

Supplementary Materials for
Comparative genomics reveals the hybrid origin of a macaque group

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Sci. Adv. **9**, eadd3580 (2023)
DOI: 10.1126/sciadv.add3580

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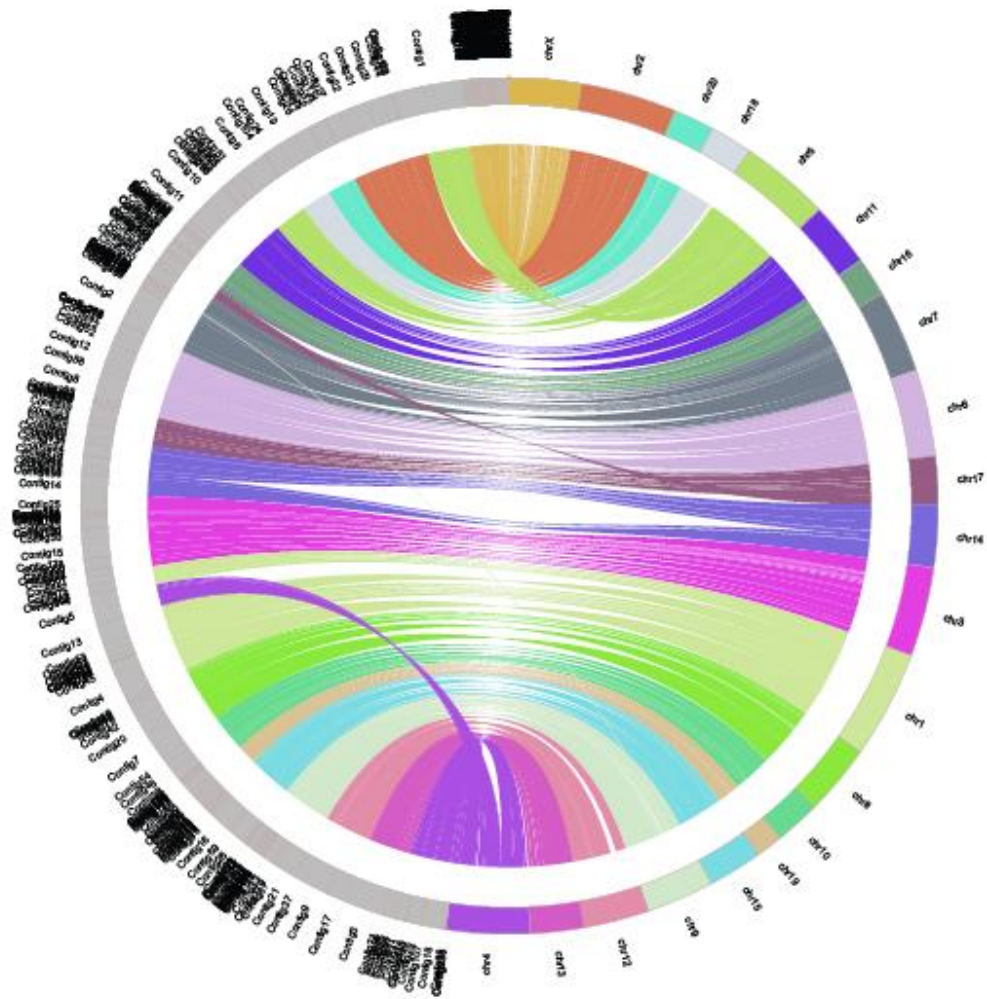


Fig. S1. An example showing the syntenic blocks between the stump-tailed macaque vs. Chinese rhesus macaque. Scaffolds larger than 10-kb were shown.

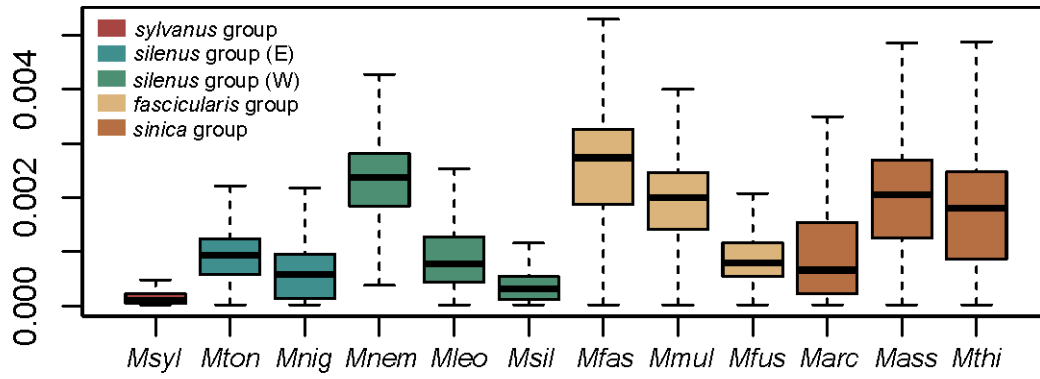


Fig. S2. Genetic diversity for different macaque species. Y-axis represents the ratio of average nucleotide differences between a pair of chromosomes in 50-kb windows. Species are abbreviated using the first letter of the genus name and the first three letters of the species name.

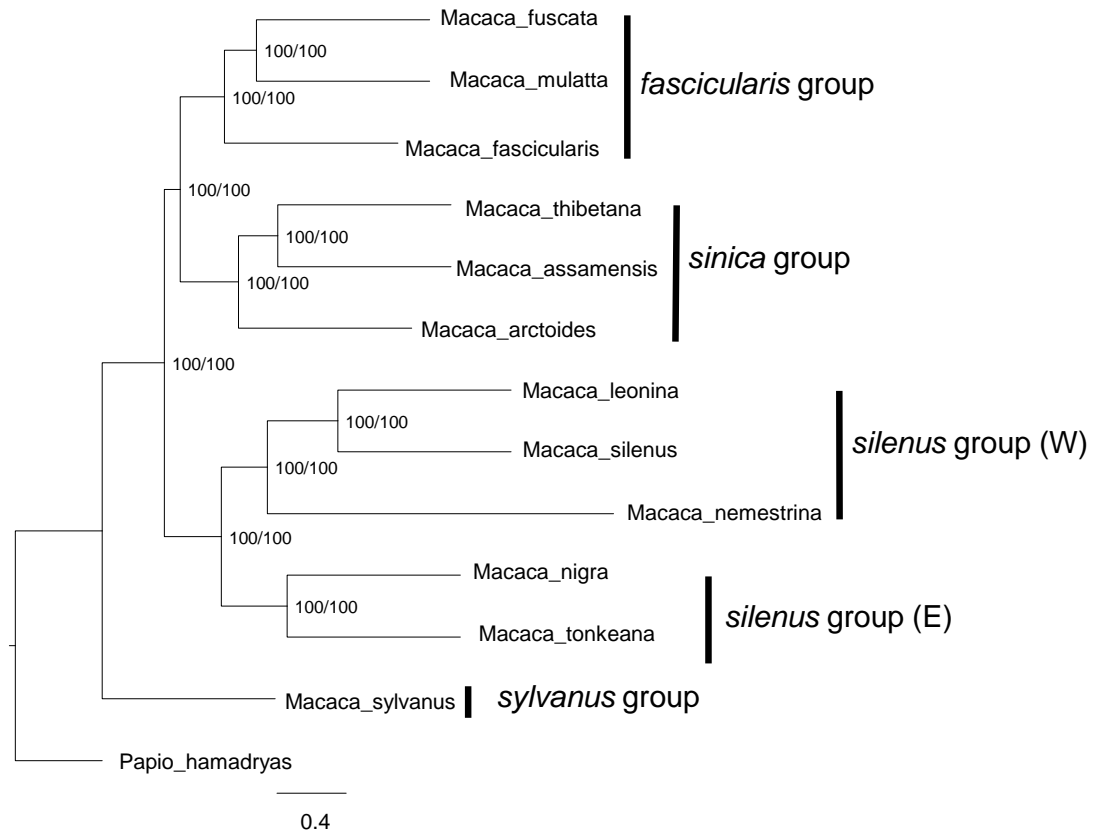


Fig. S3. Coalescent-based phylogeny of macaques inferred from 50 kb genomic windows. Branch lengths are in coalescent units as estimated by ASTRAL. Numbers at nodes refer to bootstrap values of ASTRAL and STAR, respectively.

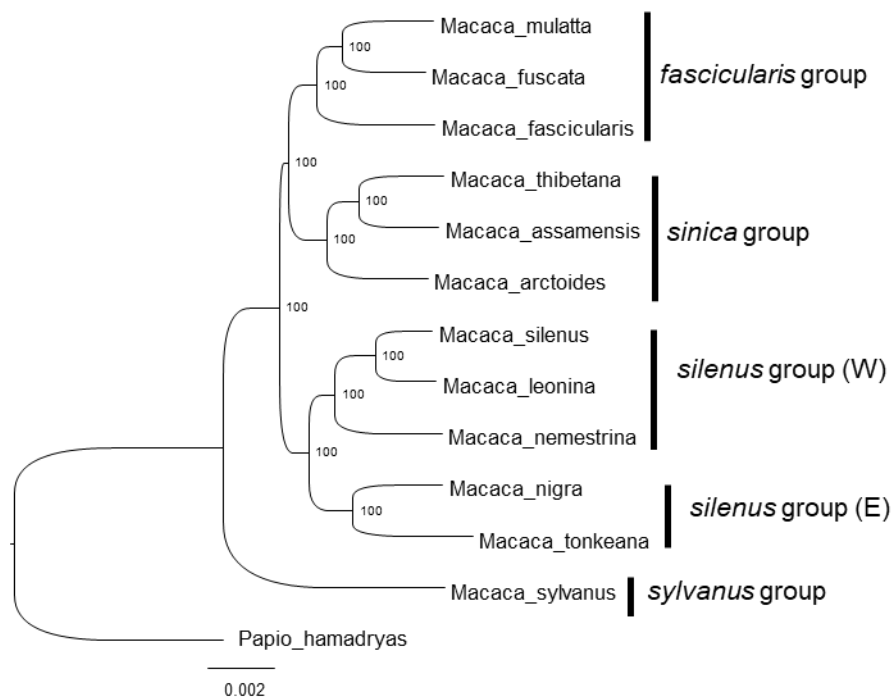


Fig. S4. Maximum Likelihood (ML) tree inferred using concatenated four-fold degenerate sites (4d) sites. We identified a total of 11,353 one-to-one orthologous genes and 4d sites were extracted and used to infer an ML phylogenetic tree by RAxML. Numbers beside nodes indicate bootstrap values.

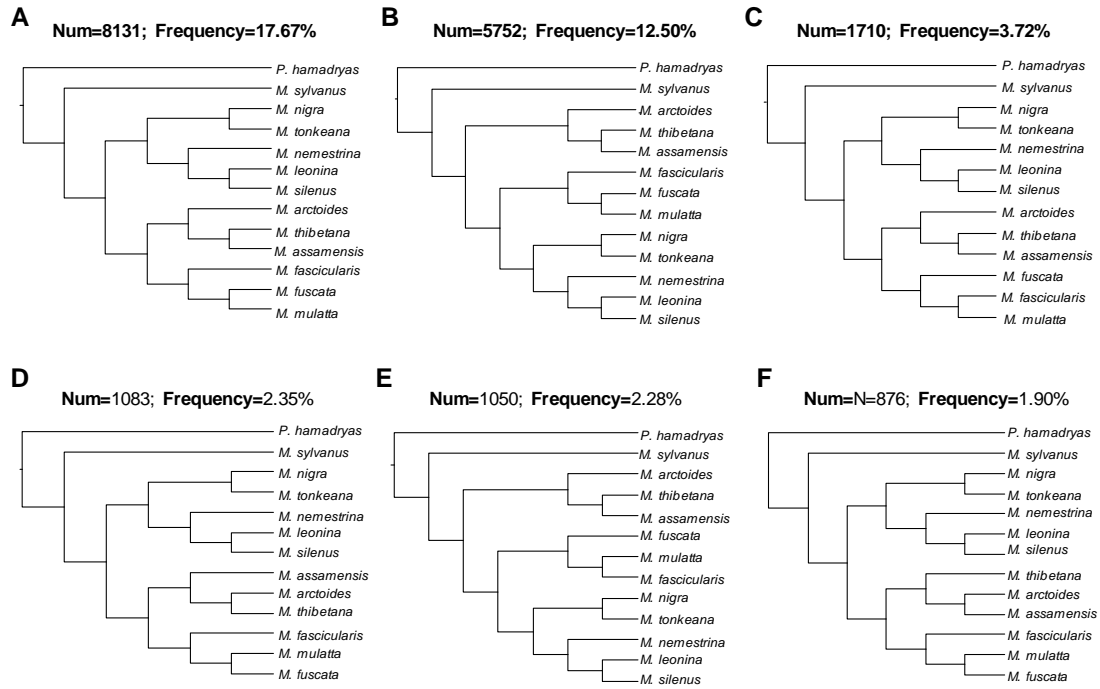


Fig. S5. The number and frequency of the six most common topologies amongst all 50-kb window trees (n=46,003 windows).

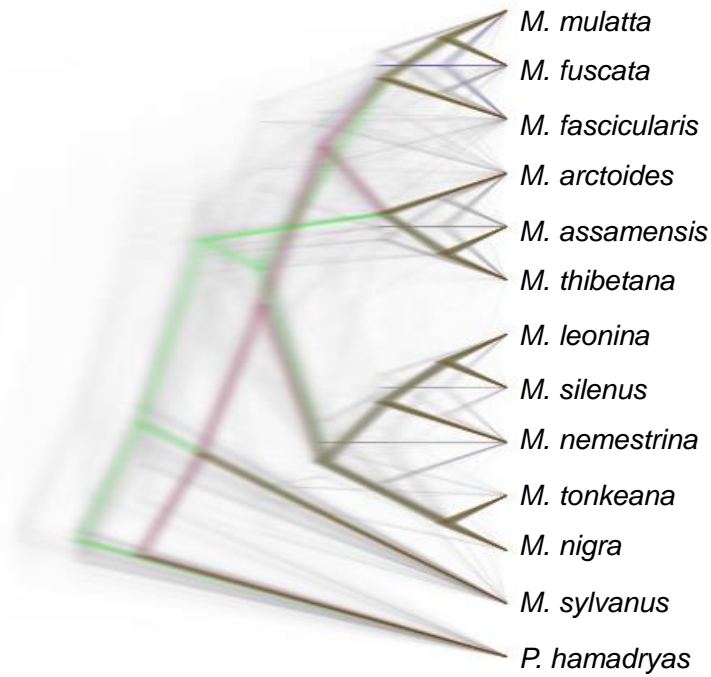


Fig. S6. DensiTree plot for 20-kb window trees. Topologies with mean bootstrap values below 80 have been removed, so that a total of 92,132 trees were retained in the results. The dark red, light green and purple colors represent the first, second and third most common topologies, respectively, whilst gray represents other topologies.

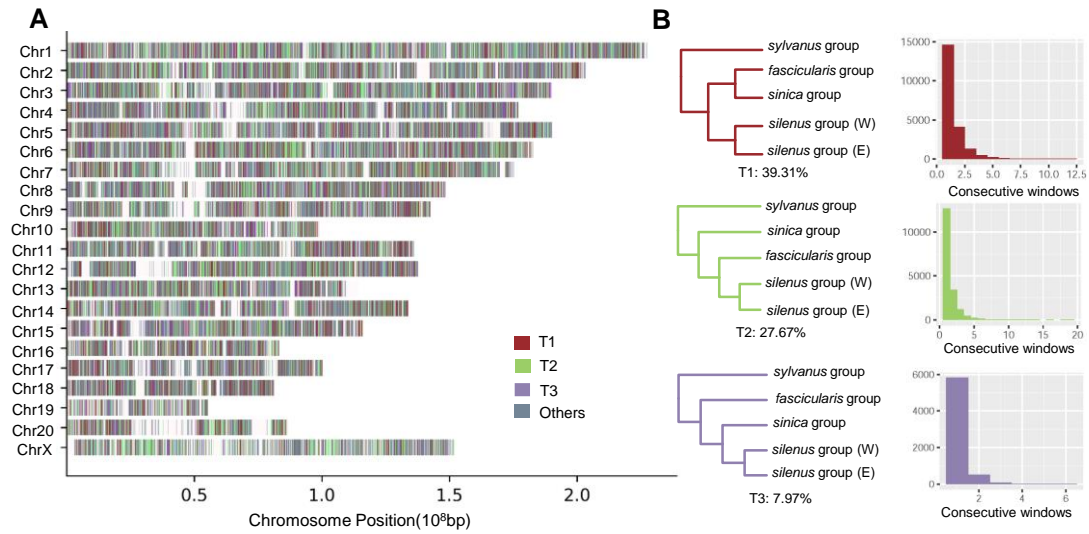


Fig. S7. Heterogeneity of the phylogenetic signals using 20-kb window sequences. (A) The distribution of the top three most common topologies by reference to the Chinese rhesus macaque (rheMacS) genome. White interval regions denote missing data. (B) The top three most common trees recovered by maximum likelihood analysis and the frequency of consecutive 20-kb windows with that topology. Values below the tree refer to the percentage of windows with that topology. The outgroup *Papio hamadryas* is not shown.

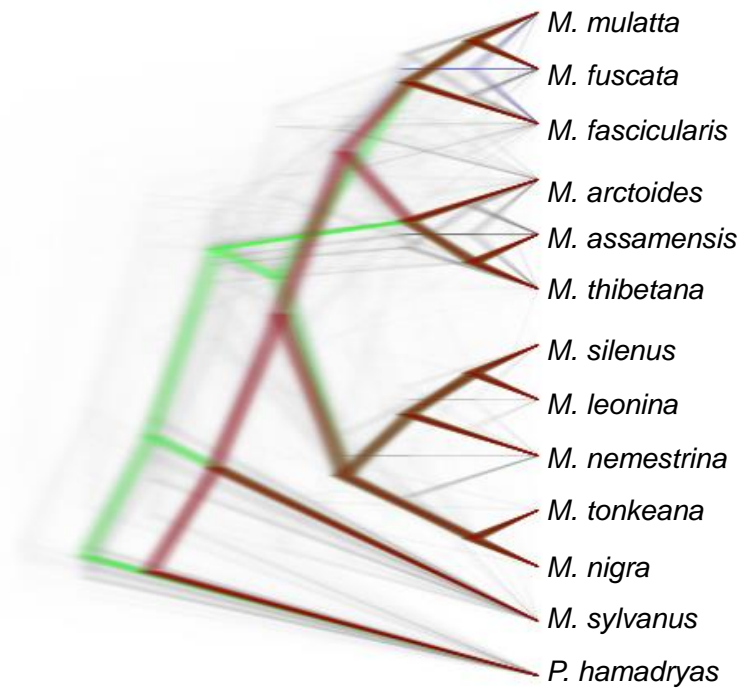


Fig. S8. DensiTree plot for 100-kb window trees. Topologies with mean bootstrap values below 80 have been removed, so that a total of 23,097 trees were retained in the results. The dark red, light green and purple colors represent the first, second and third most common topologies, respectively, whilst gray represents other topologies.

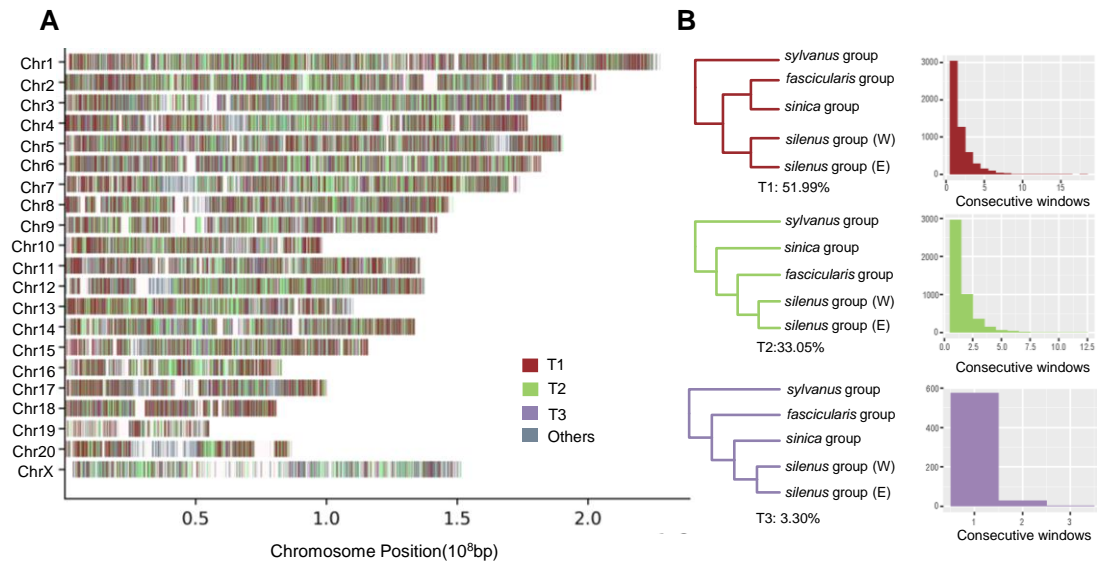


Fig. S9. Heterogeneity of phylogenetic signals using 100-kb window sequences. (A) The distribution of the three most common topologies by reference to the Chinese rhesus macaque (rheMacS) genome. White interval regions showing missing data. The outgroup *Papio hamadryas* is not shown. (B) The top three most common trees recovered by maximum likelihood analysis and the frequency of consecutive 100-kb windows with that topology. Values below the tree refer to the percentage of windows with that topology. The outgroup *Papio hamadryas* is not shown.

