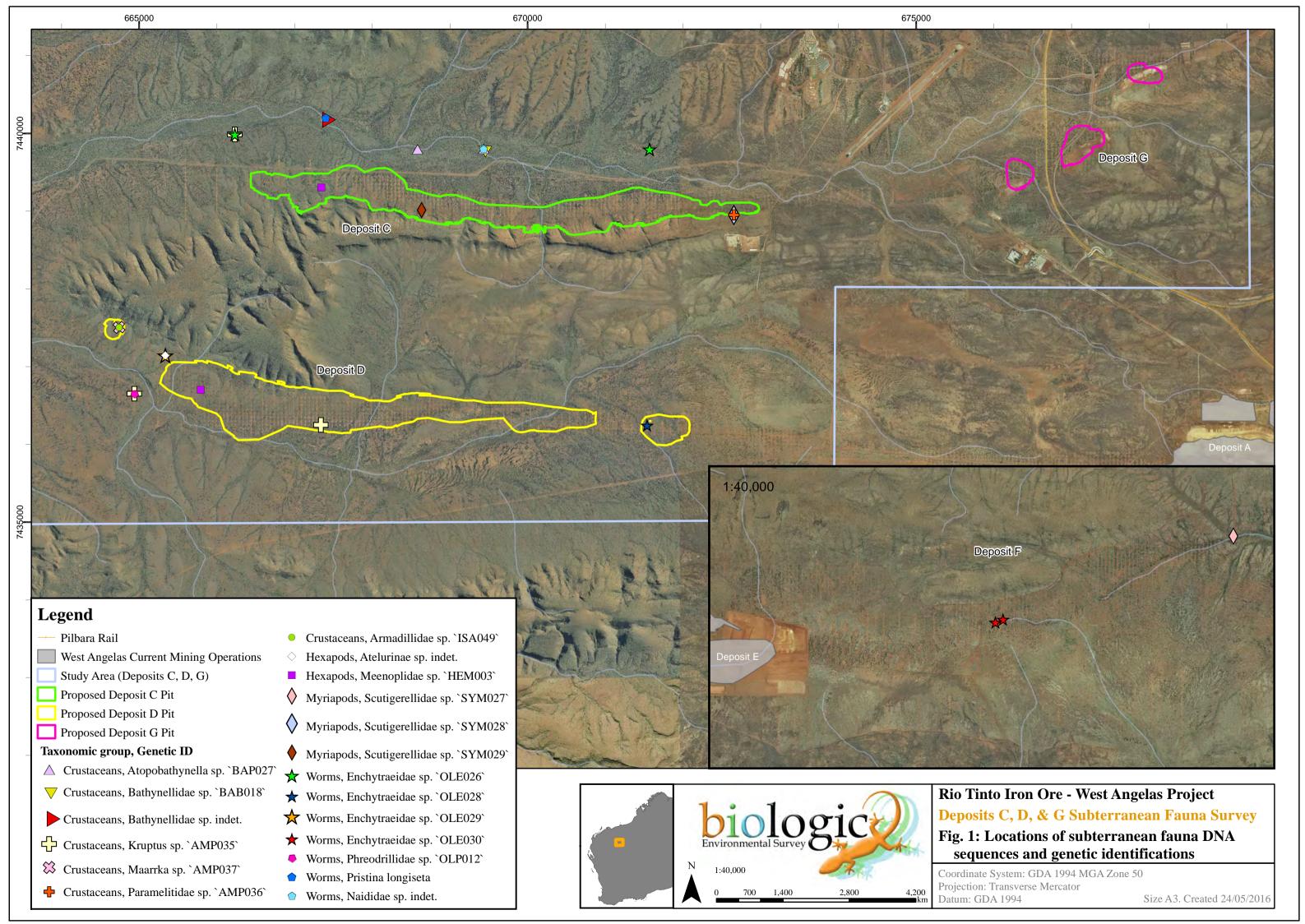
Specimen code	HIGHER TAXON Family	Preliminary ID	Bore/hole name	Local match	% div. COI	Regional match	% div. COI	Nominal species- level ID	Comment
OLIGOCHAE	TA								
BES:1849		Oligochaeta sp. indet.	RC14WAD0346	No		OLP12	<2.8%	Phreodrillidae `OLP12`	Genetic alignment to a species (OLP12) previously sampled widely across four catchments in the Pilbara (Helix 2016).
BES:2030		Oligochaeta sp. indet.	RC15WAC0384	No		Pristina longiseta	1.7%	Pristina longiseta	Genetic alignment to a cosmopolitan species previously sampled worldwide (Helix 2016).
BES:2031		Oligochaeta sp. indet.	RC15WAC0413						Sequence failed
ISOPODA									
BES:1876		Armadillidae sp. indet.	RC12WAD0295	BES:2199	0.3%	No	>18%	Armadillidae `ISA049`	Degionally distinct angular of Armadillidae
BES:2199		Isopoda sp. indet.	RC12WAD0295	BES:1876	0.3%	INO	>10%	Armaumuae 15A045	Regionally distinct species of Armadillidae.
HEMIPTERA									
BES:2139	Meenoplidae	Meenoplidae sp. indet.	RC15WAC0377	BES:2356	Identical	HEM003	1.6 -	Meenoplidae	Genetic alignment to a widespread species previously sampled at Murrays Hill, Hardy River,
BES:2356	Meenoplidae	Meenoplidae sp. indet.	RC14WAD0217	BES:2139	identical	TILIVIOUS	2.3%	`HEM003`	and Upper South Fortescue (Helix 2016).
THYSANURA	<b>\</b>								
BES:1823	Nicoletiidae	Atelurinae sp. indet.	RC14WAD0350						Sequence failed
SYMPHYLA									
BES:2112	Scutigerellidae	Scutigerellidae sp. indet.	RC14WAF0072	No	>16%	No	>16%	Scutigerellidae `SYM027`	Regionally distinct species of Scutigerellidae
BES:2117	Scutigerellidae	Scutigerellidae sp. indet.	RC15WAC0276	Possibly 2055	4.9%	No	>16%	Scutigerellidae `SYM028`	Potentially distinct, but moderate divergence from local specimens indicates more information required to separate distinct species.
BES:2055		Symphyla sp. indet.	RC15WAC0197	Possibly 2117	4.9%	No	>16%	Scutigerellidae `SYM029`	Potentially distinct, but moderate divergence from local specimens indicates more information required to separate distinct species.





# **CHANGES TO RISK ASSESSMENT**

The risk assessment has not changed for any of the taxa that were not sequenced (or not successfully sequenced), including the beetles *Hydrobiomorpha* sp. indet., and Anillini sp. indet., the silverfish Atelurinae sp. indet., the springtail Cyphoderidae sp. indet., the copepods *Australocamptus* sp. `B13` and *Parastenocaris* sp. indet., and *Thermocyclops* sp. `WA`, and the worms Aeolosomatidae sp. indet., and Turbellaria sp. indet. Biologic (2016) contains relevant details for each of these taxa.

Table 2 provides a summary of changes to the risk assessment following the results of the DNA analysis. Figure 2 shows the locations of taxa now considered to be at risk, in the context of the subterranean habitats assessed by Biologic (2016). Four taxa were found to align genetically to widespread taxa, and therefore are now considered to be at negligible risk of impact, comprising:

- The phreodrillid worm Phreodrillidae `OLP12`, found near Deposit C;
- The cosmopolitan naidid worm *Pristina longiseta*, found near Deposit C;
- The enchytraeid worm Enchytraeidae `OLE026`, found near Deposit C; and
- The meenoplid bug Meenoplidae sp. `HEM003`, found within Deposits C and D.

The remaining 13 taxa shown in Table 3 are considered to range from high to moderate low risk based on what is known about the regional occurrence of the taxon from the genetic comparisons, and whether or not the taxon occurs locally outside of the direct impact area (comprising the pit boundaries for troglofauna, and the likely extent of drawdown for stygofauna).

The genetically determined identifications were applied to specimens from the same sample and the same bore/ hole where it was reasonable to do so (such as samples where there were 17 'Enchytraeidae sp. indet.' collected and one was sent for sequencing, or bores/ holes where there were 5 'Enchytraeidae sp. indet.' from the first trip and 2 from the second trip). Nevertheless, not all of the 'sp. indet.' taxa were able to be treated this way, owing to the presence of multiple genetically determined species co-occurring in the same habitat/ deposit (particularly in the Enchytraeidae and Paramelitidae). Where a specimen from a different bore/ hole was unable to be reasonably allocated to either of multiple genetically determined species, it remained 'sp. indet.' and the risk level did not change materially.

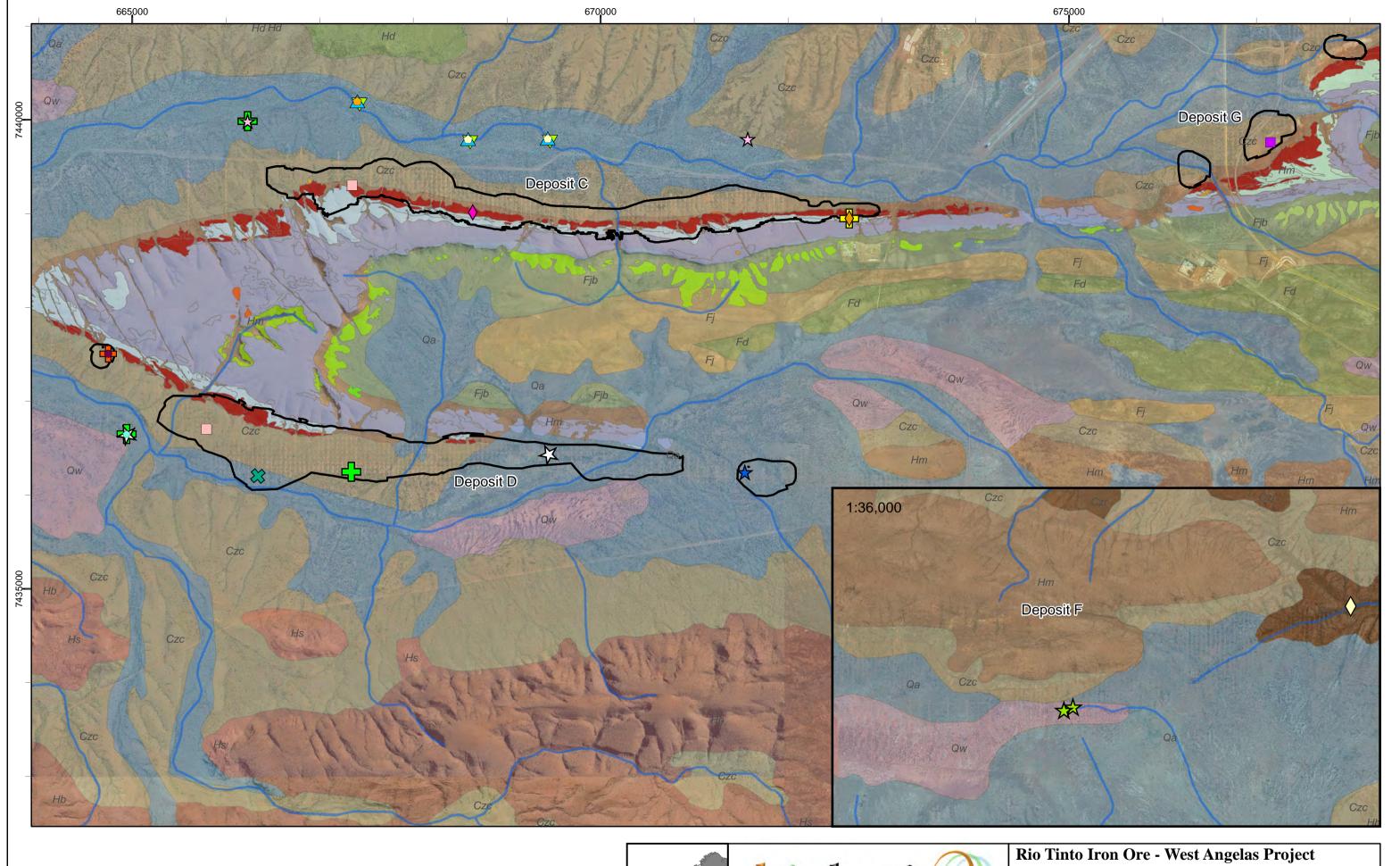
Note also that enchytraeids were assessed herein as stygofauna, because it was assumed that groundwater drawdown may possibly result in desiccation of the air-filled subterranean habitat as well as the loss of groundwater habitat within the drawdown zone.

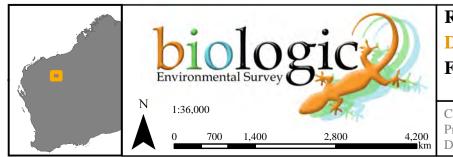
Table 3: Changes to risk assessment of subterranean taxa following DNA analysis.

Morphospecies	Current SRE status	Previous taxon	Within deposit/ impact	Out of deposit/impact	Extent of habitat beyond deposit/ likely impact area	Risk of direct impacts
Worms						
Enchytraeidae `OLE026`	Widespread	Enchytraeidae sp. indet.		Near Dep. C (29)	Regional	Negligible. Regionally widespread species
Enchytraeidae `OLE028`	Confirmed SRE (D)	Enchytraeidae sp. indet.	Dep. D (2)		Likely beyond deposit within Calcrete/ Orebody/ Mt Newman Member, but within likely drawdown	<b>High.</b> Direct impacts may include mining and drawdown.
Enchytraeidae `OLE029`	Potential SRE (A&D)	Enchytraeidae sp. indet.		Near Dep. D (11)	Beyond deposit within Orebody/ Mt Newman Member, but within likely drawdown	<b>High.</b> Direct impacts may include mining and drawdown.
Enchytraeidae `OLE030`	Potential SRE (A&D)	Enchytraeidae sp. indet.	Dep. F (26)		Likely beyond deposit within Alluvials/ Mt Newman Member	<b>Negligible</b> . Unlikely to be affected by mining at Dep. C, D, G
Enchytraeidae sp. indet.	Potential SRE (A)	Enchytraeidae sp. indet.	Dep. D (75), F (38)	Near Dep D (1), C (6)	Likely beyond Deposit D within Calcrete/ Orebody/ Mt Newman Member, but within likely drawdown	Mod / High. Specimens cannot be allocated on current information. Records in/ near Dep. C and D may be at risk from mining or drawdown
Phreodrillidae `OLP12`	Widespread	Oligochaeta sp. indet.	Near Dep. D (1)		Regional	Negligible. Regionally widespread species
Pristina longiseta	Widespread	Oligochaeta sp. indet.	Near Dep. C (6)		Worldwide	Negligible. Cosmopolitan widespread species
c.f. Pristina longiseta	Widespread	Oligochaeta sp. indet.	Near Dep. C (22)		Worldwide	<b>Negligible</b> . Likely to represent <i>P. longiseta</i> owing to location and broad morphology. Widespread.
Crustaceans						
Kruptus sp. `AMP035`	Confirmed SRE (D&E)	Kruptus sp. 'WA'	Near Dep. C (6), Dep D (3)		Beyond Deposit C/ D within Calcrete/ Alluvials, but all current records within drawdown	<b>High</b> . Species currently known only from within likely drawdown extent
Maarrka sp. `AMP037`	Confirmed SRE (D&E)	Maarka sp. 'WA'	Dep. D (1)		Likely beyond deposit within Orebody/ Mt Newman, but all current records within drawdown	<b>High</b> . Species currently known only from within likely drawdown extent
Paramelitidae sp. `AMP036`	Confirmed SRE (D&E)	Kruptus sp. 'WA'	Dep. C (1)		Likely beyond deposit within Orebody/ Mt Newman Member, but all current records within drawdown	<b>High</b> . Species currently known only from within likely drawdown extent
Paramelitidae sp. indet.	Potential SRE (A&E)	Kruptus sp. 'WA'	Near Dep. C (1)		Likely beyond Deposit D within Calcrete/ Orebody/ Mt Newman Member, but within likely drawdown	<b>Mod / High</b> . Likely to be the same as <i>K</i> . AMP035, but would not extend range beyond likely drawdown
Atopobathynella sp. `BAP027`	Confirmed SRE (D&E)	Atopobathynella sp. `WA`	Near Dep. C (200)		Unknown, but all current records within likely drawdown	<b>High</b> . Species currently known only from within likely drawdown extent
Bathynellidae sp. `BAB018`	Confirmed SRE (D&E)	Bathynellidae sp. `WA`	Near Dep. C (87)		Unknown, but all current records within likely drawdown	<b>High</b> . Species currently known only from within likely drawdown extent
Armadillidae sp. `ISA049`	Confirmed SRE (D&E)	Armadillidae sp. indet., Isopoda sp. indet.	Dep. D (2)		Recorded close to boundary, habitat likely beyond Dep. D throughout Orebody/ Mt Newman Member	<b>Mod</b> . Current records only just within pit, habitat likely to extend beyond.



Morphospecies	Current SRE status	Previous taxon	Within deposit/ impact	Out of deposit/impact	Extent of habitat beyond deposit/ likely impact area	Risk of direct impacts
Myriapods						
Scutigerellidae sp. `SYM027`	Confirmed SRE (D&E)	Scutigerellidae sp. indet.		Outside Dep. F (1)	Locally beyond Deposit F	<b>Negligible</b> . Unlikely to be affected by mining at Dep. C, D, G
Scutigerellidae sp. `SYM028`	Confirmed SRE (D&E)	Scutigerellidae sp. indet.	Dep. C (17)		Recorded close to boundary, habitat likely beyond Dep. C throughout Orebody/ Mt Newman Member	<b>Mod</b> . Current records only just within pit, habitat likely to extend beyond. Moderate genetic similarities to S. SYM029
Scutigerellidae sp. `SYM029`	Confirmed SRE (D&E)	Symphyla sp. indet.	Dep. C (1)		Likely beyond Deposit C throughout Orebody/ Mt Newman Member	<b>Mod</b> . Current records within pit, but habitat may extend beyond. Moderate genetic similarities to S. SYM028
Hexapods						
Meenoplidae sp. `HEM003`	Widespread	Meenoplidae sp. indet. (Biologic)	Dep. C (2), Dep. D (1)	Regional	Regional	Negligible. Regionally widespread species
Meenoplidae sp. indet. (Ecologia 2013)	Potential SRE (A)	Meenoplidae sp. indet. (Ecologia)	Dep. G (1)	Dep. H (1)	Likely beyond Deposit G throughout Orebody/ Mt Newman Member	<b>Mod / Low</b> . Possibly be the same as <i>M</i> . HEM003, which is regionally widespread
Atelurinae sp. indet. (Biologic 2016)	Potential troglobite	Atelurinae sp. indet. (Biologic)		Outside Dep. D (1)	Habitat outside of Dep D throughout Orebody/ Mt Newman Member	<b>Low</b> . Specimen does not occur within pit. Possibly be the same as Ecologia species, owing to proximity and connected habitats
Atelurinae sp. indet. (Ecologia 2013)	Potential troglobite	Atelurinae sp. indet. (Ecologia)	Dep D (1)		Habitat likely beyond Dep D throughout Orebody/ Mt Newman Member	<b>Mod.</b> Possibly same as Biologic species, owing to proximity and connected habitats.





Deposits C, D, & G Subterranean Fauna Survey

# Fig. 2: Subterranean fauna risk assessment changes following DNA analysis

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

Datum: GDA 1994 Size A3. Created 24/10/2016

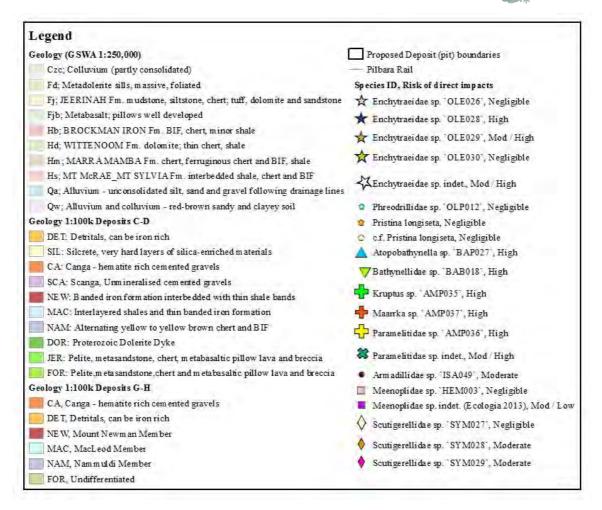


Figure 2 Legend.

## **OVERALL RISK ASSESSMENT**

This assessment considers the risk of direct impacts to subterranean fauna from the development of West Angelas Deposits C, D, and G. As defined in Biologic (2016), direct impacts on troglofauna occur as a result of the removal of habitat within the pit boundaries, while direct impacts on stygofauna include both direct removal of habitat within the pit and the associated drawdown of groundwater throughout permeable hydrogeological layers nearby (which is yet to be modelled precisely).

Including all survey results to date, the following eight troglofauna taxa were regarded to be potentially at risk from mining at Deposits C, D, and G (Figure 3):

# Moderate risk of direct impact:

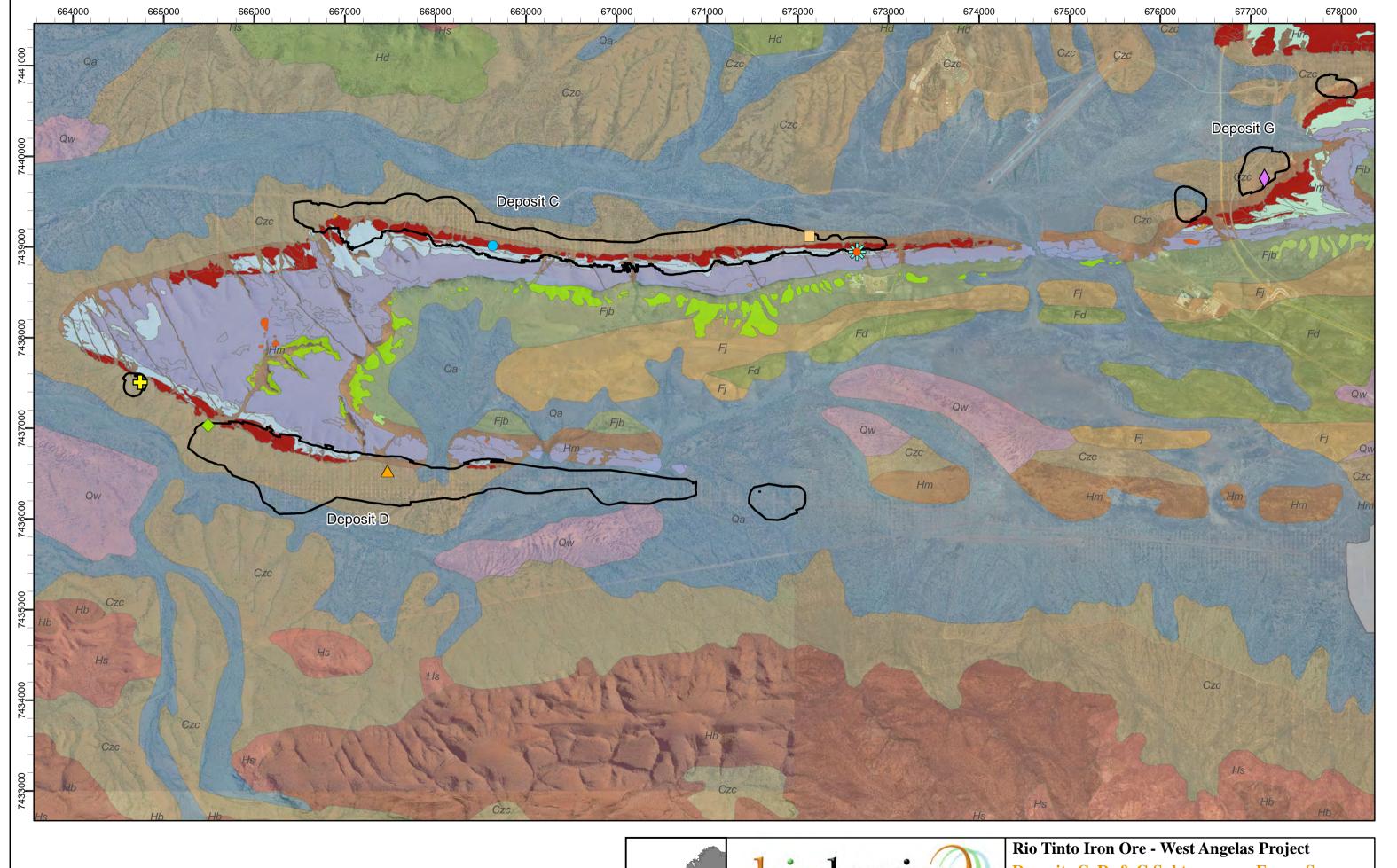
- Isopoda: Armadillidae sp. `ISA049` (Deposit D);
- Symphyla: Scutigerellidae sp. `SYM028` (Deposit C);
- Symphyla: Scutigerellidae sp. `SYM029` (Deposit C);
- Coleoptera: Anillini `sp. indet.` (Ecologia 2013) (Deposit C);
- Coleoptera: Hydrobiomorpha `sp. indet.` (Ecologia 2013) (Deposit D);
- Thysanura: Atelurinae `sp. indet.` (Ecologia 2013) (Deposit D);

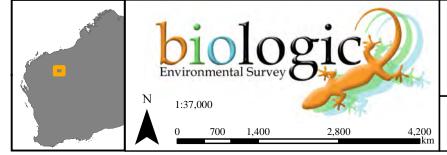
# Moderate / Low risk of direct impact:

- Collembola: Cyphoderidae `sp. indet.` (Deposit C); and
- Hemiptera: Meenoplidae `sp. indet.` (Ecologia 2013) (Deposit G).

Each of these taxa are known only from locations within the proposed mining deposits, and were therefore regarded as being potentially at risk. The potential risk level was moderated by the location of many of the records (particularly Armadillidae sp. 'ISA049', Scutigerellidae sp. 'SYM028', Cyphoderidae 'sp. indet.', Anillini 'sp. indet.', and *Hydrobiomorpha* 'sp. indet.') very close to the deposit boundaries and the lack of any clear geological or geomorphological barriers between suitable habitat layers inside and outside of the deposits (as detailed in Biologic 2016). The current records of these taxa are likely to underestimate the actual distributions of these species throughout the subterranean habitat, owing to both the inherent difficulties in sampling rarely occurring fauna with limited means of dispersal, as well as the physical limitations of accessing the wider subterranean habitat using only suitable and available drill holes.

The potential risk level for Atelurinae 'sp. indet.' and Meenoplidae 'sp. indet.' was moderated by the likelihood that these taxa (originally collected by Ecologia, and unable to be compared with current specimens) could represent the same species as other representatives of these taxa found to occur outside of the deposits in the current survey. There also remains some doubt as to the likelihood that Cyphoderidae 'sp. indet.' and Meenoplidae 'sp. indet.' represent obligate (troglobitic) subterranean fauna or potentially facultative subterranean fauna, which may be less likely to be restricted to habitats within the deposits.





Deposits C, D, & G Subterranean Fauna Survey

Fig. 3: Troglofauna taxa overall risk assessment

Coordinate System: GDA 1994 MGA Zone 50

Projection: Transverse Mercator Datum: GDA 1994

Size A3. Created 24/10/2016

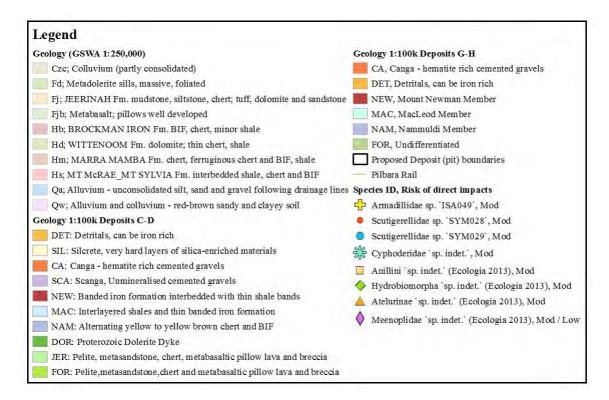


Figure 3 Legend.

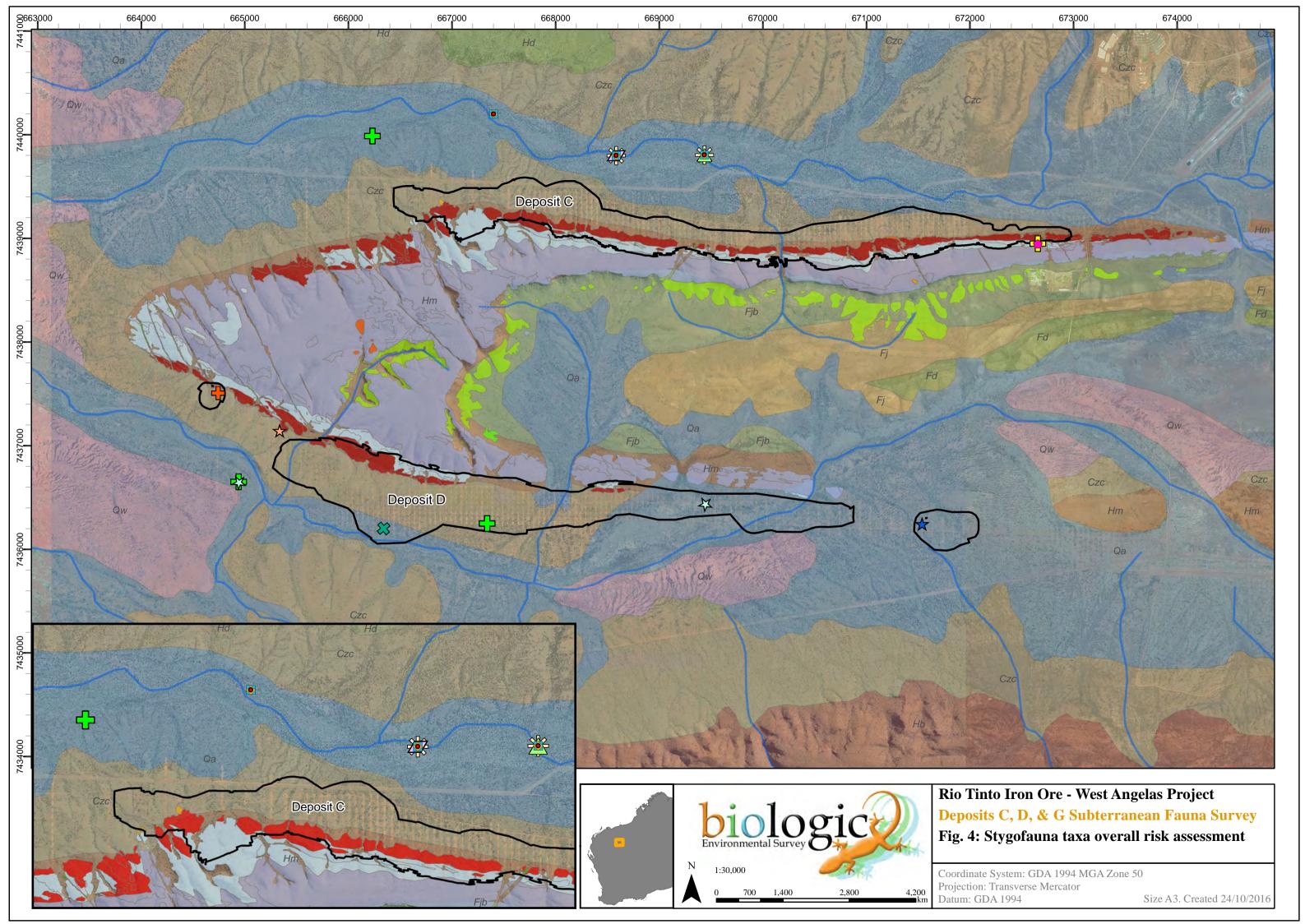
The following 14 stygofauna taxa were regarded to be potentially at risk from mining and the associated groundwater drawdown at Deposits C and D (Figure 4):

# High risk of direct impact:

- Haplotaxida: Enchytraeidae sp. `OLE028` (Deposit D);
- Haplotaxida: Enchytraeidae sp. `OLE029` (near Deposit D);
- Amphipoda: Kruptus sp. `AMP035`(near Deposit C and D);
- Amphipoda: Maarrka sp. `AMP037` (Deposit D);
- Amphipoda: Paramelitidae sp. `AMP036` (Deposit C);
- Bathynellacea: Atopobathynella sp. `BAP027` (near Deposit C);
- Bathynellacea: Bathynellidae sp. `BAB018`(near Deposit C);
- Harpacticoida: Australocamptus sp. `B13`(near Deposit C); and

# Moderate / High risk of direct impact:

- Haplotaxida: Enchytraeidae `sp. indet.` (near Deposit D);
- Turbellaria: Turbellaria `sp. indet.` (near Deposit C);
- Polychaeta: Aeolosomatidae `sp. indet.` (Deposit C);
- Amphipoda: Paramelitidae `sp. indet.` (Deposit D);
- Cyclopoida: Thermocyclops sp. 'WA' (near Deposit C); and
- Harpacticoida: Parastenocaris `sp. indet.` (near Deposit C).



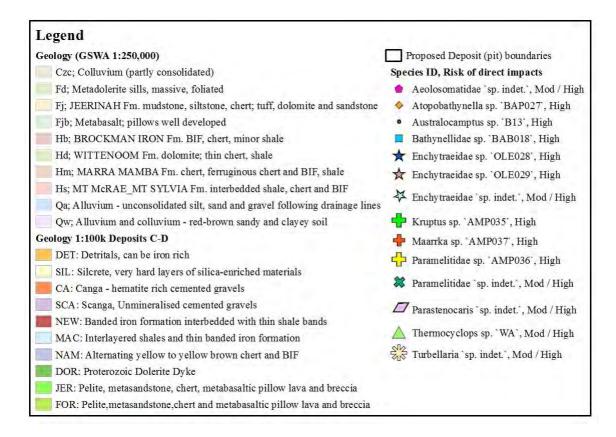


Figure 4 Legend.

The risk level for the five indeterminate taxa (identified as `sp. indet.`) was moderated by the taxonomic uncertainties regarding these taxa (or groups of specimens). Each of these nominal taxa was unable to be allocated to other existing morphospecies (or genetically determined species) on current information, and the possibility remains that they could occur more widely than the other 'high' risk taxa, as some widely occurring members of these groups are known regionally. Nevertheless, for Enchytraeidae 'sp. indet.' and Paramelitidae 'sp. indet.' in particular, it is also reasonably likely that some of the specimens could represent one of the other existing 'high' risk taxa in their respective groups.

The risk level for the 'high' risk stygofauna was primarily dependent upon the magnitude and extent of groundwater drawdown, which is yet to be modelled in detail, but which is inferred to extend throughout the orebody aquifers within the deposits and the alluvial/ detrital aquifers of the flanking valleys nearby (Biologic 2016). This is inferred to include all of the locations of stygofauna records from the current survey (which are all within 1 km of the deposit boundaries), on the basis of the available hydrogeological information. Nevertheless, it is possible that the risk of direct impact for stygofauna species may be subject to change with further information regarding groundwater drawdown.

It is also possible that the current species distributions may be partly attributed to sampling artefacts, as there has been no sampling for subterranean fauna to the immediate west of the current deposits within the same hydrogeological catchment (Turee Creek East Branch). Previous



stygofauna collected further afield (approximately 15 km to the south west at Turee Creek Borefield), and to the immediate east within the Central Plateau area of West Angelas are not able to be compared with current specimens due to old/ incomplete identifications, incompatible specimen preservation, and a lack of genetic information.

