

Supplementary Information for

Evolutionary and phylogenetic insights from a nuclear genome sequence of the extinct, giant 'subfossil' koala lemur *Megaladapis edwardsi*.

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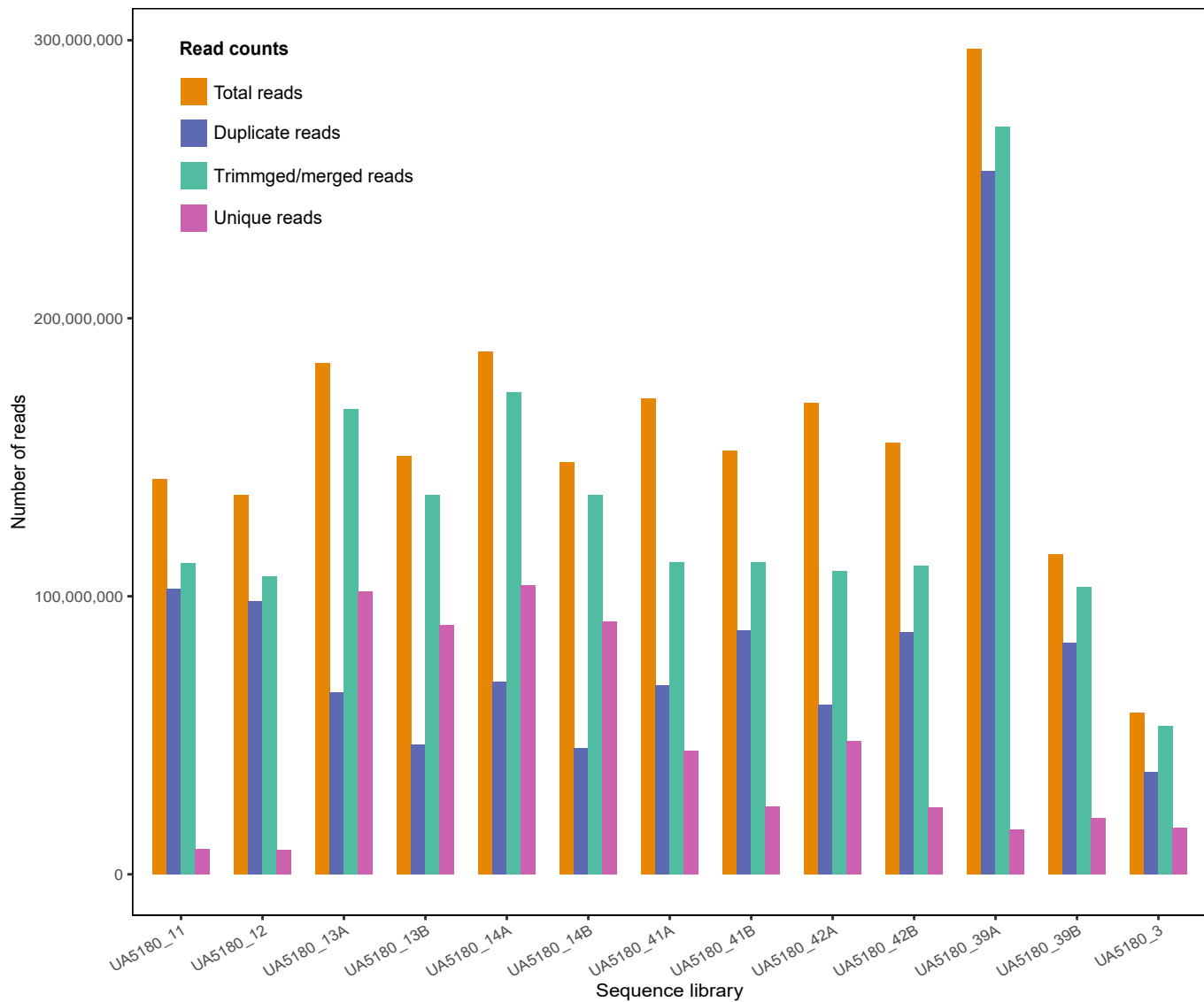


Fig. S1. Pre- and post-processed read counts for *Megaladapis edwardsi* libraries. The total counts of pre- and post-processed reads for each *Megaladapis edwardsi* library prepared from sample UA5180. “Total reads” are the raw unprocessed sequence reads; “Duplicate reads” are redundant reads based on the number of trimmed and merged reads per sequencing library; “Trimmed/merged reads” are adaptor-trimmed and merged paired-end reads; “Unique reads” are reads filtered to a minimum of 20 bp and base quality of 20 with duplicates removed.

Megaladapis edwardsi UA5180 sequence libraries

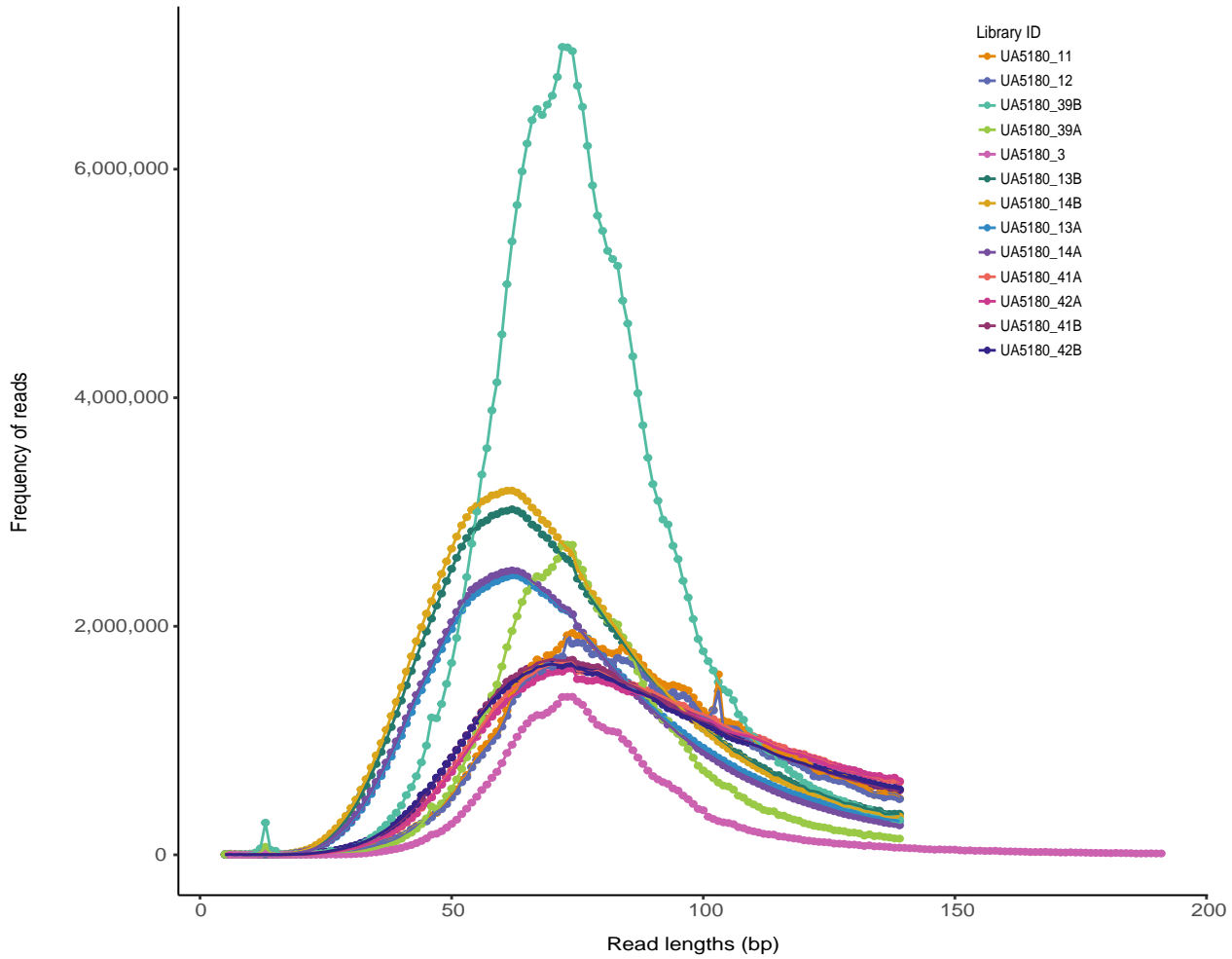


Fig. S2. Trimmed and merged read length distributions for *Megaladapis edwardsi* libraries. Read length distributions for trimmed/merged libraries without duplicate removal in each separately sequenced *M. edwardsi* library (n=9 libraries, A and B indicate those libraries sequenced twice).

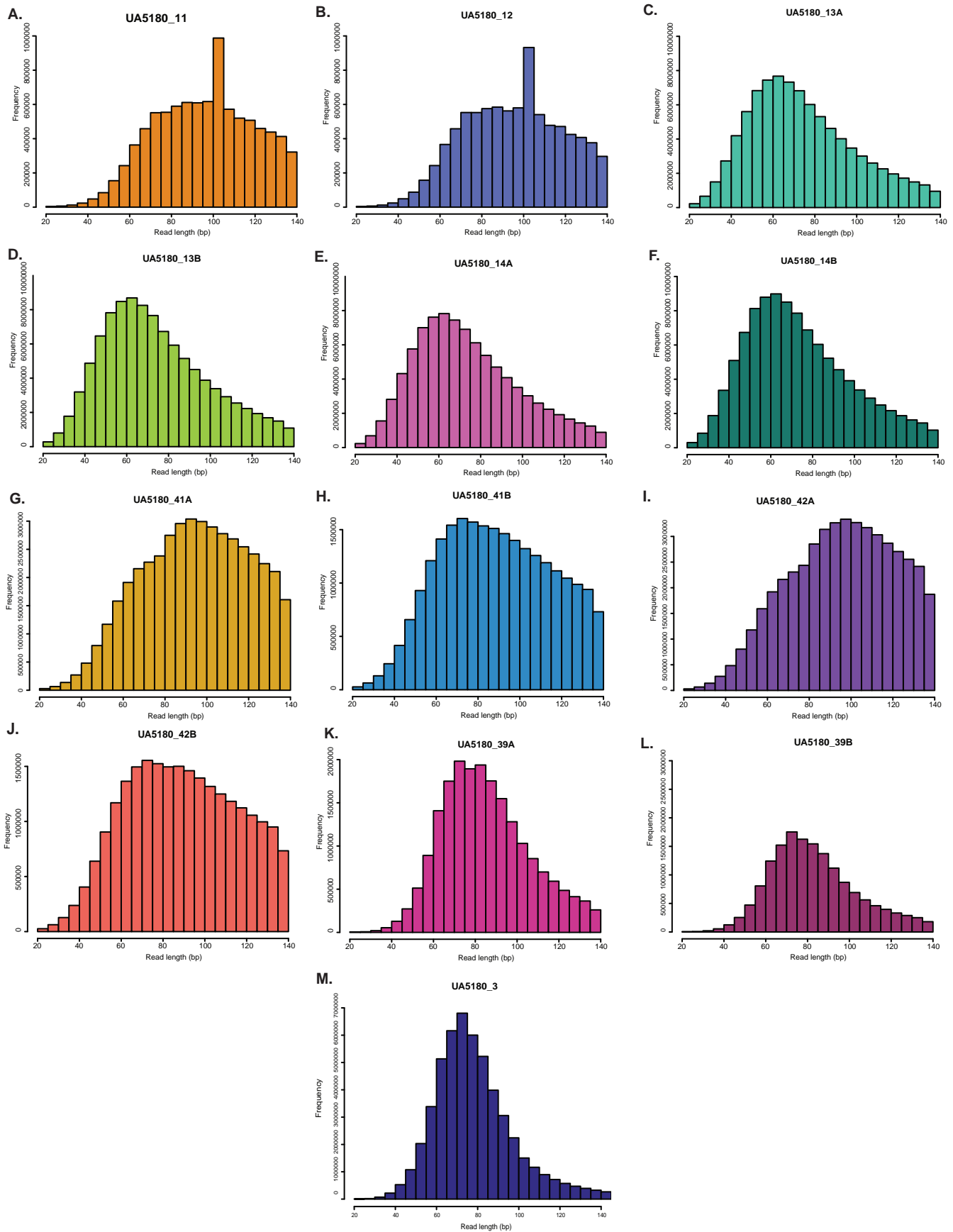


Fig. S3. Individual read length distributions for *Megaladapis edwardsi* libraries. Read length distributions (A to M) for quality filtered reads (min. 20bp and quality 20) in each separately sequenced *M. edwardsi* library (n=9 libraries, A and B indicate those libraries sequenced twice).

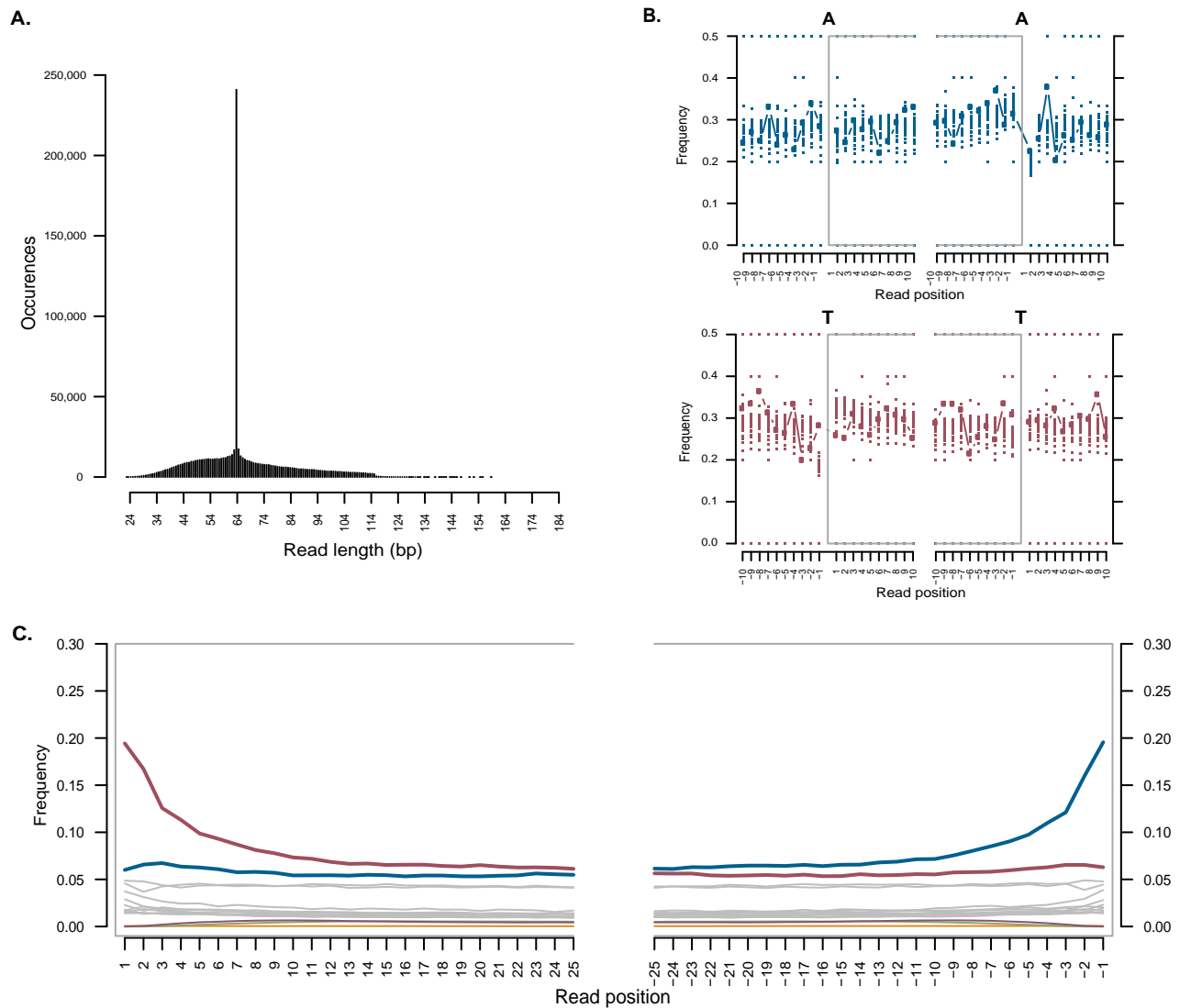


Fig. S4. Read length distribution, DNA fragmentation patterns and frequency of nucleotide misincorporation for a subset of *Megaladapis edwardsi* sequence reads. Estimates of post-mortem damage for *Megaladapis edwardsi* were generated from a BAM file of the lastZ1 alignment mapped to a modified version of hg19 (non-exons masked) using mapDamage². A) Histogram of single-end read length distribution. Note, the peak at 64 bp in the fragment size distribution is due to the presence of untrimmed 64 bp single-stranded reads remaining after trimming and merging with an 11 bp overlap. B) Base frequency DNA fragmentation patterns within the read (contained in the grey box) and outside of the read. C) The frequency of nucleotide misincorporation patterns are indicated from the 5' start (left, positive read position numbers) and 3' end (right, negative read position numbers), showing position-specific substitutions: G>A (maroon), C>T (teal), and all other substitutions (grey).

