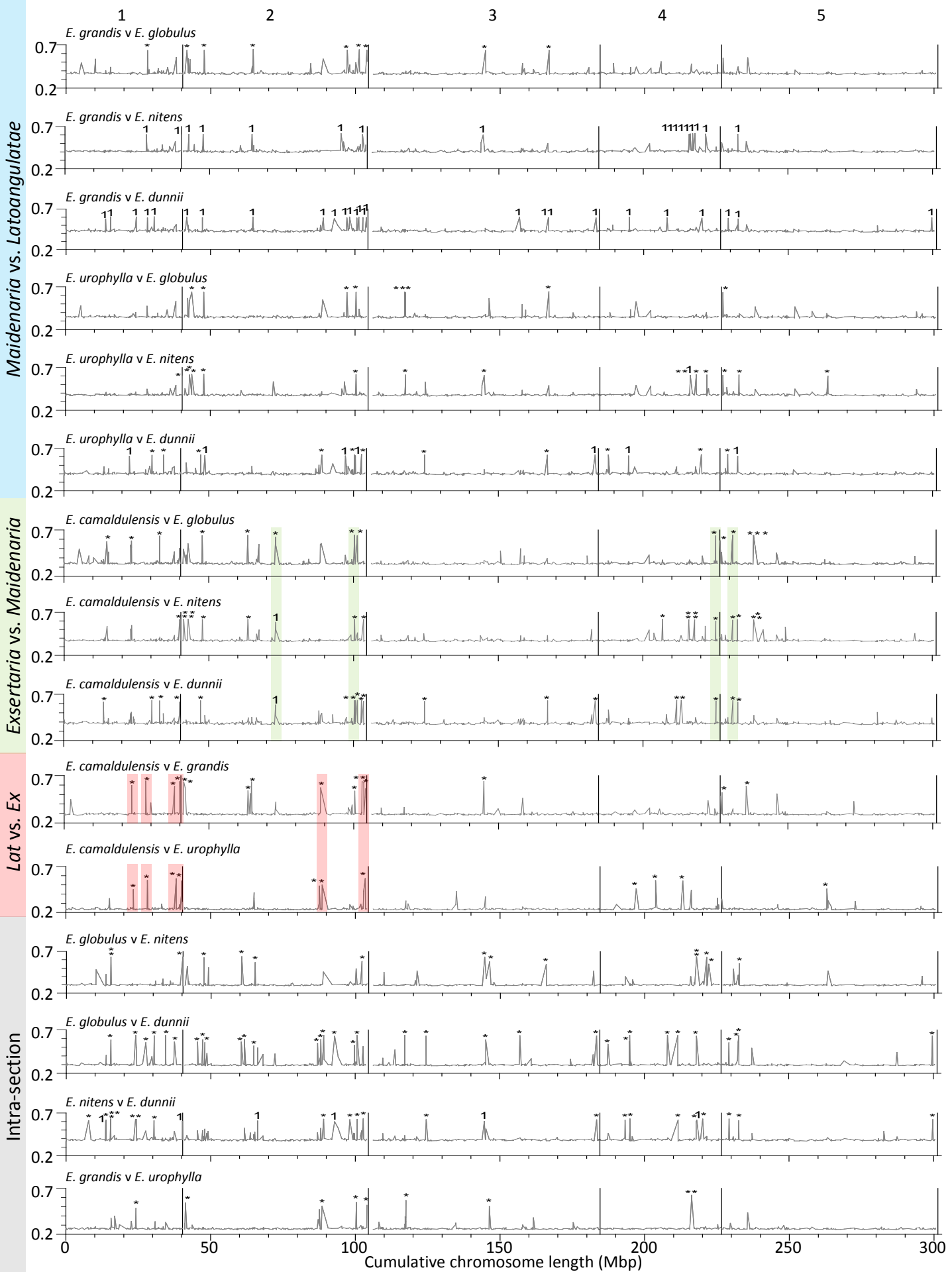


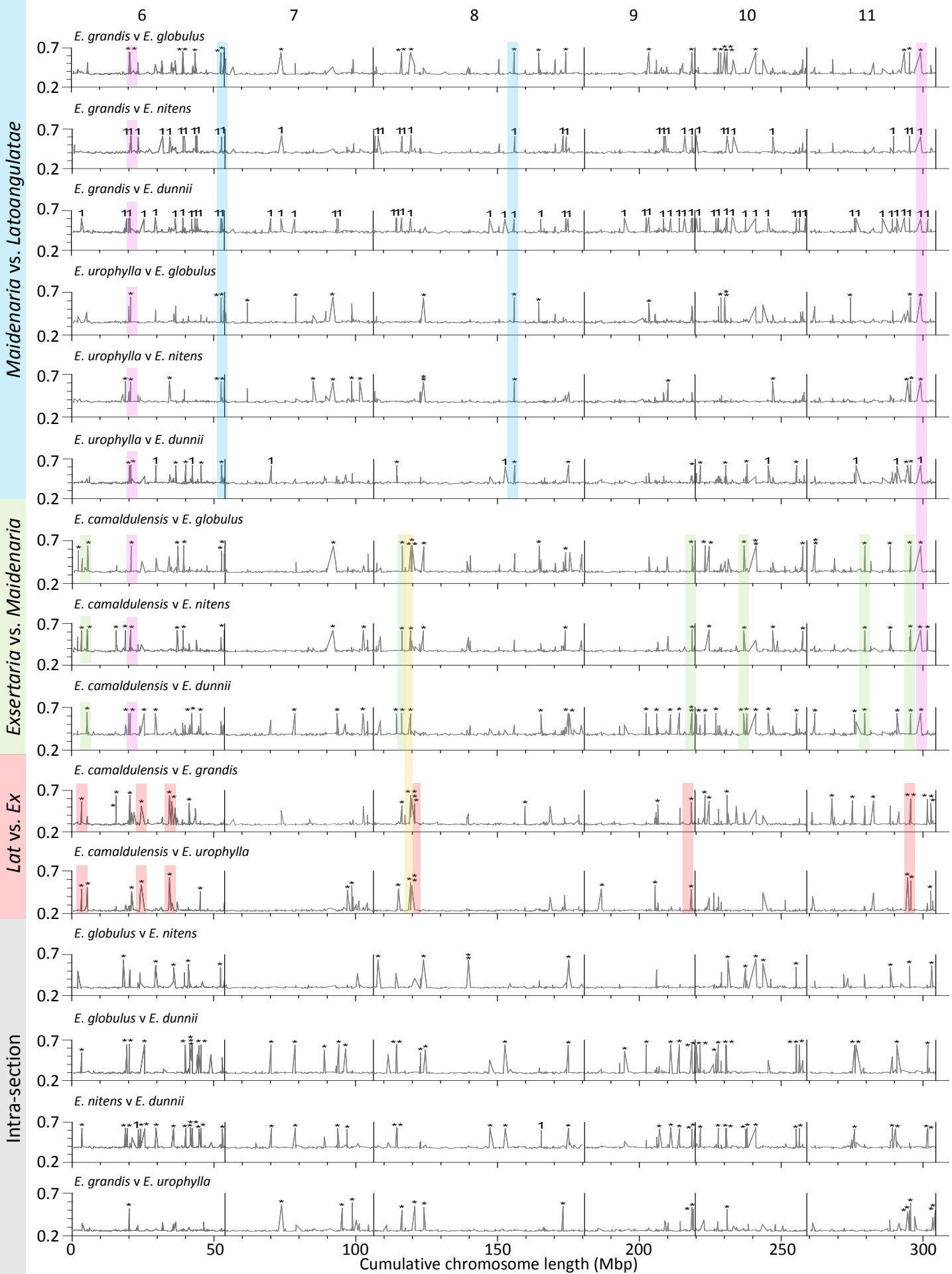
Supporting Information Figs S1-S6, Tables S1-S7, Notes S1.

Article title: Genomic patterns of species diversity and divergence in *Eucalyptus*

Authors: Corey J Hudson, Jules S Freeman, Alexander A Myburg, Brad M Potts,
and René E Vaillancourt

Following pages: Supporting Information Fig. S1 Genome-wide patterns of differentiation between six species of *Eucalyptus*. Marker F_{ST} estimates (y-axis) are plotted on the 11 eucalypt chromosomes for each of 15 pair-wise species comparisons. Graphs are grouped by intra- and inter-section comparisons as indicated on the left page margin. Chromosome numbers are given at the top of each page with black vertical lines on individual graphs indicating chromosome boundaries. Species differentiating markers (SDMs) are indicated by asterisk symbols (significant outlier marker) and '1' symbols (markers with fixed differences but not detected as an outlier marker). Section differentiating markers (SEDMs) are highlighted using the same colour coding used to indicate section comparisons. Additionally, SEDMs which differentiated, 1) section *Maidenaria* species from both *Latoangulatae* (*Lat*) and *Exsertaria* (*Ex*) species, and 2) section *Exsertaria* species from both *Maidenaria* and *Latoangulatae* species are highlighted in pink and orange, respectively.

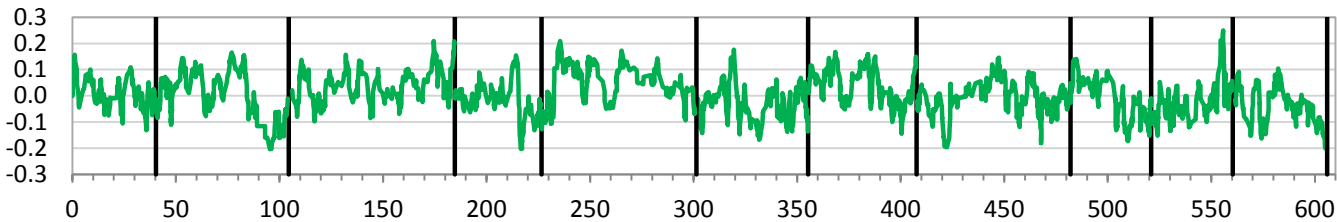




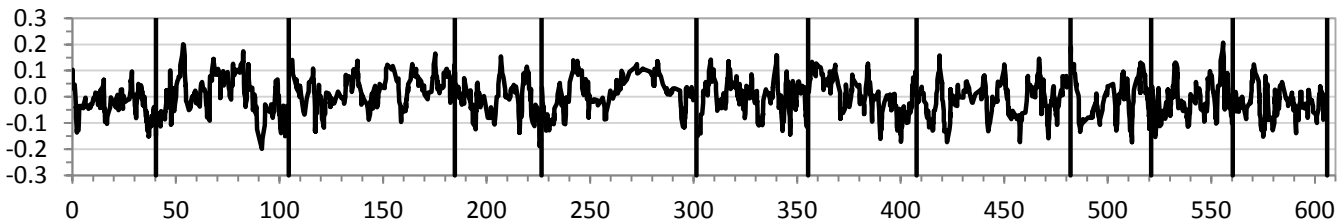
Following page: Supporting Information Fig. S2 Genome-wide patterns of genetic diversity for six eucalypt species. An 11 marker running average of standardised H_{HW} is plotted for 2408 marker estimates. The x -axis indicates cumulative chromosome positions in million base-pairs, black vertical lines indicate chromosome boundaries.