Owing to the position of the deposits within the local catchment and the direction of flow from the Central Plateau to the northern flanking valley between Deposits C and G (as discussed in Biologic 2016), there is a reasonable likelihood that some of the current stygofauna species could also occur in the Central Plateau, and/or further downstream to the west within the Turee Creek East sub-catchment.

Yours sincerely,

**Brad Durrant** 

Principal Zoologist / Managing Director

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# **REFERENCES**

- Biologic Environmental Survey (Biologic) (2016). West Angelas Deposits C, D & G Subterranean Fauna Survey 2016. Unpublished report prepared for Rio Tinto Iron Ore
- Ecologia Environmental Consultants (Ecologia) (2013). Greater West Angelas Subterranean Fauna Assessment. Unpublished report prepared for Rio Tinto Iron Ore
- Helix Molecular Solutions (2017) Report on the molecular systematics of subfauna. Unpublished report prepared for Biologic Environmental Survey c/o Alacran Environmental (Appendix I to this document)



Appendix I – Helix Molecular Solutions DNA Report



# Helix Molecular Solutions

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2 April, 2017

Frich Volschenk

Via email

# Re. Report on the molecular systematics of subfauna

Dear Erich,

Following is a summary of the results of the subfauna study we have completed on eight taxonomic groups. Sixteen distinct genetic lineages were detected among the seven groups for which sequences were obtained. We did not obtain a sequence from the one Thysanura specimen. Four of the 16 lineages have been detected previously (one each of Enchytraeidae, Naididae, Phreodrilidae and Meenoplidae), whereas the remainder appear to be new or require further investigation.

Thanks once again for collaborating on this project with Helix. We hope we can continue to provide you with useful information, and feel free to contact us if you have any questions or would like to discuss the results in detail.

Sincerely,

Dr. Terrie Finston, Yvette Hitchen and Dr. Oliver Berry Helix Molecular Solutions



## **Background and Objective**

Twenty-six specimens of subfauna (troglofauna and stygofauna) belonging to eight taxonomic groups were sequenced for variation at the mitochondrial COXI or 12s genes. The molecular data were assessed in order to determine the number of species present in each group and compare the results to those obtained during previous surveys that have been undertaken for the these groups elsewhere in the Pilbara.

# **Methods**

Twenty-six specimens of subfauna were sequenced for variation at the mitochondrial cytochrome oxidase subunit I gene (COXI) using multiple pairs of primers (LCOI/HCO2, LCOI-long/HCO2-long, NemF1/NemR1 and LCOI/CIN2341. The 12s region was amplified and sequenced using primers 12-ai and 12s-bi (Simon et al., 1994).

Sequences were edited using GENEIOUS software (Drummond et al. 2011). Alignment was performed with CLUSTAL W (Thompson et al. 1994) using default parameters. Genetic distances between unique genetic sequences (haplotypes) were measured using uncorrected p-distances (total percentage of nucleotide differences between sequences).

Genetic distances were calculated using p-distances, and neighbour-joining trees were constructed from those distances using MEGA 6.0 (Tamura et al., 2013).

For the purposes of this report, lineages were defined as haplotypes or groups of haplotypes differing from other such groups by >3% sequence divergence. This cut-off was selected based on bar-coding data, which indicates that intra-specific variation rarely exceeds 3% (Hebert et al., 2003b).

COXI is widely considered to show suitable variation to distinguish species (Hebert et al., 2003a). In a comparison of COXI sequences for over 13,000 pairs of taxa, Hebert et al (2003b) found a mean of 11.1% sequence divergence between distinct species. Nearly 80% of the comparisons showed that species pairs differed from one another by greater than 8% sequence divergence. However, a taxon by taxon approach, examining the amount of phylogenetic variation within and between species is the most widely accepted method of defining species.

## **Results and Conclusions**

# **Amphipoda**

Neighbour-joining analysis - Reference sequences and outgroups

Five specimens of amphipods, identified on the basis of morphology as belonging to the Paramelitidae, were sequenced for COI. A search of similar sequences on Genbank indicated that the specimens were most similar to sequences of Paramelitidae, thus the sequences were analysed with reference specimens representing 49 distinct genetic lineages of Paramelitidae from the Pilbara. Two specimens of Niphargidae, Niphargus fontanus (Genbank accession #KC315635) and Niphargus glenniei (Genbank accession # KC315646) were used as outgroups. In order reduce analysis time and simplify the presentation of results, a sub-set of reference lineages were selected based on the criteria that they were placed in clades containing the five target sequences in a preliminary NJ analysis.

The neighbour-joining analysis placed the five specimens into three lineages, which did not contain any reference lineages, therefore they were assigned to the new lineages AMP035 – AMP037 (Figure 1). Lineage AMP035 contained three specimens, whereas the remaining two lineages, AMP036 and AMP037, each contained a single specimen (Figure 1).

# Differentiation within and between lineages

The three lineages of Paramelitidae detected in the present study differed from one another by between 17.5 and 18.7% sequence divergence (Table 1). Individuals within lineage AMP035 differed from one another by between 0.3 and 0.9% sequence divergence (Table 1).

All three lineages differed from the closest reference lineages by >15% sequence divergence (Table 1).

#### Conclusions

Three lineages of amphipods were detected in the present study, belonging to the family Paramelitidae. The three lineages differed from one another and from the reference specimens by >15% sequence divergence, indicating that the three lineages represent three species that have so far not been detected in the Pilbara, based on the material available for comparison.

#### Paramelitidae

AMP035 = one species, new Paramelitidae AMP036 = one species, new Paramelitidae AMP037 = one species, new Paramelitidae

# Bathynellacea

Neighbour-joining analysis - Reference sequences and outgroups
Three specimens of Bathynellacea, assigned to the families Bathynellidae and
Parabathynellidae on the basis of morphology, were sequenced for COI. The sequences were
analysed with 47 reference lineages of Bathynellacea from the Pilbara, representing 65
specimens. Two species of Amphipoda were used as outgroups: Chydaekata acuminata
Genbank accession #DQ838024 and Maarka etheli GenBank accession #DQ838031.

The neighbour-joining analysis placed the three specimens into two lineages, which did not contain any reference lineages, therefore they were assigned to the new lineages BAB018 and BAP027 (Figure 2). Lineage BAB018 contained a single specimen, whereas lineage BAP027 each contained two specimens (Figure 2). Lineage BAP027 was placed in a large clade containing reference specimens of Parabathynellidae, and lineage BAB018 was placed in a clade containing reference lineages of Bathynellidae.

# Differentiation within and between lineages

Individuals within lineage BAP027 differed from one another by 0.3% sequence divergence (Table 2). Lineage BAP027 differed from the closest reference lineage (CA0084 from Callawa) by 10.8% sequence divergence (Table 2). Lineage BAB018 differed from the closest reference lineage (G456 from the Central Pilbara) by 19.6% sequence divergence (Table 2).

# Conclusions

Two lineages of Bathynellacea were detected in the present study, one each belonging to the families Bathynellidae and Parabathynellidae. The two lineages differed from the reference specimens by >10% sequence divergence, indicating that the two lineages represent two species that have so far not been detected in the Pilbara, based on the material available for comparison.

# Bathynellidae

BAB018 = one species, new Bathynellidae Parabathynellidae BAP027 = one species, new Parabathynellidae

#### Enchytraeidae

Neighbour-joining analysis - Reference sequences

Six specimens of Enchytraeidae were sequenced for COI. The sequences were analysed with 55 reference specimens of Enchytraeidae from Genbank and the Pilbara, representing 26 lineages.

The neighbour-joining analysis placed the six specimens into four lineages, three of which did not contain any reference lineages, therefore the three were assigned to new lineages OLE028 – OLE030 (Figure 3). One lineage also contained reference specimens from a previous survey in the Pilbara, and therefore was assigned to the existing lineage OLE026 (Figure 3). Lineages OLE028 and OLE029 each contained a single specimen, whereas lineage OLE030 contained two specimens (Figure 3).

Differentiation within and between lineages

The four lineages of Enchytraeidae detected in the present study differed from one another by between 7.4 and 17.1% sequence divergence (Table 3.) Individuals within lineage OLE026, which contained the two specimens from this study as well as two specimens from a previous survey, differed from one another by between 1.2 and 3.4%, and individuals within lineage OLE030 differed from one another by 1.6% sequence divergence (Table 3). Lineage OLE028 differed from the closest reference lineage (382 from Robe River) by 12.9% sequence divergence (Table 3). Lineage OLE029 differed from the closest reference lineage (EQ15) by 5.7% sequence divergence and OLE differed from the nearest reference specimen (EQ7 and GD10) by 7.8% (Table 3).

### Conclusions

Four lineages of Enchytraeidae were detected in the present study. They differed from one another by >7% sequence divergence. One of the lineages (OLE026) has been detected previously in the Pilbara. One lineage, OLE028, differed from the reference specimens by >approximately 13% indicating that it likely represents a species that has so far not been detected in the Pilbara, based on the material available for comparison. The remaining two lineages require further consideration. Lineages OLE029 and OLE030 were placed in a large clade including lineage OLE026 and containing specimens of the morphologically-defined species PST1 (Brown et al., 2015). Haplotypes within the lineage averaged 7.4% sequence divergence and cover a large geographical area covering six creek catchments and three river basins (Brown et al. 2015). Further investigation is required to resolve relationships among members of this group.

### Enchytraeidae

OLE028 = one species, new

OLE026 + OLE029 + OLE030 = species complex requiring further investigation; lineage OLE026 has been detected previously

## Naididae and Phreodrilidae

Neighbour-joining analysis - Reference sequences

Three additional specimens of Oligochaeta, which were not assigned to a taxonomic group, were sequenced for COI. A search of similar sequences on Genbank indicated that two belonged to the Naididae and one to the Phreodrilidae. For this reason, the sequences were analysed with 15 reference lineages of Naididae, representing five lineages from the Pilbara and Genbank, and 52 specimens of Phreodrilidae, representing 22 lineages from the Pilbara.

The neighbour-joining analysis placed the three specimens into two lineages, both of which also contained reference specimens (Figure 4). Two specimens were genetically identical and were placed in a lineage containing the reference specimen of *Pristina longiseta*, in the family Naididae (Figure 4). The second lineage was placed within Phreodrilidae lineage OLP012, which contained specimens from four drainage basins in the Pilbara (Brown et al., 2015).

# Differentiation within and between lineages

The two specimens of Naididae from the present study were genetically identical, and differed from the reference specimen of *Pristina longiseta* by 1.7% sequence divergence (Table 4). The specimen of Phreodrilidae from the present study differed from the remaining specimens within lineage OLP012 by between 1.9 and 2.8% sequence divergence (Table 4).

# Conclusions

One lineage each of Naididae and Phreodrilidae were detected in the present study, each corresponding to a single species. Both belong to species that have been detected previously, one to the widespread Naididae species *Pristina longiseta*, and the second to the Phreodrilidae lineage OLP012, distributed widely in the Pilbara (Brown et al., 2015). The genus *Pristina* is known from North America, Central America, Europe, Asia and Australia (Rodrigues et al., 2015).

Naididae

Pristina longiseta, world-wide distribution Phreodrilidae OLP012 = one species, previously detected

#### Hemiptera (Meenoplidae)

Neighbour-joining analysis - Reference sequences

Two specimens of Hemiptera, assigned to the family Meenoplidae, were sequenced for COI. The sequences were analysed with 26 reference specimens of Meenoplidae from the Pilbara.

The neighbour-joining analysis placed the two specimens in a single genetic lineage, which also contained reference specimens from previous surveys at Murrays Hill, Hardy River and Upper South Fortescue (Figure 5). Therefore the specimens from the present study were assigned to the existing lineage HEM003 (Figure 5).

# Differentiation within and between lineages

The two specimens of Meenoplidae from the present study were genetically identical at COI and differed from the reference specimens from Murrays Hill, Hardy River and Upper South Fortescue by between 1.6 and 2.3% sequence divergence (Table 5).

#### Conclusions

The two specimens of Meenoplidae from the present study belonged to a single species, that has been detected previously at Murrays Hill, Hardy River and Upper South Fortescue.

# Meenoplidae

HEM003 = one species, detected previously

#### Isopoda

Neighbour-joining analysis - Reference sequences

Two specimens of Isopoda were sequenced for COI. The specimens were not further assigned to family. A search of similar sequences on Genbank indicated that the specimens were most similar to sequences of Troglarmadillo, thus the sequences were analysed with reference specimens representing 48 distinct genetic lineages of presumptive Armadillidae from the Pilbara, representing 66 specimens. In order reduce analysis time and simplify the presentation of results, a sub-set of reference lineages were selected based on the criteria that they were placed in clades or near-by clades containing the two target sequences in a preliminary NJ analysis. Thirty-five lineages representing 46 specimens were used in the final NJ analysis.

The neighbour-joining analysis placed the two specimens into a single lineage, which did not contain any reference lineages, therefore it was assigned to the new lineage ISA049 (Figure 6). The lineage was placed in a clade containing reference specimens of Troglarmadillo from the Pilbara (Figure 6).

# Differentiation within and between lineages

The two specimens in lineage ISA049 differed from one another by 0.3% sequence divergence (Table 6). Lineage ISA049 differed from the closest reference lineages by >18% sequence divergence (Table 6).

#### Conclusions

A single lineage of Isopoda was detected in the present study, likely belonging to the family Armadillidae. The lineage differed from the reference specimens by >18% sequence divergence, indicating that it likely represents a new species that has so far not been detected in the Pilbara, based on the material available for comparison.

## Armadillidae

ISA049 = one species, new

# Symphyla

Neighbour-joining analysis - Reference sequences

Three specimens of Symphyla were sequenced for COI. Two were assigned to the family Scutigerellidae, on the basis of morphology, whereas the third was not further assigned. A search of similar sequences on Genbank and the Helix database indicated that the specimens were most similar to sequences of Scutigerellidae, thus the sequences were analysed with reference specimens representing 26 distinct genetic lineages of presumptive Scutigerellidae from the Pilbara.

The neighbour-joining analysis placed the three specimens into three distinct genetic lineages, which did not contain any reference lineages, and were in fact most similar to one another (Figure 7). The three lineages were therefore assigned to the new lineages SYM027, SYM028 and SYM029 (Figure 7).

# Differentiation within and between lineages

The three lineages from the present study differed from one another by between 4.9 and 17.5% sequence divergence (Table 7). The three lineages differed from the closest reference lineages by >16% sequence divergence (Table 7).

### Conclusions

Three distinct lineages of Symphyla were detected in the present study, likely belonging to the family Scutigerellidae. Two of the lineages, SYM028 and SYM029, showed moderately low genetic differentiation from one another (approximately 5%), thus require further consideration. The two lineages may represent incipient species, or differentiation within a single species between geographically separate sites, arising from the poor dispersal abilities of the taxon. Sampling of intermediate sites my help resolve their relationshps. The three lineages differed from the reference specimens by >16% sequence divergence, indicating that they are likely to represent new species that have so far not been detected in the Pilbara, based on the material available for comparison.

#### Scutiaerellidae:

SYM027 = one species, new

SYM028 + SYM029 = one or two new species, requiring further investigation

### <u>Thysanura</u>

A DNA sequence was not obtained from the specimen of Thysanura.

#### **References**

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Table 1. (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Amphipoda detected in the present study and the reference lineages as shown in Figure 1.

Table 2. (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Bathynellacea detected in the present study and the reference lineages as shown in Figure 2.

Table 3. (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Enchytraeidae detected in the present study and the reference lineages as shown in Figure 3.

Table 4. (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Naididae and Phreodrilidae detected in the present study and the reference lineages as shown in Figure 4.

Table 5. (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Meenoplidae detected in the present study and the reference lineages as shown in Figure 5.

Table 6. (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Isopoda detected in the present study and the reference lineages as shown in Figure 6.

Table 7. (attached). Genetic distances (below diagonal) and standard error (above diagonal, in blue) between specimens of Symphyla detected in the present study and the reference lineages as shown in Figure 7.

Figure 1. Neighbour-joining analysis of specimens of Amphipoda from the present study. Numbers on major nodes correspond to bootstrap support over 100 iterations. Scale bargenetic distance. The specimens from the present study are highlighted in yellow; Genbank voucher specimens are highlighted in turquoise.

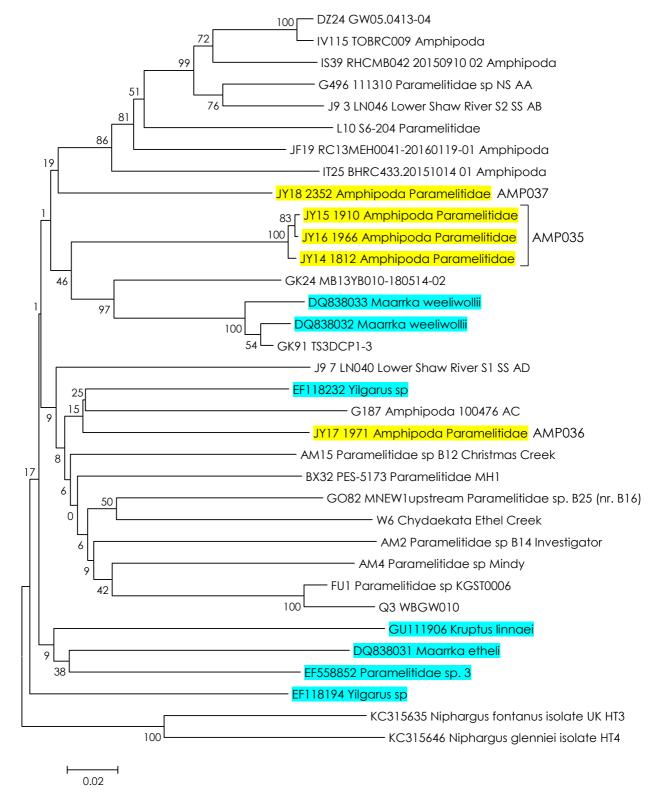


TABLE 1. Amphipod Distance Matrix																																
TABLE 1. Ampriipod bisidince Mainx																						B16)										
Specimen ID	IY14 1812 Amphipoda Paramelifidae	JY15 1910 Amphipoda Paramelitidae	JY16 1966 Amphipoda Paramelitidae	IY17 1971 Amphipoda Paramelitidae	JY18 2352 Amphipoda Paramelitidae	AM15 Paramelifidae sp B12 Christmas Creek	AM2 Paramelitidae sp B14 Investigator	AM4 Paramelitidae sp Mindy	3X32 PES-5173 Paramelitidae MH1	Q838031 Maarrka etheli	Q838032 Maarka weeliwollii	Q838033 Maarrka weeliwollii	224 GW05.0413-04	F118194 Yilgarus sp	F118232 Yilgarus sp	F558852 Paramelitidae sp.3	'U1 Paramelitidae sp KGST0006	3187 Amphipoda 100476 AC	3496 111310 Paramelitidae sp NS AA	3K24 MB13YB010-180514-02	SK91 TS3DCP1-3	3082 MNEW1 upstream Parameitidae sp. B25 (nr. B1	3U111906 Kruptus linnaei	S39 RHCMB042 20150910 02 Amphipoda	725 BHRC433.20151014 01 Amphipoda	V115TOBRC009 Amphipoda	9 3 LN046 Lower Shaw River S2 SS AB	Lower Shaw River S1 SS ,	JF19 RC13MEH0041-20160119-01 Amphipoda	10 S6-204 Paramelitidae	Q3 WBGW010	W6 Chykaeta Ethel Creek
JY14 1812 Amphipoda Paramelitidae		0.003	0.003	0.015	0.014	0.015	0.015	0.015	0.016	0.016	0.015	0.015	0.016	0.017	0.014	0.016	0.014	0.015	0.015	0.014	0.014	0.015	0.018	0.014	0.019	0.015	0.016	0.016	0.015	0.017	0.019	0.015
JY15 1910 Amphipoda Paramelitidae	0.009		0.002	0.016	0.014	0.016	0.015	0.015	0.015	0.016	0.015	0.016	0.016	0.016	0.015	0.016	0.014	0.015	0.015	0.014	0.014	0.015	0.018	0.014	0.019		0.016	0.016	0.015	0.017	0.019	0.015
JY16 1966 Amphipoda Paramelitidae	0.006	0.003		0.016	0.014	0.015	0.015	0.015	0.015	0.016	0.015	0.016	0.016	0.016	0.015	0.016	0.014	0.015	0.015	0.014	0.014	0.015	0.018	0.014	0.019	0.015	0.016	0.016	0.015	0.017	0.019	0.015
JY17 1971 Amphipoda Paramelitidae	0.181	0.181	0.181		0.014	0.015	0.015	0.015	0.015	0.016	0.015	0.015	0.015	0.015	0.014	0.015	0.015	0.015	0.015	0.014	0.014	0.015	0.016	0.014	0.019	0.015	0.016	0.017	0.014	0.015	0.020	0.014
JY18 2352 Amphipoda Paramelitidae	0.177	0.178	0.175	0.187		0.014	0.015	0.015	0.015	0.015	0.015	0.015	0.014	0.014	0.015	0.014	0.016	0.014	0.013	0.013	0.014	0.013	0.016	0.013	0.018	0.014	0.014	0.017	0.013	0.016	0.021	0.015
AM15 Paramelitidae sp B12 Christmas Creek	0.207	0.208	0.205	0.180	0.188		0.013	0.016	0.016	0.016	0.014	0.016	0.016	0.015	0.016	0.016	0.014	0.015	0.015	0.012	0.013	0.014	0.018	0.016	0.020	0.016	0.018	0.016	0.013	0.017	0.021	0.016
AM2 Paramelitidae sp B14 Investigator	0.219	0.223	0.220	0.219	0.226	0.214		0.016	0.015	0.017	0.016	0.015	0.015	0.018	0.015	0.018	0.015	0.017	0.015	0.014	0.015	0.015	0.017	0.015	0.020	0.015	0.017	0.018	0.015	0.015	0.021	0.016
AM4 Paramelitidae sp Mindy	0.226	0.228	0.225	0.207	0.222	0.193	0.211		0.016	0.015	0.014	0.015	0.017	0.017	0.017	0.015	0.016	0.017	0.017	0.016	0.014	0.016	0.019	0.015	0.019	0.017	0.016	0.017	0.017	0.018	0.020	0.017
BX32 PES-5173 Paramelitidae MH1	0.202	0.199	0.201	0.194	0.191	0.178	0.204	0.195		0.014	0.016	0.016	0.018	0.017	0.016	0.015	0.018	0.015	0.017	0.016	0.015	0.015	0.016	0.017	0.019	0.018	0.017	0.017	0.014	0.015	0.020	0.016
DQ838031 Maarrka etheli	0.233	0.236	0.236	0.245	0.214	0.231	0.229	0.231	0.233		0.017	0.018	0.018	0.014	0.015	0.014	0.016	0.016	0.015	0.015	0.017	0.015	0.017	0.017	0.022	0.018	0.018	0.017	0.017	0.019	0.024	0.016
DQ838032 Maarrka weeliwollii	0.170	0.173	0.173	0.205	0.184	0.199	0.234	0.225	0.216	0.194		0.006	0.014	0.015	0.015	0.016	0.013	0.017	0.015	0.013	0.005	0.015	0.019	0.015	0.021	0.015	0.016	0.016	0.013	0.018	0.021	0.014
DQ838033 Maarrka weeliwollii	0.178	0.183	0.182	0.219	0.190	0.201	0.234	0.229	0.224	0.201	0.030		0.015	0.016	0.015	0.016	0.015	0.017	0.015	0.013	0.007	0.016	0.018	0.015	0.021	0.015	0.017	0.016	0.014	0.018	0.021	0.015
DZ24 GW05.0413-04	0.206	0.209	0.209	0.206	0.201	0.212	0.239	0.237	0.224	0.230	0.214	0.218		0.016	0.015	0.017	0.015	0.014	0.011	0.016	0.014	0.016	0.019	0.011	0.017	0.005	0.010	0.017	0.012	0.014	0.023	0.016
EF118194 Yilgarus sp	0.197	0.199	0.199	0.217	0.191	0.216	0.254	0.243	0.202	0.236	0.211	0.221	0.209		0.016	0.015	0.017	0.015	0.017	0.014	0.014	0.016	0.019	0.016	0.019	0.016	0.016	0.018	0.016	0.016	0.021	0.016
EF118232 Yilgarus sp	0.212	0.213	0.212	0.172	0.190	0.194	0.223	0.212	0.176	0.238	0.200	0.205	0.209	0.197		0.015	0.015	0.014	0.017	0.015	0.015	0.015	0.017	0.015	0.021	0.015	0.018	0.015	0.017	0.016	0.020	0.016
EF558852 Paramelitidae sp. 3	0.199	0.196	0.198	0.222	0.191	0.213	0.242	0.236	0.219	0.202	0.194	0.203	0.207	0.211	0.202		0.018	0.015	0.015	0.016	0.015	0.014	0.018	0.015	0.022	0.017	0.016	0.015	0.017	0.017	0.025	0.014
FU1 Paramelitidae sp KGST0006	0.204	0.202	0.202	0.210	0.223	0.175	0.217	0.184	0.194	0.226	0.217	0.224	0.225	0.233	0.197	0.211		0.016	0.015	0.015	0.012	0.014	0.019	0.017	0.021	0.015	0.017	0.014	0.015	0.019	0.010	0.016
G187 Amphipoda 100476 AC	0.219	0.223	0.221	0.192	0.215	0.203	0.227	0.210	0.222	0.244	0.224	0.224	0.208	0.213	0.184	0.212	0.213		0.014	0.018	0.016	0.015	0.017	0.014	0.021	0.014	0.015	0.017	0.015	0.017	0.021	0.015
G496 111310 Paramelitidae sp NS AA	0.208	0.211	0.210	0.208	0.205	0.212	0.233	0.215	0.212	0.226	0.220	0.226	0.079	0.219	0.205	0.211	0.229	0.208		0.015	0.015	0.015	0.018	0.011	0.020	0.011	0.009	0.016	0.013	0.014	0.023	0.015
GK24 MB13YB010-180514-02	0.178	0.175	0.175	0.208	0.183	0.190	0.218	0.221	0.204	0.205	0.140	0.145	0.208	0.202	0.187	0.179	0.212	0.207	0.212		0.011	0.014	0.019	0.014	0.019	0.016	0.016	0.016	0.014	0.019	0.023	0.016
GK91 TS3DCP1-3	0.158	0.161	0.161	0.199	0.174	0.193	0.224	0.218	0.205	0.193	0.017	0.046	0.210	0.205	0.197	0.184	0.210	0.219	0.211	0.117		0.013	0.019	0.014	0.021	0.014	0.016	0.014	0.013	0.018	0.021	0.014
GO82 MNEW1upstream Paramelitidae sp. B25 (nr. B16)	0.222	0.219	0.221	0.190	0.199	0.178	0.215	0.193	0.172	0.225	0.198	0.198	0.221	0.227	0.166	0.208	0.180	0.218	0.221	0.191	0.180		0.018	0.015	0.020	0.016	0.018	0.016	0.016	0.016	0.018	0.015
GU111906 Kruptus linnaei	0.242	0.244	0.244	0.230	0.248	0.253	0.248	0.251	0.234	0.250	0.240	0.240	0.232	0.244	0.253	0.226	0.234	0.253	0.226	0.238	0.236	0.257		0.018	0.024	0.018	0.018	0.019	0.017	0.019	0.020	0.016
IS39 RHCMB042 20150910 02 Amphipoda	0.207	0.211	0.210	0.196	0.189	0.217	0.228	0.216	0.219	0.236	0.220	0.223	0.081	0.216	0.186	0.214	0.241	0.203	0.089	0.219	0.211	0.216	0.244		0.016	0.011	0.013	0.016	0.012	0.014	0.023	0.015
IT25 BHRC433.20151014 01 Amphipoda	0.195	0.195	0.195	0.200	0.173	0.238	0.240	0.228	0.209	0.214	0.183	0.195	0.155	0.195	0.224	0.214	0.231	0.244	0.173	0.195	0.180	0.221	0.244	0.166		0.017	0.017	0.023	0.016	0.017	0.022	0.023
IV115 TOBRC009 Amphipoda	0.199	0.202	0.202	0.209	0.204	0.218	0.232	0.240	0.220	0.229	0.213	0.217	0.013	0.218	0.208	0.208	0.218	0.209	0.083	0.213	0.210	0.219	0.228	0.081	0.149		0.011	0.017	0.012	0.014	0.022	0.016
J9 3 LN046 Lower Shaw River S2 SS AB	0.215	O.E.I	0.217	0.204	0.219	0.230			0.220	0.228	0.217	0.217		0.221	0.197	0.200	0.226	0.223	0.076	0.228	0.210	0.199	0.239	0.111	0.173	0.109		0.016	0.013	0.014	0.021	0.015
J9 7 LN040 Lower Shaw River S1 SS AD	0.219		0.219	0.210		0.191			0.192	0.213	0.195	0.204	_	0.215	0.182	0.208	0.182	0.219	0.221	0.193	0.189	0.213	0.243	0.232	0.223	0.215	0.224		0.017	0.018	0.018	0.018
JF19 RC13MEH0041-20160119-01 Amphipoda	0.206		0.208	0.203	0.183	0.205	0.221	0.201	0.189	0.223	0.201	0.201	0.126	0.199	0.174	0.217	0.210	0.207	0.125	0.204	0.191	0.203	0.217	0.128	0.151	0.130	0.134	0.204		0.013	0.021	0.016
L10 S6-204 Paramelitidae	0.231	0.233	0.233	0.212	0.219	0.234	0.238	0.217	0.222	0.228	0.210	0.207	0.136	0.236	0.193	0.228	0.240	0.202	0.143	0.214	0.207	0.219	0.236	0.136	0.166	0.133	0.158	0.232	0.143		0.022	0.017
Q3 WBGW010	0.231	0.231	0.228	0.225	0.255	0.210	0.218		0.225	0.236	0.231	0.241	0.239	0.241	0.225	0.249	0.037	0.223	0.241	0.252	0.231	0.204	0.239	0.268	0.228	0.231	0.240	0.191	0.233	0.255	!	0.022
W6 Chykaeta Ethel Creek Estimates of Evolutionary Divergence between Sequences	0.240	0.238	0.240	0.219	0.211	0.232	0.218	0.215	0.217	0.237	0.220	0.233	0.221	0.233	0.205	0.205	0.220	0.213	0.223	0.214	0.208	0.183	0.263	0.222	0.243	0.224	0.210	0.236	0.223	0.226	0.239	ı

Estimates of Evolutionary Divergence between Sequences

The number of base differences per site from between sequences are shown. Standard error estimate(s) are shown above the diagonal. The analysis involved 34 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for [1.] Tamura K., Stecher G., Peterson D., Filipski A., and Kumar S. (2013). MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Molecular Biology and Evolution 30: 2725-2729.