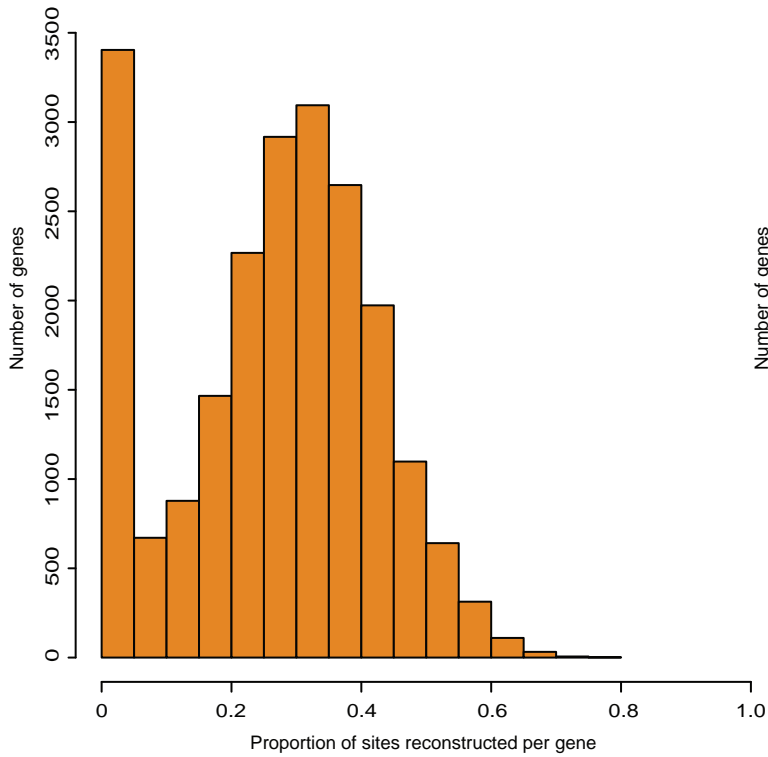
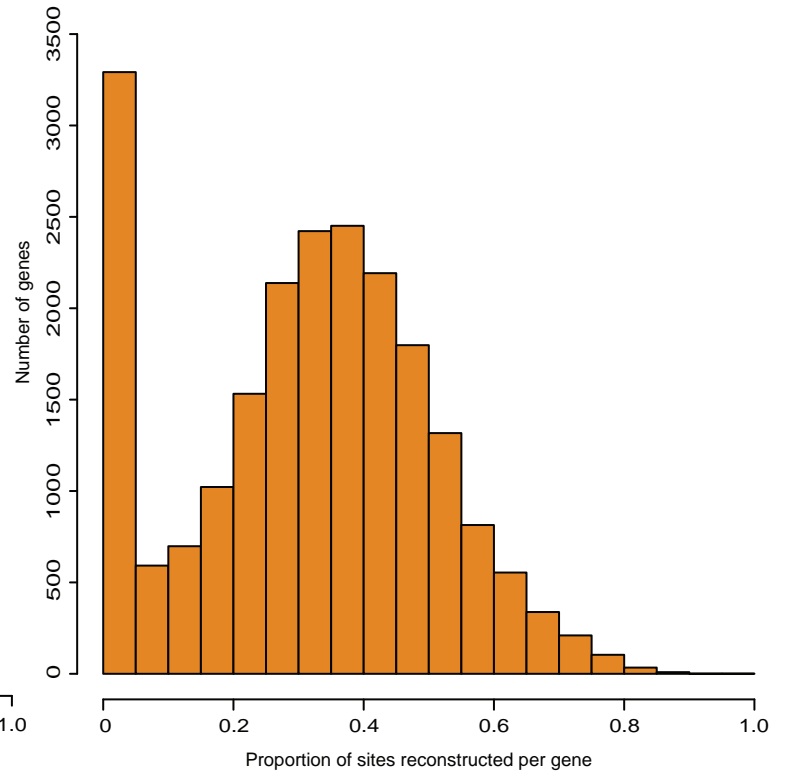
A.**B.**

Fig. S5. Proportion of sites reconstructed per gene in the 2X coverage *Megaladapis edwardsi* damage-masked and damage-unmasked nucleotide dataset. *Megaladapis edwardsi* genes were called in damage-masked and damage-unmasked 2X coverage exon sets, containing 21,519 genes total. Genes were called at: A) a median of 28.60% of sites in the damage-masked (17,448 genes called at greater than 10% of sites) and, B) median of 33.11% in the damage-unmasked (17,636 genes called at greater than 10% of sites).

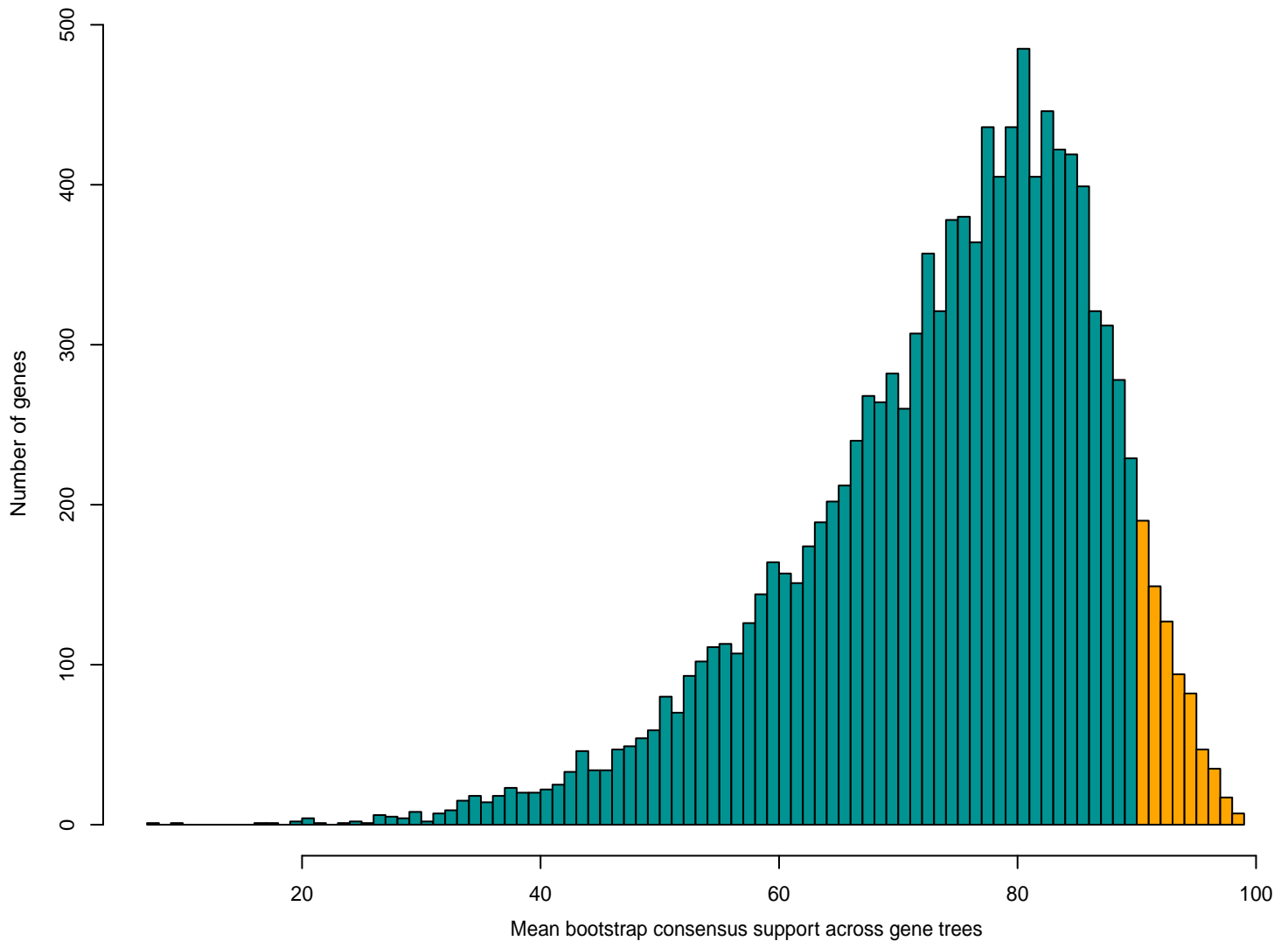
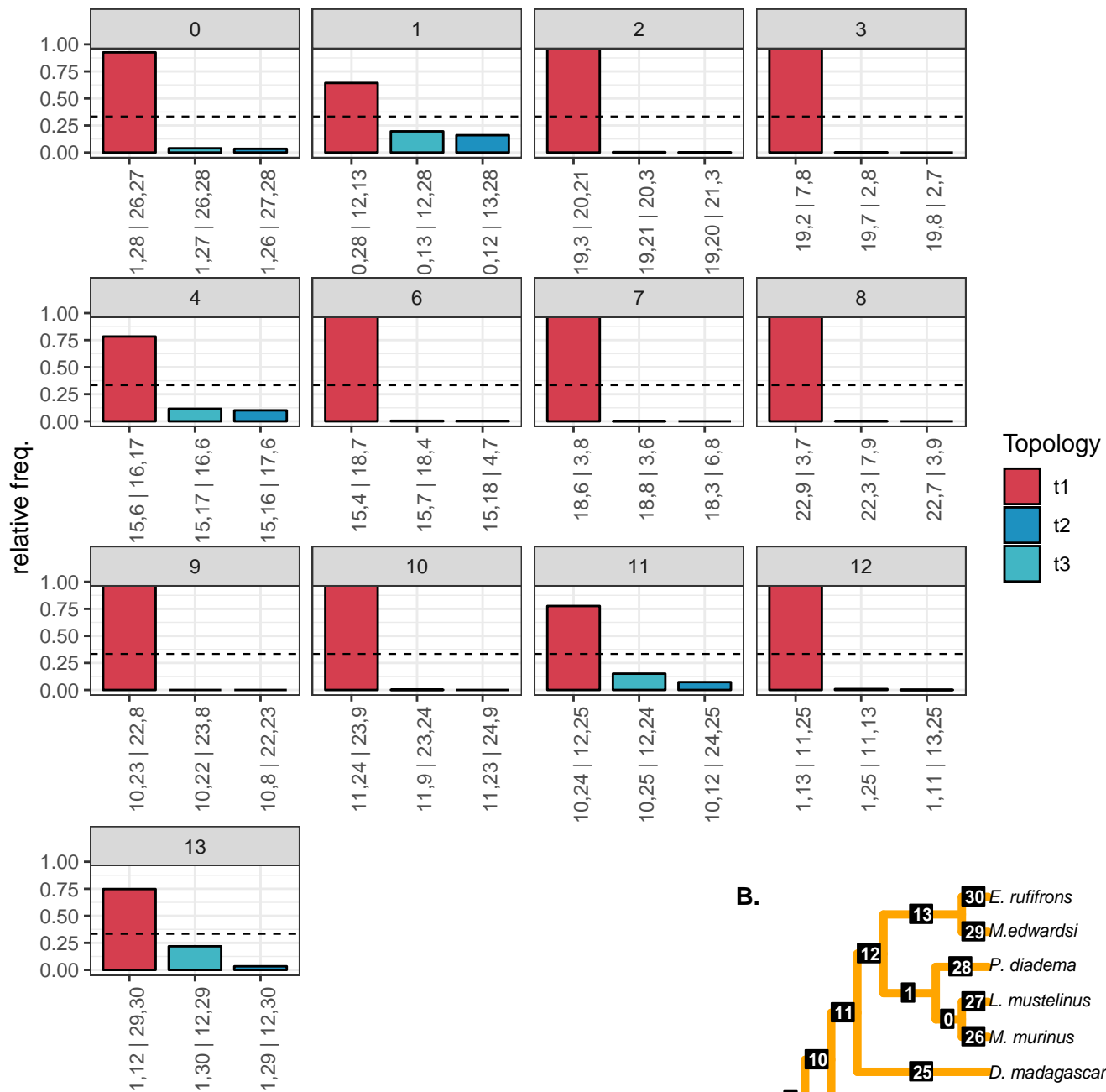


Fig. S6. Mean bootstrap support across independent gene trees. Using a database of 11,944 genes with aligned nucleotides present across at least 20% of sites, we estimated independent gene trees (100 bootstrap replicates) using the same model as the full species tree in Figure 1A. The mean level of bootstrap support across all branch bipartitions was calculated as a measure of gene tree phylogenetic signal³. The overall average mean bootstrap support value was 74.10% (s.d. = 12.65%; range = 7.69% to 98.85%). Highlighted in orange is the mean bootstrap support that exceeds 90%, representing 771 “strong phylogenetic signal” gene trees.

A.



B.

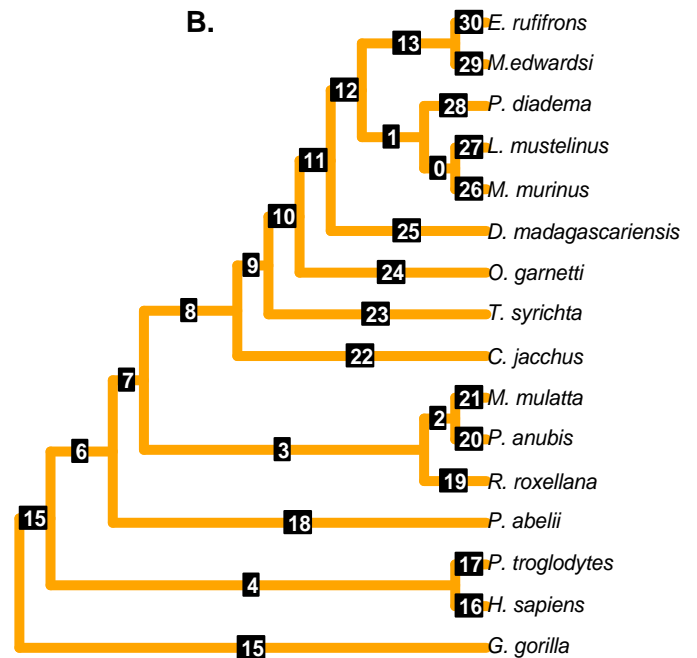
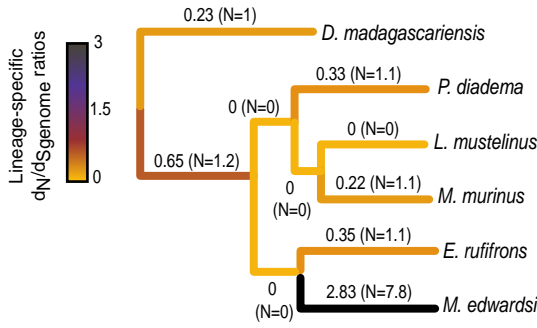


Fig. S7. Phylogenetic analyses for tree topology discordance. ASTRAL-II⁴ and DiscoVista⁵ relative frequency analysis of gene tree discordance. A) Gene-tree quartet configurations reflecting each focal internal branch with the main topology indicated in red and two alternative topologies in blue and, B) Tree topology generated by ASTRAL-II using DiscoVista.

A. *GHR* lineage-specific $d_N/d_{S_{genome}}$ ratios



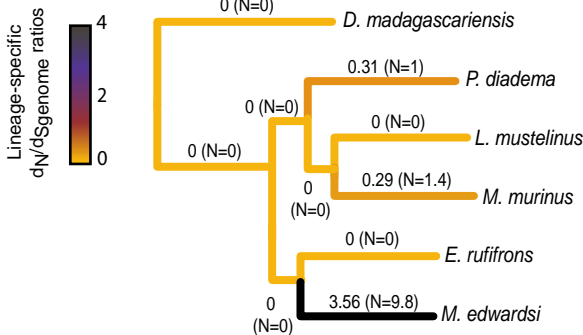
GHR variable amino acid positions

	5	6	8	9	10	41	43	45	62	63	70	71	72	73	74	76	77	78	80	81
<i>D. madagascariensis</i>	Q	L	L	T	L	P	L	T	E	T	D	G	V	H	H	L	K	S	G	S
<i>P. diadema</i>	H	.
<i>L. mustelinus</i>	H	.
<i>M. murinus</i>	E	H	.
<i>E. rufifrons</i>	H	.
<i>M. edwardsi</i>	E	.	.	.	T	.	N	.	P

	82	83	84	85	86	87	153	154	155	157	162	163	164	166	168	169	170	171	172	173
<i>D. madagascariensis</i>	V	Q	L	F	Y	I	I	G	L	W	I	S	L	G	H	A	D	I	Q	V
<i>P. diadema</i>
<i>L. mustelinus</i>
<i>M. murinus</i>
<i>E. rufifrons</i>	S
<i>M. edwardsi</i>	I	T

	186	187	207	210	211	234	235	236	237	238	239	240	243	249	251	252
<i>D. madagascariensis</i>	G	W	M	V	L	Q	R	N	S	E	K	Y	F	V	L	P
<i>P. diadema</i>	I	.
<i>L. mustelinus</i>
<i>M. murinus</i>
<i>E. rufifrons</i>
<i>M. edwardsi</i>

B. *SULT1C2* lineage-specific $d_N/d_{S_{genome}}$ ratios



SULT1C2 variable amino acid positions

	38	39	40	41	42	43	45	46	47	54	56	59	61	66	67	68	70	72	74	138
<i>D. madagascariensis</i>	K	P	D	D	L	L	C	T	Y	W	Q	V	M	G	D	V	K	Q	A	L
<i>P. diadema</i>	M	.	.	.
<i>L. mustelinus</i>
<i>M. murinus</i>
<i>E. rufifrons</i>
<i>M. edwardsi</i>	.	.	E	H	V	.	Y	L	.	.	.