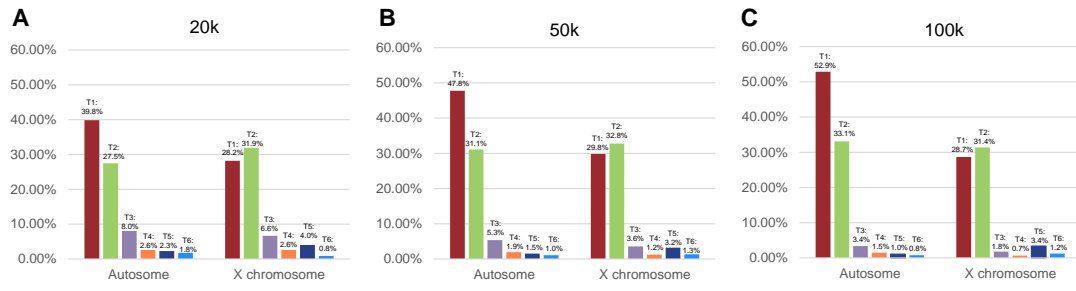


Fig. S10. Proportion of the six most common topologies (T1-T6) recovered from autosomes and the X-chromosome for 20-kb, 50-kb and 100-kb window sizes, respectively.

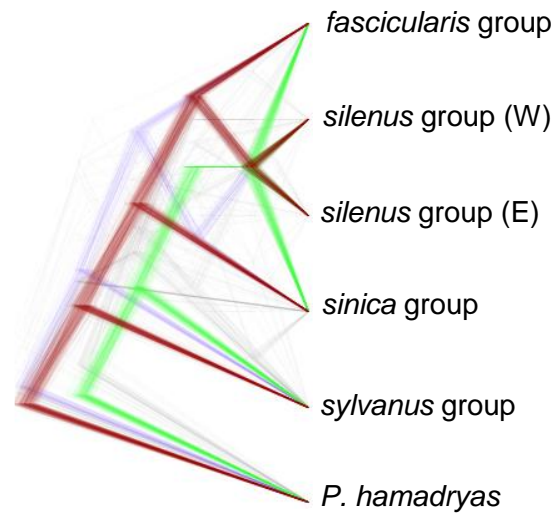


Fig. S11. DensiTree plot for the major lineage relationships in the low 1% recombination regions. The dark red color supports the sister relationship between the *fascicularis* group and the *sinica* group (tree1, 33.7 % of total), whereas the light green supports the sister relationship between the *fascicularis* group and the *silenus* group (tree2, 39.8% of total).

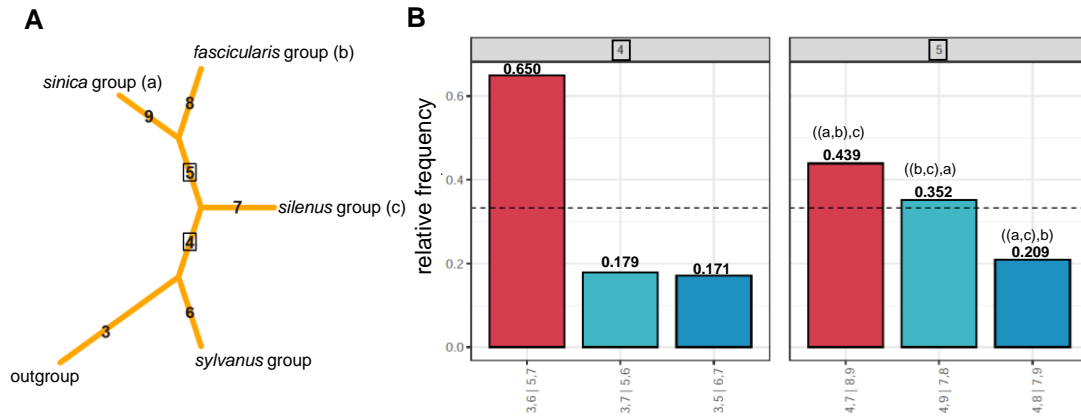


Fig. S12. DiscoVista results estimate the frequency of all three possible topologies around the internal branches. (A). The unrooted ASTRAL tree at species group level. Numbers on the tree refer to the branch number. The rectangle numbers refer to branches of interest in panel B. (B). Frequency of all three possible topologies around the interested internal branches. Each internal branch has four neighboring branches and could be used to represent all three possible topologies separated by “|”. The frequency of the main topology (consistent with the ASTRAL tree) is shown by a red bar, whereas the other two alternative topologies are depicted by blue bars. The dash line indicates the 1/3 threshold expected at random. The conflict relationships between the *fascicularis* group (b) and their two parental lineages, *sinica* (a), *silenus* (c), are also shown above the bar.

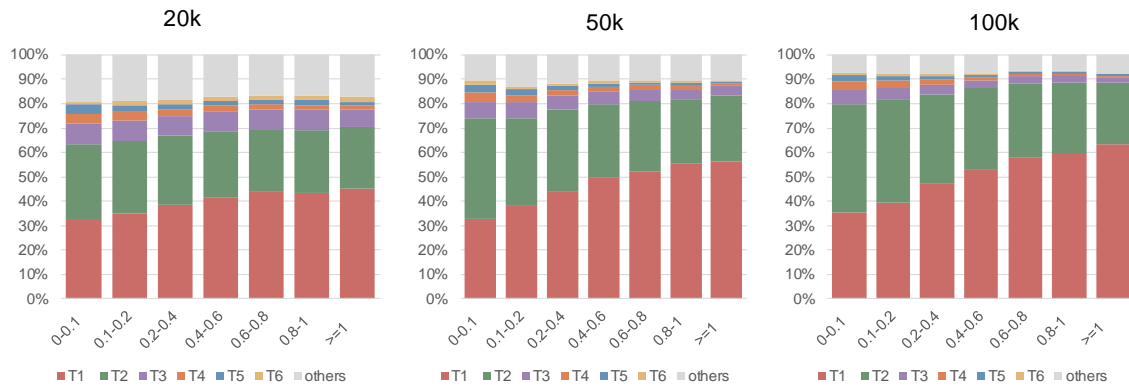


Fig. S13. Proportion of the six most common topologies (T1-T6) stratified by the recombination rate (cM/Mb, x axis) for 20-kb, 50-kb and 100-kb window sizes, respectively.

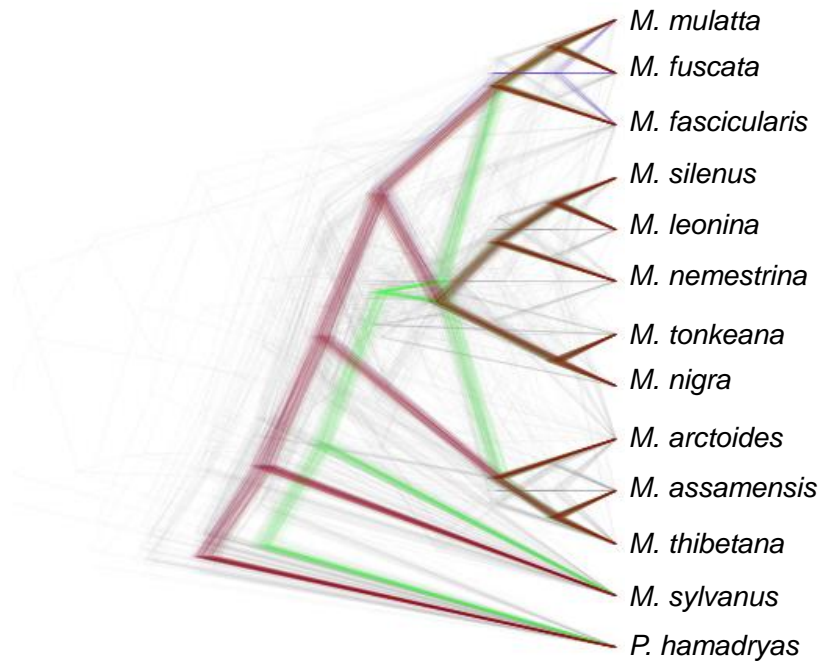


Fig. S14. DensiTree plot for all species in the low 1% recombination regions. The dark red, light green and purple colors represent the first, second and third most common topologies, respectively, whilst gray represents other topologies.

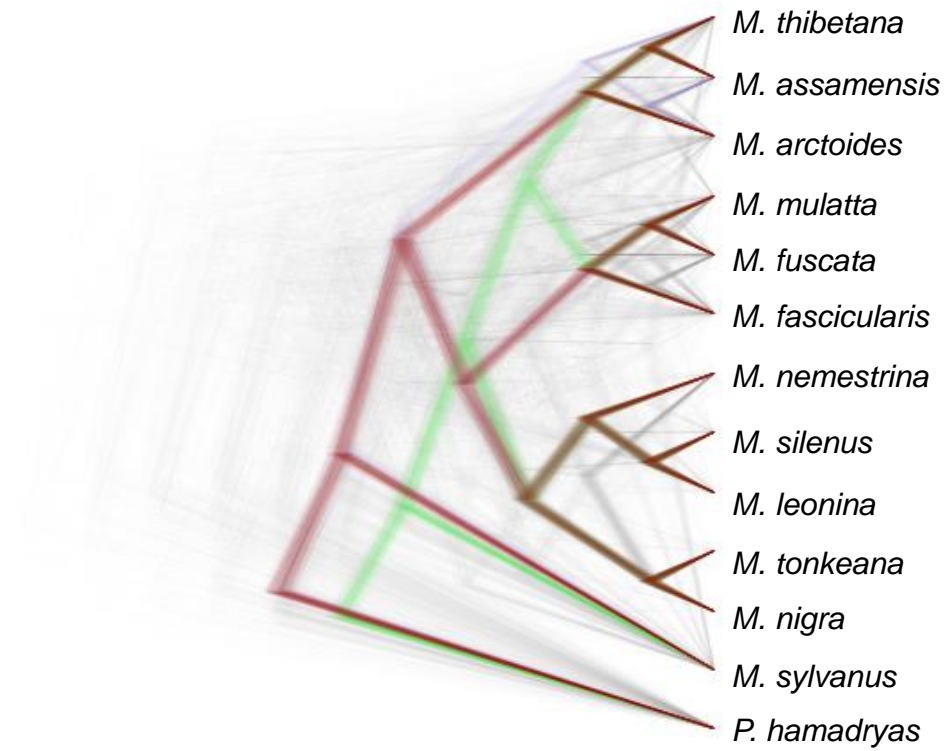


Fig. S15. DensiTree plot for topologies in the X chromosome. The dark red, light green and purple colors represent the first, second and third most common topologies, respectively, whilst gray represents other topologies.

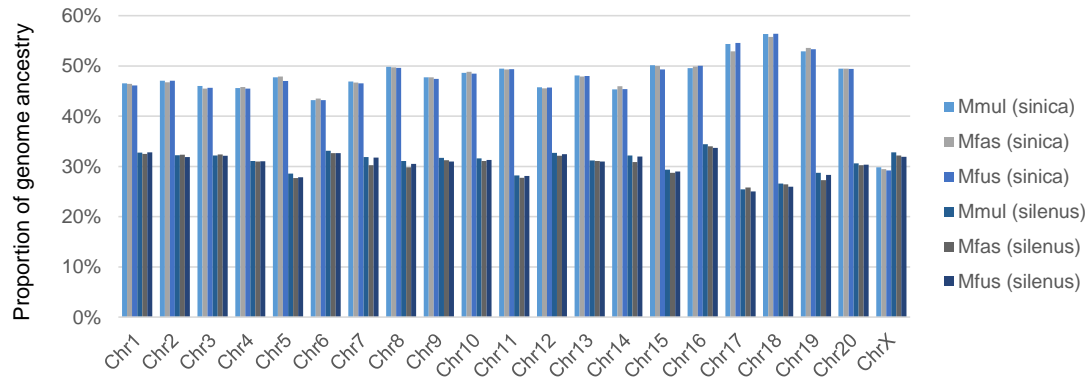


Fig. S16. Proportion of genome ancestry of two parental lineage (*sinica* group and *silenus* group) in three hybrid species. Mmul: *M. mulatta*; Mfas: *M. fascicularis* Mfus: *M. fuscata*.

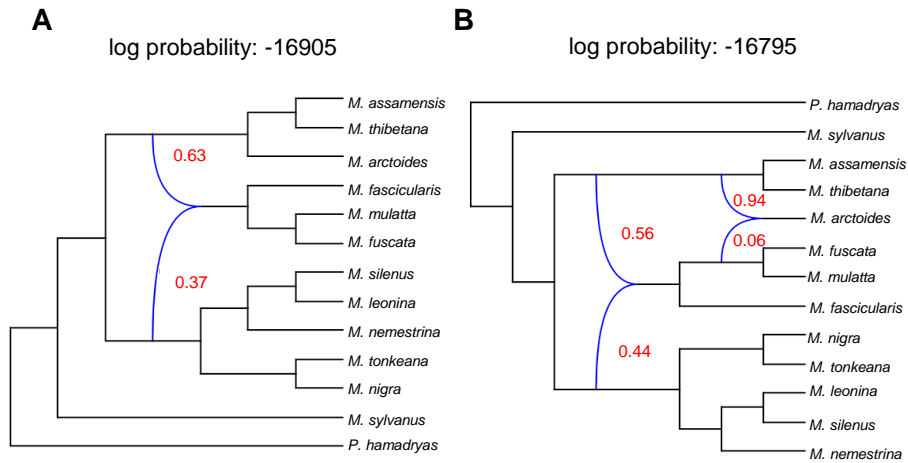


Fig. S17. Phylogenetic network inferred from PhyloNet. (A) reticulation=1; (B) reticulation=2. When more than 2 reticulation scenarios were applied, PhyloNet provided inconsistent inferences for the parental lineages involved in the reticulated evolutionary history due to excessively large search space under higher reticulation values. The blue line indicates reticulation and red numerical values indicate inheritance probabilities.

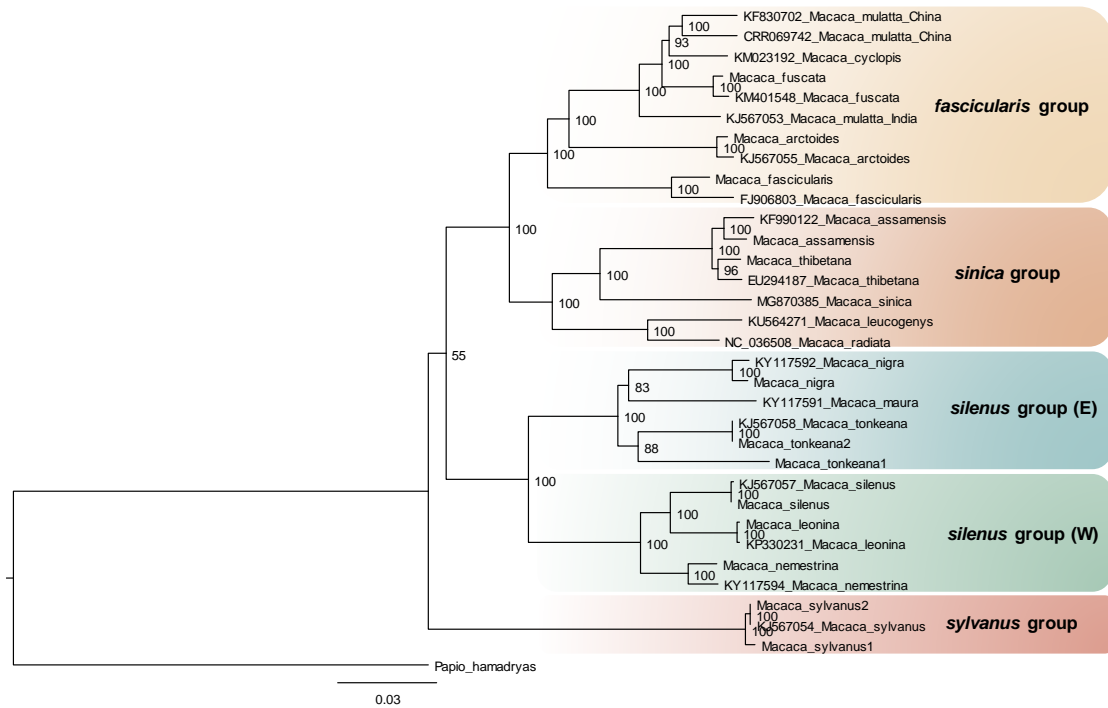


Fig. S18. Mitochondrial genome tree inferred by RAxML. Numbers beside nodes indicate bootstrap values. The labels with accession numbers refer to previously released mitochondrial genome sequences, whereas labels without an accession number refer to samples described in this study.

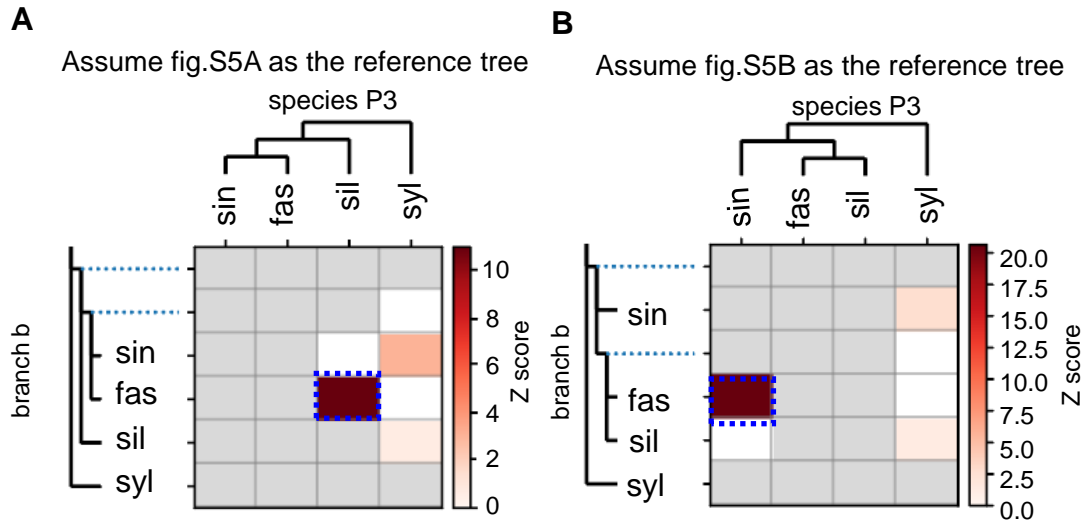


Fig. S19. Heatmap showing statistical support for introgression between pairs of species groups based on (A) species group level tree referring to fig. S5A, and (B) fig. S5B, respectively. Cells in the heatmap indicate the pairwise Z-score values between the branch b identified on the expanded tree on the Y axis (relative to its sister branch) and the taxa P3 identified on the X-axis (see Supplementary table S10-S11 for details of Z-score values). Cells having a Z-score >3 are highlighted with a blue rectangle. sin: *sinica* group; sil: *silenus* group; fas: *fascicularis* group; syl: *sylvanus* group.

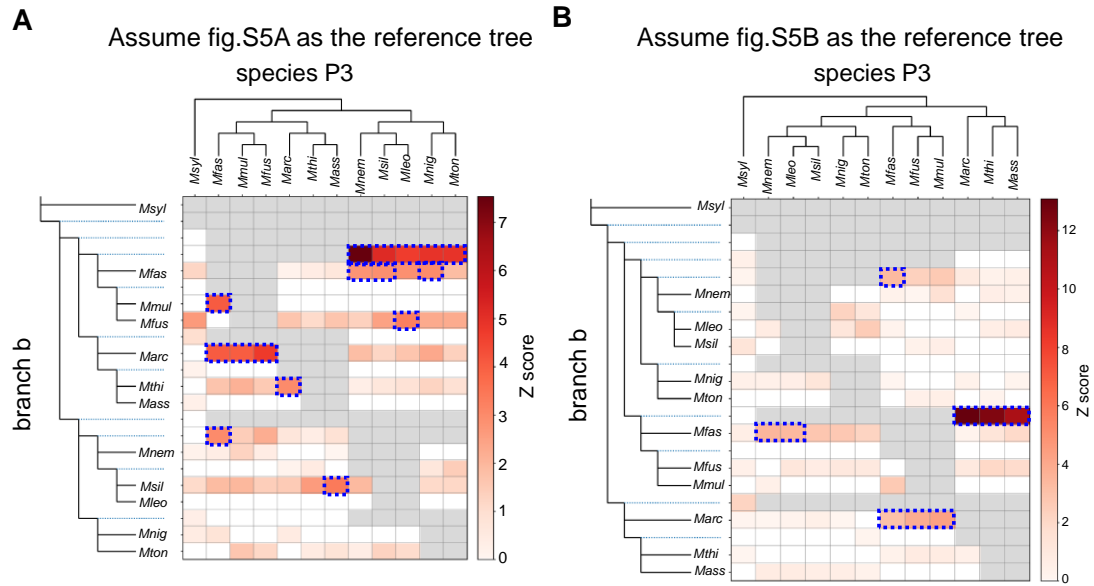


Fig. S20. Heatmap showing statistical support for introgression between pairs of species inferred from *Dsuit* package, assuming (A) fig. S5A and (B) fig. S5B as reference tree, respectively. Cells in the heatmap indicate the pairwise Z-score values between the branch b identified on the expanded tree on the Y axis (relative to its sister branch) and the species P3 identified on the X-axis (see Supplementary table S12 and S13 for details of Z-score values). Cells having a Z-score >3 are highlighted with a blue rectangle.

