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9 **Title: Hidden species diversity of Australian burrowing snakes (*Ramphotyphlops*).**

10
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1
2
3 35 **ABSTRACT**

4 36 The worm-like snakes (Scolecopidia, ~400 nominal extant species) have a conservative
5 morphology and are among the most poorly-known terrestrial vertebrates. Although
6 37 morphology and are among the most poorly-known terrestrial vertebrates. Although
7 molecular evidence has helped elucidate their higher-level relationships, such data have rarely
8 38 molecular evidence has helped elucidate their higher-level relationships, such data have rarely
9 been used to discriminate among species. We generated a molecular data set for the
10 39 been used to discriminate among species. We generated a molecular data set for the
11 continental Australian blindsnakes (genus *Ramphotyphlops*) to determine the concordance of
12 40 continental Australian blindsnakes (genus *Ramphotyphlops*) to determine the concordance of
13 molecular and morphological information in the taxonomic recognition of species. Our dataset
14 41 molecular and morphological information in the taxonomic recognition of species. Our dataset
15 included 741 specimens morphologically attributed to 27 nominal *Ramphotyphlops* species.
16 42 included 741 specimens morphologically attributed to 27 nominal *Ramphotyphlops* species.
17 We proposed species hypotheses (SHs) after analysis of sequences from a variable
18 43 We proposed species hypotheses (SHs) after analysis of sequences from a variable
19 mitochondrial gene (*cytochrome b*) and examined these SHs with additional evidence from a
20 44 mitochondrial gene (*cytochrome b*) and examined these SHs with additional evidence from a
21 nuclear gene (*prolactin receptor*) and geographic data. Although the nuclear marker was not
22 45 nuclear gene (*prolactin receptor*) and geographic data. Although the nuclear marker was not
23 as fast-evolving and discriminating as the mitochondrial marker, there was congruence among
24 46 as fast-evolving and discriminating as the mitochondrial marker, there was congruence among
25 the mitochondrial, nuclear, and geographic data, suggesting that the actual number of species
26 47 the mitochondrial, nuclear, and geographic data, suggesting that the actual number of species
27 is at least two times the current number of recognized, nominal species. Several biogeographic
28 48 is at least two times the current number of recognized, nominal species. Several biogeographic
29 barriers and complex phytogeographic and geologic patterns appeared to be involved in the
30 49 barriers and complex phytogeographic and geologic patterns appeared to be involved in the
31 division of some burrowing snake populations, and by consequence in their diversification
32 50 division of some burrowing snake populations, and by consequence in their diversification
33 and speciation through isolation.
34 51 and speciation through isolation.

35 52
36 53 **Additional keywords:** cryptic species – evolution – hidden species – *Ramphotyphlops* –
37 54 Scolecophidia – speciation
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69 INTRODUCTION

70 Species inventory and delineation are essential for assessing biodiversity, conservation
71 or biological control projects and more generally understanding the natural world (Wheeler *et*
72 *al.*, 2004). However, it is well known that the number of described species on earth is far less
73 than the total (Trontelj & Fišer 2009). Most of the species yet to be described are thought to
74 be fungi and ‘invertebrate’ animals, and particularly those living in tropical environments
75 (Pfenninger & Schwenk 2007) Over the last 12 years, the total number of nominal extant
76 species of squamates increased by 1.7 % each year (Pincheira-Donoso *et al.*, 2013) and this
77 value is much lower for mammals and birds (0.1–0.2%) (Uetz, Goll & Hallerman 2013;
78 Lepage 2012; Wilson & Reeder 2005). Cryptic species, two or more distinct species that were
79 classified as a single species due to their morphological similarity,, are almost evenly
80 distributed among major metazoan taxa and biogeographical regions (Pfenninger & Schwenk
81 2007). Therefore, the diversity of many vertebrate groups has yet to be explored (Oliver *et al.*,
82 2009).

83 Here we focus on Australian blindsnakes of the genus *Ramphotyphlops* (Scolecophidia,
84 Typhlopidae), whose systematics was little studied until recently (Aplin & Donnellan 1993;
85 Rabosky *et al.*, 2004; Vidal *et al.*, 2010). Blindsnakes typically are small (~10–30 cm),
86 burrowing species, and feed on social insects (Vidal & Hedges 2009). They comprise 402
87 named species segregated in five families: Anomalepididae, Leptotyphlopidae, Typhlopidae,
88 Xenotyphlopidae, and Gerrhopilidae (Vidal *et al.*, 2010; Uetz *et al.*, 2013). The 42 currently
89 recognized Australian scolecophidian species all belong to *Ramphotyphlops*, a genus of 66
90 species distributed across South and Southeast Asia, Australasia and Melanesia (as far east as
91 Fiji, and across the Caroline Islands from Palau to Pohnpei), and comprise one of the least-
92 known elements of the Australian herpetofauna (Rabosky *et al.*, 2004; Wynn *et al.*, 2012).

93 Previous molecular genetic studies on scolecophidian snakes, including members of the
94 families Typhlopidae and Leptotyphlopidae, have suggested a high level of hidden diversity,
95 as indicated by several recognized species being paraphyletic and polyphyletic, and
96 harbouring deep divergences (Hedges & Thomas 1991; Aplin & Donnellan 1993; Rabosky *et*
97 *al.*, 2004; Hedges 2008; Adalsteinsson *et al.*, 2009; Marin *et al.*, 2012; Kornilios *et al.*, 2013).

98 Strong selection associated with a fossorial lifestyle has led to miniaturisation, cranial
99 consolidation, and body elongation, all common features in burrowing reptile (Gauthier *et al.*,
100 2012). Moreover, there are limited characters for which inter- *versus* intraspecific variations
101 are adequately understood, partly due to the lack of interest in scolecophidians (Adalsteinsson

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3 102 *et al.*, 2009).. Here, we focus on testing and refining species boundaries within the Australian
4
5 103 radiation of *Ramphotyphlops* in light of new molecular genetic data.

6 104 Although many theoretical species concepts have been discussed over the years, there is
7
8 105 general agreement, supported by genetic data, that species are reproductively isolated from
9
10 106 one another (Coyne & Orr 2004). It is then a practical matter how to identify and delimit
11
12 107 species. If two species occur together in sympatry and are not exchanging genes, then
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14 108 identifying concordance of two or more characters (coded by unlinked genes) will usually
15
16 109 suffice in demonstrating reproductive isolation and delimitation of species. However, whether
17
18 110 or not to recognize allopatric populations as full species is a more subjective decision, often
19
20 111 requiring additional case-specific information. Padial *et al.*, (2010) discuss two different
21
22 112 approaches to distinguish species: (1) "cumulation", where only one character set (e.g.,
23
24 113 mitochondrial DNA sequences) is used, and (2) "congruence", where multiple data sets (e.g.,
25
26 114 DNA sequences and morphology) are used. Rather than alternative approaches, they could
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28 115 also be viewed as a continuum concerning level of evidence (stringency), especially because a
29
30 116 single study might diagnose some species using one character set and other species using
31
32 117 multiple sets, depending on availability.

33
34 118 In our study, we have explored species limits in Australian *Ramphotyphlops* using data
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36 119 from only one character set (mitochondrial DNA) and multiple sets (mitochondrial DNA,
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38 120 nuclear DNA, and geography). We took the general approach of defining preliminary species
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40 121 hypotheses (SHs) using the low stringency approach (mitochondrial DNA data set) and then
41
42 122 comparing the SHs with additional character sets (Padial *et al.*, 2010; Goldstein & DeSalle
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44 123 2011; Yeates *et al.*, 2011; Puillandre *et al.*, 2012b). By adding more specimens (634) to our
45
46 124 previous molecular genetic dataset (Marin *et al.*, 2012) we built a new dataset. The ABGD
47
48 125 (Automatic Barcode Gap Discovery) method (Puillandre *et al.*, 2012a) was used with
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50 126 mitochondrial gene (*cytochrome b*) sequences, and resulting SHs were then compared with
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52 127 variation from a nuclear gene (*prolactin receptor*), and geography. Genetic divergent
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54 128 population in sympatry or divided by recognized barriers was used as additional evidence.
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56 129 The goal was to test the following hypothesis: is the number of nominal species a reasonably
57
58 130 accurate reflexion of true species diversity?. This represents an initial step that could assist a
59
60 131 morphology-based taxonomic revision, providing a better delimitation of some Australian
132 *Ramphotyphlops* species.

133

134 MATERIALS AND METHODS

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3 136 **Taxon sampling**

4 137 Ingroup sampling included 741 individuals belonging to 27 nominal Australian
5
6 138 *Ramphotyphlops* species (as identified using morphology). Appendix 1 lists the taxa,
7
8 139 localities, and GenBank accession numbers of specimens used in the study. Three typhlopoid
9
10 140 snakes were used as outgroups: *Acutotyphlops subocularis* (Vuovo Camp, West New Britain,
11
12 141 Papua New Guinea, *cyt b*: JQ910524, *PRLR*: JQ910414), *Ramphotyphlops acuticaudus*
13
14 142 (Palau, *cyt b*: JQ910543, *PRLR*: JQ910412), and *R. braminus* (Florida, United States, *cyt b*:
15
16 143 JQ910548, *PRLR*: JQ910434).
17

18 144
19 145 **Molecular genetic markers**

20 146 A mitochondrial protein coding gene and one nuclear protein coding gene were used.
21 147 The mitochondrial marker, *cytochrome b* (*cyt b*), is highly variable (intraspecific variation)
22 148 and thus potentially useful to identify recent speciation events (Burbrink, Lawson &
23 149 Slowinski 2000; Adalsteinsson *et al.*, 2009). Among the nuclear genes available for squamate
24 150 phylogenies (Townsend *et al.*, 2008) we selected one of the most variable, the *prolactin*
25 151 *receptor* (*PRLR*). For this work, 83.9 % of the sequences were newly determined; 943
26 152 sequences were deposited in GenBank under accession numbers KC489799–KC490909 and
27 153 KC493653.
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34 155 **DNA extraction, amplification, and sequencing.**

35 156 DNA extraction was performed with the DNeasy Tissue Kit from Qiagen.
36 157 Amplification and sequencing was performed using primers listed in Table 1.

37 158 For the two markers, DNA amplification was performed by PCR in a final 21 μL
38 159 volume containing 1 μL DMSO, 0.8 μL of dNTP 6.6 mM, 0.12 μL of Taq DNA polymerase
39 160 (MP Biomedicals or Qiagen), using 2.5 μL of the buffer provided by the manufacturer, 100
40 161 uml^{-1} and 0.32 μL of each of the two primers at 10 pM; 1 μL of DNA extract was added.

41 162 The PCR reactions were performed with the following conditions: an initial denaturation
42 163 at 94°C for 3 min followed by 40 cycles (3 min at 94°C, 40 s at 50°C, 1 min at 72°C) and a
43 164 final elongation at 72°C for 10 min, using a PCR System 2700 thermocycler (Applied
44 165 Biosystems). Amplification products were visualised on ethidium-bromide stained agarose
45 166 gels. Sequencing was performed by the National Centre for Sequencing (Genoscope, Evry,
46 167 France) using the same primers.

47 168 The two strands obtained for each sequence were combined using the Sequencher 4.9
48 169 software (GeneCodes, Ann Arbor, Michigan). Sequence alignment was performed with
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3 170 ClustalW2 (default parameters) (Larkin *et al.*, 2007) implemented in BioEdit (Hall, 1999) and
4 171 then manually refined with MEGA 5 (Tamura *et al.*, 2011), using amino acid translations. The
5 172 absence of stop codons was checked.
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8 173

174 **Phylogenetic analysis**

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11 175 *Cyt b* analyses were performed on all the obtained sequences; *PRLR* analyses were
12 176 performed on haplotypes only to reduce computation time. We built phylogenies using
13 177 Bayesian and Maximum Likelihood (ML) methods of inference. Bayesian analyses were
14 178 performed with MrBayes 3.1.2 (Ronquist & Huelsenbeck 2003) and ML analyses were
15 179 performed with RAxML 7.2.8 (Stamatakis, 2006; Stamatakis, Hoover & Rougemont 2008).
16 180 For both *cyt b* and LRPR, the three-partition strategy (by codon position) was preferred to the
17 181 one partition strategy (by gene) using standard Bayes factors (Nylander *et al.*, 2004). Bayesian
18 182 analyses were performed by running 50,000,000 generations in four chains, saving the current
19 183 tree every 1000 generations (until convergence), with GTR+I+G model, applied to each
20 184 partition (best-fit model inferred by Modeltest (Posada & Carndall 1998)). Convergence of
21 185 ESS values were checked with Tracer 1.4.1 (Rambaut & Drummond 2009) using the default
22 186 burning (10%). The last 45,000 trees were used to construct a 50% majority rule consensus
23 187 tree. For the ML analysis, we defined the same partitions and performed 1000 bootstrap
24 188 replicates to obtain a bootstrap majority rule consensus tree. Trees were visualised with
25 189 FigTree 1.3.1 (<http://tree.bio.ed.ac.uk/software/figtree/>).
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36 190 37 191 **Species delimitation**

38 192 The ABGD method (Puillandre *et al.*, 2012a) was employed to statistically detect a
39 193 barcode gap (i.e. a gap in the pairwise genetic distance distribution, presumably between
40 194 intraspecific and interspecific distances) from the *cyt b* data set, which is then used to partition
41 195 the data set (initial partition) into species hypotheses. The resulting inferences are then
42 196 recursively applied to yield finer partitions (recursive partitions) until no further partitioning is
43 197 possible. We used the online version
44 198 (<http://www.wabi.snv.jussieu.fr/public/abgd/abgdweb.html>) to analyse the pairwise distance
45 199 matrix calculated for each dataset with PAUP (Swofford, 2003) under a GTR+I+G model, as
46 200 inferred by Modeltest (Posada & Carndall 1998) using the AIC criterion as the best-fitting
47 201 model of nucleotide substitution for the entire data set. ABGD default parameters were used,
48 202 with the exception that the relative gap width (X) was set to 1 (except for *Ramphotyphlops*
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203 *nigrescens* (Gray): 0.9), and Pmin (minimal prior intraspecific divergence) was set to 0.01 to
204 avoid the capture of intraspecific gaps due to weak sampling.

205 The number of putative species (species hypotheses, SHs) was first determined using
206 *cyt b*. Then, those *cyt b* SHs were compared with the nuclear gene data to assess concordance
207 or discordance. Major geographic features which can be barriers to gene flow (rivers,
208 mountains, climatic zones) for well-sampled groups were identified and used in further
209 comparisons of the SHs.

210

211 LRPR haplotypes

212 The software DnaSP v5 (Librado & Rozas 2009) was used to determine the haplotypes.
213 For generating the haplotypes data files, invariables sites were included and sites with gaps or
214 missing data were not considered.

215

216 RESULTS

217 For the *cyt b* gene, the alignment comprised 678 sites, with 386 variable sites among the
218 741 specimens successfully sequenced (4.6% of missing data). For the *PRLR* gene, the
219 alignment comprised 483 sites, of which 197 were variable among the 583 specimens (0.38%
220 of missing data), 158 specimens were unsuccessfully amplified. The alignments were
221 straightforward for both genes.

222

223 Phylogenetic analyses

224 Based on the *cyt b* analysis, 17 of the 27 nominal species are monophyletic in the *cyt b*
225 tree with moderate support using both methods (ML bootstrap > 75% / PP > 95) except
226 *Ramphotyphlops diversus* (Waite) (ML bootstrap = 71 / PP = 1) (see Appendix 1), and five
227 species, *R. affinis* (Boulenger), *R. howi* (Storr), *R. longissimus* (Aplin), *R. silvia* (Ingram &
228 Covacevich) and *R. troglodytes* (Storr), have one representative only. *Ramphotyphlops*
229 *ligatus* (Peters) is polyphyletic in the *cyt b* phylogram (Fig. 1), and *R. kimberleyensis* (Storr),
230 *R. leptosoma* Robb, *R. grypus* (Waite) and *R. guentheri* (Peters) are polyphyletic in both the
231 mtDNA and nDNA phylograms (Figs 1, 2).

232

233 Species delineation

234 Molecular genetic data

235 The ABGD method was applied independently to 21 monophyletic groups defined from
236 the *cyt b* phylogeny (Fig. 1), because groups including a limited number of lineages allowed

us to avoid problems linked to the heterogeneity of evolution times between lineages. This phenomenon may lead to inter- and intraspecific pairwise distributions overlapping and by consequence may prevent the barcode gap detection. These groups corresponded to 17 nominal species that are represented by at least two specimens (16 nominal species and *Ramphotyphlops guentheri* lineage 1) plus three *cyt b* clades with non-monophyletic nominal species (clade 1: *R. grypus* lineage 1, *R. leptosoma* and *R. longissimus*; clade 2: *R. kimberleyensis* and *R. troglodytes*; clade 3: *R. ganei* (Aplin) and *R. ligatus*) and *R. grypus* lineage 2. Three nominal species and the *R. guentheri* lineage 2 were represented each by only one specimen and were not analysed with ABGD. Based on the distribution of pairwise genetic distances, ABGD proposed several partitions that varied according to the different *a priori* thresholds. Apart from the two extreme *a priori* threshold values ($p = 0.009$ and $p = 0.013$), for which aberrant number of species hypotheses were obtained for some groups (almost every haplotype was considered as a different species hypothesis for $p = 0.009$ and, conversely, all the haplotypes were combined in a single species hypothesis for $p = 0.013$, as described in Puillandre et al. 2011), all the tested *a priori* thresholds lead to the same splitting. The only exception is for five groups (*R. ammodytes*, *R. bituberculatus*, *R. ganei*, *R. hamatus* and *R. ligatus*), for which ABGD proposed two different partitions. We only used initial partitions because they were stable on a wide range of values contrary to the recursive partitions (results not shown); the initial partitions are also supposed to more closely match the groups described by taxonomists (Puillandre *et al.*, 2012a).

Considering all possible initial partitions allowed the delineation of 92 partitions or *cyt b* SHs (Table 2). SHs containing more than one specimens are monophyletic and highly supported with three exceptions: SH 55 (ML bootstrap = 70 / PP = 0.93), SH 90 (ML bootstrap = 43 / PP = 0.79) and SH 91 (ML bootstrap = 61 / PP = 0.53) (Appendix 2). SH 15 and SH 11 are polyphyletic (Figure 1).

In a few cases, when ABGD splits one nominal species into several *cyt b* SHs, the divergence between these SHs is similar to the divergence between pairs of nominal species. For example, the genetic distance (*p*-distance) between *Ramphotyphlops guentheri* lineage 2 (SH 54) and *R. howi* (SH 62) is 0.10, whereas it is 0.12 among SHs 86–89 within the group of specimens identified morphologically as *R. unguirostris* (Peters).

The 92 *cyt b* SHs displayed 121 different *PRLR* haplotypes. Among them, 55 SHs are defined by their own haplotypes, i.e. their haplotypes are not shared with any other *cyt b* SHs (Table 2, Fig. 2): *Ramphotyphlops affinis* (SH 1), *R. ammodytes* (SH 3, 7), *R. australis* (Gray) (SH 12–13), *R. bicolor* (Peters) (SH 14–15), *R. bituberculatus* (SH 16–18), *R. diversus* (SH

271 24–26, 30–31), *R. grypus* (SH 40–48), *R. guentheri* (SH 49–54), *R. hamatus* (SH 61), *R. howi*
272 (SH 62), *R. kimberleyensis* (SH 65–66), *R. leptosoma* (SH 67–68), *R. ligatus* (SH 71–72), *R.*
273 *longissimus* (SH 73), *R. nigrescens* (SH 74–78), *R. pilbarensis* (Aplin & Donnellan) (SH 79),
274 *R. pinguis* (Waite) (SH 80), *R. polygrammicus* (Schlegel) (SH 81–82), *R. proximus* (Waite)
275 (SH 83), *R. silvia* (SH 84), *R. troglodytes* (SH 85), *R. unguirostris* (SH 86–89) and *R. wiedii*
276 (Peters) (SH 92). Among them, SH 15 (*R. bicolor*) was the only non-monophyletic SH in the
277 *cyt b* ABGD analysis; however, it is represented by unique *PRLR* haplotypes. Five species
278 include only one sample. The 33 remaining *cyt b* SHs share *PRLR* haplotypes, the SHs within
279 a nominal species that are sharing haplotypes are phylogenetically closely related.