	143	145	154	155	162	164	177	186	235	237	238	239	243	244	248	249	250	254	255	259
<i>D. madagascariensis</i>	N	K	D	Q	P	P	G	D	I	Q	E	T	K	M	P	M	T	T	I	I
<i>P. diadema</i>
<i>L. mustelinus</i>
<i>M. murinus</i>
<i>E. rufifrons</i>
<i>M. edwardsi</i>	I	.	M	A	.	.

	260	263	265	283	286	287	289	291
<i>D. madagascariensis</i>	L	S	S	A	E	R	E	I
<i>P. diadema</i>
<i>L. mustelinus</i>
<i>M. murinus</i>	I	.	.	.
<i>E. rufifrons</i>
<i>M. edwardsi</i>	V

Fig. S8. Lineage-specific d_N/d_S ratios for *GHR* and *SULT1C2* (full alignment). Using a maximum likelihood approach implemented in PAML⁶, lineage-specific ratios of the rates (d) of nonsynonymous (N) vs. synonymous (S) substitution along ancestral and terminal branches estimated with a maximum likelihood-based approach for A) the growth hormone receptor (*GHR*) and B) sulfotransferase 1C2 (*SULT1C2*) genes. For each branch, the d_S denominator is based on the genome-wide synonymous substitution rate. $d_N/d_{S_{genome}}$ estimates are recorded next to each branch and depicted by the heatmap. The estimated number of N substitutions for each branch are reported within the parentheses. Branch lengths shown are based on those from Figure 1A rather than these individual genes. For each gene, alignments of inferred amino acid residues for the encoded proteins are shown for all variable positions. Amino acid residues identical to those for *D. madagascariensis* are depicted with “.” and amino acid position numbers are based on the human reference sequence (hg19/GRCh37).

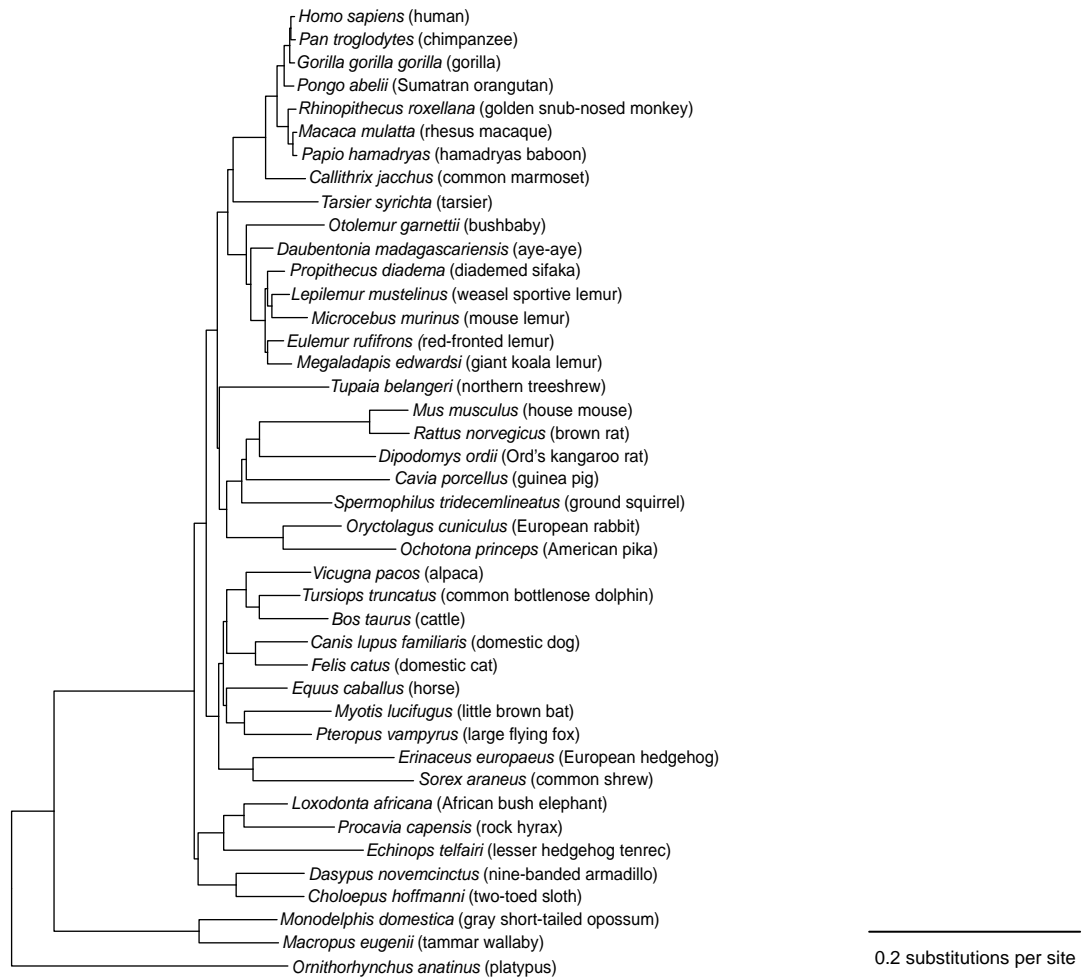


Fig. S9. Phylogenetic relationships of species used in genomic convergence analyses. Phylogenetic representation of the species from the 46-way UCSC vertebrate alignment⁷ joined with the newly sequenced *M. edwardsi*, extant lemurs and colobine⁸. For the convergence analyses, the nucleotide alignments were translated into amino acids, and queried for all possible convergences between species.

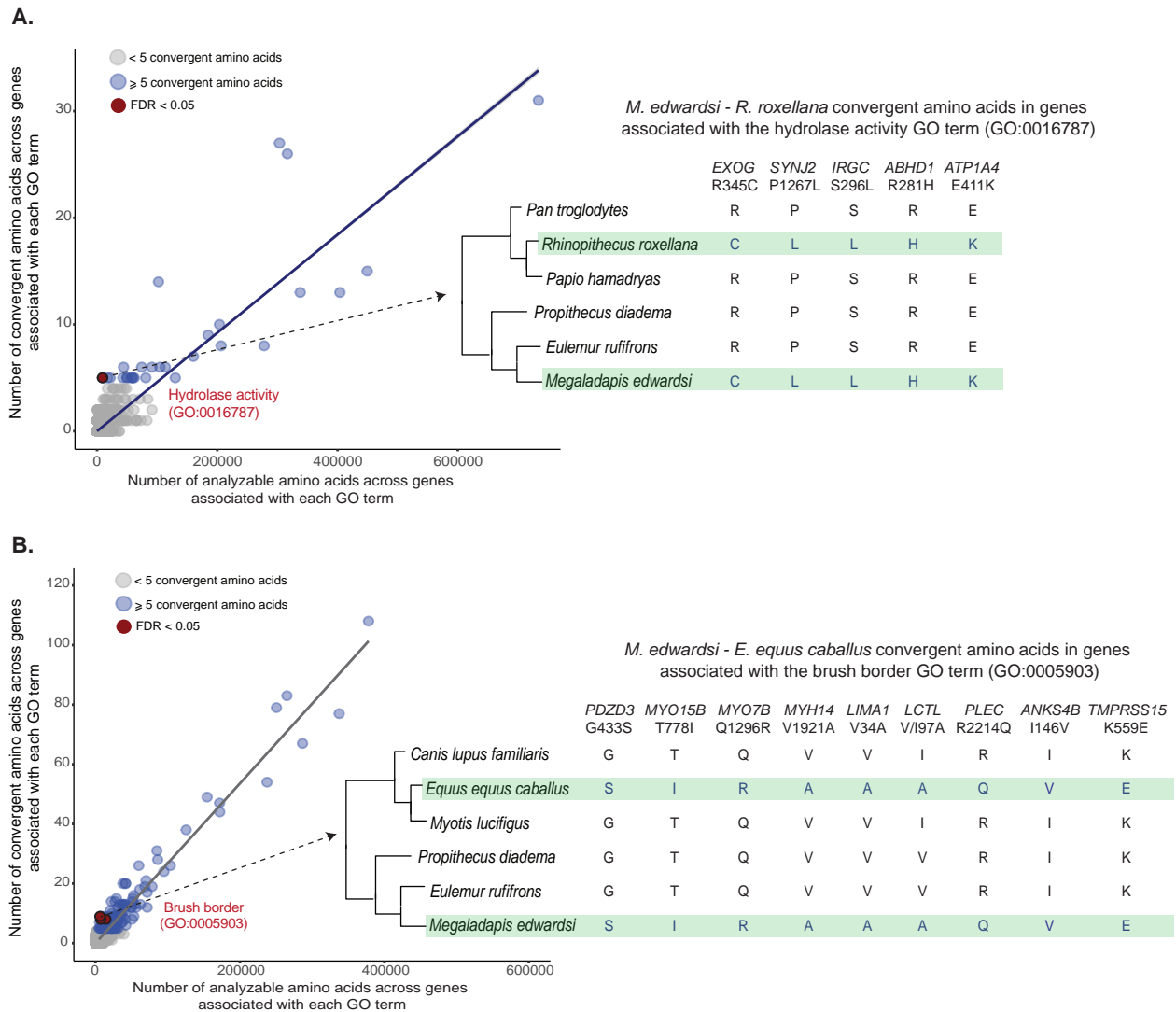
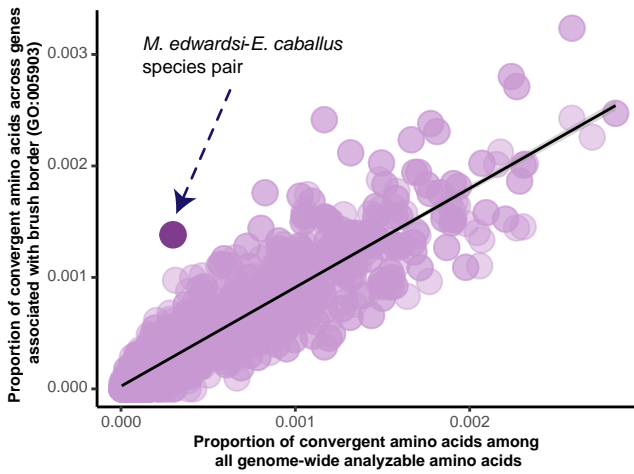
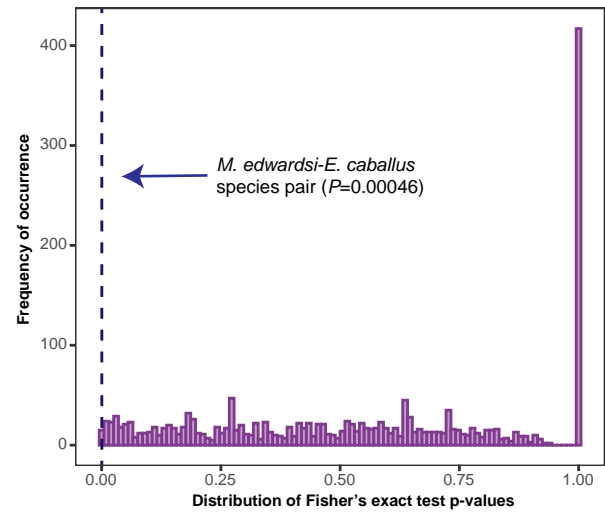


Fig. S10. *Megaladapis edwardsi* genomic convergence results with *R. roxellana* and *E. equus caballus* (*P. diadema* outgroup). Results from scans to identify Gene Ontology (GO) functional categories with unusual proportions (relative to genome-wide expectations) of inferred convergent amino acid positions⁹ between A) *M. edwardsi* and the folivore *R. roxellana* and B) *M. edwardsi* and the herbivore *E. equus caballus*. Convergent positions are those with identical residues between *M. edwardsi* and the comparison species, but for which the sister and an outgroup species (for each of the comparison species) share a distinct amino acid residue (shown at right). At left, the number of analyzable amino acid positions and convergent amino acid positions for each GO term. For terms with ≥ 5 convergent amino acids we tested whether the proportion of convergent sites was significantly different than expected based on the genome-wide ratio and computed false discovery rates (FDR)¹⁰ to account for the multiple tests. For two highlighted GO terms, all convergent amino acid positions between *M. edwardsi* and the comparison species along with gene name and position (based on the human reference sequence) are shown.

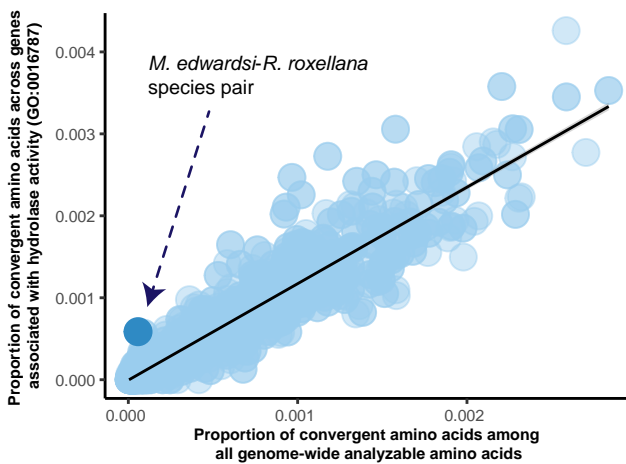
A. Proportion of convergent amino acids in the brush border (GO:005903) category relative to the proportion of sites possible genome-wide. Faded circles represent non-*Megaladapis* species pairs and *M. edwardsi-Equus caballus* is represented by an opaque circle.



B. Frequency of convergence in the brush border category (GO:005903) for non-*Megaladapis* species pairs (n=1,856 comparisons). Each bar represents the frequency of p-value occurrence.



C. Proportion of convergent amino acids in the hydrolase activity (GO:0016787) category relative to the proportion of sites possible genome-wide. Faded circles represent non-*Megaladapis* species pairs and *M. edwardsi-Rhinopithecus roxellana* is represented by an opaque circle.



D. Frequency of convergence in the hydrolase activity category (GO:0016787) for non-*Megaladapis* species pairs (n=1,856 comparisons). Each bar represents the frequency of p-value occurrence.

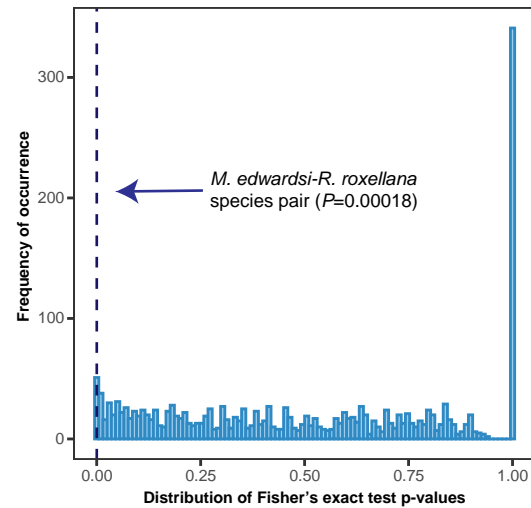


Fig. S11. Post-hoc support for genomic convergence results. A post-hoc analysis identifying the numbers of convergent and analyzable amino acid positions are shown for GO: 0005903 (brush border) and GO:0016787 (hydrolase activity) categories and also genome-wide for all possible taxonomic comparisons (excluding those involving *Megaladapis*) from the multi-species alignment (n=1,856). The ratios of the proportions of GO category:genome wide convergent evolution (A and C) and the Fisher's exact test p-values (B and D) are represented for *Megaladapis-Equus* and *Megaladapis-Rhinopithecus* species pairs.