1 2 3 4 5 6 7 8 9 10 11

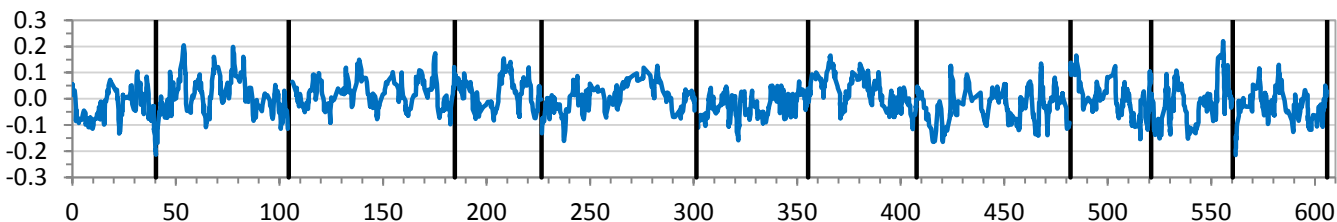
E. grandis



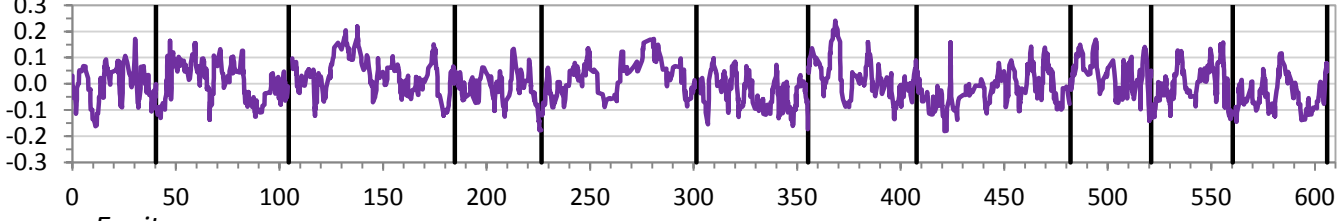
E. urophylla



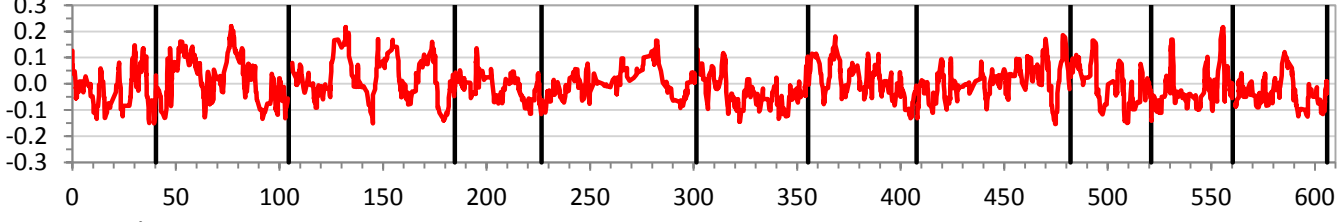
E. camaldulensis



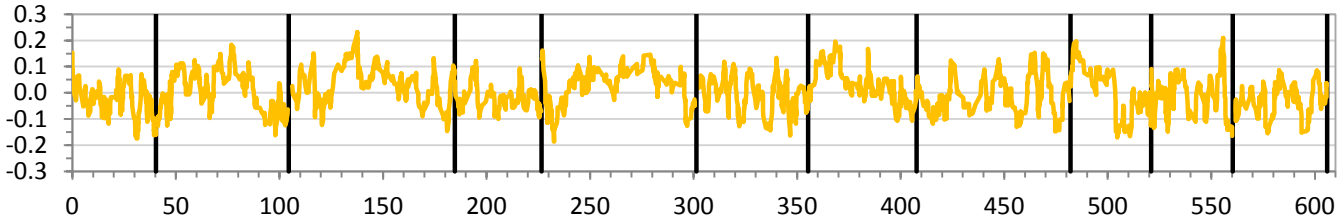
E. globulus



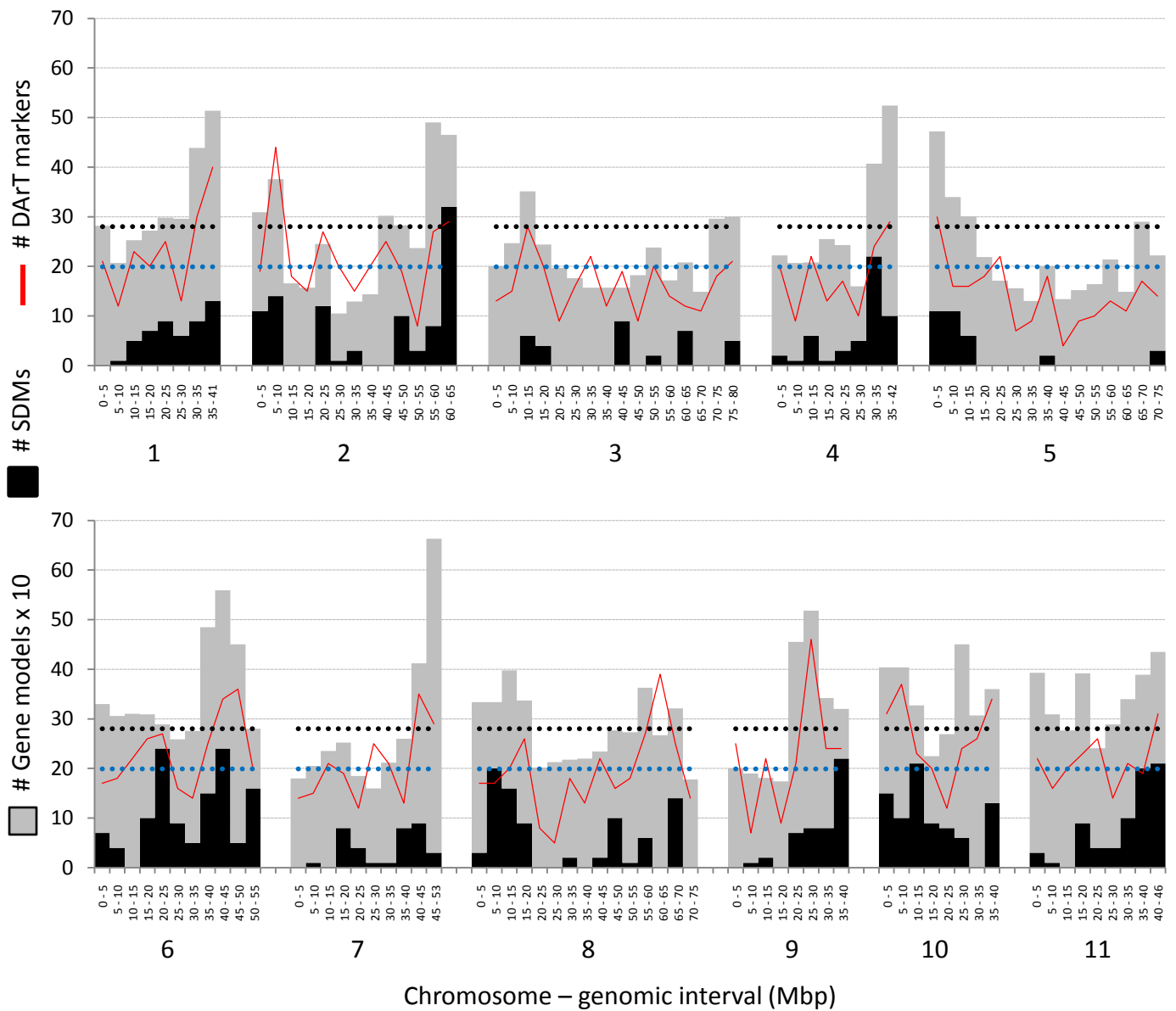
E. nitens



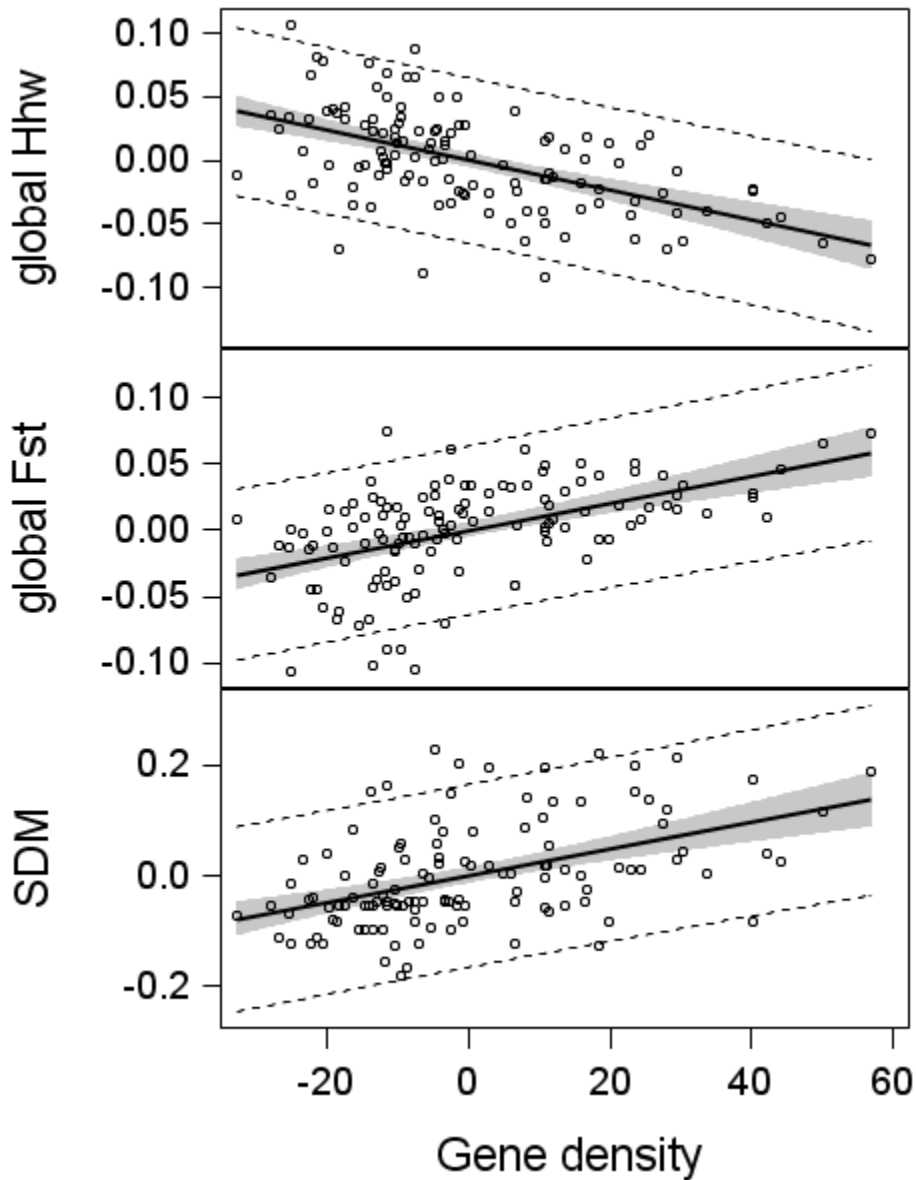
E. dunnii



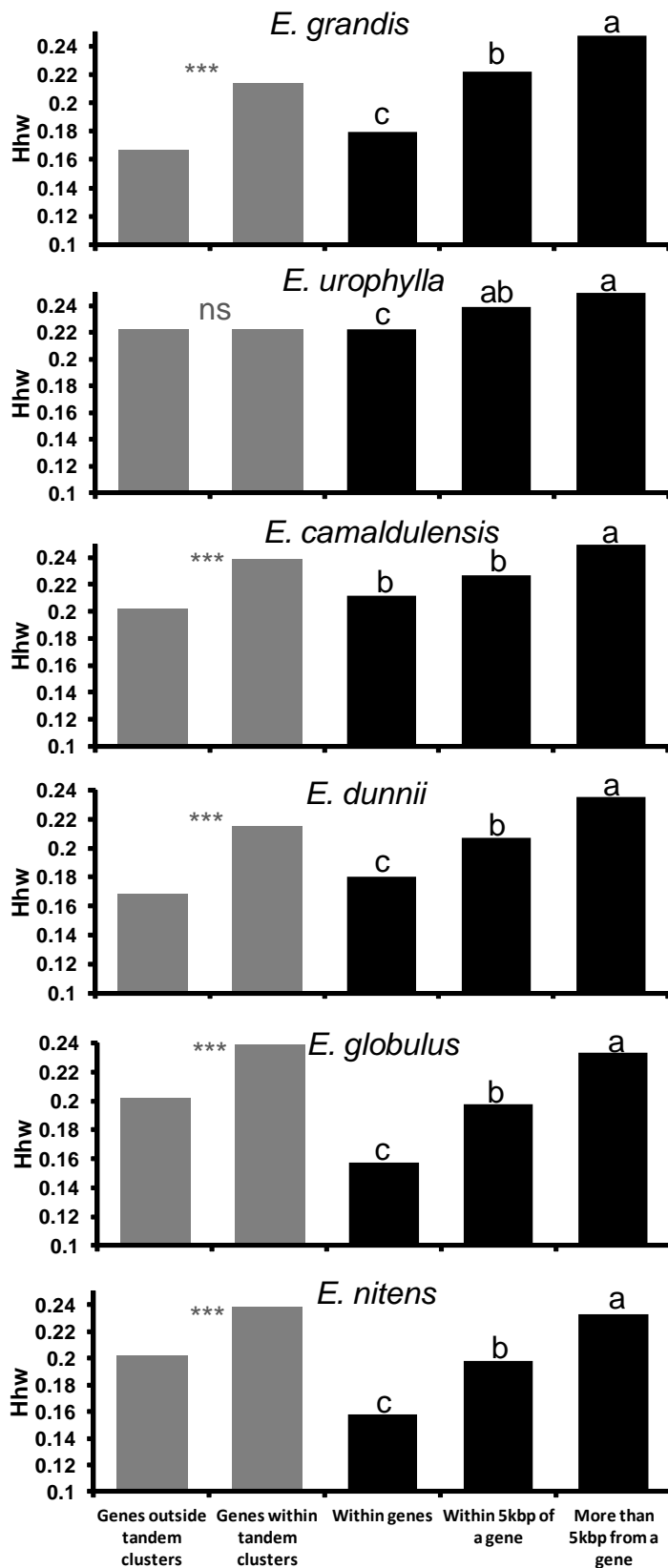
Cumulative base-pair position (Mbp)



Supporting Information Fig. S3 Genome-wide relationship between predicted gene models in the *Eucalyptus grandis* genome, annotated DArT markers of this study and detected species differentiating markers (SDMs). The 11 chromosomes of the *Eucalyptus grandis* genome were partitioned into 122 bins of (mostly) 5 Mbp, but the last two bins of chromosome 7 were combined for plotting (45 to 52.5 Mbp). For each bin, the number of predicted gene models ($\times 10$; gray bars), annotated DArT markers of this study (2408 markers; red line) and total number of SDMs detected across all pair-wise comparisons (black bars) were plotted. The average ‘per bin’ number of gene models ($\times 10$) and annotated markers are indicated by dashed black and blue lines, respectively.

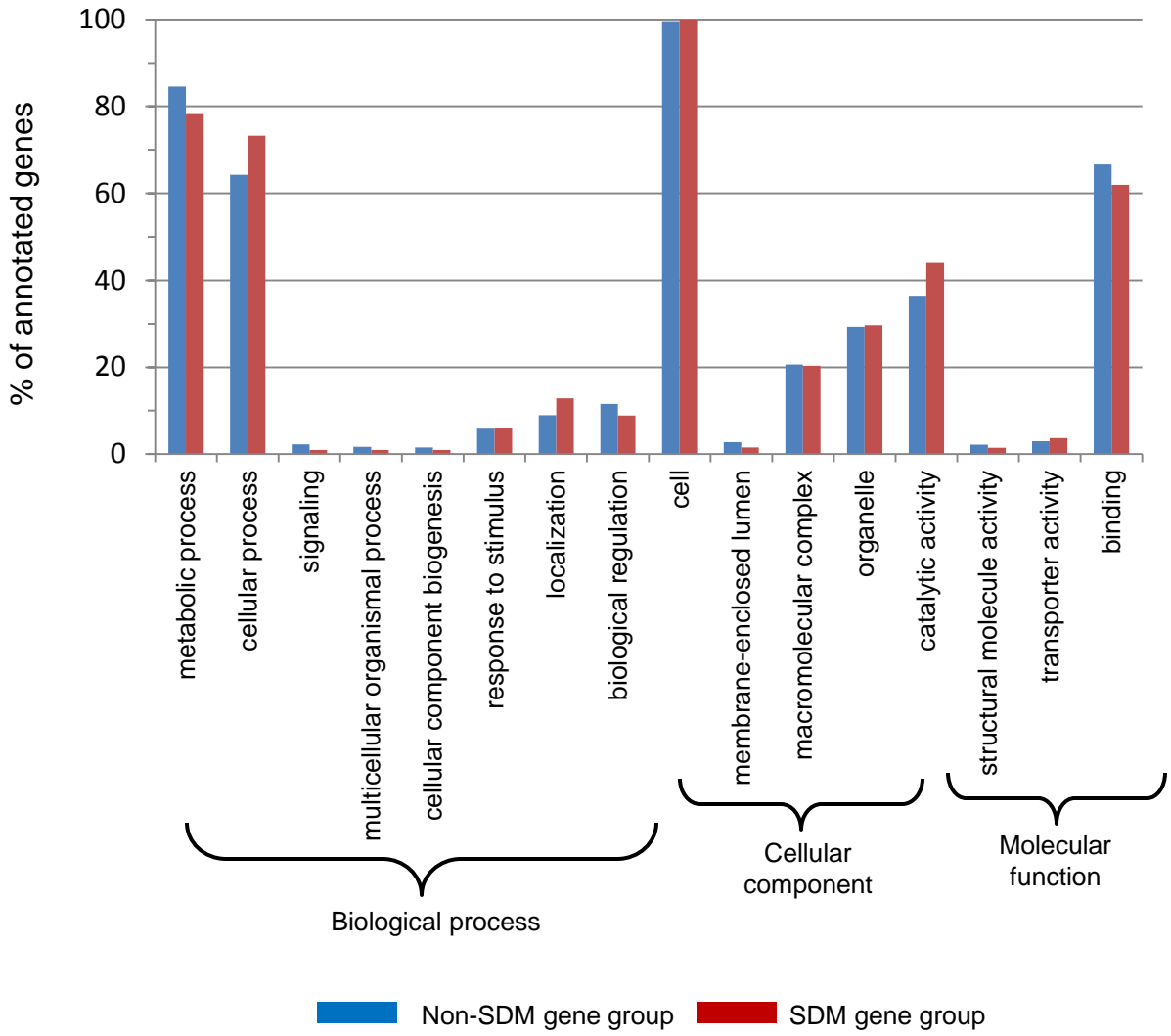


Supporting Information Fig. S4 The significant within chromosome relationships of global H_{HW} (six species H_{HW} average; top), global F_{ST} (middle) and the proportion of species differentiating markers (SDMs, bottom) with gene density (genes per Mbp). The data represents the variation amongst 5Mbp bins within chromosomes (chromosome differences were removed by standardisation of 5Mbp bin averages to a mean of zero for each chromosome). The 95% confidence intervals for the mean (shaded) and individual (dotted line) predicted values are shown.



Supporting Information Fig. S5

H_{HW} for (a) DArT markers in genes, within 5kb of a gene, and more than 5kb from a gene (black bars) and (b) DArT markers in genes which were outside and within clusters of tandemly duplicated genes (grey bars). Means with common letters (above black bars) are not significantly ($P < 0.05$) different based on pair-wise Kruskal-Wallis tests. The significance of the Kruskal-Wallis tests for the difference between DArT markers within genes which were outside and within ($n=388$) clusters of tandem duplicate genes are shown (* ns = $P \geq 0.05$; *** = $P < 0.001$). Note proximity to genes and tandem clusters is based on the *E. grandis* reference genome.



Supporting Information Fig. S6 Percentage of genes mapped to major second-level GO terms for species differentiating marker (SDM) and non-SDM gene groups. All second-level GO terms can be found in Supporting Information Table S6.

Supporting Information Table S1. Sample locality information for 533 *Eucalyptus* DNA samples.

