single site	Unique OTU, group often widespread	Not stygobite, unlikely SRE

Taxon	Data source	Taxonomic certainty	BS1	BS2	BS3	BS4	Total	Distribution comments, Linear Range (LR)	Taxonomic, ecological comments	Subterranean status, SRE status
Phreodrilidae `sp. Biologic-OLIG002`	Biologic	High, DNA	x				**1**	Singleton/ single site	Unique OTU, group often widespread	Not stygobite, unlikely SRE
Phreodrilidae `sp. Biologic-OLIG011`	Biologic	High, DNA				x	**13**	Locally restricted, LR 0.9 km	Unique OTU, group often widespread	Not stygobite, unlikely SRE
Phreodrilidae `sp. P12`	Biologic	High, DNA	x		x		**8**	Regionally widespread, LR 100+ km	Unique OTU, known to be widespread	Not stygobite, Widespread
Phreodrilus peniculus	Previous survey	High, Morpho		x			**1**	Regionally widespread	Named species, known to be widespread	Not stygobite, Widespread
Pristina aequiseta	Biologic	High, Morpho				x	**6**	Regionally widespread, LR 1000+ km	Named species, known to be widespread	Not stygobite, Widespread
Pristina leidyi	Biologic	High, Morpho				x	**2**	Regionally widespread, LR 1000+ km	Named species, known to be widespread	Not stygobite, Widespread
Nais communis	Biologic	High, Morpho				x	**1**	Regionally widespread, LR 1000+ km	Named species, known to be widespread	Not stygobite, Widespread
Total species			**21**	**10**	**20**	**30**	**76**			
Amphipoda sp. indet.	Biologic	Low, indet			x	x	**54**	n/a - indet. could be multiple sp.	Can be SRE when stygobitic	Unknown
Antarctodrilus sp. indet.	Biologic	Low, indet			x	x	**7**	n/a - indet. could be multiple sp.	Can be SRE when stygobitic	Unknown
Atopobathynella sp. indet.	Biologic	Low, indet				x	**14**	n/a - indet. could be multiple sp.	Stygobitic, never epigean, rarely widespread	Stygofauna, Potential SRE
Australocamptus sp. indet.	Biologic	Low, indet			x		**1**			
Bathynellacea sp. indet	Previous survey	Low, indet				x	**1**	singleton indet. - could represent other known species	Stygobitic, never epigean, rarely widespread	Stygofauna, Potential SRE
Bathynellidae sp. indet.	Biologic	Low, indet				x	**16**	n/a - indet. could be multiple sp.	Stygobitic, never epigean, rarely widespread	Stygofauna, Potential SRE
Bogidiellidae sp. indet.	Biologic	Low, indet	x				**1**	singleton indet. - could represent other known species	Can be SRE or widespread	Unknown
Copepoda sp. indet.	Biologic	Low, indet			x	x	**524**	singleton indet. - could represent other known species	Often widespread	Unknown
Cyclopoida sp. indet.	Biologic & Previous survey	Low, indet	x	x	x	x	**667**	n/a - indet. could be multiple sp.	Often widespread	Unknown
Diacyclops sp. indet.	Previous survey	Low, indet					**1**	singleton indet. - could represent other known species	Often widespread	Unknown
Diacyclops nr *hymphreysi*	Biologic	Low, Morpho	x			x	**8**	n/a – indet. could be multiple sp.	Often widespread	Stygofauna, Potential SRE
Enchytraeidae sp. indet.	Biologic	Low, indet	x	x	x	x	**201**	n/a - indet. could be multiple sp.	Often widespread	Unknown
Harpacticoida sp. indet.	Biologic	Low, indet				x	**7**	n/a - indet. could be multiple sp.	Often widespread	Unknown
Naididae sp. indet.	Biologic	Low, indet		x			**1**	singleton indet. - could represent other known species	Often widespread	Unknown
Nedsia sp. indet.	Biologic & Previous survey	Low, indet	x	x		x	**103**	n/a - indet. could be multiple sp.	Can be SRE or widespread	Unknown
Nematoda sp. indet.	Biologic	Low, indet	x		x		**5**	n/a - indet. could be multiple sp.	Not assessed in EIA	Unknown
Oligochaeta sp. indet.	Biologic	Low, indet	x			x	**27**	n/a - indet. could be multiple sp.	Often widespread	Unknown
Ostracoda sp. indet.	Biologic	Low, indet	x		x	x	**56**	n/a - indet. could be multiple sp	Can be SRE or widespread	Unknown
Parabathynellidae nr. Brevisomabathynella sp. indet.	Biologic	Low, indet			x		**47**	n/a - indet. could be multiple sp	Group is always stygobitic, rarely widespread	Stygofauna, Potential SRE

Taxon	Data source	Taxonomic certainty	BS1	BS2	BS3	BS4	Total	Distribution comments, Linear Range (LR)	Taxonomic, ecological comments	Subterranean status, SRE status
Parabathynellidae sp. indet.	Biologic	Low, indet	x		x	x	**41**	n/a - indet. could be multiple sp.	Typically stygobitic SRE, almost never epigean	Stygofauna, Potential SRE
Paramelitidae sp. indet.	Biologic	Low, indet	x	x	x	x	**212**	n/a - indet. could be multiple sp.	Can be SRE or widespread	Unknown
Parastenocaris sp.	3rd Party	Low, indet					**1**	singleton indet. - could represent other known species	Often widespread	Unknown
Pescecyclops sp. indet.	Biologic	Low, indet			x	x	**4**	n/a - indet. could be multiple sp.	Often widespread	Unknown
Phreodrilidae sp. indet.	Biologic	Low, indet			x	x	**44**	n/a - indet. could be multiple sp.	Often widespread	Unknown