Table S1. Sequence metrics and accession information

***Megaladapis edwardsi* shotgun sequenced libraries**

Taxon	Sample ID	Site	Tissue	Cal Yrs. BP	Library ID	Master ID	Total reads	Merged reads*	Unique reads**	% Unique reads	Duplicate reads***	Duplicate reads (%)
<i>Megaladapis edwardsi</i>	UA5180	Anavoha	Mandible	1546-1410	Bar13_Dec	UA5180_13A	183,815,699	167,293,010	101,759,510	55.36	65,533,500	39.17
					Bar13_June	UA5180_13B	150,289,729	136,466,616	89,752,467	59.72	46,714,149	34.23
					Bar14_Dec	UA5180_14A	187,934,336	173,244,552	103,995,978	55.34	69,248,574	39.97
					Bar14_June	UA5180_14B	148,344,892	136,385,993	90,997,592	61.34	45,388,401	33.28
					Bar41_July	UA5180_41A	171,073,138	112,145,675	44,267,729	25.88	67,877,946	60.53
					Bar41_Nov	UA5180_41B	152,387,056	112,120,011	24,303,403	15.95	87,816,608	78.32
					Bar42_July	UA5180_42A	169,686,911	108,941,131	47,878,427	28.22	61,062,704	56.05
					Bar42_Nov	UA5180_42B	155,204,251	110,990,589	23,972,353	15.45	87,018,236	78.40
					Bar11	UA5180_11	142,059,057	111,797,291	9,151,117	6.44	102,646,174	91.81
					Bar12	UA5180_12	136,491,202	107,080,700	8,743,143	6.41	98,337,557	91.83
					PJX039_June	UA5180_39A	296,737,001	268,882,310	15,958,787	5.38	252,923,523	94.06
					PJX039_May	UA5180_39B	115,052,998	103,300,322	20,144,369	17.51	83,155,953	80.50
					Bar3	UA5180_3	58,218,887	53,466,704	16,751,896	28.77	36,714,808	68.67

*Merged reads are adaptor-trimmed and merged paired-end reads, without duplicates removed

**Unique reads are reads filtered to min 20bp, quality 20 and duplicates removed

***Duplicate reads are redundant reads based on the difference between the raw trimmed/merged reads and trimmed/merged reads with duplicates removed

Extant lemurs shotgun sequenced libraries

Taxon	Sample ID	Site	Tissue	Date	Library ID	Total reads	Unique reads*	Average depth**
<i>Eulemur rufifrons</i>	RAN05.15	Ranomafana	Ear punch	~2016	Eulemur_S1	393,469,627	5,279,482	7.55 (+/- 7.02)
	ISA2.23	Isalo	Ear punch	~2016	Eulemur_S2	392,627,766		
<i>Lepilemur mustelinus</i>	TVY7.125	Runhua	Ear punch	~2016	Lepilemur	172,058,967	6,145,696	6.40 (+/-5.85)

*Unique reads are reads remaining after adapter trimming and read merging, filtered to min 20bp

**Average depth calculated using SAMtools depth

Accessions for lemurs and colobine used in analyses

Taxon	BioProject Accession
<i>Daubentonia madagascariensis</i>	SRA043766.1
<i>Propithecus diadema</i>	PRJNA317769
<i>Rhinopithecus roxellana</i>	PRJNA230020
<i>Microcebus murinus</i>	PRJNA285159

Table S2. Contamination estimates across libraries

Taxon	Sample ID	Library ID	Master ID	Total reads	Merged reads*	Mapped reads (<i>M. edwardsi</i> mtDNA, NC_026088)**	Mapped reads (haplotype H6A1; EU256375)**	Overlapping (shared) reads***	Reads unique to human****	% contamination estimate
<i>Megaladapis edwardsi</i>	UA5180	Bar13_Dec	UA5180_13A	183,815,699	167,293,010	38,921	1,110	319	791	2.0
		Bar13_June	UA5180_13B	150,289,729	136,466,616	31,918	1,004	285	719	1.8
		Bar14_Dec	UA5180_14A	187,934,336	173,244,552	41,069	1,118	320	798	2.5
		Bar14_June	UA5180_14B	148,344,892	136,385,993	32,158	958	275	683	2.1
		Bar41_July	UA5180_41A	171,073,138	112,145,675	29,776	378	56	322	1.1
		Bar41_Nov	UA5180_41B	152,387,056	112,120,011	30,371	382	56	326	1.1
		Bar42_July	UA5180_42A	169,686,911	108,941,131	27,467	325	41	284	1.0
		Bar42_Nov	UA5180_42B	155,204,251	110,990,589	28,731	330	39	291	1.0
		Bar11	UA5180_11	142,059,057	111,797,291	126,614	20	15	5	0.004
		Bar12	UA5180_12	136,491,202	107,080,700	120,702	19	14	5	0.004
		PJX039_June	UA5180_39A	296,737,001	268,882,310	698,966	93	80	13	0.002
		PJX039_May	UA5180_39B	115,052,998	103,300,322	276,173	115	72	43	0.016
		Bar3	UA5180_3	58,218,887	53,466,704	157,658	85	71	14	0.009

*Merged reads are adaptor-trimmed and merged paired-end reads, without duplicates removed

**Mapped (non-redundant) reads filtered to 20bp and map quality 20

***Read overlap was calculated based on the number of shared reads between the *M. edwardsi* mtDNA and H6A1 mapped BAM files

****Reads unique to human was calculated as the difference between the mapped human reads and overlapped reads

Table S3. Proportion of genes covered in the 2X damage-masked and no-masked *Megaladapis edwardsi* data set

2X damage-masked

% of sites at 2X	# of genes called at x% of sites	% of genes called at x% of sites
0%	2,763	12.84
0-9%	4,071	18.92
>10%	17,448	81.08
>15%	16,568	76.99
10-19%	2,337	10.86
>20%	15,111	70.22
>25%	12,847	59.7
20-29%	5,190	24.12
>30%	9,921	46.1
>35%	6,824	31.71
30-39%	5,733	26.64
>40%	4,188	19.46
>45%	2,206	10.25
40-49%	3,079	14.31
>50%	1,109	5.15
>55%	465	2.16
50-59%	957	4.45
>60%	152	0.71
>65%	40	0.19
60-69%	144	0.67
>70%	8	0.04
>75%	2	0.01
70-79%	8	0.04
>80%	0	0
>85%	0	0
80-89%	0	0
>90%	0	0
>95%	0	0
90-99%	0	0
100%	0	0

2X not damage-masked

% of sites at 2X	# of genes called at x% of sites	% of genes called at x% of sites
0%	2,758	12.82
0-9%	3,883	18.04
>10%	17,636	81.96
>15%	16,937	78.71
10-19%	1,718	7.98
>20%	15,918	73.97
>25%	14,390	66.87
20-29%	3,670	17.05
>30%	12,248	56.92
>35%	9,828	45.67
30-39%	4,865	22.61
>40%	7,383	34.31
>45%	5,181	24.08
40-49%	3,976	18.48
>50%	3,407	15.83
>55%	2,066	9.6
50-59%	2,153	10.01
>60%	1,254	5.83
>65%	697	3.24
60-69%	893	4.15
>70%	361	1.68
>75%	149	0.69
70-79%	315	1.46
>80%	46	0.21
>85%	11	0.05
80-89%	44	0.2
>90%	2	0.01
>95%	1	0.005
90-99%	2	0.01
100%	0	0

Table S4. Full set of genes (n=53) in *M. edwardsi* with $d_N/d_{S_{genome}} > 1.5$

Genes	t	N	S	dN	dS	dN.dS	Nsites	Ssites	dN.dSg	RefGene	Full gene name	Protein function in <i>H. sapiens</i> (NCBI ⁽¹¹⁾)
uc001aky	0.091	4.2	0	0.0401	0	999	104.3	33.7	1.564217	CEP104	Centrosomal protein 104	Ciliogenesis and ciliary integrity
uc001aoi	0.099	15.6	0	0.0451	0	999	345.9	125.1	1.759256	CAMTA1	Calmodulin binding transcription activator 1	Transcription factor, tumor suppressor
uc001cce	0.137	5.2	3.2	0.0415	0.0548	0.7577	125.5	57.5	1.618828	MTF1	Metal regulatory transcription factor 1	Maintaining metal homeostasis
uc001cix	0.121	6.3	2.2	0.0441	0.0326	1.3521	143.9	66.1	1.720249	CDC20	Cell division cycle 20	Nuclear movement and chromosome separation
uc001eoa	0.132	8.5	3	0.0459	0.0397	1.1556	184.9	76.1	1.790463	ITGA10	Integrin subunit alpha 10	Cell adhesion, cell surface signalling
uc001giz	0.139	6.9	1.5	0.0548	0.0269	2.0387	125	55	2.137633	SLC9C2	Solute carrier family 9 member C2	Not indicated
uc001glq	0.256	17.8	1.2	0.1101	0.0193	5.7069	161.2	60.8	4.29477	RASAL2	RAS protein-like activator 2	Activator of small GTPases (Ras superfamily)
uc001hly	0.158	12.9	9.5	0.0392	0.0979	0.3999	328.6	97.4	1.52911	EPRS	Glutamyl-prolyl-tRNA synthetase	Enzymes that charge tRNAs
uc001htn	0.098	12	1.6	0.0386	0.0154	2.5042	310.1	103.9	1.505705	NUP133	Nucleoporin 133	Regulates flow of macromolecules between nucleus and cytoplasm
uc001jmw	0.237	9.4	2.5	0.0846	0.063	1.3429	110.5	39.5	3.300069	CTNNA3	Catenin alpha 3	Cell adhesion in muscle cells
uc001kjk	0.12	15.1	5.9	0.04	0.0405	0.987	377.3	144.7	1.560316	PLCE1	Phospholipase C epsilon 1	Catalyzes hydrolysis in cell differentiation, growth, gene expression
uc001kqa	0.131	4.4	2.3	0.0432	0.0445	0.9715	102	51	1.685141	ENTPD7	Ectonucleoside triphosphate diphosphohydrolase 7	Hydrolyzes extracellular nucleoside triphosphate
uc001phc	0.248	10.1	2.8	0.0856	0.074	1.1578	117.5	38.5	3.339077	MMP20	Matrix metalloproteinase 20	Breakdown of amelogenin, relating to enamel formation
uc001prc	0.188	6.4	3.2	0.0596	0.0693	0.8601	106.7	46.3	2.324871	CEP164	Centrosomal protein 164	Microtubule organization, DNA damage response, chromosome segregation
uc001rfb	0.199	6.6	6.3	0.048	0.111	0.4326	138.4	56.6	1.872379	GYS2	Glycogen synthase 2	Catalyzes glycogen synthesis
uc001utj	0.155	4.8	3.9	0.0395	0.0829	0.4761	120.6	47.4	1.540812	HSPH1	Heat shock protein family H (Hsp110) member 1	Inhibits aggregation of misfolded proteins
uc001vbk	0.171	5.7	3.9	0.045	0.093	0.4842	126.2	41.8	1.755356	LRCH1	Leucine rich repeats and calponin homology domain containing 1	Polymorphisms potentially associated with osteoarthritis in knees
uc001vmk	0.138	5.1	2.1	0.0432	0.0548	0.7894	118.1	37.9	1.685141	DZIP1	DAZ interacting zinc finger protein 1	Not indicated
uc001wwf	0.153	5.2	3.1	0.0462	0.0619	0.7474	112.5	49.5	1.802165	MIS18BP1	MIS18 binding protein 1	Not indicated
uc001ygr	0.137	5	2.6	0.0421	0.0539	0.7814	119.7	48.3	1.642233	EML1	EMAP like 1	Echinoderm microtubule-associated protein-like, candidate for Usher syndrome type 1A gene (deafness, vision loss)
uc001yks	0.154	14.7	10.1	0.0398	0.0874	0.456	369.9	116.1	1.552515	DYNC1H1	Dynein cytoplasmic 1 heavy chain 1	Intracellular motility
uc002bqc	0.232	9	2.1	0.0811	0.064	1.2673	111.3	32.7	3.163541	MAN2A2	Mannosidase alpha class 2A member 2	Not indicated
uc002esm	0.095	5.5	0	0.0417	0	999	132.2	41.8	1.62663	SLC9A5	Solute carrier family 9 member A5	Not indicated
uc002hfb	0.177	8.6	4.2	0.0543	0.0719	0.7559	157.9	58.1	2.118129	CPD	Carboxypeptidase D	Metalloproteinases
uc002ktw	0.166	10.2	5.2	0.0478	0.0808	0.5911	214.3	64.7	1.864578	RBBP8	RB binding protein 8, endonuclease	Nuclear protein, potential tumor suppressor
uc002lly	0.149	7.6	3.1	0.0436	0.0741	0.5888	174.3	41.7	1.700745	TSHZ1	Teashirt zinc finger homeobox 1	Encodes colon cancer antigen; regulation of developmental processes
uc002oqb	0.145	7.4	2	0.0509	0.0413	1.2338	145.9	49.1	1.985502	HNRNPUL1	Heterogeneous nuclear ribonucleoprotein U like 1	Binds to adenovirus early-1B-55kDa oncoprotein; nucleocytoplasmic RNA transport
uc002qzh	0.17	7.2	6.7	0.042	0.0902	0.4662	171.2	74.8	1.638332	ASAP2	AirGAP with SH3 domain, ankyrin repeat and PH domain 2	Multi-domain protein
uc002tdx	0.278	9.8	3.6	0.0912	0.0975	0.9353	107.2	36.8	3.557521	SULT1C2	Sulfotransferase family 1C member 2	Catalyzes conjugation of drugs, neurotransmitters, xenobiotic compounds
uc002top	0.112	4.1	1.1	0.0406	0.0288	1.4094	101.3	39.7	1.583721	MYO7B	Myosin VIIb	Brusher border microvilli in epithelial cells of intestines and kidneys
uc002wmg	0.093	6.2	0	0.0439	0	999	141.7	59.3	1.712447	CHGB	Chromogranin B	Encodes protein abundant in endocrine cells and neurons
uc002xya	0.125	5.4	0.9	0.0461	0.0268	1.7186	117.6	35.4	1.798264	TFAP2C	Transcription factor AP-2 gamma	Activation of developmental genes associated with eyes, face, limbs, neural tube
uc002yvg	0.237	28.6	18.8	0.0696	0.0993	0.7013	410.7	189.3	2.71495	DOPEY2	Dopey family member 2	Not indicated
uc003bkb	0.265	11.9	4.5	0.0872	0.0912	0.9566	136.8	49.2	3.401489	TUBGCP6	Tubulin gamma complex associated protein 6	Microtubule nucleation at the centrosome
uc003bvt	0.186	8.9	0	0.0857	1.00E-04	999	104.4	39.6	3.342977	ATP2B2	ATPase plasma membrane Ca2+ transporting 2	Role in intracellular calcium homeostasis
uc003cvt	0.177	6.3	4.5	0.0466	0.0941	0.4947	135.3	47.7	1.817768	IMPDH2	Inosine monophosphate dehydrogenase 2	Maintaining cellular pools for DNA and RNA synthesis
uc003cwq	0.172	6.3	5.5	0.0455	0.0814	0.5586	138.9	68.1	1.77486	USP4	Ubiquitin specific peptidase 4	Maintaining endoplasmic reticulum

uc003cxh	0.312	10.2	5.7	0.0962	0.1217	0.7906	106.5	46.5	3.75256	RNF123	Ring finger protein 123	Involved in protein-protein, protein-DNA interactions
uc003iaa	0.129	6.7	2.7	0.04	0.0519	0.7711	166.9	52.1	1.560316	C4orf21	Chromosome 4 open reading frame 21	Not indicated
uc003iod	0.124	6.1	1	0.049	0.0211	2.3239	125.3	48.7	1.911387	FGA	Fibrinogen alpha chain	Involved in coagulation
uc003jmt	0.176	7.8	2	0.0725	0.0338	2.1491	107.9	60.1	2.828073	GHR	Growth hormone receptor	Transmembrane receptor for growth hormone
uc003psu	0.159	9.8	3	0.0491	0.0701	0.7004	199.6	43.4	1.915288	SESN1	Sestrin 1	Cellular response to DNA damage, oxidative stress
uc003tcv	0.274	10.5	3.7	0.0926	0.0876	1.0576	113.3	42.7	3.612132	AVL9	AVL 9 cell migration associated	Not indicated
uc003wqi	0.116	6.4	0	0.0484	0	999	132.2	32.8	1.887983	MCPH1	Microcephalin 1	DNA damage response protein
uc004bgm	0.11	4.2	1	0.0402	0.0268	1.503	105.4	38.6	1.568118	ZFP37	ZFP 37 zinc finger protein	Transcription factor for large family of zinc finger proteins
uc004cbq	0.158	11	2.4	0.0607	0.0329	1.8451	180.9	74.1	2.36778	DDX31	Deadbox helicase 31	Cellular processes, embryogenesis, spermatogenesis, cellular growth/division
uc009xdc	0.142	13.6	0	0.066	1.00E-04	999	206.3	81.7	2.574522	DTL	Denticleless E3 ubiquitin protein ligase homolog	Not indicated
uc009xug	0.128	7.3	0	0.0555	1.00E-04	999	131.5	39.5	2.164939	CEP55	Centrosomal protein 55	Not indicated
uc011dur	0.107	18.7	0	0.0482	2.00E-04	234.3107	387.2	134.8	1.880181	UBR2	Ubiquitin protein ligase E3 component n-recogin 2	Proteasome-mediated degradation; proteolytic pathway
uc011lrv	0.132	11.8	2.9	0.0497	0.0305	1.6287	237	96	1.938693	TJP2	Tight junction protein 2	Junction barrier in epithelial and endothelial cells
uc021qzu	0.147	6.2	1.2	0.0572	0.028	2.0466	107.7	42.3	2.231252	C12orf56	Chromosome 12 open reading frame 56	Not indicated
uc021ulp	0.265	10.2	3.6	0.0845	0.1015	0.8328	120.3	35.7	3.296168	ZNF516	Zinc finger protein 516	Cell proliferation, differentiation, apoptosis
uc021vwx	0.198	8.3	6.7	0.0522	0.0984	0.5304	159.9	68.1	2.036213	PLCD4	Phospholipase C delta 4	Cellular processes, including hydrolysis