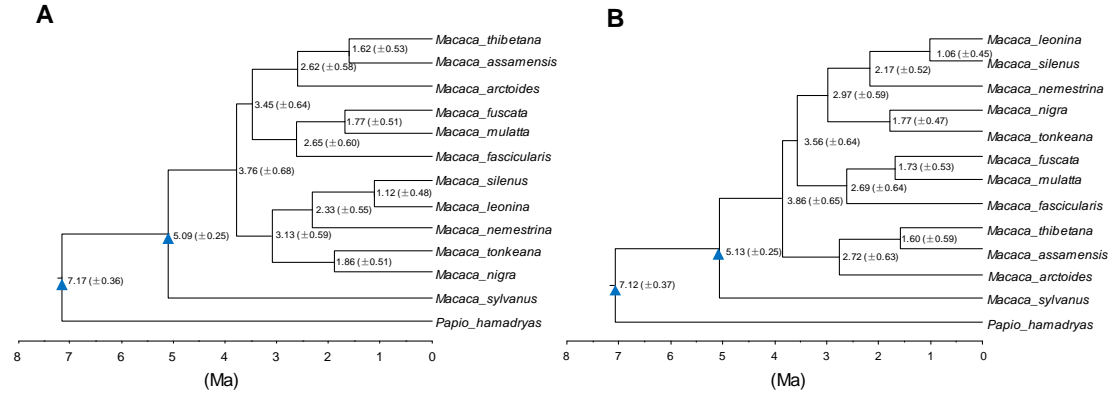


Fig. S21. The estimated divergence time for autosomal window sequences supporting **fig. 5A (left)** and **fig. 5B (right)**, respectively. Numbers at nodes refer to the average age (Ma) \pm 1 standard deviation (SD). Blue triangles indicate fossil-based calibration points.

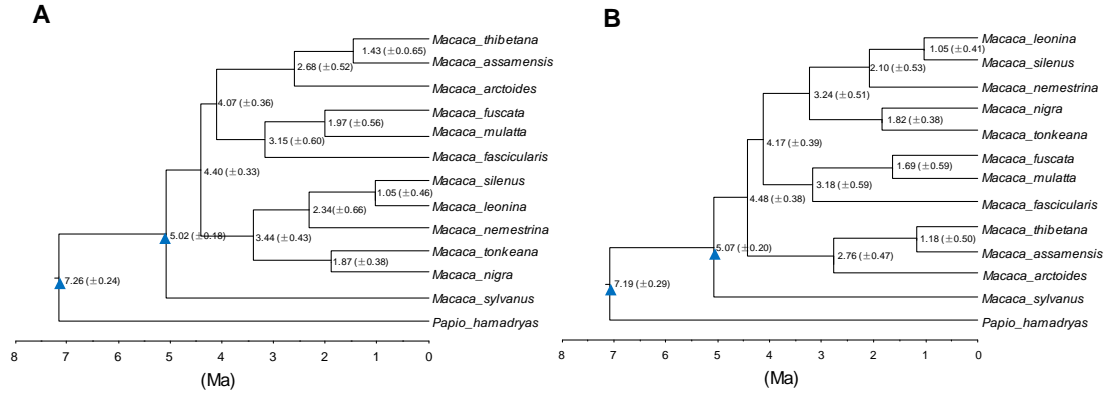


Fig. S22. The estimated divergence times for X-chromosome window sequences supporting **fig. 5A (left)** and **fig. 5B (right)**, respectively. Numbers at nodes refer to the average age (Ma) \pm 1 standard deviation (SD). Blue triangles indicate fossil record-based calibration points

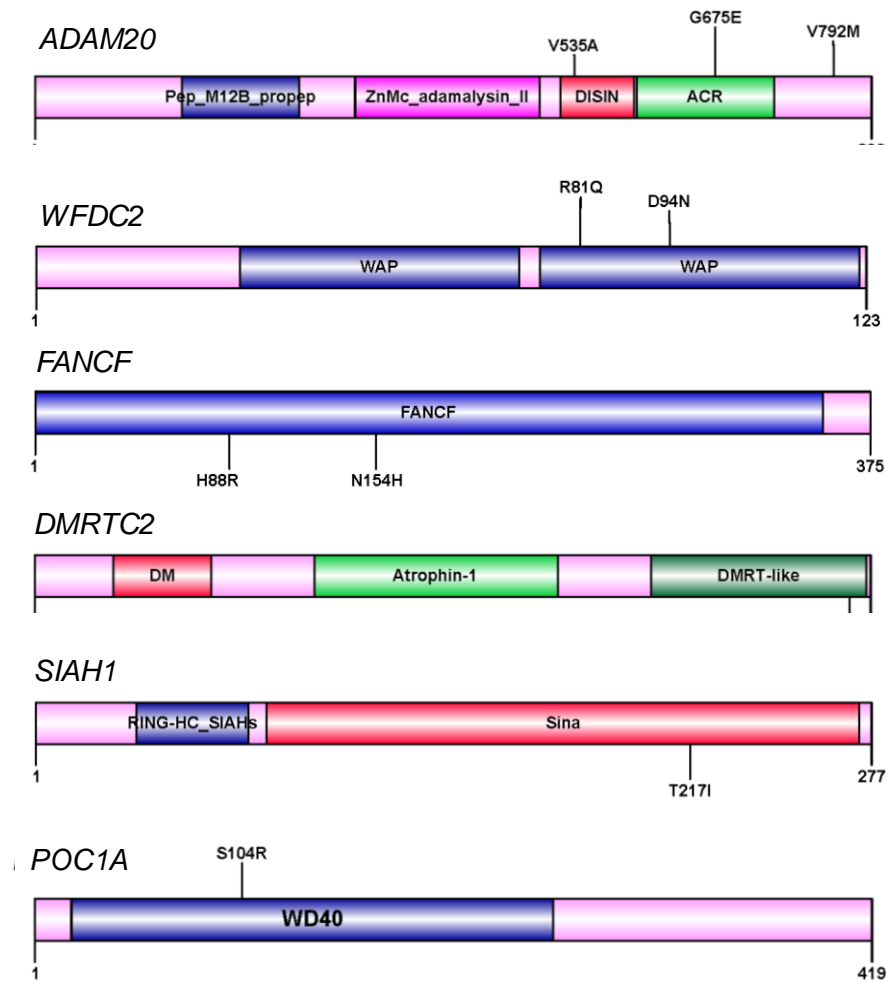


Fig. S23. The *sinica*-derived non-synonymous mutations occurring in the *fascicularis* group and their positions in relation to the functional domain regions predicted by NCBI's Conserved Domain Database.

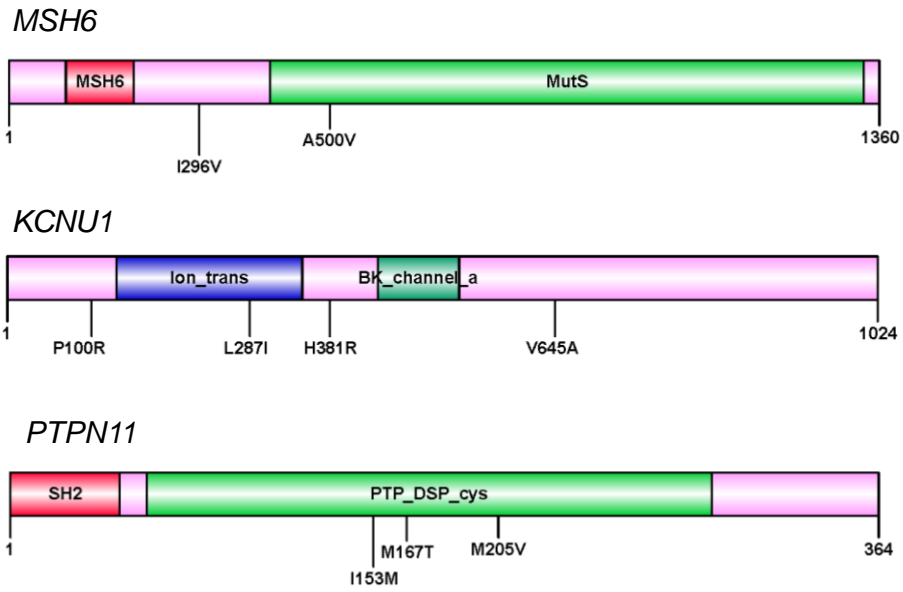


Fig. S24. The *silenus*-derived non-synonymous mutations occurring in the *fascicularis* group and their positions in relation to the functional domain regions predicted by NCBI's Conserved Domain Database.

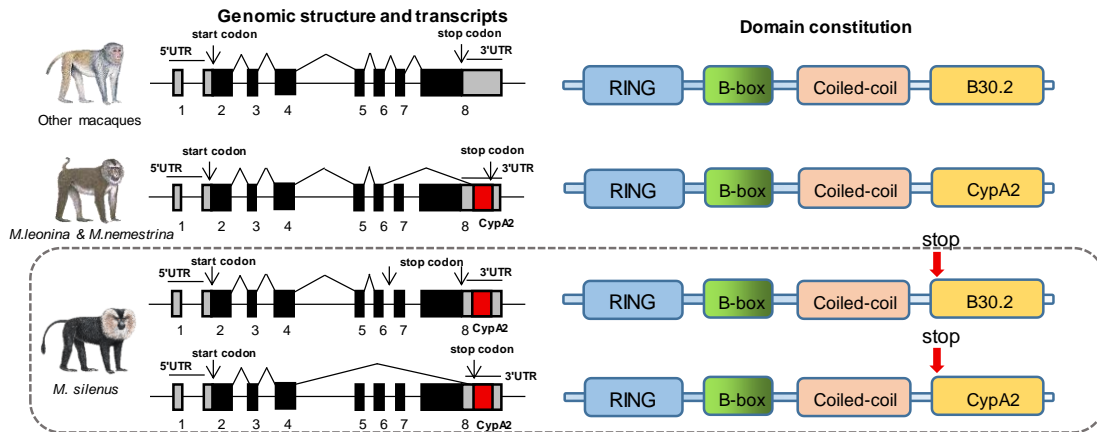


Fig. S25. The genomic structure and alternative splicing isoforms of the *TRIM5* gene and *TRIM5-CypA* fusion genes. The retrotranspositional insertion of a cyclophilin A2 (*CypA2*) gene into the 3' UTR region of the *TRIM5* locus was found in both pig-tailed macaques (*M. leonina* and *M. nemestrina*) and lion-tailed macaques (*M. silenus*), whereas other macaques (*M. mulatta* for example) lack this gene structure.

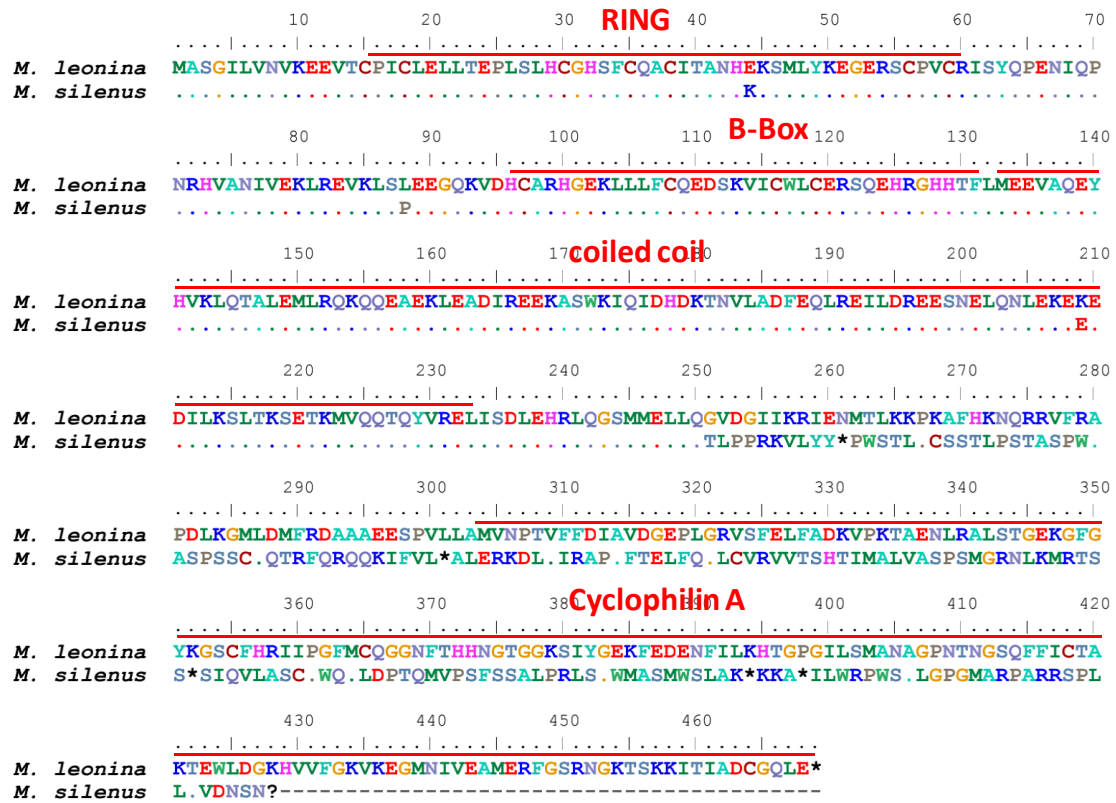


Fig. S26. Protein sequence alignment of *TRIMCyp* between the lion-tailed macaque (*M. silenus*) and the northern pig-tailed macaque (*M. leonina*). RING, B-Box, coiled coil, and cyclophilin A2 (*CypA2*) domains are shown.

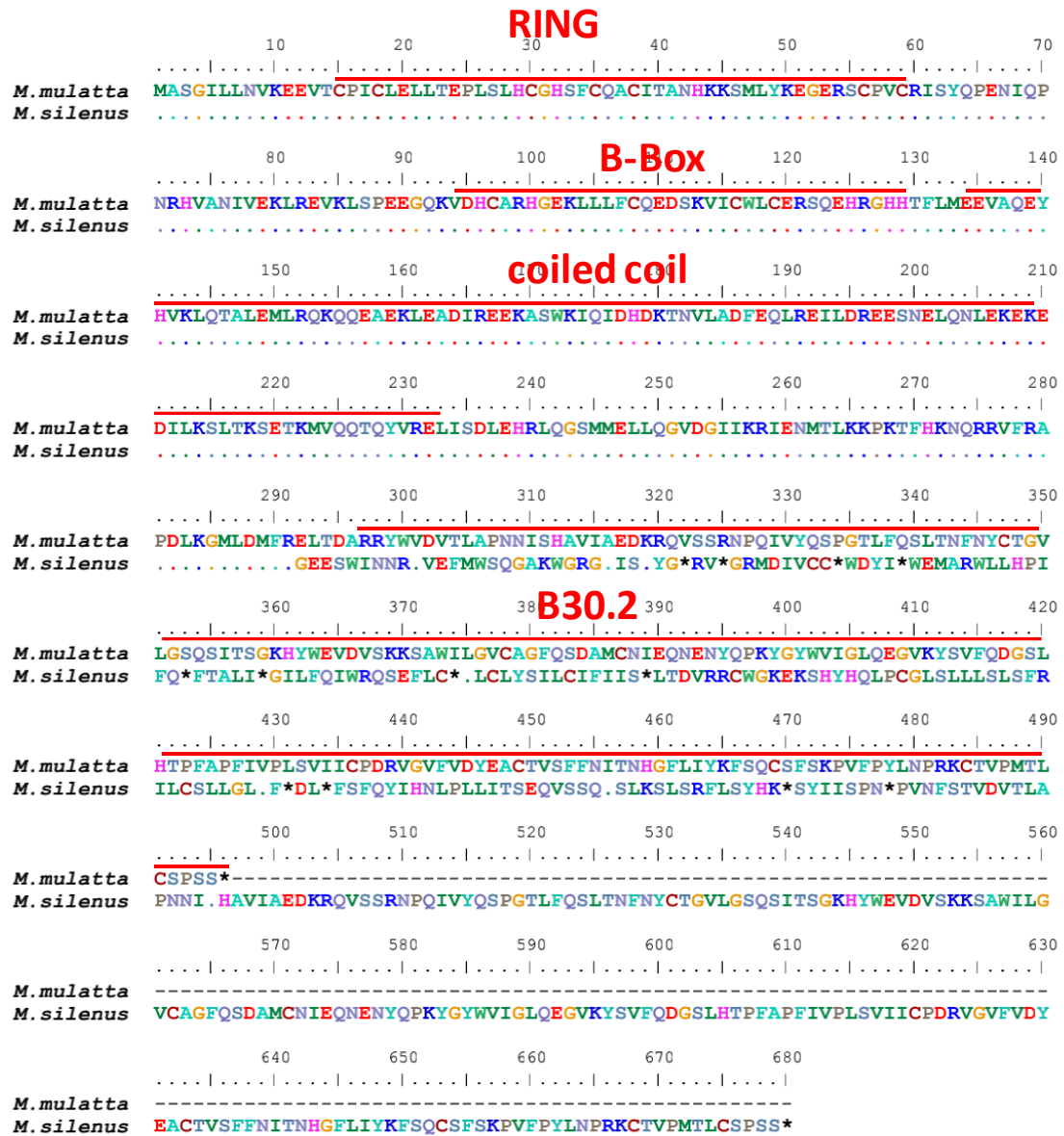


Fig. S27. Protein sequence alignment of *TRIM5a* between the lion-tailed macaque (*M. silenus*) and the rhesus macaque (*M. mulatta*). RING, B-Box, coiled coil, and B30.2 domains are shown.

Table S1. Macaque sample and sequencing information. In the "IUCN category" column, acronyms are as follows: "LC" for least concern, "NT" for near threatened, "VU" for vulnerable, "EN" for endangered, and "CR" for critically endangered. The sequencing platform and amount of data generated for each sample are also listed.

Species name	English name	IUCN category	Sex	Sample provider	Sample type	Sequencing platform and amount of data generated
<i>Macaca fuscata</i>	Japanese Macaque	LC	Male	Chengdu Zoo, China	Blood	Nanopore: 151G; MGISEQ: 178G
<i>Macaca silenus</i>	Lion-tailed Macaque	EN	Male	Guangzhou Zoo, China	Blood	Nanopore: 115G; MGISEQ: 166G
<i>Macaca thibetana</i>	Tibetan Macaque	NT	Female	Guangzhou Zoo, China	Blood	Nanopore: 147G; MGISEQ: 154G
<i>Macaca assamensis</i>	Assamese Macaque	NT	Male	Kunming Institute of Zoology, China	Blood	Nanopore: 177G; MGISEQ: 164G
<i>Macaca arctoides</i>	Stump-tailed Macaque	VU	Male	Kunming Institute of Zoology, China	Blood	Nanopore: 125G; MGISEQ: 152G
<i>Macaca fascicularis</i>	Long-tailed Macaque	VU	Male	Kunming Institute of Zoology, China	Blood	Nanopore: 153G; MGISEQ: 171G
<i>Macaca leonina</i>	Northern Pig-tailed Macaque	VU	Male	Kunming Institute of Zoology, China	Blood	Nanopore: 140G; MGISEQ: 163G
<i>Macaca nigra</i>	Crested Macaque	CR	Female	Dublin Zoo, Ireland	DNA	10x genomics: 211G
<i>Macaca tonkeana</i>	Tonkean Macaque	VU	Female	Silabe primate research center, France	DNA	StLFR:270G
<i>Macaca tonkeana2</i>	Tonkean Macaque	VU	Male	German Primate Center, German	DNA	NovaSeq 6000: 94G
<i>Macaca sylvanus</i>	Barbary Macaque	EN	Female	Barcelona Zoo, Spain	DNA	StLFR:274G
<i>Macaca sylvanus2</i>	Barbary Macaque	EN	Male	German Primate Center, German	DNA	NovaSeq 6000: 96G

Table S2. Genome statistics for the ten newly sequenced macaque genomes. The corresponding assembly strategy and number of annotated genes are also given.

