

Supplementary Table 1: Details on genes assessed in this study

Gene name	Status	Codeml Analysis Results			Position of positively selected sites <sup>1,2</sup>	P-value of positively selected sites	Population Analysis		Domains	Interactions	Pathway
		InL	Parameter estimates				SNPs tested	Unfixed sites			
<i>Genes under positive selection specifically in the human lineage</i>											
CARD6	Passed	-15625.7673	p0=0.45953 p1=0.52421 p2=0.00760 p3=0.00867 w0=0.17998 w1=1.00000 w2=70.36914	264, 346, 382, 750, 767, 805, 818, 903, 916, 937, 998, 1010, and 1031	13 > 0.50, 0 > 0.95, 0 > 0.99	38	G264E				
IRF9	Passed	-5965.31104	p0=0.66432 p1=0.33167 p2=0.00268 p3=0.00134 w0=0.07224 w1=1.00000 w2=431.16939	119, 129, and 333	3 > 0.50, 0 > 0.95, 0 > 0.99	9	None				
C1RL	Removed (R)	-7968.78747	p0=0.71660 p1=0.28084 p2=0.00183 p3=0.00072 w0=0.10272 w1=1.00000 w2=178.35256	103	1 > 0.50, 0 > 0.95, 0 > 0.99			CUB Domain			
INPP5D	Removed (R)	-32631.6355	p0=0.89627 p1=0.09099 p2=0.01157 p3=0.00117 w0=0.10134 w1=1.00000 w2=999.00000	72, 223, 227*, 228**, 235, 239, 241, 244, 249, and 250	10 > 0.50, 2 > 0.95, 1 > 0.99			SH2			
LAP2	Removed (R)	-31488.1615	p0=0.77166 p1=0.20323 p2=0.01987 p3=0.00523 w0=0.07287 w1=1.00000 w2=999.00000	714 and 1194	2 > 0.50, 0 > 0.95, 0 > 0.99						
<i>Genes under positive selection specifically in the mouse lineage</i>											
Adipoq	Passed	-3280.8125	p0=0.73898 p1=0.24047 p2=0.01550 p3=0.00505 w0=0.04219 w1=1.00000 w2=998.99930	25, 27, 29, and 82	4 > 0.50, 0 > 0.95, 0 > 0.99	9	None	Collagen-like			
Atg9a	Passed	-21083.0059	p0=0.95699 p1=0.04084 p2=0.00208 p3=0.00009 w0=0.01493 w1=1.00000 w2=26.59349	634 and 662*	2 > 0.50, 1 > 0.95, 0 > 0.99	3	None				
C1inh	Passed	-8556.45091	p0=0.54686 p1=0.43312 p2=0.01118 p3=0.00885 w0=0.10038 w1=1.00000 w2=998.99791	332*, 365, 468, 479	4 > 0.50, 1 > 0.95, 0 > 0.99				C1ra and F12	Complement	
C1ra	Passed	-19111.6792	p0=0.72843 p1=0.25840 p2=0.00972 p3=0.00345 w0=0.11188 w1=1.00000 w2=44.28694	468, 520, 574, 631, 633, and 634*	6 > 0.50, 1 > 0.95, 0 > 0.99	16	None	Peptidase S1*		Complement	
C6	Passed	-25800.2518	p0=0.61663 p1=0.34800 p2=0.02262 p3=0.01276 w0=0.11918 w1=1.00000 w2=177.5151	220, 233, 319, 353, 378, 408, 419, 430, 554, 655, 681, 703, 792, and 930	14 > 0.50, 0 > 0.95, 0 > 0.99	53	R554L	MACPF, Sushi 1, Kazal-like 1, CCP-1 and 2, Factor I module (FIM) 1 and 2		Complement	