“Genes” are the UCSC gene names

"t" is the number of nucleotide substitutions per codon

"N" is the number of non-synonymous sites

"S" is the number of synonymous sites

"dN" is the number of non-synonymous substitutions per non-synonymous site

"dS" is the number of synonymous substitutions per synonymous site

"dN.dS" is the ratio of non-synonymous to synonymous sites

"Nsites" is the genome-wide rate of non-synonymous substitutions across all genes

"Ssites" is the genome-wide rate of synonymous substitutions across all genes

"dN.dSg" is the genome-wide ratio of non-synonymous to synonymous sites across all genes

“RefGene” is the gene name

“Full gene name” is the complete name of the gene

“Protein function in *H. sapiens* (NCBI*)” is the function of the protein in *Homo sapiens* listed in NCBI

*NCBI reference: Gene [Internet]. Bethesda (MD): National Library of Medicine (US), National Center for Biotechnology Information; 2004 – [cited 2021-01-20]. Available from: <https://www.ncbi.nlm.nih.gov/gene/>

14	2156	15482	199111	2142	1978629	0.00020329	0.00138422	0.095846	1	chomf1	dm3no2	proCaf1	tau1	panoA2	mhmA1	1	Hydrolytic activity	
15	2043	15603	590909	808	497285	0.00051539	0.00134488	0.170521	3	chomf1	dm3no2	proCaf1	tubB1	slm1	slmM1	0.773380	Hydrolytic activity	
4	1033	15683	237800	1029	267807	0.00045187	0.00051487	0.94008	chomf1	dm3no2	proCaf1	tau1	panoA2	mhmA1	0.843617	Hydrolytic activity		
6	1348	13884	207760	1242	262021	0.00060356	0.00076444	0.77774	0.71523	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.712430	Hydrolytic activity	
10	1618	15618	126459	1470	262021	0.00093889	0.00073438	0.81551	0.761718	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.786317	Hydrolytic activity	
0	391	16831	160326	391	159845	0.00014411	0	0.18466	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.812836	Hydrolytic activity		
0	754	16831	450076	754	160326	0.00015813	0.00050729	0.62823	0.638433	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.828157	Hydrolytic activity	
0	798	16831	554743	793	158473	0.00014622	0.00126804	0.90048	1	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.831704	Hydrolytic activity	
13	2133	17191	512363	13	21333	0.00015091	0	0	0	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.840876	Hydrolytic activity	
6	976	18973	490239	970	496266	0.00021849	0.00020188	0.89373	0.80565	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.850027	Hydrolytic activity	
2	379	20945	281229	377	281408	0.00013794	0.00010209	0.79387	1	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.851704	Hydrolytic activity	
2	1581	19629	196299	158	184443	0.00014423	0.00015513	0.24109	0.211373	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.852700	Hydrolytic activity	
5	572	21340	350763	567	348621	0.00012979	0.00124223	0.13443	0.493928	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.843945	Hydrolytic activity	
0	1020	18170	181700	1020	181700	0.00013616	0.00015666	0.53923	0.53923	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.836008	Hydrolytic activity	
3	135	20420	344938	132	344938	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
10	952	20420	539450	927	539450	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
0	305	21242	321845	305	321845	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
3	645	22118	332158	642	332158	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
0	884	20420	526407	877	526407	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
1	56	27108	388378	55	385758	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
3	1574	235509	574	239765	1	239765	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity
3	318	17950	286458	315	279338	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
3	723	39022	543788	720	537846	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
2	288	28200	390280	286	384868	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
1	303	43350	590452	302	590452	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
2	305	13905	442760	304	470387	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
0	64	30880	444820	64	444820	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
2	115	21066	304951	113	206685	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
4	483	29337	450473	479	479336	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
1	488	28182	420286	487	420286	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
13	38	29490	321946	38	321946	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
1	385	48704	67308	384	48704	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
4	1709	590909	808	497285	1	497285	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity
5	441	38614	526974	436	526974	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
2	554	28108	420346	552	420346	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
2	1578	21789	326812	1574	326812	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
1	201	28429	378024	200	374195	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
2	202	42962	610505	202	610505	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
0	831	28429	413932	831	413932	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
0	732	28429	413932	732	413932	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
0	343	26164	364781	343	363311	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
5	1306	34324	470038	1201	467323	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
4	45327	656270	889	656270	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity		
5	859	29985	440235	854	447081	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
3	1793	24588	361625	1789	361625	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
8	870	39498	531274	862	529678	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
4	58483	862065	1163409	58483	862065	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
3	781	22275	354022	778	351225	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
4	766	32436	465139	762	460733	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
4	2936	42036	621820	2932	621820	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
9	870	31561	459478	861	456222	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
4	547	490079	670731	543	497373	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
1	539	21386	351708	534	348702	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
1	1032	13919	193924	1031	137822	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
26	2589	28429	268621	2589	268621	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
19	1905	28429	268621	1905	268621	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
13	1477	18369	274513	1464	270574	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
1	1481	17824	274513	1479	270574	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
10	1038	14750	217669	1038	217669	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
5	572	21340	350763	567	348621	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
1	17458	24588	361625	17458	361625	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
7	611	19788	281085	604	281085	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
8	109	21340	350763	109	350763	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
22	28429	29868	406209	28429	406209	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
1	599	20065	284290	598	284290	0.00013616	0.00011965	0.148319	0.079375	chomf1	dm3no2	proCaf1	tau1	panoA2	vcfA2	0.870170	Hydrolytic activity	
8	2317	9736	164749	2308														

26	2343	20555	286513	2217	283938	0.00079533	0.00120002	1.542518	0.055132	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0512385	Hydrolyse activity	
12	2214	20559	286513	2217	283938	0.00079533	0.00120002	1.542518	0.055132	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0512385	Hydrolyse activity	
12	1121	17407	371020	1309	368652	0.00031566	0.00047225	1.326211	0.313746	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0314483	Hydrolyse activity	
12	1445	16046	292326	1453	292020	0.00049468	0.00044838	1.310824	0.182234	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0317488	Hydrolyse activity	
12	1558	17566	315667	1567	315002	0.00012765	0.00012765	1.188422	0.0202028	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity	
4	470	17316	224620	466	223254	0.00020213	0.00020213	1.39353	0.380964	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0317905	Hydrolyse activity	
4	1743	18474	205641	1747	204944	0.00001729	0.00001729	1.21051	0.428243	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0312577	Hydrolyse activity	
7	1390	20725	321940	1383	320824	0.00011488	0.00011488	1.061337	0.73514	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity	
7	1516	16174	235828	1510	235102	0.00003387	0.00003387	1.049414	0.394141	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity	
20	2055	20220	270888	2055	271468	0.00001708	0.00001708	1.0054053	0.18522	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity	
7	1114	11647	180524	1107	181897	0.00006292	0.00006292	0.9992033	0.999203	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity	
7	1282	12586	422445	1281	422066	0.00001935	0.00001935	1.449714	0.139595	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0316370	Hydrolyse activity	
7	542	20489	300545	535	300381	0.00017848	0.00017848	0.00032744	1.25454	1.2544	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0317488	Hydrolyse activity
7	1840	18880	339581	1840	339181	0.00003878	0.00003878	0.00000000	0.00000000	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity	
8	1834	18417	229720	1833	229422	0.00007328	0.00007328	0.00058776	0.77203	0.67328	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
3	362	10782	1794009	359	178737	0.00012872	0.00012872	0.00078242	1.30706	0.92076	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0307354	Hydrolyse activity
3	1840	20489	300545	1840	300149	0.00001741	0.00001741	0.00017848	1.18514	1.75527	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
33	3500	39880	395543	3507	395543	0.00009394	0.00009394	0.00012872	1.47915	0.03273	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
33	14603	15214	205102	14603	205102	0.00001038	0.00001038	0.00044472	1.482026	0.00000000	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
22	2214	14177	215379	2192	214358	0.00021730	0.00021730	0.00155189	1.51988	0.03941	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
20	2055	15688	1981	200252	1981	0.00009266	0.00009266	0.00017157	1.70512	0.02581	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
4	777	14477	180550	773	180525	0.00042129	0.00042129	0.00148523	0.568617	1.5	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
2	581	22735	334009	579	333794	0.00012029	0.00012029	0.000125279	1.454204	0.45339	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
1	212	22635	366709	208	364124	0.00012029	0.00012029	0.000125279	1.454204	0.45339	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
1	199	26682	376612	198	376408	0.00012029	0.00012029	0.000125279	1.454204	0.45339	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
1	55	25028	350828	55	350432	0.00012029	0.00012029	0.000125279	1.454204	0.45339	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
5	649	21461	317024	644	314889	0.00021730	0.00021730	0.00022291	1.18077	0.63356	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
1	1975	20288	292528	1975	292528	0.00001742	0.00001742	0.000886	1.20311	0.68437	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
4	212	20559	366709	208	364124	0.00012029	0.00012029	0.000125279	1.454204	0.45339	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
13	1321	18792	291132	1308	289240	0.00041763	0.00041763	0.000969134	1.24507	0.12273	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
13	2618	26487	350626	2615	348179	0.00001704	0.00001704	0.00059711	1.72221	0.02663	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
13	1218	12946	364665	1218	364665	0.00001704	0.00001704	0.00059711	1.72221	0.02663	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
5	639	17247	261200	634	261483	0.00001774	0.00001774	0.00028995	1.04138	0.03904	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
26	2706	29487	368020	2680	368098	0.00009948	0.00009948	0.00135417	1.42705	0.07659	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0307354	Hydrolyse activity
14	2426	24724	302876	2426	302876	0.00001704	0.00001704	0.00028995	1.04138	0.03904	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
14	1641	23870	365308	1627	365124	0.00041763	0.00041763	0.0005811	1.20208	0.35721	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
14	904	11927	180484	905	119323	0.00001704	0.00001704	0.00028995	1.04138	0.03904	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
26	2713	29679	368020	2727	368107	0.00001704	0.00001704	0.00028995	1.04138	0.03904	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
13	1172	12395	192535	1172	192535	0.00001704	0.00001704	0.00028995	1.04138	0.03904	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
2	169	27824	427362	167	417938	0.045275	0.045275	1.718065	0.178928	0.30999	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0307354	Hydrolyse activity
6	530	23887	337289	524	337480	0.00021730	0.00021730	0.00025499	1.05052	0.28874	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0307354	Hydrolyse activity
10	2127	24724	327947	2127	327947	0.00021730	0.00021730	0.00025499	1.05052	0.28874	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0307354	Hydrolyse activity
19	2441	29089	295362	2422	290469	0.00001704	0.00001704	0.000995229	1.240487	0.37704	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
19	2159	230421	350181	2159	350181	0.00001704	0.00001704	0.000995229	1.240487	0.37704	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
0	185	27983	440856	185	440856	0.00001704	0.00001704	0.000995229	1.240487	0.37704	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
0	40987	429887	440856	40987	440856	0.00001704	0.00001704	0.000995229	1.240487	0.37704	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
12	2128	20200	364779	2116	362579	0.00001957	0.00001957	0.0047419	1.30839	0.13205	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
21	2798	14679	239955	2777	238923	0.00116039	0.00116039	0.0041312	1.27408	0.38741	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
21	2281	15629	243465	2262	243058	0.00001957	0.00001957	0.00094051	1.30516	0.23667	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
15	2300	1852	280339	2285	279036	0.00081815	0.00081815	0.00080838	1.08749	1.5	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
15	2845	2136	345455	2845	345455	0.00001704	0.00001704	0.000995229	1.240487	0.37704	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
10	1247	17127	280138	1237	280138	0.00041763	0.00041763	0.0005811	1.39991	0.15571	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
15	1839	14681	228453	1824	227870	0.00071744	0.00071744	0.0010893	1.444202	0.16822	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
15	3174	31024	31024	3174	31024	0.00041763	0.00041763	0.00092485	1.22939	0.47856	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
10	2580	37684	37684	2580	37684	0.00041763	0.00041763	0.00092485	1.22939	0.47856	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
10	2629	2629	404454	2629	404454	0.00041763	0.00041763	0.00092485	1.22939	0.47856	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
1	112	18684	286224	111	286070	0.4693245	0.4693245	5.9331351	1.24246	0.40394	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
20	2024	2024	291524	2024	291524	0.00001704	0.00001704	0.00028995	1.04138	0.03904	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
1	636	12147	205027	631	205210	0.00040775	0.00040775	0.0009376	0.90732	1.5	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
1	385	34264	487386	384	487422	0.7004425	0.7004425	2.91262	0.13022	0.53304	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
1	333	32599	345696	334	346066	0.00041763	0.00041763	0.00024601	1.74653	0.01568	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
2	267	14138	240388	265	142888	0.00041763	0.00041763	0.00020854	1.19933	0.70071	leaM1	prcCat1	ent1	tar1	panAa2	mMm1	0.0319466	Hydrolyse activity
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15	2462	28424	3923504	2446	3983980	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	tuTtRtL	pMvmmn	carfMzQ	0.81140179	Hydrolyase activity
16	22093	23194	3000071	2194	3000071	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	tuTtRtL	pMvmmn	carfMzQ	0.81140179	Hydrolyase activity
17	2729	17413	241696	2706	246983	0.00110196	0.00110196	0.00110196	0.00110196	0.00110196	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
18	701	23482	232640	699	232640	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
19	25790	24190	3028621	25783	3028621	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
20	335	24039	482339	333	478919	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
21	14	29400	562000	14	562000	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
22	34	28147	354884	373	353760	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
23	12107	12107	12107	12107	12107	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
24	0	19621	19621	0	19621	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
25	212	19928	280520	212	280520	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
26	75	222820	2207900	75	222820	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
27	0	13	29402	0	29402	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
28	248	19745	248173	247	248173	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
29	3	1633	4500773	3	4500773	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
30	0	23	23204	0	23204	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
31	238	12876	12876	238	12876	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
32	120	15118	227478	118	227980	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
33	179	179	179	179	179	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
34	127	20993	346418	126	346888	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
35	122	438411	438411	122	438411	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
36	21	28328	28328	21	28328	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
37	70	17381	246307	69	247956	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
38	200	170620	170620	200	170620	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
39	172	26666	368888	168	368888	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
40	3173	424840	417513	3169	424840	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
41	509	438454	448832	508	448832	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
42	164	30778	460323	163	460346	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
43	123	39596	39596	123	39596	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
44	236	21406	222052	236	222052	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
45	18	13651	13651	18	13651	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
46	345	2973	374843	342	375708	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
47	320	2833	350308	319	350308	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
48	213	45478	478841	213	478841	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
49	144	23365	291435	143	291435	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
50	400	18375	4925720	400	4925720	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
51	206	4431	557370	206	557370	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
52	373	28188	37328	373	28188	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
53	143	34271	467747	140	467747	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
54	387	33995	464802	381	464802	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
55	419	49420	588122	419	588122	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
56	180	37208	468380	176	468380	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
57	200	19044	21000208	200	21000208	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
58	311	29604	398756	309	398756	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
59	37018	37018	37018	37018	37018	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
60	306	181120	228620	304	228620	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
61	129	36005	483839	128	483839	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
62	104	42645	489567	104	489567	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
63	232	20730	296480	226	296480	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
64	133	31964	31964	133	31964	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
65	289	28118	447120	286	444032	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
66	463	33916	520333	462	519272	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
67	311	33876	481726	310	481726	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
68	20	23876	308886	18	308886	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
69	207	40020398	4159527	207	4159527	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
70	157	18688	279808	155	279848	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
71	184809	184809	184809	184809	184809	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
72	4	235	31871	4	31871	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
73	68	17805	280775	68	280775	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
74	398	33986	439846	41	439846	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
75	403	37483	511933	400	507470	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
76	232005	232005	232005	232005	232005	0.00007392	0.00056205	0.89651	0.81137	omdgnr	mmMnFr	rMmMzQ	vMmMzQ	tuTtRtL	carfMzQ	0.81140179	Hydrolyase activity
77	277	22490	327306	274	327306	0.00007392	0.00056										