Species name	Contig N50 (bp)	Scaffold N50 (bp)	Assembled Genome Size (bp)	Software	Gene Number
<i>Macaca assamensis</i>	27,348,716	27,348,716	2,759,375,986	NextDenovo + wtdbg	20960
<i>Macaca silenus</i>	25,691,658	25,691,658	2,778,791,713	NextDenovo + wtdbg	20689
<i>Macaca arctoides</i>	30,155,229	30,155,229	2,753,320,893	NextDenovo + wtdbg	20821
<i>Macaca thibetana</i>	33,225,245	33,225,245	2,775,160,973	NextDenovo + wtdbg	20838
<i>Macaca fascicularis</i>	21,239,021	21,239,021	2,770,900,045	NextDenovo + wtdbg	20502
<i>Macaca fuscata</i>	26,406,092	26,406,092	2,748,481,177	NextDenovo + wtdbg	20992
<i>Macaca leonina</i>	17,711,378	17,711,378	2,808,882,299	NextDenovo + wtdbg	20662
<i>Macaca nigra</i>	76,310	26,144,792	2,973,416,866	Supernova	21811
<i>Macaca tonkeana</i>	50,863	21,105,068	3,004,470,813	Supernova	21194
<i>Macaca sylvanus</i>	58,539	22,820,170	2,992,556,657	Supernova	21533

Table S3. Genome completeness assessed by BUSCO (version 2.0), referring to the mammalia odb9 BUSCO set.

Species name	Ratio (%)
<i>Macaca assamensis</i>	94.2
<i>Macaca silenus</i>	94.4
<i>Macaca arctoides</i>	94.4
<i>Macaca thibetana</i>	93.7
<i>Macaca fascicularis</i>	93.7
<i>Macaca fuscata</i>	94.5
<i>Macaca leonina</i>	94.0
<i>Macaca nigra</i>	93.2
<i>Macaca tonkeana</i>	93.1
<i>Macaca sylvanus</i>	93.3

Table S4. Repeat content of the assembled macaque genomes.

Species name	DNA ratio	LINE ratio	SINE ratio	LTR ratio	Unknown ratio
<i>Macaca assamensis</i>	2.70	22.41	13.56	7.83	0.20
<i>Macaca silenus</i>	3.00	22.08	13.67	7.53	0.40
<i>Macaca arctoides</i>	3.19	22.05	13.71	7.73	0.48
<i>Macaca thibetana</i>	2.75	19.71	13.97	7.30	0.19
<i>Macaca fascicularis</i>	2.69	20.51	13.17	7.73	0.45
<i>Macaca fuscata</i>	2.87	21.18	13.47	7.82	0.51
<i>Macaca leonina</i>	2.81	19.13	13.44	8.20	0.15
<i>Macaca nigra</i>	1.43	14.89	10.02	5.34	0.02
<i>Macaca tonkeana</i>	1.44	14.46	9.77	5.38	0.03
<i>Macaca sylvanus</i>	1.43	14.48	9.84	5.19	0.02

Table S5. Proportion of aligned base-pairs by reference to the Chinese rhesus macaque (*M. mulatta*) assembly.

Species name	Mapping ratio
<i>Macaca fascicularis</i>	93.6703
<i>Macaca silenus</i>	93.3064
<i>Macaca leonina</i>	93.6334
<i>Macaca assamensis</i>	93.2924
<i>Macaca nemestrina</i>	91.6092
<i>Macaca nigra</i>	93.0378
<i>Macaca sylvanus</i>	91.9538
<i>Macaca tonkeana</i>	92.3328
<i>Macaca fuscata</i>	93.6078
<i>Macaca thibetana</i>	92.6400
<i>Macaca arctoides</i>	93.2079
<i>Papio hamadryas</i>	90.1235

Table S6. HyDe results of all combinations of species groups with Z-score >3. The statistic Gamma equals 0.5 means 50:50 hybrid, whilst values close to 0 or 1 indicate a low level of asymmetrical admixture by introgression. GammaP1 and GammaP2 denote the inheritance probabilities from parental species P1 and P2, respectively.

P1	Hybrid	P2	Z-score	P-value	GammaP1	GammaP2
<i>sinica</i>	<i>fascicularis</i>	<i>silenus</i>	175.1070	~0.0	0.6447	0.3553
<i>fascicularis</i>	<i>sinica</i>	<i>sylvanus</i>	69.2458	~0.0	0.9643	0.0357
<i>silenus</i>	<i>sinica</i>	<i>sylvanus</i>	62.7978	~0.0	0.9551	0.0449
<i>fascicularis</i>	<i>silenus</i>	<i>sylvanus</i>	3.7485	0.0001	0.9978	0.0022

Table S7. HyDe results showing the combination of Z-score >3 and Gamma values ranged from 0.05 to 0.95. Extremely low level admixture signatures (gamma<0.05 and gamma>0.95) were not considered. GammaP1 and GammaP2 denote the inheritance probabilities from parental species P1 and P2, respectively.

P1	Hybrid	P2	Z-score	P-value	GammaP1	GammaP2
<i>M. fascicularis</i>	<i>M. arctoides</i>	<i>M. thibetana</i>	98.70	~0.0	0.05	0.95
<i>M. fascicularis</i>	<i>M. arctoides</i>	<i>M. assamensis</i>	103.95	~0.0	0.05	0.95
<i>M. mulatta</i>	<i>M. arctoides</i>	<i>M. thibetana</i>	120.55	~0.0	0.06	0.94
<i>M. mulatta</i>	<i>M. arctoides</i>	<i>M. assamensis</i>	131.39	~0.0	0.07	0.93
<i>M. fuscata</i>	<i>M. arctoides</i>	<i>M. thibetana</i>	142.91	~0.0	0.08	0.92
<i>M. fuscata</i>	<i>M. arctoides</i>	<i>M. assamensis</i>	158.21	~0.0	0.09	0.91
<i>M. sylvanus</i>	<i>M. assamensis</i>	<i>M. leonina</i>	70.73	~0.0	0.05	0.95
<i>M. sylvanus</i>	<i>M. assamensis</i>	<i>M. silenus</i>	73.31	~0.0	0.05	0.95
<i>M. arctoides</i>	<i>M. fascicularis</i>	<i>M. silenus</i>	194.90	~0.0	0.65	0.35
<i>M. tonkeana</i>	<i>M. fascicularis</i>	<i>M. assamensis</i>	194.94	~0.0	0.41	0.59
<i>M. arctoides</i>	<i>M. fascicularis</i>	<i>M. nigra</i>	194.98	~0.0	0.67	0.33
<i>M. arctoides</i>	<i>M. fascicularis</i>	<i>M. tonkeana</i>	195.07	~0.0	0.67	0.33
<i>M. tonkeana</i>	<i>M. fascicularis</i>	<i>M. thibetana</i>	195.09	~0.0	0.41	0.59
<i>M. nigra</i>	<i>M. fascicularis</i>	<i>M. thibetana</i>	195.82	~0.0	0.40	0.60
<i>M. nigra</i>	<i>M. fascicularis</i>	<i>M. assamensis</i>	196.00	~0.0	0.41	0.59
<i>M. nemestrina</i>	<i>M. fascicularis</i>	<i>M. assamensis</i>	197.10	~0.0	0.47	0.53
<i>M. arctoides</i>	<i>M. fascicularis</i>	<i>M. leonina</i>	197.98	~0.0	0.65	0.35
<i>M. nemestrina</i>	<i>M. fascicularis</i>	<i>M. thibetana</i>	199.84	~0.0	0.47	0.53
<i>M. silenus</i>	<i>M. fascicularis</i>	<i>M. thibetana</i>	200.44	~0.0	0.43	0.57
<i>M. leonina</i>	<i>M. fascicularis</i>	<i>M. assamensis</i>	200.88	~0.0	0.44	0.56
<i>M. leonina</i>	<i>M. fascicularis</i>	<i>M. thibetana</i>	201.06	~0.0	0.44	0.56
<i>M. silenus</i>	<i>M. fascicularis</i>	<i>M. assamensis</i>	201.66	~0.0	0.43	0.57
<i>M. arctoides</i>	<i>M. fascicularis</i>	<i>M. nemestrina</i>	208.12	~0.0	0.62	0.38
<i>M. arctoides</i>	<i>M. fuscata</i>	<i>M. silenus</i>	162.00	~0.0	0.74	0.26
<i>M. arctoides</i>	<i>M. fuscata</i>	<i>M. leonina</i>	162.74	~0.0	0.74	0.26
<i>M. arctoides</i>	<i>M. fuscata</i>	<i>M. tonkeana</i>	163.58	~0.0	0.75	0.25
<i>M. arctoides</i>	<i>M. fuscata</i>	<i>M. nigra</i>	165.58	~0.0	0.75	0.25
<i>M. nemestrina</i>	<i>M. fuscata</i>	<i>M. assamensis</i>	168.73	~0.0	0.40	0.60
<i>M. arctoides</i>	<i>M. fuscata</i>	<i>M. nemestrina</i>	169.32	~0.0	0.73	0.27
<i>M. tonkeana</i>	<i>M. fuscata</i>	<i>M. assamensis</i>	170.51	~0.0	0.36	0.64
<i>M. tonkeana</i>	<i>M. fuscata</i>	<i>M. thibetana</i>	171.06	~0.0	0.35	0.65
<i>M. nemestrina</i>	<i>M. fuscata</i>	<i>M. thibetana</i>	172.06	~0.0	0.39	0.61
<i>M. nigra</i>	<i>M. fuscata</i>	<i>M. assamensis</i>	173.01	~0.0	0.37	0.63
<i>M. nigra</i>	<i>M. fuscata</i>	<i>M. thibetana</i>	173.25	~0.0	0.35	0.65
<i>M. leonina</i>	<i>M. fuscata</i>	<i>M. assamensis</i>	174.65	~0.0	0.39	0.61
<i>M. leonina</i>	<i>M. fuscata</i>	<i>M. thibetana</i>	175.05	~0.0	0.38	0.62
<i>M. silenus</i>	<i>M. fuscata</i>	<i>M. thibetana</i>	176.09	~0.0	0.37	0.63
<i>M. silenus</i>	<i>M. fuscata</i>	<i>M. assamensis</i>	176.82	~0.0	0.39	0.61
<i>M. fuscata</i>	<i>M. mulatta</i>	<i>M. fascicularis</i>	77.23	~0.0	0.90	0.10
<i>M. arctoides</i>	<i>M. mulatta</i>	<i>M. silenus</i>	128.33	~0.0	0.75	0.25
<i>M. arctoides</i>	<i>M. mulatta</i>	<i>M. leonina</i>	134.02	~0.0	0.74	0.26
<i>M. arctoides</i>	<i>M. mulatta</i>	<i>M. tonkeana</i>	142.84	~0.0	0.74	0.26
<i>M. arctoides</i>	<i>M. mulatta</i>	<i>M. nigra</i>	146.78	~0.0	0.73	0.27
<i>M. silenus</i>	<i>M. mulatta</i>	<i>M. thibetana</i>	146.82	~0.0	0.36	0.64

<i>M. silenus</i>	<i>M. mulatta</i>	<i>M. assamensis</i>	149.54	~0.0	0.37	0.63
<i>M. leonina</i>	<i>M. mulatta</i>	<i>M. thibetana</i>	149.85	~0.0	0.37	0.63
<i>M. leonina</i>	<i>M. mulatta</i>	<i>M. assamensis</i>	151.17	~0.0	0.39	0.61
<i>M. tonkeana</i>	<i>M. mulatta</i>	<i>M. thibetana</i>	151.60	~0.0	0.36	0.64
<i>M. tonkeana</i>	<i>M. mulatta</i>	<i>M. assamensis</i>	152.50	~0.0	0.37	0.63
<i>M. nigra</i>	<i>M. mulatta</i>	<i>M. thibetana</i>	155.17	~0.0	0.36	0.64
<i>M. nigra</i>	<i>M. mulatta</i>	<i>M. assamensis</i>	156.36	~0.0	0.38	0.62
<i>M. nemestrina</i>	<i>M. mulatta</i>	<i>M. assamensis</i>	157.06	~0.0	0.43	0.57
<i>M. arctoides</i>	<i>M. mulatta</i>	<i>M. nemestrina</i>	158.29	~0.0	0.70	0.30
<i>M. nemestrina</i>	<i>M. mulatta</i>	<i>M. thibetana</i>	159.43	~0.0	0.42	0.58
<i>M. sylvanus</i>	<i>M. thibetana</i>	<i>M. leonina</i>	69.38	~0.0	0.05	0.95
<i>M. sylvanus</i>	<i>M. thibetana</i>	<i>M. silenus</i>	72.02	~0.0	0.05	0.95

Table S8. D-statistic results showing the combination of Z-score >3 as an indication of a possible signal of introgression between P2 and P3 assuming fig. S5A as the reference tree. *P. hamadryas* was used as the outgroup.

P1	P2	P3	Dstatistic	Z-score	p-value
<i>M. assamensis</i>	<i>M. fascicularis</i>	<i>M. nigra</i>	0.3739	15.4092	~0.0
<i>M. assamensis</i>	<i>M. fascicularis</i>	<i>M. nemestrina</i>	0.3918	14.5011	~0.0
<i>M. arctoides</i>	<i>M. fascicularis</i>	<i>M. nemestrina</i>	0.3279	14.3206	~0.0
<i>M. assamensis</i>	<i>M. fascicularis</i>	<i>M. leonina</i>	0.3694	12.9050	~0.0
<i>M. assamensis</i>	<i>M. fascicularis</i>	<i>M. silenus</i>	0.3591	12.6795	~0.0
<i>M. assamensis</i>	<i>M. fascicularis</i>	<i>M. tonkeana</i>	0.3408	12.6466	~0.0
<i>M. thibetana</i>	<i>M. fascicularis</i>	<i>M. nemestrina</i>	0.3823	11.7037	~0.0
<i>M. arctoides</i>	<i>M. fascicularis</i>	<i>M. silenus</i>	0.3095	10.8919	~0.0
<i>M. thibetana</i>	<i>M. fascicularis</i>	<i>M. nigra</i>	0.3361	10.5031	~0.0
<i>M. arctoides</i>	<i>M. fascicularis</i>	<i>M. nigra</i>	0.2797	10.1705	~0.0
<i>M. thibetana</i>	<i>M. fascicularis</i>	<i>M. leonina</i>	0.3473	10.1403	~0.0
<i>M. thibetana</i>	<i>M. fascicularis</i>	<i>M. silenus</i>	0.3390	9.4884	~0.0
<i>M. arctoides</i>	<i>M. fascicularis</i>	<i>M. leonina</i>	0.3002	9.3423	~0.0
<i>M. assamensis</i>	<i>M. fuscata</i>	<i>M. nigra</i>	0.3510	9.2571	~0.0
<i>M. arctoides</i>	<i>M. fascicularis</i>	<i>M. tonkeana</i>	0.2802	9.1394	~0.0
<i>M. thibetana</i>	<i>M. fascicularis</i>	<i>M. tonkeana</i>	0.3163	9.0768	~0.0
<i>M. assamensis</i>	<i>M. fuscata</i>	<i>M. nemestrina</i>	0.3459	8.2697	~0.0
<i>M. assamensis</i>	<i>M. mulatta</i>	<i>M. nemestrina</i>	0.3010	7.7672	~0.0
<i>M. arctoides</i>	<i>M. fuscata</i>	<i>M. nemestrina</i>	0.2816	7.7213	~0.0
<i>M. assamensis</i>	<i>M. mulatta</i>	<i>M. nigra</i>	0.2708	7.6451	~0.0
<i>M. assamensis</i>	<i>M. fuscata</i>	<i>M. tonkeana</i>	0.3234	7.6256	~0.0
<i>M. arctoides</i>	<i>M. mulatta</i>	<i>M. nemestrina</i>	0.2410	7.5331	~0.0
<i>M. thibetana</i>	<i>M. mulatta</i>	<i>M. nemestrina</i>	0.2926	7.4817	~0.0
<i>M. thibetana</i>	<i>M. fuscata</i>	<i>M. nemestrina</i>	0.3368	7.3266	~0.0
<i>M. arctoides</i>	<i>M. fuscata</i>	<i>M. tonkeana</i>	0.2677	7.1757	~0.0
<i>M. assamensis</i>	<i>M. fuscata</i>	<i>M. leonina</i>	0.3276	7.0628	~0.0
<i>M. assamensis</i>	<i>M. fuscata</i>	<i>M. silenus</i>	0.3150	6.7004	~0.0
<i>M. arctoides</i>	<i>M. fuscata</i>	<i>M. silenus</i>	0.2658	6.1848	~0.0
<i>M. thibetana</i>	<i>M. fuscata</i>	<i>M. leonina</i>	0.2993	6.0794	~0.0
<i>M. assamensis</i>	<i>M. arctoides</i>	<i>M. fuscata</i>	0.2095	5.9479	~0.0
<i>M. arctoides</i>	<i>M. fuscata</i>	<i>M. leonina</i>	0.2546	5.7599	~0.0
<i>M. thibetana</i>	<i>M. fuscata</i>	<i>M. silenus</i>	0.2891	5.6943	~0.0
<i>M. thibetana</i>	<i>M. fuscata</i>	<i>M. nigra</i>	0.3108	5.6345	~0.0
<i>M. assamensis</i>	<i>M. mulatta</i>	<i>M. tonkeana</i>	0.2501	5.5892	~0.0
<i>M. thibetana</i>	<i>M. fuscata</i>	<i>M. tonkeana</i>	0.2997	5.5499	~0.0
<i>M. assamensis</i>	<i>M. mulatta</i>	<i>M. leonina</i>	0.2475	5.5134	~0.0
<i>M. arctoides</i>	<i>M. fuscata</i>	<i>M. nigra</i>	0.2497	5.4793	~0.0
<i>M. assamensis</i>	<i>M. mulatta</i>	<i>M. silenus</i>	0.2422	5.2978	~0.0
<i>M. arctoides</i>	<i>M. mulatta</i>	<i>M. silenus</i>	0.1943	5.1615	~0.0
<i>M. assamensis</i>	<i>M. arctoides</i>	<i>M. mulatta</i>	0.1965	5.0952	~0.0
<i>M. thibetana</i>	<i>M. mulatta</i>	<i>M. nigra</i>	0.2315	4.9413	~0.0
<i>M. arctoides</i>	<i>M. mulatta</i>	<i>M. tonkeana</i>	0.1940	4.9214	~0.0
<i>M. assamensis</i>	<i>M. arctoides</i>	<i>M. fascicularis</i>	0.1822	4.8565	~0.0
<i>M. thibetana</i>	<i>M. mulatta</i>	<i>M. silenus</i>	0.2218	4.7476	~0.0
<i>M. thibetana</i>	<i>M. mulatta</i>	<i>M. leonina</i>	0.2253	4.6815	~0.0

<i>M. arctoides</i>	<i>M. mulatta</i>	<i>M. nigra</i>	0.1751	4.6477	~0.0
<i>M. mulatta</i>	<i>M. fascicularis</i>	<i>M. nigra</i>	0.1973	4.6210	~0.0
<i>M. thibetana</i>	<i>M. mulatta</i>	<i>M. tonkeana</i>	0.2254	4.3947	~0.0
<i>M. arctoides</i>	<i>M. mulatta</i>	<i>M. leonina</i>	0.1758	4.2984	~0.0
<i>M. mulatta</i>	<i>M. fascicularis</i>	<i>M. silenus</i>	0.2174	4.1549	~0.0
<i>M. mulatta</i>	<i>M. fascicularis</i>	<i>M. leonina</i>	0.2209	4.1322	~0.0
<i>M. tonkeana</i>	<i>M. nemestrina</i>	<i>M. fascicularis</i>	0.1854	4.1142	~0.0
<i>M. fuscata</i>	<i>M. mulatta</i>	<i>M. fascicularis</i>	0.1336	4.0828	~0.0
<i>M. nigra</i>	<i>M. silenus</i>	<i>M. fascicularis</i>	0.1798	3.8909	~0.0
<i>M. nigra</i>	<i>M. nemestrina</i>	<i>M. mulatta</i>	0.1915	3.7307	0.0001
<i>M. tonkeana</i>	<i>M. silenus</i>	<i>M. fascicularis</i>	0.2105	3.6502	0.0001
<i>M. nigra</i>	<i>M. nemestrina</i>	<i>M. fascicularis</i>	0.1542	3.5679	0.0002
<i>M. thibetana</i>	<i>M. arctoides</i>	<i>M. fuscata</i>	0.1673	3.5294	0.0002
<i>M. mulatta</i>	<i>M. fascicularis</i>	<i>M. nemestrina</i>	0.1548	3.4904	0.0002
<i>M. leonina</i>	<i>M. silenus</i>	<i>M. assamensis</i>	0.2291	3.3970	0.0003
<i>M. nigra</i>	<i>M. nemestrina</i>	<i>M. fuscata</i>	0.1464	3.3917	0.0003
<i>M. thibetana</i>	<i>M. arctoides</i>	<i>M. fascicularis</i>	0.1330	3.3062	0.0005
<i>M. mulatta</i>	<i>M. fuscata</i>	<i>M. leonina</i>	0.1571	3.2693	0.0005
<i>M. nigra</i>	<i>M. silenus</i>	<i>M. assamensis</i>	0.1787	3.1959	0.0007
<i>M. mulatta</i>	<i>M. assamensis</i>	<i>M. sylvanus</i>	0.1126	3.1323	0.0009
<i>M. nemestrina</i>	<i>M. silenus</i>	<i>M. tonkeana</i>	0.0768	3.1270	0.0009
<i>M. nigra</i>	<i>M. leonina</i>	<i>M. fascicularis</i>	0.1286	3.0884	0.0010
<i>M. assamensis</i>	<i>M. arctoides</i>	<i>M. nigra</i>	0.1767	3.0818	0.0010
<i>M. assamensis</i>	<i>M. thibetana</i>	<i>M. arctoides</i>	0.0725	3.0230	0.0013

Table S9. D-statistic results showing the combination of Z-score >3 as an indication of a possible signal of introgression between P2 and P3 assuming fig. S5B as the reference tree. *P. hamadryas* was used as the outgroup.