281 *Geographic data*

282 Geographic distributions of mtDNA clades for several well sampled species are
283 congruent with landscape features (Fig. 3). Three main climatic zones are recognized across
284 the Australian continent (Fig. 4). The monsoon tropic zone in northern Australia receives
285 heavy rainfall during the summer and dates from the Late Eocene/Early Oligocene
286 (Greenwood 1996; Pole & Bowman 1996; Alexandre *et al.*, 2004). The mesic zone, which
287 includes the Wet Tropics rainforest in the far northeast, extends south along the Great
288 Dividing Range of the eastern coast, with an isolated region in the southwest. It is the oldest
289 Australian biome, originating from the forests of the Mesozoic that were widespread until the
290 Early Miocene (Hill, 1994; Schodde, 2006). The arid zone in central and western Australia is
291 much younger, with origins from the Early Pliocene (Fujioka *et al.*, 2005; Byrne *et al.*, 2008;
292 Fujioka *et al.*, 2009).

293 In the monsoon tropic zone of northern Australia four major phylogeographic barriers
294 have been identified: the Daly River Drainage Barrier (Ford 1978), the Victoria River
295 Drainage Barrier (Joseph & Omland 2009), the Ord Arid Intrusion (Ford & Blair 2005;
296 Bowman *et al.*, 2010) and the East-West Kimberley Divide (Potter *et al.*, 2012). These
297 barriers are congruent with the distributions of *Ramphotyphlops guentheri*, *R. kimberleyensis*
298 and *R. unguirostris* (Fig. 3), with SHs restricted to each side of the barriers. The geographical
299 repartition of mitochondrial lineages of *R. diversus* can be partly explained by these
300 geographic barriers, and by the boundary between the arid and monsoon regions (Fig. 3). For
301 *R. waitii* (Boulenger), the boundary between the south-west mesic zone and the arid zone is
302 congruent with distributions of SHs 90 and 91 respectively (Fig. 3). Further south, two rivers
303 (Darling River, River Murray) and the Flinders Ranges are congruent with the three major
304 mtDNA lineages of *R. bituberculatus* (SHs 16, 19 and 20; Fig. 3) and to a lesser degree with

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3 305 those of *R. bicolor* (not shown). SH 14 and SH 15 (*R. bicolor*) are distributed on each side of
4 306 the Flinders Ranges except three specimens of the SH 15 located within the eastern SH 14
5
6 307 geographic zone. The separation by recognized barriers of allopatric SHs is additional
7
8 308 evidence for SHs 19 and 20 (*R. bituberculatus*; separated by Darling River and River
9
10 309 Murray), SHs 63–64 (*R. kimberleyensis*; separated by four major phylogeographic barriers:
11 310 the Daly River Drainage Barrier, the Victoria River Drainage Barrier, the Ord Arid Intrusion
12 311 and the East-West Kimberley Divide) and SHs 69–70 (*R. ligatus*; separated by the Victoria
13 312 River Drainage Barrier and also a huge distance (~2600 kilometers)) (Fig. 3).

14
15
16 313 Other species display different distribution patterns. Instead of observing geographically
17 314 restricted mtDNA lineages, some species harbour deep genetic divergences (0.73 between
18 315 SHs 7 and 8 (*R. ammodytes*) and 0.137 between SHs 40 and 45 (*R. grypus*)) among
19 316 geographically close and/or sympatric clades. This pattern is clearly observable for
20 317 *Ramphotyphlops ammodytes* and *R. grypus*, each with many SHs in the rocky Pilbara region,
21 318 and to a lesser degree for *R. australis* and *R. leptosoma* that are restricted to the west central
22 319 coast and for *R. nigrescens* on the east coast. Divergent genetic lineages (a SH with distinct
23 320 nuclear haplotype) found in sympatry reinforce SHs, because despite geographical proximity
24 321 there is no evidence of gene flow. But as many PRLR haplotypes are shared among the SHs
25 322 of *R. ammodytes*, is it more parsimonious to consider these SHs (2,4-6 and 8-11) as a single
26 323 species than a complex of several species with incomplete lineage sorting or hybridization.

27 324 Conversely, the four *R. endoterus* (Waite) SHs occur across the arid zone in four
28 325 allopatric mtDNA lineages but without recognized barriers between them. In this case, as with
29 326 the seven *R. hamatus* SHs (distributed across the rocky Pilbara zone and the eastern part of
30 327 the arid zone), geographic data do not suggest consolidation of SHs.

31 328 In several cases, there is strong congruence among mitochondrial, nuclear, and
32 329 geographic data, leading us to recognize 55 robust putative species using *cyt b* and *PRLR*
33 330 haplotypes and 61 putative species when adding geographic (sympatry or allopatry with
34 331 barriers) data only (Table 2). In the least conservative scheme (*cyt b* only), there are 92
35 332 putative species (Table 2).

36 333

37 334 **DISCUSSION**

38 335 The concordance of independent genes (nuclear and mitochondrial) is generally
39 336 considered valuable evidence for species delimitation (Knowlton, 2000; Barberousse &
40 337 Samadi 2010). In our data set, 55 of the 92 *cyt b* SHs are robustly defined by an independent
41 338 nuclear gene. The other *cyt b* SHs shared nuclear haplotypes, but the fact that these SHs

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3 339 remain closely related in the *cyt b* phylogram suggests a lack of variability of the *PRLR* gene
4 340 at this scale, or a nuclear gene flow. To clarify this situation the use of other more variable
5 341 nuclear markers is needed in the future. Analyzing more specimens per nominal species
6 342 should be useful as well. Indeed the probability to find rare and shared haplotypes is higher
7 343 for species that are densely sampled (several localities and several specimens per localities)
8 344 even if some nominal species appear to be genetically uniform. For example, the 9 SHs of the
9 345 nominal species *Ramphotyphlops grypus* are defined by specific haplotypes over the 59
10 346 species analyses with the nuclear marker. Concerning *R. pilbarensis*, even when the number
11 347 of nuclear sequences was relatively high (29), only 2 different haplotypes were found. If we
12 348 analyse the *cyt b* SHs on an individual basis, the number supported by different independent
13 349 sources of information increases to 61 when geographical data are considered. Therefore,
14 350 from the 27 nominal species of Australian blindsnakes studied here, our results support at
15 351 least 55 (most conservative) and up to 92 (least conservative) species. Nine nominal species
16 352 were not subdivided. The identification of new morphological characters should also help to
17 353 discriminate among the different hypotheses proposed here. The visceral anatomy traits may
18 354 be useful as they allowed the discrimination of some leptotyphlopoid species (Adalsteinsson *et*
19 355 *al.*, 2009).

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31 356 The early diversification of Australian *Ramphotyphlops* was probably driven by the
32 357 development of the arid zone ~20 Ma (Marin *et al.*, 2012). As the arid zone expanded in
33 358 central Australia, mesic-adapted lineages were confined to the east coast and southwest, to the
34 359 northern monsoonal tropics, and also to Pilbara in the arid zone which likely served as refugia
35 360 (Martin 2006; Byrne *et al.*, 2008, 2011). Occupation of areas like the Pilbara and Kimberley
36 361 (northern monsoonal tropics), that have humid refugia but are seasonally very arid may have
37 362 allowed time for this lineage of snakes that has a wet-tropical origin to acquire adaptations to
38 363 resist seasonally dry conditions which then pre-adapted them for the truly arid conditions
39 364 further inland (Fujita *et al.*, 2010).

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46 365 Several biogeographic barriers within these refugia seem to be involved in a later,
47 366 younger than eight Ma (Marin *et al.*, 2012), allopatric diversification of species (*R. bicolor*, *R.*
48 367 *bituberculatus*, *R. diversus*, *R. guentheri*, *R. kimberleyensis*, *R. ligatus* and *R. unguirostris*)
49 368 (Fig. 3). They are more subject to isolation due to their fossorial lifestyle (Vidal *et al.*, 2010).
50 369 Similar patterns of diversification were recently found for rock wallabies in the monsoon
51 370 tropic zone (Potter *et al.*, 2012) and for beaked geckos in the eastern arid zone and southeast
52 371 mesic zone (Pepper *et al.*, 2011). Some other SHs of our *Ramphotyphlops* dataset display
53 372 close and/or sympatric geographic distributions in the rocky Pilbara region. This region is
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3 373 characterized by geological heterogeneity, complex phytogeography and long-term geological
4 374 stability (Pepper, Doughty & Keogh 2006) leading to a mosaic of habitat types (Doughty *et*
5 375 *al.*, 2011). This may explain the sympatric distribution observed for *R. ammodytes*, *R. grypus*
6 376 and *R. hamatus*. Assuming that each SH may be restricted to a particular habitat, they should
7 377 have evolved independently through ecological diversification. But contrary to the results for
8 378 *R. grypus* and *R. hamatus*, nuclear haplotypes of *R. ammodytes* are shared between SHs. This
9 379 could reflect a more recent speciation event or more probably could be linked to the fact that
10 380 *R. ammodytes* is one species. One other interesting geographic pattern concerns *R. endoterus*,
11 381 which is consistent with a sandy desert expansion out of the west. Several different genetic
12 382 groups (SHs 33–35) have differentiated in the west, but only a single lineage (SH 32) has
13 383 expanded eastward into the younger central and eastern desert areas, a pattern seen in other
14 384 arid zone non-snake taxa (Moritz & Heideman 1993; Kearney *et al.*, 2006). *Ramphotyphlops*
15 385 *hamatus* shows a similar though less expansive pattern. SHs of *R. endoturus* share a common
16 386 nuclear haplotype, reflecting a recent speciation event or a single species with a polymorphic
17 387 mitochondrial marker.

18 388 Overall, our results suggest that the current complement of nominal Australian
19 389 *Ramphotyphlops* species is less than the total, with the true species diversity ranging between
20 390 210–340% of the currently described species. However, even though our dataset is large
21 391 (~740 specimens), the sampling is limited for some taxa, and adding more specimens—
22 392 especially for species with a single sequenced specimen— may help to more accurately
23 393 delimitate the current species. On a larger taxonomic scale, these new species (55–96)
24 394 represent an increase of 7–16% of the entire scolecophidian species diversity. Currently 402
25 395 scolecophidian species are described, while acknowledging that extrapolations of hidden
26 396 biodiversity from limited surveys are subject to sampling errors (Gray, 2002), taken at face
27 397 value our results suggest that up to 1200 scolecophidian species may exist, mostly hidden
28 398 from current taxonomy. If true, that would be an exceptional increase in the number of reptile
29 399 or vertebrate species.

30 400 The morphological conservativeness of blindsnakes may be responsible for this hidden
31 401 diversity, as potentially informative characters have been reduced or eliminated as an outcome
32 402 of their burrowing lifestyle (Hedges & Thomas 1991; Thomas & Hedges 2007). The limited
33 403 knowledge on the morphological characters useful for the discrimination of blindsnakes is
34 404 also likely responsible. Fortunately, in other cases where genetic analysis has revealed hidden
35 405 species of scolecophidians, non-traditional morphological characters always have been found
36 406 and used to diagnose the species (Hedges & Thomas 1991; Aplin & Donnellan 1993; Rabosky

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3 407 *et al.*, 2004; Thomas & Hedges 2007). For this reason, we suspect that most of all of the
4 408 putative new species revealed here will be diagnosed morphologically and named.

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6 409 These results also have implications for conservation, because accurate taxonomic data
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8 410 are critical for determining basic parameters of protection such as distributions and threat
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10 411 levels (Rondinini *et al.*, 2006). Also, nominal species already considered endangered or
11 412 threatened may be composed of several species, each of which are often rarer than their
12 413 "parent species," making them more susceptible to extinction (Hedges & Conn, 2012). For
13 414 these species, taxonomic revisions are urgent. Without published descriptions, these species
14 415 are essentially "off the conservation radar" and therefore cannot be considered in conservation
15 416 plans (Hedges & Conn, 2012).

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20 21 418 **CONCLUSION**

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23 419 Morphological conservativeness and the limited knowledge of useful morphological
24 420 discriminant characters seem to have prevented the recognition of numerous Australian
25 421 blindsnake species (*Ramphotyphlops*). Using several lines of independent evidence, including
26 422 mtDNA, nuclear DNA, and geography, we found that as least 55 species exist, which is twice
27 423 the currently recognized number of species. This is consistent with the results of previous
28 424 smaller-scale studies of scolecophidians elsewhere in the world, suggesting that the proportion
29 425 of species of these burrowing snakes yet to be described is greater than is typical in terrestrial
30 426 vertebrates.

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60**607 FIGURE LEGENDS**

608 **Figure 1.** Bayesian inference phylogenetic tree of Australian *Ramphotyphlops* based on
609 analysis of sequences of a mitochondrial protein-coding gene, *cytochrome b*, showing species
610 hypotheses (SHs) obtained with the ABGD method. Framed clades share common PRLR
611 haplotypes. Dashed lines join SH when they shared a PRLR haplotype. Nodes with black
612 circles are supported by posterior probabilities > 95% and ML bootstrap probabilities > 75%.
613 Nodes with white circles are supported by posterior probabilities > 90% and ML bootstrap
614 probabilities > 70%. The first set of vertical bars (Mt: mitochondrial data) corresponds to the
615 56 SHs supported by mitochondrial DNA. The second set of vertical bars (Mt & N:
616 mitochondrial and nuclear data) corresponds to the 92 SHs supported by nuclear and
617 mitochondrial DNA. Asterisks (*) indicate nominal species for which SHs are found in
618 sympatry.

620 **Figure 2.** Maximum Likelihood phylogenetic tree of Australian *Ramphotyphlops* based on the
621 analysis of a nuclear protein-coding gene, *prolactin receptor (PRLR)*. Species hypotheses
622 (SHs) shown here were obtained with the ABGD method using *cytochrome b*. Nodes with
623 black circles are supported by posterior probabilities > 95% and ML bootstrap probabilities >
624 75%. Nodes with white circles are supported by posterior probabilities > 90% and ML
625 bootstrap probabilities > 70%.

627 **Figure 3.** Sample locations of Australian *Ramphotyphlops* species for which geographic
628 patterns are discussed. Recognized biogeographic barriers – 1: Daly River, 2: Victoria River,
629 3: Ord Arid Intrusion, 4: East-West Kimberley Divide, 5: Flinders Ranges, 6: Darling River,
630 7: Murray River.

632 **Figure 4.** Map of the three main climatic zones and mountainous regions of the continental
633 Australia. Modified from Fujita *et al.*, 2010; Byrne *et al.*, 2011; Pepper *et al.*, 2011).

639 TABLES

640 Table 1. List of primers used in this study.

Gene	Primer	Authors
<i>cyt b</i>	CS1L GAAAAACCGCYRTTGTWWTCAACTA	Adalsteinsson <i>et al.</i> , 2009
	LTyph2R AGYTTGTTTGGGATKGCTCGTAGRAT	Adalsteinsson <i>et al.</i> , 2009
	L14910 GACCTGTGATMTGAAAACCAAYCGTTGT	Burbrink <i>et al.</i> , 2000
	H16064 CTTTGGTTTACAAGAACAATGCTTTA	Burbrink <i>et al.</i> , 2000
<i>PRLR</i>	PRLR_f1 GACARYGARGACCAGCAACTRATGCC	Townsend <i>et al.</i> , 2008
	PRLR_f2 AAGAGTCRCCCAYATAAAAA	This study
	PRLR_r3 GACYTTGTGRACTTCYACRTAATCCAT	Townsend <i>et al.</i> , 2008
	PRLR_r4 AAGAACYTCTCTGGAGGT	This study
	PRLR_r5 ATCCATTGGYTTTGYAGACA	This study

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642 **Table 2.** Recapitulative table of Australian *Ramphotyphlops* (*R.*) results.
 643 N hp, number of haplotypes; Nb, number; SH, Species hypotheses.
 644 Geographic patterns (sympatry and allopatry) are globally and visually assessed for each
 645 morphologically-defined species.

Species names	Number of sequences		SHs (cumulative approach)	First partition	Alternative partition	PRLR		SHs (congruent approach)	Geography
	<i>cyt b</i>	PRLR				Nb hp	Shared hp		
<i>R. affinis</i>	1	1	SH1	x		1		SH1	–
<i>R. ammodytes</i>	9	5	SH2	x	x	1	SH11	SH3 SH7	sympatry
	1	1	SH3	x	x	1			
	1	0	SH4	x	x	0			
	11	3	SH5	x	x	2	SH8		
	4	1	SH6	x		0			
	1	1	SH7	x	x	1			
	2	2	SH8	x		1	SH5		
	2	2	SH9	x		2	SH10		
	4	3	SH10	x	x	2	SH9		
	58	32	SH11	x		7	SH2		
	<i>R. australis</i>	135	116	SH12	x		14		
6		3	SH13	x		2		SH13	
<i>R. bicolor</i>	17	11	SH14	x		1		SH14	allopatry
	26	20	SH15	x		2		SH15	
<i>R. bituberculatus</i>	25	20	SH16	x		4		SH16	allopatry
	4	4	SH17	x	x	2		SH17	
	1	1	SH18	x		1		SH18	
	11	10	SH19	x	x	1	SH20		
	14	11	SH20	x	x	2	SH19		
<i>R. centralis</i> (Storr)	3	3	SH21	x		2	SH22		–
	2	2	SH22	x		1	SH21		
<i>R. diversus</i>	3	2	SH23	x		1	SH27–28–29	SH24 SH25 SH26 SH30 SH31	allopatry
	1	1	SH24	x		1			
	1	1	SH25	x		1			
	1	1	SH26	x		1			
	4	4	SH27	x		2	SH23–28–29		
	4	4	SH28	x		1	SH23–27–29		
	2	2	SH29	x		1	SH23–27–28		
	1	1	SH30	x		1			
	2	1	SH31	x		1			
<i>R. endoterus</i>	76	58	SH32	x		2	SH33–34–35	allopatry	
	7	6	SH33	x		1	SH32–34–35		
	3	3	SH34	x		1	SH32–33–35		
	10	9	SH35	x		3	SH32–33–34		
<i>R. ganei</i>	2	2	SH36	x		2	SH37–38	–	
	1	1	SH37	x		1	SH36–38		
	1	1	SH38	x	x	1	SH36–37		
	1	0	SH39	x		0			
<i>R. grypus</i>	10	8	SH40	x		2		SH40	sympatry
	4	4	SH41	x		1		SH41	
	1	1	SH42	x		1		SH42	
	1	1	SH43	x		1		SH43	
	10	5	SH44	x		2		SH44	
	21	12	SH45	x		2		SH45	
	28	22	SH46	x		6		SH46	
	2	2	SH47	x		1		SH47	
4	4	SH48	x		2		SH48		
<i>R. guentheri</i>	1	1	SH49	x		1		SH49	allopatry

	1	1	SH50	x		1		SH50	
	1	1	SH51	x		1		SH51	
	1	1	SH52	x		1		SH52	
	1	1	SH53	x		1		SH53	
	1	1	SH54	x		1		SH54	
<i>R. hamatus</i>	20	18	SH55	x		2	SH56–57–58–59		allopatry
	9	8	SH56	x		1	SH55–57–58–59		
	5	4	SH57	x		1	SH55–56–58–59		
	10	8	SH58	x	x	2	SH55–56–57–59–60		
	3	3	SH59	x		1	SH55–56–57–58		
	1	1	SH60	x		1	SH58		
	2	2	SH61	x	x	1		SH61	
<i>R. howi</i>	1	1	SH62	x		1		SH62	–
<i>R. kimberleyensis</i>	4	4	SH63	x		1	SH64		allopatry
	2	1	SH64	x		1	SH63		
	3	3	SH65	x		1		SH65	
	1	1	SH66	x		1		SH66	
<i>R. leptosoma</i>	12	12	SH67	x		4		SH67	sympatry
	2	2	SH68	x		1		SH68	
<i>R. ligatus</i>	1	1	SH69	x	x	1	SH70		allopatry
	3	3	SH70	x		1	SH69		
	1	1	SH71	x	x	1		SH71	
	1	1	SH72	x		1		SH72	
<i>R. longissimus</i>	1	1	SH73	x		1		SH73	–
<i>R. nigrescens</i>	6	6	SH74	x		2		SH74	sympatry
	3	2	SH75	x		2		SH75	
	4	3	SH76	x		1		SH76	
	8	6	SH77	x		2		SH77	
	4	4	SH78	x		1		SH78	
<i>R. pilbarensis</i>	30	29	SH79	x		2		SH79	–
<i>R. pinguis</i>	2	2	SH80	x		1		SH80	–
<i>R. polygrammicus</i>	4	4	SH81	x		1		SH81	–
	1	1	SH82	x		1		SH82	
<i>R. proximus</i>	6	3	SH83	x		2		SH83	–
<i>R. silvia</i>	1	1	SH84	x		1		SH84	–
<i>R. troglodytes</i>	1	1	SH85	x		1		SH85	–
<i>R. unguirostris</i>	4	4	SH86	x		2		SH86	allopatry
	1	1	SH87	x		1		SH87	
	1	1	SH88	x		1		SH88	
	1	1	SH89	x		1		SH89	
<i>R. waitii</i>	24	17	SH90	x		3	SH91		allopatry
	10	5	SH91	x		3	SH90		
<i>R. wiedii</i>	3	3	SH92	x		1		SH92	–

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653 **APPENDICES**

654 Table1_SuppInfo.xlsx

655 Description: Taxa, localities and accession numbers of the specimens used in the study.

656 Figure1_SuppInfo.docx

657 Description: Phylogenetic tree of Australian *Ramphotyphlops* based on the analysis of
658 sequences of *cytochrome b* (*cyt b*).