C8b	Passed	-15259.5645	p0=0.69526 p1=0.29219 p2=0.00884 p3=0.00371 w0=0.13157 w1=1.00000 w2=998.99872	242*, 263, 278, 383*, and 488	5 > 0.50, 2 > 0.95, 0 > 0.99	36	M263I	MACPF* and EGF-like		Complement	
Card6	Passed	-15610.418	p0=0.45723 p1=0.50837 p2=0.01629 p3=0.01811 w0=0.18759 w1=1.00000 w2=998.99647	394, 501, and 702	3 > 0.50, 0 > 0.95, 0 > 0.99	4	None			NOD-Like	
Cd200	Passed	-4840.43777	p0=0.65241 p1=0.33688 p2=0.00707 p3=0.00365 w0=0.11347 w1=1.00000 w2=43.04625	129 and 177	2 > 0.50, 0 > 0.95, 0 > 0.99			Ig-like V-type (Extracellular) and Ig-like C2-type (Extracellular)		Verify	
Cd63	Passed	-3469.41048	p0=0.73747 p1=0.22921 p2=0.02541 p3=0.00790 w0=0.05011 w1=1.00000 w2=15.43175	31, 118, 143, 184*, 194, and 203	6 > 0.50, 1 > 0.95, 0 > 0.99	6	None			Lysosome	
Cfh	Passed	-32274.5643	p0=0.54145 p1=0.44242 p2=0.00888 p3=0.00725 w0=0.15686 w1=1.00000 w2=54.17278	209, 243, 474, 767, 1005, 1068, 1074, 1104, 1181, and 1227	10 > 0.50, 0 > 0.95, 0 > 0.99	8	None	Sushi 4, Sushi 13, Sushi 17, Sushi 18, Sushi 19, and Sushi 20	Itgam	Complement	
Ecsit	Passed	-6653.71574	p0=0.74691 p1=0.21546 p2=0.02920 p3=0.00842 w0=0.08329 w1=1.00000 w2=9.67226	10, 12, 75, 82, 176, 325, 330**, 348, and 371	9 > 0.50, 1 > 0.95, 1 > 0.99	1	S75L			MAPK	
Eif2ak2	Passed	-9941.00706	p0=0.50390 p1=0.42346 p2=0.03947 p3=0.03317 w0=0.10192 w1=1.00000 w2=435.75819	136, 155, 181, 182*, 344, and 345	6 > 0.50, 1 > 0.95, 0 > 0.99			DRBM 2 and Protein kinase		Multiple	
F12	Passed	-12985.2912	p0=0.69339 p1=0.29338 p2=0.00930 p3=0.00393 w0=0.09174 w1=1.00000 w2=20.28259	45, 65, 166, 243**, and 454	5 > 0.50, 1 > 0.95, 1 > 0.99			Fibronectin type-II, Fibronectin type-I, Kringle**, Peptidase S1	Serping1	Coagulation	
Grn	Passed	-13333.138	p0=0.63129 p1=0.36345 p2=0.00334 p3=0.00192 w0=0.08402 w1=1.00000 w2=139.90410	18, 101, 198, 303, 375*, 382, 411, 549, and 597	9 > 0.50, 1 > 0.95, 0 > 0.99	16	None	Granulin-1, Granulin-4, Granulin-5*, and Granulin-7			
Ifit2	Passed	-6549.6695	p0=0.62755 p1=0.35886 p2=0.00865 p3=0.00495 w0=0.18240 w1=1.00000 w2=50.21497	191, 402, and 420	3 > 0.50, 0 > 0.95, 0 > 0.99	14	None	TPR 3 and TPR 7			
Il1rapl2	Passed	-9224.48778	p0=0.93075 p1=0.06482 p2=0.00414 p3=0.00029 w0=0.04513 w1=1.00000 w2=313.77759	566, 628, and 666*	3 > 0.50, 1 > 0.95, 0 > 0.99	11	None				