Sample name ^a	Source ^b	Locality	State ^c	Population / race ^d / subspecies ^e
<i>E. globulus</i>				
GL_2628	1	Recherche Bay	TAS	Recherche Bay
GL_2796	1	Recherche Bay	TAS	Recherche Bay
GL_1531	1	Dover	TAS	southern Tasmania
GL_1537	1	Dover	TAS	southern Tasmania
GL_1521	1	Geeveston	TAS	southern Tasmania
GL_1529	1	Geeveston	TAS	southern Tasmania
GL_1538	1	South Bruny Island	TAS	southern Tasmania
GL_1544	1	South Bruny Island	TAS	southern Tasmania
GL_1348	1	Tinderbox	TAS	southern Tasmania
GL_1805	1	Hobart (Chinmey Pot Hill)	TAS	southeast Tasmania
GL_1811	1	Hobart (Chinmey Pot Hill)	TAS	southeast Tasmania
GL_2913	1	Mt Dromedary Tas	TAS	Dromendary
GL_2932	1	Platform Peak	TAS	Dromendary
GL_1760	1	Jericho	TAS	northeast Tasmania
GL_1764	1	Jericho	TAS	northeast Tasmania
GL_1003	1	White Beach	TAS	southern Tasmania
GL_1046	1	Murdunna	TAS	southern Tasmania
GL_1056	1	Break-me-neck-hill	TAS	southeast Tasmania
GL_1193	1	South Buckland Military	TAS	southeast Tasmania
GL_1796	1	Maria Island South	TAS	southeast Tasmania
GL_1769	1	Maria Island North	TAS	southeast Tasmania
GL_1754	1	Triabunna	TAS	southeast Tasmania
GL_1756	1	Triabunna	TAS	southeast Tasmania

Sample name ^a	Source ^b	Locality	State ^c	Population / race ^d / subspecies ^e
GL_1745	1	Mayfield South	TAS	northeast Tasmania
GL_1750	1	Mayfield South	TAS	northeast Tasmania
GL_1736	1	Mayfield North	TAS	northeast Tasmania
GL_1740	1	Mayfield North	TAS	northeast Tasmania
GL_1655	1	Cape Tourville Tall	TAS	northeast Tasmania
GL_1345	1	Cape Tourville Dwarf	TAS	northeast Tasmania
GL_1719	1	Pepper Hill	TAS	northeast Tasmania
GL_1722	1	Pepper Hill	TAS	northeast Tasmania
GL_1726	1	Humbug Hill	TAS	northeast Tasmania
GL_1731	1	Humbug Hill	TAS	northeast Tasmania
GL_2071	1	Macquarie Harbour	TAS	western Tasmania
GL_2079	1	Macquarie Harbour	TAS	western Tasmania
GL_3403	1	Port Davey	TAS	western Tasmania
GL_3422	1	Port Davey	TAS	western Tasmania
GL_2052	1	Badgers Creek	TAS	western Tasmania
GL_2057	1	Badgers Creek	TAS	western Tasmania
GL_2058	1	Badgers Creek	TAS	western Tasmania
GL_2059	1	Little Henty River	TAS	western Tasmania
GL_2064	1	Little Henty River	TAS	western Tasmania
GL_1816	1	South King Island	TAS	King Island
GL_1821	1	South King Island	TAS	King Island
GL_2124	1	Central King Island	TAS	King Island
GL_2132	1	Central King Island	TAS	King Island
GL_2136	1	Central North King Island	TAS	King Island
GL_2137	1	Central North King Island	TAS	King Island
GL_2141	1	North King Island	TAS	King Island

Sample name ^a	Source ^b	Locality	State ^c	Population / race ^d / subspecies ^e
GL_2145	1	North King Island	TAS	King Island
GL_1406	1	Cape Barren Island	TAS	Furneaux
GL_1432	1	Cape Barren Island	TAS	Furneaux
GL_1332	1	Flinders Island South	TAS	Furneaux
GL_1334	1	Flinders Island South	TAS	Furneaux
GL_1390	1	Flinders Island Central	TAS	Furneaux
GL_1403	1	Flinders Island Central	TAS	Furneaux
GL_1391	1	Flinders Island North	TAS	Furneaux
GL_1392	1	Flinders Island North	TAS	Furneaux
GL_2577	1	Wilson's Promontory Lighthouse	VIC	Wilson Promontory
GL_2605	1	Wilson's Promontory Lighthouse	VIC	Wilson Promontory
GL_9904	1	Tidal River Wilson's Promontory	VIC	Wilson Promontory
GL_9917	1	Tidal River Wilson's Promontory	VIC	Wilson Promontory
GL_9923	1	Phillip Island	VIC	southern Gippsland
GL_9940	1	Phillip Island	VIC	southern Gippsland
GL_1254	1	Fish Creek	VIC	southern Gippsland
GL_1258	1	Fish Creek	VIC	southern Gippsland
GL_1261	1	Toora	VIC	southern Gippsland
GL_1267	1	Toora	VIC	southern Gippsland
GL_1268	1	AlbWest_Welshpool_Hedley	VIC	southern Gippsland
GL_1273	1	AlbWest_Welshpool_Hedley	VIC	southern Gippsland
GL_1139	1	Jeeralang	VIC	Strzelecki Ranges
GL_1160	1	Jeeralang	VIC	Strzelecki Ranges
GL_1554	1	Lorne	VIC	eastern Otways
GL_1558	1	Lorne	VIC	eastern Otways
GL_1572	1	Jamieson Creek	VIC	eastern Otways

Sample name ^a	Source ^b	Locality	State ^c	Population / race ^d / subspecies ^e
GL_1580	1	Cape Patton	VIC	eastern Otways
GL_1585	1	Cape Patton	VIC	eastern Otways
GL_1588	1	Cannan Spur	VIC	western Otways
GL_1593	1	Cannan Spur	VIC	western Otways
GL_1594	1	Parker Spur	VIC	western Otways
GL_1599	1	Parker Spur	VIC	western Otways
GL_1704	1	Otway State Forest	VIC	western Otways
GL_1708	1	Otway State Forest	VIC	western Otways
GL_1712	1	Lavers Hill	VIC	western Otways
<i>E. nitens</i>				
N_TO110	2	Spion Kopje	VIC	Central Victoria - south
N_TO108	2	Spion Kopje	VIC	Central Victoria - south
N_TO102	2	West Kopje	VIC	Central Victoria - south
N_TO100	2	West Kopje	VIC	Central Victoria - south
N_TO124	2	Starling Gap	VIC	Central Victoria - south
N_TO118	2	Starling Gap	VIC	Central Victoria - south
N_2087676	3	Mount Erica	VIC	Central Victoria - south
N_2087580	3	Mount Erica	VIC	Central Victoria - south
N_2087607	3	Mt St Gwinear Road	VIC	Central Victoria - south
N_2087532	3	Mt St Gwinear Road	VIC	Central Victoria - south
N_2087530	3	Newlands Rd	VIC	Central Victoria - south
N_TV53	2	Upper Thomson Valley	VIC	Central Victoria - south
N_2087596	3	Thomson Valley - Creeks	VIC	Central Victoria - south
N_2087518	3	Thomson Valley - Creeks	VIC	Central Victoria - south
N_TO11	2	Mount Horsfall	VIC	Central Victoria - south
N_TO1	2	Mount Horsfall	VIC	Central Victoria - south

Sample name ^a	Source ^b	Locality	State ^c	Population / race ^d / subspecies ^e
N_2087634	3	Marshall Spur	VIC	Central Victoria - south
N_2087514	3	Number 3 Road	VIC	Central Victoria - south
N_2087622	3	Toorongo Town	VIC	Central Victoria - south
N_H23	2	Toorongo North	VIC	Central Victoria - south
N_H14	2	Toorongo North	VIC	Central Victoria - south
N_2087716	3	Toorongo North	VIC	Central Victoria - south
N_2087570	3	Toorongo South	VIC	Central Victoria - south
N_TO135	2	Ben Cairn	VIC	Central Victoria - south
N_TO128	2	Ben Cairn	VIC	Central Victoria - south
N_TO127	2	Ben Cairn	VIC	Central Victoria - south
N_TO140	2	Bonna Buang	VIC	Central Victoria - south
N_TO138	2	Bonna Buang	VIC	Central Victoria - south
N_TO137	2	Bonna Buang	VIC	Central Victoria - south
NU103	2	Monda Road	VIC	Central Victoria - south
NU102	2	Monda Road	VIC	Central Victoria - south
Nu114	2	Mount Tanglefoot	VIC	Central Victoria - south
NU108	2	Mount Tanglefoot	VIC	Central Victoria - south
NU101	2	Mount Tanglefoot	VIC	Central Victoria - south
N_2087758	3	Royston river	VIC	Central Victoria - north
NU78	2	Quartz Ck	VIC	Central Victoria - north
N_2087603	3	Quartz Ck	VIC	Central Victoria - north
N_2087543	3	Snobs Ck	VIC	Central Victoria - north
N_2087697	3	Little River	VIC	Central Victoria - north
N_2087541	3	Little River	VIC	Central Victoria - north
N_2087630	3	Barnewall Plains	VIC	Central Victoria - north
N_2087528	3	Barnewall Plains	VIC	Central Victoria - north

Sample name ^a	Source ^b	Locality	State ^c	Population / race ^d / subspecies ^e
N_TO67	2	Mount Gregory	VIC	Central Victoria - north
N_TO64	2	Mount Gregory	VIC	Central Victoria - north
N_TO60	2	Mount Gregory	VIC	Central Victoria - north
N_2087610	3	Mount Useful - SE	VIC	Central Victoria - north
N_2087562	3	Mount Useful - SE	VIC	Central Victoria - north
N_2087567	3	Mount Useful - S	VIC	Central Victoria - north
N_MA104	2	Mount Useful - E	VIC	Central Victoria - north
N_MA101	2	Mount Useful - E	VIC	Central Victoria - north
N_MA80	2	Mount Useful - N	VIC	Central Victoria - north
N_2087694	3	Mt Skene - Lazarini Ck	VIC	Central Victoria - north
N_2087664	3	Mt Skene - Lazarini Ck	VIC	Central Victoria - north
N_2087521	3	Mt Skene - Lazarini Ck	VIC	Central Victoria - north
N_MA49	2	Mt Skene / Barkly River - E and S	VIC	Central Victoria - north
N_MA48	2	Mt Skene / Barkly River - E and S	VIC	Central Victoria - north
N_MA2	2	Connors Plains - SE	VIC	Connors Plains
N_2087536	3	Connors Plains - SE	VIC	Connors Plains
N_MA15	2	Connors Plains - Plateau	VIC	Connors Plains
N_2087721	3	Connors Plains - Plateau	VIC	Connors Plains
N_2087638	3	Connors Plains - NW	VIC	Connors Plains
N_2087544	3	Mt Wellington	VIC	Mt Wellington
N_2087526	3	Victoria - unknown	VIC	Central Victoria - unknown
N_2087525	3	Victoria - unknown	VIC	Central Victoria - unknown
N_2087524	3	Victoria - unknown	VIC	Central Victoria - unknown
N_2358996	3	Nimitabel	NSW	southern NSW
N_2358669	3	Nimitabel	NSW	southern NSW
N_2087749	3	Nimitabel	NSW	southern NSW

Sample name ^a	Source ^b	Locality	State ^c	Population / race ^d / subspecies ^e
N_2087553	3	Nimitabel	NSW	southern NSW
N_2087551	3	Nimitabel	NSW	southern NSW
N_2087635	3	Unknown	NSW	southern NSW
N_2359047	3	Tallaganda	NSW	southern NSW
N_2358790	3	Tallaganda	NSW	southern NSW
N_2358691	3	Tallaganda	NSW	southern NSW
N_2358644	3	Tallaganda	NSW	southern NSW
N_2358402	3	Tallaganda	NSW	southern NSW
N_2358698	3	Barrington Tops	NSW	northern NSW
N_2358693	3	Barrington Tops	NSW	northern NSW
N_2358626	3	Barrington Tops	NSW	northern NSW
N_2358490	3	Barrington Tops	NSW	northern NSW
N_2359035	3	Ebor	NSW	northern NSW
N_2358918	3	Ebor	NSW	northern NSW
N_2358852	3	Ebor	NSW	northern NSW
N_2358849	3	Ebor	NSW	northern NSW
N_2358346	3	Ebor	NSW	northern NSW
<i>E. camaldulensis</i>				
C_74_425C	4	Laura River	QLD	<i>simulata</i>
C_76_400	4	Normanby River	QLD	<i>simulata</i>
C_3_450	4	Gilbert River	QLD	<i>acuta</i> (northern)
C_6_415	4	Morehead River	QLD	<i>acuta</i> (northern)
C_7_390	4	Petford	QLD	<i>acuta</i> (northern)
C_7_391	4	Petford	QLD	<i>acuta</i> (northern)
C_1_MM3114	4	Adavale	QLD	<i>acuta</i> (southern)
C_2_3189	4	Angellala River	QLD	<i>acuta</i> (southern)

Sample name ^a	Source ^b	Locality	State ^c	Population / race ^d / subspecies ^e
C_5_3166	4	Moonie River	QLD	<i>acuta</i> (southern)
C_5_3170	4	Moonie River	QLD	<i>acuta</i> (southern)
C_15_3156	4	Dirrandanbi	QLD	<i>camaldulensis</i>
C_10_3340	4	Aberdeen	NSW	<i>camaldulensis</i>
C_28_CS168	4	Wellington	NSW	<i>camaldulensis</i>
C_27_163	4	Warren	NSW	<i>camaldulensis</i>
C_26_3152	4	Warraweena	NSW	<i>camaldulensis</i>
C_13_155	4	Condobolin	NSW	<i>camaldulensis</i>
C_30_125	4	Wilcannia	NSW	<i>camaldulensis</i>
C_17_SC134	4	Hillston	NSW	<i>camaldulensis</i>
C_21_114	4	Menindee	NSW	<i>camaldulensis</i>
C_29_86	4	Wentworth	NSW	<i>camaldulensis</i>
C_25_CS58	4	Towong	NSW	<i>camaldulensis</i>
C_11_77	4	Barmah	NSW	<i>camaldulensis</i>
C_31_271	4	Wirrengren Plain	VIC	<i>camaldulensis</i>
C_20_PM295	4	Lake Albacutya	VIC	<i>camaldulensis</i>
C_16_334	4	Elmhurst	VIC	<i>camaldulensis</i>
C_18_323	4	Horsham	VIC	<i>camaldulensis</i>
C_23_3026	4	Morgan	SA	<i>camaldulensis</i>
C_24_3012	4	Mypolonga	SA	<i>camaldulensis</i>
C_24_3016	4	Mypolonga	SA	<i>camaldulensis</i>
C_22_13253-1	4	Minlaton	SA	<i>camaldulensis</i>
C_19_KI2	4	Kangaroo Island	SA	<i>camaldulensis</i>
C_12_3005	4	Coffin Bay	SA	<i>camaldulensis</i>
C_32_2974	4	Boolcunda Creek	SA	<i>minima</i>
C_33_2994	4	Bunyerroo Creek	SA	<i>minima</i>

Sample name ^a	Source ^b	Locality	State ^c	Population / race ^d / subspecies ^e
C_34_2966	4	Horrocks Pass	SA	<i>minima</i>
C_35_2958	4	Huddleston	SA	<i>minima</i>
C_35_2959	4	Huddleston	SA	<i>minima</i>
C_82_2981	4	Emu Creek	SA	<i>arida</i>
C_79_107	4	Broken River	NSW	<i>arida</i>
C_88_SC92	4	Silverton	NSW	<i>arida</i>
C_80_MM3206	4	Bulloo River	QLD	<i>arida</i>
C_91_3197	4	Ward River	QLD	<i>arida</i>
C_93_3045	4	Windorah	QLD	<i>arida</i>
C_78_3109	4	Boulia	QLD	<i>arida</i>
C_85_3066	4	Muttaborra	QLD	<i>arida</i>
C_77_MM3220	4	Arthur Creek	QLD	<i>arida</i>
C_84_460B	4	Lander River	NT	<i>arida</i>
C_81_3327	4	Coongra Creek	SA	<i>arida</i>
C_86_3253	4	Palmer River	NT	<i>arida</i>
C_83_3267	4	Giles Creek	WA	<i>arida</i>
C_90_3314	4	Warbuton	WA	<i>arida</i>
C_89_2780	4	Station Creek	WA	<i>arida</i>
C_87_470C	4	Rudall River	WA	<i>arida</i>
C_92_2946	4	Wiluna	WA	<i>arida</i>
C_72_2823	4	Newman	WA	<i>refulgens</i>
C_73_2809	4	Nullagine	WA	<i>refulgens</i>
C_65_MM2867	4	Gorge Junction	WA	<i>refulgens</i>
C_70_MM2877	4	Moorarie	WA	<i>refulgens</i>
C_67_2929	4	Meeberrie	WA	<i>refulgens</i>
C_71_2798	4	Muccan	WA	<i>refulgens</i>

Sample name ^a	Source ^b	Locality	State ^c	Population / race ^d / subspecies ^e
C_62_2792	4	De Grey River	WA	<i>refulgens</i>
C_68_2835	4	Millstream	WA	<i>refulgens</i>
C_66_2858	4	Kooline	WA	<i>refulgens</i>
C_63_2888	4	Elong	WA	<i>refulgens</i>
C_60_2900	4	Bidgemia	WA	<i>refulgens</i>
C_61_2910	4	Carnarvon	WA	<i>refulgens</i>
C_69_2850	4	Mindaroo	WA	<i>refulgens</i>
C_64_2838	4	Fortescue	WA	<i>refulgens</i>
C_40_2897	4	Fitzroy River lower	WA	<i>obtusa</i>
C_39_2880	4	Fitzroy Crossing	WA	<i>obtusa</i>
C_42_2905	4	Gibb River	WA	<i>obtusa</i>
C_46_2873C	4	Margaret River	WA	<i>obtusa</i>
C_50_2861B	4	Ord River upper	WA	<i>obtusa</i>
C_49_2909B	4	Ord River lower	WA	<i>obtusa</i>
C_58_2946	4	Victoria River upper	NT	<i>obtusa</i>
C_57_2920	4	Victoria River lower	NT	<i>obtusa</i>
C_56_2937B	4	Victoria River Downs	NT	<i>obtusa</i>
C_38_ER9	4	Edith River	NT	<i>obtusa</i>
C_47_MR6	4	Mary River	NT	<i>obtusa</i>
C_51_UR2	4	Roper River	NT	<i>obtusa</i>
C_53_SgC10	4	Strangeways Creek	NT	<i>obtusa</i>
C_37_MM3236	4	Daly Waters Creek	NT	<i>obtusa</i>
C_44_HR6	4	Hodgson River	NT	<i>obtusa</i>
C_54_SC2	4	Surprise Creek	NT	<i>obtusa</i>
C_55_TC3B	4	Tennant Creek	NT	<i>obtusa</i>
C_52_SC2	4	Settlement Creek	NT	<i>obtusa</i>