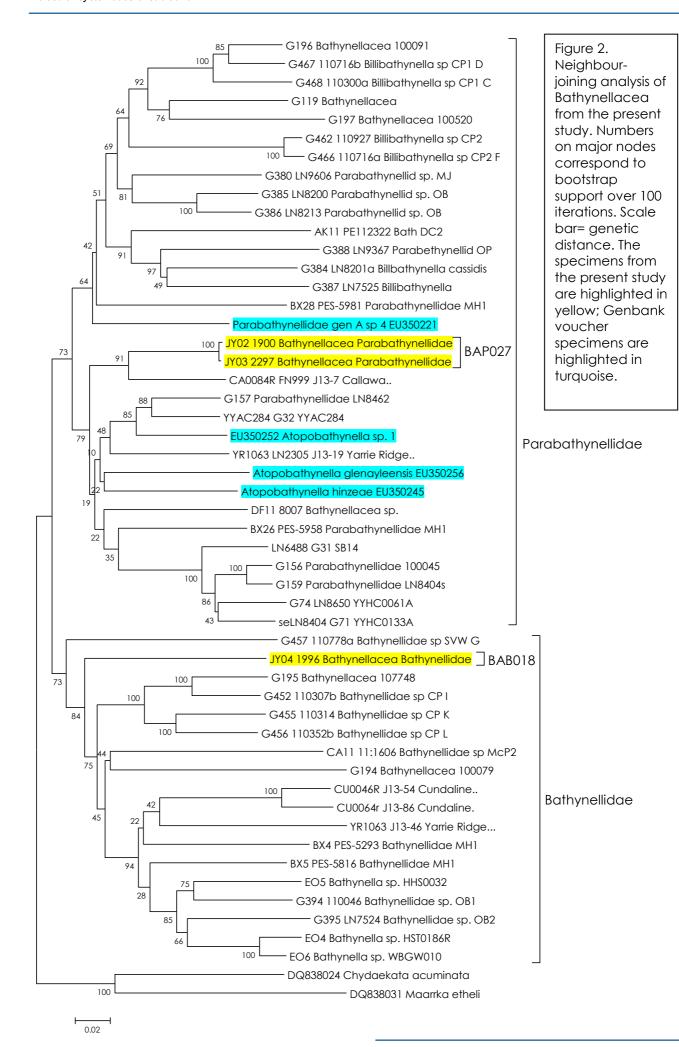
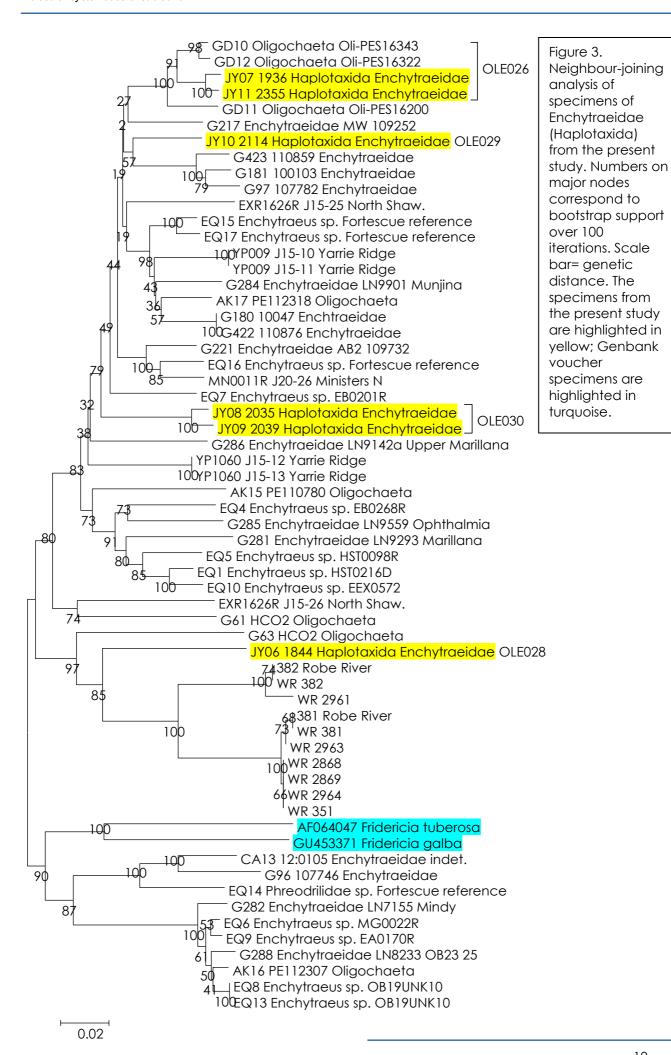


TABLE 2. Bathynellacea Distance Matrix																																													
		athynellacea Bathynellidae	ğ D	mella hinzeae EU350245	58 Parabathynellidae MH1	81 Parabathynellidae MH1	3 Bathynellidae MH1		9 J13-7 Callaw	≌ I;	-54	-86 Cundaline. athynellacea sp.	ella sp. HST0186R	əlla sp. HHS0032	iella sp. WBGW010	Atopobathynella sp. 1	Nate1C4	athynellidae 100045	athynellidae LN8462	athynellidae LN8404s	nellacea 100079	ellac	nellacea 100091	100520	6 Parabathynellid sp. MJ	Bilbathynella cassi	arabathynellid sp.	3 Parabathynellid sp. OB	7 Parabethynellid OP	s Bathynellidae sp. OB1	4 Bathynellidae sp. OB2	o Bathynellida	Bathynellidae sp C		a Bathynellida Billihothynella	a Billibathyn	Je Je	bathynella sp CP1	YYHC0061A	SB14	ellidae gen A sp 4 EU350221	71 YYHC0133A	46 Yarrie	805 J13-19 Yamie Ridge	32 YYAC284
Specimen ID	JY02 1900 Bc JY03 2297 Bc	JY04 1996 Bathy	AK11 PE112322 Atopobathynel	Atopobathy	BX26 PES-59	BX28 PES-5981	BX4 PES-5293	BX5 PES-581	CA0084R FN	CA11 11:1606		CUUU64r JII3-	Sathyn	EO5 Bathynella	EO6 Bathyne	EU350252 Aħ	G119 LCOI F	G156 Parab	G157 Parabath	G159 Parabi	G194 Bathyr	G195 Bathyr	G196 Bathyr	G197 Bathyr	G380 LN9.606 Parabat	G384 LN8201a	G385 LN8200 P.	G386 LN8213 G387 LN7525	C388 LN9367	G394 110046	G395 LN752	G452 110307	G455 110314	G456 110352b1	G457 1107780 G462 110927	G466 110716	G467 110716b Billi	G468 110300	G74 LN8650	LN6488 G31	Parabathyne	seLN8404 G7	1063 J13-	YR 1063 LN2305	YY AC284 G32 `
JY02 1900 Bathynellacea Parabathynellidae	0.002	0.016	0.019 0.0	0.01	5 0.014	0.016	0.018	0.016	0.013	0.017	0.023	.024 0.	0.0	7 0.0	6 0.01	7 0.01	6 0.01	8 0.02	0.017	7 0.020	0.020	0.017	0.018	0.019	0.017	0.015	0.016	0.015 0.0	17 0.01	0.01	6 0.015	0.017	0.015	0.015	0.015 0.	.016 0.0	0.0	0.01	0.01	7 0.018	0.017	0.018	0.018	0.017	0.016
JY03 2297 Bathynellacea Parabathynellidae JY04 1996 Bathynellacea Bathynellidae	0.003 0 0.236 0.236	0.016	0.019 0.0	0.014	4 0.014 8 0.014	0.016	0.018	0.016	0.013 (	0.017 (	0.023 (	0.024 0.0	20 0.0	18 0.0	6 0.01	6 0.01	8 0.01	9 0.01	9 0.017	7 0.019	0.019	0.017	0.018	0.019	0.016	0.015	0.015	0.015 0.0	16 0.01	18 0.01	5 0.016	0.017	0.015	0.015 0	0.014 0.	0.0 610.	17 0.0	016 0.013	0.01	7 0.018 8 0.019	0.017	0.018	0.018 (	0.017	0.018
AK11 PE112322 Bath DC2	0.233 0.231 0	0.261	0.0	019 0.02	1 0.016	0.017	0.020	0.021	0.018	0.021 0	0.024	.024 0.	024 0.0	21 0.0	9 0.02	21 0.01	9 0.02	0 0.02	0.019	9 0.020	0.021	0.019	0.021	0.020	0.017	0.017	0.015	0.016 0.0	16 0.01	17 0.02	0 0.019	0.020	0.020	0.017 0	0.018 0.	.016 0.0	0.0	020 0.019	0.019	9 0.019	0.020	0.019	0.021	0.017	0.019
Atopobathynella glenayleensis EU350256	0.177 0.175		).224	0.01	6 0.016	0.018	0.017	0.024	0.019	0.019	0.021	.021 0.	18 0.0	21 0.0	0.02	0.01	6 0.02	0.01	8 0.01	6 0.018	0.023	0.023	0.017	0.018	0.018	0.019	0.017	0.017 0.0	20 0.02	20 0.02	0.020	0.023	0.019	0.019 0	0.020 0.	.018 0.0	18 0.0	0.019	0.01	6 0.018	0.017	0.017	0.021	0.015	0.015
Atopobathynella hinzeae EU350245	0.144 0.142 0		0.240 0.1	159	0.017	0.020	0.022	0.023	0.019	0.020	0.024	.024 0.	0.0	22 0.0	22 0.02	22 0.01	6 0.01	8 0.02	0.01	6 0.020	0.025	0.024	0.019	0.021	0.017	0.019	0.017	0.019 0.0	19 0.02	20 0.02	2 0.022	0.022	0.021	0.019 0	0.018 0.	.018 0.0	0.0	0.019	0.019	9 0.018	0.016	0.019	0.025	0.020	0.015
BX26 PES-5958 Parabathynellidae MH1 BX28 PES-5981 Parabathynellidae MH1	0.168 0.168 0	U.LLU	0.236 0.1	180 0.178	8 7 0.216	0.015	0.017	0.017	0.015	0.017 0	0.021	.021 0.0	0.0	0.0	7 0.01	8 0.01	6 0.01	/ 0.01	6 0.017	/ 0.015	0.018	0.016	0.017	0.020	0.014	0.015	0.016	0.015 0.0	14 0.01	16 0.01	/ 0.017	0.015	0.016	0.015	0.015 0.	.014 0.0	0.0	0.01	0.01	5 0.015	0.017	0.015	0.018	0.014	J.016
BX4 PES-5981 Parabatnynellidae MH1 BX4 PES-5293 Bathynellidae MH1	0.259 0.258 0			219 0.20.		0.296	0.018	0.019	0.017	0.017	0.022	.023 0.1	22 0.0	14 0.0	3 0.01	5 0.01	9 0.02	1 0.01	9 0.019	9 0.019	0.017	0.018	0.018	0.021	0.018	0.015	0.019	0.018 0.0	19 0.01	17 0.01	4 0.015	0.017	0.016	0.015 0	0.016 O.	.014 0.0	0.0	0.013	7 0.02	0.020	0.018	0.020	0.017	0.018	0.020
BX5 PES-5816 Bathynellidae MH1	0.236 0.236 0			253 0.240	_				0.018	0.016	0.021	.021 0.0	24 0.0	13 0.0	4 0.01	4 0.02	0 0.02	1 0.02	0.02	1 0.021	0.018	0.018	0.021	0.021	0.019	0.018	0.019	0.018 0.0	19 0.01	19 0.01	5 0.013	0.016	0.016	0.016	0.016 0.	.018 0.0	0.0	0.01	5 0.02	2 0.021	0.021	0.022	0.014	0.020	0.022
CA0084R FN999 J13-7 Callawa	0.108 0.108 0	0.200	7.LLU U. I	74 0.17	1 0.152	0.219	0.261	0.243	(	0.019	0.021	.022 0.	20 0.0	19 0.0	7 0.01	9 0.02	0.02	1 0.02	0.019	9 0.020	0.019	0.016	0.018	0.021	0.015	0.016	0.016	0.0	17 0.01	17 0.01	7 0.017	0.017	0.017	0.015	0.015 0.	.017 0.0	0.0	0.01	0.01	7 0.020	0.017	0.020	0.016	0.015	0.020
CA11 11:1606 Bathynellidae sp McP2	0.264 0.264 0			259 0.25	3 0.263	0.274	0.234	0.235	0.279	C	0.023	.024 0.	0.0	17 0.0	8 0.01	6 0.01	9 0.02	2 0.02	0.018	8 0.019	0.020	0.019	0.021	0.021	0.017	0.017	0.017	0.017	18 0.01	19 0.01	6 0.019	0.017	0.017	0.018 0	0.019 0.	.017 0.0	0.0	0.018	0.02	1 0.019	0.020	0.021	0.018	0.017	0.019
CU0046R J13-54 Cundaline	0.274 0.271 0	0.226	0.273 0.2	260 0.27	9 0.267	0.307		0.214	0.245	).264		.010 0.0	0.0	21 0.0	0.02	0.02	1 0.02	3 0.02	4 0.022	2 0.022	0.025	0.021	0.022	0.023	0.023	0.023	0.022	0.023 0.0	24 0.02	23 0.02	0.019	0.023	0.022	0.020 0	0.022 0.	.023 0.0	0.0	0.024	4 0.02	3 0.022	2 0.023	0.023	0.021	0.023	J.021
CU0064r J13-86 Cundaline. DF11 8007 Bathynellacea sp.	0.283 0.281 0	0.224 0	0.282 0.2	78 0.2/	9 0.265 3 0.176	0.312		0.219		u	0.057	269	0.0	20 0.0	9 0.02	21 0.02	0.02	2 0.02	0.022	2 0.021	0.024	0.021	0.022	0.025	0.024	0.023	0.022 (	0.023 0.0	23 0.02	22 0.02	0 0.019	0.023	0.021	0.019 0	0.021 0.	017 0.0	122 0.0	0.023	0.02	2 0.02	0.023	0.022	0.020 0	0.022	0.020
EO4 Bathynella sp. HST0186R	0.147 0.147 0			240 0.25	5 0.176	0.243		0.233	0.167	247 0	202 0	207 0	0.0.	0.0	2 0.02	7 0.02	1 0.01	1 0.01	2 0.010	0.010	0.028	0.022	0.021	0.020	0.021	0.022	0.017	0.018 0.0	18 0.02	19 0.02	2 0.024	0.023	0.021	0.020 0	0.024 0.	018 0.0	119 0.0	0.020	7 0.01	1 0.022	0.021	0.017	0.026	0.021	0.020
EO5 Bathynella sp. HHS0032	0.246 0.244 0			244 0.25	5 0.233	0.291	0.197	0.168	0.249	0.251 0	0.205	.202 0.:	72 0.1	30	0.01	3 0.02	0 0.02	0 0.02	0.02	1 0.021	0.019	0.016	0.020	0.023	0.017	0.018	0.018	0.017 0.0	18 0.01	18 0.01	1 0.013	0.016	0.017	0.015 0	0.016 0.	.016 0.0	0.0	017 0.01	5 0.020	0 0.022	2 0.020	0.021	0.014	0.018	0.022
EO6 Bathynella sp. WBGW010	0.237 0.239 0	0.216	0.268 0.2	238 0.240	0.236	0.281	0.199	0.153	0.248	0.235	0.188	.193 0.:	255 0.0	39 0.13	33	0.02	1 0.02	0.02	2 0.020	0.021	0.018	0.016	0.021	0.022	0.017	0.018	0.017	0.0	18 0.01	18 0.01	4 0.013	0.016	0.017	0.015 0	0.015 0.	.017 0.0	0.0	0.017	7 0.02	1 0.021	0.022	0.019	0.016	0.019	0.022
EU350252 Atopobathynella sp. 1	0.154 0.152 0	0.210	,, <u>,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,</u>	59 0.14	1 0.100			0.232	0.150	0.265	0.255	.264 0.	61 0.2	0.2	0.LC	32	0.01	8 0.01	9 0.013	3 0.018	0.025	0.020	0.017	0.017	0.018	0.018	0.018	0.0	19 0.01	18 0.02	0.020	0.021	0.019	0.017 0	0.019 0.	.020 0.0	0.0	0.018	0.01	7 0.017	7 0.019	0.017	0.022	0.017	0.013
G119 LCOI Plate1C4	0.208 0.205 0		,.LLO 0.L	225 0.22	. 0.20	-		0.268	0.225 (	0.299 0		.294 0.:		, 0.2	0 0	0.21	•	0.02	0.018	8 0.020	0.025	0.021	0.019	0.017	0.016	0.020	0.015	0.016 0.0	21 0.01	19 0.02	2 0.019	0.021	0.020	0.019 0	0.018 0.	.019 0.0	020 0.0	0.018	0.020	0 0.019	0.016	0.019	0.025	0.019	0.019
G156 Parabathynellidae 100045 G157 Parabathynellidae LN8462	0.200 0.198 0		0.242 0.1	82 0.19	8 0.161 2 0.149		0.276	0.230	0.195 (	0.253 0	0.276	.267 O.	68 0.2	10 0.2	88 0.23 18 0.23	88 0.18	2 0.24	2 0 15	0.013	0.008	0.022	0.022	0.019	0.017	0.020	0.020	0.018	0.019 0.0	10 0.02	20 0.02	0.021	0.021	0.020	0.020 0	0.023 0.	010 0.0	20 0.0	0.020	0.01	7 0.013	0.020	0.012	0.022 (	0.014	0.012
G159 Parabathynellidae LN8404s	0.198 0.196 0			82 0.20	3 0.163	0.242	0.233	0.238	0.143	0.251 0	0.274	.264 0.	63 0.2	0.2	0.20	0.18	8 0.24	6 0.02	9 0.169	9	0.023	0.020	0.017	0.017	0.017	0.019	0.017	0.018 0.0	21 0.02	0.02	2 0.021	0.017	0.020	0.019 0	0.020 0.	.017 0.0	18 0.0	018 0.02	0.01	3 0.013	3 0.017	0.012	0.022	0.018	0.017
G194 Bathynellacea 100079	0.265 0.262 0	_	0.299 0.2	298 0.293	3 0.281	0.300		0.246	0.269	0.256	0.267		04 0.2	56 0.2		6 0.29	0 0.32			1 0.290	1	0.018	0.024	0.022	0.016	0.017	0.017	0.018 0.0	20 0.01	18 0.01	9 0.017	0.018	0.018	0.018 0	0.018 0.	.017 0.0	0.0	021 0.019	0.02	2 0.023	3 0.023	0.023	0.018	0.017	0.024
G195 Bathynellacea 107748	0.225 0.225 0	0.219	0.253 0.2	262 0.23	1 0.221	0.261	0.216	0.209	0.219	0.219	0.219	.214 0.:	23 0.2	30 0.23	35 0.21	5 0.22	6 0.26	9 0.22	0.207	7 0.229	0.235		0.020	0.022	0.016	0.016	0.016	0.017 0.0	18 0.01	17 0.01	7 0.018	0.010	0.014	0.014 0	0.017 0.	.020 0.0	020 0.0	0.018	0.02	2 0.022	0.020	0.022	0.019	0.016	0.022
G196 Bathynellacea 100091	0.198 0.196			200 0.21	1 0.234	0.190	0.276	0.259	0.214	0.273	0.286	.290 0.:	238 0.2	78 0.2	78 0.27	1 0.22	8 0.14	3 0.24	2 0.230	0.236	0.300	0.271		0.019	0.016	0.018	0.015	0.0	20 0.01	18 0.02	0.020	0.022	0.020	0.017 0	0.019 0.	.016 0.0	0.0	0.012	0.018	8 0.018	0.016	0.018	0.023	0.019	0.020
G197 Bathynellacea 100520	0.228 0.225 0	0.270	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	234 0.24	2 0.245	0.232	0.282	0.305	0.255 0	0.303 0	0.333 (	.331 0.:	264 0.3	0.0	1 0.29	2 0.25	3 0.15	6 0.25	9 0.242	2 0.242	0.329	0.281	0.184		0.015	0.018	0.016	0.0	20 0.01	18 0.02	2 0.022	0.021	0.019	0.019 0	0.019 0.	.020 0.0	020 0.0	0.019	0.02	1 0.019	0.017	0.020	0.024	0.019	3.019
G380 LN9606 Parabathynellid sp. MJ G384 LN8201 a Billbathynella cassidis	0.199 0.199 0	0.236	0.219 0.2	211 0.20	3 0.200 3 0.231	0.216		0.254	0.200 (	0.284 0	0.283	.298 0.:	09 0.2	J1 (0.2)	0.23	6 0.21	3 0.19 5 0.21	0 0.21	0.200	0 0.211	0.274	0.232	0.186	0.196 0.217	0.170	0.015	0.013 (	0.012 0.0	13 0.01	15 0.01	7 0.017	0.017	0.018	0.017 0	0.01/ 0.	.015 0.0	0.0	015 0.013	0.020	0 0.019	0.016	0.019	0.017 (	0.016	0.017
G385 LN8200 Parabathynellid sp. OB	0.222 0.222 0	0.257	7.17 1 0.2	96 0.22	5 0.231	0.211		0.246	0.214 (	271 0	0.295	.300 0.	21 0.2		1 0.25	4 0.21		0 0.24		0.233	0.243		0.203	0.205	0.177	0 192	0.014	0.014 0.0	15 0.01	17 0.01	7 0.017	0.016	0.018	0.013 0	0.015 0	013 0.0	114 0.0	0.013	4 0.01	8 0.017	7 0.014	0.016	0.017	0.016	0.017
G386 LN8213 Parabathynellid sp. OB	0.191 0.191 0		0.197 0.2	70 0.20	4 0.186	-			0.203	_	0.283	.293 0.:	0.2		_		_	2 0.21	9 0.203	3 0.219	0.269	_	0.159	0.198	0.144	0.172	0.066	0.0	16 0.01	16 0.01	6 0.016	0.016	0.018	0.016	0.016 0.	.015 0.0	015 0.0	015 0.013	0.01	6 0.016	0.016	0.016	0.018	0.016	0.017
G387 LN7525 Billibathynella	0.230 0.233 0			255 0.24	2 0.218	0.212	0.256		0.218		0.302	.300 0.:						2 0.24		4 0.257	0.301	0.259	0.215	0.238	0.195	0.155		0.191	0.01	14 0.01	7 0.019	0.017	0.016	0.014	0.015 0.	.016 0.0	0.0	0.01	0.020	0.022	0.019	0.020	0.019	0.018	0.018
G388 LN9367 Parabethynellid OP	0.244 0.243	0.272	0.212 0.2	246 0.25	5 0.240	0.235		0.268	0.226	0.286	0.281	.274 0.:		JO   U.L.	0.25	70 U.L.	4 0.20			2 0.259	0.273	0.253	0.194	0.230	0.202	0.164	0.216	0.221 0.1	79	0.01	8 0.017	0.017	0.016	0.015 0	0.018 0.	.017 0.0	0.0	0.01	0.02	1 0.020	0.018	0.021	0.019	0.016	ე.019
G394 110046 Bathynellidae sp. OB1	0.246 0.244 0	0.221	0.282 0.2	232 0.23	8 0.231	0.275		0.166	0.241 (	0.238 0	0.186	.200 0.:	264 0.1	42 0.1	8 0.13	0.24		7 0.24 8 0.25		8 0.244 1 0.253	0.256	0.228	0.263	0.288	0.258	0.250	0.257	0.258 0.2	59 0.25	58	0.013	0.016	0.016	0.015 0	0.016 0.	016 0.0	0.0	0.017	7 0.02	2 0.020	0.021	0.021	0.014	0.019	0.022
G395 LN7524 Bathynellidae sp. OB2 G452 110307b Bathynellidae sp CP I	0.261 0.262 0			26/ 0.2/3 263 0.24	3 0.243 2 0.224	0.288	0.200	0.164	U.∠61 (		0.212 (		38 0.1	16 0.13	22 0.13	0.26				7 0.253	0.264	0.238	U.∠8U I	0.288	0.265 0.224	0.265	0.276	0.257 0.2	35 0.25	68 0.15 48 0.21	V U 330	0.019	0.017	0.015 0	0.016	0.0 110.	119 0.0	118 U.UI.	0.02	0.02	0.020	0.020	0.014	0.018	0.020
G452 1103076 Bathynellidae sp CP K	0.221 0.214 0	0.209	0.253 0.2	251 0.23	8 0.225	0.254	0.210	0.177	0.227	).212 C	0.224	.221 0.	36 0.2	29 0.2	28 0.21	6 0.23	2 0.27	2 0.21	3 0.217	7 0.225	0.237	0.135	0.257	0.276	0.238	0.260	0.235	0.238 0.2	29 0.25	52 0.27	6 0.232	0.136	0.012	0.013 0	0.015 0.	.018 0.0	18 0.0	017 0.018	3 0.02	1 0.020	0.021	0.020	0.017	0.018	0.021
G456 110352b Bathynellidae sp CP L	0.227 0.227 0	0.196	0.253 0.2	238 0.22	8 0.221	0.247	0.215	0.199	0.229	0.212 0	0.221	.214 0.:	26 0.2	22 0.2	9 0.20	0.21	3 0.25	9 0.21	9 0.215	5 0.219	0.243	0.132	0.240	0.280	0.226	0.245	0.240	0.246 0.2	25 0.23	33 0.22	6 0.226	0.137	0.098	0	0.015 0.	.016 0.0	0.0	015 0.01	0.019	9 0.017	7 0.020	0.019	0.018	0.016	0.019
G457 110778a Bathynellidae sp SVW G	0.237 0.236 0	0.243	0.256 0.2	244 0.22	3 0.231	0.267	0.253	0.241	0.242	0.272	0.262	.269 0.:	257 0.23	38 0.2	6 0.23	0.21	1 0.24	6 0.23	6 0.217	7 0.232	0.271	0.224	0.242	0.263	0.238	0.258	0.245	0.243 0.2	47 0.26	64 0.23	8 0.255	0.217	0.224	0.214	0.	.016 0.0	0.0	0.017	0.020	0.021	0.021	0.022	0.018	0.017	0.020
G462 110927 Billibathynella sp CP2	0.211 0.211 0	0.253	0.231 0.2	232 0.240	0.209			0.269	0.213	0.272	0.305	.000 0	48 0.2	79 0.2	,, O.L,		4 0.19			. 0.2.10	0.269	0.269	0.184	0.211	0.179	0.221	0.185	0.199 0.2	12 0.23	30 0.26		0.261	0.251	0.246 0	).270	0.0	0.0	0.013	0.018	8 0.017	0.016	0.016	0.019	0.017	ე.019
G466 110716a Billibathynella sp CP2 F	0.209 0.209 0			230 0.240		0.228			0.216		0.293		252 0.2				8 0.19	_		6 0.230	0.267	0.271	0.184		0.182	0.216		0.204 0.2	10 0.23				0.248		,, · · · · ·	.022	0.0	0.013	0.01	/ 0.017	0.017	0.016	0.019	0.018	J.020
G467 110716b Billibathynella sp CP1 D G468 110300a Billibathynella sp CP1 C	0.202 0.202 (		0.231 0.2	209 0.21	5 0.227 9 0.237	0.201	0.267	0.247	0.206 (	,.L/ / O	0.286	.200	38 0.2	59 0.2			8 0.15 8 0.14	0 0.22		4 0.232 0 0.238	0.285	0.266	0.063	0.211	0.180	0.211	0.166 (	0.163 0.2	10 0.20 22 0.20	0.26		0.254	0.243 (	0.245 0	0.259 0.	192 n i	94 0.0	0.01	0.018	9 0.017	0.017	0.018	0.020 (	0.01/	0.021
G74 LN8650 YYHC0061A	0.207 0.203 0	0.200	0.233 0.2	82 0.21	9 0.237	0.226	0.287	0.251	0.217	).2/7 U	0.201	.200 U. .279 N	76 0.2	59 N 2	2 0.20	9 0.18		5 0.23	7 0.240	2 0.238	0.271	0.246	0.001	0.194	0.102	0.255	0.163	0.1/7 0.2	62 N 24	57 O.26	2 0.2//	0.259	0.234	0.234 0	).238 N	234 0.1	74 U.C	236 0 24	0.01	0.013	0.018	0.017	0.017	0.017	0.015
LN6488 G31 SB14	0.193 0.191 0	0.218	0.255 0.1	72 0.18	2 0.155	0.231	0.275	0.231	0.201	0.264	0.261	.254 0.	63 0.2	37 0.2	9 0.23	35 0.17	6 0.23	9 0.08	0.172	4 0.082	0.287	0.225	0.243	0.249	0.205	0.243	0.214	0.208 0.2	60 0.25	52 0.21	6 0.241	0.224	0.224	0.222 0	0.226 0	224 0.2	26 0.2	243 0.24	3 0.08	8	0.019	0.011	0.022	0.019	0.015
Parabathynellidae gen A sp 4 EU350221	0.165 0.163	0.209	0.200 0.1	75 0.17	1 0.197	0.190	0.265	0.242	0.157	0.265 0	0.248	.262 0.	97 0.2	51 0.2	18 0.24	8 0.18	8 0.17	0 0.21	9 0.167	7 0.213	0.314	0.238	0.167	0.207	0.167	0.200	0.167	0.154 0.2	21 0.20	0.24	6 0.259	0.236	0.248	0.234 0	0.234 0.	.209 0.2	209 0.1	177 0.184	4 0.220	0 0.222	2	0.018	0.023	0.019	0.018
seLN8404 G71 YYHC0133A	0.195 0.192		0.240 0.1	72 0.10	8 0.161	0.228	0.270	0.243	0.207	0.266	0.281	.274 0.	61 0.2	19 0.2	0.24			6 0.06		1 0.065	0.305	0.236	0.234	0.259	0.220	0.262	0.215	0.213 0.2	66 0.26	64 0.24		0.238	0.226	0.222 0	0.234 0.	.234 0.2	243 0.2	234 0.23	0.07	1 0.071	0.222		0.023	0.020	0.014
YR1063 J13-46 Yarrie Ridge	0.286 0.290		7.274 0.2	276 0.30	5 0.279	0.298	0.203	0.195	0.272	0.253	0.202	.207 0.:	98 0.20	02 0.18	36 0.20	0.29		7 0.29		2 0.298	0.248	0.256	0.283	0.314	0.296	0.282	0.293	0.283 0.2	77 0.28	31 0.17		0.240	0.254	0.251 0	).285 0.	.285 0.2	82 0.2	282 0.283	0.32	7 0.304	0.286	0.314	(	0.016	0.022
YR1063 LN2305 J13-19 Yarrie Ridge	0.165 0.165 0		0.208 0.1		0.148			0.2 10					64 0.2					0.18		2 0.179		0.217	0.219	0.236	0.200		0.195		27 0.23	32 0.25		0.222	0.232				235 0.2	216 0.23	0.10		0.171	0.181	0.272	0.116	J.018
YYAC284 G32 YYAC284 Estimates of Evolutionary Divergence between Se	0.150 0.152 0	U.219 (	J.224 (). I	154 0.13	/ [0.156	0.200	0.268	U.24/	U.14/ (	J.2/6 (	J.248 (	.255 0.	/4 U.2	oo [U.2:	)/ [U.24	io [0.09.	5 U.20	7 [0.18	4 U.U/8	810.181	0.282	U.22/	U.224	U.243	U.2U/	U.213	U.19U (	0.184 0.2	ან 0.24	17 U.24	JU.268	0.215	U.236	0.230 0	).224 ().	.232 0.2	34 U.2	234 0.230	0.1/	5[U.1/2	2 0.165	0.163	U.294 (	บ.118	

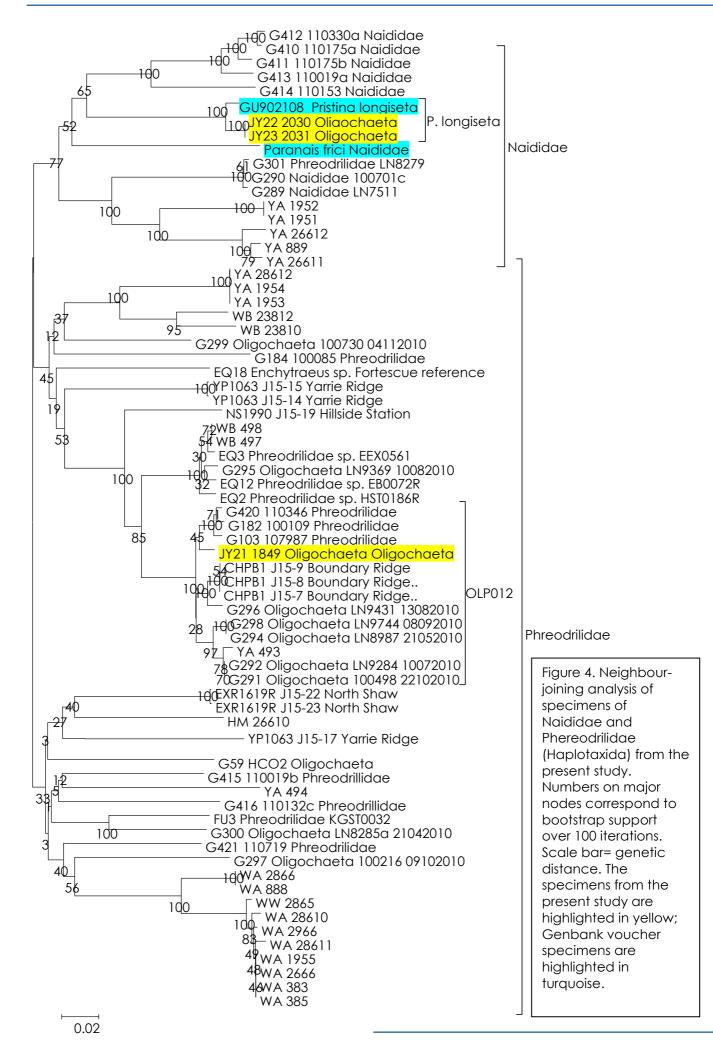
Estimates of Evolutionary Divergence between Sequences
The number of base differences per site from between sequences are shown. Standard error estimate(s) are shown above the diagonal. The analysis involved 52 nucleotide sequences. Consider a Standard error estimate(s) are shown as the diagonal and the sequence pair. There were a total of 834 positions in the final dataset. Evolutionary Genetics Analysis version 6.0. Molecular Biology and Evolution 30: 2725-2729.