3	324	16796	267025	321	265429	0.00021336	0.00078814	1.474261	4.683936	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
4	45251	17728	261025	322	213288	0.00017328	0.00354571	1.364025	0.023129	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
5	2739	17124	195163	2720	290649	0.00094878	0.00109554	1.81309	0.405564	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
6	281	11502	187482	2729	188320	0.00024982	0.00073883	1.65524	0.602743	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
7	286	12882	184555	2842	2286638	0.00028892	0.00529751	1.64712	0.020217	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
10	210	15120	161240	2100	162520	0.00017208	0.00035488	1.61069	0.095814	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
11	781	19275	178	20275	19275	0.000022068	0.00014838	1.65524	0.444633	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
12	7	985	17357	978	247811	0.00034748	0.00047997	1.534269	8.860838	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
13	3120	17437	200986	3120	200986	0.00012484	0.00024814	1.555849	0.497973	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
4	830	12026	196873	826	198923	0.00051933	0.00043239	1.632851	1.544551	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
8	951	12236	198174	950	198174	0.00047887	0.00037752	1.605208	0.401138	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
15	4211	18549	4186	4186	4186	0.00020513	0.00037752	1.622008	0.030318	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
11	1375	14482	190265	1364	189123	0.00067374	0.00058021	1.512625	1.33993	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
13	1588	18773	190385	1588	190385	0.00037155	0.00032873	1.518271	0.273802	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
15	1761	12964	216029	1736	214785	0.00082925	0.00155195	1.47512	0.242031	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
13	1900	19306	259720	1900	259720	0.00037155	0.00037155	1.5011	0.333838	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
7	159	19815	286523	152	286523	0.00014429	0.00028624	1.892142	0.012106	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
1	287	23825	200721	286	200721	0.00037155	0.00049875	1.531788	0.513788	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
1	1935	86	207856	86	207856	0.00078814	5.2143E-05	1.638909	0.448354	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
8	1348	16271	251669	1340	255893	0.00044782	0.00049127	1.514836	0.358361	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
5	290	245272	287	245272	287	0.00012568	0.00012568	1.682526	0.00012568	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
6	807	160739	861	168756	861	0.00051979	0.00048747	1.215402	0.657302	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
27	2157	14691	234407	2140	237026	0.00094659	0.0018224	1.365084	0.26292	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
22	2298	23986	2777	23986	2777	0.00016020	0.00044512	1.22748	0.18374	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
20	1935	205126	1915	207574	1915	0.00076493	0.00123363	1.634569	0.204666	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
20	3206	177025	5263	232444	5263	0.00031643	0.00042848	1.387626	1.02714	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
23	2360	18335	289721	2337	286286	0.00081782	0.00125411	1.534882	0.503274	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
29	2942	24688	2923	212483	2923	0.00021738	0.00031643	1.602519	0.021078	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
7	1231	22211	206746	1246	206746	0.00037155	0.00072516	1.593138	0.00037155	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
47	5881	18207	227379	5834	225959	0.00029726	0.00046088	1.33388	0.015866	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
44	5281	18121	211147	5287	211070	0.00029726	0.00038652	1.34855	0.025274	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
35	3523	18749	202633	3488	202633	0.00037155	0.00029256	1.609531	0.00037155	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
13	2264	21117	242294	2252	242294	0.00037155	0.00030956	1.5181	0.080795	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
14	4666	19507	247362	4632	248183	0.00088872	0.00109225	1.37862	0.300793	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
3	304	29238	301	29238	301	0.00037155	0.00031342	1.65664	0.470037	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
2	2408	344417	252	412576	252	0.00016020	0.00038102	1.92521	0.158466	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
12	889	18937	287525	877	289309	0.00031263	0.00059361	1.68641	0.023842	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
11	1870	19705	204	200275	1870	0.00037155	0.00037395	1.59635	0.00037155	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
8	4694	14683	245169	4638	244146	0.00013263	0.00048185	1.383658	0.100888	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
12	2256	19224	2146	200275	2256	0.00037155	0.00037395	1.296523	0.304827	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
27	4894	17322	291324	4867	289992	0.00017926	0.00156852	1.600363	0.855636	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
4	334	22093	348463	330	347520	8.8628E-05	0.00049494	1.210499	0.412038	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
15	1286	2311	346026	1286	346026	0.00047927	0.00094924	1.31213	0.252826	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
20	2477	18416	281478	2457	287313	0.00081665	0.00029215	1.27262	0.253577	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
20	4215	18185	262593	4215	262593	0.00037155	0.00039377	1.62631	0.374865	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
14	4732	18429	244299	4688	242981	0.00051979	0.00029256	1.376673	0.349504	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
14	4688	18185	244299	4688	244299	0.00037155	0.00029256	1.376673	0.349504	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
22	2670	18518	304720	2648	303162	0.00087799	0.00185493	1.365515	0.188463	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
13	2599	15027	259323	2586	258426	0.00037155	0.00086509	1.84526	0.09915	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
13	2798	19728	218425	2798	218425	0.00037155	0.00050451	1.63216	0.00037155	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
8	813	11478	197142	805	196427	0.00041156	0.00073244	1.737885	0.153202	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
13	31683	18463	210265	31683	210265	0.00037155	0.00032073	1.622008	0.490185	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
22	2543	23743	375183	2541	373149	0.00064207	0.00098983	1.317508	0.371533	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
25	3425	27322	388406	3401	386824	0.00081665	0.00097364	1.62061	0.839714	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
20	2612	18366	292679	2612	292679	0.00064207	0.00024885	1.25511	0.37546	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
4	766	34746	461318	762	460273	0.00081665	0.00044454	1.176522	0.512261	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
20	3129	18789	3129	3129	3129	0.00037155	0.00044454	1.176522	0.512261	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
3	822	1874	148354	819	147640	0.00031263	0.00032004	1.57872	0.59883	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
18	25868	24148	263424	25868	263424	0.00037155	0.00110509	1.60981	0.024266	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
8	839	1287	202233	831	201922	0.00041922	0.00052131	1.46002	0.270982	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
86	9068	26168	392973	8992	390565	0.00029726	0.00039511	1.32777	0.023209	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
10	2626	247996	2621	2626	2621	0.00047927	0.00029164	1.2442	0.00029164	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
19	3486	18493	3467	320365	3467	0.00011209	0.00019685	1.83155	0.486518	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
10	4057	18207	4057	4057	4057	0.00037155	0.00016492	1.66624	0.000267	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
2	493	19095	281441	491	281246	0.00017926	0.00040739	1.642696	0.777465	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
20	1960	1282	203773	1940	200051	0.00037155	0.00029256	1.595819	0.147437	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
28	3206	2734	384543	3178	381839	0.00081782	0.00031263	1.22958	0.292107	na	mnp	dndi	(wpch) tv	mycast	carfm2	0.46021737	Hydrosave activity
28	1841	18379	366407	1837	366407	0.00037155	0.00029256	1.319									

1	426	13802	281306	425	280204	0.00011289	7.246338E-05	4.78907	0.792926	galact	tarSet1	(NP)ch2	mydost	carfem2	0.77993899	Brush border	
2	15421	28454	465669	464	461120	0.00010498	0.00010288	1.010218	0.212838	carbam	tarSet1	carbam	tarSet1	carbam	0.77993899	Brush border	
3	2309	28842	420892	2296	428800	0.00051947	0.00052341	1.10994	0.658937	carfem1	carSet2	galact	carSet1	tarSet1	0.65893993	Brush border	
4	206	2072	205748	204	203996	0.70735E-05	0.00128486	1.055022	0.342729	carfem1	carSet1	carbam	tarSet1	carSet2	0.34260005	Brush border	
5	31912	43876	738925	730	717217	0.00117581	0.00116537	1.31666	0.708983	carfem1	carSet1	carbam	tarSet1	carSet2	0.70898309	Brush border	
6	1537	10567	221594	1525	220381	0.00006896	0.00018928	0.4272	0.038866	carfem1	carSet1	carbam	tarSet1	carSet2	0.03886609	Brush border	
7	24984	34984	595426	592	591432	0.00004626	0.00020028	1.4279	0.212145	carfem1	carSet1	carbam	tarSet1	carSet2	0.21214509	Brush border	
8	1114	21339	3956269	1111	3937170	0.00000186	0.00021854	0.453184	0.234054	carfem1	carSet1	carbam	tarSet1	carSet2	0.23405409	Brush border	
9	517	1733	3307739	514	3300863	0.00000186	0.00046586	1.7429	0.212145	carfem1	carSet1	carbam	tarSet1	carSet2	0.21214509	Brush border	
10	2477	172433	2461	217449	0.00000073	0.00125493	1.38055	0.184519	carfem1	carSet1	carbam	tarSet1	carSet2	0.18451909	Brush border		
11	657	11231	279493	655	278420	0.00001564	0.00037504	0.588358	0.780848	carfem1	carSet1	carbam	tarSet1	carSet2	0.78084809	Brush border	
12	17027	17027	1669	1669	0.00002187	0.00017619	1.7027	1	carfem1	carSet1	carbam	tarSet1	carSet2	0.70270000	Brush border		
13	4621	26632	431796	4604	4291304	0.00100718	0.00068303	0.156466	0.029774	carfem1	carSet1	carbam	tarSet1	carSet2	0.02977409	Brush border	
14	838	78974	30003808	835	7877443	0.00000080	0.00021418	0.76231	0.824049	carfem1	carSet1	carbam	tarSet1	carSet2	0.82404909	Brush border	
15	1838	1838	293760	1834	2930766	0.00017547	0.00011312	0.807797	0.544905	carfem1	carSet1	carbam	tarSet1	carSet2	0.54490504	Brush border	
16	2794	18380	2794	2794	0.00011752	0.00133077	1.125766	0.145407	carfem1	carSet1	carbam	tarSet1	carSet2	0.14540709	Brush border		
17	1482	1482	211341	1472	211761	0.00064474	0.00076183	1.2942	0.613887	carfem1	carSet1	carbam	tarSet1	carSet2	0.61388709	Brush border	
18	1174	24102	4509393	1167	4508831	0.00012569	0.00029042	1.01874	0.84811	carfem1	carSet1	carbam	tarSet1	carSet2	0.84811009	Brush border	
19	2559	2559	605	605	0.43336E-05	0.00015649	1.53232E-05	0.438825	0.705021	carfem1	carSet1	carbam	tarSet1	carSet2	0.70502109	Brush border	
20	334	27883	482362	334	479579	6.3424E-05	0	0	0.77995	carfem1	carSet1	carbam	tarSet1	carSet2	0.27429001	Brush border	
21	2484	462699	124	462699	2.1478E-05	0	0	0	1	carfem1	carSet1	carbam	tarSet1	carSet2	0.14288001	Brush border	
22	975	23212	387100	973	387100	0.00021058	8.6223E-05	0.234422	0.141025	carfem1	carSet1	carbam	tarSet1	carSet2	0.14128801	Brush border	
23	249	20834	3589008	248	3589004	6.3981E-05	4.7924E-05	0.039365	1	carfem1	carSet1	carbam	tarSet1	carSet2	0.35890001	Brush border	
24	1326	1326	289649	1322	289649	0.00022124	0.00022321	1.217728	0.303756	carfem1	carSet1	carbam	tarSet1	carSet2	0.30375609	Brush border	
25	1933	32043	302672	1931	320617	0.00045388	0.00039209	0.71615	0.450033	carfem1	carSet1	carbam	tarSet1	carSet2	0.45003309	Brush border	
26	3689	3689	1954745	3685	3954745	0.00015227	0.00034027	0.810123	0.306358	carfem1	carSet1	carbam	tarSet1	carSet2	0.30635809	Brush border	
27	3613	26112	418935	3599	417283	0.00008466	0.00035152	0.421302	0.028205	carfem1	carSet1	carbam	tarSet1	carSet2	0.02820509	Brush border	
28	17307	17307	17307	17304	17307	0.00014672	0.00112322	1.20495	0.521883	carfem1	carSet1	carbam	tarSet1	carSet2	0.52188309	Brush border	
29	2052	14028	340785	2050	340785	0.00019313	0.00059651	1.16992	0.64751	carfem1	carSet1	carbam	tarSet1	carSet2	0.64751009	Brush border	
30	2549	12035	210372	2541	210372	0.00121784	0.00149558	1.23871	0.354941	carfem1	carSet1	carbam	tarSet1	carSet2	0.35494109	Brush border	
31	3278	18284	340929	3273	339049	0.00012928	0.00077221	1.76322	0.238413	carfem1	carSet1	carbam	tarSet1	carSet2	0.23841309	Brush border	
32	2818	2083	494381	2817	494381	0.00006936	0.00072556	1.205225	0.39073	carfem1	carSet1	carbam	tarSet1	carSet2	0.39073009	Brush border	
33	3817	291995	100	291995	0.00051939	0.00074711	1.70747	0.162725	carfem1	carSet1	carbam	tarSet1	carSet2	0.16272509	Brush border		
34	3763	384209	3763	384209	0.00000042	0.00078793	0.688697	0.161685	carfem1	carSet1	carbam	tarSet1	carSet2	0.16168509	Brush border		
35	335	27901	482399	332	479740	6.9424E-05	0.00070759	1.149779	0.452041	carfem1	carSet1	carbam	tarSet1	carSet2	0.45204109	Brush border	
36	2111	23996	523444	2107	523444	0	0	0	0.27277	carfem1	carSet1	carbam	tarSet1	carSet2	0.27277009	Brush border	
37	1164	29622	439490	1155	432577	0.00003817	0.00038037	1.42143	0.312715	carfem1	carSet1	carbam	tarSet1	carSet2	0.31271509	Brush border	
38	3826	45428	494945	3820	454281	0.00001783	1.5339E-05	0.44219	0.482123	carfem1	carSet1	carbam	tarSet1	carSet2	0.48212309	Brush border	
39	1391	20179	391718	1380	374507	0.00004245	0.00050934	0.562348	0.02587	carfem1	carSet1	carbam	tarSet1	carSet2	0.02587009	Brush border	
40	2050	1896	42062425	2046	42062425	0.00000224	0.00024539	0.497324	0.00000224	carfem1	carSet1	carbam	tarSet1	carSet2	0.0000022409	Brush border	
41	331	29988	531575	330	531587	6.5544E-05	1.34467E-05	0.058267	1	carfem1	carSet1	carbam	tarSet1	carSet2	0.53157509	Brush border	
42	1948	2628	569798	1937	569798	0.00004936	0.00073196	1.01917	0.752038	carfem1	carSet1	carbam	tarSet1	carSet2	0.75203809	Brush border	
43	2888	42499	48004793	2884	48004793	0.00000000	0.00019788	0.89654	0.882624	carfem1	carSet1	carbam	tarSet1	carSet2	0.88262409	Brush border	
44	3426	2067	381406	3413	381394	0.00009158	0.00062867	0.70374	0.241615	carfem1	carSet1	carbam	tarSet1	carSet2	0.24161509	Brush border	
45	3826	3826	388703	3820	388703	0.00012949	0.00012949	1.48658	0.3121	carfem1	carSet1	carbam	tarSet1	carSet2	0.31210009	Brush border	
46	2962	364397	364397	2958	364397	0.00005132	0.00029768	0.388933	0.370729	carfem1	carSet1	carbam	tarSet1	carSet2	0.37072909	Brush border	
47	1714	1714	1714	1714	0.00000000	0.00072589	1.00072589	1.00072589	0.00072589	carfem1	carSet1	carbam	tarSet1	carSet2	0.0007258909	Brush border	
48	1074	206750	1074	206750	0.00000289	0.00016519	0.891258	1	carfem1	carSet1	carbam	tarSet1	carSet2	0.89125809	Brush border		
49	1251	237897	1251	237897	0.00000338	0.00088187	1.232238	0.25958	carfem1	carSet1	carbam	tarSet1	carSet2	0.25958009	Brush border		
50	1007	1007	220381	1007	220381	0.00008906	0.00038828	0.27462	0.038828	carfem1	carSet1	carbam	tarSet1	carSet2	0.03882809	Brush border	
51	95	7007	148380	95	148380	6.1320E-05	0.00028549	0.38265	0.079058	carfem1	carSet1	carbam	tarSet1	carSet2	0.07905809	Brush border	
52	1007	1007	2705128	1007	2705128	0.00013566	0.00089929	0.71645	0.158813	carfem1	carSet1	carbam	tarSet1	carSet2	0.15881309	Brush border	
53	179	281929	179	281927	0.00011784	0.00011784	0.00011784	0.00011784	0.00011784	carfem1	carSet1	carbam	tarSet1	carSet2	0.0001178409	Brush border	
54	571	9239	199153	567	198184	0.00020269	0.00040321	1.20564	0.34666	carfem1	carSet1	carbam	tarSet1	carSet2	0.34666009	Brush border	
55	1297	1297	185619	1293	185619	0.00011845	0.00039351	1.0341	0.72809	carfem1	carSet1	carbam	tarSet1	carSet2	0.72809009	Brush border	
56	318	17349	153493	316	153493	0.00018345	0.00048082	1.29582	0.87001	carfem1	carSet1	carbam	tarSet1	carSet2	0.87001009	Brush border	
57	2212	10924	21995	2212	10924	0.00012045	0.00012045	1.04264	0.36026	carfem1	carSet1	carbam	tarSet1	carSet2	0.36026009	Brush border	
58	1998	11514	247121	1992	246697	0.00081872	0.00051215	1.6304	0.327366	carfem1	carSet1	carbam	tarSet1	carSet2	0.32736609	Brush border	
59	1472	14842	2021399	1472	2021399	0.00000000	0	0	0	0	0	0	0	0	0.14842009	Brush border	
60	1622	19739	1615	19739	0.00017913	0.00115609	0.98189	0.00017913	0.00017913	carfem1	carSet1	carbam	tarSet1	carSet2	0.0001791309	Brush border	
61	867	3946	131527	864	130921	0.00009102	0.00050404	0.76382	0.00009102	carfem1	carSet1	carbam	tarSet1	carSet2	0.0000910209	Brush border	
62	1007	1007	1007	1007	0.00071814	0.00000000	0.00012244	0.247121	0.20207	carfem1	carSet1	carbam	tarSet1	carSet2	0.24712109	Brush border	
63	841	814	107825	840	107825	0.00004839	0.00012244	0.247121	0.20207	carfem1	carSet1	carbam	tarSet1	carSet2	0.24712109	Brush border	
64	1007	1007	2052198	1007	2052198	0.00000000	0.00015417	1.84858	0.3121	carfem1	carSet1	carbam	tarSet1	carSet2	0.31210009	Brush border	
65	179	10343	220627	178	220644	7.9118E-05	8.9502E-05	1.24515	0.53329	carfem1	carSet1	carbam	tarSet1	carSet2	0.53329009	Brush border	
66	1007	1007	202228	1007	202228	0.00000000	0.00012244	0.247121	0.20207	carfem1	carSet1	carbam	tarSet1	carSet2	0.24712109	Brush border	
67	34	10014	222599	34	222599	5.1574E-05	0	0	0	1	carfem1	carSet1	carbam	tarSet1	carSet2	0.22259909	Brush border
68	225	202140	202140	225	202140	0.00007921	0.00027344	0.83838	0.00007921	carfem1	carSet1	carbam	tarSet1	carSet2	0.0000792109	Brush border	
69	1888	1842	877781	1882	877781	5.1720E-05	0.00018177	0.27124	0.8477	carfem1	carSet1	carbam	tarSet1	carSet2	0.84770009	Brush border	
70	1114	888	184170	1109	184170	0.00002811	0.00050281	0.19458	1	carfem1	carSet1	carbam	tarSet1	carSet2	0.19458009	Brush border	
71	1007	1007	211948	1007													