Sample name ^a	Source ^b	Locality	State ^c	Population / race ^d / subspecies ^e
C_59_3094	4	Whistler Creek	QLD	<i>obtusa</i>
C_41_2764	4	Floraville	QLD	<i>obtusa</i>
C_45_2754	4	Kamilaroi	QLD	<i>obtusa</i>
C_48_2772	4	Mt Isa	QLD	<i>obtusa</i>
C_43_3082	4	Glen Gorge	QLD	<i>obtusa</i>
C_36_3060	4	Baroota Waterhole	QLD	<i>obtusa</i>
<i>E. grandis</i>				
GR_DP192	5	Bulahdelah	NSW	southern NSW
GR_DP109	5	Bulahdelah	NSW	southern NSW
GR_DP108	5	Bulahdelah	NSW	southern NSW
GR_DP116	5	Wang Wauk S. F.	NSW	southern NSW
GR_DP191	5	Mt. George Taree	NSW	southern NSW
GR_DP190	5	Mt. George Taree	NSW	southern NSW
GR_DP189	5	Mt. George Taree	NSW	southern NSW
GR_DP188	5	Mt. George Taree	NSW	southern NSW
GR_DP186	5	Mt. George Taree	NSW	southern NSW
GR_DP185	5	Mt. George Taree	NSW	southern NSW
GR_DP183	5	Mt. George Taree	NSW	southern NSW
GR_DP182	5	Mt. George Taree	NSW	southern NSW
GR_DP181	5	Mt. George Taree	NSW	southern NSW
GR_DP110	5	Mt. George Taree	NSW	southern NSW
GR_DP105	5	Mt. George Taree	NSW	southern NSW
GR_DP180	5	Taree	NSW	southern NSW
GR_DP102	5	Taree	NSW	southern NSW
GR_DP179	5	Lake Cathie	NSW	southern NSW
GR_DP106	5	Lake Cathie	NSW	southern NSW

Sample name ^a	Source ^b	Locality	State ^c	Population / race ^d / subspecies ^e
GR_DP103	5	Lake Cathie	NSW	southern NSW
GR_DP187	5	Wauchope	NSW	southern NSW
GR_DP184	5	Wauchope	NSW	southern NSW
GR_DP111	5	Wauchope	NSW	southern NSW
GR_DP107	5	Wauchope	NSW	southern NSW
GR_DP104	5	Wauchope	NSW	southern NSW
GR_DP101	5	Wauchope	NSW	southern NSW
GR_DP172	5	Urunga	NSW	Coffs Harbour
GR_DP171	5	Urunga	NSW	Coffs Harbour
GR_DP168	5	Urunga	NSW	Coffs Harbour
GR_DP159	5	Urunga	NSW	Coffs Harbour
GR_DP173	5	Pine Creek S. F.	NSW	Coffs Harbour
GR_DP170	5	Pine Creek S. F.	NSW	Coffs Harbour
GR_DP163	5	Pine Creek S. F.	NSW	Coffs Harbour
GR_DP176	5	Boambie Coffs Harb	NSW	Coffs Harbour
GR_DP165	5	Oraba Coffs Harb	NSW	Coffs Harbour
GR_DP164	5	Oraba Coffs Harb	NSW	Coffs Harbour
GR_DP167	5	Coffs Harbour	NSW	Coffs Harbour
GR_DP166	5	Coffs Harbour	NSW	Coffs Harbour
GR_DP161	5	Coffs Harbour	NSW	Coffs Harbour
GR_DP160	5	Coffs Harbour	NSW	Coffs Harbour
GR_DP174	5	Lower Bucca	NSW	Coffs Harbour
GR_DP162	5	Lower Bucca	NSW	Coffs Harbour
GR_DP175	5	Conglomerate S. F.	NSW	Coffs Harbour
GR_DP178	5	Toonumba	NSW	Coffs Harbour
GR_DP177	5	Yabra/Urbenville	NSW	Coffs Harbour

Sample name ^a	Source ^b	Locality	State ^c	Population / race ^d / subspecies ^e
GR_DP155	5	Belthorpe	QLD	Gympie
GR_DP154	5	Belthorpe	QLD	Gympie
GR_DP151	5	Belthorpe	QLD	Gympie
GR_DP146	5	Belthorpe	QLD	Gympie
GR_DP144	5	Belthorpe	QLD	Gympie
GR_DP141	5	Belthorpe	QLD	Gympie
GR_DP114	5	Belthorpe	QLD	Gympie
GR_DP158	5	Kenilworth	QLD	Gympie
GR_DP157	5	Kenilworth	QLD	Gympie
GR_DP156	5	Kenilworth	QLD	Gympie
GR_DP153	5	Kenilworth	QLD	Gympie
GR_DP152	5	Kenilworth	QLD	Gympie
GR_DP148	5	Kenilworth	QLD	Gympie
GR_DP145	5	Kenilworth	QLD	Gympie
GR_DP117	5	Kenilworth	QLD	Gympie
GR_DP150	5	Woondum/Gympie	QLD	Gympie
GR_DP143	5	Woondum/Gympie	QLD	Gympie
GR_DP142	5	Woondum/Gympie	QLD	Gympie
GR_DP115	5	Woondum/Gympie	QLD	Gympie
GR_DP147	5	Veteran Gympie	QLD	Gympie
GR_DP134	5	Mt Windsor	QLD	Atherton
GR_DP138	5	Townsville	QLD	Atherton
GR_DP137	5	Townsville	QLD	Atherton
GR_DP133	5	Townsville	QLD	Atherton
GR_DP124	5	Townsville	QLD	Atherton
GR_DP126	5	Kennedy	QLD	Atherton

Sample name ^a	Source ^b	Locality	State ^c	Population / race ^d / subspecies ^e
GR_DP131	5	Wandecia	QLD	Atherton
GR_DP125	5	Wandecia	QLD	Atherton
GR_DP122	5	Wandecia	QLD	Atherton
GR_DP121	5	Wandecia	QLD	Atherton
GR_DP118	5	Wandecia	QLD	Atherton
GR_DP132	5	Ravenshoe	QLD	Atherton
GR_DP129	5	Ravenshoe	QLD	Atherton
GR_DP136	5	Baldy SF	QLD	Atherton
GR_DP130	5	Baldy SF	QLD	Atherton
GR_DP120	5	Baldy SF	QLD	Atherton
GR_DP113	5	Baldy SF	QLD	Atherton
GR_DP112	5	Baldy SF	QLD	Atherton
GR_DP128	5	Atherton	QLD	Atherton
GR_DP127	5	Atherton	QLD	Atherton
GR_DP119	5	Atherton	QLD	Atherton
GR_DP140	5	Mareeba	QLD	Atherton
GR_DP139	5	Mareeba	QLD	Atherton
GR_DP135	5	Mareeba	QLD	Atherton
GR_DP123	5	Mareeba	QLD	Atherton
<i>E. urophylla</i>				
U_DP027	6	Bonleu	N/A	Timor
U_DP028	6	Bonleu	N/A	Timor
U_DP020	6	Lelobatan	N/A	Timor
U_DP021	6	Lelobatan	N/A	Timor
U_DP094	6	Leloboko	N/A	Timor
U_DP091	6	Mollo	N/A	Timor

Sample name ^a	Source ^b	Locality	State ^c	Population / race ^d / subspecies ^e
U_DP092	6	Mollo	N/A	Timor
U_DP022	6	Nuafin	N/A	Timor
U_DP023	6	Nuafin	N/A	Timor
U_DP024	6	Nuafin	N/A	Timor
U_DP096	6	Fatumnase	N/A	Timor
U_DP016	6	Naususu	N/A	Timor
U_DP017	6	Naususu	N/A	Timor
U_DP095	6	A. Esrael	N/A	Timor
U_DP093	6	Lelobatang	N/A	Timor
U_DP025	6	Tutem	N/A	Timor
U_DP026	6	Tutem	N/A	Timor
U_DP018	6	Tune	N/A	Timor
U_DP019	6	Tune	N/A	Timor
U_DP089	6	Lere-Baukrenget	N/A	Flores
U_DP090	6	Lere-Baukrenget	N/A	Flores
U_DP054	6	Natakoli	N/A	Flores
U_DP055	6	Natakoli	N/A	Flores
U_DP044	6	Ile Nggele	N/A	Flores
U_DP045	6	Ile Nggele	N/A	Flores
U_DP046	6	Ile Nggele	N/A	Flores
U_DP047	6	Kilawair	N/A	Flores
U_DP048	6	Kilawair	N/A	Flores
U_DP052	6	Kolibuluk	N/A	Flores
U_DP053	6	Kolibuluk	N/A	Flores
U_DP050	6	Hokeng	N/A	Flores
U_DP051	6	Hokeng	N/A	Flores

Sample name ^a	Source ^b	Locality	State ^c	Population / race ^d / subspecies ^e
U_DP014	6	Kawela	N/A	Adonara
U_DP015	6	Kawela	N/A	Adonara
U_DP012	6	Lamahela	N/A	Adonara
U_DP013	6	Lamahela	N/A	Adonara
U_DP008	6	Watololong	N/A	Adonara
U_DP009	6	Watololong	N/A	Adonara
U_DP010	6	Gonehama	N/A	Adonara
U_DP011	6	Gonehama	N/A	Adonara
U_DP003	6	Muda	N/A	Adonara
U_DP004	6	Muda	N/A	Adonara
U_DP001	6	Doken	N/A	Adonara
U_DP002	6	Doken	N/A	Adonara
U_DP006	6	Lamalota	N/A	Adonara
U_DP007	6	Lamalota	N/A	Adonara
U_DP066	6	Puor	N/A	Lomblen
U_DP067	6	Puor	N/A	Lomblen
U_DP058	6	Jontona	N/A	Lomblen
U_DP059	6	Jontona	N/A	Lomblen
U_DP060	6	Jontona	N/A	Lomblen
U_DP056	6	Padekluwa	N/A	Lomblen
U_DP057	6	Padekluwa	N/A	Lomblen
U_DP064	6	Ile Kerbau	N/A	Lomblen
U_DP065	6	Ile Kerbau	N/A	Lomblen
U_DP068	6	Ile Ape	N/A	Lomblen
U_DP069	6	Ile Ape	N/A	Lomblen
U_DP061	6	Labalekan	N/A	Lomblen

Sample name ^a	Source ^b	Locality	State ^c	Population / race ^d / subspecies ^e
U_DP062	6	Labalekan	N/A	Lomblen
U_DP063	6	Labalekan	N/A	Lomblen
U_DP079	6	Mauta	N/A	Pantar
U_DP080	6	Mauta	N/A	Pantar
U_DP081	6	Mauta	N/A	Pantar
U_DP085	6	Delaki	N/A	Pantar
U_DP086	6	Delaki	N/A	Pantar
U_DP087	6	Beangonong	N/A	Pantar
U_DP088	6	Beangonong	N/A	Pantar
U_DP082	6	Lalapang	N/A	Pantar
U_DP083	6	Lalapang	N/A	Pantar
U_DP084	6	Lalapang	N/A	Pantar
U_DP078	6	Watakika	N/A	Alor
U_DP075	6	Pintu Mas	N/A	Alor
U_DP076	6	Pintu Mas	N/A	Alor
U_DP077	6	Pintu Mas	N/A	Alor
U_DP070	6	Mainang	N/A	Alor
U_DP071	6	Mainang	N/A	Alor
U_DP072	6	Apui	N/A	Alor
U_DP073	6	Apui	N/A	Alor
U_DP074	6	Apui	N/A	Alor
U_DP040	6	Nesunhuhun	N/A	Wetar
U_DP041	6	Nesunhuhun	N/A	Wetar
U_DP037	6	Elun Kripas	N/A	Wetar
U_DP038	6	Elun Kripas	N/A	Wetar
U_DP042	6	Nakana Ulam	N/A	Wetar

Sample name ^a	Source ^b	Locality	State ^c	Population / race ^d / subspecies ^e
U_DP043	6	Nakana Ulam	N/A	Wetar
U_DP035	6	Alasannaru	N/A	Wetar
U_DP036	6	Alasannaru	N/A	Wetar
U_DP029	6	Puaanan	N/A	Wetar
U_DP030	6	Puaanan	N/A	Wetar
U_DP031	6	Remamea	N/A	Wetar
U_DP032	6	Remamea	N/A	Wetar
U_DP033	6	Talianan	N/A	Wetar
U_DP034	6	Talianan	N/A	Wetar
<i>E. dunnii</i>				
D_BV097	5	Bald Knob	NSW	
D_BV098	5	Moleton	NSW	
D_BV099	5	Boomi Creek	QLD	
D_BV100	5	Koreelah State Forests	NSW	
D_BV101	5	Bald Knob	NSW	
D_BV102	5	Beaury State Forest	QLD	
D_BV103	5	Moleton	NSW	
D_BV104	5	Koreelah State Forests	NSW	
D_BV105	5	Boomi Creek	QLD	
D_BV106	5	South Yabra State Forest	NSW	
D_BV107	5	Beaury State Forest	QLD	
D_BV108	5	Koreelah State Forests	NSW	
D_BV109	5	Koreelah State Forests	NSW	
D_BV110	5	Wallaby Creek	NSW	
D_BV111	5	Wallaby Creek	NSW	
D_BV112	5	Wallaby Creek	NSW	

Sample name ^a	Source ^b	Locality	State ^c	Population / race ^d / subspecies ^e
D_BV113	5	Wallaby Creek	NSW	
D_BV114	5	South Yabra State Forest	NSW	
D_BV115	5	South Yabra State Forest	NSW	
D_BV116	5	South Yabra State Forest	NSW	
D_BV117	5	Bald Knob	NSW	
D_BV118	5	Wallaby Creek	NSW	
D_BV119	5	Teviot Brk Burnett Creek	QLD	
D_BV120	5	Beaury State Forest	NSW	
D_BV121	5	Yabra State Forest	NSW	
D_BV122	5	Wallaby Creek	NSW	
D_BV123	5	Teviot Brk Burnett Creek	QLD	
D_BV124	5	Beaury State Forest	NSW	
D_BV125	5	Yabra State Forest	NSW	
D_BV126	5	Yabra State Forest	NSW	
D_BV127	5	Teviot Brk Burnett Creek	QLD	
D_BV128	5	Yabra State Forest	NSW	
D_BV129	5	Wallaby Creek	NSW	
D_BV130	5	Unknown	-	
D_BV131	5	Beaury State Forest	NSW	
D_BV132	5	Beaury State Forest	NSW	
D_BV133	5	Wallaby Creek	NSW	
D_BV134	5	Teviot Brk Burnett Creek	QLD	
D_BV135	5	Crossley	SO	
D_BV137	5	Barclay	SO	
D_BV138	5	Moleton	NSW	
D_BV139	5	Kangaroo River	NSW	

Sample name ^a	Source ^b	Locality	State ^c	Population / race ^d / subspecies ^e
D_BV140	5	Moleton	NSW	
D_BV141	5	Barclay	SO	
D_BV142	5	Moleton	NSW	
D_BV143	5	Newry	NSW	
D_BV144	5	Crossley	SO	
D_BV145	5	Kangaroo River	NSW	
D_BV146	5	Crossley	SO	
D_BV147	5	Moleton	NSW	
D_BV148	5	Newry	NSW	
D_BV149	5	Barclay	SO	
D_BV150	5	Newry	NSW	
D_BV151	5	Crossley	SO	
D_BV152	5	Newry	NSW	
D_BV153	5	Kangaroo River	NSW	
D_BV154	5	Kangaroo River	NSW	
D_BV156	5	Dead Horse Track	QLD	
D_BV157	5	Acacia Creek	NSW	
D_BV158	5	Boomi Creek	NSW	
D_BV159	5	Dead Horse Track	QLD	
D_BV160	5	Acacia Creek	NSW	
D_BV161	5	Acacia Creek	NSW	
D_BV162	5	Boomi Creek	NSW	
D_BV163	5	Dead Horse Track	QLD	
D_BV164	5	Dead Horse Track	QLD	
D_BV166	5	Oaky Creek	QLD	
D_BV167	5	South Yabra State Forest	NSW	

Sample name ^a	Source ^b	Locality	State ^c	Population / race ^d / subspecies ^e
D_BV168	5	Oaky Creek	QLD	
D_BV170	5	Oaky Creek	QLD	
D_BV172	5	Dead Horse Track	QLD	
D_BV173	5	Levuka	NSW	
D_BV174	5	Condamine	QLD	
D_BV175	5	Tooloom	NSW	
D_BV176	5	Dalman	NSW	
D_BV177	5	Condamine	QLD	
D_BV178	5	Lindesay	NSW/QLD	
D_BV179	5	Dalman	NSW	
D_BV180	5	Dalman	NSW	
D_BV181	5	Levuka	NSW	
D_BV182	5	Lindesay	NSW/QLD	
D_BV183	5	Levuka	NSW	
D_BV184	5	Tooloom	NSW	
D_BV185	5	Levuka	NSW	
D_BV186	5	Condamine	QLD	
D_BV187	5	Lindesay	NSW/QLD	
D_BV188	5	Tooloom	NSW	
D_BV189	5	Tooloom	NSW	
D_BV190	5	Dalman	NSW	

^aSample name. Samples have a species prefix (e.g. GL for *E. globulus*). *E. camaldulensis* sample names have been coded as: species prefix followed by population code from Butcher *et al.* (2009) and then CSIRO sample number. ^bSource, sample obtained from; 1) UTAS, 2) Norske Skog/Forestry Tasmania, 3) Gunns Ltd., 4) CSIRO Plant Industry, 5) Sappi, or 6) Mondi. ^cState: TAS = Tasmania, VIC = Victoria, SA = South Australia, WA = Western Australia, NT = Northern Territory, QLD = Queensland, NSW = New South Wales, SO = Seed orchards established from native open-pollinated seed lots, and N/A = not applicable. ^dRace following Dutkowski & Potts (1999) shown for *E. globulus*. ^eSubspecies shown for *E. camaldulensis*.