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TABLE 3. Enchytraeidae Distance Matrix		1 1	т т																	т т.													
Specimen ID	Y06 1844 Hapiolaxida Enchytraeidae Y07 1936 Hapiolaxida Enchytraeidae	708 2035 Haplotaxida Enchytraeidae 709 2039 Haplotaxida Enchytraeidae	Y 10 21 14 Haplotaxida Enchytraeidae	Y I I 2355 Haplotaxida Enchyltaeidae 81 Robe River	82. Robe River LF064047 Fridericia Iuberosa	.K15 PE110780 Oligochaeta	K16 PE112307 Oligochaeta K17 PE112318 Oligochaeta	CA13 12:0105 Enchytraeldae Indet. Q1 Enchytraeus sp. HST0216D		Q5 Enchytraeus sp. HST0098R Q6 Enchytraeus sp. MG0022R	Q7 Enchytraeus sp. 680201 R Q8 Enchytraeus sp. O819UnK10 Q9 Enchytraeus sp. EA0170R	Q10 Enchytraeus sp. EEX0572 Q13 Enchytraeus sp. OB 19 UNK 10	Q14 Phreodilidae sp. Fortescue reference Q15 Enchytraeus sp. Fortescue reference	Q16 Enchyltaeus sp. Fortescue reference	Q17 Enchytraeus sp. Fortescue reference XR1 626R J15-25 North Shaw.	XR1626R J15-26 North Shaw. S61 HCO2 Oligochaeta	5180 10047 Enchtraeidae	3181 100103 Enchytraeidae	2217 Enchytraeidae MW 109252 2221 Enchytraeidae AB2 109732	2281 Enchytraeidae LN9293 Marillana 5282 Enchytraeidae LN7155 Mindy Coandine	2284 Enchytraeidae LN9901 Munjina	2285 Enchytraeidae LN9559 Ophthalmia 2286 Enchytraeidae LN9142a Upper Manillanc	5288 Enchytraeidae LN8233 OB23 25 5422 1 1087 & Enchytraeidae	5423 1 10859 Enchytraeidae	59 & 1077 4& Enchytraeidae 597 107782 Enchytraeidae	5D 10 Oligachaeta Oli-PES 1 6343 5D 11 Oligachaeta Oli-PES 1 6200	5D12 Oligochaeta Oli-PES1 6322	5U45337 I Fridericia galba ANOO11R J20-26 Ministers N	VR 2869 VR 2869	VR 2961	YR 2964	rR 351 POO9 J15-10 Yorrie Ridge POO9 J15-11 Yornie Ridge	P1060 J15-12 Yarrie Ridge P1060 J15-13 Yarrie Ridge
JY06 1844 Haplotaxida Enchytraeidae	0.014	0.014 0.014	0.014	0.014 0.014	0.017 0.01	4 0.013	0.014 0.014	0.016 0.013	0.014	0.014 0.014	0.013 0.014 0.014	4 0.013 0.014	0.015 0.013	3 0.013	0.014 0.014	0.015 0.013 0	013 0.0	14 0.013 0	0.013 0.012	0.014 0.0	14 0.015	0.012 0.013	0.015 0.014	0.013	0.015 0.013	0.014 0.013	0.014	0.014 0.014	0014 0014	0.017 0	014 0.014	0.014 0.013 0.012	3 0 014 0 014
JY07 1936 Haplotaxida Enchytraeidae	0.163	0.011 0.010	0.010	0.004 0.019	0.016 0.01	7 0.011	0.014 0.010	0.014 0.011	0.014	0.011 0.014	0.010 0.014 0.01-	4 0.011 0.014	0.015 0.010	0.009	0.010 0.012	0.014 0.015 0.	014 0.0	09 0.011 0	0.009 0.010	0.011 0.0	14 0.010	0.013 0.011	0.014 0.009	0.011	0.015 0.012	0.006 0.007	0.007	0.014 0.009	0.018 0.018	0.016 0.	0.018	0.018 0.010 0.010	0.010 0.010
JY08 2035 Haplotaxida Enchytraeidae	0.167 0.080		0.011	0.010 0.019	0.017 0.01:	5 0.012	0.013 0.011	0.015 0.011	0.012	0.012 0.012	0.010 0.013 0.013	3 0.011 0.013	0.015 0.011	0.010	0.011 0.012	0.012 0.014 0.	0.0	10 0.011 0	0.011 0.010	0.013 0.0	13 0.011	0.011 0.011	0.013 0.010	0.011	0.015 0.011	0.011 0.010	0.010	0.015 0.009	0.019 0.019	0.017 0.	.019 0.019	0.019 0.011 0.011	0.010 0.010
JY09 2039 Haplotaxida Enchytraeidae	0.167 0.087		0.009	0.010 0.019	0.017 0.01:	5 0.011	0.012 0.011	0.013 0.010	0.012	0.011 0.011	0.009 0.012 0.013	2 0.010 0.012	0.014 0.011	0.010	0.011 0.012	0.012 0.013 0.	0.0	10 0.011 0	0.010 0.010	0.013 0.0	12 0.011	0.011 0.010	0.012 0.010	0.011	0.014 0.011	0.011 0.010	0.011	0.014 0.010	0.018 0.018	0.017 0.	.018 0.018	0.018 0.011 0.011	0.009 0.009
JY10 2114 Haplotaxida Enchytraeidae		0.089 0.090		0.010 0.018	0.018 0.01	6 0.011	0.013 0.009	0.013 0.010	0.012	0.011 0.013	0.009 0.013 0.013	3 0.011 0.013	0.014 0.008	0.009	0.010 0.011	0.013 0.013 0.	0.0	10 0.009 0	0.009 0.009	0.012 0.0	14 0.010	0.011 0.010	0.014 0.010	0.009	0.014 0.009	0.009 0.009	0.009	0.014 0.009	0.017 0.017	0.017 0.	.017 0.017	0.017 0.009 0.009	0.010 0.010
JY11 2355 Haplotaxida Enchytraeidae 381 Robe River	0.140 0.179	0.080 0.085	0.0/4	0.019	0.016 0.018	0.012	0.014 0.009	0.014 0.011	0.013	0.011 0.014	0.010 0.014 0.01	9 0.011 0.014	0.015 0.010	0.009	0.010 0.012	0.014   0.015   0.	014 0.0	19 0.011 0	0.009 0.009	0.012 0.0	30 0.010	0.013 0.010	0.014 0.009	0.011	0.015 0.011	0.006 0.007	0.006	0.014 0.009	0.018 0.018	0.015 0	003 0.004	0.018 0.009 0.009	0.010 0.010
381 Robe River 382 Robe River	0.140 0.178	0.183 0.175	0.186	0.183	0.015 0.01	1 0.017	0.019 0.018	0.020 0.020	0.020	0.019 0.019	0.018 0.019 0.01	1 0.019 0.019	0.019 0.013	7 0.017	0.018 0.019	0.017 0.016 0.	0.0 0.0	18 0.020 0	0.019 0.018	0.019 0.0	20 0.019	0.021 0.021	0.019 0.019	0.020	0.020 0.019	0.019 0.019	0.017	0.020 0.016	0.004 0.004	0.015 0.	015 0.004	0.004 0.018 0.018	8 0.017 0.017
AF064047 Fridericia tuberosa		0.189 0.187	0.183	0.197 0.190	0.02	0.017	0.016 0.017	0.015 0.016	0.016	0.017 0.020	0.016 0.016 0.01	7 0.016 0.014	0.015 0.015	5 0.015	0.015 0.014	0.016 0.016 0	016 0.0	16 0.015	0.015 0.014	0.017 0.0	16 0.015	0.015 0.020	0.017 0.016	0.015	0.016 0.015	0.017 0.017	0.016	0.015 0.017	0.019 0.019	0.020 0	019 0.019	0.019 0.016 0.017	5 0.016 0.016
AK15 PE110780 Oligochgeta		0.124 0.124		0.113 0.192	0.192 0.18	8	0.013 0.010	0.014 0.010	0.011	0.010 0.013	0.010 0.013 0.01	4 0.010 0.013	0.015 0.010	0.011	0.011 0.011	0.012 0.011 0.	012 0.0	11 0.011 0	0.011 0.010	0.012 0.0	13 0.011	0.010 0.011	0.014 0.011	0.010	0.014 0.011	0.011 0.011	0.011	0.013 0.011	0.017 0.017	0.018 0.	.017 0.017	0.017 0.011 0.011	0.010 0.010
AK16 PE112307 Oligochaeta	0.184 0.163	0.144 0.141	0.150	0.113 0.192 0.161 0.195	0.198 0.193	2 0.171	0.014	0.012 0.013	0.014	0.014 0.006	0.012 0.004 0.003	5 0.013 0.004	0.012 0.014	4 0.013	0.014 0.015	0.014 0.013 0.	0.0	14 0.013 0	0.013 0.013	0.015 0.0	05 0.014	0.013 0.014	0.005 0.014	0.013	0.013 0.013	0.014 0.013	0.013	0.014 0.013	0.018 0.018	0.020 0.	.019 0.018	0.018 0.013 0.013	3 0.014 0.014
AK17 PE112318 Oligochaeta		0.089 0.096			0.158 0.183		0.162	0.013 0.011	0.012	0.011 0.014	0.009 0.014 0.014	4 0.011 0.014	0.014 0.009	9 0.009	0.008 0.010	0.013 0.013 0.	0.0	07 0.011 0	0.009 0.009	0.012 0.0	14 0.008	0.011 0.011	0.014 0.007	0.010	0.014 0.010	0.010 0.010	0.009	0.013 0.009	0.017 0.017	0.017 0.	.017 0.017	0.017 0.008 0.008	0.010 0.010
CA13 12:0105 Enchytraeidae indet.		0.152 0.143					0.126 0.155		0.014	0.013 0.011	0.013 0.012 0.01	0.013 0.012	0.009 0.015	5 0.011	0.015 0.015	0.015 0.013 0.	0.0	14 0.013 0	0.013 0.013	0.016 0.0	11 0.013	0.014 0.014	0.012 0.014	0.013	0.009 0.013	0.013 0.014	0.014	0.014 0.012	0.019 0.019	0.019 0.	.019 0.019	0.019 0.014 0.014	4 0.013 0.013
EQ1 Enchytraeus sp. HST0216D		0.105 0.106					0.162 0.106		0.010	0.008 0.013	0.010 0.012 0.013	3 0.005 0.012	0.014 0.009	9 0.010	0.010 0.011	0.013 0.013 0.	0.0	11 0.010 0	0.009 0.010	0.009 0.0	13 0.011	0.009 0.011	0.013 0.011	0.010	0.013 0.010	0.011 0.010	0.010	0.014 0.010	0.019 0.019	0.017 0.	.019 0.019	0.019 0.010 0.010	0.010 0.010
EQ4 Enchytraeus sp. EB0268R EQ5 Enchytraeus sp. HST0098R	0.171 0.109	0.104 0.110						0.171 0.073		0.010 0.014	0.011 0.013 0.01	4 0.010 0.013	0.014 0.010	0.011	0.011 0.012	0.013 0.013 0.	014 0.0	11 0.010 0	0.010 0.012	0.010 0.0	14 0.011	0.009 0.010	0.015 0.011	0.010	0.013 0.011	0.012 0.012	0.012	0.014 0.011	0.020 0.020	0.018 0.	.020 0.020	0.020 0.010 0.010	0.010 0.010
EQ6 Enchytraeus sp. HS10098R EQ6 Enchytraeus sp. MG0022R	0.158 0.110	0.113 0.108			0.209 0.183		0.166 0.112 0.019 0.156		0.078	0.013	0.011 0.013 0.014	4 0.008 0.013	0.013 0.010	0.010	0.010 0.011	0.013 0.012 0.	013 0.0	14 0.010 0	0.009 0.011	0.011 0.0	0.010	0.010 0.010	0.014 0.011	0.011	0.013 0.011	0.010 0.010	0.010	0.014 0.010	0.019 0.019	0.018 0.	010 0.019	0.019 0.010 0.010	0.009 0.009
EQ7 Enchytraeus sp. EB0201R	0.166 0.136	0.144 0.141						0.123 0.138			0.012 0.003 0.00	0.013 0.003	0.012 0.013	0.013	0.013 0.014	0.014 0.013 0	013 0.0	0.013	0.013 0.013	0.013 0.0	12 0.014	0.014 0.013	0.003 0.014	0.013	0.012 0.013	0.013 0.013	0.010	0.013 0.013	0.017 0.017	0.020 0.	019 0.019	0.019 0.013 0.013	0.010 0.010
EQ8 Enchytraeus sp. OB19UNK10		0.076 0.001		0.163 0.198		4 0 169		0.137 0.007			0.011 0.01	4 0.012 0.000	0.014 0.000	3 0.007	0.007 0.010	0.014 0.012 0.	013 0.0	14 0.013 0	0.010 0.007	0.013 0.0	0.010	0.011 0.012	0.012 0.010	0.007	0.014 0.013	0.010 0.007	0.010	0.013 0.007	0.018 0.018	0.017 0.	018 0.018	0.018 0.007 0.007	3 0.013 0.013
EQ9 Enchytraeus sp. EA0170R	0.183 0.159	0.142 0.140	0.149	0.156 0.201	0.212 0.18	5 0.166	0.016 0.162	0.122 0.156	0.165	0.158 0.008	0.137 0.014	0.013 0.004	0.012 0.013	3 0.013	0.013 0.014	0.014 0.013 0.	014 0.0	14 0.013 0	0.013 0.014	0.015 0.0	05 0.015	0.014 0.014	0.004 0.014	0.014	0.013 0.013	0.013 0.013	0.013	0.013 0.014	0.019 0.019	0.020 0.	.019 0.019	0.019 0.013 0.013	3 0.013 0.013
EQ10 Enchytraeus sp. EEX0572	0.160 0.113	0.102 0.106	0.109	0.110 0.198	0.198 0.18	5 0.101	0.159 0.112	0.160 0.024	0.082	0.050 0.155	0.092 0.155 0.15	4 0.012	0.013 0.010	0.010	0.010 0.011	0.012 0.013 0.	0.0	11 0.011 0	0.010 0.010	0.010 0.0	13 0.010	0.009 0.011	0.014 0.011	0.011	0.013 0.011	0.010 0.010	0.010	0.014 0.010	0.019 0.019	0.018 0.	.019 0.019	0.019 0.010 0.010	0.010 0.010
EQ13 Enchytraeus sp. OB19UNK10	0.186 0.166	0.144 0.141	0.153		0.209 0.19	4 0.169	0.013 0.166			0.159 0.017		4 0.155	0.012 0.013	3 0.013	0.013 0.014	0.014 0.013 0.	0.0	14 0.013 0	0.013 0.013	0.014 0.0	05 0.014	0.013 0.013	0.005 0.014	0.013	0.013 0.013	0.013 0.013	0.013	0.014 0.013	0.018 0.018	0.019 0.	.018 0.018	0.018 0.013 0.013	3 0.013 0.013
EQ14 Phreodrilidae sp. Fortescue reference	0.180 0.165	0.148 0.144	0.172	0.163 0.175	0.183 0.16	7 0.181	0.128 0.153	0.079 0.149		0.159 0.124		4 0.148 0.126	0.013	3 0.012	0.014 0.015	0.015 0.014 0.	0.0	14 0.014 0	0.014 0.014	0.017 0.0	12 0.015	0.014 0.015	0.013 0.014	0.014	0.009 0.015	0.014 0.014	0.014	0.015 0.014	0.018 0.018	0.018 0.	.018 0.018	0.018 0.013 0.013	3 0.014 0.014
EQ15 Enchytraeus sp. Fortescue reference EQ16 Enchytraeus sp. Fortescue reference	0.153 0.082	0.096 0.103	0.057	0.080 0.178			0.153 0.048 0.162 0.079			0.099 0.147		0.099 0.152		0.008	0.005 0.010	0.013 0.012 0.	013 0.0	07 0.010 0	0.009 0.009	0.012 0.0	14 0.008	0.010 0.010	0.014 0.007	0.009	0.014 0.009	0.009 0.009	0.009	0.013 0.008	0.018 0.018	0.017 0.	.018 0.018	0.018 0.008 0.008	0.010 0.010
EQ17 Enchytraeus sp. Fortescue reference	0.153 0.074	0.089 0.085	0.0/3	0.075 0.195			0.162 0.079			0.092 0.152 0.105 0.145		4 0.099 0.158	0.140 0.071	0 0 072	0.008 0.011	0.013 0.012 0.	013 0.0	09 0.010 0	0.008 0.007	0.012 0.0	14 0.009	0.011 0.012	0.014 0.009	0.010	0.014 0.010	0.008 0.008	0.008	0.013 0.006	0.016 0.016	0.017 0.	017 0.017	0.017 0.009 0.009	0.009 0.009
EXR1626R J15-25 North Shaw.	0.137 0.070	0.075 0.077		0.093 0.181	0.175 0.17		0.162 0.082			0.106 0.159		3 0.109 0.165		4 0.082	0.075	0.012 0.013 0.	014 0.0	10 0.010 0	0.007 0.007	0.012 0.0	15 0.000	0.010 0.011	0.014 0.000	0.010	0.014 0.010	0.007 0.010	0.007	0.015 0.008	0.017 0.017	0.017 0.	019 0.019	0.017 0.000 0.000	2 0.011 0.011
EXR1626R J15-26 North Shaw.	0.166 0.142	0.133 0.137	0.129		0.178 0.18		0.174 0.136			0.139 0.174		2 0.129 0.174		1 0.124	0.132 0.122	0.013 0.	015 0.0	13 0.012 0	0.014 0.013	0.014 0.0	14 0.014	0.012 0.013	0.015 0.013	0.012	0.016 0.013	0.013 0.013	0.014	0.016 0.012	0.018 0.018	0.019 0.	.018 0.018	0.018 0.013 0.012	3 0.011 0.011
G61 HCO2 Oligochaeta	0.150 0.139	0.146 0.144	0.136	0.140 0.155	0.155 0.18	5 0.128	0.159 0.147	0.170 0.117	0.126	0.120 0.158	0.131 0.161 0.15	9 0.117 0.161	0.162 0.134	4 0.133	0.139 0.145	0.114	0.0	12 0.014 0	0.013 0.012	0.013 0.0	13 0.013	0.012 0.014	0.013 0.012	0.013	0.014 0.014	0.014 0.014	0.014	0.014 0.013	0.016 0.016	0.016 0.	.016 0.016	0.016 0.013 0.013	3 0.012 0.012
G63 HCO2 Oligochaeta		0.148 0.147						0.173 0.154				0.156 0.193					0.0	13 0.013 0	0.013 0.012	0.013 0.0	13 0.013	0.013 0.014	0.013 0.013	0.012	0.015 0.013	0.013 0.014	0.013	0.015 0.012	0.017 0.017	0.020 0.	.018 0.017	0.017 0.014 0.014	4 0.013 0.013
G180 10047 Enchtraeidae	0.161 0.081	0.105 0.108	0.074		0.172 0.18			0.163 0.105								0.142 0.144 0.		0.010	0.008 0.009	0.013 0.0	14 0.008	0.011 0.011	0.015 0.000	0.008	0.015 0.010	0.009 0.009	0.009	0.013 0.009	0.019 0.019	0.017 0.	.019 0.019	0.019 0.008 0.008	3 0.010 0.010
G181 100103 Enchytraeidae G217 Enchytraeidae MW 109252	0.1/1 0.090	0.099 0.097	0.068	0.087 0.201 0.068 0.178	0.178 0.19	0 0.117	0.162 0.090	0.160 0.108	0.102	0.104 0.156	0.079 0.161 0.15	7 0.114 0.161			0.076 0.093	0.137 0.142 0.	156 0.0	70 0 070	0.009 0.010	0.011 0.0	13 0.010	0.010 0.011	0.013 0.010	0.006	0.015 0.005	0.010 0.010	0.010	0.014 0.010	0.020 0.020	0.020 0.	.020 0.020	0.020 0.011 0.011	0.012 0.012
G217 Enchylraeidae AB2 109732	0.144 0.074	0.080 0.082	0.063			5 0.111		0.153 0.101	0.107	0.112 0.133		2 0.101 0.156					144 0.0	71 0.083 0	0.007	0.011 0.0	14 0.007	0.010 0.011	0.014 0.008	0.008	0.014 0.007	0.007 0.007	0.007	0.013 0.008	0.018 0.018	0.018 0	017 0.018	0.017 0.009 0.007	0.011 0.011
G281 Enchytraeidae LN9293 Marillana	0.159 0.119	0.122 0.119	0.118	0.118 0.195			0.177 0.122	0.185 0.066	0.089	0.079 0.183	0.118 0.182 0.17	7 0.076 0.182	0.174 0.115		0.119 0.123		173 0 1	25 0.122	0.122 0.112	0.0	14 0.012	0.011 0.011	0.015 0.013	0.012	0.015 0.011	0.011 0.013	0.012	0.015 0.012	0.019 0.019	0.018 0	.019 0.019	0.019 0.012 0.015	2 0.011 0.011
G282 Enchytraeidae LN7155 Mindy Coondiner	0.184 0.164	0.140 0.139	0.149	0.161 0.192	0.198 0.18	1 0.167	0.022 0.165	0.124 0.161	0.176	0.168 0.024	0.143 0.024 0.024	4 0.159 0.024	0.128 0.156	6 0.167	0.158 0.160	0.165 0.151 0.	193 0.1	64 0.159 0	0.158 0.152	0.177	0.015	0.013 0.014	0.005 0.014	0.013	0.013 0.013	0.014 0.013	0.014	0.014 0.014	0.019 0.019	0.020 0.	.020 0.019	0.019 0.014 0.014	4 0.013 0.013
G284 Enchytraeidae LN9901 Munjina	0.163 0.086	0.103 0.106	0.075	0.083 0.178	0.175 0.193	2 0.118	0.171 0.054	0.165 0.106	0.122	0.109 0.167	0.088 0.174 0.170	0.109 0.174	0.162 0.052	2 0.079	0.054 0.086	0.139 0.147 0.	164 0.0	49 0.083 0	0.067 0.072	0.125 0.1	68	0.010 0.011	0.015 0.008	0.010	0.014 0.010	0.009 0.010	0.009	0.014 0.009	0.018 0.018	0.018 0.	.018 0.018	0.018 0.008 0.009	3 0.011 0.011
G285 Enchytraeidae LN9559 Ophthalmia	0.173 0.110	0.101 0.103	0.119	0.109 0.181	0.181 0.173	3   0.109	0.174 0.118	0.173 0.073	0.076	0.077 0.171	0.112 0.171 0.170	0.079 0.171	0.161 0.119	9   0.112	0.122 0.128	0.135 0.123 0.	166 0.1	16 0.118 0	0.106 0.104	0.097 0.1	70 0.118	0.011	0.014 0.011	0.011	0.013 0.011	0.012 0.011	0.012	0.014 0.011	0.021 0.021	0.019 0.	.021 0.021	0.021 0.011 0.011	0.010 0.010
G286 Enchytraeidae LN9142a Upper Marillana G288 Enchytraeidae LN8233 OB23 25		0.098 0.098		0.089 0.201			0.149 0.107	0.170 0.092		0.086 0.151		3 0.088 0.148 5 0.162 0.016		0.071	0.097 0.109	0.126 0.128 0.		98 0.100 0			49 0.103	0.106	0.014 0.011	0.012	0.012	0.012 0.011	0.012	0.014 0.011	0.021 0.021	0.020 0.	.021 0.021	0.021 0.012 0.012	2 0.010 0.010
G288 Enchytraeidae LN8233 OB23 25 G422 110876 Enchytraeidae	0.183 0.162	0.148 0.146	0.132					0.130 0.16/		0.171 0.019	0.148 0.016 0.016				0.162 0.167			00 0.085 0	0.163   0.156			0.16/ 0.152		0.014	0.014 0.013	0.014 0.014	0.014	0.014 0.014	0.019 0.019	0.020 0.	010 0.019	0.017 0.014 0.014	0.013 0.013
G423 110859 Enchytraeidae	0.167 0.091	0.102 0.108	0.071	0.088 0.186	0.166 0.18														0.073 0.083	0.123 0.1				3.003	0.014 0.004	0.010 0.010	0.010	0.014 0.010	0.020 0.020	0.018 0	.020 0.020	0.020 0.010 0.010	0.012 0.012
G96 107746 Enchytraeidae		0.152 0.147		0.178 0.189	0.198 0.17	4 0.187	0.149 0.168	0.162 0.111 0.058 0.175	0.176	0.175 0.143	0.173 0.147 0.14	9 0.118 0.165 1 0.176 0.147	0.082 0.180	0.157	0.074 0.096 0.182 0.181	0.196 0.192 0.	187 0.1	79 0.167 0	0.172 0.169	0.185 0.1	45 0.174	0.182 0.183	0.149 0.180	0.172	0.014	0.014 0.014	0.015	0.013 0.014	0.020 0.020	0.021 0.	.020 0.020	0.020 0.014 0.014	4 0.014 0.014
G97 107782 Enchytraeidae		0.099 0.100					0.171 0.092			0.114 0.166		7 0.119 0.173			0.083 0.093					0.124 0.1	68 0.091	0.130 0.104	0.176 0.089	0.029	0.178	0.011 0.010	0.010	0.014 0.010	0.019 0.019	0.019 0.	.019 0.019	0.019 0.011 0.011	0.012 0.012
GD10 Oligochaeta Oli-PES16343		0.078 0.084					0.155 0.070			0.103 0.144		5 0.103 0.152			0.067 0.082					0.116 0.1	58 0.073	0.119 0.091	0.159 0.073	0.083	0.170 0.083	0.007	0.004	0.015 0.008	0.018	0.017 0.	.018 0.018	0.018 0.010 0.010	0.010 0.010
GD11 Oligochaeta Oli-PES16200 GD12 Oligochaeta Oli-PES16322		0.085 0.085					0.157 0.074		0.100	0.108 0.142 0.106 0.145		4 0.110 0.151 7 0.106 0.154			0.075 0.080	0.136 0.134 0.				0.124 0.1		0.110 0.107			0.164 0.089	0.038	U.007	0.014 0.009	0.019 0.019	0.018 0.	019 0.019	0.019 0.010 0.010	0.010 0.010
GU453371 Fridericia galba	0.104 0.034	0.081 0.08/	0.000	0.189 0.189			0.186 0.073		0.102		0.078 0.134 0.14	5 0.100 0.134	0.103 0.066	9 0.070	0.087 0.083	0.137 0.144 0.	195 0.0	90 0.076 0	0.060 0.069	0.113 0.1	80 0.0/6	0.121 0.094	0.101   0.0/3	0.074	0.1/2 0.0//	0.000 0.040	0.189	0.014 0.008	0.017 0.019	0.017 0.	000 0.019	0.017 0.010 0.010	3 0.014 0.014
MN0011R J20-26 Ministers N	0.161 0.074	0.081 0.093	0.068		0.166 0.18		0.169 0.073		0.120			3 0.107 0.170	0.163 0.072	2 0.036	0.071 0.075	0.120 0.137 0	154 0.0	73 0.084 0	0.077 0.046	0.115 0.1	71 0.073	0.178 0.173	0.173 0.072	0.187	0.176 0.091	0.071 0.078	0.076	0.013	0.016 0.016	0.017 0	.016 0.016	0.016 0.010 0.015	0.010 0.014
WR 2868	0.135 0.175	0.181 0.172	0.183					0.183 0.183				5 0.195 0.192		5 0.163	0.192 0.178			86 0.198 0	0.172 0.175	0.192 0.1	86 0.175	0.178 0.198						0.183 0.166	0.000	0.015 0.	.003 0.000	0.000 0.018 0.018	3 0.017 0.017
WR 2869	0.135 0.175	0.181 0.172	0.183	0.181 0.006	0.083 0.183	7 0.189	0.189 0.169	0.183 0.183		0.192 0.186	0.175 0.192 0.193	5 0.195 0.192	0.169 0.175	5 0.163	0.192 0.178	0.181 0.149 0.	152 0.1	86 0.198 0	0.172 0.175	0.192 0.1	86 0.175	0.178 0.198	0.186 0.186	0.183	0.183 0.186	0.183 0.169	0.181	0.183 0.166	0.000	0.015 0.	.003 0.000	0.000 0.018 0.018	3 0.017 0.017
WR 2961	0.138 0.158	0.178 0.172	0.192	0.175 0.095	0.014 0.21	8 0.201	0.206 0.166	0.192 0.198	0.198	0.218 0.212	0.178 0.218 0.22	0.206 0.218	0.192 0.181	0.163	0.186 0.183	0.186 0.163 0.	160 0.1	81 0.186 0	0.169 0.178	0.201 0.2	0.183	0.189 0.189	0.212 0.181	0.175	0.206 0.181	0.172 0.166	0.169	0.203 0.175	0.092 0.092	0.	.015 0.015	0.015 0.017 0.017	7 0.017 0.017
WR 2963	0.138 0.175	0.181 0.172	0.183	0.181 0.003	0.083 0.18	7 0.189	0.192 0.169	0.186 0.183	0.198	0.192 0.189	0.178 0.195 0.198	8 0.195 0.195	0.172 0.175	5   0.163	0.192 0.178	0.181 0.152 0.	155 0.1	86 0.198 0	0.175 0.178	0.192 0.1	B9 0.175	0.178 0.198	0.189 0.186	0.183	0.186 0.186	0.183 0.169	0.181	0.186 0.166	0.003 0.003	0.092	0.003	0.003 0.018 0.018	3 0.017 0.017
WR 2964	0.135 0.175	0.181 0.172	0.183	0.181 0.006		7 0.189		0.183 0.183	0.198	0.192 0.186	0.175 0.192 0.193	U.195 0.192	0.169 0.175	0.163	0.192 0.178	0.181 0.149 0.	152 0.1	86 0.198 0	U.172   0.175	0.192 0.1	86 0.175	U.178 0.198	0.186 0.186	0.183	0.183 0.186	0.183 0.169	0.181	0.183 0.166	0.000 0.000	0.092 0.	.003	0.000 0.018 0.018	0.017 0.017
WR 351 YP009 J15-10 Yarrie Ridge	0.135 0.175	0.181 0.172	0.183		0.083 0.183	7 0.107	0.189 0.169	0.100 0.100		0.192 0.186		5 0.195 0.192 3 0.115 0.165	0.169 0.175	0.163	0.192 0.178	0.181 0.149 0.	152 U.1	57 0.094 0	0.172 0.175	0.192 0.1	86 0.175 65 0.058	0.178 0.198	0.186 0.186	0.183	0.183 0.186	0.183 0.169	0.181	0.183 0.166		0.092 0.	175 0 175	0.018 0.018	0.01/ 0.017
YP009 J15-10 Yarrie Ridge	0.160 0.085	0.100 0.106	0.077	0.082 0.178	0.160 0.19	0 0.123	0.160 0.056	0.167 0.107	0.115	0.115 0.157	0.092 0.165 0.16	3 0.115 0.165	0.153 0.052	2 0.079	0.052 0.085	0.136 0.150 0.	164 0.0	57 0.094 0	0.073 0.078	0.121 0.1	65 0.058	0.121 0.101	0.164 0.056	0.088	0.177 0.094	0.079 0.086	0.078	0.180 0.082	0.175 0.175	0.169 0.	.175 0.175	0.175 0.000	0.010 0.010
YP1060 J15-12 Yarrie Ridge	0.158 0.094	0.089 0.094	0.093	0.088 0.166	0.166 0.18	5 0.115	0.150 0.090	0.160 0.091	0.104	0.095 0.155	0.094 0.153 0.153 0.094 0.153 0.153	3 0.094 0.153	0.149 0.092	2 0.090	0.098 0.096	0.112 0.114 0.	151 0.0	99 0.111 0	0.105 0.085	0.109 0.1	46 0.100	0.101 0.093	0.154 0.097	0.106	0.179 0.109	0.094 0.092	0.094	0.198 0.088	0.163 0.163	0.175 0.	.163 0.163	0.163 0.098 0.098	3 0.000
YP1060 J15-13 Yarrie Ridge		0.089 0.094	0.093	0.088 0.166	0.166 0.18	5 0.115	0.150 0.090	0.160 0.091	0.104	0.095 0.155	0.094 0.153 0.153	3 0.094 0.153	0.149 0.092	2 0.090	0.098 0.096	0.112 0.114 0.	151 0.0	99 0.111 0	0.105 0.085	0.109 0.1	46 0.100	0.101 0.093	0.154 0.097	0.106	0.179 0.109	0.094 0.092	0.094	0.198 0.088	0.163 0.163	0.175 0.	163 0.163	0.163 0.098 0.098	3 0.000
Table Estimates of Evolutionary Divergence between	n Comunance		. —		. — —				. — .			. — .								. —	-		. —	. — .		. —	. — .			. — .			

[27] 1503 [10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.78 | 10.



