

**Table S1.** Substitution models for each MtNuc<sub>24</sub> and Mt<sub>192</sub> partition, assigned in accordance with ModelFinder results obtained with IQ-TREE v1.6.10 [1]. Numbers 1,2,3 refer to codon positions for either *Cytb* or the concatenated nuclear protein coding sequences.

Partition	Model
MtNuc <sub>26</sub> – RNA stems	TVMe+I+G4
MtNuc <sub>26</sub> – RNA loops	TIM2+F+I+G4
MtNuc <sub>26</sub> –Cytb1	TIM2e+G4
MtNuc <sub>26</sub> –Cytb2	HKY+F+I
MtNuc <sub>26</sub> –Cytb3 (NT coding)	TPM3u+F+G4
MtNuc <sub>26</sub> –Cytb3 (RY coding)	GTR2+FO+I+G4
MtNuc <sub>26</sub> – Nuc1	TN+F+G4
MtNuc <sub>26</sub> – Nuc1	TN+F+G4
MtNuc <sub>26</sub> – Nuc1	K2P+G4
Mt <sub>192</sub> – 12S rRNA	GTR+F+I+G4
Mt <sub>192</sub> – 16S rRNA	TIM2+F+I+G4
Mt <sub>192</sub> – Cytb1	GTR+F+I+G4
Mt <sub>192</sub> – Cytb2	GTR+F+G4
Mt <sub>192</sub> – Cytb3 (NT coding)	GTR+F+I+G4

**Table S2.** Fossil calibrations for BEAST [2] molecular dating analyses. Maximum bounds are based on (A) a combination the absence of putative crown members from well sampled fossil faunas in relevant geographic areas that include deeper diverging (stem) members or (B) long temporal gaps preceding specimens that are close to the transition between stem and crown members. Prior distribution tails for minimum and maximum bounds are each set at 2.5%. These calibrations are discussed at length in Travouillon and Phillips [3]

Node calibrated	Minimum bound	Maximum bound
Australidelphia- Didelphimorphia <sup>1</sup>	<b>54.55 Ma</b> , based on <i>Djarthia murgonensis</i>	<b>83.8 Ma</b> , absence of crown marsupials among Campanian fossil faunas from South and North America.
Agreodontia <sup>2</sup>	<b>25.2 Ma</b> , based on <i>Bulungu minkinaensis</i>	<b>72.3 Ma</b> , absence of crown australidelphians among Maastrichtian fossil faunas from South and North America; and temporal gap back from the transitional Tingamarra Fauna.
Dasyuridae <sup>3</sup>	<b>4.36 Ma</b> , based on Hamilton fauna dasyurids	<b>23.03 Ma</b> , absence of crown dasyurids among Australian Early Miocene fossil faunas.
Dasyuromorphia <sup>1</sup>	<b>23.03 Ma</b> , based on <i>Badjcinus turnbulli</i>	<b>54.65 Ma</b> , absence of crown dasyuromorphians from the Tingamarra Fauna, and temporal gap back from the relatively transitional Late Oligocene Etadunna fossils.
<i>Isoodon</i> – <i>Perameles</i> <sup>1</sup>	<b>3.62 Ma</b> , based on <i>Perameles allinghamensis</i>	<b>18.51 Ma</b> , absence of crown peramelines from from well-sampled Riversleigh FZB sites, such as radiometrically dated Neville’s Garden and Camel Sputum sites.
Peramelidae <sup>4</sup>	<b>3.62 Ma</b> , based on <i>Perameles allinghamensis</i>	<b>23.03 Ma</b> , absence of crown peramelids among Australian Early Miocene fossil faunas.
Phascogalini <sup>1</sup>	<b>4.36 Ma</b> , based on Hamilton fauna <i>Antechinus</i>	<b>15.09 Ma</b> , absence of crown phascogalines from well-sampled Riversleigh FZC sites, such as radiometrically dated AL90 and Ringtail sites.
Didelphimorphia <sup>1</sup>	<b>12.1 Ma</b> , based on <i>Marmosa laventicus</i> [4]	<b>56.0 Ma</b> , absence of of crown didelphimorphians from well-sampled Itaborai and other Ypressian South American fossil faunas.

1. Employed as uniform bounds. 2. Truncated minimum and normal tailed maximum bounds, with a peak at 54.6 Ma, which recognises the transitional nature of several Tingamarra fossils close to this node. 3. Normal tailed minimum and maximum, with central peak, acknowledging that both bounds are highly conservative. 4. Truncated minimum and normal tailed maximum bounds, with central peak (13.325 Ma), which recognises the transitional nature of several Middle Miocene fossil taxa such as *Crash bandicoot* close to this time.

**Table S3.** BLAST identity for 150bp windows, sliding 75bp until the end of *Chaeropus* and *Macrotis* sequences. The identity ratio is a metric for the specificity of the top hit (1-I<sub>A</sub>) relative to the next most similar peramelemorphian genus (1-I<sub>B</sub>). In rare cases the first hit, which is based on the BLAST maximum score does not have the highest identity. This might occur, for example, if the first hit has greater query cover. For relevance we only include hits with similarly high query cover in identity ratio calculations. Likely non-target DNA is highlighted **red** if that window corresponds to a data point in Figure 2 that falls outside the *Macrotis* 95% distribution for BLAST identity ratio versus highest anomalous MP support and either the identity ratio is <0.30 or anomalous MP bootstrap ≥95%. Potential non-target DNA caution is highlighted **yellow** for windows when two or more of the following conditions are met: (1) The other *Chaeropus* species<sup>^</sup> is not the top hit (orange, for that column), (2) the identity ratio is below 0.7, (3) the top hit is outside of Peramelemorphia, (4) both neighbouring windows are likely or potential non-target DNA and (5) a highly unusual sequence is included that does not closely match any accession. <sup>^</sup>This also applies if *Macrotis* is the query taxon and another *Macrotis* sequence is not the top hit, when available.

***Macrotis lagotis* 12S rRNA (AJ639871), excluding any *Chaeropus* hits.**

	First hit identity (I <sub>A</sub> ) excluding <i>Macrotis</i>	Next species	1 <sup>st</sup> bandicoot (or non-bandicoot)	Identity ratio	Another <i>Macrotis</i> ?
1-150	<i>Perameles nasuta</i> (KJ868137) 92.0%	<i>Echymipera rufescens</i> (JF694111) 92.0%	<i>Marmosa murina</i> (KJ868123) 88.6%	1.00	AF131246 (100%)
76-225	<i>Perameles nasuta</i> (KJ868137) 95.4%	<i>Peram. bougainville</i> (KJ868136) 95.3%	<i>Marmosa murina</i> (KJ868123) 94.0%	0.77 <sup>1</sup>	AF131246 (99.3%)
151-300	<i>Perameles nasuta</i> (AF250022) 92.7%	<i>Echymipera kalubu</i> (JF694110) 92.6%	<i>Bettongia tropica</i> (AY245618) 91.2%	0.99	AF334773 (99.3%)
226-375	<i>Echymipera kalubu</i> (JF694110) 88.2%	<i>Echymipera rufescens</i> (AF297864) 88.2%	<i>Lasiorhinus krefftii</i> (KJ868118) 82.6%	0.96 <sup>2</sup>	AF334773 (100%)
301-450	<i>Isodon obesulus</i> (AF250011) 91.3%	<i>Isodon auratus</i> (JF694113) 90.7%	<i>Strigocuscus celebensis</i> (KJ868161) 88.1%	0.87 <sup>3</sup>	AF131246 (98.7%)
376-525	<i>Isodon obesulus</i> (KJ868116) 93.3%	<i>Isodon auratus</i> (JF694113) 93.3%	<i>Marmosops parvidens</i> (KX381537) 92.0%	0.92 <sup>4</sup>	AF131246 (99.3%)
451-600	<i>Isodon obesulus</i> (KJ868116) 96.0%	<i>Echymipera clara</i> (KJ868114) 96.0%	<i>Monodelphis domestica</i> (NC_006299) 94.0%	1.00	AF131246 (98.7%)
526-675	<i>Potorous gilberti</i> (JX104630) 92.5%	<i>Echymipera clara</i> (AF297694) 91.9%	<i>Echymipera kalubu</i> (AF334776) 93.4% <sup>C</sup>	0.86 <sup>5</sup>	AF334773 (100%)
601-750	<i>Echy. kalubu</i> (AF334776) 90.1%	<i>Echymipera rufescens</i> (JF694111) 88.7%	<i>Caenolestes fuliginosus</i> (U61072) 86.3%	0.79 <sup>6</sup>	AF334773 (99.3%)
676-825	<i>Echy. kalubu</i> (AF297690) 95.9% <sup>A</sup>	<i>Echymipera rufescens</i> (JF694111) 95.2% <sup>A</sup>	<i>Marmosa murina</i> (KJ868123) 93.2% <sup>B</sup>	0.71 <sup>7</sup>	AF131246 (96.6%)
751-924	<i>Echymipera kalubu</i> (JF694110) 92.6%	<i>Echymipera rufescens</i> (AF297864) 92.6%	<i>Acrobates pygmaeus</i> (KJ868094) 90.9%	0.94 <sup>8</sup>	AF131246 (94.9%)

<sup>A</sup> (97% complete), <sup>B</sup> (98% complete), <sup>C</sup> (94% complete) 1. I<sub>B</sub> is 0.940 for *Echymipera kalubu* (JF694110). 2. I<sub>B</sub> is 0.877 for *Perameles nasuta* (AF250022). 3. I<sub>B</sub> is 0.900 for *Echymipera kalubu* (JF694110). 4. I<sub>B</sub> is 0.927 for *Peroryctes raffrayana* (KJ868138). 5. I<sub>B</sub> is 0.913 for *Perameles bougainville* (AF250019). 6. I<sub>B</sub> is 0.875 for *Microperoryctes papuensis* (AF694100). 7. I<sub>B</sub> is 0.942 for *Microperoryctes longicauda* (KJ868126). 8. I<sub>B</sub> is 0.921 for *Rhynchomeles prattorum* (JF694112).