Il2rb	Passed	-9843.12548	p0=0.56334 p1=0.38690 p2=0.02950 p3=0.02026 w0=0.11142 w1=1.00000 w2=14.54255	4, 13, 31, 55, 174, 202, 347*, 402, 418, 491, 496, and 516	12 > 0.50, 1 > 0.95, 0 > 0.99			Extracellular, Fibronectin type-III and Cytoplasmic*		JAK-STAT	
Il4ra	Passed	-16760.2901	p0=0.57272 p1=0.40532 p2=0.01286 p3=0.00910 w0=0.16413 w1=1.00000 w2=22.51561	47, 67, 308, 330, and 626	5 > 0.50, 0 > 0.95, 0 > 0.99	51	F47S & D626G	Extracellular domains, Cytoplasmic domains, and IL4-induced gene expression		JAK-STAT	
Irf5	Passed	-7751.58473	p0=0.80862 p1=0.18466 p2=0.00547 p3=0.00125 w0=0.04140 w1=1.00000 w2=37.63417	232, 259, and 262	3 > 0.50, 0 > 0.95, 0 > 0.99	14	None			TLR	
Lbp	Passed	-7753.18236	p0=0.71414 p1=0.27262 p2=0.00958 p3=0.00366 w0=0.15781 w1=1.00000 w2=29.65659	24, 40 and 329	3 > 0.50, 0 > 0.95, 0 > 0.99	33	None			TLR	
Lgals3	Passed	-2804.56787	p0=0.78887 p1=0.19010 p2=0.01694 p3=0.00408 w0=0.09775 w1=1.00000 w2=61.54204	22, 92, 94, and 260	4 > 0.50, 0 > 0.95, 0 > 0.99	15	None	γ A γ A unimem repeats of T-γ X(3)-P-[GS]-A and Nuclear export signal			
Lrrflp1	Passed	-7901.56219	p0=0.56794 p1=0.39040 p2=0.02469 p3=0.01697 w0=0.10013 w1=1.00000 w2=232.32695	328, 449, 468, 480, and 571	5 > 0.50, 0 > 0.95, 0 > 0.99	49	None	DNA-binding			
Ltb4r1	Passed	-5596.99679	p0=0.69576 p1=0.29371 p2=0.00741 p3=0.00313 w0=0.05940 w1=1.00000 w2=286.32093	53, 101, and 175	3 > 0.50, 0 > 0.95, 0 > 0.99	16	None		Anxa1	Verify	
Nlrp14	Passed	-15100.4036	p0=0.50688 p1=0.33262 p2=0.09691 p3=0.06359 w0=0.15174 w1=1.00000 w2=2.96492	77, 79*, 186, 212, 219, 254, 257, 263, 272, 281, 284, 291, 294, 315, 319, 333, 358, 393, 415, 424, 453, 465, 530, 549, 552, 553, 584, 613, 657, 679, 684, 685, 687, 696, 782, 810, 814, 829, 846, 848, 902, 908, 912, 931, 953, 956, 958, 978, 982, 984, and 986	51 > 0.50, 0 > 0.95, 0 > 0.99	16	A613S	NACHT, LRR 1-3, LRR 6-9			
Nlrp6	Passed	-12055.1676	p0=0.70988 p1=0.20945 p2=0.06229 p3=0.01838 w0=0.08302 w1=1.00000 w2=4.16107	22, 25, 72, 77, 80, 81, 85, 96, 101, 113, 114, 190, 192, 251, 260**, 329, 344, 479, 488, 515, 553, 571, 628, 657, 727, 737, 739, 744, 771, 775*, 776, 793, 807, 865, 877, and 880	36 > 0.50, 2 > 0.95, 1 > 0.99	53	None	DAPIN, NACHT*, LRR 1, and LRR 2			
Oas2	Passed	-14212.4618	p0=0.57045 p1=0.38313 p2=0.02777 p3=0.01865 w0=0.11466 w1=1.00000 w2=999.00000	55, 56, 139, 171, 199, 211, 221, 298, 481, 549, and 711	11 > 0.50, 0 > 0.95, 0 > 0.99			OAS domain 1 and 2		Multiple	