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TABLE 4. Naididae Distance Matrix		П						1 1	1 1												s		Т		ТТ						Т	1 1				T	$\neg \neg$
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	7 88 87 80 Vitro	illo i	# SI SI B	drillic 87.1	985	900	8 8 8	8 r	8 8	8 8	8	7.5c	755	200	53	320	9 6	Ö	5	ici i	5															5 2	5 5
	849 849 Encl Physics 849	l hec	19.R	1073	<u>8</u> 8	N Sign	olio olio	Olig	olio olio	olio olio	Olig	Phre	9 3	<u> </u>	9	5 5	2 2	00 019	50	dis di	58	999	99	9 6	22	8810	812	φ .	965	52	5 4	611	612	3 0	- ·	5 5	5 5
	21 1 22 2 22 2 22 2 21 1 21 1 21 2 21 3	22 P	R16 R16	138	84 83	580	8 8 8	582	287	298	8	8 5	₹ 8	413	4	4 5	8 2	59 H	95	ron stin	A 19	A 28	88 8	8 8	8 8	A 88	B 23	B 49	× 2	61 6	8 8	A 26	7 28	1 49.	49	8 90 7	9010
Specimen ID JY21 1849 Oligochaeta Oligochaeta	5 5 5 5 5 8 8	4 0 0 10 0 01	M M M E	2 6	0 0	ου ο	0 0 00	6 6	3 3	ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο	6 0015 00	0 0	0 0	ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο	<u>0</u>	0 0	005 0014	0014 0000	20011	0022 001	2 0 002 0 0	3 3 3	3 0 000	3 3	3 0 023 0	3 3	3 3	012 0.00	33 0 031	2 3	22 0 022 00	2 2	0.022.04	22 0 000	2000	2001500	15 0 0 15
JY22 2030 Oligochaeta Oligochaeta	0.235 0.016 0.017 0.017 0.016 0.015	5 0.017 0.01	16 0.017 0.018 0.020	0.014 0.003 0.0	0.014 0.014 0.0	13 0.012 0.0	18 0.018 0.01	0.016 0.01	7 0.016 0	0.017 0.015	0.015 0.0	0.015	0.017 0.01	16 0.016 0	0.015 0.	0.013 0.014 0	.016 0.014	0.019 0.022	2 0.015	0.023 0.01	5 0.023 0.0	0.023 0.023 0.02	2 0.022	0.023 0.023	2 0.022 0.	022 0.021 0	.020 0.012 0	.021 0.02	22 0.021	0.021 0.02	22 0.022 0.0	021 0.022	0.022 0.0	22 0.000	0.021 0.02	21 0.013 0.01	13 0.017
CHPB1 J15-7 Boundary Ridge	0.025 0.229 0.000 0.000 0.011 0.014	4 0.011 0.01	10 0.016 0.015 0.024	0.015 0.007 0.0	0.014 0.0	0.017 0.0	00.0 000.0	0.011 0.00	0.016	0.007 0.014	0.014 0.0	0.016	0.01	16 0.016 0	0.015 0.	.015 0.013 0	.006 0.016	0.016 0.022	0.011	0.022 0.01	7 0.023 0.0	0.024 0.02	4 0.023	0.023 0.023	3 0.023 0.	.023 0.021 0	.023 0.014 0	.014 0.02	24 0.021	0.021 0.02	21 0.021 0.0	022 0.022	0.021 0.0	21 0.009	0.022 0.02	2 0.014 0.01	14 0.015
CHPB1 J15-8 Boundary Ridge	0.022 0.230 0.000 0.000 0.011 0.015	5 0.012 0.01	11 0.016 0.016 0.024	0.015 0.007 0.0	0.015 0.0	0.017 0.017	07 0.007 0.00	0.012 0.00	0.017	0.007 0.014	0.015 0.0	0.016	0.017 0.01	17 0.017 0	0.015 0.	.015 0.014 0	.007 0.016	0.016 0.022	0.011	0.022 0.01	7 0.023 0.0	0.024 0.02	4 0.023	0.023 0.023	3 0.023 0.	.023 0.021 0	.023 0.014 0	.014 0.02	24 0.021	0.021 0.02	21 0.021 0.0	022 0.022	0.021 0.0	21 0.009	0.022 0.02	2 0.015 0.01	15 0.015
CHPB1 J15-9 Boundary Ridge EQ12 Phreadrilidae sp. EB0072R	0.022 0.232 0.000 0.000 0.012 0.015 0.074 0.241 0.088 0.087 0.088 0.013	5 0.012 0.01	11 0.016 0.016 0.024	0.015 0.007 0.0	0.015 0.0	0.017 0.017 0.0	07 0.007 0.00	0.012 0.00	0.017	0.007 0.014	0.015 0.0	0.016	0.017 0.01	17 0.017 0	0.015 0.	0.016 0.015 0	.007 0.017	0.016 0.022	0.011	0.022 0.01	7 0.023 0.0	0.024 0.02	0.023	0.023 0.023	3 0.023 0.	023 0.021 0	.023 0.014 0	.014 0.02	24 0.021	0.021 0.02	21 0.021 0.0	022 0.022	0.021 0.0	21 0.009	0.022 0.02	2 0.015 0.01	15 0.015
EQ12 Priledaliliade sp. E800/2k EQ18 Enchytraeus sp. Fortescue	0.165 0.191 0.172 0.174 0.176 0.158	0.014 0.01	13 0.016 0.017 0.022	0.014 0.011 0.0	0.016 0.0	0.0 810.0 810	15 0.015 0.01	0.003 0.01	5 0.017 0	0.012 0.014	0.016 0.0	016 0.015 0	0.017 0.01	16 0.016 0	0.015 0.	0.014 0.016 0	.014 0.015	0.017 0.023	0.012	0.021 0.01	6 0.021 0.0	0.022 0.022 0.02	1 0.021	0.022 0.022	0.022 0.	.021 0.021 0	.021 0.007 0	.007 0.02	21 0.023	0.020 0.02	21 0.022 0.0	020 0.020	0.022 0.0	21 0.020	0.022 0.02	0.014 0.0	14 0.018
EQ2 Phreodrilidae sp. HST0186R	0.076 0.240 0.089 0.087 0.088 0.015 0.156		05 0.015 0.015 0.022	0.014 0.010 0.0	0.0 610.0 110	0.015 0.0	11 0.011 0.01	0.005 0.01	1 0.015	0.012	5 0.015 0.0	0.015	0.015 0.01	15 0.015 0	0.015 0.	.013 0.014 0	.011 0.015	0.017 0.022	0.012	0.021 0.01	7 0.022 0.0	0.022 0.022	3 0.022	0.022 0.022	2 0.022 0.	.022 0.021 0	.021 0.007 0	.007 0.02	22 0.020	0.020 0.02	22 0.022 0.0	020 0.020	0.022 0.0	22 0.016	0.022 0.02	1 0.016 0.01	16 0.016
EQ3 Phreodrilidae sp. EEX0561	0.070 0.244 0.084 0.082 0.083 0.013 0.161		0.015 0.015 0.022	0.014 0.010 0.0	0.015 0.0	0.0 610.0	11 0.011 0.01	0.006 0.01	0.015	0.014	0.015 0.0	0.015	0.01	15 0.015 0	0.015 0.	.013 0.014 0	.011 0.015	0.016 0.022	0.013	0.021 0.01	7 0.022 0.0	0.022 0.022	3 0.021	0.022 0.022	2 0.022 0.	.021 0.020 0	.020 0.004 0	.004 0.02	22 0.019	0.019 0.02	21 0.021 0.0	020 0.020	0.021 0.0	21 0.014	0.022 0.02	.0 0.016 0.01	16 0.016
EXR1619R J15-22 North Shaw EXR1619R J15-23 North Shaw	0.193 0.218 0.192 0.192 0.185 0.197 0.197 0.194 0.220 0.191 0.192 0.184 0.198 0.200			0.017 0.016 0.0	0.017 0.0	0.0 010.0 010	15 0.015 0.01	0.015 0.01	6 0.016	0.015	0.016 0.0	016 0.017 0	0.016 0.01	7 0.016 0	0.017 0.	0.016 0.016	.016 0.016	0.016 0.021	0.015	0.023 0.01	9 0.022 0.0	0.022 0.022 0.02	2 0.020	0.022 0.022	2 0.022 0.	020 0.020 0	.020 0.019 0	.019 0.02	21 0.024	0.024 0.02	21 0.021 0.0	023 0.023	0.021 0.0	0.020	0.020 0.02	3 0.016 0.01	16 0.015
EXR1619R J15-23 North Shaw Fridericia tuberosa Enchytraeidae	0.221 0.201 0.216 0.216 0.216 0.198 0.207			0.017 0.016 0.0	0.017 0.0	0.017 0.0	25 0.025 0.01	0.015 0.01	24 0,023 0	0.025 0.025	0.021 0.0	023 0.024	0.024 0.03	24 0.024 0	0.023 n	1.023 0.024 0	.025 0.016	0.017 0.021	3 0.022	0.023 0.01	0 0.024 0.0	0.024 0.024 0.03	25 0,020	0.022 0.022	4 0.024 0	022 0.020 0	.023 0.022 0	.022 0.02	24 0.024	0.023 0.03	23 0.023 0.0	025 0.023	0.023 0.0	23 0.020	0.024 0.0	24 0.023 0.0	23 0,024
FU3 Phreodrilidae KGST0032	0.179 0.225 0.191 0.189 0.191 0.180 0.187			0.014 0.0	0.017 0.0	0.0 610.0 610	15 0.015 0.01	0.015 0.01	5 0.015	0.015 0.014	0.013 0.0	0.016	0.017 0.01	17 0.016 0	0.017 0.	0.014 0.013 0	.014 0.014	0.017 0.022	0.015	0.023 0.01	7 0.020 0.0	020 0.020 0.02	0.018	0.020 0.020	0.020 0.	.018 0.022 0	.021 0.022 0	.022 0.02	20 0.019	0.019 0.02	22 0.022 0.0	021 0.021	0.022 0.0	22 0.022	0.021 0.02	0 0.016 0.0	16 0.017
G103 107987 Phreodrilidae	0.019 0.237 0.028 0.025 0.026 0.086 0.169	9 0.087 0.08	83 0.194 0.197 0.221	0.183	0.014 0.0	0.0 610.0 610	07 0.007 0.00	0.011 0.00	0.016	0.008	0.014 0.0	0.016	0.016	16 0.016 0	0.015	.015 0.013 0	.003 0.017	0.016 0.022	0.012	0.023 0.01	8 0.023 0.0	0.023 0.023	24 0.023	0.023	3 0.023 0.	023 0.022 0	.023 0.014 0	.014 0.02	24 0.022	0.022 0.02	22 0.022 0.0	022 0.022	0.022 0.0	0.009	0.022 0.02	.2 0.015 0.01	15 0.015
G182 100109 Phreodrilidae	0.025 0.234 0.026 0.025 0.026 0.094 0.170				0.014 0.0	0.0 610.0 610	07 0.007 0.00	0.012 0.00	0.016	0.008 0.014	0.014 0.0	0.016	0.016	0.016	0.015 0.	.015 0.014 0	.003 0.017	0.015 0.022	2 0.011	0.022 0.01	7 0.023 0.0	0.023 0.023	3 0.022	0.023 0.023	3 0.023 0.	.022 0.022 0	.023 0.014 0	.014 0.02	23 0.022	0.022 0.02	22 0.022 0.0	022 0.023	0.022 0.0	22 0.010	0.022 0.02	2 0.014 0.01	14 0.015
G184 100085 Phreodrilidae G289 Naididae LN7511	0.191 0.236 0.202 0.200 0.202 0.182 0.193 0.224 0.183 0.230 0.234 0.234 0.213 0.221					0.003 0.0	15 0.015 0.01	0.016 0.01	6 0.014	1016 0.015	0.0   610.0	0.016	0.017 0.01	0.017 0	0.017	0.014 0.016 0	016 0.016	0.017 0.022	0.014	0.021 0.01	4 0.022 0.0	122 0.022 0.02	2 0.022	0.022 0.022	2 0.022 0.	022 0.021 0	021 0.023 0	0.023 0.02	22 0.022	0.022 0.02	21 0.021 0.0	022 0.022	0.021 0.0	21 0.023	0.020 0.02	2 0.015 0.01	16 0.016
G290 Naididae 100701c	0.227 0.180 0.232 0.237 0.237 0.213 0.221					0.003 0.0	16 0.016 0.01	0.015 0.01	6 0.014 0	0.017 0.016	0.016 0.0	002 0.015 0	0.015 0.01	14 0.015 0	0.017 0.	0.013 0.015 0	.016 0.015	0.017 0.022	2 0.016	0.020 0.01	3 0.021 0.0	0.021 0.021 0.02	2 0.019	0.022 0.021	0.021 0	.019 0.021 0	.021 0.022 0	.022 0.02	21 0.018	0.018 0.02	22 0.022 0.0	019 0.019	0.022 0.0	22 0.020	0.021 0.0	9 0.016 0.0	16 0.018
G291 Oligochaeta 100498 22102010	0.024 0.244 0.028 0.027 0.027 0.086 0.170						0.00 0.00	0.011 0.00	0.015	0.004 0.015	0.015 0.0	0.017	0.017 0.01	17 0.017 0	0.016	.016 0.014 0	.007 0.017	0.015 0.023	0.011	0.023 0.01	8 0.023 0.0	0.023 0.02	4 0.023	0.023 0.023	3 0.023 0.	.023 0.022 0	.023 0.014 0	.014 0.02	24 0.022	0.022 0.02	23 0.023 0.0	022 0.022	0.023 0.0	23 0.004	0.022 0.02	3 0.015 0.01	15 0.015
G292 Oligochaeta LN9284 10072010	0.024 0.244 0.028 0.027 0.027 0.086 0.170							0.011 0.00	0.015	0.004	0.015 0.0	0.017	0.017 0.01	17 0.017 0	0.016	.016 0.014 0	.007 0.017	0.015 0.023	0.011	0.023 0.01	8 0.023 0.0	0.023 0.023	24 0.023	0.023	3 0.023 0.	.023 0.022 0	.023 0.014 0	.014 0.02	24 0.022	0.022 0.02	23 0.023 0.0	022 0.022	0.023 0.0	23 0.004	0.022 0.02	3 0.015 0.01	15 0.015
G294 Oligochaeta LN8987 21052010 G295 Oligochaeta LN9369 10082010	0.028 0.243 0.033 0.030 0.030 0.089 0.174 0.075 0.246 0.083 0.087 0.087 0.013 0.164	4 0.089 0.08	83 0.183 0.182 0.233	0.192 0.037 0.0	042 0.198 0.2	28 0.228 0.0	13 0.013	0.012 0.00	0.016	0.000 0.015	0.015 0.0	0.017	0.017 0.01	17 0.017 0	0.016 0.	0.014 0.014 0	.007 0.017	0.016 0.022	0.011	0.023 0.01	8 0.023 0.0	0.024 0.02	0.023	0.023 0.023	3 0.023 0.	023 0.022 0	.023 0.014 0	.014 0.02	24 0.022	0.022 0.02	23 0.023 0.0	022 0.022	0.023 0.0	23 0.007	0.022 0.02	2 0.015 0.01	15 0.015
G296 Oligochaeta LN9431 13082010	0.025 0.240 0.015 0.014 0.014 0.091 0.173								0.016	0.012 0.014	5 0.015 0.0	016 0.017 0	0.017 0.01	17 0.016 0	0.015	0.014 0.014 0	006 0.016	0.017 0.023	0.012	0.021 0.01	7 0.022 0.0	123 0.023 0.02	4 0.022	0.022 0.022	3 0 023 0	022 0.021 0	023 0.013 0	013 0.02	24 0.020	0.020 0.02	22 0.021 0.0	020 0.021	0.021 0.0	22 0.008	0.023 0.03	2 0.015 0.0	15 0.015
G297 Oligochaeta 100216 09102010	0.201 0.222 0.210 0.215 0.215 0.218 0.218	0.215 0.21	16 0.193 0.193 0.216	0.186 0.209 0.2	209 0.213 0.2	218 0.218 0.2	07 0.207 0.20	0.219 0.21	12 0	0.016	5 0.014 0.0	014 0.017	0.018 0.01	18 0.018 0	0.017 0.	.016 0.015 0	016 0.015	0.016 0.020	0.016	0.023 0.01	6 0.021 0.0	021 0.021 0.02	0 0.021	0.021 0.021	0.021 0.	021 0.022 0	.020 0.021 0	.021 0.02	21 0.021	0.021 0.02	21 0.021 0.0	021 0.022	0.021 0.0	21 0.021	0.021 0.03	1 0.015 0.01	15 0.017
G298 Oligochaeta LN9744 08092010	0.028 0.243 0.033 0.030 0.030 0.089 0.174									0.015	0.015 0.0	0.017	0.017 0.01	17 0.017 0	0.016	.016 0.014 0	.007 0.017	0.016 0.022	0.011	0.023 0.01	8 0.023 0.0	0.024 0.02	4 0.023	0.023 0.023	3 0.023 0.	.023 0.022 0	.023 0.014 0	.014 0.02	24 0.022	0.022 0.02	23 0.023 0.0	022 0.022	0.023 0.0	23 0.007	0.022 0.02	.2 0.015 0.01	15 0.015
G299 Oligochaeta 100730 04112010 G300 Oligochaeta LN8285a 21042010	0.165 0.215 0.165 0.170 0.170 0.158 0.148 0.177 0.219 0.180 0.186 0.186 0.180 0.194			0.177 0.170 0.1						1.167	0.015 0.0	0.015	0.016 0.01	16 0.016 0	0.016 0.	0.014 0.015 0	.014 0.016	0.016 0.022	0.016	0.021 0.01	6 0.022 0.0	0.022 0.022 0.02	0.020	0.022 0.022	2 0.022 0.	.020 0.019 0	.017 0.020 0	.020 0.02	21 0.020	0.020 0.02	20 0.020 0.0	023 0.023	0.020 0.0	20 0.024	0.019 0.02	2 0.014 0.01	14 0.018
G301 Phreodrilidae LN8279	0.228 0.183 0.234 0.239 0.239 0.215 0.222									230 0.180	5 0 207	0.015	0.015 0.01	14 0.014 0	1017 0.	1013 0.012 0	014 0.015	0.017 0.021	0.016	0.021 0.01	4 0.023 0.0	121 0.021 0.02	2 0.020	0.023 0.023	1 0 021 0	019 0.023 0	020 0.022 0	020 0.02	21 0.022	0.022 0.02	22 0.021 0.0	019 0.019	0.021 0.0	22 0.021	0.022 0.0	9 0.014 0.01	16 0.018
G410 110175a Naididae	0.216 0.173 0.213 0.220 0.223 0.210 0.209									0.219 0.210	0.224 0.2	203	0.005	03 0.007 0	0.011 0.	.014 0.014 0	016 0.017	0.018 0.023	0.015	0.021 0.01	6 0.023 0.0	0.023 0.023	3 0.023	0.023 0.023	3 0.023 0.	023 0.020 0	.022 0.020 0	.020 0.02	23 0.021	0.021 0.02	21 0.021 0.0	022 0.022	0.021 0.0	21 0.022	0.022 0.03	2 0.015 0.0	15 0.018
G411 110175b Naididae	0.214 0.176 0.213 0.220 0.220 0.209 0.212												0.00	0.006	0.011	.015 0.015 0	.017 0.017	0.017 0.023	0.016	0.021 0.01	6 0.022 0.0	0.022 0.022	2 0.023	0.022 0.022	2 0.022 0.	.023 0.019 0	.020 0.020 0	.020 0.02	22 0.021	0.021 0.02	20 0.020 0.0	023 0.023	0.020 0.0	20 0.020	0.020 0.02	.3 0.016 0.01	16 0.018
G412 110330a Naididae G413 110019a Naididae	0.220 0.177 0.216 0.222 0.222 0.215 0.213 0.215 0.178 0.217 0.225 0.225 0.203 0.210												0.023	0.007 0	0.012 0.	0.015 0.015 0	.017 0.017	0.018 0.023	0.015	0.021 0.01	6 0.024 0.0	0.024 0.024 0.02	0.024	0.024 0.024	4 0.024 0.	.024 0.021 0	.021 0.020 0	.020 0.02	23 0.021	0.021 0.02	20 0.020 0.0	022 0.022	0.020 0.0	20 0.021	0.021 0.02	2 0.016 0.01	16 0.018
G414 110153 Naididae	0.207 0.172 0.204 0.209 0.212 0.215 0.210												0.034 0.04	17 0 114	0.	014 0013 0	015 0.017	0.018 0.023	3 0.016	0.021 0.01	6 0.021 0.0	123 0.021 0.02	3 0.024	0.021 0.021	3 0 023 0	024 0.021 0	022 0.021 0	021 0.02	23 0.024	0.021 0.02	19 0.021 0.0	022 0.022	0.021 0.0	19 0.021	0.018 0.0	24 0.015 0.01	15 0.019
G415 110019b Phreodrillidae	0.190 0.195 0.190 0.190 0.192 0.177 0.183			0.176 0.201 0.2							0.171 0.2		0.212 0.21	16 0.205 0	0.212	0.013	016 0.015	0.014 0.020	0.016	0.021 0.01	4 0.021 0.0	021 0.020 0.02	0.021	0.021 0.021	0.021 0.	021 0.022 0	.022 0.020 0	.020 0.02	20 0.020	0.020 0.02	20 0.020 0.0	022 0.022	0.020 0.0	20 0.023	0.019 0.00	1 0.014 0.01	14 0.018
G416 110132c Phreodrillidae	0.201 0.212 0.203 0.204 0.207 0.199 0.190	0.192 0.19	99 0.201 0.204 0.216	0.173 0.199 0.2	202 0.218 0.2	0.204 0.2	06 0.206 0.20	0.197 0.20	0.182	0.203 0.192	0.168 0.2	201 0.228	0.232 0.23				.014 0.014	0.015 0.022	0.015	0.023 0.01	6 0.023 0.0	0.023 0.023	4 0.022	0.023 0.023	3 0.023 0.	.022 0.021 0	.022 0.021 0	.021 0.02	23 0.021	0.021 0.02	21 0.021 0.0	021 0.021	0.021 0.0	21 0.022	0.021 0.02	:1 0.014 0.01	14 0.018
G420 110346 Phreodrilidae G421 110719 Phreodrilidae	0.020 0.236 0.028 0.027 0.027 0.090 0.166 0.185 0.201 0.197 0.198 0.200 0.192 0.197			0.179 0.007 0.0										23 0.219 0		1.168 0.169 0	0.016	0.015 0.022	0.011	0.023 0.01	8 0.023 0.0	0.023 0.023 0.02	0.023	0.023 0.023	0.023 0.	0.023 0.022 0	.024 0.015 0	.015 0.02	23 0.022	0.022 0.02	23 0.023 0.0	022 0.022	0.023 0.0	23 0.010	0.022 0.02	2 0.014 0.01	14 0.015
G59 HCO2 Oligochaeta	0.182 0.216 0.184 0.187 0.187 0.188 0.195															1.174 0.187 0		0.017 0.019	0.015	0.022 0.01	9 0.021 0.0	121 0.021 0.02	0.018	0.021 0.021	1 0.021 0	018 0.023 0	021 0.021 0	021 0.02	20 0.022	0.022 0.02	19 0.019 0.0	024 0.024	0.022 0.0	19 0.024	0.019 0.03	3 0.014 0.01	16 0.018
HM 26610	0.218 0.226 0.218 0.218 0.218 0.226 0.206																	0.186	0.022	0.023 0.02	3 0.023 0.0	0.024 0.02	4 0.022	0.023 0.023	3 0.023 0.	022 0.025 0	.025 0.022 0	.022 0.02	23 0.020	0.020 0.02	22 0.022 0.0	021 0.022	0.022 0.0	22 0.023	0.021 0.03	1 0.023 0.00	23 0.021
NS1990 J15-19 Hillside Station	0.096 0.237 0.099 0.099 0.099 0.111 0.171	0.111 0.10	09 0.194 0.192 0.227	0.199 0.098 0.0	0.194 0.2	226 0.226 0.0	99 0.099 0.10	0.109 0.10	0.215	0.101 0.167	7 0.188 0.2	228 0.226 0	0.219 0.22	25 0.222 0	0.229 0.	.197 0.208 0	.096 0.202	0.192 0.235	5	0.024 0.01	5 0.022 0.0	0.022 0.022	2 0.022	0.022 0.022	0.022 0.	.022 0.019 0	.021 0.016 0	.016 0.02	22 0.022	0.022 0.02	21 0.021 0.0	023 0.023	0.021 0.0	21 0.015	0.021 0.02	.3 0.015 0.01	15 0.015
Paranais frici Naididae	0.246 0.192 0.232 0.232 0.232 0.226 0.223 0.232 0.017 0.229 0.229 0.229 0.238 0.194	0.226 0.22	29 0.232 0.232 0.241	0.223 0.235 0.2	235 0.252 0.2	26 0.226 0.2	44 0.244 0.24	0.229 0.23	32 0.218 0	0.198	0.212 0.2	226 0.221 0	0.212 0.21	18 0.218 0	0.195 0.	1.195 0.218 0	235 0.229	0.223 0.249	0.221	0.01	8 0.022 0.0	0.023 0.02	3 0.023	0.022 0.022	2 0.022 0.	.023 0.021 0	.021 0.021 0	.021 0.02	22 0.019	0.019 0.02	21 0.021 0.0	022 0.023	0.021 0.0	21 0.023	0.022 0.02	2 0.023 0.02	23 0.019
Pristina longiseta WA 1955	0.244 0.241 0.249 0.249 0.249 0.252 0.212															1.201 0.215 0				0.252 0.23	5 0.023 0.0	0.023 0.02	4 0.022	0.023 0.023	0.023 0.	013 0.021 0	020 0.021 0	0.021 0.02	0.021	0.021 0.02	21 0.021 0.0	021 0.022	0.021 0.0	21 0.024	0.022 0.0	23 0.020 0.01	20 0.016
WA 2666	0.244 0.241 0.249 0.249 0.249 0.252 0.212	2 0.261 0.26	61 0.209 0.209 0.233	0.192 0.244 0.2	238 0.258 0.2	21 0.218 0.2	44 0.244 0.24	0.264 0.24	6 0.178 0	0.246 0.221	0.218 0.2	218 0.266 0	0.255 0.27	72 0.252 0	0.255 0.	.201 0.215 0	241 0.186	0.192 0.198	3 0.229 0	0.252 0.23	5 0.000	0.004 0.00	4 0.013	0.003 0.000	0.000 0.	013 0.022 0	.022 0.022 0	.022 0.00	04 0.023	0.023 0.02	22 0.022 0.0	023 0.023	0.022 0.0	22 0.023	0.020 0.02	3 0.020 0.01	20 0.020
WA 28610	0.246 0.244 0.252 0.252 0.252 0.255 0.212	2 0.264 0.26	64 0.212 0.212 0.236	0.195 0.246 0.2	241 0.261 0.2	223 0.221 0.2	46 0.246 0.24	0.266 0.24	19 0.183 0	0.249 0.223	3 0.221 0.2	221 0.269	0.258 0.27	75 0.255 0	0.258 0.	.203 0.215 0	244 0.189	0.198 0.201	0.232	0.255 0.23	0.00 600.0	0.00	0.013	0.005 0.004	4 0.004 0.	.013 0.023 0	.023 0.022 0	.022 0.00	05 0.023	0.023 0.02	22 0.022 0.0	023 0.023	0.022 0.0	22 0.024	0.020 0.02	.3 0.021 0.07	21 0.020
WA 28611	0.249 0.241 0.255 0.255 0.255 0.258 0.218	0.266 0.26	66 0.215 0.215 0.239	0.198 0.249 0.2	244 0.264 0.2	226 0.223 0.2	49 0.249 0.25	0.269 0.25	0.183	0.252 0.226	0.223 0.2	223 0.272 0	0.261 0.27	78 0.258 0	0.261 0.	.206 0.221 0	246 0.192	0.198 0.203	0.235	0.258 0.23	5 0.006 0.0	0.011	0.012	0.005 0.004	4 0.004 0.	.012 0.023 0	.022 0.023 0	.023 0.00	05 0.023	0.023 0.02	22 0.022 0.0	023 0.023	0.022 0.0	22 0.024	0.020 0.02	3 0.021 0.02	21 0.020
WA 2866 WA 2966	0.241         0.238         0.246         0.246         0.246         0.232         0.195           0.246         0.241         0.252         0.252         0.252         0.252         0.252         0.252         0.252	0.244 0.24	41 0.176 0.178 0.201 61 0.212 0.212 0.23	0.176 0.241 0.3	241 0 258 0 2	23 0 221 0 2	46 0.246 0.24	0.244 0.24	19 0 178 0	249 0.206	0.206 0.2	221 0.246 0	0.241 0.25	72 0.235 0	.∠32 (). 1252 ∩	201 0.201 0	244 0 189	0.166 0.192	3 0 226	0.246 0.23	5 0.003 0.0	0.009 0.007	9 0.072	0.013	3 0.003 0	013 0 022 0	022 0 022 0	022 0.00	0.022	0.022 0.02	22 0.022 0.0	022 0.024	0.020 0.0	20 0.022	0.021 0.02	3 0.020 0.02	20 0.021
WA 383	0.244 0.241 0.249 0.249 0.249 0.252 0.212	2 0.261 0.26	61 0.209 0.209 0.233	0.192 0.244 0.2	238 0.258 0.2	21 0.218 0.2	44 0.244 0.24	0.264 0.24	6 0.178 0	0.246 0.221	0.218 0.2	218 0.266 0	0.255 0.27	72 0.252 0	0.255 0.	.201 0.215 0	241 0.186	0.192 0.198	3 0.229 (	0.252 0.23	5 0.000 0.0	00.0 0.006 0.00		0.003	0.000 0.	013 0.022 0	.022 0.022 0	.022 0.00	04 0.023	0.023 0.02	22 0.022 0.0	023 0.023	0.022 0.0	22 0.023	0.020 0.02	/3 0.020 0.01	20 0.020
WA 385	0.244 0.241 0.249 0.249 0.249 0.252 0.212	2 0.261 0.26	61 0.209 0.209 0.233	0.192 0.244 0.2	238 0.258 0.2	21 0.218 0.2	44 0.244 0.24	0.264 0.24	6 0.178	0.246 0.221	0.218 0.2	218 0.266	0.255 0.27	72 0.252 0	0.255 0.	.201 0.215 0	241 0.186	0.192 0.198	3 0.229	0.252 0.23	5 0.000 0.0	0.00 0.006 0.00	0.069	0.003		013 0.022 0	.022 0.022 0	.022 0.00	0.023	0.023 0.02	22 0.022 0.0	023 0.023	0.022 0.0	22 0.023	0.020 0.02	.3 0.020 0.07	20 0.020
WA 888 WB 23810	0.241 0.238 0.246 0.246 0.246 0.232 0.195 0.212 0.223 0.206 0.206 0.206 0.209 0.198	5 0.244 0.24	41 0.198 0.198 0.201	0.178 0.241 0.2	235 0.249 0.2	01 0.198 0.2	44 0.244 0.24	0.244 0.24	14 0.172 0	0.246 0.206	5 0.206 0.2	201 0.246 0	0.241 0.25	52 0.235 0	0.252 0.	1.178 0.201 0	238 0.160	0.166 0.192	0.221	0.246 0.23	2 0.069 0.0	0.069 0.07	4 0.000	0.072 0.069		0.021 0	.021 0.021 0	.021 0.01	13 0.022	0.022 0.02	20 0.020 0.0	022 0.024	0.020 0.0	20 0.022	0.021 0.02	3 0.020 0.02	20 0.021
WB 23812	0.209 0.206 0.209 0.209 0.209 0.201 0.201																										0.020 0	020 0.02	22 0.023	0.023 0.01	18 0.018 0.0	021 0.022	0.014 0.0	18 0.022	0.021 0.02	21 0.023 0.02	20 0.024
WB 497	0.063 0.252 0.074 0.074 0.074 0.017 0.183	3 0.020 0.00	06 0.186 0.186 0.193	0.201 0.077 0.0	080 0.221 0.2	226 0.226 0.0	72 0.072 0.07	0.011 0.07	2 0.229 0	0.077 0.181	0.186 0.2	229 0.229 0	0.218 0.22	29 0.215 0	0.226 0.	1.175 0.192 0	.080 0.203					261 0.264 0.26					.192 0	.000 0.02	22 0.020	0.020 0.02	21 0.021 0.0	021 0.021	0.021 0.0	21 0.014	0.022 0.02	1 0.022 0.01	22 0.020
WB 498	0.063 0.252 0.074 0.074 0.074 0.017 0.183																					261 0.264 0.26						0.02	22 0.020	0.020 0.02	21 0.021 0.0	021 0.021	0.021 0.0	21 0.014	0.022 0.02	.1 0.022 0.07	22 0.020
WW 2865	0.244 0.235 0.249 0.249 0.249 0.246 0.206	6 0.255 0.25	55 0.203 0.203 0.227	0.192 0.244 0.2	238 0.252 0.2	223 0.221 0.2	44 0.244 0.24	0.258 0.24	6 0.181 0	0.246 0.215	0.215 0.2	221 0.264 0	0.252 0.26								9 0.006 0.0						.221 0.255 0		0.023	0.023 0.02	21 0.021 0.0	023 0.023	0.021 0.0	21 0.024	0.020 0.02	2 0.020 0.02	20 0.020
YA 1951 YA 1952	0.246 0.218 0.244 0.244 0.244 0.244 0.226	6 0.241 0.23	38 0.218 0.218 0.216	0.201 0.246 0.3	249 0.232 0.1	58 0.155 0.2	46 0.246 0.25	0.238 0.24	14 0.209 0	1.255 0.198	0.221 0.1	155 0.192 0	0.195 0.19			1.212 0.238 0					1 0.258 0.2						198 0.232 0			0.000 0.02	23 0.023 0.0	016 0.017	0.023 0.0	23 0.021	0.021 0.0	7 0.022 0.02	22 0.019
YA 1953	0.246 0.218 0.244 0.244 0.244 0.244 0.226 0.209 0.218 0.198 0.198 0.198 0.212 0.181	0.215 0.21	12 0.201 0.201 0.207	0.215 0.212 0.2	215 0.183 0.2	38 0.238 0.2	12 0.212 0.21	0.218 0.20	0.195	1.218 0.155	5 0.198 0.2	241 0.215	0.218 0.21	15 0.218 0	0.201 0.	.201 0.232 0	215 0.189	0.183 0.221	0.198	0.218 0.22	1 0.238 0.2	238 0.241 0.24	11 0.223	0.235 0.238	3 0.238 O.	223 0.100 0	.140 0.206 0	.206 0.23	38 0.209	0.209	0.000 0.0	023 0.022	0.000 0.0	00 0.023	0.021 0.02	23 0.020 0.0	20 0.023
YA 1954	0.209 0.218 0.198 0.198 0.198 0.212 0.181	0.215 0.21	12 0.201 0.201 0.207	0.215 0.212 0.2	215 0.183 0.2	238 0.238 0.2	12 0.212 0.21	0.218 0.20	0.195	0.155	0.198 0.2	241 0.215	0.218 0.21	15 0.218 0	0.201 0.	0.232	215 0.189	0.183 0.221	0.198	0.218 0.22	1 0.238 0.2	238 0.241 0.24	11 0.223	0.235 0.238	8 0.238 0.	223 0.100 0	.140 0.206 0	.206 0.23	38 0.209	0.209 0.00	0.0	023 0.022	0.00	00 0.023	0.021 0.02	3 0.020 0.00	20 0.023
YA 26611	0.235 0.226 0.235 0.235 0.235 0.232 0.215	5 0.229 0.23	32 0.232 0.232 0.224	0.215 0.235 0.2	235 0.238 0.1	49 0.149 0.2	35 0.235 0.23	0.232 0.23	35 0.221 0	0.235 0.203	0.218 0.1	149 0.198 0	0.192 0.19	98 0.195 0	0.221 0.	.212 0.232 0	.235 0.232	0.229 0.229				238 0.241 0.24					.201 0.232 0				29 0.229	0.008	0.023 0.0	0.022	0.023 0.00	5 0.022 0.07	22 0.021
YA 26612 YA 28612	0.241 0.226 0.241 0.241 0.241 0.235 0.215																					235 0.238 0.24											0.022 0.0	0.022	0.023 0.00	7 0.023 0.07	23 0.021
YA 386 YA 386	0.209 0.218 0.198 0.198 0.198 0.212 0.181 0.209 0.218 0.198 0.198 0.198 0.212 0.181	0.215 0.21	12 0.201 0.201 0.207	0.215 0.212 0.3	215 0.183 0.2	38 0.238 0.2	12 0.212 0.21	0.218 0.20	0.195	1.218 U.155	0.198 0.2	241 0.215 0	ມ.∠18   ປ.21 ປ.218   ດ ວາ	15 0.218 0	0.201 O.	1.201 0.232 0	.∠15   U.189 .215   O.189	0.183 0.221	0.198	0.218 0.22	1 0.238 0.2	238 0.241 0.24	1 0.223	0.235 0.238 0.235 n 238	0.238 O. 3 0.238 O	223 0 100 0	.140 0.206 0	.206 0.23	38 0 209	0.209 0.00	0.000 0.5	229 0.226	0.000	0.023	0.021 0.02	23 0.020 0.02	20 0.023
YA 493	0.209 0.218 0.198 0.198 0.198 0.212 0.181 0.020 0.264 0.026 0.026 0.026 0.083 0.183	3 0.089 0.07	77 0.186 0.186 0.221	0.201 0.023 0.0	032 0.235 0.2	32 0.232 0.0	06 0.006 0.01	0.077 0.02	23 0.229 0	0.017 0.201	0.186 0.2	235 0.244 0	0.232 0.24	14 0.235 0	0.223 0.	.201 0.209 0	.026 0.223	0.189 0.229	0.095	0.238 0.24	9 0.244 0.2	244 0.246 0.24	9 0.238	0.246 0.244	4 0.244 0.	238 0.212 0	212 0.072 0	.072 0.24	44 0.246	0.246 0.20	09 0.209 0.2	232 0.238	0.209 0.2	109	0.023 0.03	2 0.022 0.0	22 0.021
YA 494	0.213 0.251 0.216 0.216 0.216 0.224 0.213	3 0.216 0.22	24 0.201 0.201 0.246	0.195 0.219 0.2	222 0.248 0.2	245 0.242 0.2	16 0.216 0.21	0.224 0.21	6 0.230 0	0.187	7 0.210 0.2	245 0.236 0	0.222 0.23	39 0.207 0	0.257 0.	1.184 0.198 0	.219 0.195	0.201 0.192	0.219	0.219 0.24	5 0.224 0.2	224 0.222 0.23	0.216	0.224 0.224	4 0.224 0.	.216 0.233 0	.230 0.219 0	.219 0.22	22 0.248	0.248 0.22	27 0.227 0.2	265 0.268	0.227 0.2	27 0.222	0.0	.3 0.022 0.07	22 0.020
YA 889	0.241 0.221 0.235 0.235 0.235 0.232 0.212	2 0.229 0.23	32 0.229 0.229 0.218	0.212 0.241 0.2	235 0.235 0.1	52 0.152 0.2	41 0.241 0.24	0.232 0.23	0.226	0.241 0.201	0.215 0.1	152 0.195	0.189 0.19	95 0.192 0	0.221 0.	.209 0.229 0	241 0.229	0.232 0.226	0.235	0.221 0.21	8 0.232 0.2	232 0.235 0.23	8 0.221	0.232 0.232	2 0.232 0.	221 0.215 0	195 0.232 0	.232 0.22	29 0.115	0.115 0.22	23 0.223 0.0	011 0.020		23 0.238		0.023 0.07	23 0.021
YP1063 J15-14 Yarrie Ridge YP1063 J15-15 Yarrie Ridge	0.167 0.184 0.165 0.162 0.163 0.170 0.169 0.167 0.186 0.165 0.162 0.163 0.170 0.169	9 0 166 0 17	70 0.187 0.189 0.204 70 0.191 0.191 0.204	0.191 0.165 0.1	170 0.206 0.2	0.206 0.1	74 0.174 0.17	1 0 170 0 17	2 0.203 0	1.174 (0.161	0.1/1 0.2	204 0.207 0	0.205 0.20	0.204 0	0.213 0. 0.214 0	1168 0 191 0	167 0.182	0.195 0.212	0.155	0.218 0.19	3 0 226 0.3	226 0.229 0.23	2 0.209	0.226 0.226	0.226 0. 6 0.226 0.	209 0 209 0	195 0 178 0	178 0.22	21 0.203	0.203 0.20	0.203 0.2 0.3 0.203 0.1	212 0.215	0.203 0.2	03 0.178	0.233 0.2	5 0 001	0.017
YP1063 J15-17 Yarrie Ridge.	0.193 0.225 0.197 0.197 0.189 0.198 0.217																																				02
Table. Estimates of Evolutionary Divergence	e between Sequences														-																		•				

Table. Estimates of Evolutionary Divergence between Sequences are shown. Standard error estimate(s) are shown above the diagonal. The analysis involved 70 nucleotide sequences. Codon positions included were 1st\*2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair. There were a total of 851 positions in the final dataset. Evolutionary analyses were conducted in MECA6 [1].

1. Tamura K., Steefar G., Peterson D., Frigiski A., and futures 3.2(013), MECA6: Molecular Evolutionary Genetics Analysis version 6.0. Molecular Biology and Evolution30: 2725-2729.

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Figure 5. Neighbour-joining analysis of specimens of Meenoplidae (Hempitera) from the present study. Numbers on major nodes correspond to bootstrap support over 100 iterations. Scale bargenetic distance. The specimens from the present study are highlighted in yellow; Genbank voucher specimens are highlighted in turquoise.