***Macrotis lagotis* 16S rRNA (AJ639871), excluding any *Chaeropus* hits.**

	First hit identity (I <sub>A</sub> ) excluding <i>Macrotis</i>	Next species	1 <sup>st</sup> bandicoot (or non-bandicoot) or next bandicoot genus	Identity ratio	Another <i>Macrotis</i> ?
1-150	<i>Microper. longicauda</i> (JF706351) 79.7% <sup>A</sup>	<i>Potorous longipes</i> (KJ868148) 77.4%	<i>Perameles bougainville</i> (KJ868136) 72.5%	0.74	NA
76-225	<i>Echymipera clara</i> (KJ868114) 87.3% <sup>C</sup>	<i>Microper. longicauda</i> (KJ868126) 87.2% <sup>C</sup>	<i>Aepyprymnus rufescens</i> (KJ868095) 86.5% <sup>C</sup>	0.99	NA
151-300	<i>Peroryctes raffrayana</i> (KJ868138) 91.3%	<i>Perameles bougainville</i> (KJ868136) 88.7%	<i>Lagostrophus fasciatus</i> (AY189935) 88.7%	0.77	NA
226-375	<i>Perameles bougainville</i> (KJ868136) 95.3% <sup>C</sup>	<i>Echymipera kalubu</i> (U97342) 95.3% <sup>C</sup>	<i>Lagostrophus fasciatus</i> (AY189935) 93.3%	1.00	NA
301-450	<i>Microper. longicauda</i> (JF706351) 92.7%	<i>Osphranter antilopinus</i> (MK211398) 92.7%	<i>Peroryctes raffrayana</i> (KJ868136) 92.1%	0.92	NA
376-525	<i>Antechinus arktos</i> (MK629605) 89.4%	<i>Thylogale stigmatica</i> (AF027991) 89.4%	<i>Peroryctes raffrayana</i> (KJ868138) 87.6%	0.93	NA
451-600	<i>Thylogale stigmatica</i> (AF027991) 88.0% <sup>D</sup>	<i>Thylogale thetis</i> (MT123587) 85.2% <sup>D</sup>	<i>Isodon obesulus</i> (KJ868116) 81.4% <sup>D</sup>	0.65	NA
526-675	<i>Peroryctes raffrayana</i> (KJ868138) 84.0%	<i>Thylamys elegans</i> (AJ508401) 83.7%	<i>Isodon obesulus</i> (KJ868116) 81.2%	0.85	NA

601-750	<i>Microper. longicauda</i> (KJ868126) 86.7% <sup>E</sup>	<i>Echymipera clara</i> (KJ868114) 85.2% <sup>E</sup>	<i>Phascolarctos cinereus</i> (NC_008133) 82.1% <sup>F</sup>	0.90	NA
676-825	<i>Dromicipo gliroides</i> (AJ508402) 83.4%	<i>Isodon obesulus</i> (KJ868116) 80.9%	See left	0.87	NA
751-900	<i>Trichosurus caninus</i> (KJ868163) 95.3%	<i>Trichosurus vulpecula</i> (AF357238) 95.3%	<i>Isodon obesulus</i> (KJ868116) 87.3%	0.37 <sup>1</sup>	NA
826-975	<i>Thylamys elegans</i> (AJ508401) 97.3%	<i>Tlacuatzin canescens</i> (KT943517) 97.3%	<i>Echymipera kalubu</i> (U97342) 95.3%	0.57 <sup>1</sup>	NA
901-1050	<i>Perameles nasuta</i> (KJ868137) 98.0%	<i>Isodon macrourus</i> (AF358864) 98.0%	<i>Lasiorninus krefftii</i> (KJ868118) 97.3%	1.00	NA
976-1125	<i>Perameles nasuta</i> (KJ868137) 92.9%	<i>Isodon macrourus</i> (AF358864) 92.8%	<i>Setonix brachyurus</i> (KJ868156) 91.9% <sup>G</sup>	0.99	NA
1051-1200	<i>Peroryctes raffrayana</i> (KJ868138) 84.7%	<i>Microper. longicauda</i> (JF706351) 83.3%	<i>Didelphis virginiana</i> (MT892666) 82.7%	0.92 <sup>2</sup>	NA
1126-1275	<i>Myrmecobius fasciatus</i> (MT712076) 94.2% <sup>H</sup>	<i>Peroryctes raffrayana</i> (KJ868138) 91.3% <sup>C</sup>	See left	0.67	NA
1201-1350	<i>Perameles nasuta</i> (KJ868137) 96.0% <sup>I</sup>	<i>Isodon obesulus</i> (KJ868116) 95.3% <sup>I</sup>	<i>Petauroides volans</i> (KJ868139) 95.3% <sup>C</sup>	0.85	NA
1276-1425	<i>Perameles nasuta</i> (KJ868137) 99.3%	<i>Perameles bougainville</i> (KJ868136) 99.3%	<i>Dactylopsila palpator</i> (KJ868106) 99.3%	1.00 <sup>2</sup>	NA
1351-1500	<i>Perameles bougainville</i> (KJ868136) 98.7%	<i>Isodon obesulus</i> (KJ868116) 98.7%	<i>Strigocuscus celebensis</i> (KJ868161) 98.6% <sup>C</sup>	1.00	NA
1426-1571	<i>Perameles bougainville</i> (KJ868136) 90.5%	<i>Microper. longicauda</i> (JF706351) 90.3%	<i>Strigocuscus celebensis</i> (KJ868161) 89.0%	0.98	NA

A (95% complete), B (96% complete), C (98% complete), D (93% complete), E (90% complete), F (89% complete), G (92% complete), H (91% complete), I (99% complete) 1. This region is apomorphic in peramelids, plesiomorphic in *Macrotis* and non-peramelemorphians, with a variety of other marsupials very close to the first hit, which lessens concern for lower identity ration resulting from a non-target inclusion. 2. I<sub>B</sub> is 0.993 for *Isodon obesulus* (KJ868116).

***Macrotis lagotis* Cytb** (AJ639871), excluding any *Chaeropus* hits.

	First hit identity (I <sub>A</sub> ) excluding <i>Macrotis</i>	Next species	1 <sup>st</sup> bandicoot (or non-bandicoot) or next bandicoot genus	Identity ratio	Another <i>Macrotis</i> ?
1-150	<i>Microper. longicauda</i> (KJ868126) 86.7%	<i>Chacodelphys formosa</i> (KU171186) 86.6% <sup>A</sup>	<i>Echymipera kalubu</i> (U34682) 85.3%	0.90	NA
76-225	<i>Philander pallidus</i> (MG491945) 89.3%	<i>Microperoryctes longicauda</i> (KJ868126) 88.7%	See left	0.95	NA
151-300	<i>Echymipera rufescens</i> (JN228213) 89.9% <sup>A</sup>	<i>Caluromys derbianus</i> (MK817305) 88%	<i>Microperor. papuensis</i> (JF718358) 86.6% <sup>A</sup>	0.75	NA
226-375	<i>Tlacuatzin canescens</i> (MG029682) 89.3%	<i>Marmosa meridae</i> (MN978642) 87.9%	<i>Echymipera rufescens</i> (JN228213) 86.7%	0.80	NA
301-450	<i>Tlacuatzin canescens</i> (MG029682) 90.0%	<i>Phascolosorex dorsalis</i> (AY533832) 89.3%	<i>Peroryctes raffrayana</i> (KJ868138) 86.7%	0.75	NA
376-525	<i>Thylamys pallidior</i> (KF164518) 89.4%	<i>Perameles bougainville</i> (KJ868136) 89.0% <sup>B</sup>	See left	0.96	NA
451-600	<i>Dactylopsila trivergata</i> (AB241054) 88.7%	<i>Spilocuscus maculatus</i> (KJ868160) 86.7%	<i>Perameles bougainville</i> (JF718361) 85.9%	0.80	NA
526-675	<i>Planigale gilesi</i> (KJ868157) 85.3%	<i>Monodelphis reigi</i> (FJ810210) 83.9% <sup>A</sup>	<i>Isodon auratus</i> (JF718353) 83.2% <sup>A</sup>	0.88	NA
601-750	<i>Echymipera clara</i> (KJ868114) 80.0%	<i>Marmosa murinao</i> (JF281050) 80.0%	<i>Perameles bougainville</i> (JF718361) 79.3%	0.93	NA
676-825	<i>Perameles bougainville</i> (JF718361) 83.9%	<i>Peroryctes raffrayana</i> (EU086682) 82.6%	<i>Dromiciops gliroides</i> (AF102815) 82.6%	0.93	NA
751-900	<i>Macropus giganteus</i> (MN746797) 89.4%	<i>Thylogale stigmatica</i> (JN638598) 88.7%	<i>Peroryctes raffrayana</i> (EU086682) 86.7%	0.80	NA
826-975	<i>Monodelph. americana</i> (KM071586) 87.3%	<i>Monodelphis diidiata</i> (KM071388) 86.7%	<i>Echymipera kalubu</i> (EU086683) 83.2% <sup>A</sup>	0.76	NA
901-1050	<i>Marmosops bishopi</i> (KT437723) 87.1% <sup>C</sup>	<i>Lestodelphys halli</i> (KF164579) 85.9% <sup>A</sup>	<i>Echymipera rufescens</i> (795975) 82.9% <sup>B</sup>	0.75	NA
976-1146	<i>Echymipera rufescens</i> (795975) 83.6%	<i>Peroryctes raffrayana</i> (KJ868138) 83.5%	<i>Thylogale browni</i> (JN202473) 81.8%	0.99	NA

A (99% complete), B (97% complete), C (98% complete).