Plec2	Passed	-5052.485198	p0=0.92757 p1=0.05944 p2=0.01220 p3=0.00078 w0=0.01231 w1=1.00000 w2=999.00000	461 and 594*	2 > 0.50, 1 > 0.95, 0 > 0.99	51	None				
Ptpn2	Passed	-6009.55698	p0=0.83598 p1=0.14967 p2=0.01217 p3=0.00218 w0=0.06919 w1=1.00000 w2=15.81386	166, 206, 319, 321, and 329	5 > 0.50, 0 > 0.95, 0 > 0.99					Verify	
Rnf31	Passed	-22413.99042	p0=0.76580 p1=0.23227 p2=0.00147 p3=0.00045 w0=0.06113 w1=1.00000 w2=999.00000	203, 431, and 1025	3 > 0.50, 0 > 0.95, 0 > 0.99	24	None				
Sirt1	Passed	-6335.55297	p0=0.77272 p1=0.21421 p2=0.01023 p3=0.00284 w0=0.03736 w1=1.00000 w2=434.93076	107, 537, 698, and 701	4 > 0.50, 0 > 0.95, 0 > 0.99			NAD-dependent protein deacetylase sirtuin-1 (long chain)			
Snap23	Passed	-1780.13675	p0=0.82284 p1=0.13205 p2=0.03887 p3=0.00624 w0=0.05350 w1=1.00000 w2=365.11678	109, 133, and 197	3 > 0.50, 0 > 0.95, 0 > 0.99	2	None	t-SNARE coiled-coil homology 2		SNARE	
Stat2	Passed	-12031.1032	p0=0.58573 p1=0.38315 p2=0.01881 p3=0.01231 w0=0.05851 w1=1.00000 w2=302.58291	21, 130, 149, 157, 195, 205, 218, 354, 623*, 869, 871, 874, 876, and 877	14 > 0.50, 1 > 0.95, 0 > 0.99	58	L874M	SH2*	Irf5	JAK-STAT	
Tcf4	Passed	-5052.485198	p0=0.92757 p1=0.05944 p2=0.01220 p3=0.00078 w0=0.01231 w1=1.00000 w2=999.00000	139	1 > 0.50, 0 > 0.95, 0 > 0.99	20	None				
Tlr3	Passed	-27528.5971	p0=0.69091 p1=0.29956 p2=0.00665 p3=0.00288 w0=0.09892 w1=1.00000 w2=16.85129	266, 297, and 603	3 > 0.50, 0 > 0.95, 0 > 0.99	4	None	LRR 8, LRR 9, and LRR 21	TICAM1	TLR	
Trif	Passed	-12203.9234	p0=0.66104 p1=0.26408 p2=0.05351 p3=0.02138 w0=0.12718 w1=1.00000 w2=4.47517	18, 327, 338, 388, 482, 556, and 711	8 > 0.50, 0 > 0.95, 0 > 0.99	3	None		TLR3	TLR	
Csf2rb	Removed (R)	-26029.902	p0=0.58565 p1=0.39059 p2=0.01425 p3=0.00951 w0=0.20770 w1=1.00000 w2=21.40825	169, 271, 288, 473, 536, 569, and 576	7 > 0.50, 0 > 0.95, 0 > 0.99	50	N536D	Fibronectin type-III I and Cytoplasmic		JAK-STAT	
Cd22	Removed (R)	-21287.1128	p0=0.51922 p1=0.46728 p2=0.00711 p3=0.00640 w0=0.13273 w1=1.00000 w2=98.82292	137, 190, 271, 474, and 812	5 > 0.50, 0 > 0.95, 0 > 0.99			Ig-like V-type, Ig-like C2-type 1, 2, and 4		Verify	
Itgam	Removed (R)	-24765.6859	p0=0.69864 p1=0.28556 p2=0.01121 p3=0.00458 w0=0.14594 w1=1.00000 w2=998.99893	23, 45, 820, 831, 844, 1035, 1089, 1092, and 1131	9 > 0.50, 1 > 0.95, 0 > 0.99			FG-GAP 1 motif	Cfh	Complement	
Ptk2	Removed (R)	-26657.7467	p0=0.96669 p1=0.03070 p2=0.00253 p3=0.00008 w0=0.03166 w1=1.00000 w2=999.00000	390* and 800	2 > 0.50, 1 > 0.95, 0 > 0.99			Region for interaction with TGFβ111		Multiple	
