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Supplementary Materials for

Genome-wide signatures of complex introgression and adaptive evolution in the big cats

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The PDF file includes:

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Other Supplementary Material for this manuscript includes the following:
(available at advances.sciencemag.org/cgi/content/full/3/7/e1700299/DC1)

- table S12 (Microsoft Excel format). Branch-site results for the tiger.
- table S13 (Microsoft Excel format). Site model results.
- table S19 (Microsoft Excel format). Annotation of nuclear insertions of mitochondrial DNA (NUMTS) in the jaguar genome.
- table S22 (Microsoft Excel format). Outlier window test results.
- table S23 (Microsoft Excel format). Outlier Window KEGG enrichment results.
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- table S30 (Microsoft Excel format). Tiger Pathway Commons enrichment results.
- table S31 (Microsoft Excel format). Tiger KEGG enrichment results.
- table S32 (Microsoft Excel format). Tiger Disease enrichment results.
- table S33 (Microsoft Excel format). Site model Pathway Commons enrichment results.
- table S34 (Microsoft Excel format). Site model KEGG enrichment results.
- table S35 (Microsoft Excel format). Site model Disease enrichment results.
- table S36 (Microsoft Excel format). Site model Biological Process enrichment results.
- table S37 (Microsoft Excel format). Site model Molecular Function enrichment results.

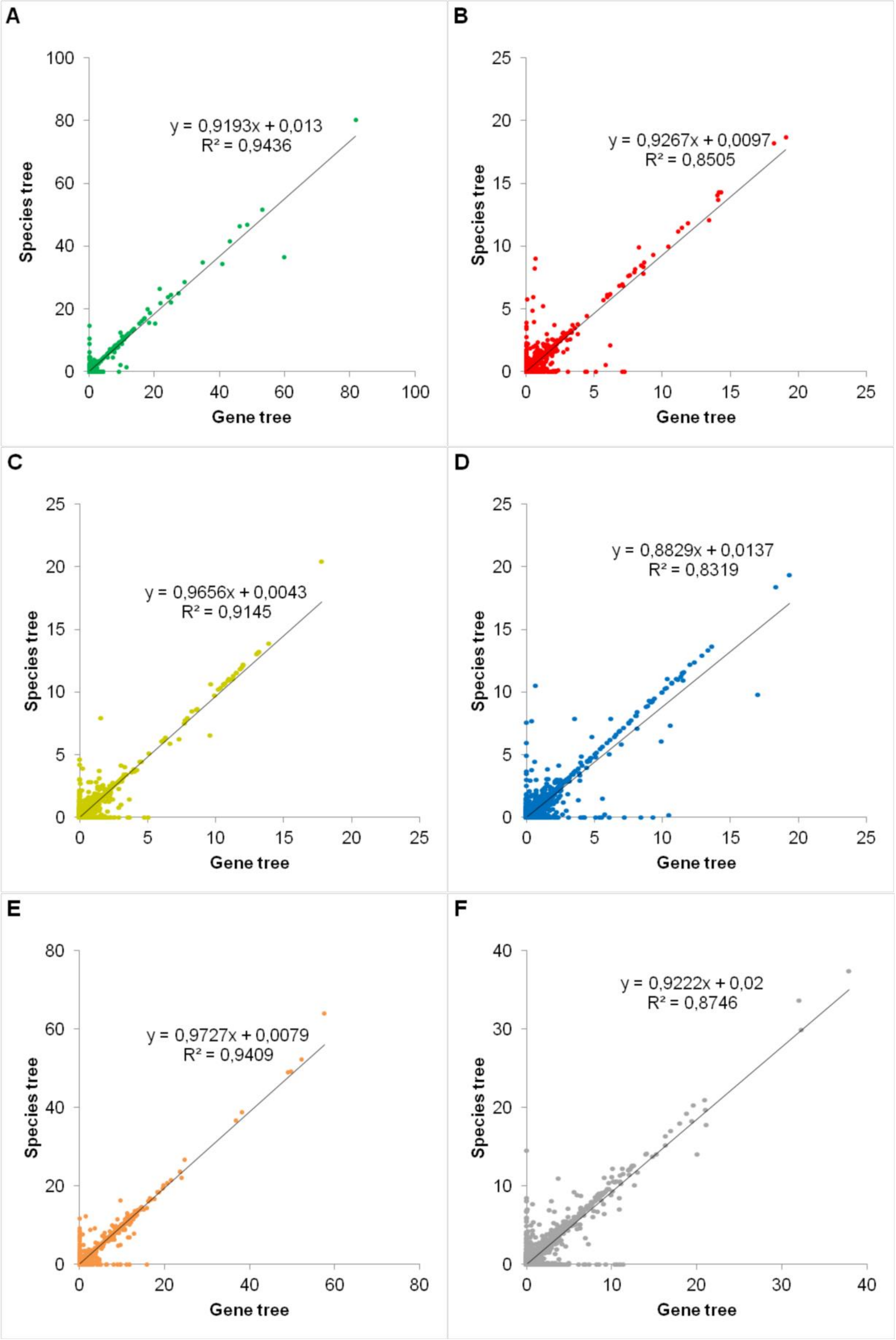

fig. S1. Assessment of the effect of genealogical discordance on branch-site tests of positive selection. Graphs depict the correlation between the calculated values (2*delta) for the branch-site likelihood ratio tests (LRTs) performed with the species tree and the equivalent values estimated with the gene tree (reconstructed for each locus – see Methods for details). (**A**) jaguar; (**B**) lion; (**C**) leopard; (**D**) snow leopard; (**E**) tiger; (**F**) domestic cat *vs. Panthera*.