***Chaeropus ecaudatus* 12S rRNA** (MK359293 and MK359294).

	First hit identity (I <sub>A</sub> )	Next species	1 <sup>st</sup> bandicoot (or non-bandicoot)	Identity ratio	<i>Chaeropus yirratji</i>
1-150	<i>Echy. clara</i> (KJ868114) 95.3%	<i>Echy. kalubu</i> (AF297691) 94.0%	<i>Petauroides volans</i> (KJ868139) 86.6%	0.87 <sup>3</sup>	85.1%
76-225	<i>Peroryctes raffrayana</i> (KJ868138) 93.2%	<i>Echy. kalubu</i> (AF297691) 92.6%	<i>Dromiciops gliroides</i> (MH363825) 92.0% <sup>9</sup>	0.92	87.0%

151-300	<i>Peroryctes raffrayana</i> (KJ868138) 98.0% <sup>1</sup>	<i>Isoodon macrourus</i> (AF358864) 97.3%	<i>Dromiciops gliroides</i> (MH363859) 94.7%	0.74	92.7%
226-375	<i>Isoodon obesulus</i> (KJ868116) 94%#	<i>Isoodon macrourus</i> (AF358864) 94.0%	<i>Notamacropus dorsalis</i> (JN003404) 89.9 %	0.82 <sup>4</sup>	88.44%
301-450	<i>Isoodon obesulus</i> (AF250011) 90.7%#	<i>Isoodon macrourus</i> (AF250009) 90.7%	<i>Thylacinus cynocephalus</i> (KY678392) 88.7% <sup>2</sup>	0.89 <sup>5</sup>	84.0%
376-525	<i>Peroryctes raffrayana</i> (KJ868138) 92.7%#	<i>Echy. clara</i> (KJ868114) 92.7%	<i>Lagor. conspicillatus</i> (KY996508) 89.3%	1.00	87.3%
451-600	<i>Isoodon obesulus</i> (KJ868116) 95.3% #	<i>Echy. clara</i> (AF297694) 95.3%	<i>Caen. fuliginosus</i> (U61072) 93.3%	1.00	91.7%
526-675	<i>Echy. kalubu</i> (JF694110) 96.1 % #	<i>Echy. rufescens</i> (AF297683) 96.1%	<i>Phalanger gymnotis</i> (KJ868142) 92.1%	0.74 <sup>6</sup>	93.7%
601-750	<i>Perameles nasuta</i> (AF250022) 92.8%	<i>Micro. longicauda</i> (KJ868126) 92.9%#	<i>Bettongia lesueur</i> (KJ868101) 87.5%	1.00	89.3%
12S 676-825	<i>Micro. longicauda</i> (KJ868126) 92.0% #	<i>Micro. papuensis</i> (JF694100) 92.0%	<i>Caen. fuliginosus</i> (U61072) 88.0%	0.92 <sup>7</sup>	88.1%
12S 751-900	<i>Isoodon macrourus</i> (AF250010) 92.1%	<i>Isoodon auratus</i> (JF694113) 91.4% #	<i>Caluromys philander</i> (AF038014) 88.4%	0.85 <sup>8</sup>	86.2%
12S 826-948	<i>Isoodon macrourus</i> (AF250010) 92.1%#	<i>Micro. longicauda</i> (AF297679) 91.2%	<i>Lagor. hirsutus</i> (AB241056) 90.4%	0.90	87.1%

\* Equal with many other macropodoids # Same as several other bandicoots 1 also *P. broadbenti*. 2. On 93% coverage 3. I<sub>B</sub> is 0.946 for *Perameles nasuta* (AF166347). 4. I<sub>B</sub> is 0.928 for *Perameles boubainville* (JF694114). 5. I<sub>B</sub> is 0.895 for *Perameles boubainville* (JF694114). 6. I<sub>B</sub> is 0.947 for *Perameles eremiana* (JF694115). 7. I<sub>B</sub> is 0.913 for *Rhynchomeles prattorum* (JF694112). 8. I<sub>B</sub> is 0.907 for *Perameles boubainville* (KJ868136). 9. 92% query coverage.

***Chaeropus ecaudatus* 16S rRNA** (MK359295 and MK359296). Note that site 931 of this sequence is site 1 of JF706364 (above).

	First hit identity (I <sub>A</sub> )	Next species	1 <sup>st</sup> bandicoot (or non-bandicoot)	Identity ratio	<i>Chaeropus yirratji</i>
1-150 <sup>^</sup>	<i>Perro. raffrayana</i> (JF706352) 84.2%# <sup>1</sup>	<i>Perameles nasuta</i> (KJ868137) 84.2% #	<i>Zalophus californianus</i> (U78350) 85% <sup>1</sup>	1.00 <sup>6</sup>	-
76-225	<i>Peram. bougainville</i> (KJ868136) 87.0%	<i>Perameles nasuta</i> (KJ868137) 85.1%	<i>Zalophus californianus</i> (U78350) 82.9%	0.90 <sup>7</sup>	-
151-300	<i>Peror. raffrayana</i> (KJ868138) 90.0% #	<i>Perameles nasuta</i> (KJ868137) 90.0%	<i>Philander frenatus</i> (KJ868146) 87.7%	1.00	-
226-375	<i>Echy. kalubu</i> (U97342) 94.0%	<i>Echy. rufescens</i> (AY795975) 93.3%#	<i>Hypsiprymnodon moschatus</i> (KJ868115) 91.2%	0.82 <sup>8</sup>	-
301-450	<i>Macrotis lagotis</i> (AJ639871) 91.2%	<i>Echy. kalubu</i> (U97342) 90.5%	<i>Petrogale xanthopus</i> (KY996509) 89.2%	0.93	-
376-525	<i>Peror. raffrayana</i> (KJ868138) 86.1% #	<i>Isoodon macrourus</i> (AF358864) 86.1%	<i>Planigale sp.</i> (KX034141) 84.6%	1.00	-
451-600	<i>Perameles nasuta</i> (AF166347) 85.0%	<i>Isoodon macrourus</i> (AF358864) 85.0%	<i>Phalanger orientalis</i> (AY228381) 85.2% <sup>2</sup>	1.00	-
526-675 <sup>3</sup>	<i>Ningau ridei</i> (JQ413968) 88.1%	<i>Sminth. psamm.</i> (KJ868159) 87.3%	<i>Perameles bougainville</i> (KJ868136) 86.6%	0.89	-
601-750 <sup>3\$</sup>	<i>Isoodon macrourus</i> (AF58864) 92.3%	<i>Isoodon obesulus</i> (KJ868116) 90.6%	No non-peramelemorph matches	0.71 <sup>9</sup>	-
676-825 <sup>3</sup>	<i>Isoodon macrourus</i> (AF358864) 98.4%	<i>Isoodon obesulus</i> (KJ868116) 95.2%	<i>Dromiciops gliroides</i> (U97341) 82.9%	0.20 <sup>10</sup>	-
751-900	<i>Isoodon macrourus</i> (AF358864) 100%	<i>Isoodon obesulus</i> (KJ868116) 98.0%	<i>Gracilinanus agilis</i> (NC_054268) 91.3%	0.00 <sup>11</sup>	-
826-975	<i>Isoodon macrourus</i> (AF358864) 100%	<i>Isoodon obesulus</i> (KJ868116) 98.7%	<i>Pseudochirulus forbesi</i> (MT123590) 95.3%	0.00 <sup>12</sup>	100% <sup>4</sup>
901-1050	<i>Perameles nasuta</i> (KJ868137) 99.3% #	<i>Isoodon macrourus</i> (AF358864) 99.3% #	<i>Petaurus breviceps</i> (AY228380) 97.3%	1.00	97.4%
976-1125	<i>Isoodon macrourus</i> (AF358864) 97.3%	<i>Perameles nasuta</i> (KJ868137) 96.0% #	<i>Pseudochirulus herbertensis</i> (KJ868153) 97.3% <sup>13</sup>	0.68	94.7%
1051-1200	<i>Chaeropus yirratji</i> (JF706364) 97.3%	<i>Isoodon obesulus</i> (KJ868116) 93.9%#	<i>Didelphis imperfecta</i> (NC_057517) 81.2%	0.62 <sup>14</sup>	97.3%
1126-1275	<i>Chaeropus yirratji</i> (JF706364) 98.0%	<i>Isoodon obesulus</i> (KJ868116) 94.0%#	<i>Parantechinus apicalis</i> (KJ868135) 94.1% <sup>16</sup>	0.76 <sup>15</sup>	98.0%
1201-1350	<i>Chaeropus yirratji</i> (JF706364) 99.3%	<i>Perameles nasuta</i> (KJ868137) 96.7% #	<i>Cercartetus concinnus</i> (KJ868105) 95.3%#	0.83 <sup>17</sup>	99.3%
1276-1425	<i>Chaeropus yirratji</i> (JF706364) 100%	<i>Wyulda semisqu.</i> (KJ868165) 99.3% #	<i>Perameles nasuta</i> (KJ868137) 98.7% #	1.00 <sup>18</sup>	100%
1351-1500	<i>Chaeropus yirratji</i> (JF706364) 98.7% #	<i>Perameles nasuta</i> (AF166347) 98.7%#	<i>Strigocuscus celebensis</i> (MH220729) 97.3%	1.00 <sup>19</sup>	98.7%
1426-1574	<i>Perameles nasuta</i> (AF166347) 89.9%	<i>Micro. longicauda</i> (KJ868126) 89.9%	<i>Lagorchestes conspicillatus</i> (KY996508) 87.3%	1.00	97.3% <sup>5</sup>