P1	P2	P3	Dstatistic	Z-score	p-value
<i>M. assamensis</i>	<i>M. fascicularis</i>	<i>M. silenus</i>	0.3185	11.0505	~0.0
<i>M. thibetana</i>	<i>M. fascicularis</i>	<i>M. nemestrina</i>	0.3173	10.9595	~0.0
<i>M. assamensis</i>	<i>M. fascicularis</i>	<i>M. nigra</i>	0.2481	10.7635	~0.0
<i>M. thibetana</i>	<i>M. fascicularis</i>	<i>M. leonina</i>	0.3237	10.5930	~0.0
<i>M. assamensis</i>	<i>M. fascicularis</i>	<i>M. leonina</i>	0.3065	10.5099	~0.0
<i>M. arctoides</i>	<i>M. fascicularis</i>	<i>M. nemestrina</i>	0.3188	10.4124	~0.0
<i>M. assamensis</i>	<i>M. fascicularis</i>	<i>M. nemestrina</i>	0.3054	10.2569	~0.0
<i>M. thibetana</i>	<i>M. fascicularis</i>	<i>M. nigra</i>	0.2613	10.1511	~0.0
<i>M. thibetana</i>	<i>M. fascicularis</i>	<i>M. tonkeana</i>	0.2549	10.0383	~0.0
<i>M. thibetana</i>	<i>M. fascicularis</i>	<i>M. silenus</i>	0.3336	9.7071	~0.0
<i>M. assamensis</i>	<i>M. fascicularis</i>	<i>M. tonkeana</i>	0.2507	8.9743	~0.0
<i>M. thibetana</i>	<i>M. fuscata</i>	<i>M. leonina</i>	0.2449	8.9695	~0.0
<i>M. assamensis</i>	<i>M. fuscata</i>	<i>M. leonina</i>	0.2229	8.4416	~0.0
<i>M. assamensis</i>	<i>M. fuscata</i>	<i>M. silenus</i>	0.2426	8.3239	~0.0
<i>M. thibetana</i>	<i>M. fuscata</i>	<i>M. silenus</i>	0.2592	8.1415	~0.0
<i>M. thibetana</i>	<i>M. fuscata</i>	<i>M. nemestrina</i>	0.2372	7.7463	~0.0
<i>M. arctoides</i>	<i>M. fascicularis</i>	<i>M. leonina</i>	0.3102	7.7277	~0.0
<i>M. arctoides</i>	<i>M. fascicularis</i>	<i>M. silenus</i>	0.3053	7.6233	~0.0
<i>M. arctoides</i>	<i>M. fascicularis</i>	<i>M. nigra</i>	0.2581	7.5484	~0.0
<i>M. arctoides</i>	<i>M. fascicularis</i>	<i>M. tonkeana</i>	0.2636	7.5263	~0.0
<i>M. assamensis</i>	<i>M. fuscata</i>	<i>M. nemestrina</i>	0.2225	7.3796	~0.0
<i>M. thibetana</i>	<i>M. mulatta</i>	<i>M. nemestrina</i>	0.2389	7.2829	~0.0
<i>M. arctoides</i>	<i>M. mulatta</i>	<i>M. nemestrina</i>	0.2430	7.2656	~0.0
<i>M. assamensis</i>	<i>M. mulatta</i>	<i>M. silenus</i>	0.2178	7.0392	~0.0
<i>M. thibetana</i>	<i>M. mulatta</i>	<i>M. silenus</i>	0.2316	6.8688	~0.0
<i>M. thibetana</i>	<i>M. mulatta</i>	<i>M. leonina</i>	0.2132	6.8588	~0.0
<i>M. assamensis</i>	<i>M. mulatta</i>	<i>M. nemestrina</i>	0.2259	6.8335	~0.0
<i>M. arctoides</i>	<i>M. fuscata</i>	<i>M. nemestrina</i>	0.2382	6.7963	~0.0
<i>M. assamensis</i>	<i>M. mulatta</i>	<i>M. leonina</i>	0.1950	6.7638	~0.0
<i>M. thibetana</i>	<i>M. mulatta</i>	<i>M. nigra</i>	0.1777	6.6106	~0.0
<i>M. arctoides</i>	<i>M. mulatta</i>	<i>M. silenus</i>	0.2134	6.5214	~0.0
<i>M. thibetana</i>	<i>M. fuscata</i>	<i>M. nigra</i>	0.2069	6.3694	~0.0
<i>M. thibetana</i>	<i>M. fuscata</i>	<i>M. tonkeana</i>	0.2075	6.3327	~0.0
<i>M. arctoides</i>	<i>M. fuscata</i>	<i>M. leonina</i>	0.2319	6.2162	~0.0
<i>M. arctoides</i>	<i>M. fuscata</i>	<i>M. silenus</i>	0.2329	6.1236	~0.0
<i>M. assamensis</i>	<i>M. fuscata</i>	<i>M. nigra</i>	0.1912	6.0300	~0.0
<i>M. arctoides</i>	<i>M. mulatta</i>	<i>M. leonina</i>	0.2055	5.9915	~0.0
<i>M. assamensis</i>	<i>M. mulatta</i>	<i>M. nigra</i>	0.1651	5.9464	~0.0
<i>M. assamensis</i>	<i>M. fuscata</i>	<i>M. tonkeana</i>	0.2014	5.8718	~0.0
<i>M. thibetana</i>	<i>M. mulatta</i>	<i>M. tonkeana</i>	0.1821	5.8375	~0.0
<i>M. assamensis</i>	<i>M. mulatta</i>	<i>M. tonkeana</i>	0.1767	5.3759	~0.0
<i>M. assamensis</i>	<i>M. arctoides</i>	<i>M. mulatta</i>	0.1569	5.2906	~0.0
<i>M. arctoides</i>	<i>M. fuscata</i>	<i>M. nigra</i>	0.2040	5.1788	~0.0
<i>M. arctoides</i>	<i>M. fuscata</i>	<i>M. tonkeana</i>	0.2174	5.0406	~0.0
<i>M. arctoides</i>	<i>M. mulatta</i>	<i>M. tonkeana</i>	0.1930	5.0222	~0.0

<i>M. arctoides</i>	<i>M. mulatta</i>	<i>M. nigra</i>	0.1781	4.9600	~0.0
<i>M. assamensis</i>	<i>M. arctoides</i>	<i>M. fuscata</i>	0.1380	4.8609	~0.0
<i>M. nigra</i>	<i>M. leonina</i>	<i>M. fascicularis</i>	0.2074	4.1347	~0.0
<i>M. tonkeana</i>	<i>M. nemestrina</i>	<i>M. fascicularis</i>	0.2084	4.0973	~0.0
<i>M. fuscata</i>	<i>M. fascicularis</i>	<i>M. nemestrina</i>	0.1313	4.0774	~0.0
<i>M. nigra</i>	<i>M. nemestrina</i>	<i>M. fascicularis</i>	0.2113	3.9581	~0.0
<i>M. tonkeana</i>	<i>M. nemestrina</i>	<i>M. mulatta</i>	0.1867	3.7155	0.0001
<i>M. assamensis</i>	<i>M. arctoides</i>	<i>M. fascicularis</i>	0.0964	3.6852	0.0001
<i>M. tonkeana</i>	<i>M. leonina</i>	<i>M. fascicularis</i>	0.1998	3.6707	0.0001
<i>M. nigra</i>	<i>M. silenus</i>	<i>M. fascicularis</i>	0.1943	3.6254	0.0001
<i>M. mulatta</i>	<i>M. fascicularis</i>	<i>M. leonina</i>	0.1748	3.6000	0.0002
<i>M. nigra</i>	<i>M. nemestrina</i>	<i>M. mulatta</i>	0.2037	3.5420	0.0002
<i>M. mulatta</i>	<i>M. arctoides</i>	<i>M. sylvanus</i>	0.1494	3.5010	0.0002
<i>M. thibetana</i>	<i>M. arctoides</i>	<i>M. mulatta</i>	0.1324	3.4363	0.0003
<i>M. nemestrina</i>	<i>M. leonina</i>	<i>M. nigra</i>	0.0913	3.4208	0.0003
<i>M. mulatta</i>	<i>M. fascicularis</i>	<i>M. nigra</i>	0.1290	3.2752	0.0005
<i>M. mulatta</i>	<i>M. assamensis</i>	<i>M. sylvanus</i>	0.1396	3.2480	0.0006
<i>M. nemestrina</i>	<i>M. leonina</i>	<i>M. tonkeana</i>	0.0842	3.2249	0.0006
<i>M. fuscata</i>	<i>M. fascicularis</i>	<i>M. leonina</i>	0.1288	3.1908	0.0007
<i>M. mulatta</i>	<i>M. thibetana</i>	<i>M. sylvanus</i>	0.1417	3.1517	0.0008
<i>M. mulatta</i>	<i>M. fascicularis</i>	<i>M. silenus</i>	0.1536	3.0738	0.0011
<i>M. tonkeana</i>	<i>M. silenus</i>	<i>M. fascicularis</i>	0.1907	3.0722	0.0011
<i>M. nigra</i>	<i>M. silenus</i>	<i>M. mulatta</i>	0.1489	3.0621	0.0011

Table S10. Z-score values between pairs of species groups inferred from the Dsuit package assuming fig. S5A as the reference tree. Cells with Z-score values >3 are given in bold. sin: *sinica* group; sil: *silenus* group; fas: *fascicularis* group; syl: *sylvanus* group.

branch_descendants	Sin	fas	sil	syl
sil,sin,fas	Nan	nan	nan	nan
sin,fas	Nan	nan	nan	0.00
sin	Nan	nan	0.00	3.08
fas	Nan	nan	10.95	0.00
sil	Nan	nan	nan	0.65
syl	Nan	nan	nan	nan

Table S11. Z-score values between pairs of species groups inferred from the Dsuit package assuming fig. S5B as the reference tree. The cell with a Z-score value >3 is given in bold. sin: *sinica* group; sil: *silenus* group; fas: *fascicularis* group; syl: *sylvanus* group.

branch_descendants	sin	fas	sil	syl
sin,fas,sil	nan	nan	nan	nan
sin	nan	nan	nan	2.78
fas,sil	nan	nan	nan	0.00
fas	20.64	nan	nan	0.00
sil	0.00	nan	nan	1.31
syl	nan	nan	nan	nan

Table S12. Z-score values between pairs of species inferred from the Dsuit package assuming fig. S5A as the reference tree. Cells with Z-score values >3 are given in bold. Species are abbreviated using the first letter of the genus name and the first three letters of the species name.

branch_descendants	Msyl	Mfas	Mfus	Mmul	Marc	Mthi	Mass	Mnem	Mleo	Msil	Mnig	Mton
Msyl	nan	nan	nan	nan	nan	nan	nan	nan	nan	nan	nan	nan
Mfas,Mmul,Mfus,Marc,Mthi,Mass,Mnig,Mton,Mnem,Msil,Mleo	nan	nan	nan	nan	nan	nan	nan	nan	nan	nan	nan	nan
Mfas,Mmul,Mfus,Marc,Mthi,Mass	0.00	nan	nan	nan	nan	nan	nan	nan	nan	nan	nan	nan
Mfas,Mmul,Mfus	0.00	nan	nan	nan	nan	nan	nan	7.53	4.68	5.16	4.94	4.92
Mfas	1.23	nan	nan	nan	0.15	0.43	0.65	3.00	3.00	2.99	3.01	1.86
Mmul,Mfus	0.00	nan	nan	nan	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Mmul	0.00	4.08	nan	nan	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Mfus	2.67	0.00	nan	nan	1.66	1.11	1.66	1.38	3.27	2.47	2.32	2.29
Marc,Mthi,Mass	1.02	nan	nan	nan	nan	nan	nan	0.00	0.00	0.00	0.00	0.00
Marc	0.00	4.08	4.74	4.03	nan	nan	nan	1.85	1.67	1.22	2.34	1.36
Mthi,Mass	0.17	0.00	0.00	0.00	nan	nan	nan	0.00	0.00	0.00	0.00	0.00
Mthi	0.00	1.70	1.55	2.13	3.02	nan	nan	0.34	0.88	0.67	1.27	0.93
Mass	0.24	0.00	0.00	0.00	0.00	nan	nan	0.00	0.00	0.00	0.00	0.00
Mnig,Mton,Mnem,Msil,Mleo	0.00	nan	nan	nan	nan	nan	nan	nan	nan	nan	nan	nan
Mnem,Msil,Mleo	0.00	3.01	2.21	1.44	0.70	0.39	0.91	nan	nan	nan	nan	nan
Mnem	0.20	0.40	0.41	1.30	0.00	0.00	0.05	nan	nan	nan	0.00	0.00
Msil	1.10	1.91	1.42	1.98	1.52	2.62	3.40	1.92	nan	nan	1.13	1.18
Mleo	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	nan	nan	0.00	0.00
Msil,Mleo	0.00	0.00	0.00	0.00	0.12	0.50	0.00	nan	nan	nan	0.66	1.46
Mnig,Mton	0.35	0.00	0.00	0.00	0.00	0.00	0.00	nan	nan	nan	nan	nan
Mnig	0.47	0.81	0.00	0.00	0.49	0.00	0.00	0.00	0.00	0.00	nan	nan
Mton	0.00	0.00	1.18	1.63	0.00	0.49	0.80	0.41	1.07	1.32	nan	nan

Table S13. Z-score values between pairs of species inferred from the Dsuit package assuming fig. S5B as the reference tree. Cells with Z-scores values >3 are given in bold. Species are abbreviated using the first letter of the genus name and the first three letters of the species name.

branch_descendants	Msyl	Mnem	Mleo	Msil	Mnig	Mton	Mfas	Mfus	Mmul	Marc	Mthi	Mass
Msyl	nan	nan	nan	nan	nan	nan	nan	nan	nan	nan	nan	nan
Marc,Mthi,Mass,Mfas,Mfus,Mmul,Mnig,Mton,Mnem,Mleo,Msil	nan	nan	nan	nan	nan	nan	nan	nan	nan	nan	nan	nan
Mfas,Mfus,Mmul,Mnig,Mton,Mnem,Mleo,Msil	0.00	nan	nan	nan	nan	nan	nan	nan	nan	nan	nan	nan
Mnig,Mton,Mnem,Mleo,Msil	0.43	nan	nan	nan	nan	nan	nan	nan	nan	0.00	0.00	0.00
Mnem,Mleo,Msil	0.18	nan	nan	nan	nan	nan	3.35	2.40	2.66	0.97	0.36	0.49
Mnem	0.00	nan	nan	nan	0.00	0.00	0.34	0.06	1.60	0.00	0.61	0.38
Mleo,Msil	0.18	nan	nan	nan	2.27	1.18	0.00	0.00	0.00	0.08	0.00	0.00
Mleo	0.00	0.78	nan	nan	1.18	2.59	0.21	0.00	0.00	0.00	0.63	0.83
Msil	1.28	0.00	nan	nan	0.00	0.00	0.00	0.33	0.58	0.00	0.00	0.00
Mnig,Mton	0.00	nan	nan	nan	nan	nan	0.00	0.00	0.00	0.00	0.00	0.00
Mnig	0.44	0.42	0.58	1.24	nan	nan	0.06	0.00	0.00	0.31	0.00	0.17
Mton	0.00	0.00	0.00	0.00	nan	nan	0.00	0.42	0.53	0.00	0.25	0.00
Mfas,Mfus,Mmul	0.00	nan	nan	nan	nan	nan	nan	nan	nan	13.08	12.39	11.14
Mfas	0.64	3.49	3.40	2.85	2.75	2.22	nan	nan	nan	0.24	1.29	1.95
Mfus,Mmul	0.00	0.00	0.00	0.00	0.00	0.00	nan	nan	nan	0.00	0.00	0.00
Mfus	0.45	0.00	1.13	0.73	1.06	0.98	0.00	nan	nan	1.02	2.02	1.85
Mmul	0.00	0.46	0.00	0.00	0.00	0.00	2.67	nan	nan	0.00	0.00	0.00
Marc,Mthi,Mass	2.20	nan	nan	nan	nan	nan	nan	nan	nan	nan	nan	nan
Marc	0.15	0.06	0.23	0.50	0.10	0.00	3.06	3.86	4.36	nan	nan	nan
Mthi,Mass	0.00	0.00	0.00	0.00	0.00	0.16	0.00	0.00	0.00	nan	nan	nan
Mthi	0.08	0.00	0.00	0.00	0.00	0.00	0.34	0.84	0.81	0.45	nan	nan
Mass	0.00	0.79	0.79	0.64	0.65	0.33	0.00	0.00	0.00	0.00	nan	nan

Table S14. PSGs identified in the comparison *fascicularis-sinica* versus *silenus* groups with *P*-value <0.01(after Yates' correction), a top 2.5% number of fixed non-synonymous mutations and fixed 1 kb upstream differences. The phylogenetic analysis supported the sister relationship between the *fascicularis* and *sinica* groups. Genes were sorted by the sum of the fixed number of non-synonymous mutations (FixNonSyn) and fixed 1-kb upstream mutations (Fix1kup).