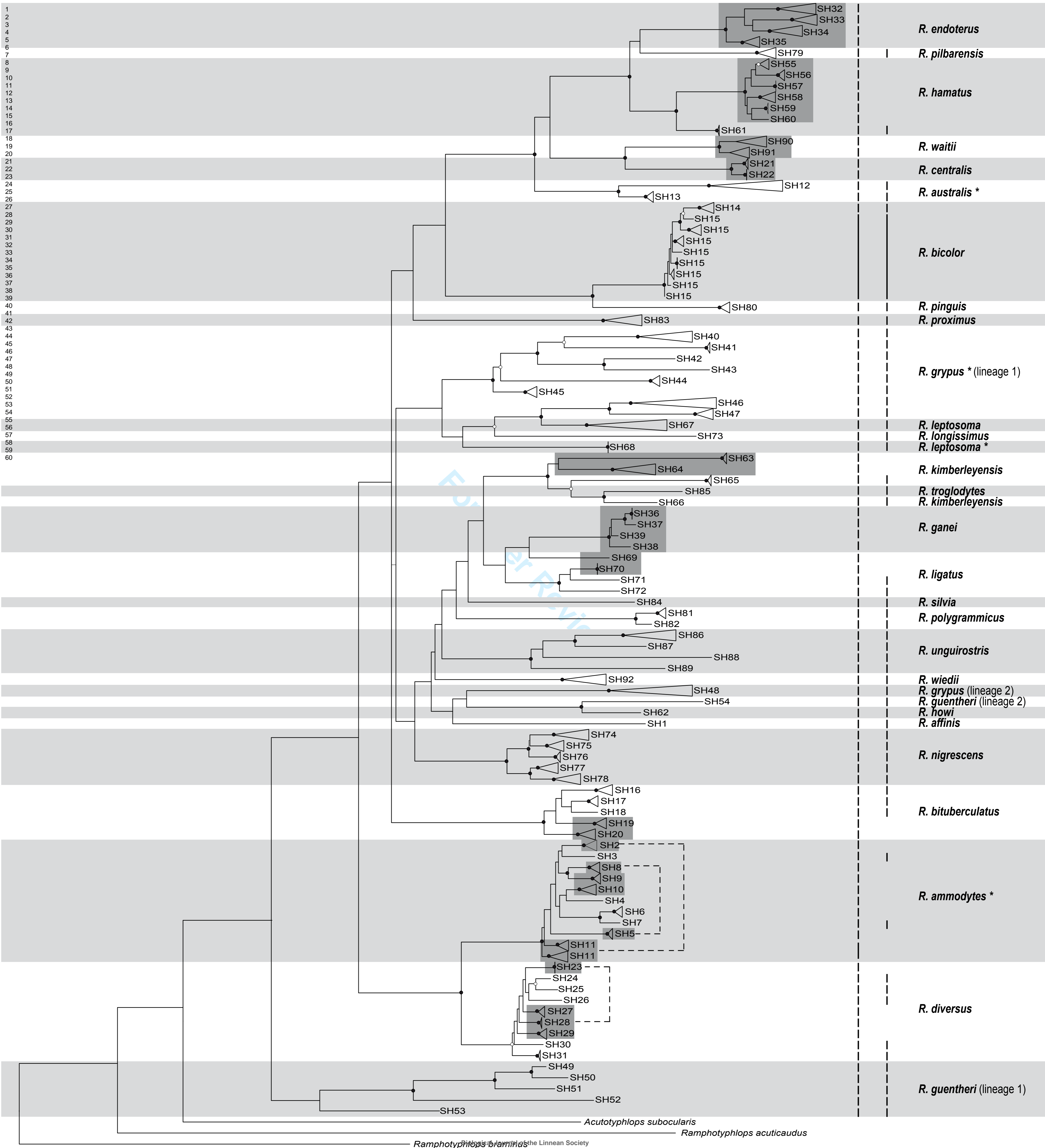
659 Figure2_SuppInfo.doc

660 Description: Phylogenetic tree of Australian *Ramphotyphlops* based on the analysis of
661 sequences of prolactine receptor (*PRLR*).

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For Peer Review



R. endoterus

R. pilbarensis

R. hamatus

R. waitii

R. centralis

R. australis *

R. bicolor

R. pinguis

R. proximus

R. grypus * (lineage 1)

R. leptosoma

R. longissimus

R. leptosoma *

R. kimberleyensis

R. troglodytes

R. kimberleyensis

R. ganei

R. ligatus

R. silvia

R. polygrammicus

R. unguirostris

R. wiedii

R. grypus (lineage 2)

R. guentheri (lineage 2)

R. howi

R. affinis

R. nigrescens

R. bituberculatus

R. ammodytes *

R. diversus

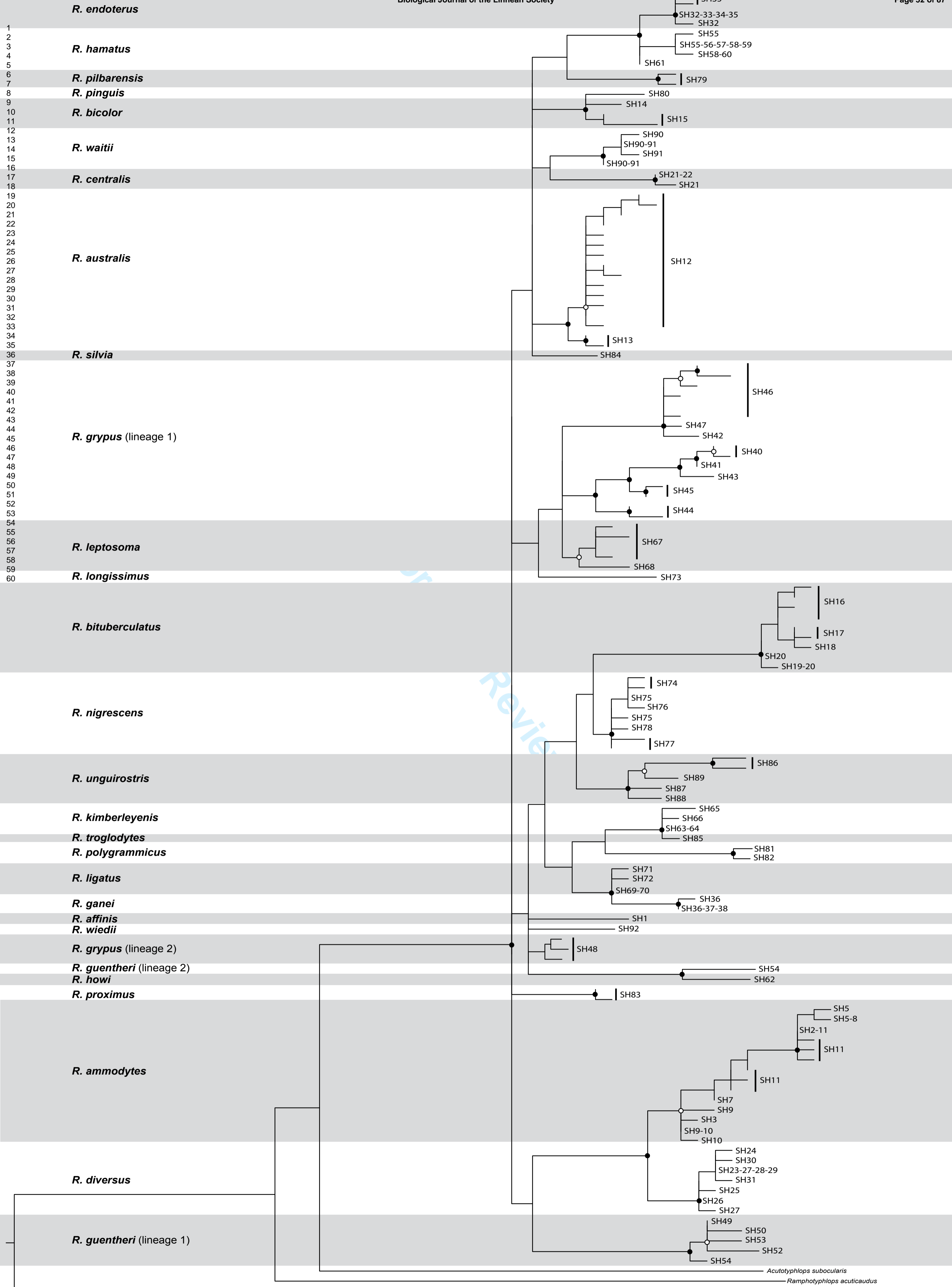
R. guentheri (lineage 1)

Acutotyphlops subocularis

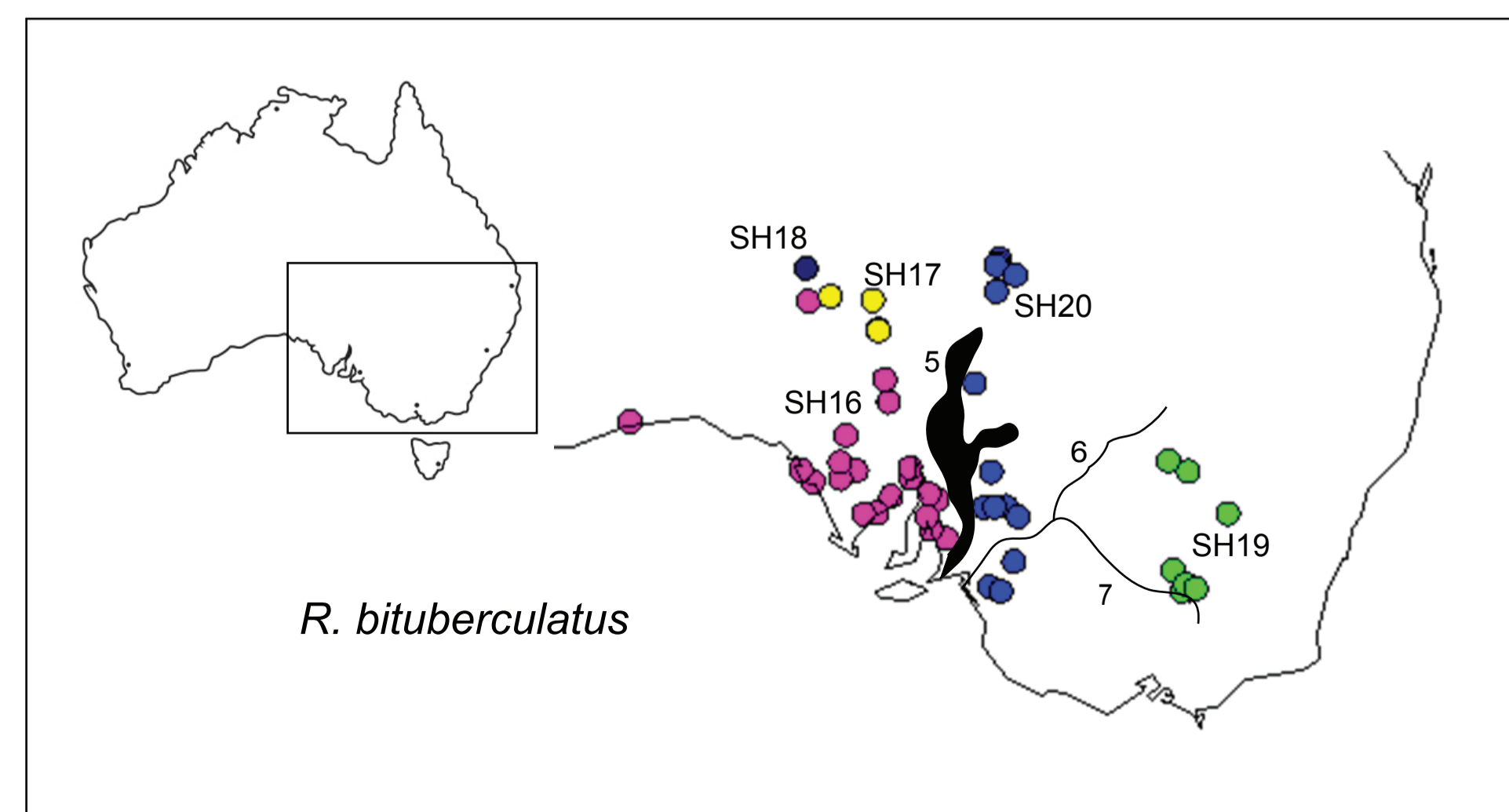
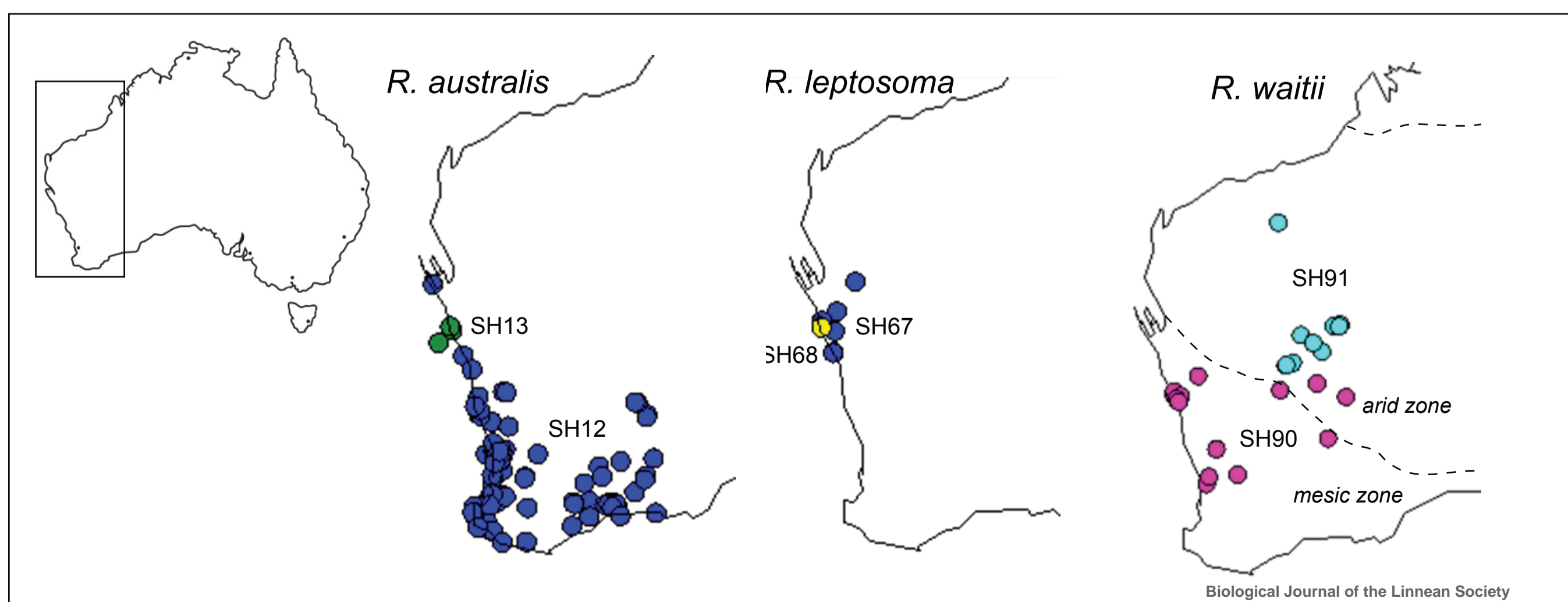
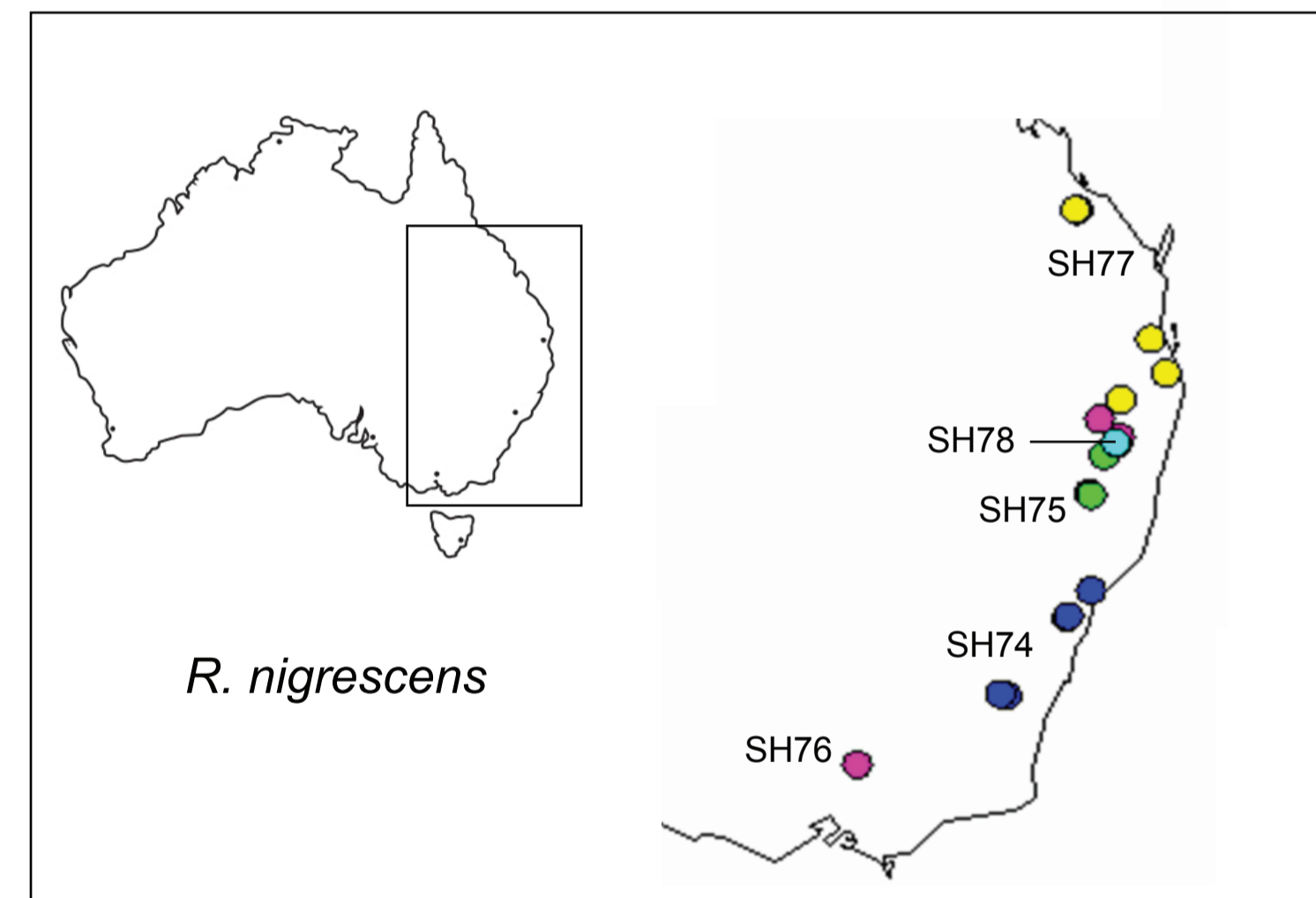
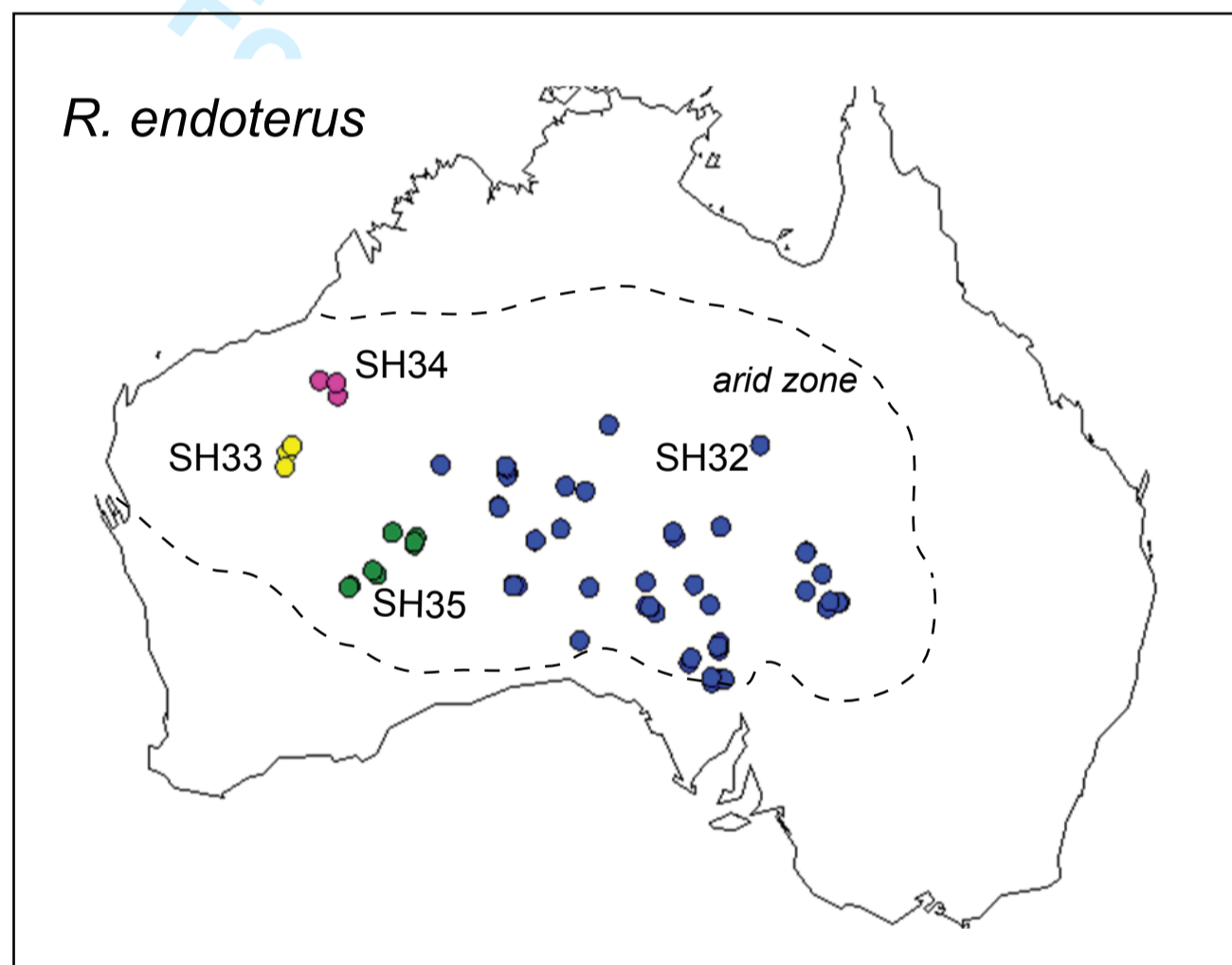
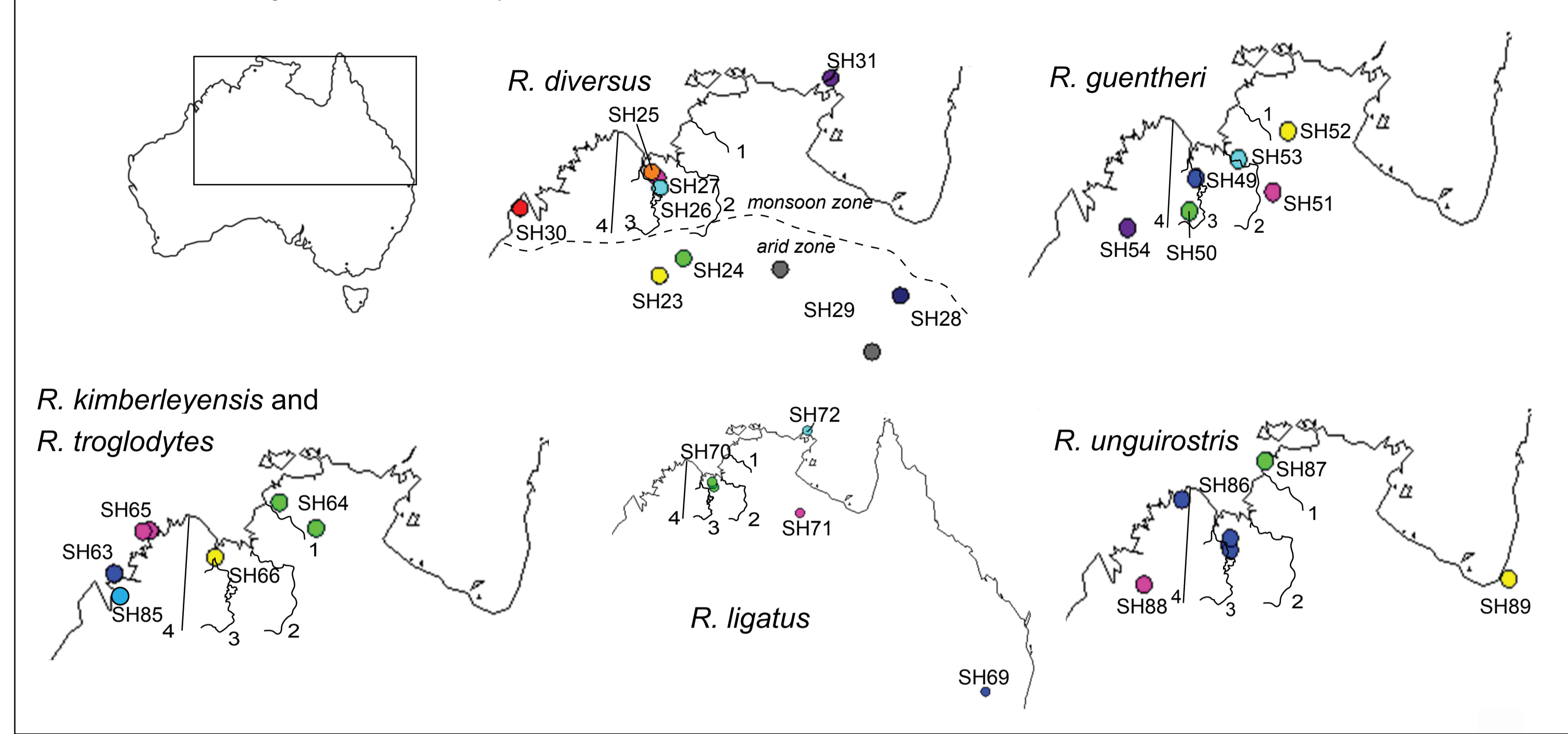
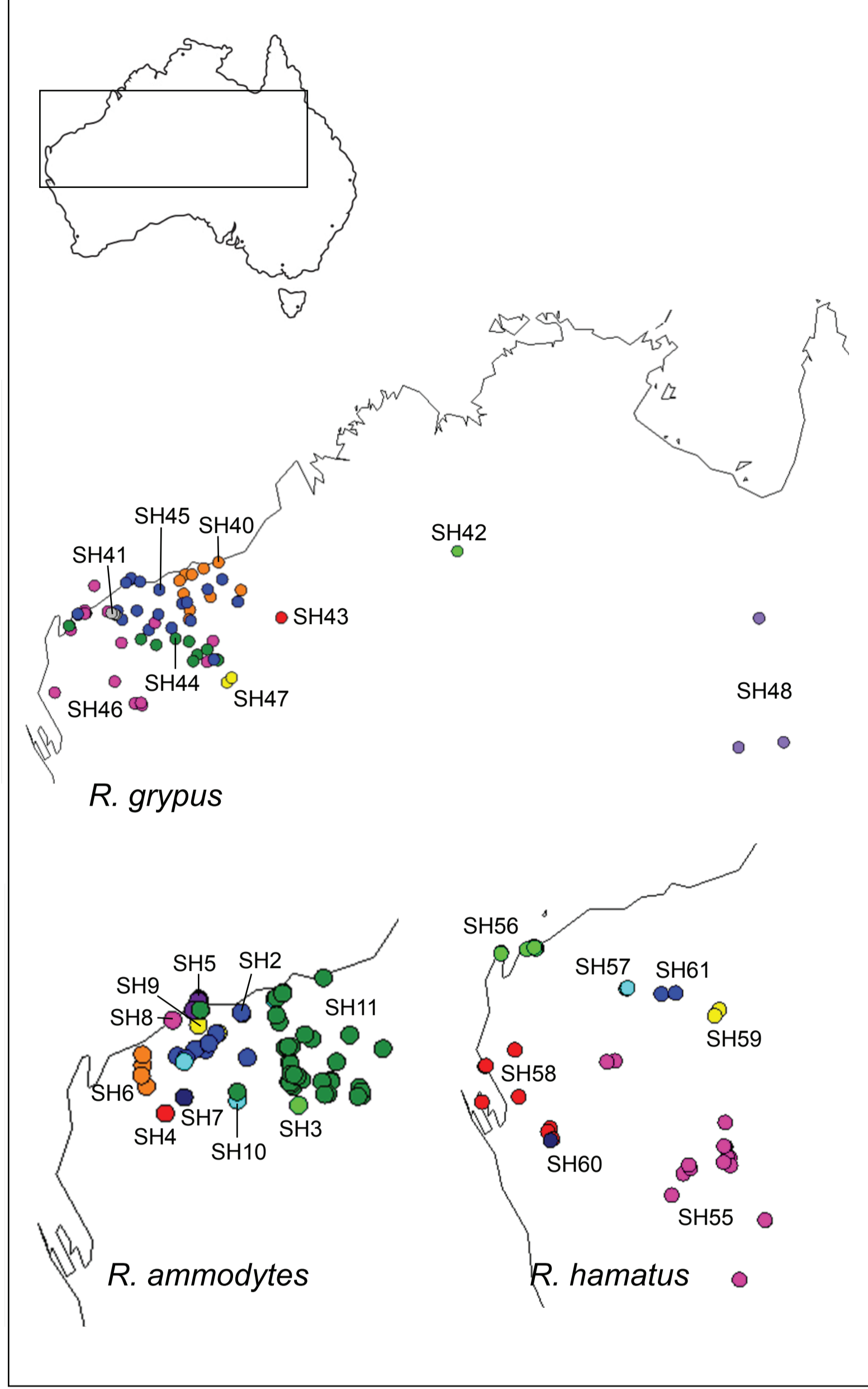
Ramphotyphlops acuticaudus