<sup>^</sup> Some anomalous sequence, as detailed in the main text, Results 3.1, last paragraph. 1. Several otariids and bandicoots close, only about 54% query coverage 2. Higher match partly due to 94% coverage 3. Last, middle and first sections of these three are ambiguities (Ns), which are excluded from the BLAST. \$ Adding two stretches cut by ambiguities (49Ns). 4. Only 30% coverage. 5. 57% coverage (5' end) and *Perameles* and *Macrotis* also 97.3 for same segment. 6. Coverage low and not exactly comparable, but very close



between bandicoots and non-bandicoots. **7.** I<sub>B</sub> is 0.855 for *Peroryctes raffrayana* (KJ868136). **8.** I<sub>B</sub> is 0.927 for *Isoodon obesulus* (KJ868116). **9.** I<sub>B</sub> is 0.892 for *Peroryctes raffrayana* (JF706352). **10.** I<sub>B</sub> is 0.919 for *Microperoryctes longicauda* (JF706351). **11.** I<sub>B</sub> is 0.967 for *Perameles bougainville* (KJ868136). **12.** I<sub>B</sub> is 0.987 for *Perameles nasuta* (KJ868137). **13.** 74% query cover. **14.** I<sub>B</sub> is 0.901 for *Perameles nasuta* (KJ868137). **15.** I<sub>B</sub> is 0.921 for *Microperoryctes papuensis* (JF706354). **16.** Only 89% query coverage. **17.** I<sub>B</sub> is 0.960 for *Isoodon obesulus* (KJ868116). **18.** I<sub>B</sub> is 0.987 for *Isoodon obesulus* (KJ868116). **19.** I<sub>B</sub> is 0.987 for *Macrotis lagotis* (AJ639871).

***Chaeropus ecaudatus* Cytb** (MK359297 and MK359298). Note that site 90 of this sequence is site 1 of JF718363 (above).

	First hit identity (I <sub>A</sub> )	Next species	1 <sup>st</sup> bandicoot (or non-bandicoot) or next bandicoot genus	Identity ratio	<i>Chaeropus yirratji</i>
1-150 <sup>A</sup>	<i>Micoureus demerae</i> (JF281087) 88.7%	<i>Micoureus paraguay.</i> (EF587308) 87.3%	<i>Isoodon macrourus</i> (AF139057) 86.7%	0.85	85.25% <sup>1</sup>
76-225 <sup>A</sup>	<i>Kerivoula titania</i> (MH137400) 89.3%	<i>Kerivoula kardwickii</i> (MH137375) 87.9%	<i>Echymipera rufescens</i> (AY95975) 86.7%	0.80	81.6%
151-300 <sup>A</sup>	<i>Hylomyscus pamfi</i> (JX893905) 89.3%	<i>Dasymys sp.</i> (KT232254) 89.7%	<i>Microper. longicauda</i> (KJ868126) 86.0%	0.76	78.5%
226-375 <sup>A</sup>	<i>Oryzomys texensis</i> (FJ971263) 89.3%	<i>Notomys alexis</i> (MH741764) 88.7%	<i>Microper. longicauda</i> (KJ868126) 86.7%	0.80	73.9%
301-450	<i>Peram. bougainville</i> (JF718361) 85.3%	<i>Dasyurus hallucatus</i> (KJ780050) 84.0%	<i>Peroryctes raffrayana</i> (KJ868136) 83.3%	0.88	80.8%
376-525 <sup>A</sup>	<i>Monodelphis kunsii</i> (KM071558) 85.2%	<i>Perameles bougainville</i> (JF718361) 83.9%	<i>Echymipera clara</i> (KJ868114) 82.6%	0.92	81.2%
451-600 <sup>A</sup>	<i>Petrogale lateralis</i> (JQ042129) 91.3%	<i>Lestoros inca</i> (KF418779) 90.0%	<i>Microper. longicauda</i> (JF718357) 88.7%	0.86	84.7%
526-675 <sup>A</sup>	<i>Myrmecobius fasciatus</i> (U82329) 87.9%	<i>Thylogale stigmatica</i> (JN638577) 89.4%	<i>Echymipera kalubu</i> (EU086683) 85.3%	0.82	85.9% <sup>2</sup>
601-750	<i>Monodelp. gardneri</i> (KM071565) 84.1%	<i>Tlacuatzin canescens</i> (MG029663) 83.2%	<i>Echymipera kalubu</i> (JF718352) 82.7%	0.92	-
676-825	<i>Notamacpus agilis</i> (KY996507) 84.4%	<i>Petrogale purpuricol.</i> (JQ042133) 83.8%	<i>Echymipera rufescens</i> (AY95975) 84.0%	0.98	-
751-856	<i>Notamacropus eugenii</i> (KJ868119) 87.6%	<i>Notamacropus parma</i> (KJ868119) 86.8%	<i>Macrotis lagotis</i> (AJ639871) 85.7%	0.87	-

**A.** Each of these yellow cautions relates to the combination of non-peramelemorphian top hits and lower congeneric *Chaeropus* hits. However, as *Macrotis* reveals below, the non-peramelemorphian top hit is not unexpected for Cytb. Moreover, with RY-coding third positions each of these windows falls withing a MP bootstrap window that places C. ecaudatus with other peramelemorphians. Such caution is instead more warranted for *C. yirratji* Cytb, for which the relevant MP windows strongly support anomalous relationships for *Chaeropus*. **1.** 40% query coverage. **2.** Reduced to 66% query coverage.

***Chaeropus yirratji* 12S rRNA** (AF131247).

	First hit identity (I <sub>A</sub> )	Next species	1 <sup>st</sup> bandicoot (or non-bandicoot)	Identity ratio	<i>Chaeropus ecaudatus</i>
1-150	<i>Potorous tridactylus</i> (JX104628) 96.0%	<i>Potorous longipes</i> (KJ868148) 94.0%	<i>Peroryctes broadbenti</i> (JF694109) 88.1%	0.34	85.1%
76-225	<i>Potorous tridactylus</i> (JX104628) 98.0%	<i>Potorous longipes</i> (KJ868148) 96.6%	<i>Peroryctes raffrayana</i> (KJ868138) 91.1%	0.22	87.0%
151-300	<i>Potorous tridactylus</i> (JX104628) 98.0%	<i>Potorous longipes</i> (KJ868148) 96.7%*	<i>Peroryctes raffrayana</i> (KJ868138) 94.7%	0.38	92.7%
226-375	<i>Notamacropus parryi</i> (AY245610) 94.7%	<i>Potorous longipes</i> (KJ868148) 93.3%*	<i>Echymipera kalubu</i> (JF694110) 92.0%#	0.66	88.44%
301-450	<i>Potorous tridactylus</i> (JX104626) 90.0%	<i>Echy. rufescens</i> (AF297683) 90.2%*	See left	1.00*	84.0%
376-525	<i>Potorous tridactylus</i> (JX104628) 90.6%	<i>Echy. clara</i> (AF297694) 90.0%	See left	0.94	87.3%
451-600	<i>Isoodon obesulus</i> (KJ868116) 93.8%#	<i>Echy. clara</i> (AF297694) 93.8%#	<i>Potorous tridactylus</i> (JX104628) 92.7%	1.00	91.7%
526-675	<i>Macrotis lagotis</i> (AF131246) 100%	<i>Echy. rufescens</i> (JF694111) 96.7%#	<i>Potorous tridactylus</i> (JX104628) 94.0%*	0.00	93.7%
601-750	<i>Macrotis lagotis</i> (AF131246) 96.7%	<i>Echy. rufescens</i> (JF694111) 96.7%#	<i>Notamacropus parma</i> (KY996504) 92.6%	1.00	89.3%
676-825	<i>Echy. rufescens</i> (JF694111) 96.0%#	<i>Echy. kalubu</i> (AF297690) 96.0%	<i>Marmosa murina</i> (KJ868123) 92.1%	0.85 <sup>2</sup>	88.1%
751-900 <sup>3</sup>	<i>Echy. rufescens</i> (JF694111) 89.7%	<i>Microper. longicauda</i> (AF297677) 88.9%	<i>Marmosa murina</i> (KJ868123) 93.5% <sup>1</sup>	0.93	86.2%
826-956 <sup>3</sup>	<i>Echy. rufescens</i> (JF694111) 89.6%	<i>Macrotis lagotis</i> (AF131246) 89.6%	<i>Dromiciops gliroides</i> (AJ508402) 86.3%	1.00	87.1%

\* Equal with many other macropodoids # Same as several other bandicoots 1. Higher % but lower BLAST score because only 74% query coverage (1<sup>st</sup> non-bandicoot with >90% coverage is *Aepyprymnus* at 86.5% match). 2. I<sub>B</sub> is 0.953 for *Macrotis lagotis* (AF131246). 3. A segment of last two windows (751-900 and 826-956), bases 863-897 (TACATCAAAAGTACATCAATGATTAATAAGAT) is not close to any other on GenBank.