Note: In their natural environments, these species extend across an extraordinary range of habitats. For example, *E. globulus* predominantly occurs in coastal, temperate forests in south-eastern Australia (~ 40-43°S; Williams & Potts, 1996), whereas *E. urophylla*, one of the few eucalypts found exclusively outside of Australia, occurs in the Sunda archipelago in eastern Indonesia (~ 8-10°S; Payn *et al.*, 2008). *Eucalyptus urophylla* also has the greatest altitudinal range of any eucalypt species; occurring from close to sea level (70 m) up to almost 3,000 m elevation (Gunn & McDonald, 1991). The remaining four species all occur on continental Australia, with *E. nitens* occurring along the Great Dividing Range in eastern Australia from the Central Highlands of Victoria (~ 37°S) to northern NSW (~ 30°S; Cook & Ladiges, 1991); where it is usually found at altitudes in excess of 1,000 m. Also occurring on the eastern seaboard of Australia, *E. grandis* has a fairly continuous distribution in coastal and sub-coastal areas from the mid-north coast of NSW (33°S) to south-east Queensland (25°S). Smaller populations are also found further north (16-19°S) in northern Queensland (Brooker & Kleinig, 2004; Jones *et al.*, 2006). This distribution overlaps with the range of *E. dunnii*, which is restricted to two small areas in north-eastern NSW and the NSW-Queensland state border region (27 - 30°S; Benson & Hager, 1993). *Eucalyptus camaldulensis* has the most widespread natural distribution of any eucalypt, ranging from ~12 to 37°S latitude and is found in all mainland Australian states (McDonald *et al.*, 2009).

References

- Benson JS, Hager TC. 1993.** The distribution, abundance and habitat of *Eucalyptus dunnii* (Myrtaceae) (Dunn's White Gum) in New South Wales. *Cunninghamia* **3**(1): 123-145.
- Brooker MIH, Kleinig DA. 2004.** *Field guide to eucalypts. Vol. 3, Northern Australia.* Melbourne: Bloomings Books.
- Butcher P, McDonald M, Bell J. 2009.** Congruence between environmental parameters, morphology and genetic structure in Australia's most widely distributed eucalypt, *Eucalyptus camaldulensis*. *Tree Genetics & Genomes* **5**(1): 189-210.
- Cook IO, Ladiges PY. 1991.** Morphological variation within *Eucalyptus nitens* s. lat. and recognition of a new species, *E. denticulata*. *Australian Systematic Botany* **4**(2): 375-390.
- Dutkowski GW, Potts BM. 1999.** Geographic patterns of genetic variation in *Eucalyptus globulus* ssp. *globulus* and a revised racial classification. *Australian Journal of Botany* **47**(2): 237-263.
- Gunn BV, McDonald MW. 1991.** *Eucalyptus urophylla* seed collections. *Forest Genetic Resources* **19**: 34-37 FAO, Rome.

- Jones M, Shepherd M, Henry R, Delves A. 2006.** Chloroplast DNA variation and population structure in the widespread forest tree, *Eucalyptus grandis*. *Conservation Genetics* **7**(5): 691-703.
- McDonald MW, Brooker MIH, Butcher PA. 2009.** A taxonomic revision of *Eucalyptus camaldulensis* (Myrtaceae). *Australian Systematic Botany* **22**(4): 257-285.
- Payn K, Dvorak W, Janse B, Myburg A. 2008.** Microsatellite diversity and genetic structure of the commercially important tropical tree species *Eucalyptus urophylla*; endemic to seven islands in eastern Indonesia. *Tree Genetics & Genomes* **4**(3): 519-530.
- Williams KJ, Potts BM. 1996.** The natural distribution of *Eucalyptus* species in Tasmania. *Tasforests* **8**: 39-165.

Supporting Information Table S2. Comparison of species-level H_{HW} (assuming Hardy-Weinberg equilibrium) and H_{PH} (complete inbreeding) genetic diversity estimates calculated using 2,840 common DArT markers in six eucalypt species. The Spearman correlation of the species-level H_{HW} with the global H_{HW} is also shown (all are significantly different from zero at the $P<0.001$ level).

Species	Genetic diversity					Correlation H_{HW} vs global H_{HW}
	H_{PH}	H_{HW}				
	Mean	Mean	Q1	Median	Q3	
<i>E. nitens</i>	0.14	0.15	0.00	0.05	0.31	0.71
<i>E. globulus</i>	0.17	0.18	0.00	0.12	0.37	0.79
<i>E. dunnii</i>	0.19	0.20	0.00	0.16	0.39	0.75
<i>E. grandis</i>	0.20	0.21	0.00	0.19	0.40	0.77
<i>E. camaldulensis</i>	0.22	0.23	0.03	0.20	0.41	0.71
<i>E. urophylla</i>	0.22	0.24	0.03	0.25	0.43	0.68

Note: As F estimates (inbreeding coefficient) could not be estimated directly from the dominant DArT markers, two H estimates (H_{HW} [assuming Hardy-Weinberg equilibrium, $F=0$] and H_{PH} [assuming no heterozygote, $F=1$]) were initially estimated for each locus within species as:

$$H_{HW} = 2\sqrt{Q} (1 - \sqrt{Q})$$

$$H_{PH} = 2Q (1 - Q)$$

(where Q is the frequency of the null homozygote; e.g. '0' scores). At the species level (mean over all loci), Kremer *et al.* (2005) has shown that H is robust to deviations in F . Furthermore, this robustness is strongest under balanced or 'U-shaped' Q frequency profiles (i.e. most markers having either low or high Q frequencies; Kremer *et al.*, 2005). All species in this study were found to have U-shaped Q frequency distributions and, as noted by Kremer *et al.* (2005), the difference between species H_{HW} and H_{PH} values was negligible (see above). Owing to the fact that eucalypts are preferentially outcrossing plants (Byrne, 2008), and species F estimates are expected to be closer to 0 (H_{HW}) than to 1 (H_{PH}), only H_{HW} marker estimates were reported.

References:

- Byrne M 2008.** Phylogeny, diversity and evolution of eucalypts. In: Sharma AK, Sharma A eds. *Plant Genome - Biodiversity and Evolution*. Enfield (NH): Science Publishers, 303-346.
- Kremer A, Caron H, Cavers S, Colpaert N, Gheysen G, Gribel R, Lemes M, Lowe AJ, Margis R, Navarro C, Salgueiro F. 2005.** Monitoring genetic diversity in tropical trees with multilocus dominant markers. *Heredity* **95**: 274-280.

Supporting Information Table S3 Markers identified as species differentiating markers (SDMs; $n = 365$) among six *Eucalyptus* species.

Markers differentiating taxonomic sections ($n = 28$) are also indicated. For each species, the frequency of '1' scores across species individuals is shown. For sections comparisons Lat. = *Latoangulatae*, Maid. = *Maidenaria* and Ex. = *Exertaria*.

Clone ID	<i>E. grandis</i> genome position		SDMs	Section differentiating markers		Species '1' score frequency					
	Chr	Base-pair coordinates	Number of pair-wise comparisons marker significant	Number of differentiated sections	Differentiated sections	<i>E. camaldulensis</i>	<i>E. globulus</i>	<i>E. nitens</i>	<i>E. dunnii</i>	<i>E. grandis</i>	<i>E. urophylla</i>
ePt-502828	11	31186849 - 31187354	1			0.06	0.20	0.00	1.00	0.01	0.01
ePt-503324	2	56896510 - 56897174	4			0.08	1.00	0.72	1.00	0.00	0.00
ePt-503517	-	-	1			1.00	1.00	1.00	0.96	0.04	0.65
ePt-503532	2	993733 - 993973	3			0.00	0.99	1.00	0.82	1.00	0.04
ePt-503550	11	36649923 - 36650811	2	1	Lat. - Ex.	0.01	0.94	0.44	0.40	1.00	1.00
ePt-503637	11	30633757 - 30634379	1			0.81	0.63	0.00	0.97	1.00	0.95
ePt-503687	-	-	1			0.48	0.26	0.50	0.13	0.00	0.94
ePt-503708	1	30429789 - 30430766	4			1.00	1.00	1.00	0.00	0.98	1.00
ePt-503709	6	52985633 - 52986742	2			0.99	0.97	1.00	0.00	1.00	0.99
ePt-503747	1	13817896 - 13818805	1			0.98	0.95	1.00	0.00	0.98	0.99
ePt-503764	11	35552478 - 35553044	4			0.00	0.02	0.00	0.00	0.08	1.00
ePt-503844	-	-	3			1.00	0.99	1.00	0.00	0.97	0.98
ePt-503869	-	-	4			1.00	1.00	1.00	0.00	0.99	1.00
ePt-503887	-	-	4			1.00	0.99	1.00	0.00	1.00	0.99
ePt-503906	9	37862728 - 37863611	4			1.00	1.00	1.00	0.00	1.00	0.99
ePt-503947	-	-	1			1.00	1.00	1.00	0.03	0.99	1.00
ePt-504026	-	-	3			0.89	1.00	0.90	0.00	1.00	1.00
ePt-504086	2	20295322 - 20295778	2			0.96	1.00	0.00	0.02	0.99	0.97
ePt-504117	5	6088437 - 6089426	4			1.00	1.00	0.40	0.00	1.00	1.00
ePt-504133	10	18223587 - 18223692	3			0.00	0.91	0.00	1.00	0.18	0.00
ePt-504144	2	21331378 - 21332104	1			0.99	1.00	1.00	0.01	0.95	0.98

ePt-504145	7	42577753 - 42578179	1			1.00	1.00	0.99	0.01	0.99	1.00
ePt-504156	3	40072131 - 40073217	4			0.63	0.00	1.00	0.00	0.00	0.00
ePt-504178	11	31777313 - 31777520	4			0.00	0.00	0.03	1.00	0.00	0.00
ePt-504181	3	19988655 - 19989012	4			1.00	1.00	1.00	0.00	0.98	1.00
ePt-504212	-	-	2			1.00	0.97	1.00	0.00	0.98	0.99
ePt-504227	5	2680298 - 2681223	4			0.98	0.99	1.00	0.00	1.00	1.00
ePt-504250	6	43566946 - 43567649	3			0.08	0.00	0.00	0.00	1.00	0.84
ePt-504251	7	16370962 - 16371625	4			0.01	0.00	0.00	1.00	0.00	0.00
ePt-504279	4	33449745 - 33450210	2			0.98	1.00	1.00	0.00	0.99	0.99
ePt-504320	7	24823517 - 24823766	4			1.00	1.00	1.00	0.00	1.00	0.98
ePt-504372	2	5180932 - 5181553	1			0.95	1.00	1.00	0.02	0.99	1.00
ePt-504403	7	31125821 - 31126737	1			0.95	0.05	0.00	0.17	0.97	1.00
ePt-504443	2	25953006 - 25954074	1			0.87	0.98	1.00	0.00	0.09	0.35
ePt-504459	1	39912285 - 39912880	4	1	Lat. - Ex.	0.00	0.99	1.00	1.00	1.00	0.98
ePt-504525	11	44022832 - 44023429	1			0.75	0.02	1.00	0.24	0.03	0.25
ePt-504527	6	35761589 - 35762026	1			0.86	0.90	0.00	1.00	0.97	0.03
ePt-504530	6	5450459 - 5451083	4	1	Ex. - Maid.	1.00	0.00	0.00	0.00	0.12	0.09
ePt-504532	4	32443772 - 32444262	1			0.66	0.81	0.00	0.41	1.00	0.54
ePt-504578	2	46693687 - 46694100	1			0.93	1.00	1.00	0.03	1.00	1.00
ePt-504655	11	2876340 - 2876723	1			1.00	0.00	0.04	0.01	0.98	0.99
ePt-504916	6	37142066 - 37142628	2			0.00	1.00	1.00	0.49	0.92	0.85
ePt-562775	2	47781939 - 47782346	1			1.00	1.00	1.00	0.01	1.00	1.00
ePt-562878	8	46347561 - 46348109	4			0.06	0.00	0.00	1.00	0.00	0.00
ePt-562917	3	78953098 - 78953649	5			0.00	0.00	0.00	1.00	0.00	0.00
ePt-562994	11	30182785 - 30183612	2			0.12	0.05	0.00	1.00	0.00	0.01
ePt-563018	2	48252883 - 48253368	2	1	Lat. - Ex.	0.99	0.00	0.46	0.00	0.00	0.02
ePt-563043	4	26979142 - 26979195	3			1.00	1.00	1.00	0.00	0.96	0.99
ePt-563110	4	8681661 - 8682258	1			0.49	0.93	0.00	1.00	0.94	0.87
ePt-563213	10	11618000 - 11618489	1			0.98	0.00	1.00	0.76	0.01	0.51
ePt-563230	4	12468425 - 12468984	1			0.98	1.00	1.00	1.00	0.05	0.02
ePt-563237	6	21101923 - 21102231	1			0.99	0.51	0.01	1.00	0.02	0.04
ePt-563423	2	7264870 - 7265373	1			0.51	0.00	1.00	0.08	0.03	0.07
ePt-563476	6	43949454 - 43950052	1			0.99	0.05	0.00	0.57	1.00	0.90
ePt-563668	-	-	2			0.04	0.01	0.02	0.00	1.00	0.96
ePt-563697	10	10424654 - 10425218	2			0.06	1.00	0.56	0.99	0.00	0.00

ePt-563710	7	48855343 - 48855959	2			1.00	0.06	0.00	0.00	0.05	0.38
ePt-564008	4	31253230 - 31253728	3			0.00	0.13	1.00	0.42	0.00	0.00
ePt-564144	6	43949671 - 43950052	1			0.99	0.05	0.00	0.30	1.00	0.85
ePt-564365	-	-	1			0.92	1.00	0.98	0.03	0.86	0.88
ePt-564519	8	33450636 - 33451157	1			0.08	0.00	1.00	0.17	0.97	0.46
ePt-564626	10	1792829 - 1793143	4			0.02	0.00	0.00	1.00	0.00	0.00
ePt-564631	4	3432124 - 3432896	1			0.01	0.95	0.80	1.00	0.06	0.00
ePt-564865	11	16829021 - 16829441	4			0.00	0.00	0.00	1.00	0.00	0.01
ePt-564938	6	44262448 - 44263003	1			0.09	0.04	0.33	1.00	0.00	0.05
ePt-565082	11	29396714 - 29397102	2			1.00	0.00	0.00	0.65	0.04	0.74
ePt-565209	6	15604679 - 15605337	1			0.04	0.94	1.00	0.94	1.00	0.69
ePt-565346	7	40210953 - 40211332	2			0.06	0.00	0.04	1.00	0.00	0.06
ePt-565453	2	1499090 - 1499473	3			0.99	1.00	0.04	1.00	0.00	0.29
ePt-565468	11	2876347 - 2876723	2			1.00	0.00	0.05	0.00	0.98	0.99
ePt-565516	4	10329874 - 10330100	4			0.05	0.00	0.00	1.00	0.00	0.00
ePt-565584	6	45301093 - 45301497	1			0.92	0.55	0.00	0.06	0.01	0.00
ePt-565738	8	13452769 - 13452999	3	1	Lat. - Ex.	1.00	0.00	0.02	0.06	0.01	0.07
ePt-565962	4	33283880 - 33284370	3			0.97	1.00	0.00	1.00	1.00	0.98
ePt-565993	6	42267730 - 42268500	3			1.00	1.00	1.00	0.00	0.95	0.99
ePt-566203	1	37435438 - 37435761	1			0.05	0.00	0.00	0.99	0.00	0.00
ePt-566371	-	-	1			1.00	1.00	1.00	0.02	1.00	1.00
ePt-566397	1	23994699 - 23995105	2			0.04	0.00	0.00	1.00	0.02	0.11
ePt-566528	4	10280622 - 10280951	1			0.01	0.00	0.00	0.99	0.01	0.03
ePt-566580	11	26688687 - 26689636	1			0.09	0.98	0.73	1.00	0.00	0.03
ePt-566607	7	41301869 - 41302694	1			0.59	0.83	0.40	0.95	0.05	1.00
ePt-566994	11	43761412 - 43761730	1			1.00	1.00	1.00	1.00	0.04	0.70
ePt-567224	-	-	4			0.00	0.90	1.00	1.00	0.01	0.00
ePt-567441	11	43628746 - 43629445	1			0.02	0.01	0.01	0.00	0.48	0.98
ePt-567529	1	23304254 - 23304880	3	1	Lat. - Ex.	0.01	1.00	1.00	1.00	1.00	0.96
ePt-567565	8	69049254 - 69049703	1			1.00	0.01	0.99	0.00	0.63	0.76
ePt-567694	11	8863458 - 8864737	1			0.01	0.94	0.88	0.72	1.00	0.57
ePt-567825	8	1525128 - 1525704	2			0.66	1.00	0.00	0.92	1.00	0.94
ePt-567863	8	8256754 - 8256968	3			0.01	0.00	0.00	1.00	0.00	0.02
ePt-567865	6	20734477 - 20734923	1			0.39	0.01	0.00	0.03	1.00	0.86
ePt-567889	-	-	4			0.00	0.03	0.08	1.00	0.00	0.00