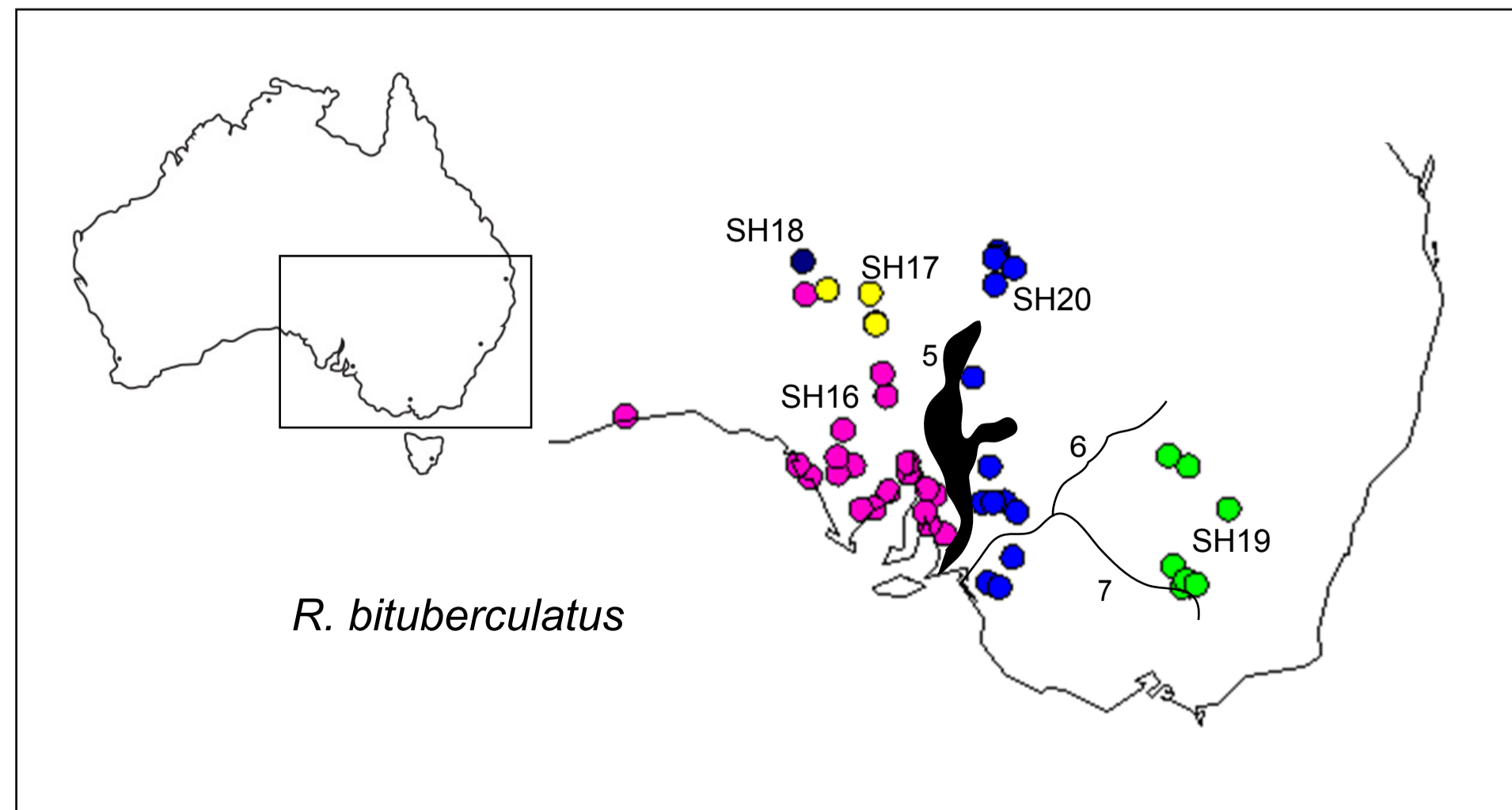
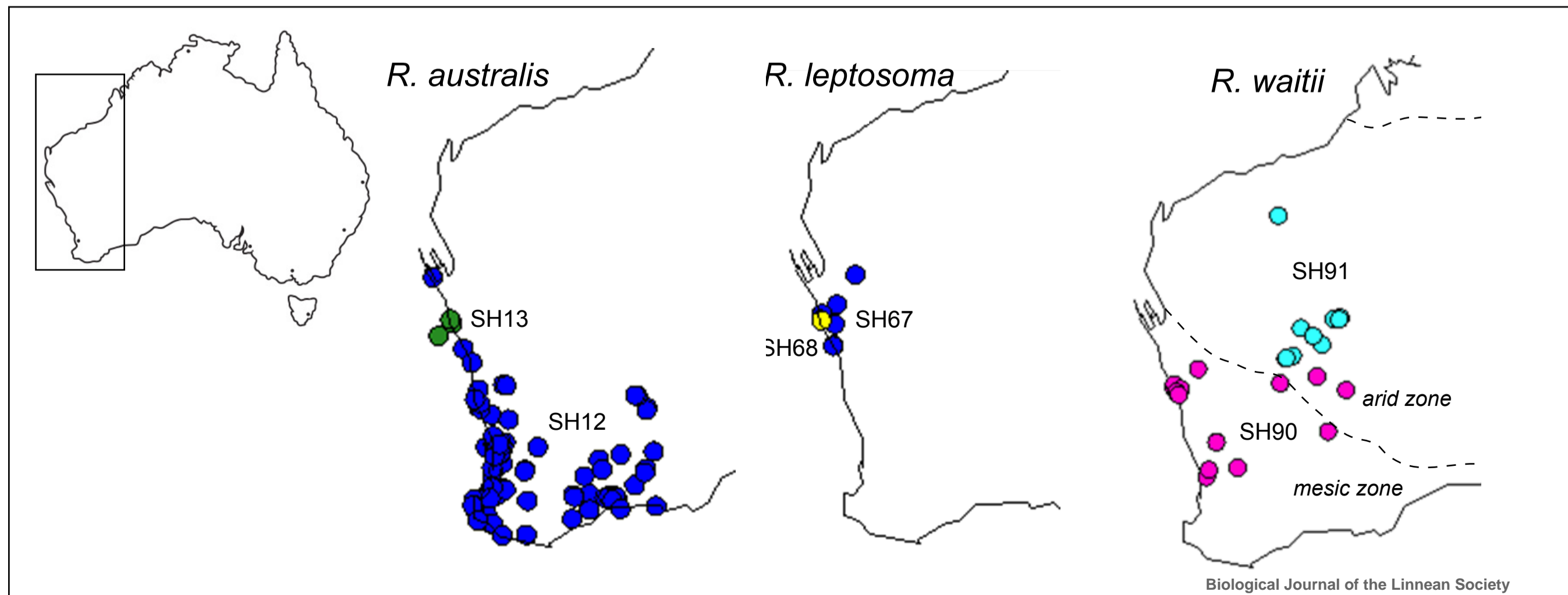
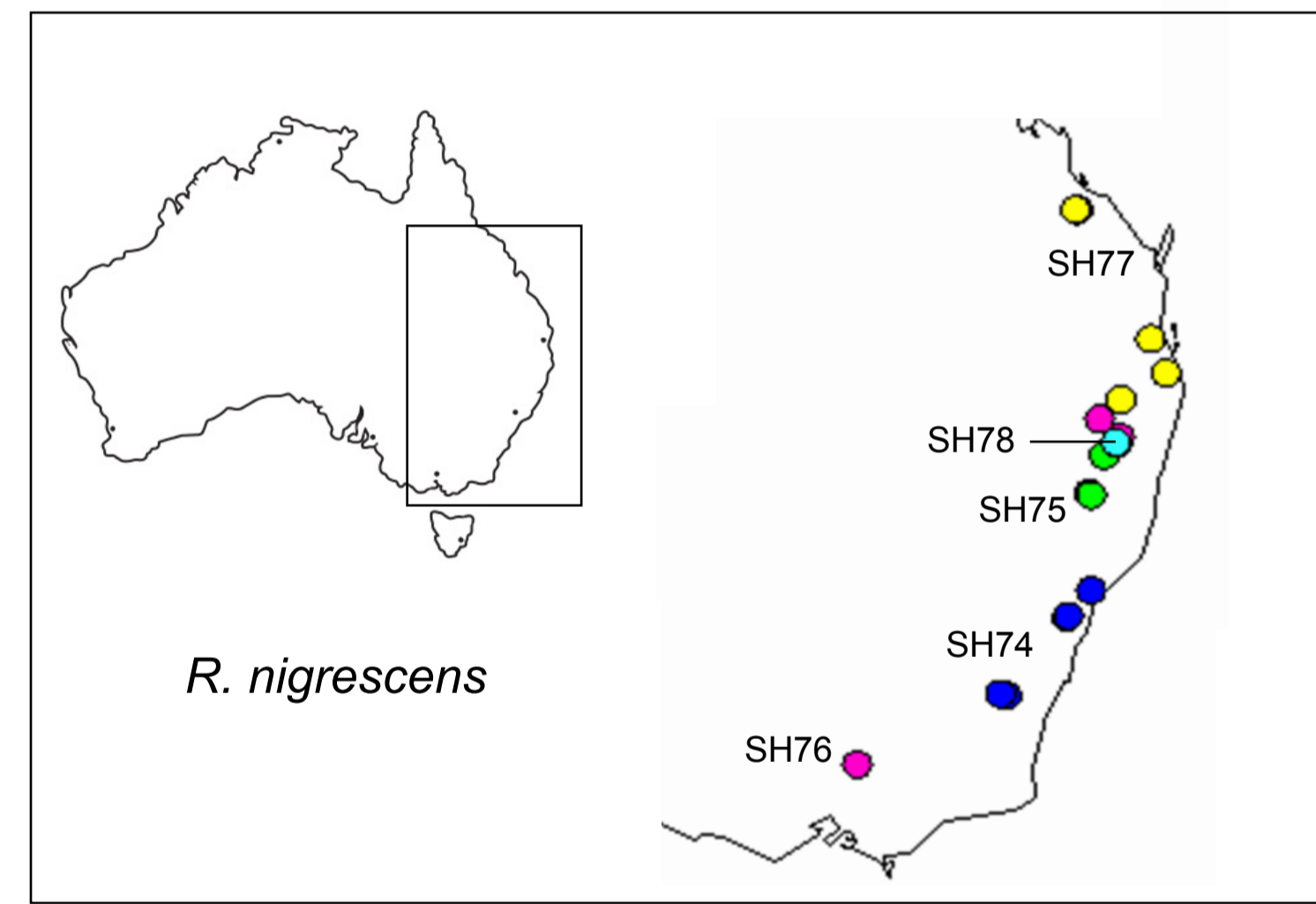
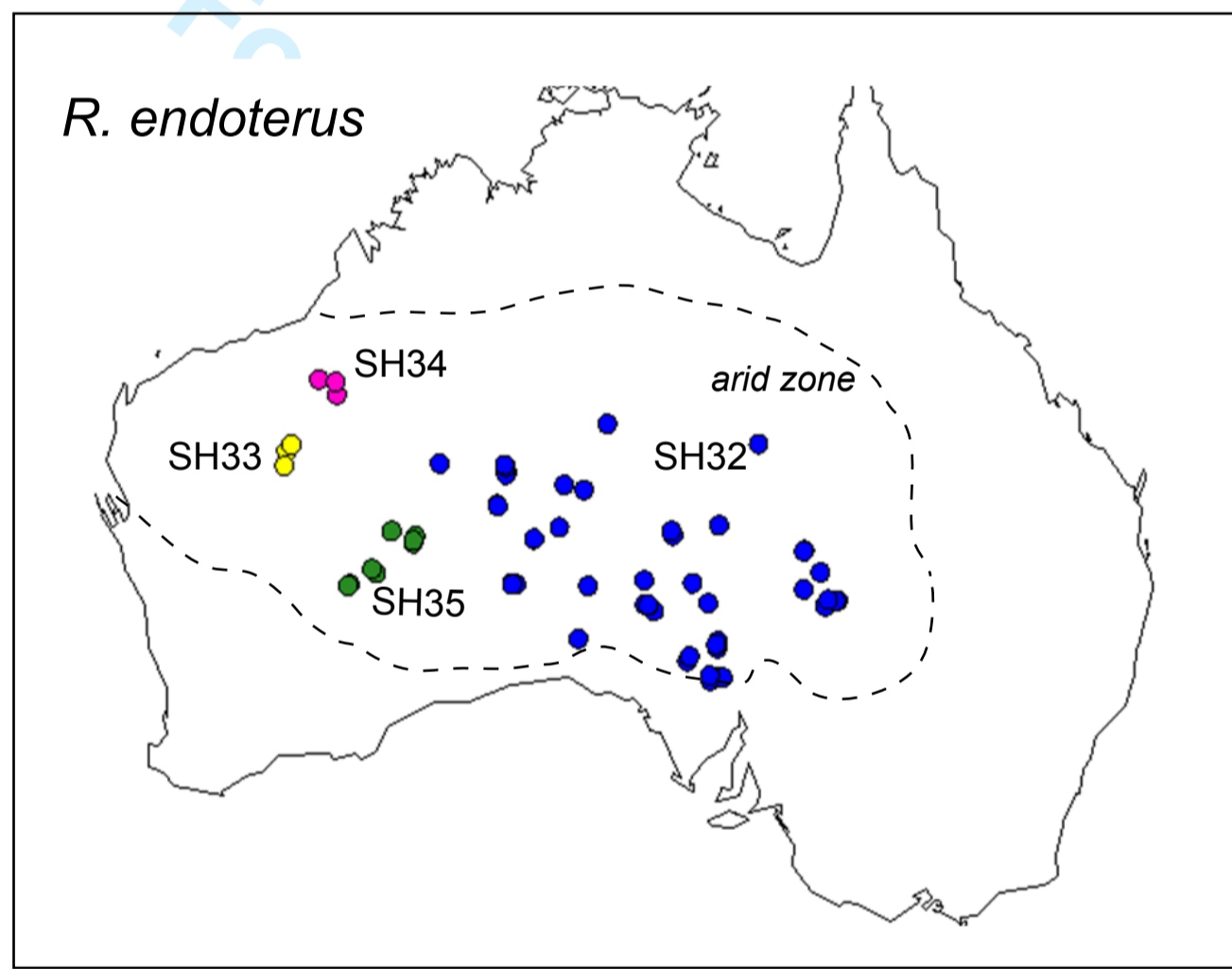
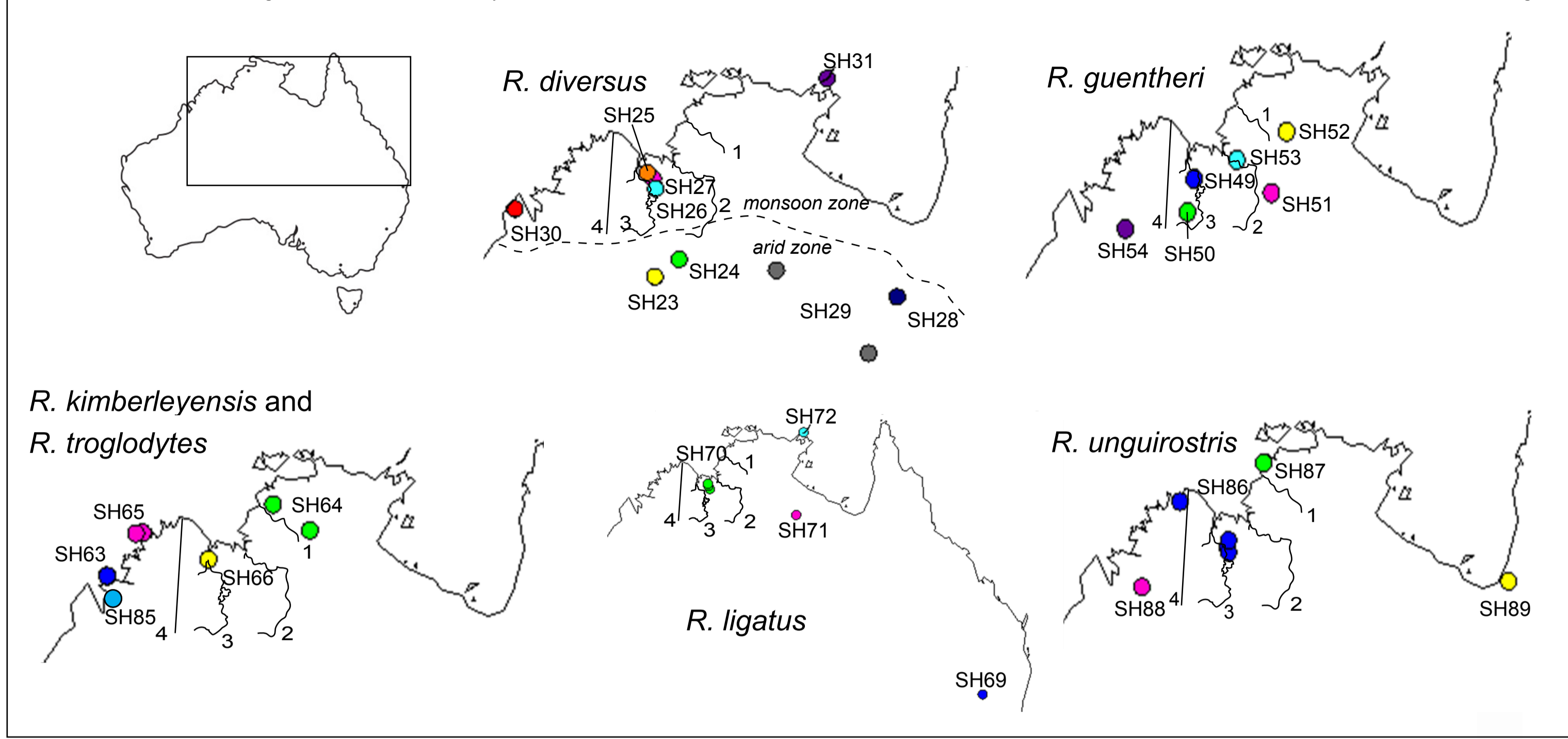
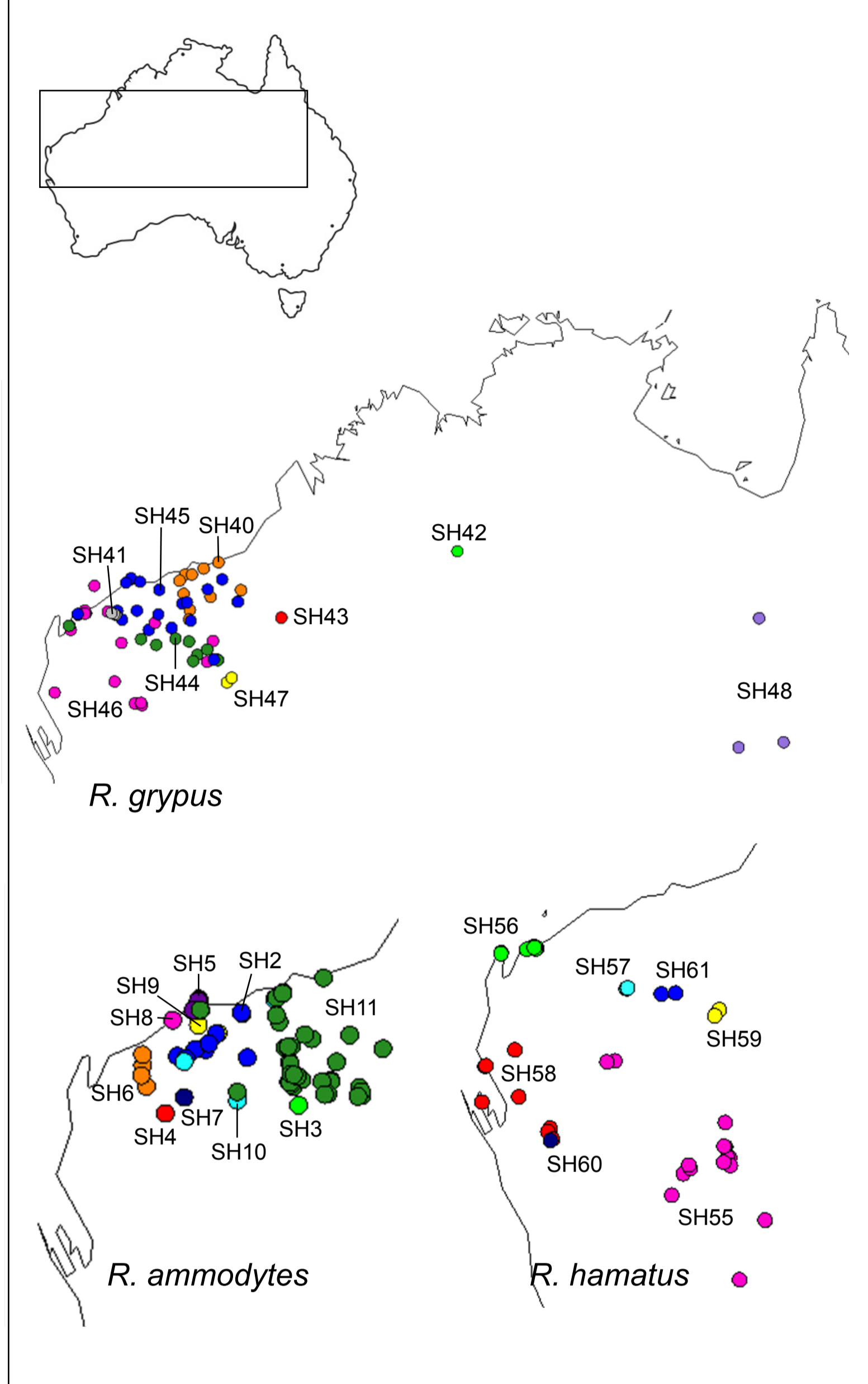
Ramphotyphlops draminus