***Chaeropus yirratji* 16S rRNA (JF706364).**

	First hit identity (I <sub>A</sub> )	Next species	1 <sup>st</sup> bandicoot (or non-bandicoot) or notable sequence	Identity ratio	<i>Chaeropus ecaudatus</i>
1-150	<i>Lasiornis krefftii</i> (KJ868118) 98.0%	<i>Perameles nasuta</i> (KJ868137) 97.3% #	<i>Vombatus ursinus</i> (MK360903) 92.7%	0.74	96.0%
76-225	<i>Chaeropus ecaudatus</i> (MK359296) 95.2%	<i>Isodon auratus</i> (JF706360) 94.0%	<i>Antechinus minimus</i> (EF011634) 83.9%	0.74 <sup>1</sup>	95.2%
151-300	<i>Chaeropus ecaudatus</i> (MK359296) 96.7%	<i>Isodon obesulus</i> (KJ868116) 92.1% #	<i>Myoictis melas</i> (AY09372) 91.0%	0.75 <sup>2</sup>	96.7%
226-375	<i>Chaeropus ecaudatus</i> (MK359296) 98.7%	<i>Perameles nasuta</i> (KJ868137) 94.0%	<i>Vombatus ursinus</i> (MK360903) 92.7%	0.90 <sup>3</sup>	98.7%
301-450	<i>Chaeropus ecaudatus</i> (MK359296) 100%	<i>Perameles nasuta</i> (AF166347) 98.0% #	<i>Vombatus ursinus</i> (MK360903) 98.0%	0.74 <sup>4</sup>	100%
376-525	<i>Chaeropus ecaudatus</i> (MK359296) 99.3%	<i>Perameles nasuta</i> (KJ868137) 98.7%	<i>Vombatus ursinus</i> (MK360903) 98.0%	1.00 <sup>5</sup>	99.3%
451-583	<i>Chaeropus ecaudatus</i> (MK359296) 98.5%	<i>Perameles nasuta</i> (KJ868137) 97.0% #	<i>Vombatus ursinus</i> (MK360903) 95.5% ^	0.79 <sup>6</sup>	98.5%

# Same as several other bandicoots. ^ Same as several other diprotodontians 1. I<sub>B</sub> is 0.919 for *Perameles nasuta* (KJ868137). 2. I<sub>B</sub> is 0.895 for *Perameles nasuta* (KJ868137). 3. I<sub>B</sub> is 0.933 for *Isodon obesulus* (KJ868116). 4. I<sub>B</sub> is 0.973 for *Isodon obesulus* (KJ868116). 5. I<sub>B</sub> is 0.987 for *Echymipera rufescens* (JF706362). 6. I<sub>B</sub> is 0.962 for *Echymipera rufescens* (JF706362).

***Chaeropus yirratji* Cytb (JF718363).**

	First hit identity (I <sub>A</sub> )	Next species	1 <sup>st</sup> bandicoot (or non-bandicoot) or note	Identity ratio	<i>Chaeropus ecaudatus</i>
1-150 <sup>1</sup>	<i>Sminthop. youngsoni</i> (AF088935) 92.6%	<i>Serinus albogularis</i> (MH307587) 91.9% <sup>1</sup>	<i>Isodon obesulus</i> (JF718354) 89.9%	0.73	81.1%
76-225 <sup>1</sup>	<i>Oreoica gutturalis</i> (EF592230) 98.0% <sup>1</sup>	<i>Sminthopsis youngsoni</i> (AF088935) 98.0%	<i>Isodon obesulus</i> (JF718354) 79.7%	0.10	79.1%
151-300 <sup>1</sup>	<i>Oreoica gutturalis</i> (EF592230) 96.0% <sup>1</sup>	<i>Sminthopsis youngsoni</i> (AF088935) 96.0%	<i>Echymipera rufescens</i> (AY95975) 78.0%	0.18	73.7%
226-375 <sup>1</sup>	<i>Peram. bougainville</i> (JF18361) 84.7%	<i>Echymipera kalubu</i> (U34682) 84.7%	<i>Pseudocheir. peregrinus</i> (AJ639870) 84.0%	1.00	81.8%
301-450	<i>Echymipera kalubu</i> (U34682) 90.1% <sup>A</sup>	<i>Echymipera kalubu</i> (EU086683) 87.9% <sup>A</sup>	<i>Pseudantechinus macdonnellensis</i> (MG251887) 86.4% <sup>B</sup>	0.74 <sup>3</sup>	83.8%
376-525	<i>Pseudantechinus ningbing</i> (U07592) 90%	<i>Pseudantechinus roryi</i> (EU086681) 89.3%	<i>Echymipera kalubu</i> (EU086683) 88.0%	0.83	83.3%
451-547	<i>Pseudantechinus roryi</i> (EU086681) 89.4%	<i>Pseudantechin. ningbing</i> (U07592) 88.5%	<i>Isodon macrourus</i> (JN228211) 89.1% <sup>2</sup>	0.97	84.7%

A. 94% query coverage. B. 93% query coverage. 1 This section includes a fragment from the crested bellbird that also appears in *S. youngsoni* and *S. ooldea* (hence the close bird matches). 2. Higher match due to lower coverage (94% cov). 3. I<sub>B</sub> is 0.866 for *Peroryctes raffrayana* (EU086682), which also had 94% query coverage.

**Table S4.** Maximum parsimony bootstrap support for 300bp windows, sliding 100bp until the end of *Chaeropus* and *Macrotis* sequences. Individual *Chaeropus* and *Macrotis* sequences were allowed to float on the backbone phylogeny shown in Figure S2. For taxonomy, we use the following clade compositions, Peramelidae includes Peramelinae (*Isoodon* and *Perameles*) and Peroryctinae (*Peroryctes*, *Echymipera*, *Rhynchomeles*, *Microperoryctes*). To gauge the extent to which the signal for the placement of *Chaeropus* or *Macrotis* departs from the expectation of placement with Peramelemorphia, but not strongly grouped with extant species/genera, we note whichever is the highest bootstrap support, that for excluding *Chaeropus* (or *Macrotis*) from Peramelemorphia + *Notoryctes* or that for grouping the *Chaeropus* (or *Macrotis*) with/within a particular genus. We chose the more conservative exclusion from Peramelemorphia + *Notoryctes* rather than exclusion only from Peramelemorphia, to make sure that instances in which *Chaeropus* (or *Macrotis*) is in a polytomy with Peramelemorphia and *Notoryctes* were not excluded. Anomalous placements with MP bootstrap support  $\geq 95\%$  are highlighted **red** and 80-95% are highlighted **yellow**.

***Macrotis lagotis* 12S rRNA (AJ639871)**

Sites	Exclusion from Peramelemorphia + <i>Notoryctes</i> (or higher genus-level affinity)	Sister taxon (BP support given for <i>Chaeropus</i> and the named taxon)	Anomaly or notable (BP support given for <i>Macrotis</i> and the named taxon)
1-300	0% (12% with <i>Peroryctes</i> )	Peroryctinae (41%)	Clade with Peramelidae 95%
101-400	23%	Peramelidae (76%)	-
201-500	5% (34% with <i>Echymipera</i> )	Peramelidae (94%)	-
301-600	33%	Peramelidae (67%)	-
401-700	36%	Peramelidae (62%)	-
501-819	49%	Peramelidae (51%)	-

***Macrotis lagotis* 16S rRNA (AJ639871)**

Sites	Exclusion from Peramelemorphia + <i>Notoryctes</i> (or higher genus-level affinity)	Sister taxon (BP support given for <i>Chaeropus</i> and the named taxon)	Anomaly or notable (BP support given for <i>Macrotis</i> and the named taxon)
1-300	19%	Peramelidae (80%)	-
101-400	29%	Peramelidae (71%)	-
201-500	20%	Peroryctinae (56%)	-
301-600	60%	Agreodontia (51%)	Peramelemorphia inc <i>Macrotis</i> (37%)
401-700	82%	Agreodontia (63%)	Peramelemorphia inc <i>Macrotis</i> (18%)
501-800	94% (non-specific, 7% with <i>Petaurus</i> )	Diprotodontia (47%)	Peramelemorphia inc <i>Macrotis</i> (6%)
601-900	65%	Agreodontia (70%)	Peramelemorphia inc <i>Macrotis</i> (35%)
701-1000	42%	Peramelidae (57%)	-
801-1100	45%	Peramelidae (55%)	-
901-1190	14% (62% with <i>Perameles</i> )	<i>Perameles</i> (62%)	Peramelemorphia inc <i>Macrotis</i> (86%)

***Macrotis lagotis* Cytb (AJ639871) Standard nucleotide coding**

Sites	Exclusion from Peramelemorphia + <i>Notoryctes</i> (or higher genus-level affinity)	Sister taxon (BP support given for <i>Chaeropus</i> and the named taxon)	Anomaly or notable (BP support given for <i>Macrotis</i> and the named taxon)
1-300	42%	Echymiperinae (49%)	Peramelemorphia inc <i>Macrotis</i> (57%)
101-400	82%	Diprotodontia (36%)	Peramelemorphia inc <i>Macrotis</i> (18%)
201-500	88%	Agreodontia (43%)	Peramelemorphia inc <i>Macrotis</i> (12%)



301-600	96%	Eomarsupialia (51%)	Peramelemorphia inc <i>Macrotis</i> (4%)
401-700	94%	Eomarsupialia (59%)	Peramelemorphia inc <i>Macrotis</i> (5%)
501-800	72%	<i>Notoryctes</i> + all other peramelemorphians (52%)	Peramelemorphia inc <i>Macrotis</i> (17%)
601-900	70%	<i>Notoryctes</i> + all other peramelemorphians (39%)	Peramelemorphia inc <i>Macrotis</i> (27%)
701-1000	34%	Peramelidae (45%)	-
801-1140	48%	Peramelidae (50%)	-

***Macrotis lagotis* Cytb (AJ639871) RY coding 3<sup>rd</sup> codon positions**

Sites	Exclusion from Peramelemorphia + <i>Notoryctes</i> (or higher genus-level affinity)	Sister taxon (BP support given for <i>Chaeropus</i> and the named taxon)	Anomaly or notable (BP support given for <i>Macrotis</i> and the named taxon)
1-300	25% (54% with <i>Echymipera</i> )	<i>Echymipera clara</i> (52%)	Peramelemorphia inc <i>Macrotis</i> (73%)
101-400	70%	Agreodontia (43%)	Peramelemorphia inc <i>Macrotis</i> (30%)
201-500	91% (non-specific, 14% with <i>Potorous</i> )	Eomarsupialia (59%)	Peramelemorphia inc <i>Macrotis</i> (9%)
301-600	91% (non-specific, 17% with <i>Dactylopsila</i> )	Dasyuromorphia (50%)	Peramelemorphia inc <i>Macrotis</i> (9%)
401-700	90%	Eomarsupialia (62%)	Peramelemorphia inc <i>Macrotis</i> (7%)
501-800	48%	<i>Notoryctes</i> + all other peramelemorphians (50%)	Peramelemorphia inc <i>Macrotis</i> (50%)
601-900	32%	Peroryctinae (44%)	Peramelemorphia inc <i>Macrotis</i> (67%)
701-1000	52%	<i>Notoryctes</i> + all other peramelemorphians (48%)	Peramelemorphia inc <i>Macrotis</i> (48%)
801-1140	44%	Peramelidae (56%)	-

1. Despite the reduced phylogenetic signal incurred by RY coding 3<sup>rd</sup> positions, exclusion from target Peramelemorphia+*Notoryctes* falls from an average of 70% to 60%, indicating overall noise reduction or bias reduction.