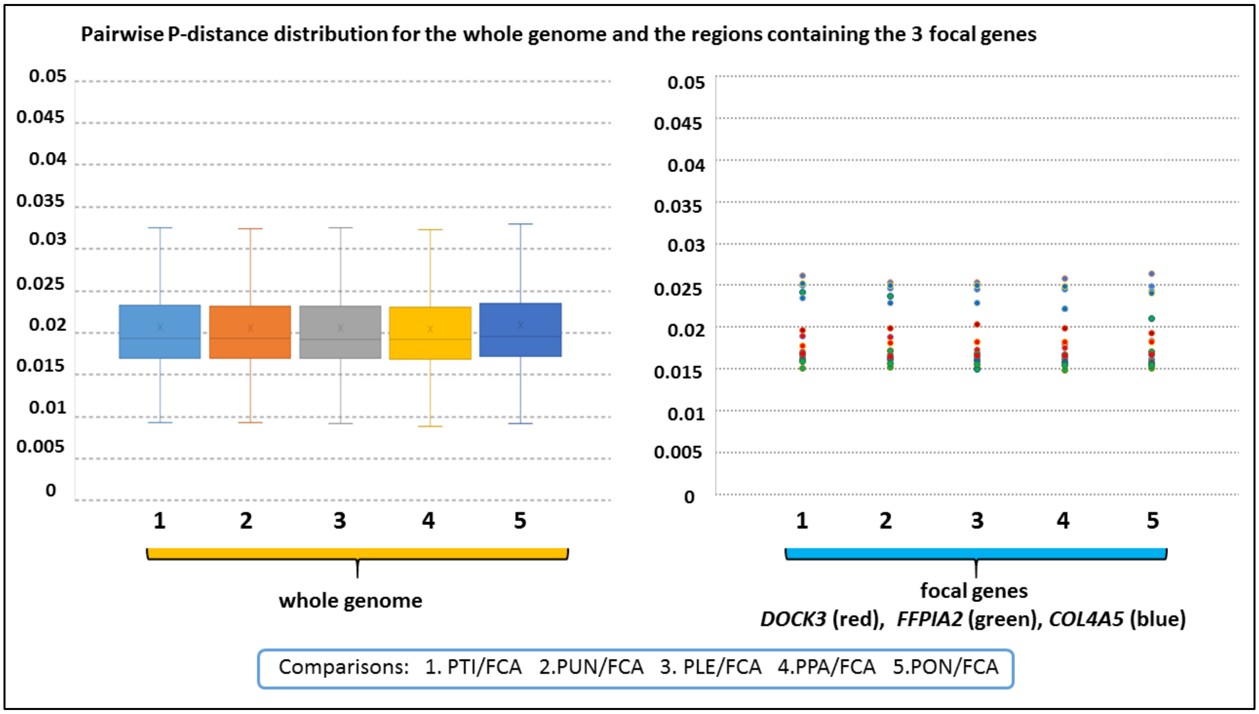

fig. S2. Assessment of divergence between domestic cat and *Panthera* species in windows containing genes with signatures of interspecies introgression and positive selection. The genome wide p-distance (estimated in non-overlapping 100 kb windows) between each *Panthera* species and the domestic cat is shown in the left panel: boxes range from the upper bound of quartile 1 (Q1) to the upper bound of quartile 3 (Q3); the line inside each box is the median; whisker lines represent the full range of the data). The right panel shows p-distances for the same taxon comparisons, with each dot representing a single non-overlapping 100 kb window containing one of the three focal genes [*DOCK3* (red), *PPFIA2* (green) and *COL4A5* (blue)].

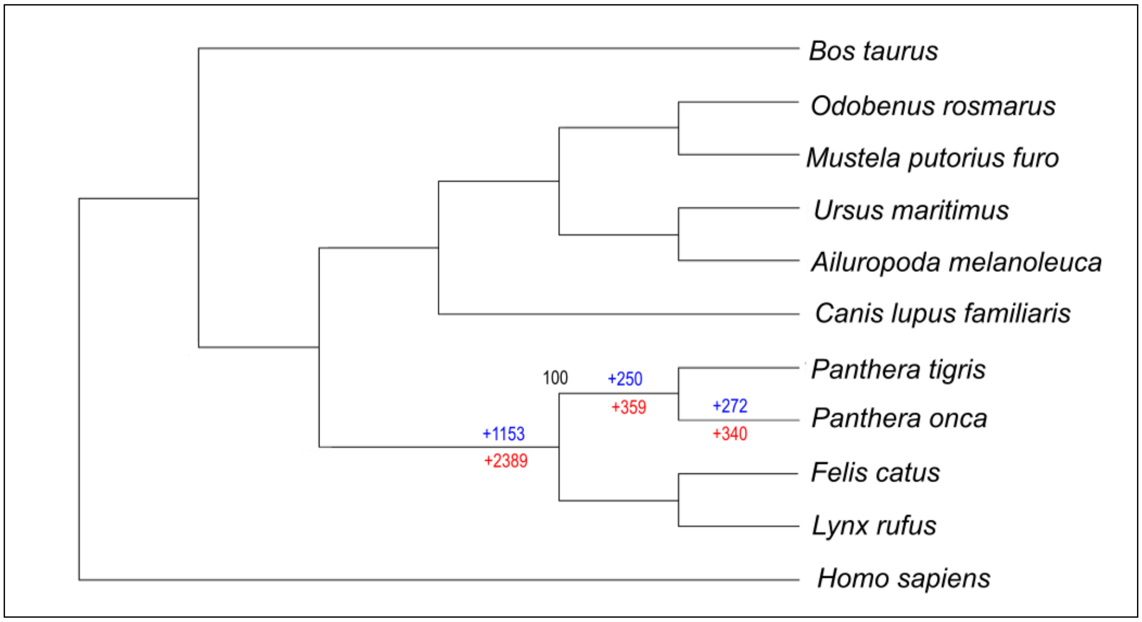

fig. S3. Maximum-likelihood phylogeny constructed with a supermatrix consisting of 2151 concatenated single-copy orthologs for 11 mammals, derived from our phylome analysis. All nodes were supported by 100% bootstrap values. For three felid branches (leading to the base of Felidae, the base of *Panthera*, and the jaguar lineage), values above branches (in blue) indicate the number of identified duplication events, and values below branches (in red) indicate the resulting number of novel genes.