0.3 substitution/site



Acutotyphlops subocularis
Ramphotyphlops acuticaudus
Ramphotyphlops braminus





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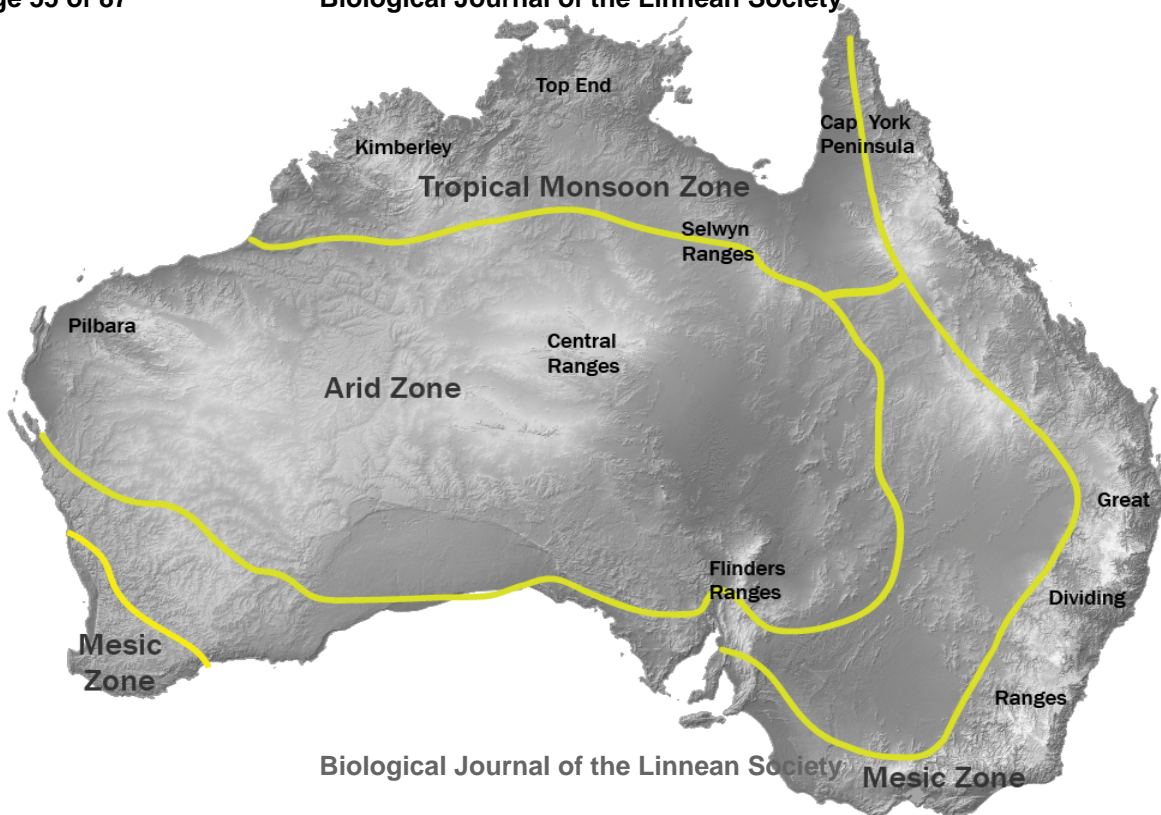


Table1_SupplInfo: Taxa, localities and accession numbers of the specimens used in the study.

Genus	species	GenBank numbers		SH	Museum catalogue
		Cytb	PRLR		
<i>Ramphotyphlops</i>	<i>affinis</i>	JQ910526	JQ910417	1	SAMAR55645
<i>Ramphotyphlops</i>	<i>ammodytes</i>	KC489799	KC490434	11	WAMR114541
		KC489800		4	WAMR102560
		KC489801		5	WAMR102805
		JQ910527	JQ910418	11	WAMR104109
		KC489802		11	WAMR108831
		KC489803		5	WAMR110068
		KC489804		2	WAMR110144
		KC489805		2	WAMR110185
		KC489806	KC490435	2	WAMR110199
		KC489807	KC490436	11	WAMR110244
		KC489808		11	WAMR110247
		KC489809		11	WAMR110279
		KC489810	KC490437	11	WAMR110290
		KC489811		11	WAMR110318
		KC489812		11	WAMR110319
		KC489813	KC490438	10	WAMR110856
		KC489814	KC490439	2	WAMR110858
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		KC489816	KC490440	11	WAMR111958
		KC489817		11	WAMR111969
		KC489818		11	WAMR111995
		KC489819	KC490441	11	WAMR111996
		KC489820	KC490442	11	WAMR114541
		JQ910528	JQ910419	3	WAMR121995
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		KC489823		5	WAMR132643
		KC489824	KC490445	5	WAMR132647
		KC489825	KC490446	5	WAMR132666
		KC489826	KC490447	11	WAMR135908
		KC489827		11	WAMR139373
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		JQ910531	JQ910422	8	WAMR141306
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		KC489829	KC490449	11	WAMR145549
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		KC489840	KC490457	11	WAMR146623

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		JQ910532	JQ910423	9	WAMR158097	
		KC489855		11	WAMR158159	
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KC489911	KC490500	12	WAMR115969
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		KC490286	KC490792	46	WAMR166004
		KC490287		44	WAMR166215
		KC490288	KC490793	44	WAMR166895
		KC490289		45	WAMR170781
<i>Ramphotyphlops</i>	<i>guentheri</i>	JQ910574	JQ910461	52	NTMR13611
		JQ910575	JQ910462	51	NTMR16488
		JQ910576	JQ910463	53	ABTC67980
		JQ910577	JQ910460	54	SAMAR53885
		JQ910578	JQ910464	49	WAMR105974
		JQ910579	JQ910465	50	WAMR108431
<i>Ramphotyphlops</i>	<i>hamatus</i>	KC490290	KC490794	55	WAMR113176
		KC490291	KC490795	56	WAMR108348
		KC490292	KC490796	56	WAMR110669
		KC490293		56	WAMR110678
		KC490294	KC490797	55	WAMR110954
		KC490295	KC490798	55	WAMR110955
		KC490296	KC490799	55	WAMR110956
		KC490297	KC490800	55	WAMR110958
		KC490298	KC490801	59	WAMR111744
		KC490299	KC490802	59	WAMR111763
		JQ910580	JQ910467	59	WAMR111862
		KC490300	KC490803	56	WAMR112181
		KC490301	KC490804	56	WAMR112182
		KC490302	KC490805	56	WAMR112504
		KC490303	KC490806	58	WAMR112742
		KC490304	KC490807	58	WAMR112743
		JQ910581	JQ910468	58	WAMR120619
		KC490305	KC490808	58	WAMR120654
		KC490306	KC490809	58	WAMR120970
		KC490307	KC490810	55	WAMR121395
		KC490308	KC490811	57	WAMR127804
		KC490309		57	WAMR127878
		JQ910582	JQ910469	61	WAMR131753

		KC490310	KC490812	56	WAMR132221
		KC490311	KC490813	58	WAMR136262
		KC490312		58	WAMR136275
		JQ910583	JQ910470	60	WAMR136276
		KC490313	KC490814	58	WAMR136278
		KC490314		58	WAMR136304
		KC490315	KC490815	55	WAMR136654
		KC490316		55	WAMR136664
		KC490317	KC490816	55	WAMR136677
		JQ910584	JQ910471	55	WAMR136817
		KC490318	KC490817	58	WAMR137443
		KC490319	KC490818	57	WAMR145264
		KC490320	KC490819	57	WAMR145265
		JQ910585	JQ910472	57	WAMR145266
		KC490321	KC490820	55	WAMR156176
		KC490322	KC490821	55	WAMR156185
		JQ910586	JQ910473	56	WAMR156249
		KC490323	KC490822	55	WAMR156990
		KC490324	KC490823	56	WAMR157986
		KC490325	KC490824	61	WAMR162241
		KC490326		55	WAMR164354
		KC490327	KC490825	55	WAMR164355
		KC490328	KC490826	55	WAMR164357
		KC490329	KC490827	55	WAMR165304
		KC490330	KC490828	55	WAMR165617
		KC490331	KC490829	55	WAMR167496
		KC490332	KC490830	55	WAMR167499
<i>Ramphotyphlops</i>	<i>howi</i>	JQ910587	JQ910474	62	WAMR141536
<i>Ramphotyphlops</i>	<i>kimberleyensis</i>	KC490333		64	ABTC28167
		JQ910588	JQ910475	64	ABTC29484
		JQ910589	JQ910476	66	WAMR125981
		KC490334	KC490831	63	WAMR133192
		KC490335	KC490832	63	WAMR133193
		KC490336	KC490833	63	WAMR158055
		KC490337	KC490834	65	WAMR164213
		JQ910590	JQ910477	63	WAMR165559
		JQ910591	JQ910478	65	WAMR165885
		KC490338	KC490835	65	WAMR165886
<i>Ramphotyphlops</i>	<i>leptosoma</i>	KC490339	KC490836	67	WAMR114892
		KC490340	KC490837	67	WAMR114892
		KC490341	KC490838	67	WAMR114893
		JQ910592	JQ910479	67	WAMR114894
		JQ910593	JQ910480	67	WAMR119241
		JQ910594	JQ910481	67	WAMR125964
		KC490342	KC490839	67	WAMR125963
		JQ910625	JQ910512	68	WAMR129778
		JQ910595	JQ910482	67	WAMR135647
		JQ910624	JQ910511	67	WAMR136311
		KC490343	KC490840	68	WAMR146400
		KC490344	KC490841	67	WAMR146454
		JQ910596	JQ910483	67	WAMR146455
		KC490345	KC490842	67	WAMR146456