***Chaeropus ecaudatus* 12S rRNA (MK359293 and MK359294)**

Sites	Exclusion from Peramelemorphia + <i>Notoryctes</i> (or higher genus-level affinity)	Sister taxon (BP support given for <i>Chaeropus</i> and the named taxon)	Anomaly or notable (BP support given for <i>Chaeropus</i> and the named taxon)
1-300	0% (17% with <i>Microperoryctes</i> )	<i>Echymipera</i> + <i>Microperoryctes</i> (40%)	Clade with Peramelidae 90%
101-400	14% (51% with <i>Peroryctes</i> )	<i>Peroryctes</i> (51%)	Clade with Peramelidae 76%
201-500	23%	Peramelidae (45%)	-
301-600	28%	Peramelidae (58%)	-
401-700	23%	All other peramelemorphians (76%)	-
501-819	6% (20% with <i>Echymipera</i> )	Peramelidae (63%)	-

***Chaeropus ecaudatus* 16S rRNA (MK359295 and MK359296)**

Sites	Exclusion from Peramelemorphia + <i>Notoryctes</i> (or higher genus-level affinity)	Sister taxon (BP support given for <i>Chaeropus</i> and the named taxon)	Anomaly or notable (BP support given for <i>Chaeropus</i> and the named taxon)
1-300	13% (17% with <i>Peroryctes</i> )	All other peramelemorphians (87%)	-
101-400	3% (14% with <i>Macrotis</i> )	All other peramelemorphians (94%)	-
201-500	5% (58% with <i>Echymipera</i> )	<i>Echymipera</i> (58%)	Clade with Peramelidae 63%
301-600	4% (34% with <i>Echymipera</i> )	Peroryctinae + Echymiperinae (50%)	Clade with Peramelidae 51%

401-700	1% (47% with <i>Isoodon</i> )	<i>Isoodon</i> (47%)	Clade with Peramelidae 94%
501-800	0% (54% with <i>Isoodon</i> )	<i>Isoodon</i> (54%)	Clade with Peramelidae 100%; with Peramelinae 87%
601-900	0% (43% with <i>Isoodon</i> )	<i>Isoodon</i> (43%)	Clade with Peramelidae 100%; with Peramelinae 77%
701-1000	1% (32% with <i>Perameles</i> )	Peramelinae (58%)	Clade with Peramelidae 85%
801-1100	7% (28% with <i>Perameles</i> )	Peramelinae (58%)	Clade with Peramelidae 81%
901-1190	13% (28% with <i>Perameles</i> )	Peramelinae (47%)	Clade with Peramelidae 70%

***Chaeropus ecaudatus* Cytb** (MK359297 and MK359298) Standard nucleotide coding

Sites	Exclusion from Peramelemorphia + <i>Notoryctes</i> (or higher genus-level affinity)	Sister taxon (BP support given for <i>Chaeropus</i> and the named taxon)	Anomaly or notable (BP support given for <i>Chaeropus</i> and the named taxon)
1-300	66%	Eomarsupialia (47%)	Excluded from Peramelemorphia also 66%
101-400	73%	Dasyuromorphia (43%)	Excluded from Peramelemorphia 74%
201-500	68%	Eomarsupialia (52%)	Excluded from Peramelemorphia 70%
301-600	34%	Peramelidae (58%)	Clade with all other peramelemorphians (62%)
401-700	42%	Peramelidae (57%)	Clade with all other peramelemorphians (58%)
501-853	47%	All other peramelemorphians (52%)	-

***Chaeropus ecaudatus* Cytb** (MK359297 and MK359298) **RY coding** 3<sup>rd</sup> codon positions

Sites	Exclusion from Peramelemorphia + <i>Notoryctes</i> (or higher genus-level affinity) <sup>1</sup>	Sister taxon (BP support given for <i>Chaeropus</i> and the named taxon)	Anomaly or notable (BP support given for <i>Chaeropus</i> and the named taxon)
1-300	30%	Peroryctinae (59%)	Clade with Peramelidae 65%
101-400	44%	Agreodontia (50%)	-
201-500	24% (27% with <i>Echymipera</i> )	Peramelidae (62%)	-
301-600	44%	All other peramelemorphians (54%)	-
401-700	35%	Peroryctinae (50%)	Clade with Peramelidae 63%
501-853	30%	Eomarsupialia (57%)	-

1. Despite the reduced phylogenetic signal incurred by RY coding 3<sup>rd</sup> positions, exclusion from target Peramelemorphia+*Notoryctes* falls from an average of 55% to 35%, indicating overall noise reduction or bias reduction.

***Chaeropus yirratji* 12S rRNA** (AF131247)

Sites	Exclusion from Peramelemorphia + <i>Notoryctes</i> (or higher genus-level affinity)	Sister taxon (BP support given for <i>Chaeropus</i> and the named taxon)	Anomaly or notable (BP support given for <i>Chaeropus</i> and the named taxon)
1-300	100%	<i>Potorous longipes</i> (71%)	Clade with <i>Potorous</i> 96%
101-400	100%	<i>Potorous</i> (51%)	Clade with Diprotodontia 92%
201-500	44% (14% with <i>Microperoryctes</i> )	All other peramelemorphians (56%)	-
301-600	3% (34% with <i>Macrotis</i> )	All other peramelemorphians (97%)	-
401-700	0% (42% with <i>Macrotis</i> )	All other peramelids (43%)	-
501-819	1% (48% with <i>Macrotis</i> )	<i>Macrotis lagotis</i> (48%)	-

***Chaeropus yirratji* 16S rRNA (JF706364)**

Sites	Exclusion from Peramelemorphia + <i>Notoryctes</i> (or higher genus-level affinity)	Sister taxon (BP support given for <i>Chaeropus</i> and the named taxon)	Anomaly or notable (BP support given for <i>Chaeropus</i> and the named taxon)
1-300	16% (34% with <i>Perameles</i> )	All other peramelemorphians (74%)	-
101-400	3% (61% with <i>Perameles</i> )	<i>Perameles nasuta</i> (58%)	Clade with Peramelidae 88%
201-490	41%	All other peramelemorphians (49%)	-

***Chaeropus yirratji* Cytb (JF718363) Standard nucleotide coding**

Sites	Exclusion from Peramelemorphia + <i>Notoryctes</i> (or higher genus-level affinity)	Sister taxon (BP support given for <i>Chaeropus</i> and the named taxon)	Anomaly or notable (BP support given for <i>Chaeropus</i> and the named taxon)
1-300	100%	<i>Sminthopsis youngsoni</i> + <i>S. ooldea</i> (100%)	Nested within <i>Sminthopsis</i>
101-400	96%	<i>Sminthopsis youngsoni</i> + <i>S. ooldea</i> (95%)	Nested within <i>Sminthopsis</i>
201-547	84%	Dasuromorphia (43%)	-

***Chaeropus yirratji* Cytb (JF718363) RY coding 3<sup>rd</sup> codon positions**

Sites	Exclusion from Peramelemorphia + <i>Notoryctes</i> (or higher genus-level affinity)	Sister taxon (BP support given for <i>Chaeropus</i> and the named taxon)	Anomaly or notable (BP support given for <i>Chaeropus</i> and the named taxon)
1-300	100%	<i>Sminthopsis youngsoni</i> + <i>S. ooldea</i> (100%)	Nested within <i>Sminthopsis</i>
101-400	96%	<i>Sminthopsis youngsoni</i> + <i>S. ooldea</i> (92%)	Nested within <i>Sminthopsis</i>
201-547	53%	<i>Notoryctes</i> + all other peramelemorphians (46%)	-

**Table S5.** Maximum likelihood hypothesis testing for the placement of *Chaeropus* with the MtNuc<sub>26</sub> data under the favoured treatment, with *Cytb* 3<sup>rd</sup> codon positions RY coded. Partitioning and models as given in Table S1. The favoured  $-\ln L$  (or difference from the best tree) are shown along with RELL bootstrap and the approximately unbiased test p-value.