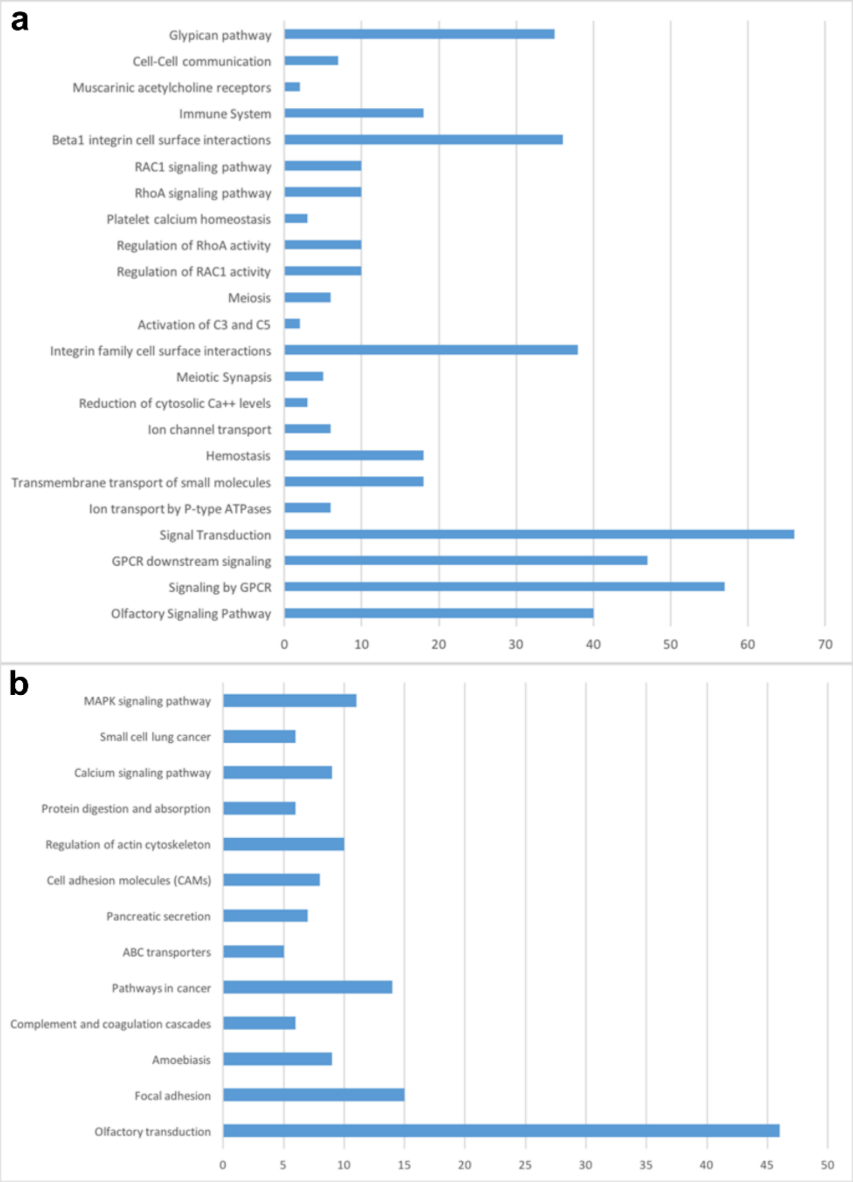

fig. S4. Enrichment analysis for the site model test. (**a**) Results against the Pathway Commons database; (**b**) Results against the KEGG database.

table S1. DNA sequencing information for the reference jaguar individual. Sequenced libraries with number of reads, insert size, sequence length and GC content information.

Species	Number of reads	Direction	Insert Size	Seq Length	% GC
Jaguar	908,465,441	R1	180bp	101	44
Jaguar	908,465,441	R2	180bp	101	41
Jaguar	211,010,191	R1	3kb	101	41
Jaguar	211,010,191	R2	3kb	101	41
Jaguar	183,752,503	R1	8kb	101	40
Jaguar	183,752,503	R2	8kb	101	40
Total	2,606,456,270				

table S2. Jaguar genome assembly quality metrics.

Metric	Contigs	Scaffolds
CEGMA partial	86.29%	93.15%
CEGMA full	49.60%	56.05%
#contigs	158329	7521
#contigs >1kb	156436	7442
Total length	2,284,631,488	2,405,344,986
Total length >1kb	2,282,949,125	2,405,268,288
Largest contig	338,209	8,985,697
GC (%)	41.51	41.51%
N50	28.53 kb	1.52 Mb
L50	23,26	474
%gaps	0%	5%

table S3. Annotated protein-coding genes.

Feature	Number
Base pairs	32,384,308
N50	1,827
Longest gene	26,310
Median gene size	927
% genes > 100 b	99.56%
% genes > 200 b	97.27%
% genes > 500 b	73.65%
% genes > 1 kb	46.56%

table S4. Summary of the jaguar transcriptome sequencing results. Sequenced tissues used for the transcriptome analysis and annotation. Number of reads, insert size, sequence length and GC content for each library.

Tissue	Library ID	Direction	Number of Reads	Insert Size	Seq Length	% GC
Gum	Gum_1_R1	R1	26672756	180bp	101	49
Gum	Gum_1_R2	R2	26672756	180bp	101	49
Tongue	Tongue_1_R1	R1	20298080	180bp	101	50
Tongue	Tongue_1_R2	R2	20298080	180bp	101	50
Testicle	Testicle_1_R1	R1	26912880	180bp	101	50
Testicle	Testicle_1_R2	R2	26912880	180bp	101	50
Skin	Skin1_R1	R1	24363734	180bp	101	49
Skin	Skin_1_R2	R2	24363734	180bp	101	49
Skin	Skin_2_R1	R1	1473959	180bp	50	52
Skin	Skin_3_R1	R1	4000000	180bp	50	51
Skin	Skin_4_R1	R1	899518	180bp	50	51
Skin	Skin_5_R1	R1	4000000	180bp	50	52
Skin	Skin_6_R1	R1	1942875	180bp	50	52
Skin	Skin_7_R1	R1	2422274	180bp	50	51
Blood	Blood_1_R1	R1	4000000	180bp	50	52
Blood	Blood_2_R1	R1	1805834	180bp	50	52
Muscle	Muscle_1_R1	R1	1807474	180bp	50	51

table S5. DNA sequencing information for the leopard genome. Sequenced libraries with number of reads, direction, insert size, sequenced length and GC content information.

Species	Number of reads	Direction	Insert Size	Seq Length	% GC
Leopard	94016735	R1	180bp	20-125	41
Leopard	94016735	R2	180bp	20-125	41
Total	188033470				

table S6. Tree topology frequencies in window- and gene-based analyses.