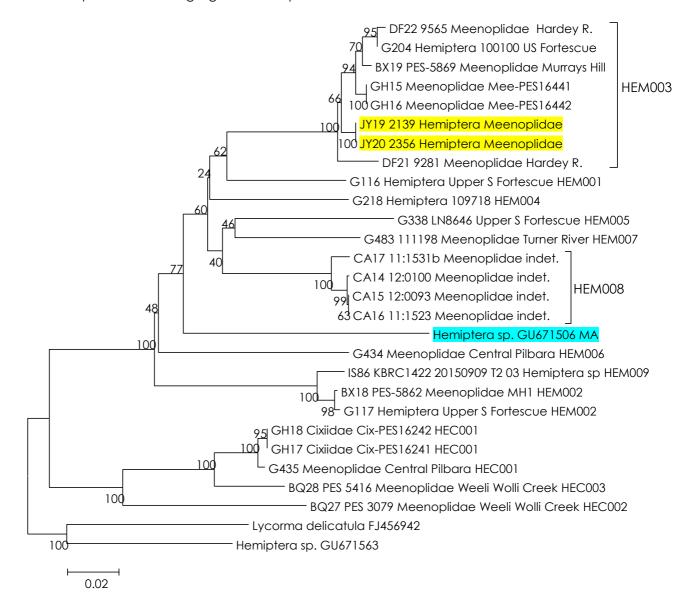


TABLE 5. Meenoplidae Distance Matrix																										
	Y19 2139 Hemiptera Meenoplidae	20 2356 Hemiptera Meenoplidae	Q27 PES 3079 Meenoplidae Weeli Wolli Creek MH	Q28 PES 5416 Meenoplidae Weeli Wolli Creek MI	BX18 PES-5862 Meenoplidae MH1 MG	3X19 PES-58 <i>69</i> Meenoplidae MH1 MB	A14 12:0100 Meenoplidae indet.	CA15 12:0093 Meenoplidae indet.	A16 11:1523 Meenopiidae indet.	CA17 11:1531b Meenoplidae indet.	:21 9281 Meenoplidae sp.	:22 9565 Meenoplidae sp.	G116 Hemiptera Upper S Fortescue MC(2)	117 Hemiptera Upper S Fortescue MG(2)	204 Hemiptera 100100 widespread MB(2)	218 Hemiptera 109718(2)	338 Hemiptera LN8646 Upper S Fortescue ME(2)	434 Meenoplidae Central Pilbara MF	5435 Meenoplidae Central Pilbara MJ	483 111198 Meenoplidae Turner River MD	GH15 Meenoplidae Mee-PES16441	GH16 Meenoplidae Mee-PES16442	3H17 Cixiidae Cix-PES16241	ЭН18 Сіхіїдае Сіх-РЕS16242	lemiptera sp. GU671506 MA	86 KBRC 1 422 201 50909 12 03 Hemiptera sp
Specimen ID	₹	<u></u> 5 0.000	0.014	0.016		0.005	0.012	ට 0.012	ර 0.012	ට 0.012	0.005	占 0.008	0.010	<u>0</u>	0.006	ර 0.012	0.014	<u>ර</u> 0.014	ර 0.015	<u>ර</u> 0.014	0.005	0.005	ত 0.016	0.016	<u>半</u> 0.015	0.014
JY19 2139 Hemiptera Meenoplidae  JY20 2356 Hemiptera Meenoplidae	0.000	0.000	0.014	0.016	0.013	0.005	0.012	0.012	0.012	0.012	0.005	0.008	0.010	0.013	0.006	0.012	0.014	0.014	0.015	0.014	0.005	0.005	0.016	0.016	0.015	0.014
BQ27 PES 3079 Meenoplidae Weeli Wolli Creek MH	0.220	0.221	0.014	0.018	0.016	0.003	0.012	0.012	0.012	0.012	0.003	0.008	0.015	0.016	0.006	0.012	0.014	0.014	0.013	0.014	0.003	0.003	0.014	0.014	0.013	0.017
BQ28 PES 5416 Meenoplidae Weeli Wolli Creek MI	0.217	0.216	0.127	0.012	0.015	0.014	0.016	0.016	0.016	0.015	0.014	0.020	0.016	0.015	0.016	0.016	0.015	0.015	0.008	0.017	0.016	0.016	0.008	0.008	0.017	0.017
BX18 PES-5862 Meenoplidae MH1 MG	0.146	0.146	0.216	0.206		0.014	0.015	0.015	0.015	0.015	0.014	0.018	0.015	0.002	0.014	0.015	0.015	0.014	0.015	0.016	0.014	0.014	0.016	0.016	0.015	0.005
BX19 PES-5869 Meenoplidae MH1 MB	0.016	0.016	0.226	0.224	0.149		0.012	0.012	0.012	0.012	0.007	0.005	0.010	0.014	0.004	0.012	0.015	0.014	0.015	0.014	0.004	0.004	0.016	0.016	0.015	0.015
CA14 12:0100 Meenoplidae indet.	0.115	0.115	0.210	0.211	0.149	0.120		0.001	0.001	0.004	0.012	0.015	0.012	0.015	0.012	0.012	0.013	0.014	0.015	0.014	0.010	0.010	0.016	0.016	0.015	0.014
CA15 12:0093 Meenoplidae indet.	0.115	0.115	0.210	0.211	0.147	0.120	0.001		0.000	0.004	0.012	0.015	0.012	0.015	0.012	0.012	0.013	0.013	0.015	0.014	0.010	0.010	0.016	0.016	0.015	0.014
CA16 11:1523 Meenoplidae indet.	0.115	0.115	0.210	0.211	0.147	0.120	0.001	0.000		0.004	0.012	0.015	0.012	0.015	0.012	0.012	0.013	0.013	0.015	0.014	0.010	0.010	0.016	0.016	0.015	0.015
CA17 11:1531b Meenoplidae indet.	0.115	0.115	0.209	0.207	0.144	0.118	0.015	0.013	0.013		0.012	0.014	0.012	0.016	0.012	0.013	0.012	0.013	0.015	0.013	0.012	0.012	0.016	0.016	0.015	0.016
DF21 9281 Meenoplidae sp.	0.023	0.023	0.228	0.227	0.153	0.031	0.117	0.117	0.117	0.117		0.010	0.010	0.014	0.007	0.012	0.015	0.014	0.016	0.014	0.006	0.006	0.017	0.017	0.015	0.015
DF22 9565 Meenoplidae sp.	0.022	0.022	0.241	0.226	0.168	0.012	0.130	0.130	0.130	0.135	0.036		0.013	0.018	0.002	0.016	0.018	0.020	0.020	0.019	0.006	0.006	0.020	0.020	0.018	0.019
G116 Hemiptera Upper S Fortescue MC(2)	0.095	0.095	0.221	0.203	0.132	0.101	0.111	0.111	0.111	0.105	0.107	0.111		0.015	0.010	0.012	0.016	0.014	0.014	0.014	0.010	0.010	0.015	0.015	0.014	0.014
G117 Hemiptera Upper S Fortescue MG(2)	0.148	0.148	0.218	0.204	0.003	0.151	0.148	0.150	0.150	0.148	0.156	0.168	0.130		0.014	0.015	0.015	0.014	0.015	0.017	0.014	0.014	0.016	0.016	0.015	0.005
G204 Hemiptera 100100 widespread MB(2)	0.019	0.019	0.231	0.224	0.153	0.009	0.117	0.117	0.117	0.117	0.031	0.002	0.104	0.153		0.012	0.014	0.014	0.016	0.014	0.004	0.004	0.016	0.016	0.015	0.015
G218 Hemiptera 109718(2)	0.110	0.110	0.218	0.209	0.148	0.116	0.107	0.107	0.107	0.108	0.119	0.125	0.110	0.147	0.119		0.014	0.016	0.016	0.015	0.012	0.012	0.016	0.016	0.016	0.015
G338 Hemiptera LN8646 Upper S Fortescue ME(2)	<mark>0.136</mark>	0.136	0.223	0.189	0.168	0.137	0.112	0.112	0.112	0.114	0.142	0.139	0.128	0.167	0.136	0.127		0.016	0.014	0.014	0.014	0.014	0.014	0.014	0.015	0.015
G434 Meenoplidae Central Pilbara MF	<mark>0.153</mark>	0.154	0.210	0.207	0.138	0.156	0.152	0.150	0.150	0.146	0.162	0.171	0.138	0.144	0.159	0.147	0.158		0.015	0.015	0.015	0.015	0.016	0.016	0.016	0.014
G435 Meenoplidae Central Pilbara MJ	0.206	0.205	0.137	0.045	0.204	0.216	0.195	0.194	0.194	0.192	0.213	0.204	0.203	0.206	0.213	0.200	0.187	0.208		0.015	0.015	0.015	0.003	0.003	0.018	0.017
G483 111198 Meenoplidae Turner River MD	<mark>0.117</mark>	0.117	0.227	0.212	0.162	0.120	0.109	0.108	0.108	0.104	0.126	0.135	0.107	0.166	0.121	0.124	0.111	0.142	0.191		0.014	0.014	0.016	0.016	0.016	0.016
GH15 Meenoplidae Mee-PES16441	<mark>0.016</mark>	0.016	0.229	0.226	0.150	0.012	0.110	0.110	0.112	0.116	0.025	0.014	0.103	0.150	0.010	0.116	0.139	0.163	0.214	0.121		0.000	0.016	0.016	0.015	0.013
GH16 Meenoplidae Mee-PES16442	<mark>0.016</mark>	0.016	0.229	0.226	0.150	0.012	0.110	0.110	0.112	0.116	0.025	0.014	0.103	0.150	0.010	0.116	0.139	0.163	0.214	0.121	0.000		0.016	0.016	0.015	0.013
GH17 Cixiidae Cix-PE\$16241	0.204	0.205	0.133	0.050	0.204	0.215	0.200	0.200	0.200	0.190	0.212	0.200	0.202	0.205	0.210	0.202	0.184	0.206	0.006	0.193	0.219	0.219		0.000	0.019	0.017
GH18 Cixiidae Cix-PE\$16242	0.204	0.205	0.133	0.050	0.204	0.215	0.200	0.200	0.200	0.190	0.212	0.200	0.202	0.205	0.210	0.202	0.184	0.206	0.006	0.193	0.219	0.219	0.000		0.019	0.017
Hemiptera sp. GU671506 MA	<mark>0.169</mark>	0.169	0.250	0.234	0.191	0.167	0.178	0.178	0.178	0.179	0.170	0.161	0.163	0.193	0.167	0.158	0.163	0.178	0.236	0.157	0.169	0.169	0.234	0.234		0.016
IS86 KBRC 1422 20150909 T2 03 Hemiptera sp	0.155	0.154	0.223	0.199	0.020	0.158	0.145	0.143	0.146	0.152	0.166	0.178	0.130	0.017	0.159	0.151	0.169	0.152	0.199	0.166	0.147	0.147	0.212	0.212	0.194	

Table. Estimates of Evolutionary Divergence between Sequences

The number of base differences per site from between sequences are shown. Standard error estimate(s) are shown above the diagonal. The analysis involved 28 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair. There were a total of 834 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 [1].

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<sup>1.</sup> Tamura K., Stecher G., Peterson D., Filipski A., and Kumar S. (2013). MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Molecular Biology and Evolution30: 2725-2729.

Figure 6. Neighbour-joining analysis of specimens of Isopoda from the present study. Numbers on major nodes correspond to bootstrap support over 100 iterations. Scale bar= genetic distance. The specimens from the present study are highlighted in yellow; Genbank voucher specimens are highlighted in turquoise.

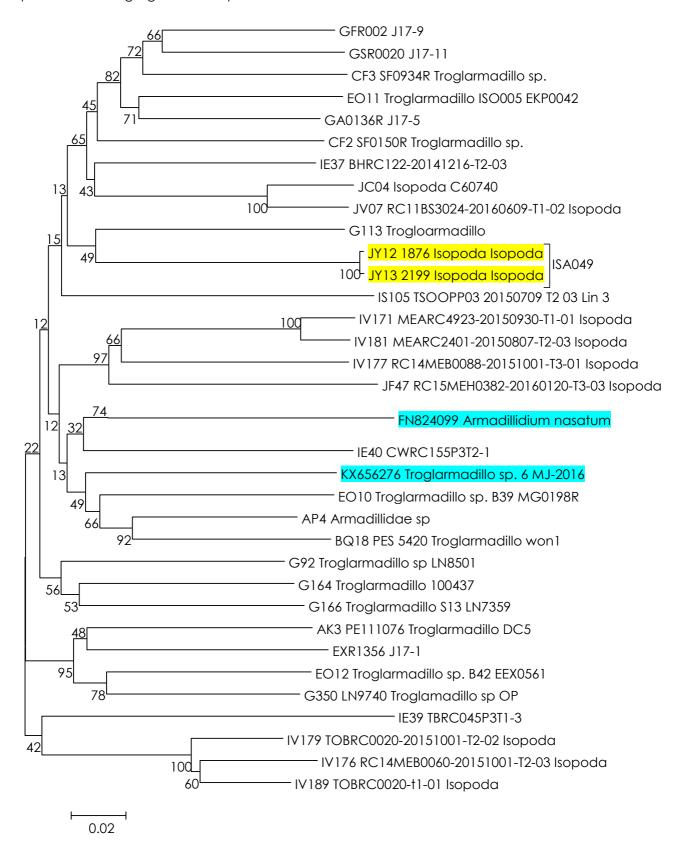


TABLE 6. Isopoda Distance Matrix	1																																
Lineage ID	JY12 1876 Isopoda Isopoda	JY13 2199 Isopoda Isopoda	AK3 PE111076 Troglam DC5	AP4 Armadilidae sp	BQ18 PES 5420 Troglamadillo won1	CF2 SF0150R Troglamadillo sp.	CF3 SF0934R Traglarmadillo sp.	EO10 Troglarmadillo sp. B39 MG0198R	EO11 Troglamadillo ISO005 EKP0042	EO12 Troglamadillo sp. B42 EEX0561	EXR1356 J17-1	FN824099 Armadillidium nasatum	G113 Trogloarmadillo	G164 Troglarmadillo 100437	G166 Troglarmadillo S13 LN7359	0 Troglame	GY2 Iroglamadillo sp LN8501	GA0136R J17-5	GSR0020 J17-11	IE37 BHRC 122-20141216-T2-03	45P3T1-3	IE40 CWRC155P3T2-1	IS105 TSOOPP03 20150709 T2 03 Lin 3	IV 171 MEARC 4923-20150930-T1-01 Isopoda	IV 176 RC 14MEB0060-20151001-T2-03 Isopod	IV 177 RC 14MEB0088-20151001-T3-01 Isopod	IV 179 TOBR C0020-20151001-T2-02 Isopoda	IV 181 MEARC 2401-20150807-12-03 Isopoda	IV 189 TOBR C0020-11-01 Isopoda	JC04 Isopoda C60740	JF47 RC15MEH0382-20160120-T3-03 Isopodd	JV07 RC11BS3024-20160609-T1-02 Isopoda	KX656276 Troglarmadillo sp. 6 MJ-2016
JY12 1876 Isopoda Isopoda		0.002	0.017	0.016	0.016	0.014	0.017	0.016	0.017	0.015	0.016	0.014	0.015	0.016	0.016	0.016 0.0	13 0.	.016 0.01	5 0.017	0.015	0.020	0.015	0.016	0.018	0.015	0.014	0.015	0.018	0.014	0.016	0.016	0.016	0.017
JY13 2199 Isopoda Isopoda	0.003		0.017	0.015	0.016	0.014	0.017	0.016	0.017	0.015	0.016	0.014	0.015	0.016	0.016	0.016 0.0	13 0.	.016 0.01	5 0.017	0.015	0.020	0.015	0.016	0.018	0.015	0.014	0.015	0.018	0.014	0.016	0.016	0.016	0.017
AK3 PE111076 Troglarm DC5		0.224		0.014	0.016		0.016	0.016	0.014	0.016	0.015	0.015	0.017	0.016	0.015	0.015 0.0	_	.015 0.01	5 0.015	0.016	0.024	0.017	0.017	0.015		0.016	0.016	0.015	0.016	0.016	0.014	0.015	0.015
AP4 Armadillidae sp		0.187	0.183		0.014			0.016	0.013		0.015	0.014	0.015	0.014	0.013	0.016 0.0	_	.013 0.01	5 0.014	0.014	0.021	0.015	0.015	0.016		0.015	0.012	0.015	0.013	0.012	0.013	0.012	0.014
BQ18 PES 5420 Troglarmadillo won1		0.190						0.016	0.015		0.017	0.014	0.016	0.016	0.016	0.017 0.0	_	.015 0.01	6 0.015	0.016	0.025	0.016	0.017	0.018		0.017	0.015	0.018	0.016	0.015	0.015	0.013	0.017
CF2 SF0150R Troglarmadillo sp.	0.203	0.000	0.199		0.213			0.015	0.015		0.016	0.014	0.016	0.013	0.014	0.016 0.0		.014 0.01	4 0.013	0.012	0.020	0.017	0.015	0.016		0.015	0.015	0.016	0.015	0.015	0.012	0.016	0.015
CF3 SF0934R Troglarmadillo sp.		0.197	0.204	0.205				0.016	0.015	0.016	0.016	0.015	0.015	0.015	0.016	0.016 0.0	_	.013 0.01	3 0.014	0.014	0.022	0.018	0.015	0.017	0.019	0.015	0.016	0.017	0.017	0.014	0.015	0.015	0.017
EO10 Troglarmadillo sp. B39 MG0198R	0.225	_	0.221	0.160		0.217			0.015		0.016	0.014	0.016	0.013	0.015	0.016 0.0		.015 0.01	5 0.016	0.015	0.024	0.017	0.015	0.016		0.016	0.014	0.016	0.013	0.015	0.014	0.014	0.015
EO11 Troglarmadillo ISO005 EKP0042	0.221		0.204	0.190	000			0.197		0.015	0.016	0.015	0.015	0.015	0.014	0.015 0.0		.013 0.01	6 0.015	0.015	0.021	0.018	0.014	0.018		0.016	0.016	0.018	0.015	0.015	0.014	0.015	0.015
EO12 Troglarmadillo sp. B42 EEX0561	0.219		0.187	0.183				0.190			0.017	0.016	0.014	0.015	0.014	0.014 0.0		.014 0.01	4 0.015	0.013	0.023	0.015	0.015	0.014		0.015	0.014	0.014	0.015	0.015		0.015	0.014
EXR1356 J17-1	0.237	0.00	0.170	0.193	0.220		0.220	0.209		0.176		0.016	0.017	0.016	0.015	0.014 0.0		.016 0.01	3 0.016	0.013	0.023	0.014	0.017	0.015		0.016	0.014	0.016	0.014	0.016		0.016	0.016
FN824099 Armadillidium nasatum	0.242		0.245	0.212				0.209			0.228		0.014	0.012	0.015	0.015 0.0		.015 0.01	5 0.015	0.015	0.021	0.015	0.017	0.016	0.014	0.015	0.013	0.016	0.014	0.014	0.015	0.015	0.015
G113 Trogloarmadillo	0.189		0.215	0.174	0.200			0.225	0.217	0.225	0.230			0.016	0.014	0.016 0.01		.015 0.01	6 0.014	0.016	0.020	0.014	0.015	0.017	0.014	0.017	0.014	0.017	0.014	0.015	0.016	0.014	0.015
G164 Troglarmadillo 100437	0.216	_	0.191	0.203	0.200			0.199		0.215	0.220	0.228	0.206		0.014	0.015 0.0	_	.015 0.01	4 0.013	0.016	0.022	0.014	0.017	0.016	0.016	0.014	0.015	0.015	0.015	0.014	0.015	0.015	0.015
G166 Troglarmadillo S13 LN7359	0.222		0.197	0.182	0.210	0.203	0.203	0.215	0.193	0.201	0.200	0.235	0.210	0.161		0.014 0.0	13 0.	.015 0.01	5 0.014	0.015	0.021	0.014	0.016	0.015	0.013	0.014	0.013	0.016	0.014	0.015	0.013	0.014	0.015
G350 LN9740 Troglamadillo sp OP	0.233	0.200	0.173	0.178	0.210			0.198	0.204		0.164	0.210	0.222	0.189		0.0		.015 0.01	5 0.015	0.015	0.020	0.015	0.015	0.016	0.014	0.015	0.015	0.016	0.015	0.017	0.014	0.016	0.015
G92 Troglarmadillo sp LN8501	0.215		0.205	0.203				0.196		0.182		0.234	0.210		0.162			.015 0.01	4 0.015	0.015	0.021	0.015	0.016	0.015	0.015	0.014	0.015	0.015	0.015	0.014	0.013	0.012	0.013
GA0136R J17-5		0.211	0.213	0.193	0.194	0.170	0.148		0.141		0.217	0.229	0.213	0.203	0.182	0.193 0.18	_	0.01	3 0.013	0.015	0.023	0.017	0.014	0.017	0.016	0.016	0.015	0.017	0.015	0.015	0.014	0.013	0.016
GFR002 J17-9	0.203	0.000	0.205	0.195	0.206	0.180	0.153	0.203	0.168		0.217	0.252	0.196	_	0.182	0.221 0.19	_	.148	0.012	0.015	0.022	0.017	0.015	0.017		0.017	0.015	0.017	0.013	0.014	0.015	0.015	0.016
GSR0020 J17-11	0.205	0.000	0.219	0.191	0.217	****			0.174		0.232	0.251	0.202	_		0.223 0.20		.150 0.13	-	0.014	0.021	0.016	0.014	0.018		0.016	0.017	0.017	0.016	0.014	0.014	0.014	0.015
IE37 BHRC122-20141216-T2-03		0.189	0.207	0.187			0.174			0.204		0.227	0.199	0.196		0.209 0.19	_	.167 0.16		_	0.022	0.016	0.015	0.016		0.015	0.015	0.016	0.014	0.014	0.014	0.014	0.016
IE39 TBRC045P3T1-3	0.246		0.245	0.232	0.243	0.246			0.251	0.243		0.262	0.243	_	0.253	0.236 0.24	_	.222 0.26	_	_		0.018	0.019	0.022	0.019	0.021	0.020	0.022	0.021	0.023	0.019	0.021	0.020
IE40 CWRC155P3T2-1	0.217	_	0.213	0.189				0.192	0.214		0.212	0.221	0.188	0.226	0.214	0.204 0.20	_	.222 0.22	_	0.218			0.018	0.014	0.014	0.015	0.014	0.014	0.015	0.017	0.014	0.016	0.015
IS 105 TSOOPP03 20150709 T2 03 Lin 3		0.228	0.248	0.228		0.208			0.226		0.238	0.242	0.216			0.235 0.20	_	.198 0.21		0.216		0.258		0.016		0.017	0.016	0.017	0.016	0.016		0.015	0.014
IV171 MEARC4923-20150930-T1-01 Isopoda		0.237	0.243	0.222		0.217			0.219		0.237	0.215	0.225	-	0.203	0.225 0.19	_	.206 0.22		0.223	0.267	0.214	0.216			0.016	0.014	0.006	0.015	0.015	0.014	0.015	0.015
IV176 RC14MEB0060-20151001-T2-03 Isopoda		0.231	0.230	0.198				0.215	0.250		0.209	0.223	0.225	0.188	0.207	0.188 0.20	_	.236 0.22		1 0.218	0.219	0.223	0.230	0.231		0.015	0.010	0.016	0.010	0.014	0.016	0.015	0.016
IV177 RC14MEB0088-20151001-T3-01 Isopoda		0.219	0.235	0.201	0.201	0.00		0.200	0.223	0.232		0.219	0.216	_	0.207	0.220 0.20	_	.217 0.22	_	1 0.214	0.258	0.218	0.232	0.166	0.218		0.013	0.016	0.014	0.014	0.015	0.015	0.017
IV179 TOBRC0020-20151001-T2-02 Isopoda	0.211		0.213	0.198	0.2.0	0.00	*·	0.198	0.227		0.187	0.212	0.222		0.191	0.200 0.18	_	.216 0.21			0.217	0.204	0.218	0.201		0.207		0.013	0.009	0.015		0.015	0.015
IV181 MEARC2401-20150807-T2-03 Isopoda	0.236	000	0.232	0.216		0.220		0.198	0.219		0.236	0.212	0.225	0.215	0.200	0.216 0.19	_	.205 0.21	_	0.217	0.267	0.217	0.220	0.038		0.169			0.014	0.016		0.015	0.015
IV189 TOBRC0020-t1-01 Isopoda	0.221	_	0.221	0.195	0.210		0.234		0.227		0.203	0.212	0.224		0.197	0.197 0.18		.214 0.20		0.202	0.229	0.205	0.226	0.216		0.211	0.067			0.014		0.013	0.015
JC04 Isopoda C60740	0.214	_	0.205	0.192		0.192	0.185	0.210	0.192	0.210	0.222	0.252	0.199	0.193	0.212	0.233 0.22		.200 0.19	_	0.180	0.251	0.226	0.213	0.230		0.224			0.213		0.014	0.010	0.017
JF47 RC15MEH0382-20160120-T3-03 Isopoda		0.246	0.237	0.211	0.216	0.219	0.228	0.220	0.224	0.229	0.239	0.236	0.227	0.219	0.219	0.225 0.2	_	.219 0.22		0.220	0.267	0.221	0.231	0.191		0.185	•	0.185		0.238	0.07	0.013	0.014
JV07 RC11BS3024-20160609-T1-02 Isopoda	0.212	_	0.208	0.195	+	_		0.197		0.223	0.232	0.252	0.193	-	0.215	0.231 0.20	_	.191 0.18	_			0.218		0.229		0.223		0.232		0.061	0.224		0.016
KX656276 Troglarmadillo sp. 6 MJ-2016	0.203	0.203	0.201	0.170	0.184	0.211	0.230	0.181	0.209	0.208	0.222	0.220	0.200	0.222	0.225	0.216 0.19	77 0.	.211 0.20	0.217	0.211	0.234	0.206	0.221	0.211	0.226	0.206	0.220	0.201	0.217	0.228	0.226	0.223	

Table. Estimates of Evolutionary Divergence between Sequences

The number of base differences per site from between sequences are shown. Standard error estimate(s) are shown above the diagonal. The analysis involved 35 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair. There were a total of 714 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 [1].

1. Tamura K., Stecher G., Peterson D., Filipski A., and Kumar S. (2013). MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Molecular Biology and Evolution30: 2725-2729.

Figure 7. Neighbour-joining analysis of specimens of Symphyla from the present study. Numbers on major nodes correspond to bootstrap support over 100 iterations. Scale bar= genetic distance. The specimens from the present study are highlighted in yellow; Genbank voucher specimens are highlighted in turquoise.

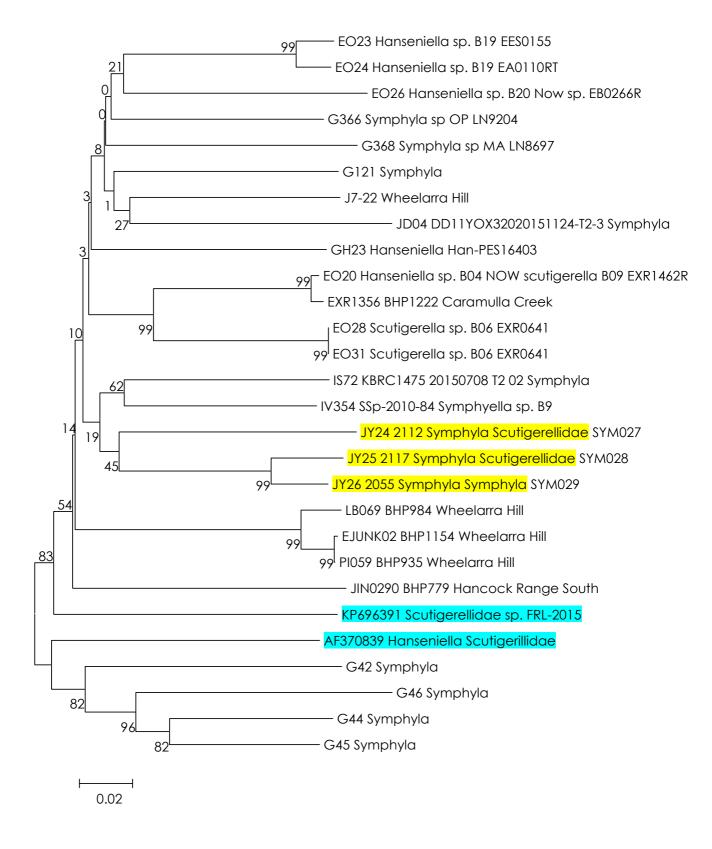


TABLE 7. Symphyla Distance Matrix																												
Specimen ID	1Y24 21 12 Symphyla Scutigerellidae	1725 2117 Symphyla Scutigerellidae	JY26 2055 Symphyla Symphyla	AF370839 Hanseniella Scutigerillidae	EJUNK02 BHP1154 Jimblebar E	EO20 Hanseniella sp. 804 NOW scutigerella 809 EXR14621	EO23 Hanseniella sp. B19 EES0155	EO24 Hanseniella sp. B19 EA0110RT	EO26 Hanseniella sp. B20 Now sp. EB0266R	EO28 Scutigerella sp. B06 EXR0641	EO31 Scutigerella sp. B06 EXR0641	EXR1356 BHP1222 Caramulla Creek	3121 Symphyla	3366 Symphyla sp OP LN9204	G368 Symphyla sp MA LN8697	G42 Symphyla	G44 Symphyla	G45 Symphyla	G46 Symphyla	GH23 Hanseniella Han-PES16403	S72 KBRC1475 20150708 T2 02 Symphyla	V354 SSp-2010-84 Symphyella sp. B9	77-22 Wheelarra Hill	JD04 DD11YOX32020151124-12-3 Symphyla	JIN0290 BHP779 Hancock Range South	P696391 Scutigerellidae sp. FRL-2015	LB069 BHP984 Hashimoto	PIOS9 BHP935 Hashimoto
JY24 2112 Symphyla Scutigerellidae		0.014	0.014	0.015	0.012		<u>ш</u> 0.015	0.014	0.013	0.01 <i>7</i>	0.017	0.013	0.013	0.012	0.015	0.018	0.017	0.013	0.021	0.015	0.014	0.011	0.012	0.015	0.016	0.018	0.011	0.012
JY25 2117 Symphyla Scutigerellidae	0.175	0.014	0.010		0.012					0.013	0.013	0.016			0.014	0.019		0.013			0.014	0.015	0.014		0.017			0.013
JY26 2055 Symphyla Symphyla	0.166	0.049		0.017	0.013			_	0.012	0.013	0.013	0.015	0.013	0.013	0.015	0.018	0.019	0.015	0.025		0.014	0.015	0.012	0.020	0.018	0.018	0.013	0.013
AF370839 Hanseniella Scutigerillidae	0.211	0.224	0.220		0.014	0.017	0.015	0.013	0.013	0.016	0.016	0.017	0.012	0.014	0.014	0.019	0.017	0.015	0.017	0.011	0.017	0.015	0.015	0.018	0.014	0.016	0.014	0.014
EJUNK02 BHP1154 Wheelarra Hill	0.194	0.192	0.198	0.209		0.013	0.016	0.013	0.014	0.016	0.016	0.014	0.014	0.017	0.016	0.021	0.017	0.016	0.018	0.014	0.016	0.015	0.013	0.017	0.016	0.017	0.006	0.001
EO20 Hanseniella sp. B04 NOW scutigerella B09 EXR1462R	0.172	0.209	0.203	0.226	0.192		0.015	0.015	0.012	0.012	0.012	0.003	0.012	0.014	0.014	0.020	0.019	0.014	0.021	0.013	0.016	0.012	0.015	0.017	0.014	0.018	0.015	0.014
EO23 Hanseniella sp. B19 EES0155	0.202	0.178	0.172	0.223	0.197	0.181		0.005	0.014	0.013	0.013	0.017	0.013	0.012	0.011	0.019	0.017	0.016	0.022	0.015	0.012	0.012	0.014	0.017	0.015	0.018	0.013	0.015
EO24 Hanseniella sp. B19 EA0110RT	0.206	0.175	0.166	0.218	0.194	0.183	0.027		0.013	0.013	0.013	0.017	0.015	0.014	0.012	0.019	0.016	0.014	0.023	0.013	0.013	0.013	0.013	0.016	0.016	0.018	0.012	0.014
EO26 Hanseniella sp. B20 Now sp. EB0266R	0.211	0.195	0.192	0.240	0.228	0.181	0.173	0.168		0.015	0.015	0.013	0.014	0.012	0.014	0.015	0.020	0.011	0.017	0.012	0.012	0.015	0.015	0.015	0.016	0.020	0.014	0.014
EO28 Scutigerella sp. B06 EXR0641	0.203	0.187	0.191	0.217	0.195	0.125	0.176	0.180	0.197		0.000	0.013	0.013	0.011	0.015	0.020	0.016	0.016	0.017	0.013	0.014	0.012	0.012	0.015	0.015	0.020	0.017	0.017
EO31 Scutigerella sp. B06 EXR0641	0.203	0.187	0.191	0.217	0.195	0.125	0.176	0.180	0.197	0.000		0.013	0.013	0.011	0.015	0.020	0.016	0.016	0.017	0.013	0.014	0.012	0.012	0.015	0.015	0.020	0.017	0.017
EXR1356 BHP1222 Caramulla Creek	0.179	0.212	0.206	0.226	0.191	0.008	0.183	0.183	0.180	0.133	0.133		0.012	0.014	0.016	0.022	0.019	0.015	0.021	0.014	0.018	0.014	0.015	0.017	0.013	0.018	0.015	0.014
G121 Symphyla	0.196	0.191	0.176	0.216				0.180			0.177			0.013	0.013	0.020	0.016	0.012	0.021	0.011	0.016	0.012	0.013	0.014	0.016	0.018		0.013
G366 Symphyla sp OP LN9204	0.203		0.190		0.190			0.164			0.171		0.174		0.012	0.020	0.015	0.016			0.015	0.012	0.014		0.015	0.020		0.016
G368 Symphyla sp MA LN8697	0.186	0.211	0.206	0.220	0.202			0.188			0.196		0.185			0.016	0.018	0.016			0.015	0.014	0.014		0.014	0.017	0.016	0.016
G42 Symphyla	0.238	0.216	0.201		0.260			0.212			0.228				0.239		0.017	0.014			0.020	0.022	0.017		0.019	0.017	0.021	0.021
G44 Symphyla	0.241	0.231	0.227	0.208	0.218			_		0.245		0.224			0.224			0.012			0.021	0.019	0.021	0.030	0.021	0.021	0.018	0.017
G45 Symphyla	0.226	0.227	0.224	0.200	0.236					0.231		0.224				0.182	_		0.017		0.015	0.017	0.017	0.020	0.015	0.017	0.017	0.016
G46 Symphyla	0.253	0.267	0.258	0.217	0.240		0.244			0.216	0.216			0.252		0.215	0.178			0.020	0.025	0.023	0.019	0.026	0.018	0.022	0.020	0.018
GH23 Hanseniella Han-PE\$16403	0.191		0.191		0.189			0.179		0.182	0.182					0.224	_	0.227			0.013	0.013	0.015	0.020	0.013	0.018		0.014
IS72 KBRC1475 20150708 T2 02 Symphyla	0.174		0.163		0.205			0.163		0.187	0.187					0.207	0.229			0.181		0.014	0.012	0.020	0.016	0.017	0.015	0.016
IV354 SSp-2010-84 Symphyella sp. B9	0.194		0.163	0.221	0.186			0.185			0.177					0.239	_	0.218		0.186		0.170	0.014	0.017	0.014	0.017	0.015	0.015
J7-22 Wheelarra Hill	0.221		0.191		0.202			0.165		0.185	0.185					0.254		0.223			0.197		0.175		0.013	0.017		0.014
JD04 DD11YOX32020151124-T2-3 Symphyla	0.189	0.212	0.210	0.228	0.216			0.195			0.199					0.255	_	0.228			0.210				0.020	0.021	0.017	0.017
JIN0290 BHP779 Hancock Range South	0.221	0.170	0.197	0.229				0.195		0.203	0.203			0.186		0.212		0.224		0.196		0.208	0.205		0.01-	0.017		0.016
KP696391 Scutigerellidae sp. FRL-2015	0.237	0.207	0.201	0.220	0.215					0.207		0.195	0.216		-	0.221	0.247	0.238				0.204	0.198	0.241			0.019	0.017
LB069 BHP984 Wheelarra Hill	0.187	0.196	0.201		0.029			0.192		0.201	0.201	0.192				0.258		0.240			0.199		0.212		0.195			0.006
PI059 BHP935 Wheelarra Hill	0.192	0.191	0.197	0.209	0.002	0.191	0.195	0.195	0.228	0.194	0.194	0.189	0.203	0.189	0.200	0.260	0.218	0.236	0.240	0.189	0.203	0.185	0.200	0.216	0.209	0.214	0.028	1

Table. Estimates of Evolutionary Divergence between Sequences

The number of base differences per site from between sequences are shown. Standard error estimate(s) are shown above the diagonal. The analysis involved 28 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair. There were a total of 14667 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 [1].

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<sup>1.</sup> Tamura K., Stecher G., Peterson D., Filipski A., and Kumar S. (2013). MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Molecular Biology and Evolution30: 2725-2729.

# Orebody Knowledge & Planning - Water Resource Evaluation & Services

# West Angelas – Deposits C and D Hydrogeological Conceptual Model

RTIO-PDE-0150624 - WANG Deposit B Conceptual hydro model.docx: <a href="http://iodms/iodms/drl/objectId/090188a380a6c711">http://iodms/iodms/drl/objectId/090188a380a6c711</a>

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### 1. Introduction

This report details a conceptual hydrogeological model over the area encompassing West Angelas Deposits C and D (Figure 1). The model described herein will form the foundation for subsequent mathematical modelling to be completed to support assessment of Life-of-Mine (LOM) dewatering and water supply options considered as part of a Pre-Feasibility Study (PFS).

The West Angelas deposits are located approximately 100 km north-west of Newman and are covered by mining lease AML70/00248, as part of the HI State Agreement. The main structural feature of the West Angelas region is the regional, east-west trending Wonmunna Anticline. The Wonmunna Anticline hosts a series of discontinuous deposits; (from west to east) Deposits C, G, B and H occur along the northern limb and Deposits D, Awest, A, E and F along the southern limb. Deposits C and D are located to the southwest of the main West Angelas village as shown in Figure 1.

On the basis of a regional groundwater elevation of 625m RL, the maximum depth of dewatering required at Deposit D is  $\sim$ 130 m (compared to  $\sim$ 70 m at Deposit C). This equates to  $\sim$ 30% of the total reserve below the water table (BWT) at Deposit C and  $\sim$ 50% of the total reserve BWT at Deposit D.

Mining at Deposits C and D is due to commence in 2020, and BWT mining due to commence in 2023 and 2022 respectively.

Hydrogeological investigations conducted to-date have been carried out to enable assessment of the following:

- Available water supply options to satisfy construction and dust suppression demand,
- · Determination of dewatering requirements to facilitate BWT mining,
- Drawdown associated with dewatering activities for the duration of LOM
- Most appropriate management strategy, including discharge of surplus dewatering.

Hydrogeological field investigations at Deposit C and D initially targeted the deepest sections of each orebody. This enabled assessment of hydraulic characteristics of key hydrostratigraphic units, specifically, mineralised fractured rock aquifer of the Marra Mamba Iron Formation and West Angela Member of the Wittenoom Formation.