<i>Chaeropus</i> placement	$-\ln L$ (or $\Delta$ )	BP-RELL	AU p-value
Sister to Peramelemorphia	8.11	0.157	0.199
Sister to Peramelidae	< 43067.41 >	0.819	—
Sister to <i>Macrotis</i>	11.42	0.011	0.030
Sister to <i>Perameles</i>	45.60	0.000	<0.001
Sister to <i>Isoodon</i>	42.69	0.000	<0.001
Sister to Peramelinae	19.28	0.002	0.010
Sister to Peroryctinae <sup>^</sup>	18.46	0.010	0.018

<sup>^</sup>Considered here as *Peroryctes*, *Microperoryctes*, *Echymipera* (and *Rhynchomeles*, which was not included in MtNuc<sub>26</sub> due to missing data)

**Table S6.** Foraging ecospace among Australidelphian marsupial genera. Foraging height categories: (0) fossorial, (1) semi-fossorial, (2) terrestrial, (3) mostly terrestrial but some arboreal foraging, (4) scansorial, (5) arboreal. Diet categories: (0) herbivorous, (1) plant-specialized omnivorous, (2) generalized omnivorous, (3) animalivorous. Marsupials that rarely (e.g. only opportunistically) eat animals are regarded here as herbivorous. Similarly, Marsupials that occasionally eat plant material, but for which it is not a key dietary component are regarded here as animalivorous. The distinction between the two omnivore categories is between plant-specialized omnivores with a plant dietary component requiring more specialization for tough, fibrous or abrasive material, such as harder seeds/nuts, grasses and certain fungi, and generalized omnivores with less specialization for such foods. The former tend to have molars with more grinding or horizontal shear and the latter tend to have molars with more vertical shear and piercing cusps. Note that *Dromicops* was not included in Figure 6A, because its distribution does not include Australia, New Guinea or surrounding islands. Scoring for diet and foraging height is primarily drawn from [5-7]. Inconsistencies and uncertainty are retained in the scoring as variation or resolved in accordance with primary literature and personal observations (MJP).

Taxon	Foraging height	Notes	Diet	Notes
<a href="#">Microbiotheria</a> <i>Dromicops</i>	5 (4?)	Mainly arboreal foraging, but uncertain. Sometimes on ground, including collecting nest grass.	2	Mainly invertebrates, but many fruits in summer. Important seed dispersers [8]
<a href="#">Notoryctemorphia</a> <i>Notoryctes</i>	0		3	Some suggestions of seeds also in diet, but likely incidental?
<a href="#">Peramelemorphia</a> <i>Chaeropus</i> <i>Echymipera</i>	1 or 2 1-1.5?	See main text Many above ground fruits/seeds suggest 1-1.5.	0 or 1 2	See main text
<i>Isoodon</i>	1		2-2.5	Mostly generalized omnivores. Some more animalivorous (hence 2-2.5)
<i>Macrotis</i>	1		2	
<i>Microperoryctes</i>	1		2-2.5	Mostly generalized omnivores. Some more animalivorous (hence 2-2.5)
<i>Perameles</i>	1		2-2.5	Mostly generalized omnivores. Some more animalivorous (hence 2-2.5)
<i>Peroryctes</i>	1		2	
<a href="#">Dasyuromorphia</a> <i>Antechinomys</i>	2		3	
<i>Antechinus</i>	1.5-3.5	Most 3. <i>Swainsonii</i> group tends to be mixed scratch diggers/terrestrial (1.5). <i>leo</i> and maybe <i>godmani</i> 3.5	3	Some plant material, but a minor component.
<i>Dasyercus</i>	2		3	
<i>Dasykaluta</i>	2		3	Some plant material, but a minor component.[9]



<i>Dasyuroides</i>	2	Seen climbing, but seems to be a terrestrial forager	3	
<i>Dasyurus</i>	2-3.5	Varies from <i>viverrinus</i> (2) to <i>albopunctatus</i> & <i>maculatus</i> (3.5)	3	Some plant material, but a minor component.
<i>Murexia</i>	3-4	Several spp. (4), <i>habbema</i> (3)	3	
<i>Myoictis</i>	2-3	Wooley [10] suggests most largely terrestrial, <i>wavicus</i> some arboreal foraging	3	
<i>Myrmecobuius</i>	1		3	
<i>Neophascogale</i>	1.5-4	Considerable uncertainty. Claws adapted for climbing and digging? Seen on ground and in trees – but foraging?	3	
<i>Ningau</i>	3	Tail semi-prehensile	3	
<i>Parantechinus</i>	3		2.5	20% diet fruit and nectar
<i>Phascogale</i>	4-4.5	<i>calura</i> (4), <i>tapoatafa</i> (4.5)	3	Occasional nectar
<i>Phascosorex</i>	2	More information required (maybe 3?) [11]	3	
<i>Pseudantechinus</i>	2		3	
<i>Sarcophilus</i>	2	Juveniles climb more, but little foraging	3	Some plant material, but a minor component.
<i>Sminthopsis</i>	2		3	
<i>Thylacinus</i>	2		3	
<b>Diprotodontia</b>				
<i>Acrobates</i>	5	Some ground feeding observed but typical behaviour and adaptation highly arboreal	2	
<i>Ailurops</i>	5		0	
<i>Aepyprymnus</i>	1		0-1 (0.5?)	Digs for larvae – invertebrates some importance, but less so than others given (1)
<i>Bettongia</i>	1-1.5	Most spp. (1). <i>lesueur</i> sometimes even climbs into low shrubs for food, but predominantly semi-fossorial/terrestrial foraging	0.5-1	Most spp. (1), <i>lesueur</i> more herbivorous, still some animalivory (e.g. termites)
<i>Burramys</i>	3		1	(1) rather than (2), given specialized plagiaulacoid premolars, hard seeds etc.
<i>Caloprymnus</i>	1?		0.5 or 1?	Poorly known
<i>Cercartetus</i>	4-5	Spp. vary from scansorial (4) to predominantly arboreal (5)	2	
<i>Dactylopsila</i>	5		2-2.5?	<i>D. palpator</i> may be more predominantly animalivorous than <i>D. trivirgata</i>
<i>Dendrolagus</i>	3-4.5	<i>dorianus</i> , <i>mbaiso</i> , <i>scottae</i> mainly terrestrial	0	Reports of opportunistic animalivory, but minor component
<i>Distoechurus</i>	5		2	
<i>Dorcopsis</i>	2?	More information required, some reports of turning over stones for insects	0-0.5?	More information required, some reports of turning over stones for insects
<i>Dorcopsulus</i>	2?	More information required	0?	

<i>Gymnobelidius</i>	5		2	
<i>Hemibelideus</i>	5		0	
<i>Hypsiprymnodon</i>	1	Substantial leaf litter/surface foraging as well as shallow digging (could be 1.5?)	1	Importance of seeds, related herbivory dental adaptations and perhaps less importance on animals places diet at (1) or possibly (1.5?) relative to most bandicoots at (2) [12]
<i>Lagorchestes</i>	2		0	
<i>Lagostrophus</i>	2		0	
<i>Lasiorhinus</i>	2	Burrow, but foraging is mostly terrestrial	0	
<i>Macropus</i>	2		0	
<i>Notamacropus</i>	2		0	
<i>Onychogalea</i>	2		0	
<i>Osphranter</i>	2		0	
<i>Petauroides</i>	5		0	
<i>Petaurus</i>	5		2	
<i>Petrogale</i>	2	Some foraging in low trees, but predominantly terrestrial	0	
<i>Petropseudes</i>	5	Terrestrial (rock shelter) much of time, but foraging is almost exclusively arboreal	0	Occasionally observed feeding on termites, but a minor component
<i>Phalanger</i>	5	<i>gymnotis</i> tends to nest in terrestrial dens but forages mostly in trees	0-0.5	At least <i>gymnotis</i> eats eggs and preys on live rats and lizards in captivity
<i>Phascolarctos</i>	5		0	
<i>Potorous</i>	1		1	
<i>Pseudocheirus</i>	5		0	
<i>Pseudochirops</i>	5		0	
<i>Pseudochirulus</i>	5		0	
<i>Setonix</i>	2	Can climb to get food - up to 1.5m. Too poorly adapted and too little climbing to be comparable to other taxa listed as (3). A possibility is (2.5)	0	
<i>Spilocuscus</i>	5		0-0.5	<i>rufoniger</i> and <i>maculatus</i> both omnivorous to some extent – uncertain whether sub-herv (still 0) or 0.5 perhaps moreso for <i>maculatus</i>
<i>Strigocuscus</i>	5		0	
<i>Tarsipes</i>	5		0 (?)	Purely nectar and pollen (so herbivory distinct from other marsupials, likely derived from (3), perhaps treated as ?
<i>Thylogale</i>	2		0	Occasional animalivory (e.g. <i>stigmatica</i> ), but a minor component
<i>Trichosurus</i>	4		0	Sub-herbivorous, some argument for (0.5)
<i>Wallabia</i>	2		0	
<i>Wyulda</i>	4		0	
<i>Vombatus</i>	2	Burrow, but foraging is mostly terrestrial	0	

**Table S7.** Body mass of hopping mammals averaged over adult males and females. The principal source is the PanTHERIA dataset Jones et al. [13]. Body mass of additional taxa was included from the primary literature, with the reference list available upon request to the corresponding author. Mass of recently extinct species is included only if estimates unambiguously fall within one of the time bins used in Figure 6B.