Tree	Topology	% Windows	% Windows post-AU	% Genes	% Genes post-AU
1	(FCA,(((PLE,PPA),PON),(PTI,PUN)));	63.362	81.992	23.390	57.421
2	(FCA,(((PLE,PON),PPA),(PTI,PUN)));	10.706	5.345	3.893	1.549
3	(FCA,((PLE,(PON,PPA)),(PTI,PUN)));	5.553	2.705	2.861	1.028
4	(FCA,((((PLE,PPA),PON),PTI),PUN));	3.642	1.171	3.080	0.954
5	(FCA,((((PLE,PPA),PON),PUN),PTI));	2.93	0.895	15.904	11.905
6	(FCA,((PLE,PPA),(PON,(PTI,PUN))));	2.697	0.684	2.633	0.683
7	(FCA,((((PLE,PON),PPA),PTI),PUN));	1.103	0.754	0.989	0.235
8	(FCA,((((PLE,PON),PPA),PUN),PTI));	0.975	0.627	3.876	2.628
9	(FCA,(((PLE,PPA),(PTI,PUN)),PON));	0.949	0.232	1.996	0.470
10	(FCA,((PLE,PON),(PPA,(PTI,PUN))));	0.707	0.557	0.641	0.286
11	(FCA,(((PLE,(PON,PPA)),PTI),PUN));	0.663	0.43	0.761	0.242
12	(FCA,(((PLE,PON),(PTI,PUN)),PPA));	0.633	0.526	0.619	0.294
13	(FCA,(((PLE,PPA),(PON,PTI)),PUN));	0.633	0.329	2.930	1.901
14	(FCA,(((PLE,(PON,PPA)),PUN),PTI));	0.58	0.346	2.629	1.813
15	(FCA,((PLE,(PTI,PUN)),(PON,PPA)));	0.422	0.364	0.5377501	0.234879624
16	(FCA,(PUN,(PTI,PON)),(PLE,PPA));	0.409	0.241	0	0
17	(FCA,(PTI,PON),(PUN,(PLE,PPA)));	0.404	0.197	0	0
18	(FCA,((PTI,(PLE,PPA)),(PON,PUN)));	0.343	0.219	0	0
19	(FCA,(((PLE,PPA),(PON,PUN)),PTI));	0.259	0.153	1.1056141	0.616559014
20	(FCA,(PTI,PPA),(PUN,(PON,PLE)));	0.246	0.193	0	0
21	(FCA,(PLE,((PON,PPA),(PTI,PUN))));	0.22	0.145	0.460314	0.146799765
22	(FCA,((PLE,PPA),((PON,PUN),PTI)));	0.202	0.132	0.555	0.176
23	(FCA,((((PLE,PON),PUN),PTI),PPA));	0.171	0.158	0.185	0.081
24	(FCA,((((PLE,PPA),PTI),PON),PUN));	0.136	0.088	0.314	0.081
25	(FCA,((((PLE,PON),PUN),PPA),PTI));	0.132	0.123	0.452	0.374
26	(FCA,((((PLE,PPA),PUN),PON),PTI));	0.114	0.057	4.427	3.743
27	(FCA,(((PLE,PON),(PPA,PTI)),PUN));	0.114	0.088	0.172	0.044
28	(FCA,(((PLE,PON),PTI),(PPA,PUN)));	0.114	0.101	0.202	0.059
29	(FCA,((((PLE,PON),PTI),PPA),PUN));	0.083	0.07	0.228	0.044
30	(FCA,((PLE,PUN),((PON,PPA),PTI)));	0.079	0.053	0.215	0.132
31	(FCA,((((PLE,PPA),PTI),PUN),PON));	0.075	0.048	0.396	0.095
32	(FCA,((PLE,((PON,PTI),PPA)),PUN));	0.075	0.053	0.275	0.132
33	(FCA,((((PLE,PPA),PUN),PTI),PON));	0.066	0.044	0.912	0.382
34	(FCA,(((PLE,PUN),(PON,PPA)),PTI));	0.066	0.048	0.559	0.308
35	(FCA,((PLE,(PON,(PTI,PUN))),PPA));	0.062	0.031	0.224	0.066
36	(FCA,((((PLE,PON),PTI),PUN),PPA));	0.057	0.057	0.155	0.051
37	(FCA,((PLE,((PON,PPA),PTI)),PUN));	0.053	0.035	0.159	0.044
38	(FCA,(((PLE,PON),(PPA,PUN)),PTI));	0.048	0.048	0.581	0.286
39	(FCA,(((PLE,PTI),(PON,PPA)),PUN));	0.048	0.044	0.181	0.044
40	(FCA,(((PLE,PUN),PTI),(PON,PPA)));	0.035	0.031	0.237	0.103
41	(FCA,((PLE,PON),((PPA,PUN),PTI)));	0.035	0.031	0.267	0.073
42	(FCA,((PLE,PUN),((PON,PTI),PPA)));	0.035	0.026	0.262	0.125
43	(FCA,((PLE,((PON,PPA),PUN)),PTI));	0.031	0.022	0.297	0.139
44	(FCA,((PLE,PUN),(PON,(PPA,PTI))));	0.031	0.022	0.039	0.007

45	(FCA,(PLE,(((PON,PPA),PTI),PUN)));	0.026	0.018	0.108	0.015
46	(FCA,(PLE,(((PON,PPA),PUN),PTI)));	0.026	0.018	0.103	0.007
47	(FCA,((((PLE,PUN),PON),PPA),PTI));	0.022	0.013	0.172	0.066
48	(FCA,(((PLE,(PON,PTI)),PPA),PUN));	0.022	0.018	0.361	0.125
49	(FCA,(((PLE,(PTI,PUN)),PON),PPA));	0.022	0.009	0.198	0.044
50	(FCA,(((PLE,PTI),PPA),(PON,PUN)));	0.022	0.013	0.056	0.007
51	(FCA,((PLE,(PON,(PPA,PTI))),PUN));	0.022	0.009	0.116	0.022
52	(FCA,(PLE,((PON,(PTI,PUN)),PPA)));	0.022	0.004	0.267	0.037
53	(FCA,((((PLE,PUN),PPA),PON),PTI));	0.018	0.013	0.503	0.257
54	(FCA,(PLE,(PON,(PPA,(PTI,PUN)))));	0.018	0.009	0.142	0.022
55	(FCA,((((PLE,PUN),PON),PTI),PPA));	0.013	0.013	0.065	0.015
56	(FCA,(((PLE,(PPA,PTI)),PON),PUN));	0.013	0.009	0.090	0.015
57	(FCA,(((PLE,PUN),PON),(PPA,PTI)));	0.013	0.009	0.026	0.015
58	(FCA,(((PLE,PUN),PPA),(PON,PTI)));	0.013	0.013	0.533	0.330
59	(FCA,((PLE,((PON,PTI),PUN)),PPA));	0.013	0.009	0.323	0.110
60	(FCA,((PLE,((PON,PUN),PPA)),PTI));	0.013	0.009	0.211	0.051
61	(FCA,((PLE,(PON,PUN)),(PPA,PTI)));	0.013	0.013	0.043	0.015
62	(FCA,((PLE,(PPA,(PTI,PUN))),PON));	0.013	0.004	0.361	0.059
63	(FCA,((PLE,(PPA,PUN)),(PON,PTI)));	0.013	0.013	0.546	0.272
64	(FCA,((PLE,PTI),((PON,PUN),PPA)));	0.013	0.004	0.034	0.015
65	(FCA,(PLE,(((PON,PTI),PPA),PUN)));	0.013	0.013	0.120	0.037
66	(FCA,((((PLE,PTI),PPA),PUN),PON));	0.009	0.004	0.099	0.015
67	(FCA,((((PLE,PTI),PUN),PON),PPA));	0.009	0.009	0.043	0.015
68	(FCA,((((PLE,PUN),PTI),PON),PPA));	0.009	0.004	0.090	0.015
69	(FCA,(((PLE,(PON,PUN)),PPA),PTI));	0.009	0	0.202	0.037
70	(FCA,(((PLE,(PPA,PUN)),PON),PTI));	0.009	0.009	0.602	0.286
71	(FCA,(((PLE,PUN),(PON,PTI)),PPA));	0.009	0.009	0.211	0.110
72	(FCA,(((PLE,PUN),(PPA,PTI)),PON));	0.009	0.004	0.099	0.007
73	(FCA,((PLE,(PON,(PPA,PUN))),PTI));	0.009	0.009	0.189	0.066
74	(FCA,((PLE,(PON,PTI)),(PPA,PUN)));	0.009	0.009	0.189	0.103
75	(FCA,(PLE,(((PON,PTI),PUN),PPA)));	0.009	0	0.301	0.088
76	(FCA,((((PLE,PUN),PPA),PTI),PON));	0.004	0.004	0.163	0.044
77	(FCA,((((PLE,PUN),PTI),PPA),PON));	0.004	0.004	0.133	0.015
78	(FCA,(((PLE,(PON,PTI)),PUN),PPA));	0.004	0	0.176	0.081
79	(FCA,(((PLE,(PON,PUN)),PTI),PPA));	0.004	0.004	0.073	0.007
80	(FCA,(((PLE,(PPA,PTI)),PUN),PON));	0.004	0.004	0.116	0.022
81	(FCA,(((PLE,PTI),PON),(PPA,PUN)));	0.004	0.004	0.047	0.022
82	(FCA,((PLE,PTI),(PON,(PPA,PUN))));	0.004	0.004	0.047	0.015
83	(FCA,(PLE,(((PON,PUN),PPA),PTI)));	0.004	0.004	0.039	0.007
84	(FCA,(PLE,(((PON,PUN),PTI),PPA)));	0.004	0.004	0.116	0.022
85	(FCA,(PLE,((PON,(PPA,PTI)),PUN)));	0.004	0.004	0.069	0.015
86	(FCA,(PLE,((PON,PTI),(PPA,PUN))));	0.004	0.004	0.198	0.059
87	(FCA,(PLE,((PON,PUN),(PPA,PTI))));	0.004	0	0.069	0.015