<i>Ramphotyphlops</i>	<i>ligatus</i>	JQ910597	JQ910484	69	SAMAR31019
		JQ910598	JQ910485	71	NTMR35156
		JQ910599	JQ910486	70	NTMR13753
		JQ910600	JQ910487	72	NTMR19109
		KC490346	KC490843	70	WAMR137952
		KC490347	KC490844	70	WAMR137954
<i>Ramphotyphlops</i>	<i>longissimus</i>	JQ910525	JQ910416	73	WAMR120049
<i>Ramphotyphlops</i>	<i>nigrescens</i>	KC490348		75	SAMAR31020
		KC490349	KC490845	77	SAMAR31022
		KC490350	KC490846	76	SAMAR31023
		KC490351	KC490847	76	SAMAR31024
		JQ910602	JQ910489	75	SAMAR31025
		JQ910603	JQ910490	77	ABTC03939
		KC490352		77	ABTC03940
		JQ910604	JQ910491	77	ABTC100162
		KC490353	KC490848	77	QMJ83805
		KC490354	KC490849	77	ABTC100627
		KC490355	KC490850	74	SAMAR40863
		KC490356	KC490851	77	QMJ54856
		KC490357		76	SAMAR40954
		KC490358		77	SAMAR55640
		KC490359	KC490852	74	AMSR145555
		JQ910605	JQ910492	74	AMSR146228
		KC490360	KC490853	74	AMSR152666
		JQ910606	JQ910493	75	AMSR157050
		JQ910607	JQ910494	78	AMSR157114
		JQ910601	JQ910488	78	SAMAR31022
		JQ910608	JQ910495	76	AMSR157200
		KC490361	KC490854	78	AMSR157265
		JQ910609	JQ910496	78	AMSR157267
		JQ910610	JQ910497	74	ANWCR05614
		KC490362	KC490855	74	ANWCR06776
<i>Ramphotyphlops</i>	<i>pilbarensis</i>	KC490363	KC490856	79	WAMR90643
		KC490364	KC490857	79	WAMR90864
		KC490365	KC490858	79	WAMR108989
		KC490366		79	WAMR102604
		KC490367	KC490859	79	WAMR108813
		KC490368	KC490860	79	WAMR108989
		KC490369	KC490861	79	WAMR110733
		KC490370	KC490862	79	WAMR110734
		JQ910611	JQ910498	79	WAMR110744
		KC490371	KC490863	79	WAMR110860
		KC490372	KC490864	79	WAMR110938
		JQ910628	JQ910515	79	WAMR110939
		KC490373	KC490865	79	WAMR110940
		KC490374	KC490866	79	WAMR110942
		KC490375	KC490867	79	WAMR110943
		KC490376	KC490868	79	WAMR120727
		KC490377	KC490869	79	WAMR124836
		KC490378	KC490870	79	WAMR135459
		KC490379	KC490871	79	WAMR139141
		KC490380	KC490872	79	WAMR139387

		KC490381	KC490873	79	WAMR139388
		KC490382	KC490874	79	WAMR139400
		KC490383	KC490875	79	WAMR140330
		KC490384	KC490876	79	WAMR141303
		KC490385	KC490877	79	WAMR156309
		KC490386	KC490878	79	WAMR156814
		KC490387	KC490879	79	WAMR156822
		KC490388	KC490880	79	WAMR160167
		KC490389	KC490881	79	WAMR166182
		KC490390	KC490882	79	WAMR166501
<i>Ramphotyphlops</i>	<i>pinguis</i>	JQ910633	JQ910520	80	WAMR125664
		JQ910627	JQ910514	80	WAMR146995
<i>Ramphotyphlops</i>	<i>polygrammicus</i>	JQ910612	JQ910499	82	QMJ60625
		KC490391	KC490883	81	ABTC51251
		JQ910613	JQ910500	81	ABTC51252
		KC490392	KC490884	81	ABTC58999
		KC490393	KC490885	81	ANWCR06771
<i>Ramphotyphlops</i>	<i>proximus</i>	KC490394		83	ABTC100639
		KC490395		83	SAMAR22713
		KC490396	KC490886	83	AMSR132486
		KC490397		83	AMSR132486
		JQ910630	JQ910517	83	AMSR151562
		JQ910629	JQ910516	83	ANWCR06668
<i>Ramphotyphlops</i>	<i>silvia</i>	KC493653	JQ910501	84	QMJ46128
<i>Ramphotyphlops</i>	<i>trogodytes</i>	JQ910614	JQ910466	85	WAMR146048
<i>Ramphotyphlops</i>	<i>unguirostris</i>	JQ910615	JQ910502	87	NTMR21669
		KC490398	KC490887	86	WAMR115861
		JQ910616	JQ910503	88	SAMAR54430
		JQ910617	JQ910504	86	WAMR115861
		JQ910618	JQ910505	89	WAMR117861
		JQ910619	JQ910506	86	WAMR146958
		KC490399	KC490888	86	WAMR151036
<i>Ramphotyphlops</i>	<i>waitii</i>	KC490400	KC490889	90	WAMR97215
		KC490401		90	WAMR104279
		KC490402		90	WAMR120289
		KC490403		90	WAMR104279
		KC490404	KC490890	91	WAMR110957
		KC490405	KC490891	90	WAMR113302
		KC490406	KC490892	90	WAMR113321
		KC490407		90	WAMR113392
		KC490408	KC490893	90	WAMR114891
		KC490409	KC490894	90	WAMR115123
		KC490410	KC490895	90	WAMR119239
		KC490411		90	WAMR119296
		KC490412	KC490896	90	WAMR119299
		KC490413		90	WAMR120289
		JQ910620	JQ910507	90	WAMR120315
		KC490414	KC490897	91	WAMR135251
		KC490415	KC490898	90	WAMR136448
		KC490416	KC490899	90	WAMR136679
		KC490417	KC490900	91	WAMR136738
		KC490418		91	WAMR136739

		KC490419		91	WAMR136741
		KC490420		91	WAMR136761
		KC490421	KC490901	90	WAMR136815
		KC490422	KC490902	90	WAMR140423
		KC490423	KC490903	90	WAMR144088
		KC490424	KC490904	90	WAMR144089
		KC490425	KC490905	90	WAMR145181
		KC490426	KC490906	90	WAMR145346
		KC490427		91	WAMR151432
		KC490428		91	WAMR151490
		KC490429		90	WAMR164356
		JQ910636	JQ910523	91	WAMR165022
		KC490430	KC490907	90	WAMR165623
		KC490431	KC490908	91	WAMR166685
<i>Ramphotyphlops</i>	<i>wiedii</i>	KC490432	KC490909	92	QMJ59020
		JQ910621	JQ910508	92	AMSR154152
		JQ910631	JQ910518	92	ANWCR05533

Locality	State	Latitude	Longitude
Blackdown Tableland Road, 2k S Jcnctn	Qld	-23.6294444	149.1997222
28k ESE Port Headland	WA	-20.3934	118.8437
Barlee Range Nature Reserve	WA	-23.0958	116.0097
Burrup Peninsula	WA	-20.5383	116.8186
1.4k NNE Woodstock	WA	-21.6094	118.9619
8k S Karratha	WA	-20.7833	116.8500
6k S Karratha	WA	-20.7945	116.857
14.5k SE Mt Florance Homestead	WA	-21.8562	117.98
Python Pool	WA	-21.33	117.23
12.5k SW Millstream	WA	-21.6772	116.975
14k WSW Roy Hill Station	WA	-22.6757	119.841
6k SW Roy Hill Station	WA	-22.6611	119.919
14k WSW Roy Hill Station	WA	-22.6757	119.841
14k WSW Roy Hill Station	WA	-22.6757	119.841
6k SW Roy Hill Station	WA	-22.6611	119.919
6k SW Roy Hill Station	WA	-22.6611	119.919
37.9k SSE Pannawonica	WA	-21.9483	116.4636
20.6k S Pannawonica	WA	-21.8188	116.2997
18k NW Balfour Downs Homestead	WA	-22.7006	120.737
36k NW Balfour Downs Homestead	WA	-22.5181	120.678
36k NW Balfour Downs Homestead	WA	-22.5181	120.678
25k NW Balfour Downs Homestead	WA	-22.6111	120.729
23k WNW Balfour Downs Homestead	WA	-22.7183	120.646
28k ESE Port Hedland	WA	-20.5166	118.6833
Weeli Wolli Spring	WA	-22.9166	119.2167
32k N Port Hedland, Great Nothern Highway	WA	-20.4166	118.8333
5k S Mount Tom Price Mine	WA	-22.8080	117.7489
5k S Mount Tom Price Mine	WA	-22.8080	117.7489
Burrup Peninsula	WA	-20.5963	116.8108
Burrup Peninsula	WA	-20.5602	116.8053
Burrup Peninsula	WA	-20.5847	116.8000
Pardoo Roadhouse	WA	-20.0666	119.8167
Meentheena	WA	-21.3511	120.4469
Mount Minnie Homestead	WA	-22.0333	115.4667
Cape Preston area	WA	-21.0152	116.1872
69k S Port Hedland	WA	-20.9100	118.6800
69k S Port Hedland	WA	-20.9100	118.6800
86k S Port Hedland	WA	-21.0600	118.7500
69k S Port Hedland	WA	-20.9100	118.6800
69k S Port Hedland	WA	-20.9100	118.6800
27k S Port Hedland	WA	-20.5400	118.6400
231k SSW Port Hedland	WA	-22.3600	119.9900
248k SSW Port Hedland	WA	-22.5000	119.0900
Munni Munni	WA	-21.1297	116.8039
235k SSW Port Hedland	WA	-22.3900	118.9800
231k SSW Port Hedland	WA	-22.3600	119.9900
235k SSW Port Hedland	WA	-22.3900	119.9900
Hesta Rail siding	WA	-22.1819	119.0214

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3	Yule River, 7.2k WSW Woodstock	WA	-21.6341	118.8872
4	Tom Price area	WA	-22.6202	117.7436
5	Fortescue Marsh	WA	-22.2991	119.0228
6	Fortescue Marsh	WA	-22.2591	119.0264
7	Fortescue Marsh	WA	-22.4144	119.0067
8	Fortescue Marsh	WA	-22.2591	119.0264
9	Mulga Downs Station	WA	-22.3497	119.2911
10	Fortescue Marsh	WA	-22.4144	119.0067
11	Fortescue Marsh	WA	-22.4591	119.0364
12	Fortescue Marsh	WA	-21.9538	118.9958
13	Fortescue Marsh	WA	-21.9880	119.0219
14	Fortescue Marsh	WA	-22.3466	119.0100
15	Fortescue Marsh	WA	-22.4144	119.0067
16	6k N Millstream	WA	-21.5402	117.057
17	5k NNE Python Pool	WA	-21.3104	117.276
18	6k SW Roy Hill Station	WA	-22.6611	119.919
19	16k N Cowra Line Camp	WA	-22.2217	119.025
20	32.6k SE Roy Hill	WA	-22.3894	119.7753
21		WA		
22	6k S Karratha	WA	-20.7945	116.857
23	6k S Karratha	WA	-20.7945	116.857
24	14k WSW Roy Hill Station	WA	-22.6757	119.841
25	6k SE Whim Creek Hotel	WA	-20.8699	117.859
26	1k SE Mt Murray	WA	-22.4984	115.558
27	21.5k NE Mt Mary	WA	-22.2554	115.437
28	16k W Mt De Courcey	WA	-22.7402	116.461
29	Newman	WA	-22.2680	119.1892
30	Newman	WA	-22.2400	119.1031
31	Newman	WA	-22.2400	119.1031
32	20k NNW Mt Elvire	WA	-21.6728	116.725
33	16.6k ENE Karratha	WA	-20.7986	116.6814
34	13.8k ENE Karratha	WA	-20.7802	116.7019
35	16.4k ENE Karratha	WA	-20.7922	116.6806
36	16k ENE Karratha	WA	-20.7927	116.6850
37	Nullagine	WA	-21.9519	120.1317
38	Nullagine	WA	-21.9541	120.1242
39	Woodie Woodie	WA	-21.6594	121.2417
40	Whim Creek	WA	-20.8497	117.8394
41	17k WNW Peedamulla Homestead	WA	-21.7914	115.464
42	31k WSW Mt Elvire	WA	-21.8736	116.503
43	Spear Hill Mine	WA	-29.492	119.412
44	35.5k SW Marble Bar	WA	-21.4381	119.541
45	4k SE The Island Hill	WA	-21.3403	119.366
46	Woodstock	WA	-21.6169	118.9536
47	Woodstock Station	WA	-21.6111	119.0397
48	Woodstock Station	WA	-21.6097	118.9622
49	Rottneest Island	WA	-	115.5
50	near Dandalup	WA	-32.53	115.94
51	Bold Park	WA	-31.94	115.77
52	Bold Park	WA	-31.94	115.77
53	Victoria Park, Perth	WA	-31.9709	115.9018
54	Bold Park	WA	-31.94	115.77
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Bold Park	WA	-31.94	115.77
Kalgoorlie Nickel Smelter	WA	-	121.488611111111
Bold Park	WA	-31.94	115.77
Dandaragan area	WA	-30.9952	115.6958
Rottnest Island	WA	-32.0150	115.4750
Muddy Lakes	WA	-33.4208	115.6053
Mount Helena.	WA	-31.8666	116.2000
Mount McMahon, Ravensthorpe Range	WA	-33.5500	120.1000
Kalgoorlie Nickel Smelter, 10k S Kalgoorlie	WA	-30.8333	121.4667
Kalgoorlie Nickel Smelter, 10k S Kalgoorlie	WA	-30.8333	121.4667
Kalgoorlie Nickel Smelter, 10k S Kalgoorlie	WA	-30.8333	121.4667
10k S Kalgoorlie	WA	-30.8333	121.4667
Kings Park	WA	-31.9666	115.8333
Kings Park	WA	-31.9666	115.8333
Kings Park	WA	-31.9666	115.8333
Bold Park	WA	-31.9333	115.7667
11k ESE North Dandalup	WA	-32.5333	116.1000
11k ESE North Dandalup	WA	-32.5333	116.1000
11k ESE North Dandalup	WA	-32.5333	116.1000
Wanneroo	WA	-31.7500	115.8000
Byford	WA	-32.2166	116.0000
Edel Land	WA	-26.5000	113.5000
20k NE Newdegate	WA	-32.9333	119.1500
1k N Cape Burney	WA	-28.8500	114.6333
Talbot Road Reserve, Swan View	WA	-31.8736	116.0508
Rolystone	WA	-32.1166	116.0667
Talbot Road Reserve, Swan View	WA	-31.8666	116.0511
Bold Park, Perth	WA	-31.9538	115.7711
Kings Park, Perth	WA	-31.9666	115.8333
Bungendore, Perth	WA	-32.1911	116.0356
Masons Bay, 36k E Hopetoun	WA	-33.9500	120.5000
Bandalup Hill	WA	-33.6500	120.3667
Ravensthorpe	WA	-33.5833	120.0500
SE corner Lake Magenta Reserve	WA	-33.5000	119.3333
Bungendore Park	WA	-32.1833	116.0167
Bungendore Park	WA	-32.1833	116.0167
Talbot Road, Perth	WA	-31.8730	116.0461
Cocanarup Homestead	WA	-33.6000	119.9167
Corackerup	WA	-34.2666	118.7000
Cooliabberra Spring, Bungendore Park	WA	-32.1833	116.0333
Cooliabberra Spring, Bungendore Park	WA	-32.1833	116.0333
Cooliabberra Spring, Bungendore Park	WA	-32.1833	116.0333
Bungendore Park	WA	-32.1833	116.0333
Bungendore Park	WA	-32.1833	116.0333
23k N Black Point	WA	-34.1666	115.5333
18k SW Ravensthorpe	WA	-33.2144	121.0300
Lesueur National Park	WA	-30.1833	115.2000
Bandalup Hill	WA	-33.6819	120.3022
20k W Waroona	WA	-32.8666	115.7000
Bandalup Hill	WA	-33.6819	120.3022
Bandalup Hill	WA	-33.6819	120.3022
20k WNW Waroona	WA	-32.8166	115.7167

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3	20k W Waroona	WA	-32.8666	115.7000
4	Bungendore, School Site	WA	-32.1833	116.0333
5	Brickwood Reserve	WA	-32.0638	116.0189
6	Brickwood Reserve	WA	-32.2338	116.0019
7	Brickwood Reserve	WA	-32.2311	116.0033
8	Brickwood Reserve	WA	-32.2311	116.0033
9	1.8k from Twertup, along Twertup Track	WA	-33.9833	119.3333
10	Bungendore Park	WA	-32.1833	116.0333
11	Hepburn Heights	WA	-31.8158	115.7808
12	8k W Esperance	WA	-33.8666	121.8333
13	16k NNW Ongerup	WA	-33.7000	117.0167
14	Lake Jasper area	WA	-34.4166	115.6833
15	8k WNW Maggie Hayes Hill	WA	-32.2500	120.5000
16	8k WNW Maggie Hayes Hill	WA	-32.2500	120.5000
17	Shannon Basin	WA	-34.7500	116.9833
18	Shannon Basin	WA	-34.7500	116.9833
19	Kalamunda	WA	-31.9666	116.0500
20	6k NE Margaret River	WA	-33.9666	115.0500
21	Lake Jasper	WA	-34.4013	115.6436
22	Ravensthorpe	WA	-33.5833	120.0500
23	Hay Park, Bunbury	WA	-33.3166	115.6333
24	5k NE Morehead	WA	-33.2969	116.0928
25	5k NW Dryandra	WA	-32.7433	116.9400
26	4k W Dryandra Settlement	WA	-32.7758	116.9211
27	Jangardup study area, Dentrecaux Na	WA	-34.4166	115.7500
28	2k NE Wonnerup Siding	WA	-33.6166	115.4453
29	30k W Southwest Calingiri	WA	-31.1433	116.3217
30	8k NW Norseman	WA	-32.1602	121.7417
31	Gracetown	WA	-33.8500	114.9833
32	Lake Mealup	WA	-32.6833	115.7000
33	Cervantes area	WA	-30.7508	115.2031
34	Cervantes area	WA	-30.7988	115.2708
35	Donnybrook-Collie Road	WA	-33.5500	115.8500
36	~15k WNW Cataby	WA	-30.6138	115.2508
37	~10k NE Marchagee	WA	-30.0205	116.1197
38	Ludlow Drive	WA	-33.6480	115.4164
39	Ludlow Drive	WA	-33.6480	115.4164
40	Point Douro, Australind	WA	-33.3000	115.7000
41	5k E Ora Banda	WA	-30.3788	121.1242
42	5k E Ora Banda	WA	-30.3788	121.1242
43	5k E Ora Banda	WA	-30.3788	121.1242
44	5k E Ora Banda	WA	-30.3788	121.1242
45	5k E Ora Banda	WA	-30.3788	121.1242
46	4k S Collie	WA	-33.3533	116.2064
47	Bandalup Hill	WA	-33.5861	120.3275
48	Lot 52, Burns Beach Road	WA	-31.7183	115.7661
49	Marchagee area	WA	-30.0500	116.2333
50	23k S Kalbarri	WA	-27.9219	114.1633
51	23k S Kalbarri	WA	-27.9219	114.1633
52	35k S Kalbarri	WA	-28.0166	114.2167
53	23k S Kalbarri	WA	-27.9000	114.1500
54	7k S Dongara	WA	-29.3138	114.9483
55	Lake Cooloongup Nature Reserve	WA	-32.3000	115.7833
56	Australind	WA	-33.2833	115.7000
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Australind	WA	-33.2833	115.7000
Ravensthorpe area	WA	-33.6616	120.3953
Ravensthorpe area	WA	-33.5652	120.3175
Ravensthorpe area	WA	-33.5652	120.3175
Ravensthorpe area	WA	-33.5861	120.3275
Salmon Gums area	WA	-32.7000	121.4467
Salmon Gums area	WA	-32.8200	121.4100
Cervantes	WA	-30.5000	115.0667
Cervantes	WA	-30.5000	115.0667
East Wallabi Island	WA	-28.4333	113.7167
Kundip	WA	-33.6819	120.1989
Kundip	WA	-33.6800	120.1933
Pingrup area	WA	-33.5266	118.7422
Pingrup area	WA	-33.5808	118.7653
Australind	WA	-33.2805	115.7217
Australind	WA	-33.2805	115.7217
Australind	WA	-33.2805	115.7217
Canal Rocks	WA	-33.6627	115.0125
Quairading	WA	-32.0166	117.4000
Ora Banda	WA	-30.3666	121.0500
East Wallabi Island	WA	-28.4333	113.7167
Neerabup	WA	-31.6666	115.7500
Forrestania	WA	-32.4108	119.6950
Digger Rocks	WA	-32.7158	119.8017
Digger Rocks	WA	-32.7158	119.8017
Digger Rocks	WA	-32.7286	119.8081
Digger Rocks	WA	-32.7286	119.8081
3k SW Ludlow	WA	-33.6208	115.6375
Mount Chudalup	WA	-34.7666	116.0833
1k NE Augusta	WA	-34.3041	115.1708
Perth Airport	WA	-31.9233	115.9778
16.7k NNE Fig Tree Corner	SA	-31.5389	132.7144
Gawler Ranges	SA	-32.616667	136.35
Red Band Tank	SA	-	140.599444444444
Hideaway Hut	SA	-	140.622222222222
Theodolite Dam	SA	-33.4	139.936111111111
Theodolite Dam	SA	-33.4	139.936111111111
Theodolite Dam	SA	-33.4	139.936111111111
Burra Creek	SA	-33.8166666666666	139.016666666667
6k SE Keyneton	SA	-34.6	139.2
4k NW Courtabie	SA	-	134.822222222222
3k E Tailem Bend	SA	-	139.480833333333
2.5k NW Iron Chieftain	SA	-	137.133333333333
17k NW Witera, Flinders Highway	SA	-	134.483333333333
Swan Reach	SA	-	139.6
W boundary track Karte CP	SA	-	140.685
W boundary track Karte CP	SA	-	140.685
Peebinga CP, Mootatunga	SA	-	140.833333333333
24k SW Canopus HS	SA	-	140.483333333333
4k NE Kalgoorlie	WA	-34.1322	146.5048
8.5k W Pinjarra dam	WA	-	134.704444444444
5k N Blanchetown	SA	-	139.6