ePt-568021	3	40417872 - 40418125	2			0.00	0.00	0.02	0.81	1.00	0.88
ePt-568093	6	42441007 - 42441260	5			0.00	0.00	0.00	1.00	0.00	0.00
ePt-568370	7	43076619 - 43077174	1			0.73	0.58	0.00	1.00	0.99	0.89
ePt-568410	9	30387273 - 30387545	4			0.00	0.00	0.00	1.00	0.00	0.11
ePt-568543	-	-	3			0.00	1.00	0.04	0.25	0.00	0.02
ePt-568565	6	52666604 - 52667266	7	1	Lat. - Maid.	0.01	1.00	1.00	1.00	0.00	0.00
ePt-568620	10	17180538 - 17180971	3	1	Ex. - Maid.	0.00	1.00	1.00	1.00	0.95	0.49
ePt-568676	7	44715795 - 44716632	1			0.95	0.66	0.00	0.81	0.40	1.00
ePt-568774	2	61877770 - 61878725	1			0.98	1.00	0.01	1.00	1.00	0.98
ePt-568788	9	35359394 - 35359978	2			0.09	0.82	1.00	1.00	0.00	0.63
ePt-568878	8	68652471 - 68652816	5			0.00	0.00	0.00	1.00	0.00	0.00
ePt-568907	-	-	1			0.99	1.00	0.97	0.02	1.00	1.00
ePt-568915	-	-	4			0.07	1.00	0.71	1.00	0.00	0.00
ePt-568986	11	20448362 - 20448695	3	1	Ex. - Maid.	0.00	1.00	1.00	1.00	0.98	0.75
ePt-569359	6	20221876 - 20222749	4			1.00	1.00	0.61	0.00	1.00	1.00
ePt-569366	9	27920171 - 27920470	2			0.47	0.95	1.00	1.00	0.00	0.02
ePt-569377	1	24272055 - 24273310	2			0.97	0.98	1.00	0.00	1.00	0.95
ePt-569385	5	73099527 - 73100341	3			0.98	1.00	1.00	0.00	1.00	0.93
ePt-569485	10	445393 - 445880	3			0.00	0.00	0.04	1.00	0.00	0.01
ePt-569670	-	-	1			0.44	0.68	0.53	1.00	0.00	0.59
ePt-569689	-	-	3			0.95	1.00	1.00	0.00	1.00	0.99
ePt-569786	-	-	4			1.00	1.00	1.00	0.00	0.96	1.00
ePt-569822	-	-	3			1.00	1.00	1.00	0.00	0.98	0.99
ePt-569878	10	35547277 - 35547445	2			0.98	1.00	1.00	0.00	0.96	0.99
ePt-569904	6	41633349 - 41634080	2			0.99	1.00	1.00	0.00	0.96	0.98
ePt-569921	2	60327743 - 60328330	5			1.00	1.00	1.00	0.00	1.00	1.00
ePt-570025	2	24637505 - 24638075	1			1.00	1.00	1.00	0.04	1.00	1.00
ePt-570096	5	6065840 - 6066010	5			1.00	0.99	0.00	1.00	1.00	1.00
ePt-570195	6	41098007 - 41098334	1			0.96	1.00	0.01	0.18	0.98	0.09
ePt-570274	5	11650717 - 11651070	2			0.00	1.00	1.00	0.98	0.48	0.06
ePt-570414	1	15385725 - 15386099	2			0.05	1.00	0.00	1.00	0.05	0.79
ePt-570452	9	38305972 - 38306849	1			0.43	0.83	0.06	0.73	0.99	0.01
ePt-570545	2	57819410 - 57819907	2			0.89	0.86	0.00	1.00	0.00	0.02
ePt-570580	6	29552634 - 29553887	5			0.00	0.99	0.00	1.00	0.00	0.00
ePt-570716	5	477563 - 478242	2			0.37	1.00	1.00	0.65	0.01	0.00

ePt-570774	7	47596482 - 47597147	1			0.91	0.83	0.00	0.85	0.98	1.00
ePt-570860	9	29516549 - 29516882	1			0.01	0.28	1.00	0.08	0.03	0.00
ePt-571051	1	34370826 - 34371740	2			0.99	1.00	0.85	0.00	0.98	1.00
ePt-571109	6	23351368 - 23351454	2			0.04	0.19	1.00	0.00	0.00	0.04
ePt-571161	-	-	1			0.10	0.00	1.00	0.30	0.88	0.13
ePt-571164	11	36305894 - 36306244	2			0.01	0.02	1.00	0.04	0.00	0.24
ePt-571200	-	-	2			0.00	0.56	1.00	1.00	0.12	0.11
ePt-571227	10	38936244 - 38936583	1			0.09	0.98	0.96	1.00	0.00	0.29
ePt-571236	10	35531081 - 35531332	1			0.04	0.00	0.99	0.00	0.01	0.02
ePt-571237	1	7763353 - 7763733	1			0.92	0.49	1.00	0.00	0.98	0.97
ePt-571292	4	33283069 - 33283775	4			0.00	0.00	1.00	0.42	0.00	0.00
ePt-571353	5	5859548 - 5860074	1			0.32	0.02	0.48	1.00	0.01	0.20
ePt-571444	11	29467970 - 29468429	1			0.00	0.00	0.99	0.00	0.00	0.00
ePt-571455	10	13099737 - 13100274	1			0.07	0.96	0.14	1.00	0.00	0.06
ePt-571464	8	68868496 - 68869113	1			0.44	0.00	1.00	0.10	0.03	0.02
ePt-571574	9	22695871 - 22696815	3			0.03	1.00	0.98	1.00	0.00	0.01
ePt-571575	8	17619277 - 17619634	4			0.00	1.00	1.00	0.93	0.62	0.00
ePt-571631	8	66765136 - 66765610	2			0.12	0.80	1.00	0.13	0.00	0.98
ePt-571640	4	31253202 - 31253489	3			0.00	0.13	1.00	0.44	0.00	0.00
ePt-571679	7	7972535 - 7972925	1			0.24	1.00	1.00	0.99	0.43	0.01
ePt-571768	4	28522685 - 28523027	2			0.00	0.48	0.98	1.00	0.32	0.98
ePt-571818	2	6890981 - 6891379	4			0.00	0.01	0.01	1.00	0.00	0.00
ePt-571849	4	35478484 - 35479217	3			0.22	0.86	0.00	1.00	0.00	0.00
ePt-572163	10	8119121 - 8119295	3			0.99	1.00	1.00	0.00	1.00	0.99
ePt-572182	-	-	1			1.00	1.00	1.00	0.04	1.00	0.96
ePt-572304	1	14851576 - 14851981	1			0.01	1.00	1.00	0.93	0.66	0.75
ePt-572379	6	40007565 - 40008380	3			0.99	1.00	1.00	0.00	0.99	1.00
ePt-572381	6	39216724 - 39217348	3			0.98	0.00	0.00	0.00	1.00	0.40
ePt-572411	-	-	1			1.00	0.01	0.99	0.00	0.63	0.77
ePt-572645	-	-	1			0.02	0.00	1.00	0.18	0.99	0.52
ePt-572702	10	7410971 - 7411457	3			1.00	0.99	0.97	0.00	1.00	0.98
ePt-572873	5	91121 - 91795	1			0.01	1.00	0.99	0.95	0.99	0.92
ePt-572883	6	34430192 - 34430614	4	1	Lat. - Ex.	0.00	0.25	0.00	0.01	1.00	1.00
ePt-572918	4	37510795 - 37511287	1			0.83	1.00	0.02	0.43	1.00	1.00
ePt-572981	-	-	2			0.97	0.93	1.00	0.00	1.00	0.96

ePt-573103	10	11209256 - 11210168	2			0.72	0.00	0.00	0.06	1.00	0.86
ePt-573119	7	38149334 - 38150056	4			1.00	0.00	0.00	0.46	0.98	1.00
ePt-573190	3	61348704 - 61349337	1			0.40	1.00	0.03	0.93	0.73	0.88
ePt-573316	10	35734686 - 35735255	4			0.00	0.00	0.11	1.00	0.00	0.00
ePt-573491	6	52424629 - 52425311	1			0.95	0.04	1.00	0.69	0.77	0.95
ePt-573579	5	4405287 - 4405667	3	1	Ex. - Maid.	1.00	0.00	0.00	0.00	0.18	0.54
ePt-573791	5	615428 - 615761	1			0.05	1.00	1.00	0.90	1.00	0.72
ePt-573833	2	7448226 - 7448556	6			1.00	0.00	0.00	0.64	1.00	1.00
ePt-573990	6	20731260 - 20731690	9	2	Maid. from both Ex. and Lat.	1.00	0.00	0.00	0.00	1.00	1.00
ePt-574065	11	34378109 - 34378505	2			0.59	0.00	0.07	0.00	1.00	0.97
ePt-574160	-	-	2			0.08	0.00	0.00	0.01	1.00	0.30
ePt-574213	6	2116439 - 2116930	1			0.01	1.00	1.00	0.99	0.91	0.23
ePt-574296	3	52429693 - 52430129	2			0.97	1.00	0.92	0.00	1.00	0.97
ePt-574332	10	3453632 - 3454061	3			0.00	1.00	0.87	1.00	1.00	0.65
ePt-574348	7	35032771 - 35033454	1			0.49	1.00	1.00	0.01	0.98	1.00
ePt-574352	8	67871491 - 67871774	3			0.62	0.00	0.00	0.00	1.00	0.91
ePt-574375	11	23558475 - 23558778	1			0.00	0.00	0.00	0.00	0.99	0.92
ePt-574478	6	35959337 - 35959919	1			0.94	0.04	1.00	0.32	1.00	1.00
ePt-574488	2	24392217 - 24392435	4			0.00	0.00	0.00	0.00	1.00	0.63
ePt-574558	4	40560173 - 40560523	3	1	Ex. - Maid.	0.00	1.00	1.00	1.00	0.03	0.87
ePt-574618	11	17362894 - 17363257	3			0.01	0.00	0.03	1.00	0.00	0.00
ePt-574621	6	18739076 - 18740139	1			0.84	0.81	1.00	0.00	0.99	0.76
ePt-574631	11	42438626 - 42439162	3			1.00	0.83	0.00	1.00	0.01	0.27
ePt-574757	7	39672619 - 39673447	3			1.00	0.90	1.00	0.00	1.00	0.97
ePt-574780	8	67626164 - 67626877	2			1.00	0.01	0.00	0.02	0.92	0.98
ePt-574815	10	11005641 - 11006674	3			0.98	1.00	1.00	0.00	1.00	0.99
ePt-574848	2	48798089 - 48799029	4			0.99	1.00	1.00	0.00	1.00	1.00
ePt-574866	6	24074690 - 24075306	1			0.02	0.96	0.00	1.00	0.94	0.97
ePt-574890	8	9997254 - 9997876	5			0.05	0.00	0.00	0.00	1.00	0.08
ePt-574912	8	18280418 - 18280995	1			0.98	1.00	0.99	0.01	1.00	0.78
ePt-574967	8	13124212 - 13124615	3			0.15	0.00	0.00	0.00	1.00	0.73
ePt-574973	-	-	1			0.98	0.99	0.89	0.00	0.98	0.84
ePt-574985	-	-	2			0.98	0.95	1.00	0.00	1.00	0.95
ePt-575044	4	23393470 - 23394826	2			0.99	1.00	0.92	0.00	1.00	0.95

ePt-575077	6	45519628 - 45520175	4			1.00	1.00	1.00	0.00	0.98	1.00
ePt-575211	10	21407284 - 21407543	1			1.00	0.00	0.01	0.60	0.07	0.86
ePt-575216	3	12943257 - 12943484	3			0.27	0.00	0.00	0.07	0.02	1.00
ePt-575224	9	37667705 - 37668093	3	1	Lat. - Ex.	0.03	0.04	0.67	0.00	1.00	0.99
ePt-575292	8	8077482 - 8077797	5			1.00	1.00	1.00	0.00	1.00	1.00
ePt-575300	-	-	4			0.54	0.00	0.00	0.00	0.01	1.00
ePt-575357	5	9008242 - 9008501	1			1.00	1.00	1.00	1.00	0.01	0.97
ePt-575467	-	-	2			0.04	1.00	0.00	1.00	0.07	0.77
ePt-575490	-	-	3			1.00	1.00	1.00	0.00	0.99	0.93
ePt-575575	3	62471683 - 62473044	2			1.00	0.18	0.04	0.00	1.00	0.99
ePt-575587	2	60078293 - 60078594	8	1	Ex. - Maid.	1.00	0.00	0.00	0.00	0.03	1.00
ePt-575640	-	-	2			0.01	0.00	1.00	0.00	0.02	0.82
ePt-575679	-	-	1			0.27	0.00	0.00	0.00	0.00	0.98
ePt-575745	10	25707047 - 25707325	3			1.00	0.96	0.53	0.00	1.00	1.00
ePt-575769	3	12658747 - 12659097	1			0.83	0.00	0.28	0.24	0.27	1.00
ePt-599530	2	63752070 - 63752875	2			0.00	0.00	0.00	0.00	0.99	0.01
ePt-599538	6	31936178 - 31936913	1			0.16	0.01	0.00	0.03	1.00	0.22
ePt-599605	9	24944742 - 24945438	1			0.00	0.00	0.00	0.00	0.92	0.97
ePt-599659	-	-	4			0.00	1.00	1.00	0.00	0.67	0.14
ePt-599692	9	28269131 - 28269535	1			0.76	0.30	0.00	0.04	1.00	0.20
ePt-599755	-	-	3			1.00	0.71	0.62	0.00	1.00	1.00
ePt-599844	6	39622771 - 39623248	1			0.37	0.62	0.00	0.80	1.00	0.68
ePt-599901	7	43249147 - 43249832	1			0.93	0.00	0.85	0.00	0.24	0.00
ePt-599923	-	-	3			0.87	1.00	1.00	0.00	0.99	1.00
ePt-599987	2	32787514 - 32787907	3	1	Ex. - Maid.	1.00	0.00	0.00	0.00	0.07	0.82
ePt-600173	11	43761412 - 43761730	1			1.00	1.00	1.00	1.00	0.03	0.61
ePt-600341	5	11650717 - 11651028	2			0.00	1.00	1.00	0.99	0.53	0.06
ePt-600394	6	3513758 - 3514185	1			0.33	0.12	0.84	0.00	1.00	0.22
ePt-600416	9	38290674 - 38291227	1			0.53	0.07	0.02	0.00	1.00	0.13
ePt-600497	3	40647470 - 40648509	1			0.99	1.00	1.00	0.01	0.99	0.65
ePt-600541	10	8310265 - 8310822	2			0.08	0.00	0.24	0.00	1.00	0.99
ePt-600560	11	16052831 - 16053425	1			0.02	0.72	0.24	0.25	1.00	0.63
ePt-600658	2	24940948 - 24941553	1			0.38	0.99	0.00	0.99	0.99	0.27
ePt-600691	7	25039462 - 25039887	1			0.97	0.00	0.79	0.43	0.99	1.00
ePt-600709	1	39910659 - 39911653	1			0.00	0.96	1.00	0.99	0.58	0.89