table S7. Tree topology frequencies for 3732 genes and their introns. The frequency of each observed topology (numbered as in table S6) is shown for a data set in which each gene is represented solely by its introns (i.e. CDs excluded), as well as for the full data set (Genes) comprising introns+exons.

Tree	Topology	% Introns	% Introns post-AU	% Genes	% Genes post-AU
1	(FCA,(((PLE,PPA),PON),(PTI,PUN)))	33.69	99.57	33.69	99.57
2	(FCA,(((PLE,PON),PPA),(PTI,PUN)))	2.78	0	2.78	0
3	(FCA,((PLE,(PON,PPA)),(PTI,PUN)))	2.18	0	2.18	0
4	(FCA,((((PLE,PPA),PON),PTI),PUN))	2.64	0.09	2.64	0.09
5	(FCA,((((PLE,PPA),PON),PUN),PTI))	22.36	0.17	22.36	0.17
6	(FCA,((PLE,PPA),(PON,(PTI,PUN))))	2.26	0.03	2.26	0.03
7	(FCA,((((PLE,PON),PPA),PTI),PUN))	0.37	0	0.37	0
8	(FCA,((((PLE,PON),PPA),PUN),PTI))	3.1	0	3.1	0
9	(FCA,(((PLE,PPA),(PTI,PUN)),PON))	1.12	0.06	1.12	0.06
10	(FCA,((PLE,PON),(PPA,(PTI,PUN))))	0.43	0	0.43	0
11	(FCA,(((PLE,(PON,PPA)),PTI),PUN))	0.17	0	0.17	0
12	(FCA,(((PLE,PON),(PTI,PUN)),PPA))	0.14	0	0.14	0
13	(FCA,(((PLE,PPA),(PON,PTI)),PUN))	2.58	0	2.58	0
14	(FCA,(((PLE,(PON,PPA)),PUN),PTI))	2.21	0	2.21	0
15	(FCA,((PLE,(PTI,PUN)),(PON,PPA)))	0.32	0	0.32	0
19	(FCA,(((PLE,PPA),(PON,PUN)),PTI))	1.06	0	1.06	0
21	(FCA,(PLE,((PON,PPA),(PTI,PUN))))	0.23	0	0.23	0
22	(FCA,((PLE,PPA),((PON,PUN),PTI)))	0.2	0	0.2	0
23	(FCA,((((PLE,PON),PUN),PTI),PPA))	0.03	0	0.03	0
24	(FCA,((((PLE,PPA),PTI),PON),PUN))	0.17	0	0.17	0
25	(FCA,((((PLE,PON),PUN),PPA),PTI))	0.37	0	0.37	0
26	(FCA,((((PLE,PPA),PUN),PON),PTI))	4.56	0	4.56	0
27	(FCA,(((PLE,PON),(PPA,PTI)),PUN))	0.03	0	0.03	0
28	(FCA,(((PLE,PON),PTI),(PPA,PUN)))	0.06	0	0.06	0
29	(FCA,((((PLE,PON),PTI),PPA),PUN))	0.03	0	0.03	0
30	(FCA,((PLE,PUN),((PON,PPA),PTI)))	0.2	0	0.2	0
31	(FCA,((((PLE,PPA),PTI),PUN),PON))	0.14	0	0.14	0
32	(FCA,((PLE,((PON,PTI),PPA)),PUN))	0.11	0	0.11	0
33	(FCA,((((PLE,PPA),PUN),PTI),PON))	0.69	0	0.69	0
34	(FCA,(((PLE,PUN),(PON,PPA)),PTI))	0.32	0	0.32	0
35	(FCA,((PLE,(PON,(PTI,PUN))),PPA))	0.17	0	0.17	0
36	(FCA,((((PLE,PON),PTI),PUN),PPA))	0.09	0	0.09	0
38	(FCA,(((PLE,PON),(PPA,PUN)),PTI))	0.37	0	0.37	0
39	(FCA,(((PLE,PTI),(PON,PPA)),PUN))	0.09	0	0.09	0
40	(FCA,(((PLE,PUN),PTI),(PON,PPA)))	0.11	0	0.11	0
41	(FCA,((PLE,PON),((PPA,PUN),PTI)))	0.06	0	0.06	0
42	(FCA,((PLE,PUN),((PON,PTI),PPA)))	0.14	0	0.14	0
43	(FCA,((PLE,((PON,PPA),PUN)),PTI))	0.2	0	0.2	0
45	(FCA,(PLE,(((PON,PPA),PTI),PUN)))	0.03	0	0.03	0
47	(FCA,((((PLE,PUN),PON),PPA),PTI))	0.09	0	0.09	0
48	(FCA,(((PLE,(PON,PTI)),PPA),PUN))	0.11	0	0.11	0
49	(FCA,(((PLE,(PTI,PUN)),PON),PPA))	0.17	0	0.17	0
50	(FCA,(((PLE,PTI),PPA),(PON,PUN)))	0.03	0	0.03	0
52	(FCA,(PLE,((PON,(PTI,PUN)),PPA)))	0.2	0	0.2	0
53	(FCA,((((PLE,PUN),PPA),PON),PTI))	0.37	0	0.37	0
58	(FCA,(((PLE,PUN),PPA),(PON,PTI)))	0.37	0	0.37	0
59	(FCA,((PLE,((PON,PTI),PUN)),PPA))	0.23	0	0.23	0
60	(FCA,((PLE,((PON,PUN),PPA)),PTI))	0.03	0	0.03	0