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3	14k WNW Gluepot Homestead	SA	-	139.98
4	18k NNW Barellan	NSW	-34.1322	146.5048
5	Budgeree Station	NSW	-32.8838888888	141.170833333333
6	Yathong NP	NSW	-32.59	145.4
7	JERILDERIE, McCAUGHEE INST./OLD	NSW	-35.3474	145.5408
8	near Boolcoomata HS	SA	-31.9683	140.5451
9	5.2k E Paney shearers quarters	SA	-	135.699805555556
10	10k NE Kalbrae	SA	-	135.035333333333
11	3.7k ENE Corrobinnie Hill	SA	-	135.771944444444
12	13.4k NE Fig Tree Corner	SA	-31.6042	132.8303
13	4k NE Kalgoorlie	WA	-30.7333	121.4667
14	Kalgoorlie	WA	-30.7333	121.4667
15	Goongarrie Station	WA	-29.9833	121.0333
16	25k S Widgiemooltha	WA	-31.7000	121.5333
17	Leinster Downs Station	WA	-27.9647	120.3892
18	Leinster Downs Station	WA	-27.9647	120.3892
19	Marvel Loch	WA	-31.4830	119.5292
20	Windarling Hill	WA	-30.0130	119.2872
21	Goongarrie Station	WA	-29.8997	121.1764
22	Ora Banda	WA	-30.3972	121.1225
23	Ora Banda	WA	-30.3666	121.0500
24	Ora Banda	WA	-30.3666	121.0500
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27	Welbourne Hill Station	SA	-27.5561111	134.425
28	11.5 km SSW Winninowie homestead	SA	-32.7236	137.8972
29	10.3 km SSW Winninowie homestead	SA	-32.6997	137.8511
30	6k NE Culburra	SA	-35.755	139.988888888889
31	7.5k NNW Rabbit Island Dam	SA	-	140.315833333333
32	5.2k ESE Strangways Springs	SA	-	136.596944444444
33	3.5k NW Beresford Rail Station	SA	-	136.630833333333
34	Peake Station	SA	-	136.446388888889
35	6.3k NNW Wimma Hill	SA	-	140.290555555556
36	10.3k SW Wimma Hill	SA	-	140.228888888889
37	19.6k SW Wimma Hill	SA	-	140.178055555556
38	Hideaway Hut	SA	-	140.478333333333
39	Balah Station	SA	-	139.816666666667
40	Diamond Dam	SA	-	140.033333333333
41	Port Kenny	SA	-	134.639166666667
42	near Arno Bay	SA	-	136.566666666667
43	20k N Cowell	SA	-33.5	137
44	Burke's Grave, near Innamincka	SA	-27.7333333	140.7666667
45	N end Stock Route	SA	-32.85	135.95
46	SW Olympic Dam	SA	-30.5	136.8
47	Moomba	SA	-	140.183333333333
48	Wudinna	SA	-33.05	135.466666666667
49	37.5k NE Minnipa	SA	-	135.45
50	7k E Koolunga	SA	-	138.4
51	7k S Crystal Brook	SA	-	138.15
52	7k S Crystal Brook	SA	-	138.15
53	Lake Richardson, 10k ENE Woomera	SA	-	136.933333333333
54	Kangaroo Flat, Sec 78	SA	-	138.7
55	2.9k ESE Mulga Bore	SA	-30.6	139.533333333333
56	E boundary Karte CP	SA	-35.1258333	140.7241667
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2k NNE Whyalla	SA	-	137.576944444444
3.5k W Inkerman	SA	-34.275	138.2
Dept of Defence Firing Range, Port	SA	-	138.2
1.5k ENE Gluepot HS	SA	-	140.1375
9.2k WNW Wharminda	SA	-	136.163888888889
West Wyalong	NSW	-33.93	147.2
Yathong NP	NSW	-32.59	145.4
JERILDERIE, OLD COREE STATION	NSW	-35.3474	145.5408
Yarra property, 35k Mt Hope on	NSW	-32.8687	145.9979
Yathong NP	NSW	-32.59	145.4
Ashleigh Park, 21k S Berrigan,	NSW	-	145.821388888889
BERRIGAN STATE FOREST, 11k E	NSW	-	145.923888888889
Pine Lodge, 18k N Mulwala, Savernake	NSW	-	146.009444444444
Ashleigh Park, 21k S Berrigan,	NSW	-	145.821388888889
Berrigan State Forest, 11k E Berrigan	NSW	-35.6883333	145.9238889
Fairfield 29k NE Mulwala, Savernake	NSW	-	146.221388888889
8.4k NE Border Village	SA	-	129.086944444444
Cornish Well, 22.9k WNW Moonaree	SA	-31.9414	135.6344
20k NE Mount Penrhyn	SA	-29.305	135.1716667
6.8k NNE Kulpara	SA	-34.013056	138.085
11.8k NE Yarnerby Hill	SA	-	134.271111111111
11.8k NE Yarnerby Hill	SA	-	134.271111111111
7.1k WNW Ant Hill	SA	-28.433889	134.500278
6.1k ENE Hunchee	SA	-	140.850277777778
30.3k N Whyalla	SA	-32.775556	137.572778
MacDonnell Ranges	NT	-	
Lawrence Gorge	NT	-23.9977	133.4291
Mount Barry Station	SA	-	134.706666666667
9.4k SSW Granite Downs HS	SA	-	133.47
8k ENE Mount Chandler	SA	-26.9891667	133.4055556
Cravens Peak property, approximately	Qld	-23.0165765	138.2344608
176 Camooweal Street, Mount Isa	Qld	-20.7265	139.4909
Mount Isa area	Qld	-	
176 Camooweal Street, Mount Isa	Qld	-20.7265	139.4909
176 Camooweal Street, Mount Isa	Qld	-20.7265	139.4909
Hidden Valley Caravan Park, Kununurra	WA	1546 S	12844 E
Supplejack Station, 8 Mile Bore	NT	-19.1735	129.9219
Guluwuru Island	NT	-11.5243	136.4231
Guluwuru Island	NT	-11.5243	136.4231
Tennant Creek	NT	-19.6269	134.191
117k NNW Tanami Downs Homestead	WA	-19.8894	128.8600
Beagle Bay Aboriginal Community	WA	-17.0597	122.7167
Beagle Bay Aboriginal Community	WA	-17.0766	122.7072
Mirima National Park	WA	-15.7833	128.7833
Mirima National Park	WA	-15.7833	128.7833
~5k S Carlton Hill Homestead	WA	-15.5386	128.5233
Lake Argyle	WA	-16.2166	128.9000
Tanami Desert	WA	-19.8986	128.8658
Tanami Desert	WA	-19.8891	128.8600
Ethabuka Station	Qld	-23.8627	138.4794
70k E Moomba	SA	-	140.866666666667
Mabel Creek HS	SA	-	134.108333333333

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3	Mabel Creek HS	SA	-	134.466666666667
4	Mabel Creek HS	SA	-	134.25
5	Yulara	NT	-	131.016666666667
6	Curtin Springs	NT	-	131.766666666667
7	4.6k N Strangways Springs	SA	-	136.545
8	86k SW Approdirna Attora Knolls	SA	-	136.953611111111
9	8.4k SW Wimma Hill	SA	-	140.245
10	11.5k SW Wimma Hill	SA	-	140.229166666667
11	Musgrave Ranges	SA	-26.65	130.816666666667
12	38k ENE Laverton	WA	-28.513	122.7621
13	4k W Mt Lindsay	SA	-	129.839166666667
14	3.1k WNW Mt Lindsay	SA	-	129.850277777778
15	N Olympic Dam	SA	-	136.916666666667
16	Olympic Dam area	SA	-30.55	136.883333333333
17	Olympic Dam Site	SA	-	136.9
18	Olympic Dam Site	SA	-	136.9
19	Olympic Dam Site	SA	-	136.883333333333
20	Olympic Dam Site	SA	-	136.883333333333
21	Olympic Dam Site	SA	-30.4333333	136.85
22	near Mundibarcooloo WH	SA	-	140.216666666667
23	25k SSW Mabel Creek HS	SA	-	134.233333333333
24	Yalymboo Station	SA	-	136.625833333333
25	Mt Vivian Station	SA	-	135.821666666667
26	Glendambo near Hotel	SA	-	135.733333333333
27	near Crows Nest Bore Mt Vivian Station	SA	-	135.821666666667
28	Oakden Hills Station	SA	-	136.911388888889
29	Mt Gunson Paddock Oakden Hills Station	SA	-31.4925	137.105833333333
30	15k S Yuendumu Road	NT	-23.1823	132.6566
31	10k SSW Maralinga	SA	-	131.545833333333
32	Davenport Range	SA	-	135.941111111111
33	Wirraminna Station	SA	-	136.591944444444
34	24.4k SSE Hamilton HS	SA	-	135.196111111111
35	6.8k SE Hamilton HS	SA	-	135.118888888889
36	Yamarna Station	WA	-	123.783388888889
37	Sturt NP, Camerons Corner Road, 3.4k N	NSW	-29.0908	141.2051
38	Sturt NP, 13.5k E on Middle Road from	NSW	-29.0063	141.1436
39	Sturt NP, Camerons Corner Road, 3.4k N	NSW	-29.0908	141.2051
40	Sturt NP, 5.7k W along Whitecatch Gate	NSW	-29.1414	141.1343
41	Sturt NP, 1.8k W along Whitecatch Gate	NSW	-29.1163	141.173
42	Sturt NP, Camerons Corner Road, 3.4k N	NSW	-29.0908	141.2051
43	Sturt NP, Whitecatch Gate Road	NSW	-29.2125	141.0252
44	Sturt NP, 2.7k W Binerah Downs HS on	NSW	-29.0319	141.5249
45	Sturt NP, 9.8k W Binerah Downs HS on	NSW	-29.0317	141.4511
46	Sturt NP, 13.7k E on Middle Road from	NSW	-29.0063	141.1436
47	4.2k SSE Pungkulpirri Waterhole	WA	-24.6964	128.7628
48	5.3k SSE Pungkulpirri Waterhole	WA	-24.7072	128.7603
49	4.2k SSE Pungkulpirri Waterhole	WA	-24.6964	128.7628
50	3.2k N Pungkulpirri Waterhole, Walter	WA	-24.6286	128.7556
51	5.3k SSE Pungkulpirri Waterhole	WA	-24.7072	128.7603
52	5.6k SE Mt Ant	WA	-24.8006	128.7972
53	Kutjuntari Rockhole	WA	-24.8914	128.7692
54	3.2k N Pungkulpirri Waterhole, Walter	WA	-24.6286	128.7556
55	3.2k N Pungkulpirri Waterhole, Walter	WA	-24.6286	128.7556
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3	12.2k N Pungkulpirri Waterhole, Walter	WA	-24.5594	128.7097
4	12.2k N Pungkulpirri Waterhole, Walter	WA	-24.5594	128.7097
5	12.2k N Pungkulpirri Waterhole, Walter	WA	-24.5594	128.7097
6	Morgan Range, 18.5k ENE Blackstone	WA	-25.9306	128.4525
7	Morgan Range, 18.5k ENE Blackstone	WA	-25.9306	128.4525
8	Morgan Range, 16.8k ENE Blackstone	WA	-25.9353	128.4378
9	18.4k NE Blackstone	WA	-25.8917	128.4269
10	Morgan Range, 16.8k ENE Blackstone	WA	-25.9353	128.4378
11	Morgan Range, 17.3k ENE Blackstone	WA	-25.9325	128.4411
12	Morgan Range, 17.3k ENE Blackstone	WA	-25.9325	128.4411
13	Morgan Range, 17.3k ENE Blackstone	WA	-25.9325	128.4411
14	Morgan Range, 17.3k ENE Blackstone	WA	-25.9325	128.4411
15	Morgan Range, 18.5k ENE Blackstone	WA	-25.9306	128.4525
16	Morgan Range, 18.5k ENE Blackstone	WA	-25.9306	128.4525
17	Morgan Range, 16.8k ENE Blackstone	WA	-25.9353	128.4378
18	Morgan Range, 18.5k ENE Blackstone	WA	-25.9306	128.4525
19	179k SSW Watarru	SA	-28.46277	129.01026
20	Anne Beadel Highway, 15.4k E SA/WA	SA	-28.5112	129.1582
21	184k SSW Watarru	SA	-28.50788	129.00473
22	184k SSW Watarru	SA	-28.50788	129.00473
23	28.8k WNW Emu	SA	-	131.923333333333
24	29.1k SSW England Hill	SA	-28.383333	134.083333
25	29.1k SSW England Hill	SA	-28.383333	134.083333
26	Little Sandy Desert	WA	-24.1047	120.3250
27	Little Sandy Desert	WA	-24.1047	120.3250
28	Little Sandy Desert	WA	-24.1047	120.3250
29	Little Sandy Desert	WA	-23.8883	120.5217
30	Little Sandy Desert	WA	-23.8794	120.5033
31	Little Sandy Desert	WA	-23.8883	120.5217
32	Willies Soak, Little Sandy Desert	WA	-24.5930	120.2500
33	8k WSW Yamana Hs	WA	-28.0166	123.6167
34	38k ENE Laverton	WA	-28.5500	122.7000
35	38k ENE Laverton	WA	-28.5500	122.7000
36	Nifty Mine	WA	-21.6666	121.5833
37	near Telfer Dome	WA	-22.1833	122.2667
38	Telfer	WA	-21.7611	122.2233
39	Officer Basin area	WA	-27.1675	125.2000
40	Officer Basin area	WA	-26.9327	125.2789
41	Officer Basin area	WA	-26.9327	125.2789
42	Officer Basin area	WA	-27.0750	125.2028
43	Empress Spring	WA	-26.7666	124.3661
44	Clutterbuck Hills	WA	-24.5172	126.2178
45	30k W Newman, Cathedral Gorge	WA	-23.2916	119.4667
46	Millstream	WA	-21.5833	117.0667
47	Chichester Range	WA	-22.2302	118.9814
48	27k ESE Mt De Courcey	WA	-22.7892	116.571
49		WA		
50	6.4k ENE Invasion Tank	SA	-26.075	140.896667
51	Onslow	WA	-21.6533	115.1131
52	Phosphate Hill, Buffel site	Qld	-21.9002778	139.9969444
53	3k SSW Karrathunka Waterhole	SA	-	139.235833333333
54	3k SSW Karrathunka Waterhole	SA	-	139.235833333333
55	10k NW Mt Windell, Hamersley Range (Ka	WA	-22.6027	118.4597
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3	Withnell Bay, Burrup Peninsula	WA	-20.5750	116.7903
4	Little Sandy Desert	WA	-24.0752	120.3606
5	Little Sandy Desert	WA	-23.9233	120.5314
6	3.7k ENE Woodstock	WA	-21.6094	118.9878
7	Onslow area	WA	-21.6813	115.0942
8	8k E Yarra Bluff	WA	-21.7833	116.2500
9	8k E Yerra Bluff, ~12k SW Pannawonica	WA	-21.7833	116.2500
10	25k SE Telfer	WA	-21.8833	122.3667
11	67.5k S Fortescue River crossing	WA	-22.0592	117.693
12	5k NW Mt Florance Homestead	WA	-21.7665	117.825
13	6k SW Millstream	WA	-21.6424	117.037
14	14k WSW Roy Hill Station	WA	-22.6757	119.841
15	Brockan Mine	WA	-22.6133	117.1881
16	18.5k SW Pannawonica	WA	-21.7563	116.1964
17	37.5k W Pannawonica	WA	-21.6711	115.9622
18	25.3k WSW Pannawonica	WA	-21.7280	116.0983
19	Onslow area	WA	-21.7308	115.1569
20	Onslow area	WA	-21.7308	115.0978
21	Onslow area	WA	-21.7308	115.0978
22	10k SSE Onslow	WA	-21.7200	115.1508
23	10k SSE Onslow	WA	-21.7200	115.1508
24	Pannawonica Townsite	WA	-21.6500	116.3167
25	Wittenoom	WA	-22.2333	118.3167
26	26k ENE Port Hedland	WA	-20.4000	118.8167
27	Marble Bar	WA	-21.1666	119.7500
28	13k SW Cooralya HS	WA	-24.4166	114.0000
29	Onslow	WA	-21.6333	115.1167
30	30k E Newman	WA	-23.3166	120.0333
31	Gifford Creek Homestead	WA	-24.0500	116.2167
32	10k S Onslow	WA	-21.7333	115.0833
33	5k S Mount Tom Price Mine	WA	-22.8072	117.7500
34	Urala Station	WA	-21.7850	114.8631
35	Urala Station	WA	-21.7541	114.8508
36	Burrup Peninsula	WA	-20.5277	116.8197
37	25k WNW Abydos	WA	-21.4000	118.7061
38	Cape Lambert	WA	-20.6472	117.1522
39	Urala Station	WA	-21.7536	114.8522
40	Urala Station	WA	-21.7766	114.8719
41	36k WSW Pardoo	WA	-20.1902	119.4978
42	26k ENE Pardoo	WA	-19.9769	120.0467
43	50k E South Hedland	WA	-20.4000	119.0667
44	34k S Port Hedland	WA	-20.6100	118.6100
45	Chichester Range	WA	-21.9400	118.9608
46	Abydos Station	WA	-21.3580	118.8831
47	Brockan Ridge	WA	-23.3069	119.8767
48	Waldburg Station	WA	-24.8444	117.2236
49	Waldburg Station	WA	-24.7611	117.1903
50	Waldburg Station	WA	-24.7811	116.9589
51	Onslow area	WA	-21.7411	115.1139
52	Upper Marillana Creek	WA	-22.6927	118.9564
53	Cundaline Gap	WA	-20.5669	120.1850
54	Fortescue Marsh	WA		
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Fortescue Marsh	WA	-21.9880	119.0219
Yanrey Station	WA	-22.2997	114.5931
Yanrey Station	WA	-22.1577	114.5286
Yanrey Station	WA	-22.1538	114.5508
Tanami Desert	WA	-19.5933	128.8611
Barrow Island	WA	-20.7833	115.4667
32.5k ESE Meentheena Outcamp	WA	-21.3337	120.752
35k ESE Meentheena Outcamp	WA	-21.3377	120.77
11k SSE Whim Creek Hotel	WA	-20.9198	117.861
14k WSW intersection of Coongan and Ta	WA	-20.9108	119.65
14k WSW intersection of Coongan and Ta	WA	-20.9108	119.65
20k ESE Warrawagine Homestead	WA	-20.9356	120.876
16k W Mt De Courcey	WA	-22.7402	116.461
13k SSW Giles Point	WA	-23.3611	119.112
11.5k SW Rhodes Ridge	WA	-23.146	119.266
15k NNE Wodgina	WA	-21.0636	118.761
55k NNW Tom Price	WA	-22.295	117.473
West Intercourse Island	WA	-20.6811	116.6317
Mount Whaleback	WA	-23.3825	119.6253
Mount Whaleback	WA	-23.3825	119.6253
Mount Whaleback	WA	-23.3283	120.0192
Newman	WA	-22.9680	119.6306
8.5k NE Mt Rica	WA	-21.9522	116.488
Katherine Gorge	NT	-14.31	132.46
Top Springs, Tanami Desert	NT	-16.5436	131.7947
Bradshaw Station	NT	-15.34	130.27
40k S Tunnel Creek Gorge	WA	-17.8275	125.3744444
Kingston Rest	WA	-16.0333	128.4000
32k N Ord River crossing	WA	-17.2286	128.0994
Atley Station	WA	-28.2267	119.0744
Onslow area	WA	-21.6777	115.0594
North West Cape	WA	-21.8433	114.1100
North West Cape	WA	-21.8513	114.1058
17.7k W Lake Way	WA	-26.9813	120.6417
44.7k NW Lake Way	WA	-27.2525	120.7578
14.9k W Lake Way	WA	-26.9700	120.6150
40.7k NW Lake Way	WA	-27.2483	120.6967
33.5k E Wheelarra Hill	WA	-23.3725	120.458
33.5k E Wheelarra Hill	WA	-23.3725	120.458
26k SE Wheelarra Hill	WA	-23.5356	120.326
Onslow area	WA	-21.7208	115.1508
Onslow area	WA	-21.7408	115.1139
Urala Station	WA	-21.7536	114.8511
2k W Carnarvon	WA	-24.8738	113.6369
6k NE Carnarvon	WA	-24.8600	113.6689
	WA		
6k NW Mardathuna	WA	-24.4430	114.5117
1.7k SSW Meedo	WA	-25.6805	114.6217
Jundee	WA	-26.3500	120.6333
5k S Mount Tom Price Mine	WA	-22.8080	117.7489
5k S Mount Tom Price Mine	WA	-22.8077	117.7858
Mount Robinson, West Angelas	WA	-22.9552	118.7706