Chromosome	Num FixNonSyn+Fix1kup	Num FixNonSyn	Num Fix1kup	P-value	Gene Symbol	Full Name
Chr9	10	0	10	2.20E-16	<i>MKX</i>	Homeobox protein Mohawk
Chr11	9	3	6	2.20E-16	<i>TAS2R64</i>	Taste receptor type 2 member 64
ChrY	8	4	4	2.20E-16	<i>MXRA5</i>	Matrix-remodeling-associated protein 5
Chr13	8	6	2	2.20E-16	<i>ASPRV1</i>	Retroviral-like aspartic protease 1
Chr3	8	6	2	1.53E-14	<i>NACAD</i>	NAC-alpha domain-containing protein 1
Chr2	7	0	7	1.13E-11	<i>WDR48</i>	WD repeat-containing protein 48
Chr16	7	1	6	5.21E-13	<i>OR4D2</i>	Olfactory receptor 4D2
Chr15	7	1	6	1.26E-12	<i>KDM4C</i>	Lysine-specific demethylase 4C
Chr8	7	4	3	2.20E-16	<i>MTUS1</i>	Microtubule-associated tumor suppressor 1 homolog
Chr12	7	6	1	3.82E-11	<i>ZDBF2</i>	DBF4-type zinc finger-containing protein 2
Chr14	7	6	1	0.000431	<i>PHRF1</i>	PHD and RING finger domain-containing protein 1
Chr12	7	7	0	3.42E-08	<i>TTN</i>	Titin
Chr12	7	7	0	0.003575	<i>FSIP2</i>	Fibrous sheath-interacting protein 2
Chr10	6	0	6	2.40E-10	<i>GPCPD1</i>	Glycerophosphocholine phosphodiesterase GPCPD1
Chr1	6	0	6	2.01E-08	<i>ANKRD65</i>	Ankyrin repeat domain-containing protein 65
Chr14	6	1	5	9.94E-14	<i>KIF18A</i>	Kinesin-like protein KIF18A
Chr7	6	1	5	3.34E-12	<i>MLH3</i>	DNA mismatch repair protein Mlh3
Chr11	6	2	4	2.20E-16	<i>IFT81</i>	Intraflagellar transport protein 81 homolog
Chr12	6	2	4	6.61E-15	<i>TRAF3IP1</i>	TRAF3-interacting protein 1
Chr14	6	2	4	1.26E-12	<i>LYVE1</i>	Lymphatic vessel endothelial hyaluronic acid receptor 1
Chr12	6	3	3	2.20E-16	<i>WIPF1</i>	WAS/WASL-interacting protein family member 1
Chr1	6	3	3	1.06E-15	<i>DNAJB6</i>	DnaJ homolog subfamily B member 6
Chr10	6	3	3	2.64E-11	<i>SUSD2</i>	Sushi domain-containing protein 2

Chr16	6	5	1	7.42E-14	<i>KIF2B</i>	Kinesin-like protein KIF2B
Chr7	6	5	1	1.58E-07	<i>KNL1</i>	Kinetochore scaffold 1
Chr12	5	0	5	4.65E-14	<i>PGAP1</i>	GPI inositol-deacylase
Chr6	5	0	5	1.50E-11	<i>PLPP1</i>	Phospholipid phosphatase 1
Chr4	5	0	5	7.87E-11	<i>EGFL8</i>	Epidermal growth factor-like protein 8
Chr6	5	0	5	1.49E-09	<i>RAB24</i>	Ras-related protein Rab-24
Chr14	5	0	5	3.99E-08	<i>TMEM126B</i>	Complex I assembly factor TMEM126B, mitochondrial
Chr4	5	0	5	9.78E-08	<i>TGas006m08.1</i>	Histone H4
Chr9	5	0	5	9.78E-08	<i>MORN4</i>	MORN repeat-containing protein 4
Chr12	5	0	5	9.78E-08	<i>GPR35</i>	G-protein coupled receptor 35
Chr19	5	1	4	1.49E-09	<i>DMRTC2</i>	Doublesex- and mab-3-related transcription factor C2
Chr14	5	1	4	1.49E-09	<i>BTG4</i>	Protein BTG4
Chr19	5	1	4	3.99E-08	<i>MUM1</i>	PWWP domain-containing protein MUM1
Chr4	5	1	4	2.64E-07	<i>PRDM13</i>	PR domain zinc finger protein 13
Chr8	5	1	4	5.24E-06	<i>TRPA1</i>	Transient receptor potential cation channel subfamily A member 1
Chr7	5	2	3	7.87E-11	<i>NGDN</i>	Neuroguidin
Chr8	5	2	3	8.40E-11	<i>LRRC24</i>	Leucine-rich repeat-containing protein 24
Chr6	5	2	3	1.49E-09	<i>APBB3</i>	Amyloid beta A4 precursor protein-binding family B member 3
Chr19	5	2	3	4.99E-09	<i>ZNF256</i>	Zinc finger protein 256
Chr7	5	2	3	1.44E-05	<i>Ino80</i>	DNA helicase INO80
Chr15	5	3	2	3.80E-08	<i>DENND1A</i>	DENN domain-containing protein 1A
ChrX	5	3	2	0.000189	<i>ARMCX4</i>	Armadillo repeat-containing X-linked protein 4
Chr10	5	3	2	0.002678	<i>ZSWIM3</i>	Zinc finger SWIM domain-containing protein 3
Chr16	5	4	1	6.83E-16	<i>GEMIN4</i>	Gem-associated protein 4
Chr10	5	4	1	0.002248	<i>TRIOBP</i>	TRIO and F-actin-binding protein
Chr3	4	0	4	2.20E-16	<i>ZYX</i>	Zyxin
Chr12	4	0	4	2.81E-13	<i>DYNC1I2</i>	Cytoplasmic dynein 1 intermediate chain 2
Chr12	4	0	4	1.42E-12	<i>AGPS</i>	Alkyldihydroxyacetonephosphate synthase, peroxisomal

ChrX	4	0	4	4.84E-09	<i>MAGT1</i>	Magnesium transporter protein 1
Chr8	4	0	4	9.78E-08	<i>CA8</i>	Carbonic anhydrase-related protein
Chr7	4	0	4	2.22E-07	<i>FLVCR2</i>	Feline leukemia virus subgroup C receptor-related protein 2
Chr5	4	0	4	3.23E-07	<i>HNRNPD</i>	Heterogeneous nuclear ribonucleoprotein D0
Chr8	4	0	4	9.40E-07	<i>Naca</i>	Nascent polypeptide-associated complex subunit alpha
Chr2	4	0	4	1.25E-06	<i>ZNF620</i>	Zinc finger protein 620
Chr16	4	0	4	1.78E-06	<i>PIGS</i>	GPI transamidase component PIG-S
Chr1	4	0	4	5.36E-06	<i>SLC30A10</i>	Zinc transporter 10
Chr19	4	0	4	1.13E-05	<i>SAE1</i>	SUMO-activating enzyme subunit 1
Chr4	4	0	4	5.28E-05	<i>HIST1H2AJ</i>	Histone H2A type 1-J
Chr18	4	0	4	0.000115	<i>Kctd1</i>	BTB/POZ domain-containing protein KCTD1
Chr6	4	0	4	0.000115	<i>SKIV2L2</i>	Superkiller viralicidic activity 2-like 2
Chr10	4	0	4	0.000182	<i>C20orf204</i>	Chromosome 20 open reading frame 204
Chr3	4	0	4	0.000412	<i>EIF3B</i>	Eukaryotic translation initiation factor 3 subunit B
Chr7	4	0	4	0.000412	<i>CRIP1</i>	Cysteine-rich protein 1
Chr1	4	0	4	0.000477	<i>ECE1</i>	Endothelin-converting enzyme 1
Chr4	4	0	4	0.00083	<i>OSTM1</i>	Osteopetrosis-associated transmembrane protein 1
Chr2	4	0	4	0.001136	<i>CRBN</i>	Protein cereblon
Chr1	4	0	4	0.001522	<i>PFKFB2</i>	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2
Chr7	4	1	3	2.81E-13	<i>ZC2HC1C</i>	Zinc finger C2HC domain-containing protein 1C
ChrY	4	1	3	1.42E-12	<i>USP9Y</i>	Probable ubiquitin carboxyl-terminal hydrolase FAF-Y
Chr5	4	1	3	4.16E-09	<i>Cpeb2</i>	Cytoplasmic polyadenylation element-binding protein 2
Chr11	4	1	3	4.84E-09	<i>VPS29</i>	Vacuolar protein sorting-associated protein 29
Chr3	4	1	3	4.08E-08	<i>PVRIG</i>	Transmembrane protein PVRIG
Chr8	4	1	3	3.22E-06	<i>CEBPD</i>	CCAAT/enhancer-binding protein delta
Chr5	4	1	3	5.36E-06	<i>PEF1</i>	Peflin
Chr13	4	1	3	5.57E-06	<i>TGOLN2</i>	Trans-Golgi network integral membrane protein 2
Chr2	4	1	3	4.01E-05	<i>POCIA</i>	POC1 centriolar protein homolog A

Chr2	4	1	3	0.000108	<i>EIF4B</i>	Eukaryotic translation initiation factor 4B
Chr2	4	1	3	0.000115	<i>LRR1Q4</i>	Leucine-rich repeat and IQ domain-containing protein 4
Chr4	4	1	3	0.000115	<i>TJAP1</i>	Tight junction-associated protein 1
Chr19	4	1	3	0.000412	<i>ABHD17A</i>	Protein ABHD17A
Chr7	4	1	3	0.000592	<i>SLTM</i>	SAFB-like transcription modulator
Chr16	4	1	3	0.002591	<i>MKS1</i>	Meckel syndrome type 1 protein
Chr12	4	1	3	0.003299	<i>UGT1A1</i>	UDP-glucuronosyltransferase 1-1
Chr14	4	2	2	3.02E-11	<i>TIGD3</i>	Tigger transposable element-derived protein 3
Chr7	4	2	2	1.49E-09	<i>Irf2bpl</i>	Interferon regulatory factor 2-binding protein-like
Chr5	4	2	2	1.73E-09	<i>LIAS</i>	Lipoyl synthase, mitochondrial
Chr2	4	2	2	1.73E-09	<i>CEP63</i>	Centrosomal protein of 63 kDa
Chr6	4	2	2	2.20E-08	<i>HMGXB3</i>	HMG domain-containing protein 3
Chr3	4	2	2	7.91E-08	<i>IFNAR2</i>	Interferon alpha/beta receptor 2
Chr4	4	2	2	9.25E-07	<i>ZKSCAN4</i>	Zinc finger protein with KRAB and SCAN domains 4
Chr20	4	2	2	6.19E-05	<i>SRCAP</i>	Helicase SRCAP
Chr8	4	2	2	0.000149	<i>RECQL4</i>	ATP-dependent DNA helicase Q4
Chr3	4	2	2	0.000151	<i>RPL3</i>	60S ribosomal protein L3
Chr11	4	2	2	0.000278	<i>FAM186B</i>	Protein FAM186B
Chr7	4	2	2	0.000366	<i>CATSPERB</i>	Cation channel sperm-associated protein subunit beta
Chr1	4	2	2	0.00083	<i>SYNC</i>	Syncoilin
Chr4	4	2	2	0.00083	<i>GAPDH</i>	Glyceraldehyde-3-phosphate dehydrogenase
Chr2	4	2	2	0.002591	<i>Tnik</i>	Traf2 and NCK-interacting protein kinase
Chr14	4	2	2	0.004142	<i>FANCF</i>	Fanconi anemia group F protein
Chr7	4	3	1	8.93E-09	<i>ADAM21</i>	Disintegrin and metalloproteinase domain-containing protein 21
Chr14	4	3	1	5.36E-06	<i>UBE4A</i>	Ubiquitin conjugation factor E4 A
Chr2	4	3	1	1.13E-05	<i>Krt8</i>	Keratin, type II cytoskeletal 8
Chr11	4	3	1	0.000182	<i>SLC9A7</i>	Sodium/hydrogen exchanger 7
Chr6	4	3	1	0.000278	<i>KIF4B</i>	Chromosome-associated kinesin KIF4B

Chr4	4	3	1	0.002003	<i>CCDC170</i>	Coiled-coil domain-containing protein 170
Chr10	4	3	1	0.002591	<i>MAVS</i>	Mitochondrial antiviral-signaling protein
Chr7	4	4	0	9.94E-14	<i>BDKRB1</i>	B1 bradykinin receptor
Chr12	4	4	0	3.80E-08	<i>RBM44</i>	RNA-binding protein 44
ChrX	4	4	0	1.47E-07	<i>CXorf49</i>	Uncharacterized protein CXorf49
Chr4	4	4	0	9.29E-06	<i>PLG</i>	Plasminogen
Chr12	4	4	0	0.000614	<i>UGT1A9</i>	UDP-glucuronosyltransferase 1-9
Chr6	4	4	0	0.003299	<i>SLCO6A1</i>	Solute carrier organic anion transporter family member 6A1
Chr10	4	4	0	0.009938	<i>LAMA5</i>	Laminin subunit alpha-5
Chr8	3	0	3	2.20E-16	<i>JPH1</i>	Junctophilin-1
Chr3	3	0	3	2.20E-16	<i>GET4</i>	Golgi to ER traffic protein 4 homolog
ChrY	3	0	3	6.23E-15	<i>RPS4Y1</i>	40S ribosomal protein S4, Y isoform 1
Chr7	3	0	3	1.50E-11	<i>GALNT16</i>	Polypeptide N-acetylgalactosaminyltransferase 16
Chr14	3	0	3	9.71E-08	<i>LRRRC10B</i>	Leucine-rich repeat-containing protein 10B
Chr1	3	0	3	3.23E-07	<i>POU3F1</i>	POU domain, class 3, transcription factor 1
Chr16	3	0	3	9.25E-07	<i>GHDC</i>	GH3 domain-containing protein
Chr4	3	0	3	1.55E-06	<i>Nfya</i>	Nuclear transcription factor Y subunit alpha
Chr17	3	0	3	1.55E-06	<i>Mab21l1</i>	Putative nucleotidyltransferase MAB21L1
ChrX	3	0	3	1.55E-06	<i>SUV39H1</i>	Histone-lysine N-methyltransferase SUV39H1
Chr7	3	0	3	5.36E-06	<i>AP3S2</i>	AP-3 complex subunit sigma-2
Chr9	3	0	3	6.59E-06	<i>Atad1</i>	ATPase family AAA domain-containing protein 1
Chr16	3	0	3	6.59E-06	<i>HOXB6</i>	Homeobox protein Hox-B6
Chr4	3	0	3	2.16E-05	<i>RNF5</i>	E3 ubiquitin-protein ligase RNF5
Chr4	3	0	3	2.19E-05	<i>ELOVL4</i>	Elongation of very long chain fatty acids protein 4
Chr5	3	0	3	5.80E-05	<i>ARSJ</i>	Arylsulfatase J
Chr20	3	0	3	6.95E-05	<i>C16orf90</i>	Uncharacterized protein C16orf90
Chr18	3	0	3	6.95E-05	<i>DCC</i>	Netrin receptor DCC
Chr4	3	0	3	6.95E-05	<i>RARS2</i>	Probable arginine--tRNA ligase, mitochondrial

Chr4	3	0	3	6.95E-05	<i>TRAPPC3L</i>	Trafficking protein particle complex subunit 3-like protein
Chr8	3	0	3	0.000277	<i>PPP1R42</i>	Protein phosphatase 1 regulatory subunit 42
Chr4	3	0	3	0.000278	<i>SCAF8</i>	Protein SCAF8
Chr2	3	0	3	0.000519	<i>SS18L2</i>	SS18-like protein 2
Chr11	3	0	3	0.000519	<i>Myl6</i>	Myosin light polypeptide 6
Chr16	3	0	3	0.00083	<i>FADS6</i>	Fatty acid desaturase 6
ChrX	3	0	3	0.000899	<i>RAB5A</i>	Ras-related protein Rab-5A
Chr1	3	0	3	0.000899	<i>DCLRE1B</i>	5' exonuclease Apollo
Chr2	3	0	3	0.000899	<i>RASSF1</i>	Ras association domain-containing protein 1
Chr6	3	0	3	0.000899	<i>PPP2CA</i>	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform
Chr14	3	0	3	0.001462	<i>SLC25A22</i>	Mitochondrial glutamate carrier 1
Chr7	3	0	3	0.002256	<i>SUSD6</i>	Sushi domain-containing protein 6
Chr16	3	0	3	0.003299	<i>HID1</i>	Protein HID1
Chr5	3	0	3	0.003299	<i>PCDH10</i>	Protocadherin-10
Chr1	3	0	3	0.003328	<i>AP4B1</i>	AP-4 complex subunit beta-1
Chr14	3	0	3	0.003328	<i>GATD1</i>	Glutamine amidotransferase-like class 1 domain-containing protein 1
Chr7	3	0	3	0.006491	<i>MIPOL1</i>	Mirror-image polydactyly gene 1 protein
Chr2	3	0	3	0.006491	<i>SLC25A20</i>	Mitochondrial carnitine/acylcarnitine carrier protein
Chr5	3	0	3	0.008669	<i>RPL9</i>	60S ribosomal protein L9
Chr7	3	0	3	0.008669	<i>FURIN</i>	Furin
Chr11	3	0	3	0.008669	<i>KLRC4</i>	NKG2-F type II integral membrane protein
Chr9	3	0	3	0.008669	<i>SLC16A9</i>	Monocarboxylate transporter 9
Chr10	3	0	3	0.008669	<i>RSPH14</i>	Radial spoke head 14 homolog
Chr19	3	0	3	0.008669	<i>YJEFN3</i>	YjeF N-terminal domain-containing protein 3
Chr1	3	1	2	6.42E-14	<i>SUCO</i>	SUN domain-containing ossification factor
Chr4	3	1	2	9.25E-07	<i>GPANK1</i>	G patch domain and ankyrin repeat-containing protein 1
Chr11	3	1	2	9.40E-07	<i>NR4A1</i>	Nuclear receptor subfamily 4 group A member 1
Chr14	3	1	2	2.34E-06	<i>OR51I2</i>	Olfactory receptor 51I2

Chr10	3	1	2	3.07E-06	<i>INPP5J</i>	Phosphatidylinositol 4,5-bisphosphate 5-phosphatase A
Chr19	3	1	2	5.57E-06	<i>VAV1</i>	Proto-oncogene vav
Chr6	3	1	2	2.16E-05	<i>CENPK</i>	Centromere protein K
Chr1	3	1	2	2.19E-05	<i>TDRD10</i>	Tudor domain-containing protein 10
Chr1	3	1	2	2.34E-05	<i>JAK1</i>	Tyrosine-protein kinase JAK1
Chr13	3	1	2	0.000182	<i>MTIF2</i>	Translation initiation factor IF-2, mitochondrial
ChrX	3	1	2	0.000277	<i>CLDN2</i>	Claudin-2
Chr4	3	1	2	0.000278	<i>ZNF322</i>	Zinc finger protein 322
Chr4	3	1	2	0.000519	<i>HIST1H1B</i>	Histone H1.5
ChrX	3	1	2	0.000519	<i>SIAH1</i>	E3 ubiquitin-protein ligase SIAH1
Chr12	3	1	2	0.000592	<i>ALPI</i>	Intestinal-type alkaline phosphatase
Chr19	3	1	2	0.000592	<i>EMC10</i>	ER membrane protein complex subunit 10
Chr10	3	1	2	0.001136	<i>SEC14L4</i>	SEC14-like protein 4
Chr4	3	1	2	0.001136	<i>TBC1D32</i>	Protein broad-minded
Chr8	3	1	2	0.001462	<i>TMEM68</i>	Transmembrane protein 68
Chr1	3	1	2	0.001842	<i>INTS11</i>	Integrator complex subunit 11
Chr6	3	1	2	0.002256	<i>CSF2</i>	Granulocyte-macrophage colony-stimulating factor
Chr8	3	1	2	0.003328	<i>SPAG1</i>	Sperm-associated antigen 1
Chr16	3	1	2	0.003328	<i>GGNBP2</i>	Gametogenetin-binding protein 2
Chr9	3	1	2	0.003328	<i>EBLN1</i>	Endogenous Bornavirus-like nucleoprotein 1
Chr19	3	1	2	0.004443	<i>ERCC2</i>	TFIIH basal transcription factor complex helicase XPD subunit
Chr17	3	1	2	0.004724	<i>ZIC5</i>	Zinc finger protein ZIC 5
Chr19	3	1	2	0.006491	<i>ZNF844</i>	Zinc finger protein 844
Chr14	3	1	2	0.008669	<i>FOXRED1</i>	FAD-dependent oxidoreductase domain-containing protein 1
Chr19	3	1	2	0.008669	<i>SYT5</i>	Synaptotagmin-5
Chr3	3	1	2	0.008669	<i>SLC25A13</i>	Calcium-binding mitochondrial carrier protein Aralar2
Chr9	3	2	1	3.84E-10	<i>JMJD1C</i>	Probable JmjC domain-containing histone demethylation protein 2C
ChrY	3	2	1	6.59E-06	<i>RBMY1F</i>	RNA-binding motif protein, Y chromosome, family 1 member F/J

Chr11	3	2	1	1.13E-05	<i>NEUROD4</i>	Neurogenic differentiation factor 4
Chr19	3	2	1	1.44E-05	<i>SBNO2</i>	Protein strawberry notch homolog 2
Chr10	3	2	1	0.000135	<i>WFDC2</i>	WAP four-disulfide core domain protein 2
Chr9	3	2	1	0.000182	<i>USP54</i>	Inactive ubiquitin carboxyl-terminal hydrolase 54
Chr11	3	2	1	0.000278	<i>CSRNP2</i>	Cysteine/serine-rich nuclear protein 2
Chr4	3	2	1	0.001136	<i>PRSS16</i>	Thymus-specific serine protease
Chr20	3	2	1	0.001136	<i>RNF40</i>	E3 ubiquitin-protein ligase BRE1B
Chr20	3	2	1	0.001462	<i>SPATA33</i>	Spermatogenesis-associated protein 33
Chr14	3	2	1	0.002256	<i>ZFPL1</i>	Zinc finger protein-like 1
Chr10	3	2	1	0.002475	<i>CABIN1</i>	Calcineurin-binding protein cabin-1
Chr17	3	2	1	0.003328	<i>EFNB2</i>	Ephrin-B2
Chr11	3	2	1	0.004142	<i>B3GNT4</i>	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase 4
Chr9	3	2	1	0.006491	<i>VSIR</i>	V-type immunoglobulin domain-containing suppressor of T-cell activation
Chr11	3	2	1	0.008669	<i>C3AR1</i>	C3a anaphylatoxin chemotactic receptor
Chr17	3	2	1	0.009463	<i>AKAP11</i>	A-kinase anchor protein 11
Chr10	3	3	0	1.07E-13	<i>SBF1</i>	Myotubularin-related protein 5
Chr7	3	3	0	2.64E-07	<i>ADAM20</i>	Disintegrin and metalloproteinase domain-containing protein 20
Chr14	3	3	0	2.26E-05	<i>DNHD1</i>	Dynein heavy chain domain-containing protein 1
Chr14	3	3	0	7.64E-05	<i>DNHD1</i>	Dynein heavy chain domain-containing protein 1
Chr10	3	3	0	0.000151	<i>FASTKD5</i>	FAST kinase domain-containing protein 5, mitochondrial
Chr1	3	3	0	0.000412	<i>THBS3</i>	Thrombospondin-3
Chr2	3	3	0	0.000614	<i>VILL</i>	Villin-like protein
Chr3	3	3	0	0.002678	<i>CYP3A7</i>	Cytochrome P450 3A7
Chr19	3	3	0	0.004443	<i>CD22</i>	B-cell receptor CD22
Chr9	3	3	0	0.004724	<i>PTCHD3</i>	Patched domain-containing protein 3

Table S15. Gene ontology enrichment analyses based on the 216 PSGs identified in the comparison *fascicularis-sinica* versus *silenus* group. The top 40 most significant categories (P -value <0.05) from the over-representation analysis are reported. The categories related to reproductive functions are highlighted in red.