Additional drilling outside the proposed footprint of each orebody was conducted to target underlying and adjacent Wittenoom Formation. In particular, drilling in the area west of Deposit C and D has enabled the establishment of a groundwater monitoring network directly adjacent Karijini National Park (KNP), where a potential groundwater dependent ecosystem (GDE) has been identified approximately 3.5 km's from the western perimeter.

Hydrogeological investigations completed to-date within and in the immediate vicinity of Deposits C and D have resulted in the installation of 32 vibrating wire piezometers, 69 monitoring bores and five production bores.

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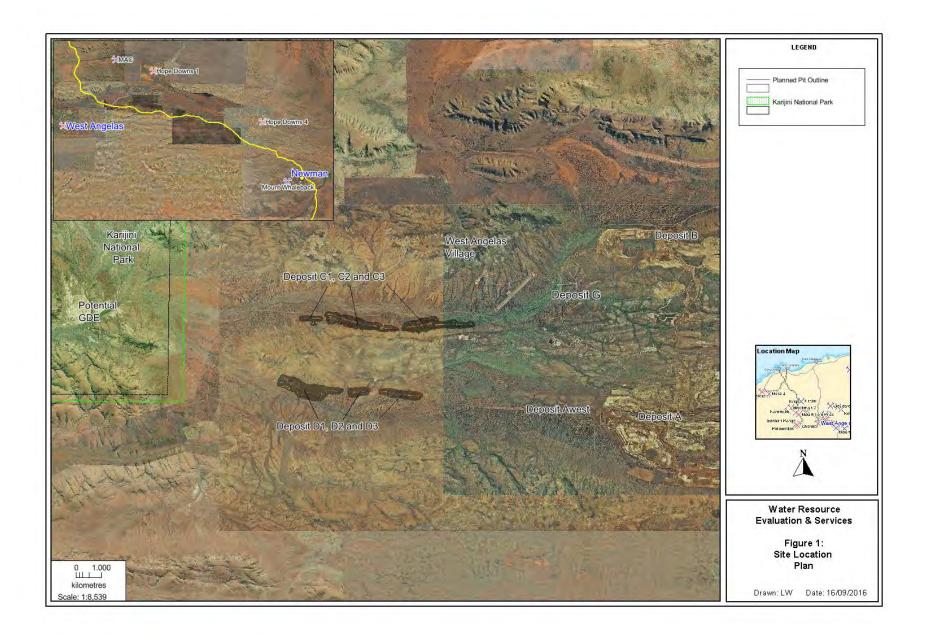


Figure 1: Site location plan

# 2. Regional setting

### 2.1 Climate

Rainfall at West Angelas is typically associated with tropical low pressure systems and thunderstorm activity from the monsoonal trough that develops over northern Australia during summer.

Analysis of Bureau of Meteorology (BoM) recorded daily rainfalls (BoM, 2012), shows that on average there are 37 rain event days per year for the area, with only 8 of those rain event days having a rainfall total greater than 10 mm.

The long term mean annual rainfall (1907 to 2015) for West Angelas is 317 mm, estimated based on gridded rainfall data, with a historical annual range of 75 to 820 mm illustrating the high inter-annual variability (Figure 2).

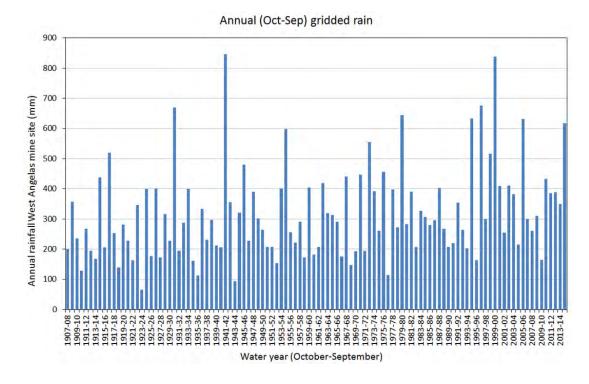


Figure 2: Annual (October to September) gridded rainfall for West Angelas

As depicted in Figure 3, the monthly rainfall is highly seasonal with approximately 72% of the annual total occurring between December and April. Winters are typically dry and mild though winter rain events can occur in June and July as a result of tropical cloud bands that intermittently affect the area.

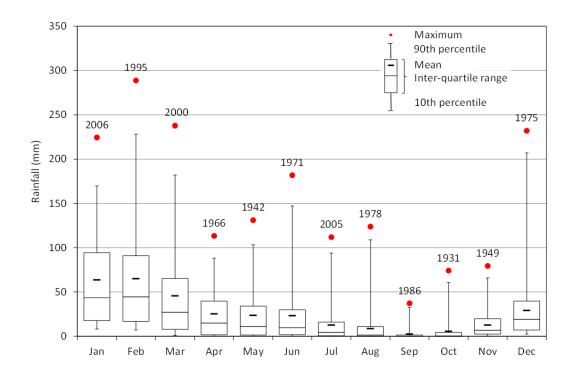


Figure 3: Monthly gridded rainfall distribution for West Angelas

# 2.2 Hydrology

Deposits C and D are located in the catchment of Turee Creek East (TCE), with a catchment area of approximately 213 km² (Figure 4). Although surface water management infrastructure has been proposed to divert TCE entering Deposit C and D, run-off from local catchments will still be intercepted by the pits and require active management (e.g. sump and pump).

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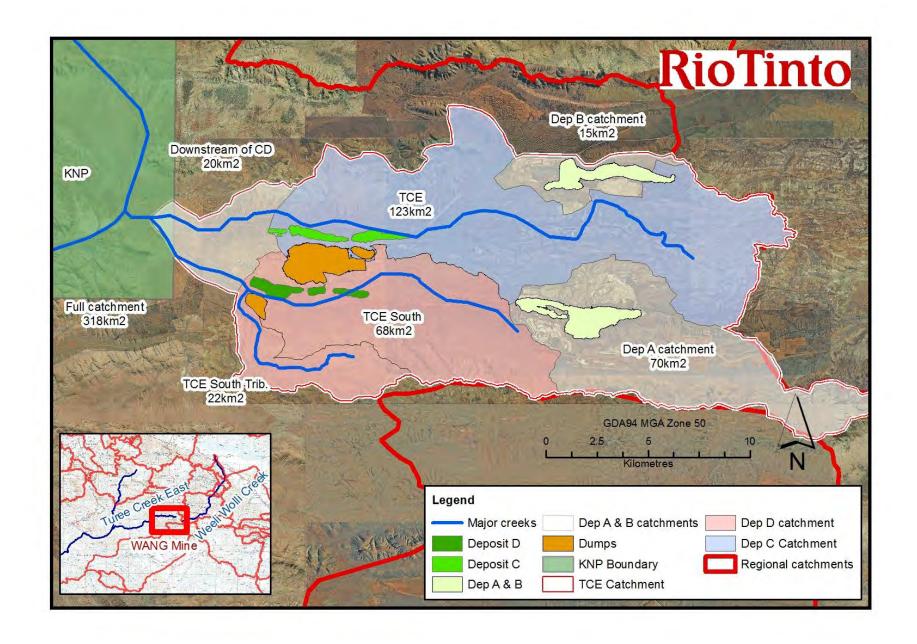


Figure 4: Major creeks and catchments at West Angelas Deposit C and D

# 2.3 Geology

Deposits C and D are principally Marra Mamba Iron Formation deposits (Mount Newman Member), with minor mineralisation present in the MacLeod Member as well as the Wittenoom Formation (West Angela Member) and Tertiary Detritals (RTIO, 2017a). A summary of the regional stratigraphy is presented in Figure 5.

### 2.3.1 Stratigraphy

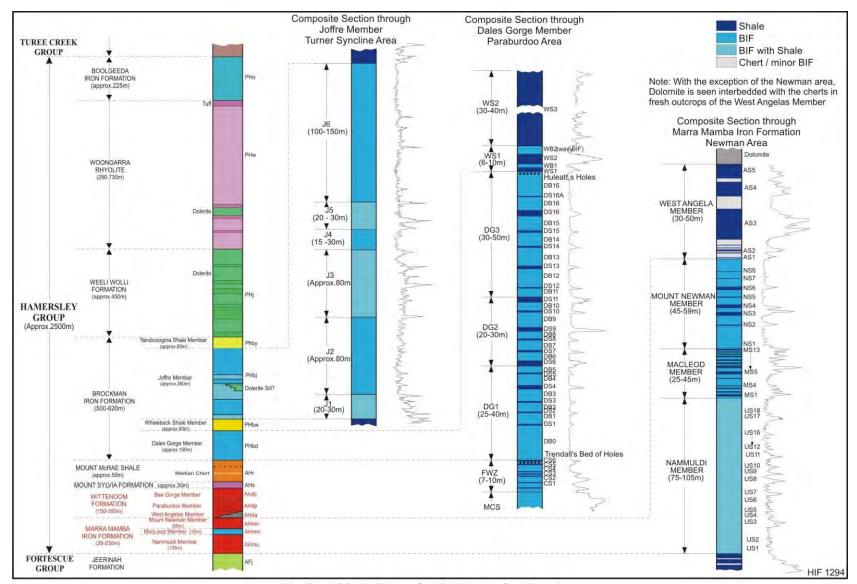
Table 1 presents a summary of the stratigraphy encountered in the area of Deposits C and D on the basis of resource and hydrogeological drilling investigations conducted todate.

Table 1: Summary of stratigraphy encountered

Stratigraphy	Max. thickness encountered (m)
Nammuldi Member (BIF, chert)	33
MacLeod Member (BIF, shale, chert)	63
Mount Newman Member (ore, BIF, chert, shale)	93
Un-differentiated Wittenoom Formation (shale, chert, ore, BIF, clay, silcrete, dolomite)	164
Detritals (hematite, goethite, chert, BIF with clay, calcrete, limonite, shale)	130

### 2.3.2 Structure

Deposits C and D are located on the northern and southern limbs respectively of the east west trending, west plunging Wonmunna anticline. Deposit C is dominated by lithologies dipping to the north for the most part at around 30 degrees. Deposit D is dominated by lithologies dipping to the south for the most part at around 35 degrees. However, the western area of Deposit D is structurally more complex, with an open syncline interpreted in this area (RTIO, 2017). Similar to other iron ore deposits in the Pilbara, operating mine the area has been subject to intrusion by NE/SW and NW/SE trending Dolerite dykes.



Stratigraphic Columns for the Hamersley Group

Figure 5: Summary of the regional stratigraphy

# 3. Hydrogeology

# 3.1 Bore network

Data acquisition has been on-going since 2004, with the main phase of fieldwork carried out in 2016 (RTIO, 2016b). Hydrogeological investigations completed to-date within and in the immediate vicinity of Deposits C and D have resulted in the installation of 32 vibrating wire piezometers, 69 monitoring bores and five production bores. The locations of bores in the area are presented in (Figure 6), with a summary of the stratigraphy encountered in Appendix 1.

Hydrogeological drilling has generally targeted a combination of the Mount Newman Member, Wittenoom Formation (un-differentiated) and the orebody (i.e. mineralised Mount Newman Member and Wittenoom Formation), as well as multiple stratigraphic units, to obtain representative groundwater levels in the area.

# 3.2 Data sources and previous studies

The area in and around Deposits C and D has been subject to borehole drilling and pumping testing programs to investigate the presence of groundwater as outlined in Table 2.

Table 2: Summary of previous hydrogeological investigations

Date of Issue	Document Name	Summary	IODMS link
17/09/2015	RTIO-PD-0135550: West Angelas - Deposit C Hydrogeological Conceptual Model Report	Summary of the hydrogeological conceptual model at West Angelas Deposit C. Results indicate the water table sits between 635m RL in the east and 623m RL in the west, with the presence of a groundwater divide up to 12m in the central area of the site, possibly associated with a dyke. In addition, it was noted that groundwater abstraction associated with dewatering activities might extend off site and beneath the area of the KNP.	http://iodms/iodms/drl/objectId/0 90188a380959287
01/10/2015	RTIO-PDE-0136009: Deposit C Analytical Modelling (9.1 base case)	Memo presenting results of analytical modelling solutions to approximate dewatering Deposit C. Results indicated that up to 13GL of groundwater might need to be abstracted to facilitate BWT mining.	http://iodms/iodms/drl/objectld/0 90188a38096343d
12/09/2016	RTIO-PDE-0145302 - Deposit C Analytical Modelling (Option 5A).doc	Memo presenting results of analytical modelling solutions to approximate dewatering Deposit C3. Results indicated that up to 17GL of groundwater might need to be abstracted to facilitate BWT mining. Increase in predicted volume from previous work associated with increase in duration and planned depth BWT mining.	http://iodms/iodms/drl/objectId/0 90188a380a1359b
29/09/2015	RTIO-PD-0135949: West Angelas - Deposit D Hydrogeological Conceptual Model Report	Summary of the hydrogeological conceptual model at West Angelas Deposit D. Results indicate the groundwater elevation varies between 624 and 625m RL. In addition, it was noted that groundwater abstraction associated with dewatering activities might extend off site and beneath the area of the KNP.	http://iodms/iodms/drl/objectld/0 90188a380960e52

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Date of Issue	Document Name	Summary	IODMS link
30/09/2015	RTIO-PDE-0135997: Deposit D Analytical Modelling (9.1 base case)	Memo presenting results of analytical modelling solutions to approximate dewatering at Deposit D. Results indicated that up to 38GL of groundwater might need to be abstracted to facilitate BWT mining.	http://iodms/iodms/drl/objectId/0 90188a380962d7c
14/10/16	RTIO-PDE-0146330 - 2016 Deposit C & D and Western End PFS Field Program Report_06102016 (Final).doc:	Borehole drilling and pumping testing program in the area of Deposit C and D and the area between Deposit C / D and the nearby Karijini National Park (KNP). 30 monitoring bores and five 12" test production bores were installed. Results corroborate groundwater divide identified earlier between Deposit C2 and C3. Recommended pumping rates varied between 8 and 30L/s.	http://iodms/iodms/drl/objectId/0 90188a380a2166e
28/11/16	RTIO-PDE-0147252 - West Angelas Deposits C&D Regional Groundwater model	Numerical modelling exercise to estimate the dewatering required at Deposits C2 and D for BWT mining and associated aquifer drawdown. The results indicated a maximum abstraction rate of between 9 and 25ML/day would be required, with between 10 and 53GL of groundwater removed. It was predicted that groundwater drawdown beneath the nearby KNP would be between 3 and 8m over a 100 year post mining time frame.	http://iodms/iodms/drl/objectId/0 90188a380a3561b

# 3.3 Hydrostratigraphy

Figure 7 presents a geological map covering key focus areas, with Figure 8 to Figure 17 inclusive presenting conceptual cross sections in the area.

The following section describes the geology and groundwater characteristics encountered during the course of drilling undertaken in these respective areas.

### Nammuldi Member

The Nammuldi Member is the oldest member of the Marra Mamba Iron Formation. On the basis of field mapping, in weathered outcrop, the Nammuldi Member consists of predominantly yellow and brown chert with thin hematite bands. It has distinctive and extensive development of chert pods, especially in the upper part of the unit.

Observations made during the 2016 hydrogeological drilling program show the Nammuldi Member consisted of hard, blue-grey-black BIF and chert, which was magnetic in places. The drilling method adopted did not permit acquisition of groundwater quality or airlift yield information during drilling.

The Nammuldi Member is considered to have low primary porosity.

### MacLeod Member

On the basis of observations made during resource drilling, the boundary between the MacLeod Member and the underlying Nammuldi Member is at the base of a chert horizon within the MacLeod Member, consisting of large (up to 70 cm long and 30 cm diameter) distorted ellipsoidal chert pods. This boundary is approximately 17 m above the well-defined podded chert horizon within the

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Nammuldi Member known as the "potato beds". The MacLeod Member consists of shale, chert and minor bands of hematite or goethite.

Observations made during the 2016 hydrogeological drilling program show the MacLeod Member consisted of BIF, chert, and shale, described as hard to very hard, magnetic in paces and with traces of weathering. The drilling method adopted did not permit acquisition of groundwater quality or airlift yield information during drilling.

The MacLeod Member is considered to have low primary porosity.

### Mount Newman Member

The Mount Newman Member is at the top of the Marra Mamba Iron Formation and is the main ore-bearing member of the formation. Observations made from resource drilling show it consists of nine macro bands of magnetite-rich, oxide-type BIF (with a significant silicate-carbonate content) alternating with eight macro bands of ferroan dolomite and limestone, with shaly intercalations and occasional chert beds (shaly bands NS1 – NS8.

Observations made during hydrogeological drilling investigations completed in 2016 varied, depending on whether bores were drilled either in-pit or ex-pit. In-pit bores revealed ore with interbedded shales and chert, highly weathered with low to moderate strength and evidence of faulting (with hardness and magnetism typically increasing with depth, with associated decreasing mineralisation). Ex-pit bores revealed hard siliceous BIF, chert and shale.

Airlift yields obtained during development of monitoring bores in the Mount Newman Member ranged from 5 to <0.1 L/s, indicating enhanced permeability associated with mineralised sections within the orebody. Outside of the orebody, unmineralised sequences of the Mount Newman Member have limited permeability and constrain groundwater flow. Groundwater quality is fresh ranging from EC values between 496 to 1,975  $\mu$ S/cm.

### Wittenoom Formation (un-differentiated)

The Wittenoom Formation conformably overlies the Marra Mamba Iron Formation. Elsewhere in the Pilbara it is divided into three distinct Members: West Angela (bottom), Paraburdoo (middle) and Bee Gorge (top). Only the West Angela Member has been intersected in RE drill holes in the area, consisting of shale, dolomite and minor chert increasing towards the base. Near the base of the West Angela Member, there is a 10 to 20 m thick sequence of chert, BIF and shales.

Based on observations made during the 2016 hydrogeological drilling program, it was not been possible to subdivide the Wittenoom Formation in the area. Lithologies encountered consist of BIF, Ore with inter-bedded shales, clay, chert, dolomite and silcrete, with evidence of mineralisation increasing with depth. Although evidence of weathering/fractures, vugs etc. was encountered in the dolomite towards the top of the profile, with increasing depth, the dolomite was in turn in places described as hard.

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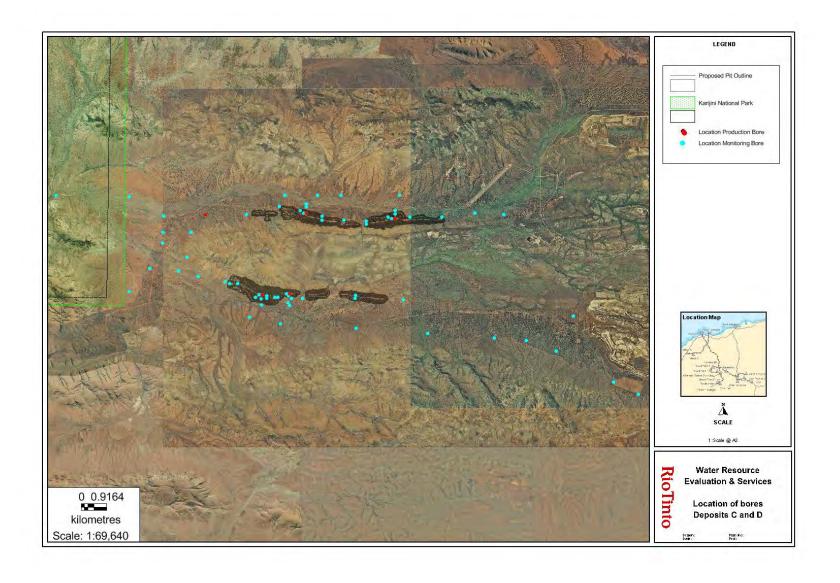


Figure 6: Location of bores area Deposit C and D

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Airlift yields obtained during development of monitoring bores in the Wittenoom Formation ranged from 5 to zero L/s. An increase in yield was typically associated with mineralisation or weathering and erosion indicating enhanced permeability in these horizons. Outside of the areas of mineralisation and/or weathering and erosion, the Wittenoom Formation will have limited permeability and constrain groundwater flow. Groundwater quality is fresh ranging from EC values between 1,192 to 1,219  $\mu$ S/cm.

### Mount Sylvia Formation and Mt McRae Shale

Although not encountered during borehole drilling, the Mount Sylvia Formation (consisting of BIF bands separated by shales, cherts and dolomite) and the Mount McRae Shale (consisting of a sequence of shales and cherts), conformably overlie the Wittenoom Formation. Based on RTIO experience of other sites in the Pilbara (e.g. Nammuldi, Marandoo etc.), the Mount Sylvia Formation/Mount McRae Shale is anticipated to act as a barrier to groundwater flow.

### **Dolerite**

Based on observations during drilling and surface geological mapping, there is evidence for intrusion of Dolerite dykes in the area. Based on RTIO observations during pumping testing at Deposit C (RTIO, 2016A), observed groundwater elevations in the area, as well as experience of other sites in the Pilbara (e.g. Nammuldi), Dolerite dykes may act as barriers to groundwater flow.

### Detrital Material

The area in the vicinity of Deposits C and D is covered by a layer of Tertiary Detritals, comprising clay, with mineralised detritals occurring close to bedded mineralisation. Based on observations made during the 2016 hydrogeological drilling program, Detritals were encountered BWT at approximately 50% of locations tested, in particular, in the west, between Deposits C and D and the area of the KNP. Athough the Detritals were encountered up to a maximum thickness of 130 m, in some places, the majority of locations tested they were significantly less than 100 m and are not considered to represent a significant aquifer in the area.

Based on observed groundwater levels, presence of recorded mineralisation close to the bedded mineralisation, presence of a layer of Calcrete at the base of the Detritals to the west of Deposit C and D, it is anticipated that the groundwater in the Detritals and bedrock is interconnected and will behave the same to dewatering (i.e. no delayed yield anticipated during dewatering Detritals and bedrock). The drilling method adopted did not permit acquisition of groundwater quality or airlift yield information during drilling.

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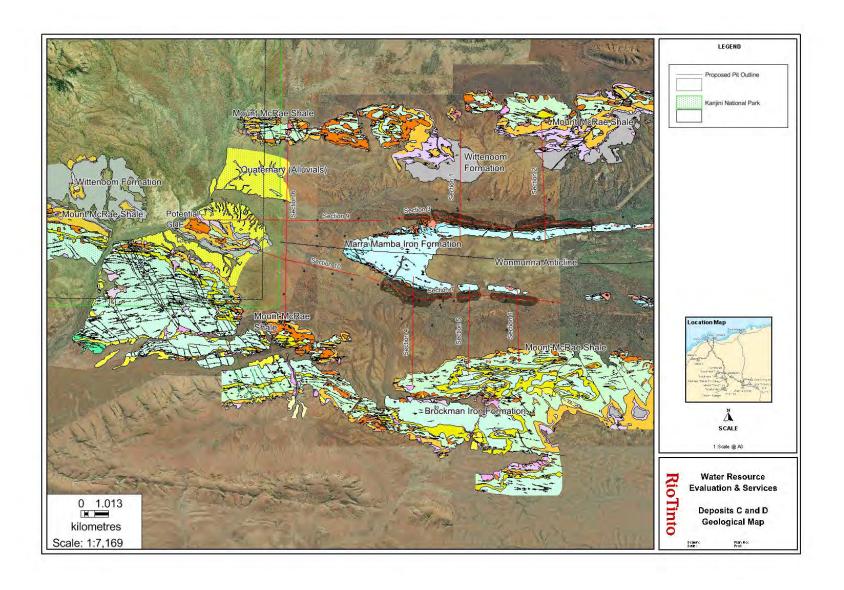