4	533	9306	1978305	529	188999	0.002029423	0.004292813	1.595376	0.325687	delNo2nd	chomNo1	locuA01	locuP01m	mydloc	carfA02	1.83247931	Bush	border	
4	750	2053	2093355	402	10024021	0.000300522	0.002030822	0.232028	0.173521	delNo2nd	chomNo1	locuA01	locuP01m	mydloc	carfA02	1.93702823	Bush	border	
2	579	10294	232895	571	281801	0.000246675	0.000180278	0.730931	1.1	Deluobio	deluobio	deluobio	deluobio	deluobio	deluobio	1.79062441	TarSert	1	
2	657	11121	218429	655	212828	0.00025666	0.00019474	0.588358	0.78068	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
4	689	17	142327	57	4055178	0.00010138	0.000076	0.76417	0	1	1	carfA01	carfA01	carfA01	carfA01	0.73763083	carfA01	1	
3	949	8884	173242	946	1724078	0.000567775	0.000397324	0.533322	0.538194	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
4	103	143	129665	103	100033846	0.000139511	0.000039511	0.728629	1.1	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
3	170	1040	288124	167	287754	1.56115E-05	0.00012322	1.57862	0.554514	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.57228384	carfA02	1	
4	296	1911	296195	296	191131	0.000104945	0.00007111	0.730931	1.1	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
2	168	422	92526	166	925067	0.000116167	0.000042	2.54824	0.188386	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.81635792	carfA02	1	
2	161	7299	158885	609	1943542	0.00030455	0.00027401	0.712549	1	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
4	693	7433	193101	689	1884642	0.00023348	0.00016205	0.730931	1.1	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
10	1018	10004	213188	1008	2123877	0.00047005	0.00034078	1.04888	0.674577	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
4	104	1683	145208393	104	16830445	0.000100483	0.000032963	0.611661	0.177865	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.77321073	carfA02	1	
4	364	1043	238742	364	238740	0.00010404	0.00003404	0.730931	1.1	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
4	104	8839	1600206	104	1611338	0.00012708	0.00007628	0.730931	1.1	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
4	605	118989	290913	605	118983	0.00047269	0.00031033	1.04888	0.674577	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
4	878	136428	878	136428	878	136428	0.00047269	0.00031033	1.04888	0.674577	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
4	1296	1594	245828	1296	245828	0.00017815	0.00012524	0.650044	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
4	356	8632	162135	356	162135	0.00021077	0.00014883	0.730931	1.1	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
4	334	295595	334	295595	334	295595	0.00012642	0.00008752	0.620251	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
4	87	10796	218477	87	218771	0.00021077	0.00014883	0.730931	1.1	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
4	80	12167	202789	80	221520	0.00012642	0.00008752	0.620251	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
4	18	10276	224294	18	224294	8.13888E-06	0.00001517	0.730931	1.1	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
4	187	130647	187	130647	187	130647	0.00013137	0.00009417	0.730931	1.1	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1
4	107	1908	162195	107	162195	0.00013137	0.00009417	0.730931	1.1	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
2	382	18737	174509	380	178932	0.00012642	0.00008752	0.620251	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
4	860	10810	208171	860	207785	0.00012642	0.00008752	0.620251	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
4	369	21748	236668	366	236608	0.00012642	0.00008752	0.620251	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
1	423	17684	17684	423	172888	0.00012642	0.00008752	0.620251	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
4	240	8840	165986	240	165986	0.00013137	0.00009417	0.730931	1.1	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
4	167	19784	19784	167	199997	0.00012642	0.00008752	0.620251	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
2	773	18075	178071	771	177521	0.00014009	0.000102345	0.538342	0.597461	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.9576638	carfA02	1	
3	612	11850	221370	609	220980	0.00027427	0.00020322	0.533934	0.587011	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.9576638	carfA02	1	
4	127	16135	16135	127	166505	0.00027427	0.00020322	0.533934	0.587011	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.9576638	carfA02	1	
4	75	11265	224294	73	223255	3.37318E-05	0.00017754	1.26331	0.078088	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.05588883	carfA02	1	
4	68	11927	224294	68	224294	4.42786E-05	0.00017754	1.26331	0.078088	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.05588883	carfA02	1	
4	330	10128	204425	336	204547	0.00013137	0.00009417	0.730931	1.1	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
4	118	1040	204425	118	204425	0.00013137	0.00009417	0.730931	1.1	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
2	781	9214	185029	779	184835	0.00041018	0.00030455	1.04888	0.674577	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
2	813	11487	221570	811	221024	0.00012642	0.00008752	0.620251	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
2	812	11790	288878	812	278429	2.30021E-02	0.00012642	0.620251	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
3	448	18785	282227	448	282844	0.00012642	0.00008752	0.620251	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
4	121	12105	12105	121	12105	0.00012642	0.00008752	0.620251	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
4	830	150873	830	150873	830	150873	0.00012642	0.00008752	0.620251	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
4	167	1908	202733	167	1908	0.00012642	0.00008752	0.620251	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
5	1206	9047	159467	1201	164132	0.00012642	0.00008752	0.620251	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
12	1199	10733	209472	1187	208429	0.00012642	0.00008752	0.620251	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
4	1216	13126	13126	1216	130251	0.00012642	0.00008752	0.620251	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
3	507	9917	204790	504	203873	0.00012642	0.00008752	0.620251	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
4	107	1908	1908	107	1908	0.00012642	0.00008752	0.620251	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
2	183	21769	157609	181	156280	0.00013137	0.00009417	0.730931	1.1	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
22	4321	18198	340779	4309	338997	0.00012642	0.00008752	0.620251	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
20	3255	42954	996827	3247	996827	0.00012642	0.00008752	0.620251	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
17	2612	10617	491304	2608	491304	0.00012642	0.00008752	0.620251	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
17	2212	12192	219012	2212	219012	0.00012642	0.00008752	0.620251	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
7	932	30183	518805	925	513738	0.00013137	0.00009417	0.730931	1.1	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
9	2495	14617	272724	2491	272724	0.00012642	0.00008752	0.620251	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
9	909	10118	155158	900	154970	0.00012642	0.00008752	0.620251	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
18	3500	12086	266375	3482	265375	0.00012642	0.00008752	0.620251	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
13	2018	10184	212877	2017	212877	0.00012642	0.00008752	0.620251	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
15	5066	25435	5066	25435	5066	0.00012642	0.00008752	0.620251	0.377553	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	Deluobio	1.6497544	carfA02	1	
15	5066	25435	5066	25435	5066	0.00012642	0.00008752												

1	975	2512	386420	973	387200	0.00020388	6.85623E-05	0.34542	0.14055	Lepidoptera	miMura	Protopse	facialis	caerul	euCa2	0.1425843	Bush border	
2	1202	1929	28212	68	219078	0.00021428	7.7814E-05	0.57079	0.21646	Lepidoptera	miMura	Protopse	caurivis	caerul	euCa1	0.1212121	Bush border	
3	1461	1580	290213	162	207683	0.00048627	0.0008576	1.19474	0.57902	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1579676	Bush border	
4	535	202	202409	523	220201	0.00021428	0.0002734	0.08638	1	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1	Bush border	
5	402	402	402700	405	413824	0	0	0	0	0	0	0	0	0	0	0	0	
6	394	2007	340700	391	347083	0.0001237	0.0004949	1.32429	0.48704	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1489013	Bush border	
7	484	484	484700	482	484700	0.00020388	0.00020388	0.20037	0.1227	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1202020	Bush border	
8	741	2418	241813	737	246435	0.0001748	0.0003557	0.58467	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1489013	Bush border		
9	1461	1580	290213	1461	290213	0.00020388	0.00020388	0.20037	0.1227	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1202020	Bush border	
10	9401	12367	379257	1392	379200	0.0001748	0.0003557	0.58467	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1489013	Bush border		
11	992	2193	219317	989	220324	0.0004390	0.0002110	0.10257	0.32029	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1502044	Bush border	
12	1217	40270	402700	1217	402700	0.00021428	0.0004222	1.36864	0.14787	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1502044	Bush border	
13	74	1796	280977	74	287191	2.5607E-05	0	0	0	1	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1	Bush border
14	1347	1347	134700	82	140717	0.0003875	0.0003077	0.18848	0.0003875	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1	Bush border	
15	938	2310	231000	939	230950	0.0004020	0.0003861	1.40748	0.13914	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1379240	Bush border	
16	482	1770	291796	479	291796	0.0001547	0.0002266	0.39083	0.04607	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1422020	Bush border	
17	482	1770	291796	479	291796	0.0001547	0.0002266	0.39083	0.04607	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1422020	Bush border	
18	149	2142	415428	148	402837	0.0001916	0.0004832	0.51287	0.04124	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1504924	Bush border	
19	120	2396	412976	129	412976	0.0001916	0.0004832	0.51287	0.04124	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1504924	Bush border	
20	30	2548	402589	30	398821	7.4796E-06	0	0	0	1	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1	Bush border
21	245	21264	212640	244	212544	0.0001428	8.846E-05	0.77408	0	0	0	0	0	0	0	0	0	
22	640	17399	613668	633	610629	0.0002487	0.0004022	1.26325	0.09889	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1097817	Bush border	
23	640	17399	613668	633	610629	0.0002487	0.0004022	1.26325	0.09889	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1097817	Bush border	
24	640	17399	613668	633	610629	0.0002487	0.0004022	1.26325	0.09889	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1097817	Bush border	
25	1220	2829	368798	1216	369298	0.00021428	0.0002249	0.10413	0.78814	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.7882020	Bush border	
26	556	2648	385403	552	383043	0.0001748	0.0001758	0.32904	0.26885	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1287602	Bush border	
27	611	15627	156270	607	151017	0.0001428	0.0001718	1.18832	0.5848	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1584386	Bush border	
28	3	350	17860	347	278429	0.0001462	0.0001781	1.18859	0.48324	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1482179	Bush border	
29	1116	1846	387246	1112	387286	0.00020388	0.0001865	0.56861	0.16128	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1422020	Bush border	
30	1116	1846	387246	1112	387286	0.00020388	0.0001865	0.56861	0.16128	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1422020	Bush border	
31	7	1152	303511	7	312646	0.0001916	0.0004866	1.14702	0.61127	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1489013	Bush border	
32	885	2263	387407	879	381404	0.0002844	0.0002627	1.16998	0.05578	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1645081	Bush border	
33	140	2456	474064	140	474064	2.3938E-05	0	0	0	1	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1	Bush border
34	7	415	20081	7	415000	0.0001428	0	0	0	1	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1	Bush border
35	7	415	20081	7	415000	0.0001428	0	0	0	1	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1	Bush border
36	238	2007	396821	236	398830	0.0001428	0.0004868	1.17824	0.00782	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.0071834	Bush border	
37	1159	1746	398830	1159	398830	0.0001428	0.0004868	1.17824	0.00782	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.0071834	Bush border	
38	1218	2293	380210	1210	381794	0.0001547	0.0005888	1.18664	0.70201	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.7020079	Bush border	
39	432	432	432700	432	432700	0	0	0	0	1	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1	Bush border
40	653	2286	500478	649	499885	0.0001748	0.0005888	1.18664	0.70201	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.7020079	Bush border	
41	513	2007	340700	513	340700	0.0001748	0.0005888	1.18664	0.70201	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.7020079	Bush border	
42	1248	1248	124800	1236	125071	0.0004473	0.0001916	0.56861	0.16128	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1422020	Bush border	
43	6061	1708	342524	6055	339486	0.0003907	0.0003573	1.12802	0.62472	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1642246	Bush border	
44	1054	19004	190040	1054	190040	0.00020388	0.00020388	0.20037	0.1227	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1202020	Bush border	
45	636	2479	402739	634	402739	0.0001748	0.0008006	0.51168	0.02933	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1603307	Bush border	
46	61	1024	102400	61	102400	0.0001748	0.0008006	0.51168	0.02933	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1603307	Bush border	
47	661	1827	251405	661	250790	0.0002127	0.0001718	1.18832	0.5848	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1584386	Bush border	
48	1024	1024	102400	1024	102400	0.0001748	0.0001718	1.18832	0.5848	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1584386	Bush border	
49	2004	1578	291518	1996	291627	0.0004390	0.0002079	0.77093	0.67483	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.6748300	Bush border	
50	1422	1845	339878	1419	338231	0.0001865	0.0001790	0.42505	0.19664	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1379240	Bush border	
51	2003	2003	200300	2003	200300	0.0001865	0.0002009	0.71413	0.40023	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.4002300	Bush border	
52	127	1578	220000	127	219487	5.7568E-05	0	0	0	1	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1	Bush border
53	2147	2147	214700	2147	214700	0.0001428	0.0011231	0.31366	0.17635	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1763500	Bush border	
54	2	483	483071	2	483071	0.0001211	0.0001211	0.31366	0.17635	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1763500	Bush border	
55	849	1917	307586	844	303829	0.0002708	0.0001748	1.19474	0.09994	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1821807	Bush border	
56	1054	1054	105400	1054	105400	0.0002708	0.0001748	1.19474	0.09994	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1821807	Bush border	
57	433	1343	237916	432	236985	0.0001203	0.0001203	0.43736	0.57305	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.7392745	Bush border	
58	2030	2030	203000	2030	203000	0.0001203	0.0004703	0.51838	0.08864	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.0886400	Bush border	
59	127	2014	374431	127	373209	0.0001748	0.0005888	1.18664	0.70201	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.7020079	Bush border	
60	344	1645	264500	344	264500	0.0001748	0.0005888	1.18664	0.70201	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.7020079	Bush border	
61	1727	10675	106750	1718	106875	0.0001748	0.0004868	1.17824	0.00782	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.0071834	Bush border	
62	1003	1003	100300	1003	100300	0.0001748	0.0004868	1.17824	0.00782	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.0071834	Bush border	
63	1003	1003	100300	1003	100300	0.0001748	0.0004868	1.17824	0.00782	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.0071834	Bush border	
64	1185	1674	264739	1179	264303	0.0004759	0.0004009	0.81241	0.79609	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.7960900	Bush border	
65	1185	1674	264739	1179	264303	0.0004759	0.0004009	0.81241	0.79609	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.7960900	Bush border	
66	1185	1674	264739	1179	264303	0.0004759	0.0004009	0.81241	0.79609	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.7960900	Bush border	
67	1185	1674	264739	1179	264303	0.0004759	0.0004009	0.81241	0.79609	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.7960900	Bush border	
68	247	1871	306396	246	305255	0.0001748	0	0	0	1	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1	Bush border
69	207	207	207000	207	207000	0.0001748	0	0	0	1	Lepidoptera	miMura	Protopse	caerul	caerul	euCa1	0.1	Bush border
70	16	1811	356461	16	356461	5.7568E-05	0	0	0	1	Lepidoptera	miMura	Protopse	caerul	caerul			