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3	Urala Station	WA	-21.7541	114.8508
4	Muggon Station	WA	-26.5269	115.5250
5	Muggon Station	WA	-26.4888	115.5308
6	Muggon Station	WA	-26.8169	115.5439
7	Muggon Station	WA	-26.5777	115.4689
8	Muggon Station	WA	-26.7800	115.6039
9	Lake Mason Station	WA	-27.5277	119.5839
10	Lake Mason Station	WA	-27.6733	119.4086
11	Lake Mason Station	WA	-27.5413	119.6186
12	Lake Mason Station	WA	-27.4505	119.5758
13	2.5k N Peron Homestead	WA	-25.8172	113.5472
14	5k S Mount Tom Price Mine	WA	-22.7961	117.7900
15	5k S Mount Tom Price Mine	WA	-22.7961	117.7900
16	5k S Mount Tom Price Mine	WA	-22.7961	117.7900
17	Waldburg Station	WA	-24.7330	117.4186
18	Waldburg Station	WA	-24.7608	117.1903
19	Onslow area	WA	-21.7050	115.0733
20	51.2k S Leinster	WA	-27.4630	120.7825
21	North West Cape	WA	-21.8719	114.1033
22	3k SW Weeli Wollie Spring	WA	-22.9312	119.185
23	Leonora	WA	-28.8641	121.7947
24	Leonora	WA	-28.8641	121.7947
25	Leonora	WA	-28.8605	121.7906
26	Lake Way	WA	-27.3766	120.5861
27	Ora Banda	WA	-30.3666	121.0500
28	12.8k W Lake Way	WA	-26.9622	120.5956
29	12.8k W Lake Way	WA	-26.9622	120.5956
30	Kalumburu	WA	-14.3000	126.6333
31	Katherine Gorge	NT	-14.31	132.46
32	Litchfield NP	NT	-13.283	130.8752
33	Wyndham	WA	-15.4666	128.1000
34	Koolan Island	WA	-16.1272	123.7414
35	Koolan Island	WA	-16.1322	123.7633
36	Koolan Island	WA	-16.1391	123.7481
37	Prudhoe Island	WA	-14.4161	125.2722
38	Koolan Island	WA	-16.1291	123.7458
39	South Maret Island	WA	-14.4447	124.9861
40	South Maret Island	WA	-14.4363	124.9844
41	Geraldton	WA	-28.7474	114.6362
42	Geraldton	WA	-28.7666	114.6167
43	Geraldton	WA	-28.7666	114.6167
44	Geraldton	WA	-28.7666	114.6167
45	Kalbarri	WA	-27.7000	114.1667
46	Kalbarri	WA	-27.7000	114.2000
47	Kalbarri	WA	-27.7000	114.2000
48	22k S Kalbarri	WA	-27.8977	114.1669
49	31k SSE Nerren Nerren	WA	-27.3905	114.7528
50	Muggon Station	WA	-26.3827	115.4639
51	23k S Kalbarri	WA	-27.9219	114.1633
52	Binnu	WA	-28.0333	114.6667
53	Binnu	WA	-28.0333	114.6667
54	Binnu	WA	-28.0333	114.6667
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4	21k E Narrabri	NSW	-30.1833333	149.9333333
5	Tableland Highway	NT	-17.705	135.696
6	Keep River NP	NT	-15.8113	129.1074
7	Raragala Island	NT	-11.61	136.26
8	~35k NNE Kununurra	WA	-15.4166	128.9500
9	~35k NNE Kununurra	WA	-15.5888	128.9833
10	Bandicoot Bay, Barrow Island	WA	-20.9000	115.3667
11	8k W Woolbrook	NSW	-	151.3
12	30k E Tenterfield	NSW	-28.8	152.083333333333
13	38k E Glen Innes	NSW	-29.65	152.05
14	38k W Glenn Innes	NSW	-29.65	152.05
15	8k W Woolbrook	NSW	-30.9666667	151.35
16	8k W McAfees Lookout	Qld	-27.4009	152.8131
17	8k W McAfees Lookout	Qld	-27.4009	152.8131
18	Kroombit Forest Drive, Kroombit Forest	Qld	-24.3757769	150.9858102
19	Kroombit Forest Drive, Kroombit Tops	Qld	-24.3597804	150.9636134
20	Egg Rock Firetrail, Lamington NP	Qld	-28.187436	153.1866493
21	Watagan SF	NSW	-	151.35
22	Kroombit Tops	Qld	-24.36	151.03
23	5k S Euroa, Mansfield Road	SA	-	145.583333333333
24	Kroombit Tops forestry hut	Qld	-	150.960555555556
25	Castlereagh SF, near Penrith	NSW	-33.68	150.75
26	Castlereagh waste depot, near Penrith	NSW	-33.68	150.75
27	WINDSOR DOWNS NATURE	NSW	-33.64	150.79
28	Llangothlin to Ben Lomond Road	NSW	-30.0707	151.6738
29	Kingsgate Road	NSW	-29.8016667	151.9825
30	30k E Tenterfield	NSW	-28.8	152.0833333
31	Torrington State Recreation area, Butler	NSW	-29.2403	151.5577
32	Red Range to Kingsgate Road	NSW	-29.7739	151.9574
33	Red Range to Kingsgate Road	NSW	-29.7739	151.9574
34	Captains Flat Road, E Queanbeyan	NSW	-35.3583333	149.2666667
35	Red Hill, Canberra	ACT	-35.325	149.116666666667
36				
37	Woodstock Station	WA	-21.6226	118.9562
38	Woodstock Station	WA	-21.6226	118.9562
39	Lesley Salt Works	WA	-20.3432	118.6336
40	no locality data	WA		
41	20k E South Hedland	WA	-20.3833	118.8000
42	Lesley Salt Works	WA	-20.2833	118.8944
43	Brockan Mine	WA	-22.6133	117.1881
44	Brockan Mine	WA	-22.6175	117.1814
45	Brockan Mine	WA	-22.5730	117.1911
46	50.1k W Pannawonica	WA	-21.6666	115.8353
47	42.9k W Pannawonica	WA	-21.6561	115.9078
48	22.1k WSW Pannawonica	WA	-21.6938	116.1178
49	37.5k W Pannawonica	WA	-21.6711	115.9622
50	16k SW Pannawonica	WA	-21.7461	116.2200
51	29.1k WSW Pannawonica	WA	-21.6991	116.0489
52	Boodarie Hill	WA	-20.4000	118.5167
53	39k W Munjina	WA	-22.4333	118.7500
54	Mt Brockan	WA	-22.2975	117.2878
55	Meentheena	WA	-21.2038	120.4731
56	Meentheena	WA	-21.2252	120.3556
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4	Meentheena	WA	-21.2902	120.4664
5	Meentheena	WA	-21.4216	120.4267
6	Millstream-Chichester Range NP	WA	-21.4619	117.1625
7	Cape Preston area	WA	-21.0163	116.1956
8	Chichester Range	WA	-22.2305	118.9794
9	Port Hedland area	WA	-20.3513	118.7186
10	Port Hedland area	WA	-20.3811	118.6853
11	52.5k N Nullagine	WA	-21.4077	120.071
12	Nullagine	WA	-21.9541	120.1219
13	Woodie Woodie	WA	-21.6847	121.2308
14	Carabooda	WA	-31.5675	115.7114
15	Helena Valley	WA	-31.9333	116.0333
16	Mt Hartley	Qld	-15.76	145.33
17	Charmillan Creek	Qld	-17.6856	145.5224
18	Charmillan Creek	Qld	-17.6856	145.5224
19	7.5k W Paluma	Qld	-19.0237	146.1395
20	Julatten	Qld	-	145.333333333333
21	Pine Creek Road, Numinbah Valley	Qld	-28.1119517	153.2441232
22	Arcadia Valley, 20k NNE Injune	Qld	-	148.833333333333
23	CLARENCE TOWN, 2.5k S - RAYMOND	NSW	-32.5937	151.7587
24	CLARENCE TOWN, 2.5k S - RAYMOND	NSW	-32.5937	151.7587
25	Goonoo SF near Dubbo	NSW	-32.08	148.9
26	Sloane Reserve, 28.5k N Mulwala,	NSW	-35.7383333	146.0483333
27	25k N Pomona	Qld	-26.1437	152.8415
28	Oobagooma Homestead	WA	-16.7500	123.9853
29	Dundee Beach, Fog Bay	NT	-12.7597	130.3553
30	Lake Argyle	WA	-16.1163	128.7303
31	Burke Development Road 10k ENE	Qld	-17.4347222	141.2763889
32	Lake Argyle	WA	-16.3000	128.8000
33	near Mount Percy	WA	-17.6630	124.9333
34	Kalumburu	WA	-14.3000	126.6333
35	10k SE Kununurra	WA	-15.8333	128.8000
36	25k N Dongara	WA	-29.033	114.8328
37	2k SE Gabalong	WA	-30.7266	116.4026
38	16k ESE Moonyoonooka	WA	-	114.916666666667
39	2k SE Gabalong	WA	-30.7500	116.4000
40	41.7k NW Lake Way	WA	-27.1894	120.7867
41	Moresby, Geraldton	WA	-28.7666	114.6167
42	Forrestfield	WA	-31.9833	115.9833
43	Geraldton	WA	-	-
44	Waggrakine Pass	WA	-28.7000	114.6667
45	Tallering Peak	WA	-28.1000	115.6333
46	near Walyunga National Park	WA	-31.7333	116.0833
47	Buller River, Geraldton	WA	-28.7666	114.6167
48	Spalding Park, Geraldton	WA	-28.6500	114.6333
49	16K ESE Moonyoonooka	WA	-28.8166	114.9167
50		WA	-	-
51	31k W Wiluna	WA	-26.5833	119.9167
52	Yuinmery Station	WA	-28.6166	119.0667
53	Lake Mason Station	WA	-27.6975	119.2800
54	Lorna Glen Station	WA	-26.2625	121.5108
55	Lorna Glen Station	WA	-26.2350	121.2811
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3	Lorna Glen Station	WA	-26.1852	121.5644
4	Lake Mason Station	WA	-27.6133	119.5697
5	Lake Mason Station	WA	-27.6877	119.3042
6	Pinnacles Station	WA	-28.3722	120.5831
7	5k E Cunderdin	WA	-31.6500	117.2833
8	5k E Cunderdin	WA	-31.6500	117.2833
9	Greenough area	WA	-28.9333	114.7333
10		WA		
11	Lorna Glen Station	WA	-26.2702	121.4975
12	Lorna Glen Station	WA	-26.2625	121.5108
13	Leonora	WA	-28.8591	121.8036
14	1k N Mulga Downs Outcamp	WA	-22.3175	118.98
15	Ora Banda	WA	-30.3666	121.0500
16	Wiluna	WA	-26.8708	120.4167
17				
18	Bundaburg	Qld	-24.86	152.34
19	Poison Gate road, on road to Poison	NSW	-29.5778	149.2256
20	Shoalwater Bay Army Training Reserve	Qld	-22.6491667	150.4594444
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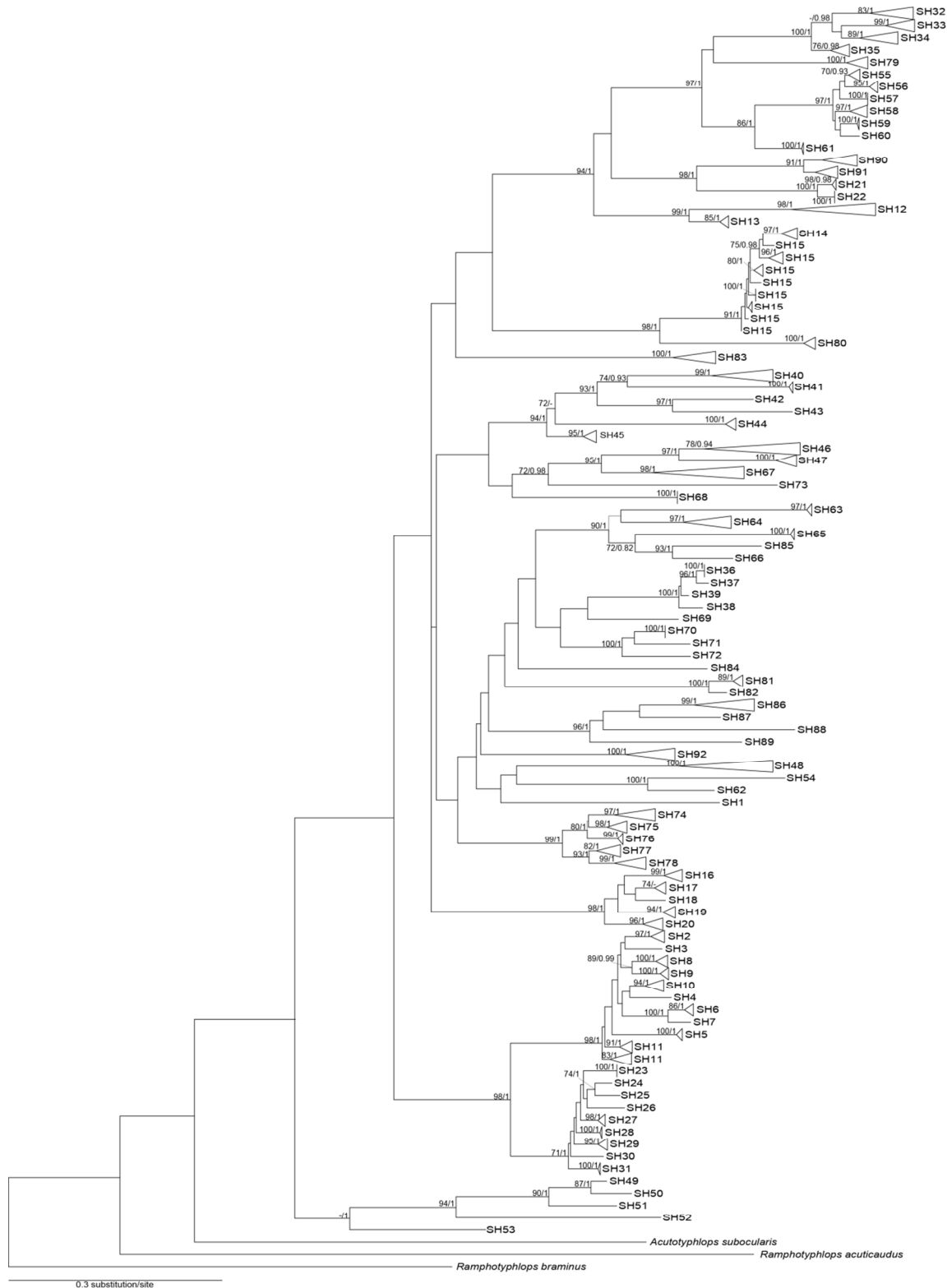


Figure 1. Bayesian inference phylogenetic tree of Australian *Ramphotyphlops* based on analysis of sequences of a mitochondrial protein-coding gene, *cytochrome b*, showing species hypotheses (SHs) obtained with the ABGD method, with bootstraps (>70) and posterior probabilities (>0.9) indicated next to each node

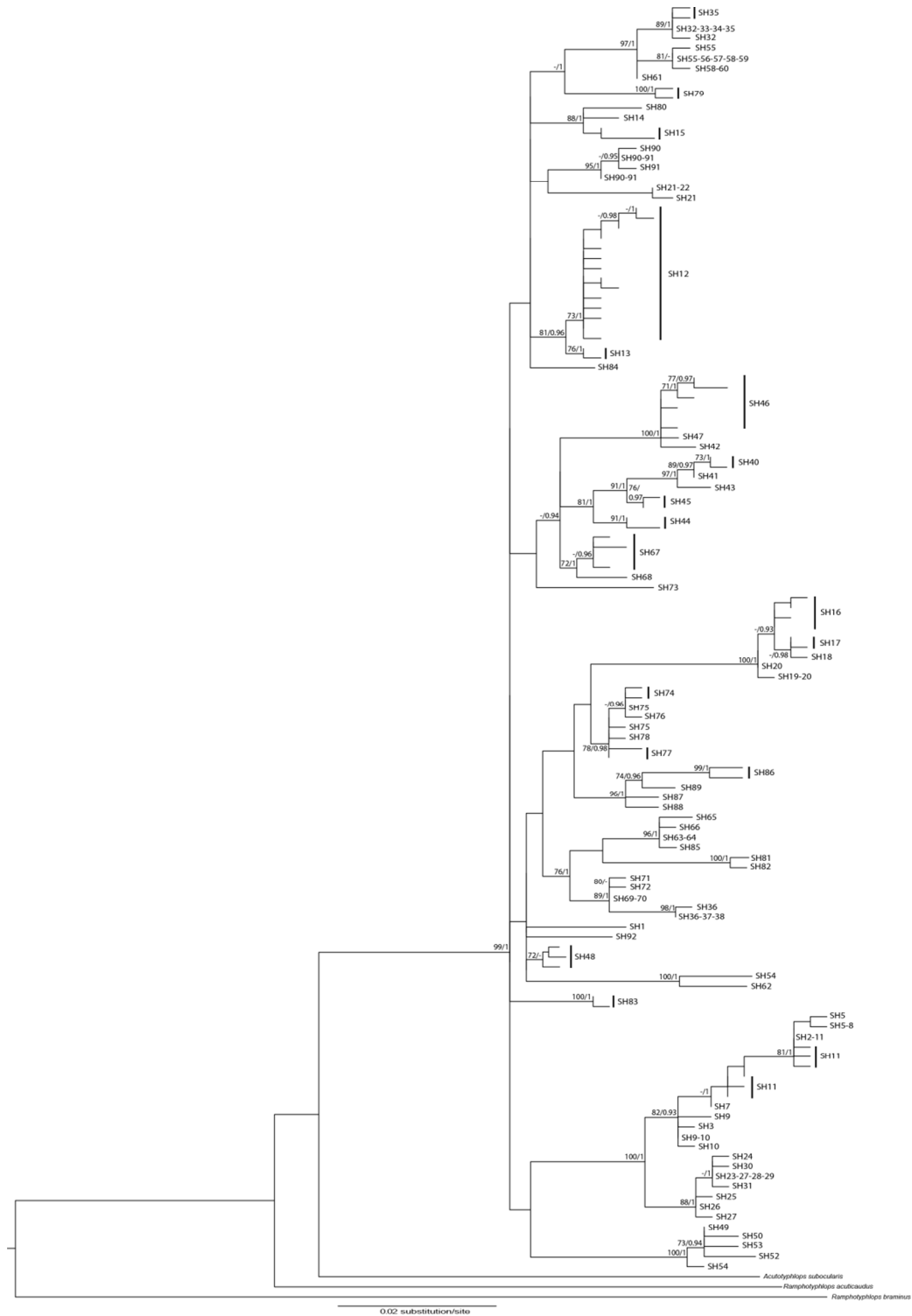


Figure 2. Maximum Likelihood phylogenetic tree of Australian *Ramphotyphlops* based on the analysis of a nuclear protein-coding gene, *prolactin receptor (PRLR)*. Species hypotheses (SHs) reported here were obtained with the ABGD method using *cytochrome b*. Bootstraps (>70) and posterior probabilities (>0.9) are indicated next to each node.