Figure 7: Geological map Deposit C and D

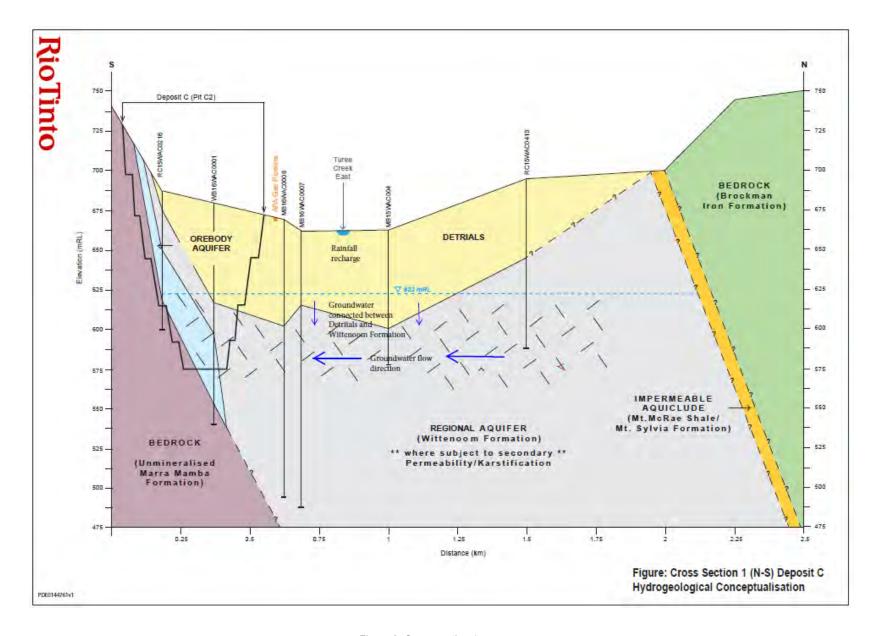


Figure 8: Cross section 1

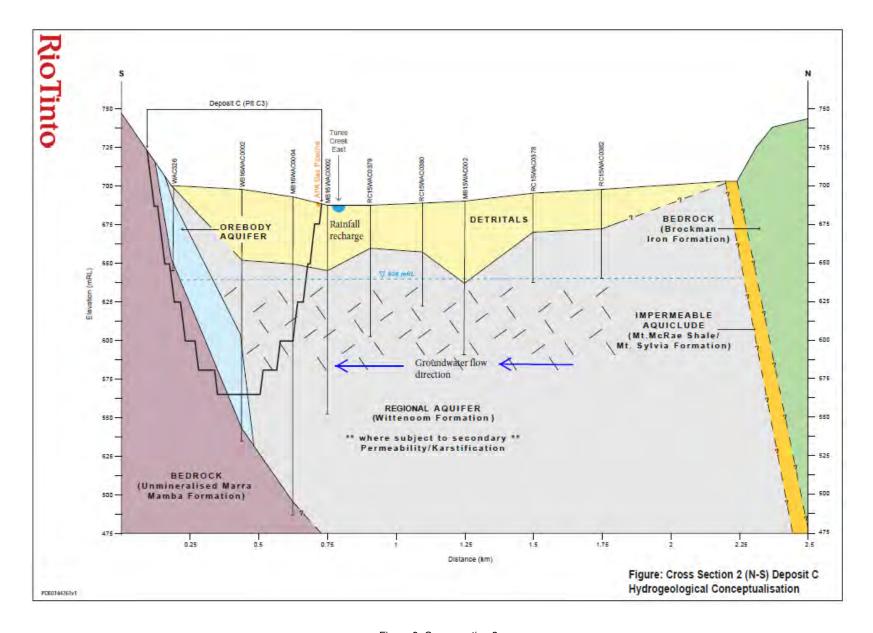


Figure 9: Cross section 2

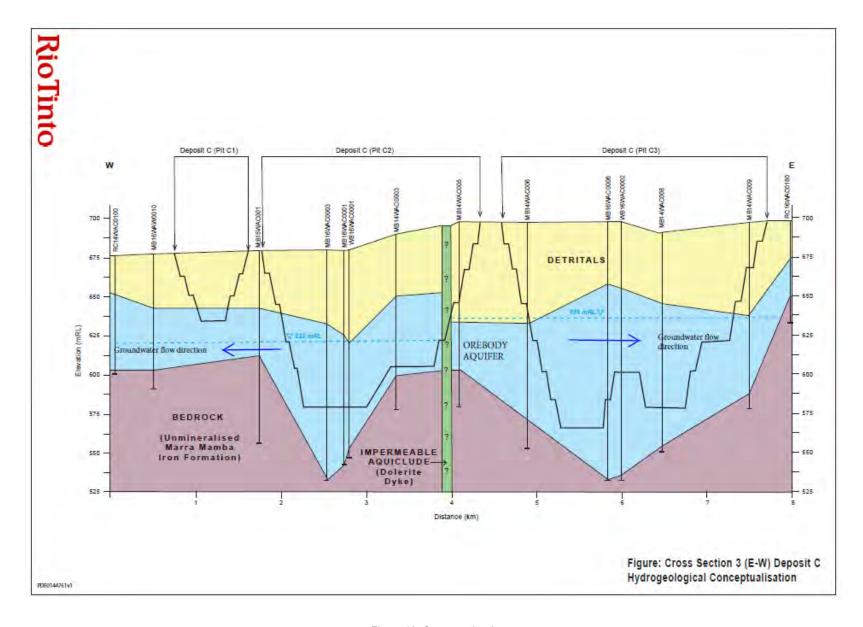


Figure 10: Cross section 3

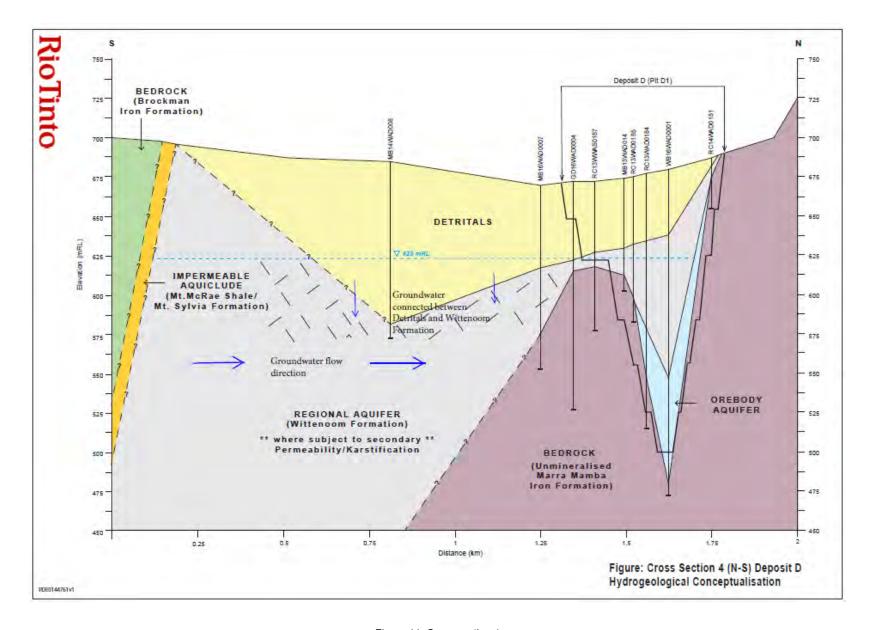


Figure 11: Cross section 4

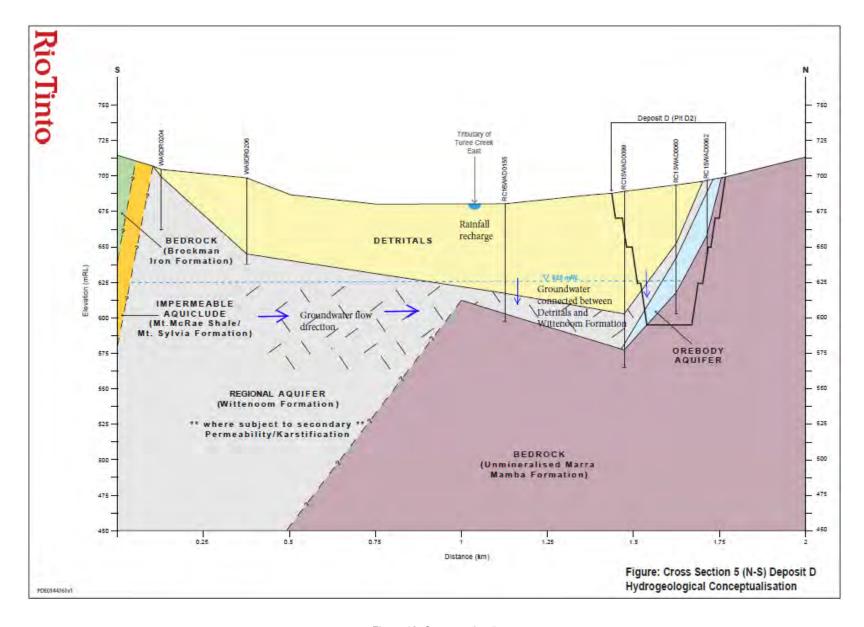


Figure 12: Cross section 5

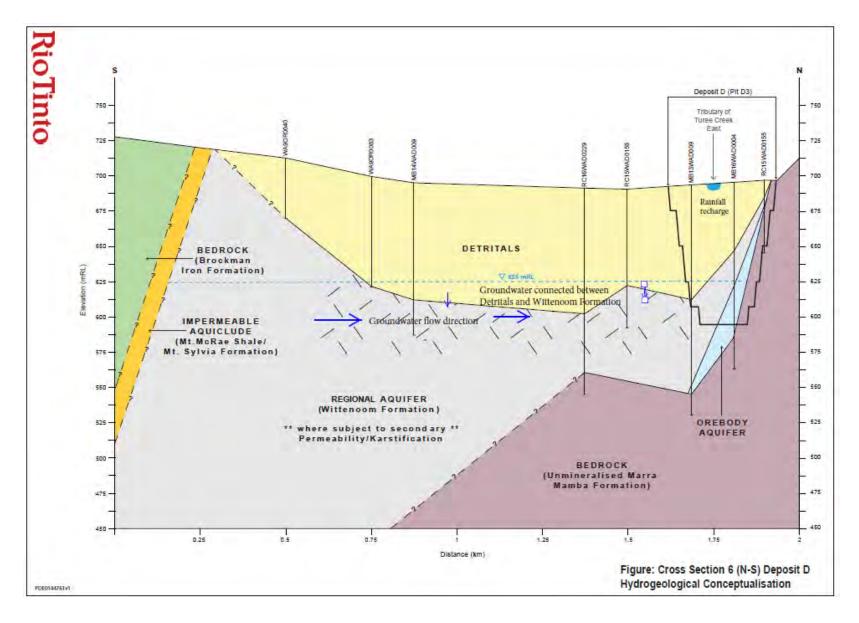


Figure 13: Cross section 6

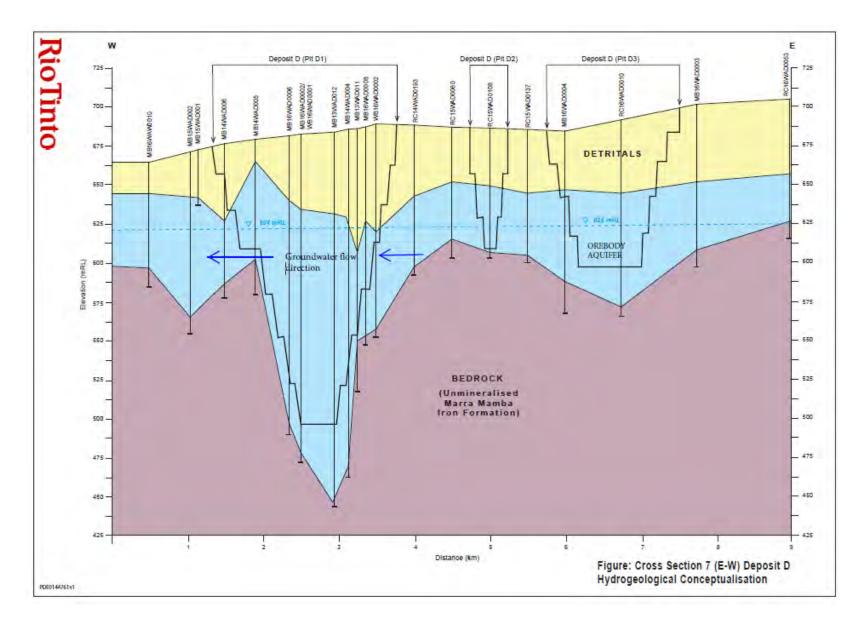


Figure 14: Cross section 7

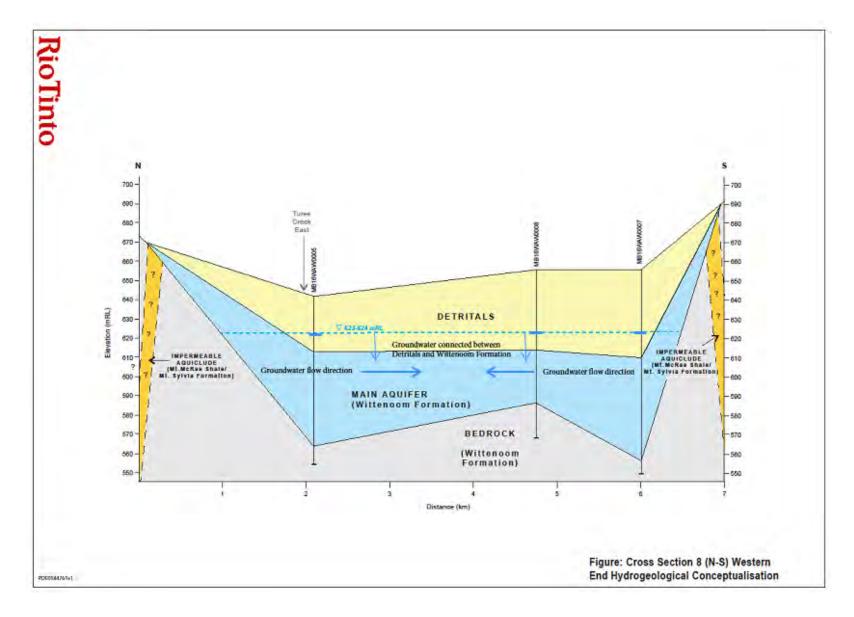


Figure 15: Cross section 8

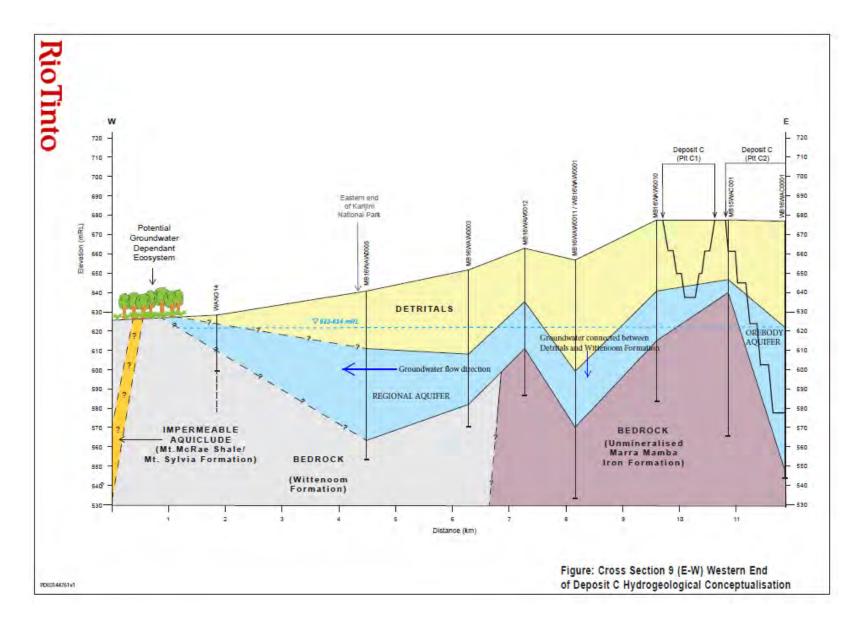


Figure 16: Cross section 9

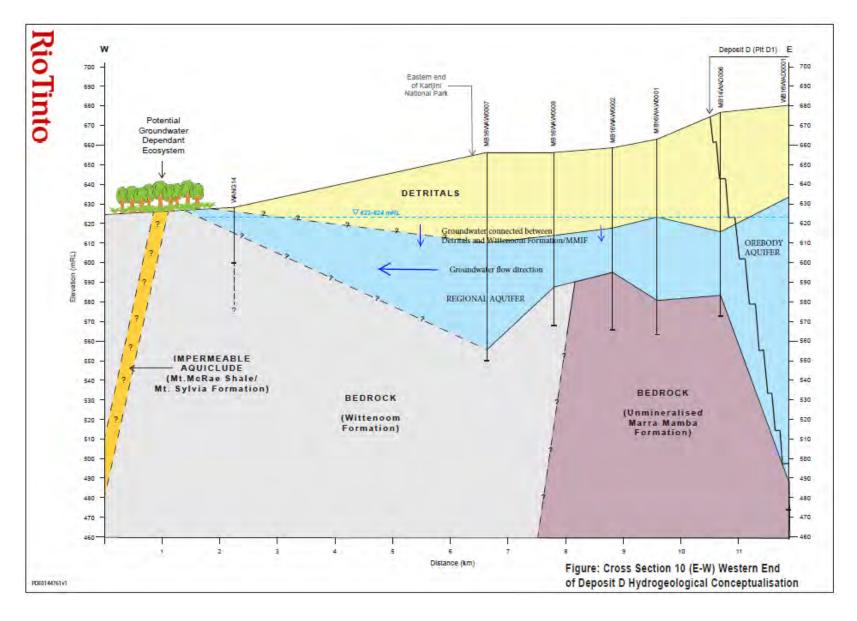


Figure 17: Cross section 10

# 3.4 Aquifer

Based on the local hydrostratigraphy, the principal aquifer in the region is associated with mineralised sections of the Marra Mamba Iron Formation and the overlying Wittenoom Formation (orebody aquifer), the Wittenoom Formation (regional aquifer), where subjected to weathering resulting in secondary permeability and in hydraulic continuity with the orebody and the overlying Detritals material.

# 3.5 Recharge

Based on a review of available hydrographs with rainfall data (Figure 18, Figure 19 and Figure 20), there is negligible response to rainfall events across the area, except in the location of WANG14 (~1.3m rise in groundwater level recorded in February 2017 and located to the west of the site in area of KNP and potential GDE). The observed response of groundwater level to rainfall at this location is assumed to be associated with the shallow depth to groundwater ~7m bgl.

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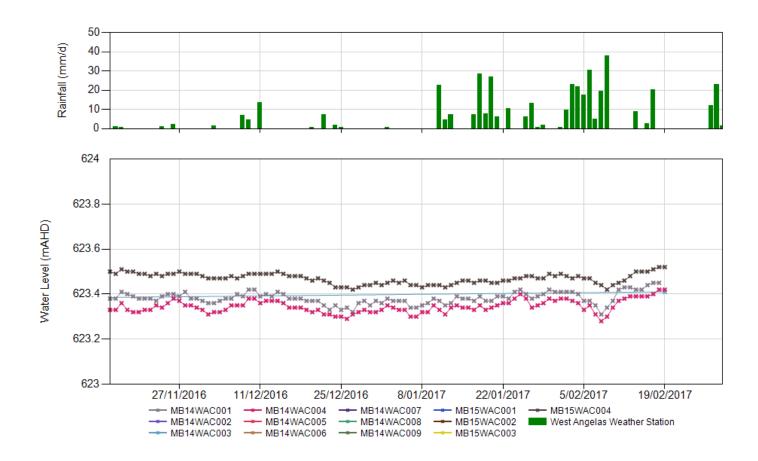


Figure 18: Hydrograph/rainfall data area Deposit C

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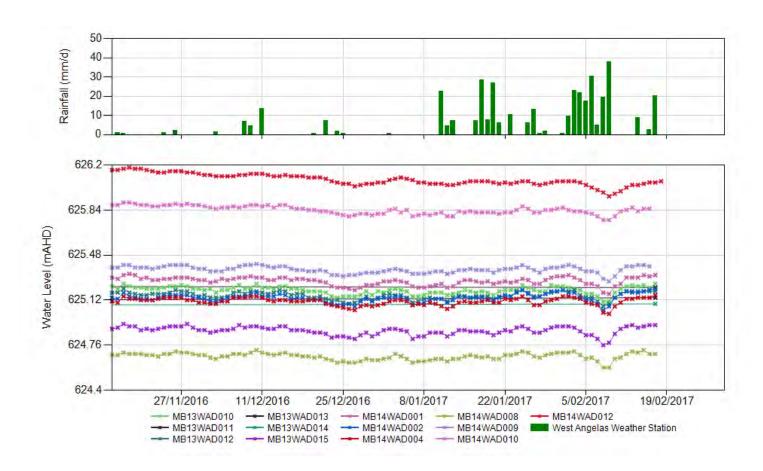


Figure 19: Hydrograph/rainfall data area Deposit D

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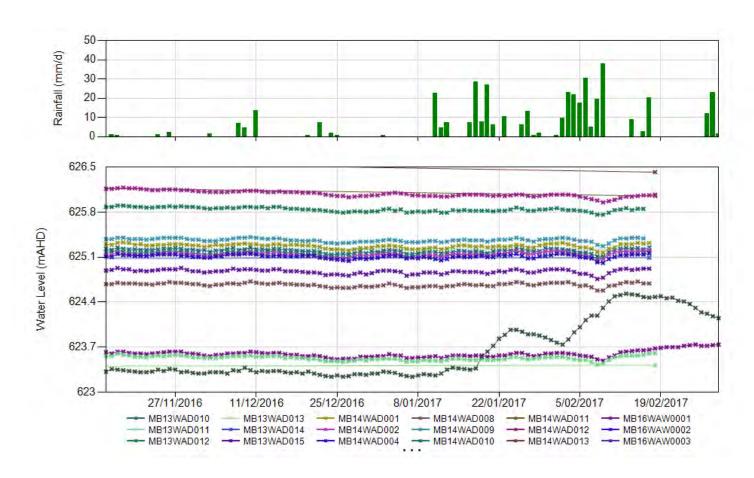


Figure 20: Hydrograph/rainfall data area west of Deposit C and D

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### 3.6 Groundwater flow

Groundwater level data obtained from the monitoring bores in the vicinity of Deposits C and D are presented in Figure 21 and Figure 22 respectively and Appendix 2.

The groundwater level in the vicinity of Deposit C shows the water table sits between ~636m RL in the east and 623m RL in the west, with evidence of a groundwater divide between MB14WAC005 and MB14WAC004, in the area of a dyke, possibly forming a barrier to groundwater flow in the area. To the west of the divide, it is assumed that groundwater flow is toward the west, and the direction of KNP, with a shallow gradient. To the east of the divide, and based on regional data, including nearby Deposit B with an observed groundwater elevation of ~630m RL, it is assumed that the groundwater flow direction is to the east, again with a shallow gradient.

Based on a groundwater elevation of ~625m RL in and around Deposit D, and the flat groundwater gradient in this area, it is apparent that there is a groundwater divide in the east between MB14WAE005 and MB14WAE006, with an associated change in groundwater elevation ~30m, in an area of dyke, possibly forming a barrier to groundwater flow. To the west of the divide, it is assumed that groundwater flow is toward the west, and the direction of KNP, with a shallow gradient.

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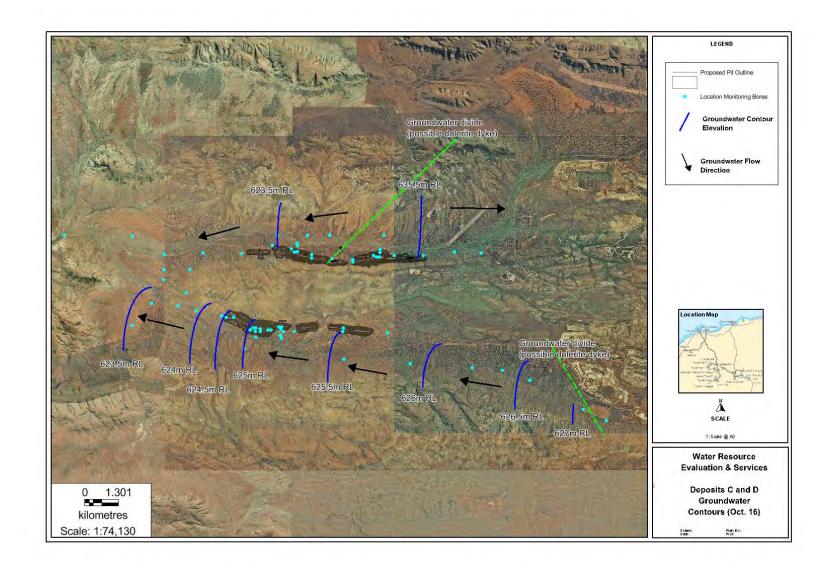


Figure 21: Groundwater contours (Oct. 16)

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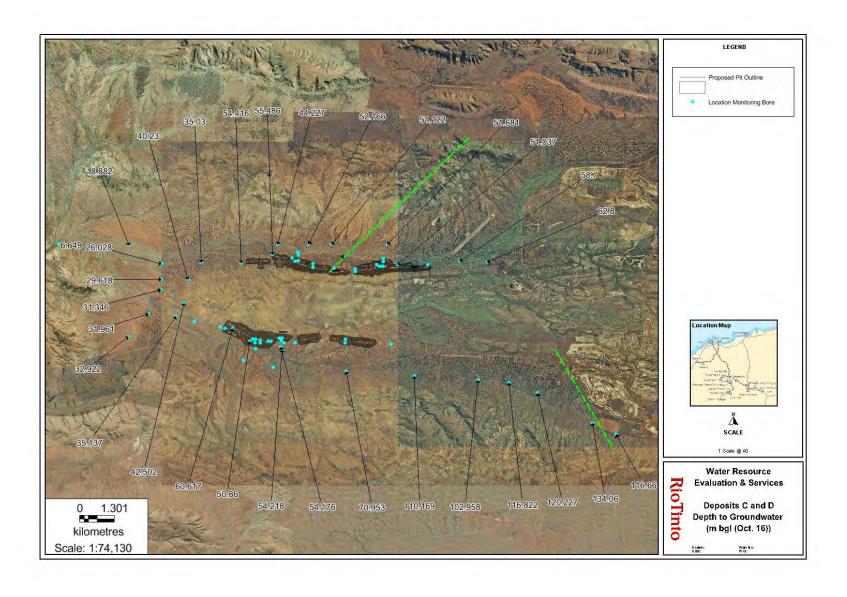


Figure 22: Depth to groundwater (Oct. 16)

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# 3.7 Discharge

Based on the depth to groundwater across the area, the closed groundwater catchment (i.e. no inflow boundaries associated with un-mineralised Marra Mamba Iron Formation, groundwater divides in the area etc.), the only discharge is assumed to be associated with evapotranspiration in the area of the potential GDE to the west, and the area of KNP. Based on RTIO Environment Team information (pers. coms. J. Naaykens to Simon Page, 2016), it is currently estimated that the potential GDE may generate an evapotranspiration rate of 0.05 GL/year.

# 3.8 Hydrochemistry

The results of the analysis of filtered samples during the course of the 2016 field program (RTIO, 2016a), revealed that groundwater samples showed similar values for major cations and anions (Figure 23).

Results of pH analysis ranged from 7.75 to 7.91. Groundwater was fresh with EC values ranging between 968 to 1,790  $\mu$ S/cm.

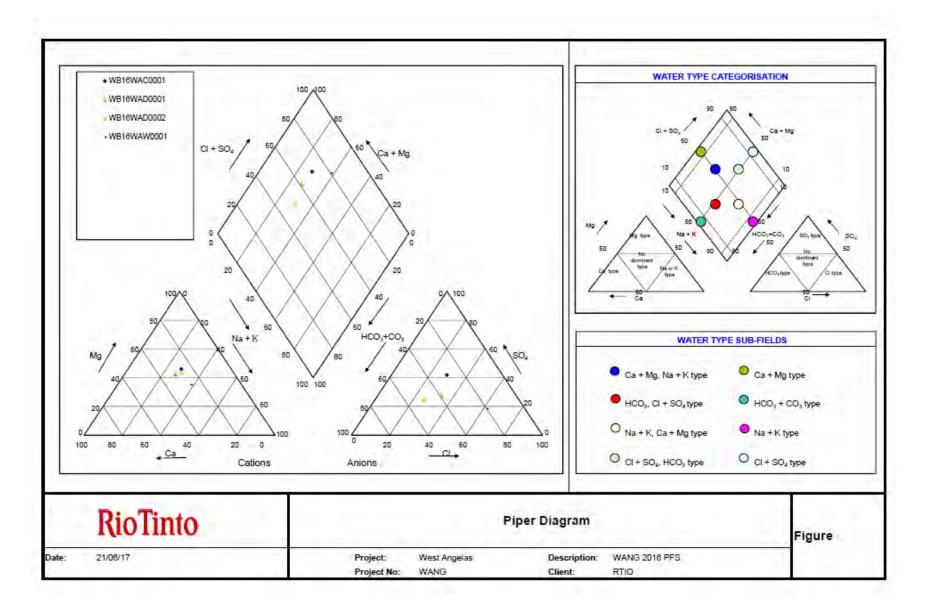


Figure 23: Piper diagram WB16WAC0001, WB16WAD0001, WB16WAD0002 and WB16WAW0001

### 3.9 Water balance

A catchment scale water balance was undertaken to help refine the conceptualisation and to determine the likely volumetric inputs for each of the processes identified in the balance.

Components of the water balance can be expressed as follows:

Total inflow – total outflow =  $\Delta S/\Delta t$ 

where  $\Delta S$  = change in storage, and  $\Delta t$  = change in time.

Under natural long-term (steady state) conditions, the change in storage is zero relative to time, and hence:

Total inflow = Total outflow

Including the specific water balance components for the catchment results in the following equation:

$$P = ET + R + Q$$

where P = precipitation, ET = evapotranspiration, R = recharge and Q = run-off outflow.

If the basic water balance equation is combined to include the solute chloride, then:

where Cl<sub>p</sub>, Cl<sub>et</sub>, Cl<sub>gw</sub>, and Cl<sub>q</sub> refer to chloride concentrations in rainfall, recharge, evapotranspiration and runoff respectively. The chloride ion is considered to behave conservatively. That is it does not participate in any hydrochemical reactions with other ions in groundwater or undergo rock interaction.

Aquifer recharge (R) can be calculated using the chloride mass balance method as follows:

$$R = (P*Cl_p)/Cl_{gw}$$

Based on an assumed annual rainfall of 317 mm/year, a chloride concentration in rainwater of 1 mg/l (Dogramaci et al, 2012), and an observed range of chloride concentration in groundwater between 87 and 422 mg/l, recharge can be calculated between 3.4 and 0.75 mm/year. Assuming even recharge across the catchment area, and based on the measured catchment of 298 km², recharge across the entire area is calculated between 0.9 to 0.2 GL/year.

## 4. Conceptual hydrogeological model

The conceptual hydrogeological model in the area of Deposits C and D is summarised in representative cross-sections Figure 8 to Figure 17 and is guided by the following key themes that describe groundwater occurrence and flow:

- Enhanced permeability associated with mineralised successions of the Mount Newman Member of the Marra Mamba Iron Formation as well as the West Angela Member of the Wittenoom Formation (permeability within these successions is relatively enhanced due to supergene processes related to the enrichment of iron within the orebody and typical of the Pilbara region).
- A locally significant aquifer is anticipated to be associated with the Wittenoom Formation in the valley to the north of Deposit C, south of Deposit D and the area to the west of Deposit C and D (Dolomite currently assumed to have been subjected to weathering, resulting in secondary permeability and in hydraulic continuity with the orebody).
- There is evidence for compartmentalisation associated with two groundwater divides in the area, up to 13m between MB14WAC005 and MB14WAC006 (Deposits C2 and C3) and 30m between MB14WAE005 and MB14WAE006 (Deposits D and E).
- Based on groundwater level data, it is anticipated that un-mineralised Marra Mamba Iron Formation (MacLeod and Nammuldi Members) will form an effective hydraulic barrier to the base of Deposits C and D.
- Based on RTIO experience at other mine sites in the Pilbara, it is anticipated that
  the Mount McRae Shale to the north, south and west will form an effective barrier
  to groundwater flow.
- Rainfall recharge to the orebody aquifer and in the immediate vicinity of Deposits
  C and D is considered low. This is inferred largely on the basis of the significant
  depth to groundwater, site water balance, observed hydrograph data, and the
  thickness of the detritals intersected during drilling.
- A greater contribution from rainfall recharge to the aquifers in the vicinity of the
  potential GDE is likely due to the relatively shallow depth to groundwater in
  comparison to Deposits C and D (Figures 17 and 19). Similarly,
  evapotranspiration will higher and it is therefore considered likely inflow of water
  by recharge will be offset by outflow from evapotranspiration at this location.
- Based on the assumed site boundary conditions adopted and minimal recharge, it is assumed that groundwater abstraction will from storage, with no flow across boundaries.

A summary of the conceptual site hydrogeology is presented in Figure 24.

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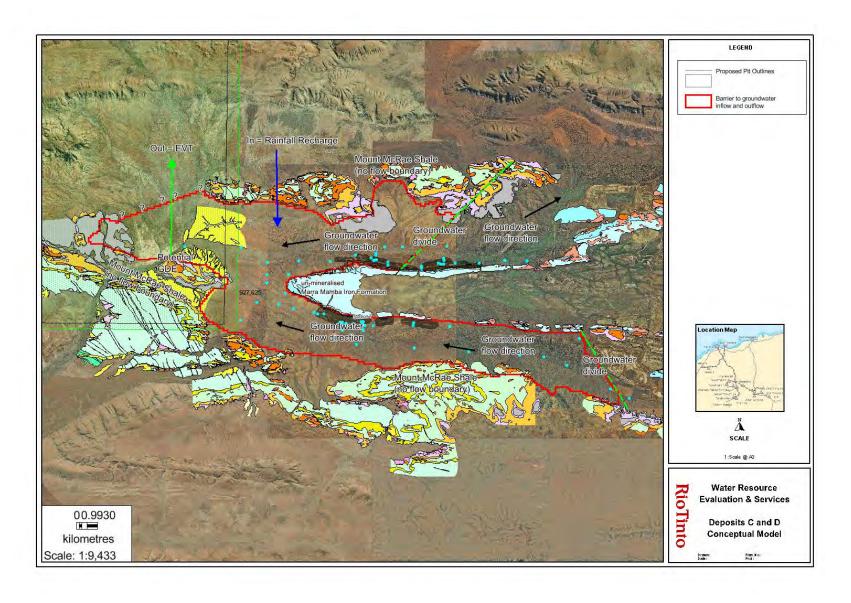


Figure 24: Conceptual hydrogeology Deposits C and D

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# 5. Model uncertainty and future work

In order to validate the current conceptual site model, it is recommended that the following work is undertaken during the course of the RTIO Feasibility Study (FS):

- Carry out surface geological mapping, to confirm the presence of the Mount McRae Shale – area to the to the north-west of Deposit C where current uncertainty exists (Figure 24):
- Undertake a review of RTIO geophysical database in the area north-west of Deposit C, to increase certainty around stratigraphy in the area and basement geometry;
- Review site conceptualisation and run alternative groundwater model(s) to test impact of absence of Mount McRae Shale north-west of Deposit C;
- Undertake water quality sampling of available surface water in TCE and bore WANG14 to better understand local surface-groundwater interaction;
- Undertake desk top review of possible mitigation for drawdown extending beneath the potential GDE;
- Borehole drilling program to evaluate the effectiveness of ex-pit dewatering at Deposit C and D.

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#### 6. References

BOM, 2012: High resolution daily rainfall gridded datasets from 1900 onwards, (http://www.bom.gov.au/climate/how/newproducts/images/daily rainfall metadata.pdf).

Dogramaci et al, 2012, Stable isotope and hydrochemical evoluation of groundwater in the semi-arid Hamersley Basin of subtropical northwest Australia

RTIO, 2016a: West Angelas Deposit C and D hydrogeological conceptual review, Anne-Audrey Latscha, February 2016

RTIO, 2016b: RTIO-PDE-0146330 - 2016 Deposit C & D and Western End PFS Field Programme Report\_06102016 (Final).doc: http://iodms/iodms/drl/objectId/090188a380a2166e

RTIO, 2017: <a href="http://riopersql13:8090/display/RHTS/West+Angelas+-+Deposit+C">http://riopersql13:8090/display/RHTS/West+Angelas+-+Deposit+C</a>, <a href="http://riopersql13:8090/display/RHTS/West+Angelas+-+Deposit+D">http://riopersql13:8090/display/RHTS/West+Angelas+-+Deposit+C</a>, <a href="http://riopersql13:8090/display/RHTS/West+Angelas+-+Deposit+D">http://riopersql13:8090/display/RHTS/West+Angelas+-+Deposit+C</a>, <a href="http://riopersql13:8090/display/RHTS/West+Angelas+-+Deposit+D">http://riopersql13:8090/display/RHTS/West+Angelas+-+Deposit+D</a>

RTIO, undated: An Introduction to the Structure and Stratigraphy of the Pilbara, Excursion Guide 1, D J Mason

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# Appendix 1



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# Appendix 2



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Robe River Mining Co. Pty Ltd

ABN: 71 008 694 246

# West Angelas Closure Plan July 2017

Mineral Field 47 - West Pilbara

FDMS No RTIO-HSE-0228290

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#### **EXECUTIVE SUMMARY**

#### Overview

West Angelas is an open cut iron ore mine located in the Eastern Pilbara region of Western Australia, approximately 105km north-west of Newman. The mine uses conventional drill-and-blast and load-and-haul mining methods to remove iron ore from above and below the water table.

#### Scope

This closure plan covers currently approved deposits and associated infrastructure at West Angelas (Deposits A, A West, B, E and F) and the proposed C, D and G deposits that have been referred to the Environmental Protection Authority (EPA) for environmental approval. It is an update of the February 2015 version of the West Angelas closure plan, and will supersede that document once it has been formally approved.

The closure plan has been developed to meet the requirements of the Rio Tinto Closure Standard and the joint Department of Mines and Petroleum (DMP) and EPA *Guidelines for Preparing Mine Closure Plans* (May 2015).

#### Post-mining land use

As West Angelas is underlain by Vacant Crown Land, and is located in close proximity to Karijini National Park, the return of a native ecosystem is considered to be the most appropriate final land use. This is consistent with advice provided by the OEPA in November 2014.

#### Closure objectives

The following closure objectives have been set for the site:

- Final landform is stable and considers ecological and hydrological issues;
- Vegetation on rehabilitated land is self-sustaining and compatible with the final land use;
- Public safety hazards have been managed;
- Contamination risks have been appropriately managed; and
- Infrastructure has been appropriately managed.

These objectives have evolved from those in the approved May 2015 plan.

#### Anticipated closure outcome

The shape of the landscape at West Angelas is still evolving, with the final mine void areas and waste dump locations and dimensions still in development across all of the deposits.

Mine voids will be backfilled to prevent the formation of permanent pit lakes, although water may temporarily pool at the base of the voids following heavy rainfall. The proposal to develop Deposits C, D and G assumes water levels beneath a potentially groundwater dependent ecosystem at Karijini National Park will be lowered between 3 to 8 metres over a 100 year post-mining timeframe, and that there will be no attempt at closure to reinstate pre-mining levels. Lowering the water table will also result in a permanent loss of subterranean fauna habitat. The area around pit voids may be unstable as pit walls are expected to collapse over time, and inadvertent access will be restricted by the use of physical barriers (e.g. abandonment bunds).

Waste dumps will be reshaped so as to be stable, and all disturbed areas except pit voids will be rehabilitated with native vegetation with the aim of creating self-sustaining ecosystems that function in a similar fashion to those present in the pre-mining environment.

It is assumed that all infrastructure will be removed, but this will be subject to negotiation with the Western Australian State Government as per State Agreement obligations. Creek diversions have been designed to be permanent structures, and there are no plans to reinstate original surface water flow paths.

# **CLOSURE PLAN CHECKLIST**

The following table provides cross reference to the requirements of the Department of Mines and Petroleum / Environmental Protection Authority *Guidelines for preparing mine closure plans* (2015).

	Mine Closure Plan (MCP) Checklist	Y/N/ NA	Page No.	Comments	Change from previous version (Y/N)	Page No.	Comments
1	Has the Checklist been endorsed by a senior representative within the operating company?	Y	-		-		
Publ	ic Availability						
2	Are you aware that from 2015 all MCPs will be made publically available?	Y	-				
3	Is there any information in this MCP that should not be publicly available?	Y	-	Appendix C is considered confidential			
4	If "Yes" to Q3, has confidential information been submitted in a separate document / section?	Y	-				
Cove	er page, table of contents						
5	Does the MCP cover page include: Project Title, Company Name, Contact Details (including telephone numbers and email address) Document ID and version number, Date of submission (needs to match the date of this checklist)	Y	-		-		
Scop	pe and purpose						
6	State why the MCP is submitted (e.g. as part of a Mining Proposal, a reviewed MCP or to fulfil other legal requirement)	-	-	Support Part IV referral of Deposit C/D/G	-		
Proje	ect overview						
7	Does the project summary include land ownership details, location of the project, comprehensive site plans and background information on the history and status of the project?	Y	3		N		
Lega	al obligations and commitments						
8	Does the MCP include a consolidated summary or register of closure obligations and commitments been included?	Y	Appen dix A		N		

Stak	eholder engagement						
9	Have all stakeholders involved in closure been identified?	Y	5		N		
10	Does the MCP included a summary or register of historic stakeholder engagement been provided, with details on who has been consulted and the outcomes?	Y	Appen dix B		Y		Update with consultation undertaken to support Part IV referral
11	Does the MCP include a stakeholder consultation strategy to be implemented in the future?	Y	24		N		
Post	mining land use(s) and closure objective	S					
12	Does the MCP include agreed post- mining land use, closure objectives and conceptual landform design diagram?	Y	26		Y	26	Changes from last version explain in Section 7.2
13	Does the MCP identify all potential (or pre-existing) environmental legacies which may restrict the post mining land use (including contaminated sites)?	Y	14		N		
14	Has any soil or groundwater contamination that occurred, or is suspected to have occurred, during the operation of the mine, been reported to DER as required under the Contaminated Sites Act 2003?	N	-		N		
Deve	elopment of completion criteria			'			
15	Does the MCP include an appropriate set of specific completion criteria and closure performance indicators?	Y	27		Y	30	Changes explained in Section 8.1
Colle	ection and analysis of closure data			'			
16	Does the MCP include baseline data (including pre-mining studies and environmental data)	Y	32	Also Appendix C	Y	-	Information updated to incorporate discussion on Deposit C,D and G where relevant
17	Has materials characterisation been carried out consistent with applicable standards and guidelines (e.g. GARD Guide)?	Y	39		N		
18	Does the MCP identify applicable closure learnings from benchmarking against other comparable mine sites?	N	-	Information learnt from other sites (particularly other Pilbara mines managed by Rio Tinto) is incorporated into	N		

				the closure plan, but there has been no formal benchmarking exercise			
19	Does the MCP identify all key issues impacting mine closure objectives and outcomes (including potential contamination impacts)?	Y	Appen dix D		Y		Closure risk assessment updated to incorporate Deposits C D and G
20	Does the MCP include information relevant to mine closure for each domain or feature?	Y	Appen dix E		Y		Updated to incorporate Deposits C D and G
Ident	ification and management of closure issu	ies					
21	Does the MCP include a gap analysis / risk assessment to determine if further information is required in relation to closure of each domain or feature?	Y	69	Risk assessment and gap analysis is based on issues management rather than specific domains	Y	69	Updated to consider Deposits C D and G.
22	Does the MCP include the process, methodology and has the rationale been provided to justify identification and management of the issues?	Y	57		N		
Clos	ure Implementation						
23	Does the MCP include a summary of closure implementation strategies and activities for the proposed operations or for the whole site?	Y	71		Y	71	Updated to consider Deposits C D and G.
24	Does the MCP include a closure work program for each domain or feature?	Y	71		N		
25	Does the MCP contain site layout plans to clearly show each type of disturbance as defined in Schedule 1 of the MRF Regulations?	Y	71		Y	71	Updated to consider Deposits C D and G.
26	Does the MCP contain a schedule of research and trial activities?	Y	69		Y	69	Table of actions was not included in previous closure plan
27	Does the MCP contain a schedule of progressive rehabilitation activities?	N		Progressive rehabilitation will be conducted when areas become available			
28	Does the MCP include details of how unexpected closure and care and maintenance will be handled?	Y	75		N		

29	Does the MCP contain a schedule of decommissioning activities?	N		This will be developed as the site approaches closure	
30	Does the MCP contain a schedule of closure performance monitoring and maintenance activities?	Y	76	Indicative monitoring program. The program will be further developed as the site approaches closure	
Clos	ure monitoring and maintenance				
31	Does the MCP contain a framework, including methodology, quality control and remedial strategy for closure performance monitoring including post-closure monitoring and maintenance?	Y	76		
Fina	ncial provisioning for closure				
32	Does the MCP include costing methodology, assumptions and financial provision to resource closure implementation and monitoring?	Y	78		
33	Does the MCP include a process for regular review of the financial provision?	Y	78		
Man	agement of information and data			1	
34	Does the MCP contain a description of management strategies including systems and processes for the retention of mine records?	Y	80		

#### Corporate endorsement:

I hereby certify that to the best of my knowledge, the information within this Mine Closure Plan is true and correct and addresses the relevant requirements of the *Guidelines for Preparing Mine Closure Plans* approved by the Director General of Mines and Petroleum.

Santi Pal

General Manager - Orebody Knowledge and Planning

Date:

5/7/17

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#### **SCOPE AND PURPOSE**

### 1. Purpose

Planning for closure of a site is a critical business process that demonstrates Rio Tinto's commitment to sustainable development. This closure plan has been prepared in accordance with the Department of Mines and Petroleum (DMP) / Environmental Protection Authority (EPA) *Guidelines for preparing mine closure plans* (2015).

This closure plan has been updated to achieve the following goals:

- support environmental impact assessment of West Angelas Deposits C, D and G;
- approval of the closure plan during the course of Part IV assessment of the Deposit C, D and G project;
- submission to the Department of State Development, to satisfy a request from that Department;
- submission to the Office of the EPA for approval under condition 9 of Ministerial Statement 970 issued in relation to the West Angelas Iron Ore Project (this submission will occur following confirmation that environmental approval of Deposits C, D and G has been granted);
- meet the internal requirements of the Rio Tinto Closure Standard (2015) mandated for all Rio Tinto businesses;
- reflect the current knowledge and requirements for closure of West Angelas mine and identify the future requirements to continue to progress towards a planned and managed closure of the site; and
- inform the development of closure provisions.

## 2. Scope

This plan covers development of Deposits A, A West, B, C, D, E, F and G, and applies to the following:

- Mine development within the following leases<sup>1</sup>;
  - ML248SA Sections 067-084 (mining lease issued pursuant to the Robe River State Agreement)
  - o G47/01235;
  - o G47/01236;
  - L47/41 (Turee B borefield);
  - o L47/52 (road);
  - o L47/53 (road);
  - L47/54 (gas pipeline);
  - L47/61 (repeater station);
  - L47/62 (repeater station);
  - L47/63 (rail);
  - o L52/75 (gas pipeline)

The plan excludes the following:

- potential future expansions at West Angelas or the surrounding area; and
- the mainline rail.

<sup>&</sup>lt;sup>1</sup> Note that the scope of the closure plan has been aligned to tenure boundaries, which may differ from the footprint approved or referred under Part IV of the *Environmental Protection Act 1986*.