ePt-636573	11	36165604 - 36166310	4			0.22	0.00	0.00	0.00	1.00	0.10
ePt-636638	6	35309480 - 35310267	1			0.00	0.00	0.00	0.00	0.99	0.84
ePt-636736	2	52558946 - 52559427	3			0.02	0.00	0.00	1.00	0.00	0.01
ePt-636783	11	40132816 - 40133456	9	2	Maid. from both Ex. and Lat.	0.00	1.00	1.00	1.00	0.00	0.00
ePt-636828	6	36604173 - 36604654	2			0.98	0.01	0.21	0.00	1.00	1.00
ePt-636880	4	36760455 - 36760990	1			0.72	1.00	0.00	0.96	0.42	0.09
ePt-636956	6	19423508 - 19424262	3			0.05	0.00	0.00	1.00	0.00	0.29
ePt-637106	3	41745216 - 41745560	2			0.25	1.00	0.01	0.78	0.99	0.01
ePt-637233	11	45272900 - 45273724	1			0.48	0.24	0.46	0.13	0.00	0.95
ePt-637257	4	2837151 - 2837734	1			1.00	1.00	1.00	0.03	1.00	1.00
ePt-637567	10	10744963 - 10745635	3			0.97	1.00	1.00	0.00	0.98	1.00
ePt-637643	10	416384 - 416833	2			0.70	0.07	0.00	0.00	1.00	0.46
ePt-637835	6	43949460 - 43949748	1			0.99	0.06	0.00	0.57	1.00	0.90
ePt-638074	1	24253591 - 24254095	1			0.68	0.00	0.00	0.02	0.00	0.95
ePt-638154	-	-	4			0.01	1.00	0.01	0.00	0.00	0.03
ePt-638162	8	13452769 - 13452974	3	1	Lat. - Ex.	1.00	0.00	0.01	0.06	0.01	0.08
ePt-638305	4	31553755 - 31554220	2			0.46	0.12	0.00	0.10	1.00	0.00
ePt-638325	9	28580499 - 28580893	1			0.76	0.33	0.00	0.02	1.00	0.22
ePt-638596	9	37863608 - 37863712	1			0.38	1.00	0.76	1.00	1.00	0.05
ePt-638618	1	28182327 - 28182655	5	1	Lat. - Ex.	0.00	0.00	0.00	0.00	1.00	0.98
ePt-638693	-	-	4			1.00	1.00	1.00	0.00	1.00	0.99
ePt-638726	-	-	6			1.00	0.00	1.00	0.00	1.00	0.99
ePt-638871	-	-	5			0.00	0.00	0.00	0.00	1.00	0.00
ePt-638901	4	19170203 - 19170879	1			0.98	0.05	0.00	0.12	0.26	0.00
ePt-639040	6	20457309 - 20457709	3			1.00	1.00	0.04	1.00	0.00	0.31
ePt-639134	2	63150230 - 63150796	4	1	Lat. - Ex.	0.00	0.85	1.00	1.00	1.00	0.99
ePt-639336	10	4946231 - 4946380	3			1.00	0.00	0.00	0.53	0.02	0.18
ePt-639434	3	12658394 - 12659097	1			0.82	0.00	0.26	0.24	0.26	1.00
ePt-639436	10	27331855 - 27332083	3			0.00	0.98	1.00	0.99	0.00	0.00
ePt-639448	1	30488625 - 30489294	1			0.27	0.85	0.07	1.00	0.00	0.11
ePt-639564	9	37998377 - 37998818	6	1	Ex. - Maid.	1.00	0.00	0.00	0.00	1.00	0.99
ePt-639625	9	25489792 - 25490672	1			0.00	0.16	0.01	1.00	0.91	0.14
ePt-639634	6	41416137 - 41416699	1			0.98	0.01	0.00	0.00	0.00	0.40
ePt-639726	10	17783877 - 17784403	3			0.07	0.98	0.00	1.00	0.00	0.02

ePt-639757	3	62426065 - 62426640	4			0.93	0.00	0.01	0.00	1.00	1.00
ePt-639838	2	23173362 - 23173701	3			1.00	0.00	0.00	0.11	0.03	0.60
ePt-639853	5	11650717 - 11650992	2			0.00	1.00	1.00	0.97	0.49	0.05
ePt-639954	11	45266135 - 45266980	1			0.46	0.25	0.50	0.16	0.00	0.95
ePt-639987	9	14168059 - 14169124	2			0.99	0.99	0.99	0.00	1.00	0.95
ePt-640029	2	62586747 - 62587260	2			0.00	0.58	0.00	0.69	1.00	0.91
ePt-640042	8	13112669 - 13113178	5	2	Ex. from both Lat. and Maid.	0.00	1.00	1.00	1.00	1.00	0.99
ePt-640051	2	59441552 - 59442173	1			0.99	1.00	1.00	0.04	0.97	1.00
ePt-640083	1	27512604 - 27512891	1			0.33	1.00	1.00	0.02	0.97	0.93
ePt-640200	6	53749879 - 53750207	6			1.00	0.00	0.00	0.64	1.00	1.00
ePt-640389	6	39211057 - 39211650	4			1.00	0.00	0.00	0.01	1.00	0.93
ePt-640436	10	23940438 - 23940926	1			0.14	0.01	1.00	0.16	1.00	1.00
ePt-640499	2	55163968 - 55164450	1			0.29	0.61	1.00	0.20	0.00	0.04
ePt-640610	-	-	2			0.99	1.00	1.00	0.99	0.98	0.01
ePt-640676	-	-	2			0.74	0.99	1.00	0.00	0.99	0.84
ePt-640713	9	25848610 - 25849297	1			1.00	0.75	0.01	0.02	0.03	0.25
ePt-640742	10	37958875 - 37959245	2			0.00	1.00	1.00	0.08	0.01	0.04
ePt-640772	6	44768681 - 44769677	2			0.99	1.00	1.00	0.00	0.99	0.65
ePt-640828	8	59037881 - 59039101	3			1.00	0.51	1.00	0.00	1.00	0.95
ePt-641020	8	40968043 - 40968806	2			0.98	0.96	1.00	0.00	1.00	0.99
ePt-641068	10	21388436 - 21389178	6			1.00	0.00	1.00	0.00	1.00	0.99
ePt-641085	-	-	1			0.98	0.02	0.01	1.00	0.99	0.97
ePt-641088	1	38125875 - 38126727	2	1	Lat. - Ex.	1.00	1.00	1.00	1.00	0.01	0.02
ePt-641150	10	10424654 - 10425218	2			0.08	1.00	0.56	0.99	0.00	0.00
ePt-641176	4	31253249 - 31253728	3			0.00	0.11	1.00	0.75	0.00	0.00
ePt-641191	2	63637892 - 63638251	2			0.96	1.00	0.44	1.00	0.00	0.53
ePt-641343	2	2540372 - 2540656	3			1.00	0.01	0.00	0.18	1.00	1.00
ePt-641448	8	533975 - 534485	1			0.76	0.18	0.00	0.24	1.00	0.99
ePt-641474	-	-	3			0.98	1.00	1.00	0.00	1.00	0.75
ePt-641496	-	-	1			0.71	0.08	0.00	0.02	1.00	0.49
ePt-641499	-	-	3			1.00	1.00	1.00	0.00	0.99	0.99
ePt-641504	2	47291472 - 47291829	1			1.00	1.00	0.99	0.99	1.00	0.11
ePt-641538	8	16559647 - 16560246	1			0.83	0.99	0.99	0.00	0.99	0.99
ePt-641547	-	-	3			0.53	1.00	1.00	0.00	1.00	0.82

ePt-641548	-	-	5			1.00	1.00	1.00	0.00	1.00	1.00
ePt-641577	-	-	2			0.98	1.00	1.00	0.00	0.96	0.98
ePt-641587	6	24537087 - 24537495	2	1	Lat. - Ex.	0.05	1.00	1.00	1.00	1.00	1.00
ePt-641617	6	15604648 - 15604819	2			0.00	0.96	1.00	0.94	1.00	0.77
ePt-641620	-	-	5			1.00	1.00	1.00	0.00	1.00	1.00
ePt-641636	1	40259717 - 40260152	5			0.00	0.00	1.00	0.00	0.00	0.00
ePt-641637	-	-	1			0.98	1.00	0.99	0.00	0.99	0.97
ePt-641642	6	3457775 - 3458066	5	1	Lat. - Ex.	0.00	0.99	1.00	0.00	0.99	0.94
ePt-641656	-	-	2			0.07	1.00	0.96	1.00	0.01	0.00
ePt-641659	1	15385725 - 15386099	2			0.05	1.00	0.00	1.00	0.07	0.80
ePt-641671	4	36889844 - 36890292	2			0.01	0.75	1.00	0.07	0.00	0.00
ePt-641678	8	8781788 - 8782310	1			1.00	0.90	0.94	0.84	0.30	0.10
ePt-641682	-	-	4			1.00	1.00	1.00	0.00	0.99	1.00
ePt-641689	2	62441158 - 62441624	4			1.00	0.98	1.00	0.00	1.00	1.00
ePt-641712	5	36706179 - 36706848	1			0.44	0.07	1.00	0.11	0.12	0.00
ePt-641739	-	-	3			0.99	0.99	1.00	0.00	1.00	0.98
ePt-641749	10	36759693 - 36760083	3			0.98	1.00	1.00	0.00	1.00	0.98
ePt-641762	-	-	1			0.78	1.00	0.03	0.96	0.44	0.09
ePt-641766	-	-	5			1.00	1.00	1.00	0.00	1.00	1.00
ePt-641781	-	-	5			1.00	1.00	1.00	0.00	1.00	1.00
ePt-641791	6	25593162 - 25593179	4			1.00	1.00	1.00	0.00	1.00	0.99
ePt-641798	8	58276080 - 58276672	3			0.00	1.00	0.31	0.85	0.00	0.01
ePt-641819	-	-	4			1.00	1.00	1.00	0.00	0.96	1.00
ePt-641823	-	-	4			1.00	1.00	1.00	0.00	0.97	1.00
ePt-641827	-	-	3			1.00	1.00	1.00	0.00	0.97	0.98
ePt-641828	-	-	4			1.00	1.00	1.00	0.00	1.00	0.99
ePt-641831	-	-	5			1.00	1.00	1.00	0.00	1.00	1.00
ePt-641833	-	-	4			0.99	1.00	1.00	0.00	1.00	1.00
ePt-641835	-	-	2			1.00	1.00	0.99	0.00	0.99	0.99
ePt-641954	-	-	1			0.87	1.00	0.96	0.00	0.95	0.89
ePt-642223	9	21811654 - 21812750	3			1.00	1.00	0.99	0.00	1.00	0.99
ePt-642295	6	18158146 - 18158445	1			0.10	0.00	1.00	0.30	0.91	0.13
ePt-642408	-	-	2			0.00	0.95	0.81	1.00	0.08	0.00
ePt-642447	11	15424791 - 15425194	1			0.30	1.00	0.65	0.62	0.06	0.00
ePt-642471	1	15429581 - 15430014	3			0.05	0.01	0.00	1.00	0.00	0.03

ePt-642562	9	33491547 - 33491869	4			1.00	1.00	1.00	0.00	1.00	0.96
ePt-642570	11	36548715 - 36549111	8	1	Ex. - Maid.	1.00	0.00	0.00	0.00	0.01	1.00
ePt-642748	8	33450636 - 33450936	1			0.01	0.00	1.00	0.18	0.98	0.47
ePt-642862	8	17626303 - 17626498	3			0.65	1.00	0.00	0.79	0.05	1.00
ePt-642864	4	22158383 - 22158974	1			1.00	0.13	0.00	0.16	0.38	0.95
ePt-642873	8	49702301 - 49702648	6	1	Lat. - Maid.	0.99	0.00	0.00	0.00	1.00	1.00
ePt-642970	8	14512766 - 14512981	2			1.00	1.00	1.00	1.00	0.03	1.00
ePt-642976	6	20123958 - 20124636	1			0.16	0.00	0.00	0.00	0.01	0.99
ePt-642994	7	19927586 - 19928160	4			0.09	0.00	0.00	0.00	1.00	0.02
ePt-643010	7	44839187 - 44840127	2			0.99	1.00	1.00	1.00	1.00	0.01
ePt-643208	9	6020882 - 6021330	1			0.10	0.24	0.98	0.38	0.97	1.00
ePt-643303	5	36350274 - 36350291	1			0.02	0.01	0.01	0.78	0.44	0.98
ePt-643412	9	38929203 - 38929688	4			0.99	0.99	1.00	0.00	1.00	1.00
ePt-643444	1	13720802 - 13720874	3			1.00	0.09	1.00	0.00	1.00	0.95
ePt-643553	9	26344501 - 26344928	1			0.85	0.93	1.00	0.00	0.99	0.93
ePt-643595	2	7655440 - 7656191	1			0.98	0.02	0.01	1.00	0.99	0.97
ePt-643603	2	48215890 - 48216423	1			0.74	0.00	0.00	0.24	0.00	0.96
ePt-643644	6	18860500 - 18861126	2			1.00	0.28	0.00	0.78	0.49	1.00
ePt-643763	2	8371853 - 8372124	1			0.99	0.96	0.99	0.00	0.97	1.00
ePt-643799	2	3295967 - 3296445	2			0.82	0.00	0.00	0.54	0.28	1.00
ePt-643941	10	9054079 - 9054555	2			0.08	1.00	0.17	0.98	0.00	0.00
ePt-643956	2	61080704 - 61081373	4			0.00	1.00	0.99	1.00	0.00	0.49
ePt-643963	10	11215132 - 11215778	5			0.00	0.00	0.00	0.00	1.00	0.08
ePt-643991	8	9998403 - 9998634	6	1	Ex. - Maid.	1.00	0.00	0.00	0.00	1.00	0.56
ePt-644024	1	22620997 - 22621429	1			0.08	0.54	0.89	1.00	0.88	0.00
ePt-644040	8	53455710 - 53456481	1			0.05	0.53	0.05	0.39	1.00	0.93
ePt-644086	-	-	1			0.09	0.92	1.00	0.00	0.04	0.18
ePt-644176	10	13484978 - 13485787	2			0.44	0.01	0.00	0.00	1.00	0.28
ePt-644182	4	31515580 - 31516212	1			0.14	1.00	0.99	1.00	0.03	1.00
ePt-644338	11	42683869 - 42684909	3			0.97	1.00	1.00	0.00	1.00	0.95
ePt-644345	1	33110988 - 33112002	2			1.00	0.00	0.06	0.00	0.93	0.33
ePt-644384	3	12574722 - 12575703	1			0.79	1.00	0.98	0.00	0.94	0.81

Supporting Information Table S4. Spearman correlations (r_s) of chromosome average global H_{HW} (six species H_{HW} average), global F_{ST} and the proportion of species differentiating markers (SDMs) with chromosome features (n=11) for different DArT marker classes. The chromosome features include: chromosome length (Mbp), recombination rate (cM/Mbp), gene density (genes per Mbp), density of retrotransposons, DNA transposons and uncategorised transposons (per Mbp); as well as the number of clusters of tandemly duplicated genes, segmental duplications and duplications attributable to lineage specific whole genome duplication (WGD) and more ancient hexaploidization relative to the number of genes on the chromosome. Data on chromosome features was derived from Myburg *et al.* (2014), except the recombination rate which is from Petroli *et al.* (2012). The significance of correlations after Bonferroni adjustment for multiple comparisons within each population parameter and marker class (n=10) is shown (* = P<0.05; ** = P<0.01; *** = P<0.001).