9	1150	20259	400499	1183	407140	0.00029098	0.00042717	1.470151	0.22358	mm	rd	du0r1	calcat	panT2	tarT1	0.2718886	Brush border
2	1217	20260	440199	1184	407141	0.00029102	0.00042721	1.470151	0.22358	mm	rd	du0r1	calcat	panT2	tarT1	0.2718886	Brush border
5	946	1016	224473	941	273437	0.00045269	0.00064835	1.067289	0.81433	mm	rd	du0r1	chm04	d4m20	zncA1	0.8142874	Brush border
2	441	3017	530970	439	530927	0.8424825	0.8424825	0.70734	1	mm	rd	du0r1	colobae	panT2	panT2	0.70734	Brush border
1	3192	13192	37981	3183	377829	0.00021389	0.00021389	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
2	347	1817	150676	345	150745	0.00021392	0.00021392	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
1	1283	1833	270447	1276	270447	0.00021393	0.00021393	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
3	369	1836	217434	366	216088	0.00021394	0.00021394	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
1	1717	21718	270123	1710	270123	0.00021395	0.00021395	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
6	2030	1885	261347	2024	209652	0.00021397	0.00021397	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
12	1818	2071	460780	1846	460378	0.00021398	0.00021398	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
7	3279	3279	3279	3279	3279	0.00021399	0.00021399	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
7	1647	1835	241322	1640	239887	0.00064774	0.00064774	0.797329	0.61837	mm	rd	du0r1	colobae	panT2	panT2	0.61837	Brush border
4	1335	1807	220084	1328	220084	0.00021400	0.00021400	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
7	1689	2463	444375	1682	440852	0.00021401	0.00021401	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
7	2076	2076	2076	2076	2076	0.00021402	0.00021402	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
4	157	157	157	157	157	0.00021403	0.00021403	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
3	152	2329	459242	149	427474	0.00021404	0.00021404	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
4	127	1040	465336	127	453226	0.00021405	0.00021405	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
0	48	2468	44833	48	444875	0.00021406	0.00021406	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
4	156	2362	385465	152	375041	0.00021407	0.00021407	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
1	119	2118	353463	118	353533	0.00021408	0.00021408	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
0	100	1224	241651	99	240537	0.00021409	0.00021409	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
1	2076	2076	2076	2076	2076	0.00021410	0.00021410	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
4	1238	2004	364465	1234	362374	0.00021411	0.00021411	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
1	843	1308	180648	840	180246	0.00021412	0.00021412	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
7	1287	1803	357155	1280	356852	0.00021413	0.00021413	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
1	1277	2127	217136	1270	215049	0.00021414	0.00021414	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
3	400	2004	317449	400	314441	0.00021415	0.00021415	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
7	2151	2223	347448	2144	346235	0.00021416	0.00021416	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
7	2386	1899	342749	2384	338849	0.00021417	0.00021417	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
10	207	2236	373014	206	370914	0.00021418	0.00021418	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
12	164	4633	364926	164	463329	0.00021419	0.00021419	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
1	187	3030	521748	186	520548	0.00021420	0.00021420	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
4	583	2043	403339	579	418274	0.00021421	0.00021421	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
1	4732	4732	4732	4732	4732	0.00021422	0.00021422	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
6	1859	2143	363395	1853	362525	0.00021423	0.00021423	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
4	54	204	483150	54	484115	0.00021424	0.00021424	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
5	1981	2578	439878	1976	437222	0.00021425	0.00021425	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
1	120	120	120	120	120	0.00021426	0.00021426	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
4	98	3036	567146	94	566990	0.00021427	0.00021427	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
12	2360	20718	248771	2348	248703	0.00021428	0.00021428	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
1	2014	17464	306827	2007	304893	0.00021429	0.00021429	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
2	1033	2913	460335	1031	460234	0.00021430	0.00021430	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
1	2044	1041	448123	2041	448123	0.00021431	0.00021431	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
8	1189	1466	274454	1181	274938	0.00021432	0.00021432	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
1	1197	1197	1197	1197	1197	0.00021433	0.00021433	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
7	1840	1800	278263	1833	277423	0.00021434	0.00021434	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
7	1627	1627	1627	1620	329440	0.00021435	0.00021435	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
1	1028	1028	1028	1020	370817	0.00021436	0.00021436	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
0	93	1158	271389	93	270481	0.00021437	0.00021437	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
1	156	156	156	156	156	0.00021438	0.00021438	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
4	1056	1884	181947	1052	180763	0.00021439	0.00021439	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
4	554	2106	420446	550	421440	0.00021440	0.00021440	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
1	308	308	308	302	321361	0.00021441	0.00021441	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
6	419	619	131328	405	130769	0.00021442	0.00021442	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
1	3025	1029	22007134	3024	22007134	0.00021443	0.00021443	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
1	433	798	176084	422	175288	0.00021444	0.00021444	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
1	483	1548	288470	480	288400	0.00021445	0.00021445	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
11	3255	10248	355224	3244	354817	0.00021446	0.00021446	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
5	627	1230	228109	622	228779	0.00021447	0.00021447	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
1	213	213	213	213	213	0.00021448	0.00021448	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
22	2186	16817	368221	2184	368221	0.00021449	0.00021449	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
1	1028	1028	1028	1028	1028	0.00021450	0.00021450	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
8	2033	925	198494	2032	199389	0.00021451	0.00021451	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
9	1882	1882	1882	1882	1882	0.00021452	0.00021452	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
8	807	1463	264375	806	264342	0.00021453	0.00021453	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
1	1048	1048	1048	1048	1048	0.00021454	0.00021454	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
0	216	1968	368028	216	368042	0.00021455	0.00021455	0.128122	0.277795	mm	rd	du0r1	colobae	panT2	panT2	0.277795	Brush border
1	1411	1411	1411	1411	1411	0.00021456											

2	151	12375	279641	149	2776684	5.41327E-05	0	0	0.000516777	2.89554	154881	rMmAd2	pupMm1	colobM	chomM	dMmNoM	prcMm1	0.152300029	Brush border	
5	152	12376	279642	150	2776685	5.41327E-05	0	0	0.000516777	2.89554	154882	rMmAd2	pupMm1	colobM	chomM	dMmNoM	prcMm1	0.152300029	Brush border	
1	222	15369	3465267	221	3447578	4.45842E-05	0	0	6.44978E-05	1.004435	1	rMmAd2	pupMm1	colobM	dMmNoM	chomM	hAdM1	1	Brush border	
0	82	138070	2803870	82	279428	2.00202E-05	0	0	0	0	1	rMmAd2	pupMm1	colobM	DaubMm1	pupMm1	dMmNoM	dMmNoM	Brush border	
1	84	138072	2803892	84	279428	1.99999E-05	0	0	0	0	1	rMmAd2	pupMm1	colobM	dMmNoM	chomM	hAdM1	1	Brush border	
0	426	30061	516621	426	508663	8.25381E-05	0	0	0	0.188917	rMmAd2	pupMm1	colobM	dMmNoM	rMm1	carMm1	0.189874643	Brush border		
1	18068	60	124950	18068	60	124950	0	0	0	0	1	rMmAd2	pupMm1	colobM	carMm1	carMm1	carMm1	carMm1	Brush border	
3	294	15940	317520	291	315563	9.26718E-05	0	0	0.00038206	2.03896	rMmAd2	pupMm1	colobM	ehM1	ehM1	dMmNoM	0.185144731	Brush border		
6	30098	366	108540	30098	366	108540	0	0	6.64966E-05	0.181164	rMmAd2	pupMm1	colobM	carMm1	carMm1	carMm1	0.176142773	Brush border		
0	27	20410	382741	27	380331	7.04517E-04	0	0	0	0	1	rMmAd2	pupMm1	colobM	leuMm2	leuMm2	leuMm2	1	Brush border	
0	247	10398	288750	247	287225	8.55441E-05	0	0	0	0.048483	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	ehM1	ehM1	Brush border	
0	158	11885	273846	158	273846	5.99662E-05	0	0	0	0	1	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	ehM1	Brush border	
5	334	30095	538335	329	538320	6.22181E-05	0	0	0.00066141	1.070739	0.042797	rMmAd2	pupMm1	colobM	leuMm1	leuMm1	carMm1	0.140424384	Brush border	
1	163	19903	457044	163	457044	4.18702E-05	0	0	8.93066E-05	0.119519	rMmAd2	pupMm1	colobM	leuMm1	leuMm1	leuMm1	leuMm1	0.143823614	Brush border	
0	94	20440	584370	94	582228	2.48221E-05	0	0	0	0	1	rMmAd2	pupMm1	colobM	gMm1	gMm1	gMm1	gMm1	1	Brush border
0	94	20440	584370	94	582228	1.98680E-05	0	0	0	0	1	rMmAd2	pupMm1	colobM	gMm1	gMm1	gMm1	gMm1	1	Brush border
0	95	20441	584371	95	582229	4.30087E-05	0	0	0	0	1	rMmAd2	pupMm1	colobM	gMm1	gMm1	gMm1	gMm1	1	Brush border
0	155	20512	478278	155	474126	2.42228E-05	0	0	0	0	1	rMmAd2	pupMm1	colobM	leuMm1	leuMm1	leuMm1	leuMm1	1	Brush border
0	24989	36	438826	24989	36	438826	0	0	0	0	1	rMmAd2	pupMm1	colobM	leuMm1	leuMm1	leuMm1	leuMm1	1	Brush border
1	57	14028	280320	56	280308	1.97778E-05	0	0	6.69882E-05	0.378708	0.258933	rMmAd2	pupMm1	colobM	leuMm1	leuMm1	ehM1	0.252323260	Brush border	
1	2284	423265	220	423265	1.59825E-05	0	0	4.28376E-05	0.182854	1	rMmAd2	pupMm1	colobM	leuMm1	leuMm1	leuMm1	leuMm1	0.153190221	Brush border	
1	185	423987	184	424648	1.96351E-05	0	0	4.30226E-05	0.197836	1	rMmAd2	pupMm1	colobM	leuMm1	leuMm1	leuMm1	leuMm1	0.153190221	Brush border	
1	174	26477	483063	174	478436	3.61697E-05	0	0	3.77688E-05	1.044238	0.673176	rMmAd2	pupMm1	colobM	leuMm1	leuMm1	leuMm1	0.167226266	Brush border	
2	202	2929	49529	202	49286	6.39822E-05	0	0	6.82899E-05	0.198651	1	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	ehM1	1	Brush border
2	170	30313	532126	168	529993	3.24668E-05	0	0	6.63724E-05	0.20432	0.258411	rMmAd2	pupMm1	colobM	mMm1	rMm1	ehM1	0.256243431	Brush border	
2	222	29707	433045	222	431628	5.14620E-05	0	0	4.88286E-05	0.698937	1	rMmAd2	pupMm1	colobM	mMm1	mMm1	mMm1	0.153190221	Brush border	
0	232	13407	256329	232	255192	9.04871E-05	0	0	0	0.818377	rMmAd2	pupMm1	colobM	mMm1	mMm1	mMm1	mMm1	0.638513889	Brush border	
0	37205	30	399860	37205	30	399860	2.11811E-05	0	0	0	1	rMmAd2	pupMm1	colobM	leuMm1	leuMm1	leuMm1	leuMm1	1	Brush border
0	339	20275	417225	339	414810	5.0	0	0	0.0729790	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	ehM1	ehM1	0.274799951	Brush border	
3	394	21729	400920	391	406827	9.63266E-05	0	0	0.000318071	1.431916	0.471888	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.471745039	Brush border	
1	107	10324	592676	107	590420	1.26448E-05	0	0	0	0	0.431920	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.520760260	Brush border	
1	141	18788	394662	140	379789	3.92440E-05	0	0	5.54866E-05	0.136839	0.521213	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.520760260	Brush border	
1	207	13254	592676	207	590420	1.26448E-05	0	0	0	0	0.431920	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.520760260	Brush border	
2	354	24937	434988	352	432661	8.18190E-05	0	0	8.41870E-05	1.03484	0.72005	rMmAd2	pupMm1	colobM	prcMm1	ehM1	ehM1	0.720002051	Brush border	
2	152	20359	540290	150	537485	7.81312E-05	0	0	7.00202E-05	0.248022	0.194443	rMmAd2	pupMm1	colobM	PrMm1	leuMm1	leuMm1	0.191271238	Brush border	
2	2029	18778	527718	2029	524767	6.84725E-05	0	0	6.84725E-05	0.120882	1	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.451941614	Brush border	
1	191	30021	534029	190	527428	3.84432E-05	0	0	3.31155E-05	0.908855	1	rMmAd2	pupMm1	colobM	rMm1	mMm1	ehM1	1	Brush border	
1	184	19481	438613	184	437023	8.48623E-05	0	0	0.000396419	1.04347	0.520073	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.920455454	Brush border	
1	437	22737	459889	437	457566	7.48806E-05	0	0	0	0	0	1	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	1	Brush border
1	409	22827	432071	409	430531	6.55241E-05	0	0	0	0	0	1	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.512042480	Brush border
2	385	24413	4505417	383	451004	7.17838E-05	0	0	1.93265E-05	1.11055	0.702009	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.702468939	Brush border	
1	167	32736	540290	166	547006	3.04446E-05	0	0	3.07523E-05	0.102407	0.628313	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.628302610	Brush border	
1	224	18286	445012	224	443188	5.30088E-05	0	0	4.09283E-05	0.182926	1	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.471745039	Brush border	
0	220	17546	347718	220	346925	6.22696E-05	0	0	0	0.633203	0.643718	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.643404831	Brush border	
1	181	13849	338499	181	337178	1.14855E-05	0	0	0	0	0	1	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.471745039	Brush border
6	1698	18116	347312	1692	346016	0.00040831	0	0	0.00027382	0.071203	0.402117	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.402143603	Brush border	
1	2076	22076	420714	2076	419024	0.00042432	0	0	0.00024242	0.127211	0.312163	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.312163163	Brush border	
10	1838	460628	460628	1838	459709	0.00041713	0	0	0.00037946	0.096134	0.880354	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.88031822	Brush border	
3	946	11037	222778	943	221611	0.00044753	0	0	0.00072306	0.041904	0.692924	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.692404402	Brush border	
3	1096	12064	23066	1096	23066	0.00041713	0	0	8.97847E-05	0.204219	0.520248	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.520248000	Brush border	
1	574	21318	379229	573	377601	0.00011308	0	0	4.22189E-05	0.28006	0.278312	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.278305705	Brush border	
1	104	104	104	104	104	0.00041713	0	0	0.00031673	0.00066	0.000265	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.000265141	Brush border	
3	1243	127086	1240	127084	0.00045483	0	0	0.000370734	1.55057	0.30382	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.301290793	Brush border		
2	388	11035	214287	388	213232	0.00027848	0	0	0.00018054	1.03181	0.72044	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.720252007	Brush border	
2	178	20538	378265	178	376805	0.00029612	0	0	0.00029612	1.38823	0.402713	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.402713000	Brush border	
7	1978	26158	460289	1971	460289	0.00017599	0	0	0.000205525	0.684262	0.354345	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.3512447	Brush border	
0	2054	460289	460289	2054	460289	0.00040831	0	0	0.00029612	1.38823	0.402713	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.402713000	Brush border	
0	163	26565	337151	163	336550	4.97388E-05	0	0	0	0	0.613209	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.613147434	Brush border	
0	1683	18085	245243	1683	245243	0.00041713	0	0	0.00039041	1.84817	0.74517	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.745170000	Brush border	
0	1972	20943	442473	1972	442473	0.00041713	0	0	0.00039041	1.84817	0.74517	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.745170000	Brush border	
3	628	2748	396479	625	393421	0.00019038	0	0	0.00029612	1.38823	0.402713	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.402713000	Brush border	
1	161	46043	46043	161	459525	4.14815E-05	0	0	7.88521E-05	0.427592	0.28362	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	0.283620000	Brush border	
0	161	28169	46043	161	46043	3.49756E-05	0	0	0	0	1	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	1	Brush border	
0	161	28169	46043	161	46043	3.49756E-05	0	0	0	0	1	rMmAd2	pupMm1	colobM	ehM1	ehM1	ehM1	1	Brush border	
4	53	2447	388280	540	388463	0.00013137	0	0	0.0007816	1										

*Proportion of genome-wide convergent sites to genome-wide possible sites" is based on the counts from column 2 and column 4
*Proportion of convergent sites convergent in the GO term to sites possible in the GO term" is based on the counts from column 1 and column 3
*Odds ratio" is the strength of the association between the GO term and number of convergent sites
*Pval" is the probability of association between the GO term and number of convergent sites
*Species1or_group1[OUT1,OUT1]" and *Species2or_group2[OUT2,OUT2]" represent the comparison between Species 1 and Species 2 with respective outgroups
*Fisher pval" is the p-value from the Fisher's exact test
*GO pathway" is the data from the hydrolyase activity or brush border species comparisons

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