GeneSet ID	Description	Enrichment Ratio	P-value	Database	No. of genes	Genes
GO:0048232	Male gamete generation	3.034933822	8.02E-05	Biological_Process	16	<i>WDR48;KIF18A;MLH3;IFT81;KNL1;DMRTC2;USP9Y;POC1A;CATSPERB;FANCF;SIAH1;GGNBP2;RBMY1F;WFDC2;SBF1;PTCHD3</i>
GO:0019953	Sexual reproduction	2.507521542	1.42E-04	Biological_Process	20	<i>WDR48;KIF18A;MLH3;IFT81;KNL1;PLPP1;DMRTC2;USP9Y;POC1A;CATSPERB;FANCF;ADAM21;SIAH1;SPAG1;GGNBP2;RBMY1F;WFDC2;SBF1;ADAM20;PTCHD3</i>
HP:0012447	Abnormal myelination	3.720040183	1.95E-04	Human_Ontology	11	<i>PGAP1;TMEM126B;GEMIN4;SLC30A10;LIAS;JPH1;ELOVL4;SLC25A22;ERCC2;FOXRED1;SBF1</i>
GO:0051567	Histone H3-K9 methylation	12.8510479	2.51E-04	Biological_Process	4	<i>KDM4C;DMRTC2;SUV39H1;HIST1H1B</i>
GO:0060831	Smoothed signaling pathway involved in dorsal/ventral neural tube patterning	22.03036784	3.04E-04	Biological_Process	3	<i>TRAF3IP1;MKS1;TBC1D32</i>
GO:0007276	Gamete generation	2.58924817	3.19E-04	Biological_Process	17	<i>WDR48;KIF18A;MLH3;IFT81;KNL1;PLPP1;DMRTC2;USP9Y;POC1A;CATSPERB;FANCF;SIAH1;GGNBP2;RBMY1F;WFDC2;SBF1;PTCHD3</i>
HP:0100326	Immunologic hypersensitivity	6.493161046	3.29E-04	Human_Ontology	6	<i>GPR35;SRCAP;ELOVL4;KLRC4;ERCC2;JMJD1C</i>
GO:0036124	Histone H3-K9 trimethylation	18.14265586	5.56E-04	Biological_Process	3	<i>KDM4C;DMRTC2;SUV39H1</i>
GO:0007283	Spermatogenesis	2.746788865	6.15E-04	Biological_Process	14	<i>WDR48;IFT81;KNL1;DMRTC2;USP9Y;POC1A;CATSPERB;FANCF;SIAH1;GGNBP2;RBMY1F;WFDC2;SBF1;PTCHD3</i>
HP:0100022	Abnormality of movement	1.892593511	7.43E-04	Human_Ontology	28	<i>TTN;MLH3;DNAJB6;KNL1;TMEM126B;GEMIN4;CA8;FLVCR2;SLC30A10;CRBN;POC1A;MKS1;UGT1A1;LIAS;CEP63;FANCF;PLG;JPH1;ELOVL4;DCC;RARS2;SLC25A22;AP4B1;KLRC4;ERCC2;FOXRED1;JMJD1C;SBF1</i>
HP:0002921	Abnormality of the cerebrospinal fluid	3.150117592	7.93E-04	Human_Ontology	11	<i>TMEM126B;FLVCR2;OSTM1;MKS1;RECL4;FANCF;PLG;RARS2;ERCC2;FOXRED1;JMJD1C</i>
HP:0100513	Vitamin E deficiency	41.12335329	9.23E-04	Human_Ontology	2	<i>GPR35;SLC30A10</i>
GO:0061647	Histone H3-K9 modification	9.138522954	9.43E-04	Biological_Process	4	<i>KDM4C;DMRTC2;SUV39H1;HIST1H1B</i>
HP:0003819	Death in childhood	14.01932499	0.001215	Human_Ontology	3	<i>RARS2;SLC25A22;ERCC2</i>
HP:0100514	Abnormality of vitamin E metabolism	34.26946108	0.001375	Human_Ontology	2	<i>GPR35;SLC30A10</i>

GO:1902525	Regulation of protein monoubiquitination	34.26946108	0.001375	Biological_Process	2	<i>WDR48;PEF1</i>
GO:0016255	Attachment of GPI anchor to protein	34.26946108	0.001375	Biological_Process	2	<i>PGAP1;PIGS</i>
GO:0051552	Flavone metabolic process	34.26946108	0.001375	Biological_Process	2	<i>UGT1A1;UGT1A9</i>
GO:0051570	Regulation of histone H3-K9 methylation	13.40978912	0.001387	Biological_Process	3	<i>KDM4C;DMRTC2;HIST1H1B</i>
GO:0044703	Multi-organism reproductive process	2.085362743	0.001468	Biological_Process	20	<i>WDR48;KIF18A;MLH3;IFT81;KNLI;PLPP1;DMRTC2;USP9Y;POC1A;CATSPERB;FANCF;ADAM21;SIAH1;SPAG1;GGNBP2;RBMY1F;WFDC2;SBF1;ADAM20;PTCHD3</i>
GO:0021904	Dorsal/ventral neural tube patterning	12.8510479	0.001574	Biological_Process	3	<i>TRAF3IP1;MKS1;TBC1D32</i>
HP:0012759	Neurodevelopmental abnormality	1.696338323	0.001582	Human_Ontology	33	<i>TTN;MLH3;TRAF3IP1;WIPF1;KNLI;PGAP1;TMEM126B;GEMIN4;MAGT1;CA8;FLVCR2;ECE1;CRBN;POC1A;MKS1;UGT1A1;LIAS;CEP63;SRCAP;RECQL4;FANCF;PLG;ELOVL4;DCC;RARS2;SLC25A22;AP4B1;SLC25A20;KLRC4;ERCC2;FOXRED1;JMJD1C;SBF1</i>
HP:0000240	Abnormality of skull size	2.045937975	0.001839	Human_Ontology	20	<i>IFT81;KNLI;PGAP1;TMEM126B;SLC30A10;POC1A;MKS1;LIAS;CEP63;FANCF;PLG;ELOVL4;RARS2;SLC25A22;AP4B1;SLC25A20;ERCC2;FOXRED1;JMJD1C;SBF1</i>
GO:0036123	Histone H3-K9 dimethylation	29.37382378	0.001913	Biological_Process	2	<i>DMRTC2;SUV39H1</i>
HP:0001263	Global developmental delay	1.887145103	0.002385	Human_Ontology	23	<i>TRAF3IP1;KNLI;PGAP1;TMEM126B;GEMIN4;FLVCR2;CRBN;POC1A;MKS1;LIAS;CEP63;SRCAP;FANCF;PLG;ELOVL4;DCC;RARS2;SLC25A22;AP4B1;SLC25A20;ERCC2;FOXRED1;JMJD1C</i>
GO:0048609	Multicellular organismal reproductive process	2.149744791	0.002449	Biological_Process	17	<i>WDR48;KIF18A;MLH3;IFT81;KNLI;PLPP1;DMRTC2;USP9Y;POC1A;CATSPERB;FANCF;SIAH1;GGNBP2;RBMY1F;WFDC2;SBF1;PTCHD3</i>
HP:0002672	Gastrointestinal carcinoma	11.01518392	0.002476	Human_Ontology	3	<i>MLH3;GPR35;DCC</i>
HP:0006749	Malignant gastrointestinal tract tumors	11.01518392	0.002476	Human_Ontology	3	<i>MLH3;GPR35;DCC</i>
HP:0012758	Neurodevelopmental delay	1.793971788	0.002486	Human_Ontology	26	<i>TTN;TRAF3IP1;KNLI;PGAP1;TMEM126B;GEMIN4;MAGT1;FLVCR2;CRBN;POC1A;MKS1;UGT1A1;LIAS;CEP63;SRCAP;FANCF;PLG;ELOVL4;DCC;RARS2;SLC25A22;AP4B1;SLC25A20;ERCC2;FOXRED1;JMJD1C</i>
GO:1901620	Regulation of smoothed signaling pathway involved in dorsal/ventral neural tube patterning	25.70209581	0.002534	Biological_Process	2	<i>TRAF3IP1;MKS1</i>
GO:0070778	L-aspartate transmembrane transport	25.70209581	0.002534	Biological_Process	2	<i>SLC25A22;SLC25A13</i>

HP:0031826	Abnormal reflex	2.067654635	0.002785	Human_Ontology	18	<i>TTN;MLH3;KNL1;TMEM126B;CA8;CEP63;FANCF;PLG;JPH1;ELOVL4;DCC;RARS2;SLC25A22;AP4B1;KLRC4;ERCC2;FOXRED1;SBF1</i>
HP:0007364	Aplasia/Hypoplasia of the cerebrum	2.013772455	0.002855	Human_Ontology	19	<i>KNL1;PGAP1;FLVCR2;SLC30A10;POCIA;MKS1;LIAS;CEP63;RECQL4;FANCF;ELOVL4;DCC;RARS2;SLC25A22;AP4B1;SLC25A20;ERCC2;JMJD1C;SBF1</i>
GO:0042733	Embryonic digit morphogenesis	6.741533327	0.002928	Biological_Process	4	<i>TRAF3IP1;ECE1;MKS1;TBC1D32</i>
HP:0002242	Abnormal intestine morphology	2.421211924	0.002932	Human_Ontology	13	<i>MLH3;WIPF1;GPR35;ECE1;MKS1;SRCAP;RECQL4;FANCF;PLG;DCC;KLRC4;ERCC2;JMJD1C</i>
GO:0032504	Multicellular organism reproduction	2.110800139	0.002955	Biological_Process	17	<i>WDR48;KIF18A;MLH3;IFT81;KNL1;PLPP1;DMRTC2;USP9Y;POCIA;CATSPERB;FANCF;SIAH1;GGNBP2;RBMY1F;WFDC2;SBF1;PTCHD3</i>
HP:0011446	Abnormality of higher mental function	1.884820359	0.003019	Human_Ontology	22	<i>TTN;MLH3;DNAJB6;PGAP1;TMEM126B;GEMIN4;CA8;SLC30A10;MKS1;UGT1A1;SRCAP;ELOVL4;DCC;RARS2;SLC25A22;AP4B1;SLC25A20;KLRC4;ERCC2;FOXRED1;SLC25A13;JMJD1C</i>
HP:0100021	Cerebral palsy	10.28083832	0.003026	Human_Ontology	3	<i>CA8;UGT1A1;DCC</i>
GO:0015810	Aspartate transmembrane transport	22.84630739	0.003237	Biological_Process	2	<i>SLC25A22;SLC25A13</i>
GO:0052696	Flavonoid glucuronidation	22.84630739	0.003237	Biological_Process	2	<i>UGT1A1;UGT1A9</i>

Table S16. PSGs identified in the comparison *fascicularis-silenus* versus *sinica* groups with *P*-value <0.01(after Yates' correction), a top 2.5% number of fixed non-synonymous mutations and fixed 1 kb upstream differences. The phylogenetic analysis supports the sister relationship between the *fascicularis* and *silenus* groups. Genes were sorted by the sum of the fixed number of non-synonymous mutations (FixNonSyn) and fixed 1-kb upstream mutations (Fix1kup).

Chromosome	Num FixNonSyn+Fix1kup	Num FixNonSyn	Num Fix1kup	P-value	Gene Symbol	Full Name
Chr1	14	11	3	2.20E-16	<i>SYDE2</i>	Rho GTPase-activating protein SYDE2
Chr19	13	12	1	2.81E-12	<i>WDR87</i>	WD repeat-containing protein 87
Chr4	13	6	7	2.20E-16	<i>ZNF318</i>	Zinc finger protein 318
Chr1	12	2	10	2.20E-16	<i>PRG4</i>	Proteoglycan 4
Chr13	10	9	1	1.81E-07	<i>C2orf16</i>	Uncharacterized protein C2orf16
Chr7	10	1	9	2.20E-16	<i>NEK9</i>	Serine/threonine-protein kinase Nek9
Chr14	10	0	10	2.20E-16	<i>TEX12</i>	Testis-expressed protein 12
Chr18	10	0	10	2.20E-16	<i>CABYR</i>	Calcium-binding tyrosine phosphorylation-regulated protein isoform c
Chr10	9	9	0	2.20E-16	<i>CHD6</i>	Chromodomain-helicase-DNA-binding protein 6
Chr10	9	0	9	2.82E-15	<i>GSTT1</i>	Glutathione S-transferase theta-1
Chr1	8	8	0	0.000614	<i>AHCTF1</i>	Protein ELYS
Chr13	8	7	1	1.62E-07	<i>RAD51AP2</i>	RAD51-associated protein 2
Chr3	8	3	5	6.40E-14	<i>Upk3b</i>	Uroplakin-3b
Chr15	8	1	7	1.03E-05	<i>EML2</i>	Echinoderm microtubule-associated protein-like 2
Chr1	8	0	8	2.20E-16	<i>ZC3H12A</i>	Endoribonuclease ZC3H12A
Chr7	8	0	8	1.21E-14	<i>EMC4</i>	ER membrane protein complex subunit 4
Chr12	8	0	8	3.98E-13	<i>COL5A2</i>	Collagen alpha-2(V) chain
Chr20	8	0	8	8.19E-11	<i>VPS35</i>	Vacuolar protein sorting-associated protein 35
Chr19	7	7	0	2.20E-16	<i>ZNF274</i>	Neurotrophin receptor-interacting factor homolog
Chr16	7	5	2	0.0018	<i>GPR179</i>	Probable G-protein coupled receptor 179

Chr15	7	4	3	5.02E-14	<i>PIGO</i>	GPI ethanolamine phosphate transferase 3
Chr7	7	4	3	2.34E-12	<i>MGA</i>	MAX gene-associated protein
Chr9	7	4	3	3.92E-08	<i>EIF4B</i>	Eukaryotic translation initiation factor 4B
Chr14	7	4	3	3.61E-07	<i>PITPNM1</i>	Membrane-associated phosphatidylinositol transfer protein 1
Chr15	7	3	4	3.95E-13	<i>C9orf131</i>	Uncharacterized protein C9orf131
Chr12	7	2	5	2.20E-16	<i>MFSD6</i>	Major facilitator superfamily domain-containing protein 6
Chr14	7	2	5	2.20E-16	<i>PIDD1</i>	p53-induced death domain-containing protein 1
Chr9	7	2	5	2.82E-15	<i>ZFYVE27</i>	Protrudin
Chr7	7	2	5	4.82E-08	<i>HERC1</i>	Probable E3 ubiquitin-protein ligase HERC1
Chr5	7	2	5	9.19E-08	<i>SHROOM3</i>	Protein Shroom3
Chr7	7	1	6	1.21E-15	<i>TOGARAM1</i>	TOG array regulator of axonemal microtubules protein 1
Chr3	7	1	6	7.37E-08	<i>AIRE</i>	Autoimmune regulator
Chr16	7	0	7	2.20E-16	<i>PSMD12</i>	26S proteasome non-ATPase regulatory subunit 12
Chr2	7	0	7	2.39E-14	<i>GHSR</i>	Growth hormone secretagogue receptor type 1
Chr7	7	0	7	2.02E-12	<i>USP3</i>	Ubiquitin carboxyl-terminal hydrolase 3
Chr10	7	0	7	3.80E-11	<i>PROKR2</i>	Prokineticin receptor 2
Chr10	7	0	7	1.54E-09	<i>PAK5</i>	Serine/threonine-protein kinase PAK 5
Chr7	7	0	7	2.20E-08	<i>NEIL1</i>	Endonuclease 8-like 1
Chr6	6	6	0	0.002642	<i>PCDHA3</i>	Protocadherin alpha-3
Chr7	6	3	3	1.63E-13	<i>RPGRIP1</i>	X-linked retinitis pigmentosa GTPase regulator-interacting protein 1
Chr3	6	2	4	3.98E-14	<i>LHFPL3</i>	Lipoma HMGIC fusion partner-like 3 protein
Chr17	6	2	4	2.38E-09	<i>SUPT20H</i>	Transcription factor SPT20 homolog
Chr8	6	2	4	3.13E-06	<i>Eppk1</i>	Epiplakin
Chr3	6	2	4	0.005234	<i>SDK1</i>	Protein sidekick-1
Chr3	6	1	5	3.92E-08	<i>EPHA1</i>	Ephrin type-A receptor 1
Chr2	6	1	5	2.20E-07	<i>LPP</i>	Lipoma-preferred partner
Chr6	6	1	5	0.000181	<i>GEMIN5</i>	Gem-associated protein 5
Chr19	6	0	6	8.19E-11	<i>LMNB2</i>	Lamin-B2

Chr10	6	0	6	1.31E-10	<i>OVOL2</i>	Transcription factor Ovo-like 2
Chr10	6	0	6	8.97E-10	<i>ERGIC3</i>	Endoplasmic reticulum-Golgi intermediate compartment protein 3
Chr6	6	0	6	1.34E-08	<i>TCF7</i>	Transcription factor 7
Chr19	6	0	6	5.98E-08	<i>IZUMO4</i>	Izumo sperm-egg fusion protein 4
Chr9	6	0	6	3.96E-07	<i>TMEM72</i>	Transmembrane protein 72
Chr5	6	0	6	1.16E-06	<i>PDHA2</i>	Pyruvate dehydrogenase E1 component subunit alpha, testis-specific form, mitochondrial
Chr14	6	0	6	3.05E-05	<i>TKFC</i>	Triokinase/FMN cyclase
Chr6	5	5	0	2.20E-08	<i>PRLR</i>	Prolactin receptor
Chr6	5	5	0	6.60E-05	<i>PCDHA13</i>	Protocadherin alpha-13
Chr7	5	5	0	0.000817	<i>AKAP13</i>	A-kinase anchor protein 13
ChrX	5	4	1	4.05E-06	<i>GVQW1</i>	Protein GVQW1
Chr2	5	4	1	0.002376	<i>BSN</i>	Protein bassoon
Chr13	5	3	2	4.68E-06	<i>RANBP2</i>	E3 SUMO-protein ligase RanBP2
Chr16	5	3	2	4.21E-05	<i>AATF</i>	Protein AATF
Chr7	5	3	2	6.95E-05	<i>C8orf44</i>	Putative uncharacterized protein C8orf44
Chr7	5	2	3	2.20E-16	<i>DDHD1</i>	Phospholipase DDHD1
Chr7	5	2	3	3.11E-10	<i>TRIP4</i>	Activating signal cointegrator 1
Chr18	5	2	3	8.97E-10	<i>CABYR</i>	Calcium-binding tyrosine phosphorylation-regulated protein
Chr7	5	2	3	3.01E-08	<i>TP53BP1</i>	TP53-binding protein 1
Chr20	5	2	3	2.17E-05	<i>PRSS53</i>	Serine protease 53
Chr9	5	2	3	4.21E-05	<i>C10orf142</i>	Uncharacterized protein C10orf142
Chr15	5	2	3	0.004178	<i>GBGT1</i>	Globoside alpha-1,3-N-acetylgalactosaminyltransferase 1
Chr12	5	2	3	0.005788	<i>TIGD1</i>	Tigger transposable element-derived protein 1
Chr11	5	1	4	1.49E-13	<i>FMNL3</i>	Formin-like protein 3
Chr16	5	1	4	4.30E-08	<i>SP6</i>	Transcription factor Sp6
Chr8	5	1	4	5.98E-08	<i>TM2D2</i>	TM2 domain-containing protein 2
Chr5	5	1	4	1.14E-07	<i>LARP7</i>	La-related protein 7
Chr20	5	1	4	9.04E-07	<i>SRRM2</i>	Serine/arginine repetitive matrix protein 2