62	(FCA,((PLE,(PPA,(PTI,PUN))),PON))	0.09	0.03	0.09	0.03
63	(FCA,((PLE,(PPA,PUN)),(PON,PTI)))	0.29	0	0.29	0
65	(FCA,(PLE,(((PON,PTI),PPA),PUN)))	0.03	0	0.03	0
66	(FCA,((((PLE,PTI),PPA),PUN),PON))	0.03	0	0.03	0
69	(FCA,(((PLE,(PON,PUN)),PPA),PTI))	0.03	0	0.03	0
70	(FCA,(((PLE,(PPA,PUN)),PON),PTI))	0.23	0	0.23	0
71	(FCA,(((PLE,PUN),(PON,PTI)),PPA))	0.09	0	0.09	0
73	(FCA,((PLE,(PON,(PPA,PUN))),PTI))	0.11	0	0.11	0
74	(FCA,((PLE,(PON,PTI)),(PPA,PUN)))	0.11	0	0.11	0
75	(FCA,(PLE,(((PON,PTI),PUN),PPA)))	0.11	0	0.11	0
76	(FCA,((((PLE,PUN),PPA),PTI),PON))	0.06	0	0.06	0
78	(FCA,(((PLE,(PON,PTI)),PUN),PPA))	0.09	0	0.09	0
80	(FCA,(((PLE,(PPA,PTI)),PUN),PON))	0.03	0	0.03	0
86	(FCA,(PLE,((PON,PTI),(PPA,PUN))))	0.03	0	0.03	0

table S8. Detailed results of the ABBA/BABA tests.

P1	**P2**	**P3**	**nABBA**	**nBABA**	***D***	**jackEst**	**s.e.**	***Z***	**p-value**
Lion	Jaguar	Snow leopard	1,219,639	1,921,731	-0.22	-0.22	0.0043	-52.5	0
Leopard	Jaguar	Snow leopard	1,334,215	1,921,658	-0.18	-0.18	0.0042	-43.3	0
Leopard	lion	Snow leopard	1,079,821	963,890	0.06	0.06	0.0034	16.7	1.31E-62
Lion	Jaguar	Tiger	1,328,409	1,887,613	-0.17	-0.17	0.0055	-31.6	3.69E-219
Leopard	Jaguar	Tiger	1,430,119	1,887,678	-0.14	-0.14	0.0051	-27.2	6.49E-163
Leopard	Lion	Tiger	1,077,955	978,765	0.05	0.05	0.0037	13.1	3.29E-39
Tiger	Snow leopard	Jaguar	1,165,436	1,483,318	-0.12	-0.12	0.0040	-30.0	9.81E-198
Tiger	Snow leopard	Leopard	1,235,405	1,433,574	-0.07	-0.07	0.0028	-26.8	3.23E-158
Tiger	Snow leopard	Lion	1,250,134	1,434,106	-0.07	-0.07	0.0026	-26.0	4.95E-149
Leopard	Lion	Jaguar	1,311,090	1,169,855	0.06	0.06	0.0048	11.8	3.90E-32

table S9. Branch-site results for the jaguar. Candidate genes under positive selection, p-values for the gene tree and species tree analysis (significance threshold: alpha<0.05) and gene description. Genes are ordered based on the p-values for the gene tree dataset.

Gene	P-value		Description
	Gene tree	Species tree	
LOC102957369	3.22E-13	6.78E-13	Uncharacterized protein c1orf167-like
LOC102957355	3.52E-12	7.62E-12	Olfactory receptor 3A1-like
LOC102952669	1.05E-11	1.05E-11	Repetin-like
LOC102968863	3.52E-09	3.52E-09	60S ribosomal protein L35-like
SLC8A3	4.12E-09	4.12E-09	Sodium/calcium exchanger 3 isoform X1
SSTR4	6.59E-08	8.89E-08	Somatostatin receptor type 4
LOC102971194	1.65E-07	5.95E-07	Zinc finger protein 135-like
ESRP1	5.31E-07	7.16E-07	Epithelial splicing regulatory protein 1 isoform X1
LOC102950007	5.41E-07	2.49E-06	Protein FAM47A-like
ZFP3	2.98E-06	2.98E-06	Zinc finger protein 3 homolog
LOC102956118	3.29E-06	2.92E-07	Mucin-16-like
LOC102955222	7.04E-06	8.59E-05	Uncharacterized protein LOC102955222 isoform X1
CNTNAP1	1.59E-05	1.47E-05	Contactin-associated protein 1
LOC102948925	1.79E-05	7.68E-05	Olfactory receptor 10H1-like
LOC102948654	2.38E-05	8.36E-06	KH domain-containing protein 3-like
AKAP13	3.64E-05	3.64E-05	A-kinase anchor protein 13-like
ABTB2	4.37E-05	4.37E-05	Ankyrin repeat and BTB/POZ domain-containing protein 2
TPM3	8.75E-05	8.75E-05	Tropomyosin alpha-3 chain isoform X6
PPP1R15A	0.0001794	0.000179405	Protein phosphatase 1 regulatory subunit 15A isoform X7
KDM3B	0.0002056	0.000226917	Lysine-specific demethylase 3B
LOC102953722	0.0002392	0.000241142	Uncharacterized protein LOC102953722
GFI1	0.000315	0.000315011	Zinc finger protein Gfi-1
FOXJ2	0.0004935	0.00049352	Forkhead box protein J2
LOC102963291	5.30E-04	5.30E-04	Melanoma-associated antigen B4-like isoform X1
CAPG	6.19E-04	6.19E-04	Macrophage-capping protein isoform X1
BAHD1	6.59E-04	7.22E-04	Bromo adjacent homology domain-containing 1 protein
SLC26A3	0.0006776	0.236785196	Chloride anion exchanger
LOC102964920	0.0007984	0.000798578	Uncharacterized protein LOC102964920
BIRC2	8.06E-04	7.92E-04	Baculoviral IAP repeat-containing protein 2
LOC102956679	0.0008665	0.000866455	Olfactory receptor 2B6-like
LOC102965607	0.0010403	0.001350757	Cyclic AMP-dependent transcription factor ATF-5-like

table S10. Branch-site results for the lion. Candidate genes under positive selection, p-values for the gene tree and species tree analysis (significance threshold: alpha<0.05) and gene description. Genes are ordered based on the p-values for the gene tree data set.

Gene	P-value		Description
	Gene tree	Species tree	
LOC102951325	3.36E-07	0.998871621	Complement C3-like
KRT40	1.26E-05	1.55E-05	Keratin, type I cytoskeletal 40
ART3	1.96E-05	1.00E+00	Ecto-ADP-ribosyltransferase 3 isoform X2
KRT76	2.00E-05	2.00E-05	Keratin, type II cytoskeletal 2 oral isoform X2

table S11. Branch-site results for the snow leopard. Candidate genes under positive selection, p-values for the gene tree and species tree analysis (significance threshold: alpha< 0.05) and gene description. Genes are ordered based on the p-values for the gene tree data set. No statistically significant enrichment was observed in the Gene Ontology analysis.