Family	Species	Body mass (g)	Family	Species	Body mass (g)
(Marsupials)			(Rodents)		
Macropodidae	<i>Dendrolagus bennettianus</i>	10473.9	Dipodidae	<i>Allactaga balikunica</i>	72.5
Macropodidae	<i>Dendrolagus dorianus</i>	8976.4	Dipodidae	<i>Allactaga bullata</i>	87
Macropodidae	<i>Dendrolagus goodfellowi</i>	7954.6	Dipodidae	<i>Allactaga elater</i>	60
Macropodidae	<i>Dendrolagus inustus</i>	12626	Dipodidae	<i>Allactaga euphratica</i>	90
Macropodidae	<i>Dendrolagus matschiei</i>	8425.1	Dipodidae	<i>Allactaga firouzi</i>	98.6
Macropodidae	<i>Dendrolagus mbaiso</i>	9405.6	Dipodidae	<i>Allactaga hotsoni</i>	76.5
Macropodidae	<i>Dendrolagus lumholtzi</i>	6651.0	Dipodidae	<i>Allactaga major</i>	350
Macropodidae	<i>Dendrolagus pulcherrimus</i>	7400	Dipodidae	<i>Allactaga severtzovi</i>	159
Macropodidae	<i>Dendrolagus scottae</i>	9958.2	Dipodidae	<i>Allactaga sibirica</i>	117.5
Macropodidae	<i>Dendrolagus spadix</i>	8490.6	Dipodidae	<i>Allactaga tetradactyla</i>	53.0
Macropodidae	<i>Dendrolagus stellarum</i>	7674.4	Dipodidae	<i>Allactaga vinogradovi</i>	58.7
Macropodidae	<i>Dendrolagus ursinus</i>	13251	Dipodidae	<i>Allactaga williamsi</i>	232
Macropodidae	<i>Dorcopsis atrata</i>	6206.2	Dipodidae	<i>Allactodipus bobrinskii</i>	65
Macropodidae	<i>Dorcopsis hageni</i>	5501	Dipodidae	<i>Cardiocranius paradoxus</i>	196.8
Macropodidae	<i>Dorcopsis luctuosa</i>	5098.8	Dipodidae	<i>Dipus sagitta</i>	90
Macropodidae	<i>Dorcopsis muelleri</i>	5375.1	Dipodidae	<i>Eremodipus lichtensteini</i>	51
Macropodidae	<i>Dorcopsulus macleayi</i>	2788.5	Dipodidae	<i>Euchoreutes naso</i>	24.1
Macropodidae	<i>Dorcopsulus vanheurni</i>	1894.3	Dipodidae	<i>Jaculus blanfordi</i>	54.7
Macropodidae	<i>Lagorchestes asomatus</i>	1501	Dipodidae	<i>Jaculus jaculus</i>	60.9
Macropodidae	<i>Lagorchestes conspicillatus</i>	2832.7	Dipodidae	<i>Jaculus orientalis</i>	139.3
Macropodidae	<i>Lagorchestes hirsutus</i>	1409.1	Dipodidae	<i>Paradipus ctenodactylus</i>	109
Macropodidae	<i>Lagorchestes leporides</i>	3001	Dipodidae	<i>Pygeretmus platyurus</i>	26.4
Macropodidae	<i>Lagostrophus fasciatus</i>	1935.7	Dipodidae	<i>Pygeretmus pumilio</i>	53.2
Macropodidae	<i>Macropus fuliginosus</i>	25842.0	Dipodidae	<i>Pygeretmus zhitkovi</i>	56.5
Macropodidae	<i>Macropus giganteus</i>	33432.7	Dipodidae	<i>Salpingotulus michaelis</i>	3.9
Macropodidae	<i>Notamacropus agilis</i>	11823.9	Dipodidae	<i>Salpingotus crassicauda</i>	12
Macropodidae	<i>Notamacropus dorsalis</i>	11251.0	Dipodidae	<i>Salpingotus heptneri</i>	9.6
Macropodidae	<i>Notamacropus eugenii</i>	5283.6	Dipodidae	<i>Salpingotus kozlovi</i>	9.5
Macropodidae	<i>Notamacropus rufogriseus</i>	16755.8	Dipodidae	<i>Salpingotus pallidus</i>	9
Macropodidae	<i>Notamacropus greyi</i>	10001	Dipodidae	<i>Salpingotus thomasi</i>	3.9
Macropodidae	<i>Notamacropus irma</i>	8001.0	Dipodidae	<i>Stylodipus andrewsi</i>	57.5
Macropodidae	<i>Notamacropus parma</i>	4157.0	Dipodidae	<i>Sicista armenica</i>	6.5
Macropodidae	<i>Notamacropus parryi</i>	12662.5	Dipodidae	<i>Sicista betulina</i>	10.0
Macropodidae	<i>Onychogalea fraenata</i>	4957.3	Dipodidae	<i>Sicista caucasica</i>	10
Macropodidae	<i>Onychogalea lunata</i>	3501	Dipodidae	<i>Sicista caudata</i>	8
Macropodidae	<i>Onychogalea unguifera</i>	6494.8	Dipodidae	<i>Sicista concolor</i>	6.5
Macropodidae	<i>Osphranter antilopinus</i>	27251.1	Dipodidae	<i>Sicista kazbegica</i>	7
Macropodidae	<i>Osphranter bernardus</i>	17001	Dipodidae	<i>Sicista kluchorica</i>	7.5
Macropodidae	<i>Osphranter robustus</i>	25976.6	Dipodidae	<i>Sicista napaea</i>	11

Macropodidae	<i>Osphranter rufus</i>	38964.5	Dipodidae	<i>Sicista pseudonapaea</i>	7.3
Macropodidae	<i>Petrogale assimilis</i>	4622.7	Dipodidae	<i>Sicista severtzovi</i>	11.7
Macropodidae	<i>Petrogale brachyotis</i>	4014.4	Dipodidae	<i>Sicista strandi</i>	8.9
Macropodidae	<i>Petrogale burbidgei</i>	1259	Dipodidae	<i>Sicista subtilis</i>	12.7
Macropodidae	<i>Petrogale coenensis</i>	4375	Dipodidae	<i>Stylodipus sungorus</i>	76.9
Macropodidae	<i>Petrogale concinna</i>	1399.6	Dipodidae	<i>Stylodipus telum</i>	61.0
Macropodidae	<i>Petrogale godmani</i>	4751	Dipodidae	<i>Sicista tianshanica</i>	11.5
Macropodidae	<i>Petrogale herberti</i>	6465.8	Heteromyidae	<i>Dipodomys agilis</i>	61.2
Macropodidae	<i>Petrogale inornata</i>	4558.1	Heteromyidae	<i>Dipodomys californicus</i>	86.0
Macropodidae	<i>Petrogale lateralis</i>	4570.6	Heteromyidae	<i>Dipodomys compactus</i>	50.2
Macropodidae	<i>Petrogale mareeba</i>	4150	Heteromyidae	<i>Dipodomys deserti</i>	108.7
Macropodidae	<i>Petrogale penicillata</i>	6936.7	Heteromyidae	<i>Dipodomys elator</i>	112.0
Macropodidae	<i>Petrogale persephone</i>	5590.0	Heteromyidae	<i>Dipodomys elephantinus</i>	85.9
Macropodidae	<i>Petrogale purpureicollis</i>	5283.9	Heteromyidae	<i>Dipodomys gravipes</i>	85.0
Macropodidae	<i>Petrogale rothschildi</i>	4546.6	Heteromyidae	<i>Dipodomys heermanni</i>	64.1
Macropodidae	<i>Petrogale sharmani</i>	4250	Heteromyidae	<i>Dipodomys ingens</i>	114.7
Macropodidae	<i>Petrogale xanthopus</i>	8501	Heteromyidae	<i>Dipodomys merriami</i>	38.9
Macropodidae	<i>Setonix brachyurus</i>	3033.3	Heteromyidae	<i>Dipodomys microps</i>	57.3
Macropodidae	<i>Thylogale billardieri</i>	5876.4	Heteromyidae	<i>Dipodomys nelsoni</i>	88.9
Macropodidae	<i>Thylogale browni</i>	5479	Heteromyidae	<i>Dipodomys nitratooides</i>	42.6
Macropodidae	<i>Thylogale thetis</i>	5401	Heteromyidae	<i>Dipodomys ordii</i>	51.4
Macropodidae	<i>Thylogale lanatus</i>	5316.1	Heteromyidae	<i>Dipodomys panamintinus</i>	74.7
Macropodidae	<i>Thylogale brunii</i>	4796	Heteromyidae	<i>Dipodomys phillipsii</i>	42
Macropodidae	<i>Thylogale stigmatica</i>	4515.2	Heteromyidae	<i>Dipodomys simulans</i>	57.5
Macropodidae	<i>Thylogale calabyi</i>	4326.1	Heteromyidae	<i>Dipodomys spectabilis</i>	125.6
Macropodidae	<i>Wallabia bicolor</i>	15001	Heteromyidae	<i>Dipodomys stephensi</i>	69.5
Potoroidae	<i>Aepyprymnus rufescens</i>	2815.9	Heteromyidae	<i>Dipodomys venustus</i>	82.6
Potoroidae	<i>Bettongia gaimardi</i>	1686.1	Heteromyidae	<i>Microdipodops megacephalus</i>	13.3
Potoroidae	<i>Bettongia lesueur</i>	1449.7	Heteromyidae	<i>Microdipodops pallidus</i>	14.3
Potoroidae	<i>Bettongia penicillata</i>	1191.4	Zapodidae	<i>Eozapus setchuanus</i>	32.6
Potoroidae	<i>Bettongia tropica</i>	1258.4	Zapodidae	<i>Napaeozapus insignis</i>	23.2
Potoroidae	<i>Caloprymnus campestris</i>	929.3	Zapodidae	<i>Zapus hudsonius</i>	19.43
Potoroidae	<i>Potorous gilbeti</i>	1573	Zapodidae	<i>Zapus princeps</i>	28.23
Potoroidae	<i>Potorous longipes</i>	1837.7	Zapodidae	<i>Zapus trinotatus</i>	28.45
Potoroidae	<i>Potorous tridactylus</i>	1057.6	Muridae	<i>Notomys longicaudatus</i>	101
			Muridae	<i>Notomys alexis</i>	33.3
			Muridae	<i>Notomys amplus</i>	91
			Muridae	<i>Notomys aquilo</i>	40
			Muridae	<i>Notomys cervinus</i>	35.8
			Muridae	<i>Notomys fuscus</i>	40.4
			Muridae	<i>Notomys macrotis</i>	91
			Muridae	<i>Notomys mitchellii</i>	43.8
			Muridae	<i>Notomys mordax</i>	91
			Pedetidae	<i>Pedetes capensis</i>	2551.6
			Pedetidae	<i>Pedetes surdaster</i>	2774.6

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