Chr20	5	1	4	1.89E-06	<i>ADAT1</i>	tRNA-specific adenosine deaminase 1
Chr14	5	1	4	2.21E-06	<i>HARB11</i>	Putative nuclease HARB11
Chr1	5	1	4	4.05E-06	<i>TTC13</i>	Tetratricopeptide repeat protein 13
Chr19	5	1	4	6.95E-05	<i>RASGRP4</i>	RAS guanyl-releasing protein 4
Chr1	5	1	4	0.000101	<i>MPL</i>	Thrombopoietin receptor
Chr3	5	1	4	0.000351	<i>EPHB4</i>	Ephrin type-B receptor 4
Chr10	5	1	4	0.003512	<i>BCR</i>	Breakpoint cluster region protein
Chr15	5	0	5	2.20E-16	<i>VCP</i>	Transitional endoplasmic reticulum ATPase
Chr14	5	0	5	7.67E-16	<i>RCN1</i>	Reticulocalbin-1
Chr7	5	0	5	3.20E-15	<i>LTBR2</i>	Leukotriene B4 receptor 2
Chr19	5	0	5	4.65E-15	<i>TIMM13</i>	Mitochondrial import inner membrane translocase subunit Tim13
Chr14	5	0	5	5.77E-13	<i>CRTAM</i>	Cytotoxic and regulatory T-cell molecule
Chr7	5	0	5	7.18E-12	<i>SIN3A</i>	Paired amphipathic helix protein Sin3a
ChrX	5	0	5	6.16E-11	<i>VGLL1</i>	Transcription cofactor vestigial-like protein 1
Chr14	5	0	5	1.34E-09	<i>STX5</i>	Syntaxin-5
Chr6	5	0	5	1.34E-09	<i>FBLL1</i>	rRNA/tRNA 2'-O-methyltransferase fibrillarin-like protein 1
Chr2	5	0	5	2.38E-09	<i>IP6K2</i>	Inositol hexakisphosphate kinase 2
Chr1	5	0	5	4.84E-09	<i>TSACC</i>	TSSK6-activating co-chaperone protein
Chr6	5	0	5	2.91E-08	<i>MRPL22</i>	39S ribosomal protein L22, mitochondrial
Chr1	5	0	5	1.10E-07	<i>LRRC40</i>	Leucine-rich repeat-containing protein 40
Chr10	5	0	5	6.89E-07	<i>SF3A1</i>	Splicing factor 3A subunit 1
Chr1	5	0	5	1.15E-06	<i>ZNF326</i>	DBIRD complex subunit ZNF326
Chr1	5	0	5	1.15E-06	<i>ARV1</i>	Protein ARV1
Chr19	5	0	5	4.05E-06	<i>TGFB1</i>	Transforming growth factor beta-1
Chr7	5	0	5	7.10E-06	<i>CPSF2</i>	Cleavage and polyadenylation specificity factor subunit 2
Chr1	5	0	5	8.99E-06	<i>AHDC1</i>	AT-hook DNA-binding motif-containing protein 1
Chr20	5	0	5	1.20E-05	<i>TXNL4B</i>	Thioredoxin-like protein 4B
Chr12	5	0	5	3.05E-05	<i>SMARCAL1</i>	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A-like protein 1

Chr10	5	0	5	3.06E-05	<i>SPATA2</i>	Spermatogenesis-associated protein 2
Chr19	5	0	5	0.0002	<i>FSTL3</i>	Follistatin-related protein 3
Chr20	5	0	5	0.000367	<i>ORC6</i>	Origin recognition complex subunit 6
Chr16	5	0	5	0.000485	<i>COIL</i>	Coilin
Chr1	5	0	5	0.000633	<i>ADGRL4</i>	Adhesion G protein-coupled receptor L4
Chr2	4	4	0	5.68E-07	<i>CFAP44</i>	Cilia- and flagella-associated protein 44
ChrX	4	4	0	0.0002	<i>FRMPD4</i>	FERM and PDZ domain-containing protein 4
Chr19	4	4	0	0.000273	<i>ICAM1</i>	Intercellular adhesion molecule 1
Chr1	4	4	0	0.000327	<i>CFAP74</i>	Cilia- and flagella-associated protein 74
Chr15	4	4	0	0.00163	<i>DENND4C</i>	DENN domain-containing protein 4C
Chr8	4	4	0	0.001988	<i>KCNU1</i>	Potassium channel subfamily U member 1
Chr20	4	4	0	0.009006	<i>PRMT7</i>	Protein arginine N-methyltransferase 7
Chr13	4	3	1	5.98E-08	<i>ODC1</i>	Ornithine decarboxylase
Chr13	4	3	1	2.45E-07	<i>PUM2</i>	Pumilio homolog 2
ChrX	4	3	1	1.89E-06	<i>FRMPD3</i>	FERM and PDZ domain-containing protein 3
Chr18	4	3	1	1.52E-05	<i>OSBPL1A</i>	Oxysterol-binding protein-related protein 1
Chr5	4	3	1	0.000143	<i>PTPN11</i>	Tyrosine-protein phosphatase non-receptor type 11
Chr4	4	3	1	0.000315	<i>DTNBP1</i>	Dysbindin
ChrX	4	3	1	0.000436	<i>SHROOM2</i>	Protein Shroom2
Chr13	4	3	1	0.001327	<i>PRR30</i>	Proline-rich protein 30
Chr8	4	3	1	0.001349	<i>WDR97</i>	WD repeat-containing protein 97
ChrX	4	3	1	0.004934	<i>FAM47C</i>	Putative protein FAM47C
Chr16	4	2	2	1.63E-13	<i>AKAP1</i>	A-kinase anchor protein 1, mitochondrial
ChrX	4	2	2	3.11E-10	<i>P2RY10</i>	Putative P2Y purinoceptor 10
Chr13	4	2	2	1.16E-06	<i>MSH6</i>	DNA mismatch repair protein Msh6
Chr2	4	2	2	2.17E-05	<i>PLXNB1</i>	Plexin-B1
Chr19	4	2	2	7.48E-05	<i>ZNF570</i>	Zinc finger protein 570
Chr16	4	2	2	0.0002	<i>GGA3</i>	ADP-ribosylation factor-binding protein GGA3

Chr12	4	2	2	0.001035	<i>SCLY</i>	Selenocysteine lyase
Chr18	4	2	2	0.003063	<i>CCDC178</i>	Coiled-coil domain-containing protein 178
Chr5	4	2	2	0.004918	<i>RELL1</i>	RELT-like protein 1
Chr10	4	2	2	0.004934	<i>GGT1</i>	Gamma-glutamyltranspeptidase 1
Chr2	4	1	3	2.20E-16	<i>GSK3B</i>	Glycogen synthase kinase-3 beta
Chr15	4	1	3	6.82E-15	<i>FAM214B</i>	Protein FAM214B
ChrY	4	1	3	1.89E-11	<i>TSPY10</i>	Testis-specific Y-encoded protein 10
Chr14	4	1	3	1.34E-09	<i>OTUB1</i>	Ubiquitin thioesterase OTUB1
Chr10	4	1	3	2.38E-09	<i>CSDC2</i>	Cold shock domain-containing protein C2
Chr1	4	1	3	4.30E-08	<i>MRPL55</i>	39S ribosomal protein L55, mitochondrial
Chr1	4	1	3	4.30E-08	<i>HFE2</i>	Hemojuvelin
Chr14	4	1	3	1.17E-07	<i>TTC9C</i>	Tetratricopeptide repeat protein 9C
Chr16	4	1	3	1.87E-07	<i>MED24</i>	Mediator of RNA polymerase II transcription subunit 24
Chr11	4	1	3	2.08E-06	<i>Phlda1</i>	Pleckstrin homology-like domain family A member 1
Chr14	4	1	3	2.21E-06	<i>FADS1</i>	Fatty acid desaturase 1
Chr1	4	1	3	2.21E-06	<i>LRIF1</i>	Ligand-dependent nuclear receptor-interacting factor 1
Chr20	4	1	3	1.05E-05	<i>ATXN1L</i>	Ataxin-1-like
ChrX	4	1	3	2.23E-05	<i>CXorf23</i>	Uncharacterized protein CXorf23
Chr10	4	1	3	0.000143	<i>GAS2L1</i>	GAS2-like protein 1
Chr2	4	1	3	0.0002	<i>DAG1</i>	Dystroglycan
Chr20	4	1	3	0.000203	<i>CCDC113</i>	Coiled-coil domain-containing protein 113
Chr2	4	1	3	0.000273	<i>VTCN1</i>	V-set domain-containing T-cell activation inhibitor 1
Chr13	4	1	3	0.000315	<i>ATRAID</i>	All-trans retinoic acid-induced differentiation factor
Chr16	4	1	3	0.000315	<i>NDUFS5</i>	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5
Chr19	4	1	3	0.000367	<i>KCNK6</i>	Potassium channel subfamily K member 6
Chr16	4	1	3	0.000471	<i>IFI35</i>	Interferon-induced 35 kDa protein
Chr14	4	1	3	0.000485	<i>TUT1</i>	Speckle targeted PIP5K1A-regulated poly(A) polymerase
Chr16	4	1	3	0.000801	<i>MTMR4</i>	Myotubularin-related protein 4

Chr6	4	1	3	0.004918	<i>WDR70</i>	WD repeat-containing protein 70
Chr20	4	1	3	0.004918	<i>MLST8</i>	Target of rapamycin complex subunit LST8
Chr9	4	1	3	0.009066	<i>NEBL</i>	Nebulette
Chr15	4	0	4	2.20E-16	<i>TEKT4</i>	Tektin-4
Chr3	4	0	4	3.16E-10	<i>Tra2a</i>	Transformer-2 protein homolog alpha
Chr1	4	0	4	6.28E-09	<i>WDTC1</i>	WD and tetratricopeptide repeats protein 1
Chr7	4	0	4	4.30E-08	<i>CIB1</i>	Calcium and integrin-binding protein 1
Chr16	4	0	4	2.58E-07	<i>MRPL45</i>	39S ribosomal protein L45, mitochondrial
Chr19	4	0	4	7.67E-07	<i>ZNF569</i>	Zinc finger protein 569
Chr1	4	0	4	7.67E-07	<i>PIGC</i>	Phosphatidylinositol N-acetylglucosaminyltransferase subunit C
Chr2	4	0	4	4.05E-06	<i>NCKIPSD</i>	NCK-interacting protein with SH3 domain
Chr16	4	0	4	4.71E-06	<i>SLC16A11</i>	Monocarboxylate transporter 11
ChrY	4	0	4	5.04E-06	<i>CDY2A</i>	Testis-specific chromodomain protein Y 2
Chr11	4	0	4	5.04E-06	<i>FAM60A</i>	Protein FAM60A
Chr8	4	0	4	1.20E-05	<i>SPIDR</i>	DNA repair-scaffolding protein
Chr15	4	0	4	1.20E-05	<i>UBQLN1</i>	Ubiquilin-1
Chr19	4	0	4	1.20E-05	<i>MATK</i>	Megakaryocyte-associated tyrosine-protein kinase
Chr9	4	0	4	1.94E-05	<i>DEPP</i>	Protein DEPP
Chr16	4	0	4	4.21E-05	<i>HCRT</i>	Orexin
Chr17	4	0	4	4.21E-05	<i>EXOSC8</i>	Exosome complex component RRP43
Chr18	4	0	4	0.000101	<i>MPPE1</i>	Metallophosphoesterase 1
Chr19	4	0	4	0.000126	<i>ZNF570</i>	Zinc finger protein 570
Chr5	4	0	4	0.000143	<i>GATB</i>	Glutamyl-tRNA(Gln) amidotransferase subunit B, mitochondrial
Chr13	4	0	4	0.000315	<i>MTHFD2</i>	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial
Chr3	4	0	4	0.000471	<i>BAZ1B</i>	Tyrosine-protein kinase BAZ1B
Chr20	4	0	4	0.000471	<i>C16orf70</i>	UPF0183 protein C16orf70
Chr2	4	0	4	0.000471	<i>MRPL47</i>	39S ribosomal protein L47, mitochondrial
Chr16	4	0	4	0.000682	<i>KCTD2</i>	BTB/POZ domain-containing protein KCTD2

Chr1	4	0	4	0.000682	<i>TCTEX1D4</i>	Tctex1 domain-containing protein 4
Chr14	4	0	4	0.000963	<i>MRPL49</i>	39S ribosomal protein L49, mitochondrial
Chr10	4	0	4	0.002361	<i>PI4KA</i>	Phosphatidylinositol 4-kinase alpha
Chr7	4	0	4	0.002361	<i>ADSSL1</i>	Adenylosuccinate synthetase isozyme 1
Chr3	4	0	4	0.003063	<i>SLC25A40</i>	Solute carrier family 25 member 40
Chr7	4	0	4	0.00391	<i>SSTR1</i>	Somatostatin receptor type 1
Chr8	4	0	4	0.004918	<i>Sorbs3</i>	Vinexin

Table S17. Gene ontology enrichment analyses based on the 195 PSGs identified in the comparison *fascicularis-silenus* versus *sinica* group. The top 40 most significant categories (P -value <0.05) from the over-representation analysis are reported. The categories related to reproductive functions are highlighted in bold.

GeneSet ID	Description	Enrichment Ratio	P-value	Database	No. of genes	Genes
GO:0006661	Phosphatidylinositol biosynthetic process	5.280865	3.76E-04	Biological_Process	7	<i>PIGO;PITPNM1;PTPN11;MTMR4;PIGC;MPPE1;PI4KA</i>
HP:0003307	Hyperlordosis	5.039257	4.99E-04	Human_Ontology	7	<i>HERC1;BCR;VCP;TGFB1;SMARCAL1;DAG1;BAZ1B</i>
HP:0100785	Insomnia	18.35729	5.42E-04	Human_Ontology	3	<i>SIN3A;HCRT;BAZ1B</i>
GO:1902074	Response to salt	17.39112	6.40E-04	Biological_Process	3	<i>ZC3H12A;GHSR;TGFB1</i>
GO:0007010	Cytoskeleton organization	2.033423	6.77E-04	Biological_Process	24	<i>EML2;SHROOM3;TOGARAM1;GHSR;PAK5;EPHA1;AKA P13;FMNL3;BCR;VCP;TGFB1;CFAP44;FRMPD4;ICAM1 ;CFAP74;DTNBP1;SHROOM2;PLXNB1;GSK3B;DAG1;M LST8;NEBL;CIB1;NCKIPSD</i>
GO:0030220	Platelet formation	16.52156	7.47E-04	Biological_Process	3	<i>MPL;PTPN11;CIB1</i>
HP:0005506	Chronic myelogenous leukemia	44.0575	8.05E-04	Human_Ontology	2	<i>MPL;BCR</i>
GO:0002513	Tolerance induction to self antigen	44.0575	8.05E-04	Biological_Process	2	<i>AIRE;TGFB1</i>
GO:0036344	Platelet morphogenesis	15.73482	8.66E-04	Biological_Process	3	<i>MPL;PTPN11;CIB1</i>
HP:0001760	Abnormality of the foot	2.219227	9.31E-04	Human_Ontology	19	<i>PRG4;NEK9;COL5A2;PIGO;ZFYVE27;HERC1;PROKR2; RPGRI1;DDHD1;TRIP4;BCR;VCP;SIN3A;TGFB1;ORC6 ;PRMT7;DAG1;BAZ1B;PI4KA</i>
GO:0001954	Positive regulation of cell-matrix adhesion	8.8115	0.0010889 63	Biological_Process	4	<i>EPHA1;GSK3B;DAG1;CIB1</i>
HP:0004859	Amegakaryocytic thrombocytopenia	36.71458	0.0011996 9	Human_Ontology	2	<i>MPL;PTPN11</i>
GO:0090325	Regulation of locomotion involved in locomotory behavior	36.71458	0.0011996 9	Biological_Process	2	<i>VPS35;GHSR</i>
GO:0046488	Phosphatidylinositol metabolic process	3.765598	0.0013570 66	Biological_Process	8	<i>PIGO;PITPNM1;IP6K2;PTPN11;MTMR4;PIGC;MPPE1;P I4KA</i>
HP:0002814	Abnormality of the lower limb	2.03253	0.0015091 34	Human_Ontology	21	<i>PRG4;NEK9;COL5A2;PIGO;ZFYVE27;HERC1;PROKR2; RPGRI1;DDHD1;TRIP4;BCR;VCP;SIN3A;TGFB1;SMAR CAL1;ORC6;PRMT7;DAG1;BAZ1B;PI4KA;ADSSL1</i>
HP:0000134	Female hypogonadism	12.70889	0.0016379 76	Human_Ontology	3	<i>AIRE;PROKR2;PRLR</i>
GO:0045830	Positive regulation of isotype switching	12.70889	0.0016379 76	Biological_Process	3	<i>TP53BP1;TGFB1;MSH6</i>

GO:0097327	Response to antineoplastic agent	5.85871	0.0016607 32	Biological_Process	5	<i>ZC3H12A;GHSR;TGFB1;ICAM1;SPIDR</i>
GO:1903003	Positive regulation of protein deubiquitination	31.46964	0.0016695 54	Biological_Process	2	<i>ZC3H12A;VCP</i>
GO:0022603	Regulation of anatomical structure morphogenesis	2.103247	0.0017350 37	Biological_Process	19	<i>ZC3H12A;COL5A2;VPS35;ZFYVE27;SHROOM3;GHSR;E PHA1;AKAP13;DDHD1;FMNL3;SP6;MPL;BCR;TGFB1;I CAM1;PLXNB1;GSK3B;DAG1;CIB1</i>
GO:1990778	protein localization to cell periphery	3.293335	0.0017457 39	Biological_Process	9	<i>VPS35;ZFYVE27;GHSR;TGFB1;DENND4C;GGA3;DAG1; CIB1;C16orf70</i>
HP:0010674	Abnormality of the curvature of the vertebral column	2.268082	0.0019111 51	Human_Ontology	16	<i>NEK9;COL5A2;HERC1;LMNB2;DDHD1;TRIP4;LARP7;M PL;BCR;VCP;SIN3A;TGFB1;SMARCAL1;PTPN11;DAG1; BAZ1B</i>
HP:0005922	Abnormal hand morphology	3.553024	0.0019559 95	Human_Ontology	8	<i>NEK9;PIGO;HERC1;PSMD12;LMNB2;BCR;SIN3A;PI4KA</i>
HP:0000137	Abnormality of the ovary	3.933705	0.0021090 84	Human_Ontology	7	<i>AIRE;PROKR2;PRLR;PTPN11;MSH6;SPIDR;BAZ1B</i>
GO:0002562	Somatic diversification of immune receptors via germline recombination within a single locus	7.342917	0.0021495 83	Biological_Process	4	<i>TCF7;TP53BP1;TGFB1;MSH6</i>
GO:0016444	Somatic cell DNA recombination	7.342917	0.0021495 83	Biological_Process	4	<i>TCF7;TP53BP1;TGFB1;MSH6</i>
HP:0011729	Abnormality of joint mobility	2.169691	0.0022061 23	Human_Ontology	17	<i>PRG4;NEK9;COL5A2;HERC1;PROKR2;TRIP4;BCR;VCP; SIN3A;TGFB1;ORC6;PTPN11;MSH6;DAG1;EXOSC8;BAZ 1B;PI4KA</i>
HP:0005558	Chronic leukemia	27.53594	0.0022128 13	Human_Ontology	2	<i>MPL;BCR</i>
GO:0060312	Regulation of blood vessel remodeling	27.53594	0.0022128 13	Biological_Process	2	<i>BCR;TGFB1</i>
GO:1904468	Negative regulation of tumor necrosis factor secretion	27.53594	0.0022128 13	Biological_Process	2	<i>ZC3H12A;GHSR</i>
GO:0035418	Protein localization to synapse	7.222541	0.0022843 77	Biological_Process	4	<i>VPS35;GHSR;BSN;DAG1</i>
HP:0040068	Abnormality of limb bone	2.002614	0.0023323 68	Human_Ontology	20	<i>PRG4;NEK9;COL5A2;PIGO;HERC1;PSMD12;RPGRIPI; LMNB2;BCR;VCP;SIN3A;TGFB1;SMARCAL1;ORC6;PRM T7;PTPN11;DAG1;SPIDR;BAZ1B;PI4KA</i>
HP:0040064	Abnormality of limbs	1.822365	0.0024134 79	Human_Ontology	25	<i>PRG4;NEK9;COL5A2;PIGO;ZFYVE27;HERC1;PSMD12; PROKR2;RPGRIPI;LMNB2;DDHD1;TRIP4;BCR;VCP;SI N3A;TGFB1;SMARCAL1;ORC6;PRMT7;PTPN11;DAG1;S PIDR;BAZ1B;PI4KA;ADSSL1</i>

HP:0012379	Abnormal enzyme/coenzyme activity	5.24494	0.0026979 99	Human_Ontology	5	<i>PIGO;BCR;VCP;TGFB1;DAG1</i>
GO:0033554	Cellular response to stress	1.710856	0.0027292 26	Biological_Process	29	<i>TEX12;CHD6;ZC3H12A;PIDD1;USP3;PAK5;NEIL1;AATF;TP53BP1;MPL;VCP;SIN3A;SMARCAL1;ICAM1;PTPN11;DTNBP1;MSH6;RELL1;GSK3B;OTUB1;FADS1;GAS2L1;DAG1;WDR70;MLST8;CIB1;SPIDR;UBQLN1;BAZ1B</i>
GO:0006506	GPI anchor biosynthetic process	10.65907	0.0027393 93	Biological_Process	3	<i>PIGO;PIGC;MPPE1</i>
GO:0006974	Cellular response to DNA damage stimulus	2.186476	0.0027545 46	Biological_Process	16	<i>TEX12;ZC3H12A;PIDD1;USP3;NEIL1;AATF;TP53BP1;VCP;SMARCAL1;PTPN11;MSH6;OTUB1;WDR70;CIB1;SPIDR;BAZ1B</i>
GO:0098696	Regulation of neurotransmitter receptor localization to postsynaptic specialization membrane	24.47639	0.0028281 11	Biological_Process	2	<i>GHSR;DAG1</i>
GO:0033689	Negative regulation of osteoblast proliferation	24.47639	0.0028281 11	Biological_Process	2	<i>PLXNB1;ATRAID</i>
GO:1990314	Cellular response to insulin-like growth factor stimulus	24.47639	0.0028281 11	Biological_Process	2	<i>GHSR;TGFB1</i>