Gene	P-value		Description
	Gene tree	Species tree	
IKBKG	1.09E-05	1.09E-05	NF-kappa-B essential modulator
LOC102958616	1.83E-05	1.83E-05	Uncharacterized protein LOC102958616
UHRF1	3.65E-05	0.001758798	E3 ubiquitin-protein ligase UHRF1

table S14. Results of coalescent simulations based on jaguar exome data. focusing on the 25 captured genes with significant signatures of interspecies introgression (based on the outlier window test). *DOCK3* and *COL4A5* retained significance after Bonferroni correction for all four demographic/recombination scenarios.

Gene	Length (bp)	No. of SNPs	p-values for different demographic/recombination scenarios			
			No recombination	No recombination with bottleneck	Chromosome recombination	Chromosome recombination with bottleneck
DOCK3	**6088**	**0**	**0.0024**	**0**	**0**	**0**
COL4A5	**5026**	**0**	**0.0144**	**0.0072**	**0.0072**	**0.0096**
PPFIA2	3828	1	0.0648	0.0576	0.0744	0.06
AMER1	3447	0	0.096	0.0792	0.0528	0.0912
COL4A6	5836	2	0.1104	0.0936	0.0984	0.0912
IRS4	3004	0	0.1368	0.144	0.1248	0.12
EXOC2	3223	1	0.156	0.1752	0.1872	0.192
AR	2722	0	0.2136	0.2136	0.2184	1.02
MID2	2430	0	0.3192	0.3744	0.3504	0.372
UBE3A	3350	1	0.5568	0.5832	0.4848	0.4896
NXF2	1849	0	0.9144	0.8904	0.9408	0.9864
PJA1	2660	1	1.3008	1.308	1.164	1.224
DACH2	1558	0	1.4448	1.428	1.44	1.4496
PLP1	1355	0	2.1528	2.052	2.0376	2.1936
CNGA2	2003	1	2.964	3.2016	3.0288	3.0216
SH3BGRL	1041	0	3.5616	3.5568	3.4632	3.4704
ASB12	1469	1	5.7984	5.8224	5.6568	5.9016
HMGN5	675	0	7.1112	6.7656	7.0368	7.0224
RAB9B	1204	1	8.2704	7.944	8.1192	8.28
POU3F4	1201	1	8.3016	8.2848	8.3328	8.1504
MC2R	895	1	8.6568	8.616	8.6904	8.8152
FATE1	1063	1	9.588	9.6168	9.4944	9.2664
SULT1C4	1041	1	10.0104	9.8448	9.8184	10.0224
BEX5	377	5	24	23.9832	23.9928	23.9808

table S15. Summary of repeat annotation for the jaguar genome.

Tool	Repeat type	Contigs	Scaffolds
WindowMasker	Any repeated fragments	31.23%	29.66%
TRF	Tandem repeats	2.10%	2.12%
DUST	Simple sequence	6.50%	11.20%
RepeatMasker	Known repeats	38.63%	37.48%
	SINEs	10.65%	10.40%
	LINEs	19.38%	18.92%
	LTR elements	5.41%	5.11%
	DNA elements	3.01%	2.86%
	Other	0.18%	0.19%

table S16. Tandem repeat annotation for the jaguar genome.

Category	Contigs	Scaffolds
All TRs	854704	856590
Microsatellites	344251	343205
Perfect microsatellites	145457	144563
Complex TRs	3097	3091
Large TRs >1 kbp	590	1685
Large TRs >3 kbp	76	341
Large TRs >10 kbp	2	4

table S17. Forty largest microsatellite families in the jaguar genome.

s	Copy number	Total length (bp)	Imperfect (%)	Perfect (%)
(AG)n	114588	5367594	68.72	31.28
(AC)n	95656	3857060	37.9	62.1
(A)n	27547	1017208	40.77	59.23
(AT)n	18112	1422474	78.57	21.43
(AAAT)n	17070	735046	58.6	41.4
(AAAG)n	14927	1285059	81.18	18.82
(AAGG)n	7867	812581	86.18	13.82
(AAAAC)n	7663	284497	52.72	47.28
(AAAC)n	6572	228002	52.77	47.23
(AAAAT)n	6226	331755	71.86	28.14
(AGAT)n	5991	442948	80.3	19.7
(AAT)n	4971	187591	54.09	45.91
(AATG)n	4706	173181	57.65	42.35
(AAC)n	4445	159310	46.19	53.81
(ATCC)n	3084	411443	83.82	16.18
(C)n	3011	111414	40.42	59.58
(AAAAG)n	2914	226321	86.51	13.49
(AAG)n	2538	174700	60.44	39.56
(ACAT)n	2512	116237	68.39	31.61
(AGG)n	2252	154900	79.97	20.03
(ATC)n	1498	78208	56.81	43.19
(AGGG)n	1385	103320	89.39	10.61
(AAAGG)n	795	80569	82.77	17.23
(ACAG)n	698	26012	84.1	15.9
(AATAT)n	602	38234	80.4	19.6
(AAGGG)n	564	44792	80.14	19.86
(AATT)n	525	16903	38.86	61.14
(AAATT)n	494	22558	61.34	38.66
(AATC)n	486	14553	33.54	66.46
(AGC)n	453	19032	43.05	56.95
(ACC)n	441	24983	51.47	48.53
(AAGAG)n	408	37429	82.35	17.65
(CCG)n	380	14521	70.53	29.47
(AGAGG)n	324	22916	78.4	21.6
(AATAG)n	317	19019	64.67	35.33
(AGGGG)n	315	17641	76.83	23.17
(AACC)n	297	12244	61.62	38.38
(AAATG)n	268	15104	67.54	32.46
(ACTC)n	192	9116	69.79	30.21
(ACCT)n	178	7407	76.97	23.03

table S18. Statistics on noncoding RNA annotation in the jaguar genome.

Type	Subtype	Copy Number	Total length (bp)
miRNA		1,626	130,589
tRNA	All	169,838	4,257,400
	Without repeats	3,299	313,405
rRNA	rRNA	510	94,238
snRNA	snRNA	3454	419,792
	snoRNA	973	106,012
miscRNA		1640	323,969

table S20. Previously reported genomic resources used in our multispecies analyses.

Common name	Scientific Name	Type of Data	Accession Number
Tiger	*Panthera tigris*	High-coverage genome	ATCQ01
Lion	*Panthera leo*	Low-coverage genome (raw reads)	SRX273034
Snow Leopard	*Panthera uncia*	Low-coverage genome (raw reads)	SRX273036
Cat	*Felis catus*	High-coverage genome	AANG03

table S21. Consensus genome information (using the tiger assembly as a reference).