Parameter and chromosome feature	All DArT markers	DArT markers within genes	DArT markers within 5kbp of genes	DArT markers more than 5 kbp of a gene	DArT markers within genes outside of tandem duplicate clusters	DArT markers within genes within tandem duplicate clusters
	r_s	r_s	r_s	r_s	r_s	r_s
Global H_{HW}						
Chromosome length	0.51	0.29	0.45	0.23	0.28	0.45
Recombination rate	-0.72	-0.44	-0.34	-0.42	-0.58	-0.32
Gene density	-0.88**	-0.54	-0.50	-0.66	-0.60	-0.34
Retrotransposon density	-0.18	-0.07	-0.25	-0.18	0.05	-0.35
DNA transposon density	0.65	0.43	0.42	0.32	0.38	0.48
Uncategorised transposon density	0.76	0.45	0.47	0.57	0.61	0.12
Tandem duplicates	0.85*	0.68	0.48	0.57	0.82*	0.30
Segmental duplicates	0.55	0.57	0.43	0.23	0.27	0.80
Lineage WGD duplicates	-0.73	-0.59	-0.52	-0.60	-0.60	-0.07

Hexaploidization duplicates	-0.39	-0.45	-0.36	0.00	-0.24	-0.63
Global F_{ST}						
Chromosome length	-0.70	-0.64	-0.80*	-0.80*	-0.38	-0.89**
Recombination rate	0.76	0.81*	0.68	0.70	0.64	0.55
Gene density	0.92***	0.95***	0.65	0.75	0.79*	0.44
Retrotransposon density	0.34	0.22	0.56	0.55	0.01	0.78*
DNA transposon density	-0.81*	-0.81*	-0.72	-0.78*	-0.54	-0.67
Uncategorised transposon density	-0.85*	-0.84*	-0.65	-0.74	-0.89**	-0.38
Tandem duplicates	-0.78*	-0.85**	-0.59	-0.69	-0.87**	-0.31
Segmental duplicates	-0.65	-0.69	-0.74	-0.50	-0.39	-0.52
Lineage WGD duplicates	0.75	0.73	0.51	0.65	0.84*	0.04
Hexaploidization duplicates	0.63	0.57	0.65	0.69	0.35	0.71
SDMs						
Chromosome length	-0.49	-0.62	-0.17	-0.08	-0.43	-0.49
Recombination rate	0.65	0.76	0.16	0.27	0.65	0.37
Gene density	0.75	0.75	0.38	0.53	0.67	0.22
Retrotransposon density	0.10	0.15	0.11	-0.14	0.13	0.13
DNA transposon density	-0.65	-0.73	-0.25	-0.37	-0.55	-0.41
Uncategorised transposon density	-0.75	-0.74	-0.39	-0.39	-0.81*	-0.16
Tandem duplicates	-0.85**	-0.90**	-0.48	-0.53	-0.95***	0.17
Segmental duplicates	-0.72	-0.62	-0.73	-0.68	-0.48	-0.14
Lineage WGD duplicates	0.75	0.65	0.45	0.67	0.76	-0.22
Hexaploidization duplicates	0.57	0.60	0.31	0.38	0.45	0.39

References:

- Myburg AA, Grattapaglia D, Tuskan GA, Hellsten U, Hayes RD, Grimwood J, Jenkins J, Lindquist E, Tice H, Bauer D *et al.* 2014.** The genome of *Eucalyptus grandis*. *Nature* **510** (7505): 356-362.
- Petroli CD, Sansaloni CP, Carling J, Steane DA, Vaillancourt RE, Myburg AA, da Silva OB, Jr., Pappas GJ, Jr., Kilian A, Grattapaglia D. 2012.** Genomic characterization of DArT markers based on high-density linkage analysis and physical mapping to the *Eucalyptus* genome. *PLoS ONE* **7**: e44684.

Supporting Information Table S5. Number of Pfam codes and GO terms for genes identified within species differentiating marker (SDM) and non-SDM 10 Kbp regions.

10 Kbp region by marker type	Number of genes within region	Pfam codes		GO terms	
		<i>n</i>	% ^a	<i>n</i>	% ^a
SDM	378	266	70.4	187	49.5
Non-SDM	2352	1694	72.0	1272	54.1
Overlapping SDM and non-SDM marker regions	74	57	77.0	38	51.4
Total	2804	2017	71.9	1497	53.4

^aPercentage of 'number of genes identified'

Supporting Information Table S6. Number and percentage of genes within species differentiating marker (SDM) and non-SDM groups mapped to second level GO terms. The ‘Graphed’ column indicates the ‘major’ (= YES) GO terms presented in Supporting Information Fig. S6

GO term ID	Description	GO category ^a	Non-SDM gene group (1272 genes)			SDM gene group (225 genes)			Graphed
			<i>N</i> genes having GO category annotations	Genes assigned to GO terms		<i>N</i> genes having GO category annotations	Genes assigned to GO terms		
				<i>n</i>	Percent		<i>n</i>	Percent	
GO:0008152	metabolic process	BP	582	492	84.5	101	79	78.2	YES
GO:0009987	cellular process	BP	582	374	64.3	101	74	73.3	YES
GO:0023052	signaling	BP	582	13	2.2	101	1	1.0	YES
GO:0032501	multicellular organismal process	BP	582	10	1.7	101	1	1.0	YES
GO:0044085	cellular component biogenesis	BP	582	9	1.5	101	1	1.0	YES
GO:0050896	response to stimulus	BP	582	34	5.8	101	6	5.9	YES
GO:0051179	localization	BP	582	52	8.9	101	13	12.9	YES
GO:0065007	biological regulation	BP	582	67	11.5	101	9	8.9	YES
GO:0000003	reproduction	BP	582	9	1.5	101	0	0.0	NO
GO:0016043	cellular component organization	BP	582	10	1.7	101	0	0.0	NO
GO:0051704	multi-organism process	BP	582	9	1.5	101	0	0.0	NO

GO:0071554	cell wall organization or biogenesis	BP	582	6	1.0	101	0	0.0	NO
GO:0016265	death	BP	582	0	0.0	101	1	1.0	NO
GO:0016032	viral reproduction	BP	582	2	0.3	101	1	1.0	NO
GO:0032502	developmental process	BP	582	1	0.2	101	1	1.0	NO
GO:0005623	cell	CC	252	251	99.6	64	64	100.0	YES
GO:0031974	membrane-enclosed lumen	CC	252	7	2.8	64	1	1.6	YES
GO:0032991	macromolecular complex	CC	252	52	20.6	64	13	20.3	YES
GO:0043226	organelle	CC	252	74	29.4	64	19	29.7	YES
GO:0003824	catalytic activity	MF	867	314	36.2	134	59	44.0	YES
GO:0005198	structural molecule activity	MF	867	19	2.2	134	2	1.5	YES
GO:0005215	transporter activity	MF	867	26	3.0	134	5	3.7	YES
GO:0005488	binding	MF	867	578	66.7	134	83	61.9	YES
GO:0009055	electron carrier activity	MF	867	8	0.9	134	0	0.0	NO
GO:0060089	molecular transducer activity	MF	867	4	0.5	134	0	0.0	NO
GO:0016209	antioxidant activity	MF	867	2	0.2	134	1	0.7	NO
GO:0030234	enzyme regulator activity	MF	867	7	0.8	134	1	0.7	NO
GO:0045735	nutrient reservoir activity	MF	867	5	0.6	134	1	0.7	NO

^aGO category: BP = biological process; CC = cellular component; MF = molecular function

Supporting Information Table S7. Gene ontology (GO) terms detected as being significantly over- or under-represented ($P \leq 0.05$) for genes in the species differentiating marker (SDM) 10kb region gene group (test set) relative to genes within all DArT marker 10kb regions (reference set). GO enrichment was tested in Blast2GO using a Fishers exact test. No GO terms remained significant when applying a false discovery rate of 0.05 to account for multiple testing.

Gene ontology			Number of genes annotated with GO term		Number of genes not annotated with GO term		Enrichment test results	
Term	Description	Category ^a	Test set	Ref. set	Test set	Ref. set	<i>P</i> -value	Direction of enrichment
GO:0005515	protein binding	F	36	311	189	961	0.006	under
GO:0044425	membrane part	C	23	70	202	1202	0.010	over
GO:0016021	integral to membrane	C	19	56	206	1216	0.019	over
GO:0005488	binding	F	83	578	142	694	0.020	under
GO:0031224	intrinsic to membrane	C	19	57	206	1215	0.020	over
GO:0016151	nickel cation binding	F	2	0	223	1272	0.023	over
GO:0005622	intracellular	C	36	137	189	1135	0.031	over
GO:0016491	oxidoreductase activity	F	14	41	211	1231	0.034	over
GO:0005623	cell	C	36	140	189	1132	0.042	over
GO:0044464	cell part	C	36	140	189	1132	0.042	over
GO:0044424	intracellular part	C	29	107	196	1165	0.043	over
GO:0016020	membrane	C	33	128	192	1144	0.047	over

^aGO category: C = cellular component; F = molecular function.

Supporting Information Note S1 Ascertainment bias in DArT markers according to species of origin

The species from which the DArT markers were derived may affect estimates of diversity and divergence. While Steane *et al.*, (2011) reported no evidence for strong ascertainment bias, they did note the possibility of greater polymorphisms in DArTs originating from the same taxonomic section as those from which the markers were derived (e.g. section *Maidenaria* versus section *Latoangulatae*). While 68 phylogenetically diverse species were used to construct the DArT array used in the present study (Sansaloni *et al.*, 2010; Steane *et al.*, 2011), species from the section *Latoangulatae* were the dominant source of DArT clones (S1 Table 1).

Supporting Information Note S1 Table 1. Species from which DArT markers used in the present study originated and the number of DArT markers they contributed to the data set.

Genus/subgenus	Section	Species of origin	N DArT Markers
<i>Corymbia</i>		<i>Corymbia</i> sp.	33
<i>subg Eucalyptus</i>		<i>E. pilularis</i>	56
<i>Latoangulatae</i>	<i>Latoangulatae</i>	<i>E. grandis</i>	966
<i>Latoangulatae</i>	<i>Latoangulatae</i>	<i>E. grandis x urophylla</i>	185
<i>Latoangulatae</i>	<i>Latoangulatae</i>	<i>E. urophylla</i>	175
<i>Symphyomyrtus</i>	<i>Exsertaria</i>	<i>E. camaldulensis</i>	59
<i>Symphyomyrtus</i>	<i>Maidenaria</i>	<i>E. globulus</i>	494
<i>Symphyomyrtus</i>	<i>Maidenaria</i>	<i>E. nitens</i>	156
<i>Unknown</i> ¹	<i>Unknown</i>	<i>Unknown</i>	716
TOTAL			2840

¹Species of origin is unknown since DNA from 64 species was pooled together.

To test whether the species of origin affected diversity (global H_{HW}) and divergence (global F_{ST} and SDMs) parameters, a linear model was fitted to the DArT data (n=2840) which included species of origin (9 levels as listed in S1 Table 1), gene proximity (4 levels - intragenic outside of tandemly repeated gene clusters, intragenic within tandemly repeated gene clusters, within 5 Kbp of a gene and greater than Kbp of a gene), chromosome (11 levels)

and their interactions as fixed effects. The model was fitted using PROC GLIMMIX of SAS™.

A normal distribution fitted for global H_{HW} and global F_{ST} , and Poisson model with a log link function was fitted for the proportion of SDMs. Due to sparse presences, only main effects were tested for SDMs. All main effects were significant for global H_{HW} , whereas species of DArT origin did not have a significant ($P < 0.05$) effect on global F_{ST} or SDMs (S1 Table 2).

Supporting Information Note S1 Table 2. Results of linear models fitted testing the effects of gene proximity (DArT_position), species of origin (Species), chromosome and their interactions on marker global H_{HW} , global F_{ST} and proportion of species differentiating markers (SDMs).

Term	df	Global Hhw		Global Fst		SDM	
		F	Prob	F	Prob	F	Prob
DArT_position	3	7.6	<0.001	8.58	<0.001	7.0	0.000
Species	8	3.7	0.000	1.82	0.069	0.6	0.789
Chromosome	10	2.4	00.007	3.6	<0.001	2.5	0.007
DArT_position*Species	24	1.1	0.315	1.17	0.262	NA	NA
Species*Chromosome	78	1.0	0.611	1.06	0.341	NA	NA
DArT_position*Chromosome	30	1.4	0.059	0.84	0.712	NA	NA
DArT_position*Species*Chromosome	162	1.1	0.243	0.91	0.780	NA	NA

To examine the extent to which ascertainment bias affected individual species diversity, the average H_{HW} for the six species using subsets of the DArT markers based on their species or section of origin (S1 Table 3). There was a clear trend for DArT markers to be more diverse in the species or section in which they were developed.

Supporting Information Note S1 Table 3. DArT marker diversity (H_{HW}) within the six eucalypts species according to the species or section (*Latoangulatae* or *Maidenaria*) of origin of the DArT markers.

	DArT origin							
	ALL DArTs	<i>E. grandis</i>	<i>E. globulus</i>	<i>E. nitens</i>	<i>E. urophylla</i>	<i>E. camaldulensis</i>	<i>Latoangulatae</i>	<i>Maidenaria</i>
<i>E. grandis</i>	0.21	0.22	0.19	0.18	0.20	0.16	0.22	0.19
<i>E. urophylla</i>	0.24	0.22	0.24	0.19	0.31	0.23	0.24	0.23
<i>E. camaldulensi</i>	0.23	0.22	0.24	0.20	0.23	0.32	0.22	0.23
<i>E. globulus</i>	0.18	0.16	0.25	0.22	0.15	0.14	0.16	0.24
<i>E. nitens</i>	0.15	0.14	0.20	0.25	0.14	0.11	0.14	0.21
<i>E. dunnii</i>	0.20	0.19	0.24	0.24	0.19	0.19	0.19	0.24
N DArT marker	2840	966	494	156	175	59	1326	650

Despite ascertainment bias in marker diversity (S1 Tables 1 and 2), the associations of diversity and divergence with chromosome features and gene proximity reported based on all markers were stable across diverse subsets of the DArT markers (S1 Table 4). A reduction in the number of markers used is confounded with species differences between marker subsets, and would partly explain differences in the strength and significance of these chromosome level correlations.

References:

Steane DA, Nicolle D, Sansaloni CP, Petroli CD, Carling J, Kilian A, Myburg AA, Grattapaglia D, Vaillancourt RE. 2011. Population genetic analysis and phylogeny reconstruction in *Eucalyptus* (*Myrtaceae*) using high-throughput, genome-wide genotyping. *Molecular Phylogenetics and Evolution* **59**: 206-224.

Supporting Information Note S1 Table 4. Spearman correlations (r_s) and their unadjusted probabilities (P) of gene density and the number of clusters of tandem duplicated genes relative to the number of genes on a chromosome with global H_{HW} , global F_{ST} and the proportion of SDMs for different sets of the DArT markers and different gene proximity classes. The sets of DArT markers include all DArTs and those originating from (i) only species used the present study, (ii) only *Latoangulatae* species and their hybrids, and (iii) only *Maidenaria* species.

	DArT marker origin	N DArTs	All DArT markers		DArT markers within genes		DArT markers within 5 Kbp of genes		DArT markers more than 5 Kbp of a gene		DArT markers within genes outside of tandem duplicate gene clusters		DArT markers within genes within tandem duplicate gene clusters	
			r_s	P	r_s	P	r_s	P	r_s	P	r_s	P	r_s	P
a) global Hhw														
Gene density	all DArTs	2408	-0.88	***	-0.54		-0.50		-0.66	*	-0.60		-0.34	
	only species used in study	1683	-0.79	**	-0.54		-0.20		-0.69	*	-0.45		-0.39	
	Latoangulatae only	1085	-0.85	***	-0.53		-0.08		-0.79	**	-0.50		-0.13	
	Maidenaria only	544	-0.75	**	-0.34		-0.21		-0.36		-0.32		0.15	
Tandem duplication	all DArTs	2408	0.85	**	0.68	*	0.48		0.57		0.82	**	0.30	
	only species used in study	1683	0.83	**	0.69	*	0.32		0.38		0.76	**	0.35	
	Latoangulatae only	1085	0.77	**	0.67	*	0.25		0.49		0.75	**	0.25	

	Maidenaria only	544	0.43		0.37		-0.13		0.09		0.48		-0.28
b) global Fst													
Gene density	all DArTs	2408	0.92	***	0.95	***	0.65	*	0.75	**	0.79	**	0.44
	only species used in study	1683	0.82	**	0.79	**	0.39		0.78	**	0.61	*	0.45
	Latoangulatae only	1085	0.88	***	0.75	**	0.57		0.90	***	0.52		0.41
	Maidenaria only	544	0.53		0.45		0.39		0.27		0.25		0.59
Tandem duplication	all DArTs	2408	-0.78	**	-0.85	**	-0.59		-0.69	*	-0.87	***	-0.31
	only species used in study	1683	-0.76	**	-0.87	***	-0.43		-0.63	*	-0.84	**	-0.30
	Latoangulatae only	1085	-0.85	**	-0.85	**	-0.25		-0.76	**	-0.72	*	-0.28
	Maidenaria only	544	-0.55		-0.61	*	-0.47		-0.10		-0.56		-0.37
c) SDMs													
Gene density	all DArTs	2408	0.75	**	0.75	**	0.38		0.53		0.67	*	0.22
	only species used in study	1683	0.82	**	0.58		0.28		0.50		0.41		0.24
	Latoangulatae only	1085	0.76	**	0.55		0.20		0.28		0.44		0.09
	Maidenaria only	544	0.56		0.20		0.42		0.42		0.28		0.28
Tandem duplication	all DArTs	2408	-0.85	***	-0.90	***	-0.48		-0.53		-0.95	***	0.17
	only species used in study	1683	-0.88	***	-0.87	***	-0.35		-0.52		-0.83	**	0.13
	Latoangulatae only	1085	-0.92	***	-0.78	**	-0.25		-0.36		-0.75	**	0.19
	Maidenaria only	544	-0.68	*	-0.48		-0.55		-0.16		-0.63	*	0.03

(* = P<0.05; ** = P<0.01; *** = P<0.001)