Feature	*Panthera leo*	*Panthera pardus*	*Panthera uncia*
Number of contigs	1,379	1,375	1,379
Number of bases in all contigs	2,390,883,613	2,390,829,645	2,390,861,245
N50	8,860,407	8,860,407	8,860,407
Longest contig	41,607,841	41,607,841	41,607,841
Median contig size	15,815	16,235	16,148
Number of contigs > 100 b	1,376	1,372	1,374
Total of bases into contigs > 100 b	2,390,883,383	2,390,829,405	2,390,860,856
% contigs > 100 b	99	99	99
Number of contigs > 200 b	1,348	1,354	1,351
Total of bases into contigs > 200 b	2,390,878,923	2,390,826,466	2,390,856,977
% contigs > 200 b	97	98	98
Number of contigs > 500 b	1,191	1,187	1,187
Total of bases into contigs > 500 b	2,390,822,375	2,390,766,351	2,390,797,568
% contigs > 500 b	86	86	86
Number of contigs > 1 kb	962	961	962
Total of bases into contigs > 1 kb	2,390,656,905	2,390,603,429	2,390,635,250
% contigs > 1 kb	69	69	69

table S27. Detailed information on the samples used in the exome capture experiment. Sample identification, geographic location, assigned population, collectors and mean depth

Sample ID	Municipality	State	Biome/Region	Collector	Sequencing Depth
bPon-167	Tefé	Amazonas	Amazon	Emiliano Ramalho	5.57
bPon-354	Caseara	Tocantins	Amazon	Leandro Silveira	7.01
bPon-404	Uarini	Amazonas	Amazon	Emiliano Ramalho	9.46
bPon-403	Uarini	Amazonas	Amazon	Emiliano Ramalho	9.56
bPon-402	Uarini	Amazonas	Amazon	Emiliano Ramalho	10.32
bPon-401	Uarini	Amazonas	Amazon	Emiliano Ramalho	10.53
bPon-353	Caseara	Tocantins	Amazon	Leandro Silveira	14.71
bPon-338	Chapadão do Céu	Goiás	Cerrado	Leandro Silveira	9.03
bPon-148	Corumbá	Mato Grosso do Sul	North Pantanal	Fernando Azevedo	8.61
bPon-144	Corumbá	Mato Grosso do Sul	North Pantanal	Fernando Azevedo	8.71
bPon-170	Corumbá	Mato Grosso do Sul	North Pantanal	Fernando Azevedo	10.53
bPon-171	Corumbá	Mato Grosso do Sul	North Pantanal	Fernando Azevedo	12.67
bPon-465	Cáceres	Mato Grosso	North Pantanal	Daniel Kantek	13.48
bPon-428	Cáceres	Mato Grosso	North Pantanal	Daniel Kantek	13.86
bPon-412	Cáceres	Mato Grosso	North Pantanal	Daniel Kantek	15.84
bPon-463	Cáceres	Mato Grosso	North Pantanal	Daniel Kantek	16.09
bPon-423	Cáceres	Mato Grosso	North Pantanal	Daniel Kantek	17.9
bPon-076	Miranda	Mato Grosso do Sul	South Pantanal	Fernando Azevedo	4.6
bPon-069	Miranda	Mato Grosso do Sul	South Pantanal	Fernando Azevedo	4.61
bPon-068	Miranda	Mato Grosso do Sul	South Pantanal	Fernando Azevedo	5.91
bPon-340	Miranda	Mato Grosso do Sul	South Pantanal	Leandro Silveira	8.32
bPon-163	Miranda	Mato Grosso do Sul	South Pantanal	Leandro Silveira	9.25
bPon-333	Miranda	Mato Grosso do Sul	South Pantanal	Leandro Silveira	9.74
bPon-339	Miranda	Mato Grosso do Sul	South Pantanal	Leandro Silveira	9.77
bPon-343	Miranda	Mato Grosso do Sul	South Pantanal	Leandro Silveira	9.89
bPon-074	Miranda	Mato Grosso do Sul	South Pantanal	Fernando Azevedo	10.64
bPon-350	Miranda	Mato Grosso do Sul	South Pantanal	Leandro Silveira	10.93
bPon-344	Miranda	Mato Grosso do Sul	South Pantanal	Leandro Silveira	11.02
bPon-071	Miranda	Mato Grosso do Sul	South Pantanal	Fernando Azevedo	12.73
bPon-342	Miranda	Mato Grosso do Sul	South Pantanal	Leandro Silveira	13.19

table S28. Enrichment results for the jaguar branch-site test. Analysis refers to the analysis performed in WebGestalt with a significance threshold of alpha<0.05 and a correction for multiple comparisons. Characteristic refers to the enriched category found. Parameters describes enrichment details. C (Genes presented in the category); O (Genes observed in the dataset); R (Ratio of enrichment); rawP (p-value for the hypergeometric test); adjP (adjusted P value by the multiple correction test).

Database	**Category**	**Parameters**	**Genes**
Disease	Hyperpituitarism	C=26;O=2;E=0.01;R=174.60;rawP=5.94e-05;adjP=7.92e-05	*SSTR4; ESRP1*
	Adenoma	C=157;O=3;E=0.07;R=43.37;rawP=4.39e-05;adjP=7.92e-05	*SLC26A3; SSTR4; ESRP1*
	Acromegaly	C=20;O=2;E=0.01;R=226.98;rawP=3.48e-05;adjP=7.92e-05	*SSTR4; ESRP1*
	Brenner tumor of ovary	C=222;O=2;E=0.10;R=20.45;rawP=0.0043;adjP=0.0043	*CNTNAP1; FOXJ2*
KEGG	Pathways in cancer	C=326;O=2;E=0.20;R=10.18;rawP=0.0164;adjP=0.0164	*TPM3; BIRC2*

table S29. Enrichment results for the lion branch-site test. Analysis refers to the analysis performed in WebGestalt with a significance threshold < 0.05 and multiple correct testing (FDR). Characteristic refers to the enriched category found. Parameters describes enrichment details. C (Genes presented in the category); O (Genes observed in the dataset); R (Ratio of enrichment); rawP (p-value for the hypergeometric test); adjP (adjusted P value by the multiple correction test).

Category	Gene Ontology	Parameters	Genes
Molecular Function	Structural Molecule Activity	C=621;O=2;E=0.12;R=16.41;rawP=0.0048;adjP=0.0096	KRT40; KRT76
Cellular Component	Intermediate Filament Cytoskeleton	C=230;O=2;E=0.04;R=49.43;rawP=0.0005;adjP=0.0043	KRT40; KRT76
	Intermediate Filament	C=190;O=2;E=0.03;R=59.84;rawP=0.0004;adjP=0.0043	KRT40; KRT76