Sirpa	Removed (R)	-10063.2315	p0=0.55941 p1=0.37830 p2=0.03716 p3=0.02513 w0=0.09496 w1=1.00000 w2=19.05016	51, 52*, 69, 77, 83, 91, 193, 202, 221, 224, 226, 237, 238, 250, 276, 297, 305, 307, 338*, 344, and 490	21 > 0.50, 2 > 0.95, 0 > 0.99			Ig-like V-type* and Ig-like C1-type 1 and 2*		Verify	
Tlr8	Removed (R)	-26914.2776	p0=0.64539 p1=0.34225 p2=0.00807 p3=0.00428 w0=0.07990 w1=1.00000 w2=11.83741	44, 751, 764*, 778, 802*, 864, and 1003	7 > 0.50, 2 > 0.95, 0 > 0.99			LRR 1, LRR 23, LRR 26*, and TIR		TLR	
Traf5	Removed (R)	-11832.62	p0=0.79115 p1=0.15526 p2=0.04480 p3=0.00879 w0=0.09787 w1=1.00000 w2=681.22327	133, 308, 309, and 339	4 > 0.50, 0 > 0.95, 0 > 0.99	3	None	TRAF-type 1		Multiple	
Tyro3	Removed (R)	-24726.15312	p0=0.77200 p1=0.20790 p2=0.01584 p3=0.00427 w0=0.08897 w1=1.00000 w2=998.99820	85, 101, 825, and 826	4 > 0.50, 0 > 0.95, 0 > 0.99						
Zp3r	Removed (R)	-19249.87608	p0=0.38277 p1=0.51708 p2=0.04260 p3=0.05755 w0=0.15358 w1=1.00000 w2=8.54244	3, 7, 39, 110, 174, 179, 206, 212, 219, 244, 311, 454, 460, 461, 470, 485, 488, 510, 514, 518*, 524, 528, 537, 541, and 546	25 > 0.50, 1 > 0.95, 0 > 0.99			Sushi 2, 3, 5, and 7			
<i>Genes under positive selection specifically in the primate lineage</i>											
ACHE	Passed	-12717.91667	p0=0.85629 p1=0.12361 p2=0.01756 p3=0.00254 w0=0.03849 w1=1.00000 w2=105.25786	23**, 171, 429, 488, 494, 604**, and 605**	7 > 0.50, 3 > 0.95, 3 > 0.99						
APOA1	Passed	-2855.996221	p0=0.81375 p1=0.15102 p2=0.02971 p3=0.00551 w0=0.10502 w1=1.00000 w2=27.92713	119*, 151, 260*	3 > 0.50, 2 > 0.95, 0 > 0.99						

Gene name	Status	Codeml Analysis Results				Population Analysis		Domains	Interactions	Pathway
		InL	Parameter estimates	Position of positively selected sites <sup>1,2</sup>	P-value of positively selected sites	SNPs tested	Unfixed sites			
<i>Genes under positive selection specifically in the rodent lineage</i>										
Bear1	Passed	-16655.27502	p0=0.83443 p1=0.14246 p2=0.01973 p3=0.00337 w0=0.03543 w1=1.00000 w2=999.00000	666, 691, 722, 740, 870, 944	6 > 0.50, 0 > 0.95, 0 > 0.99					
Inpp5d	Passed	-32669.65616	p0=0.90623 p1=0.09080 p2=0.00270 p3=0.00027 w0=0.10264 w1=1.00000 w2=997.43640	760, 1022	2 > 0.50, 0 > 0.95, 0 > 0.99					
Mst1r	Passed	-46793.76024	p0=0.63668 p1=0.35667 p2=0.00426 p3=0.00239 w0=0.12113 w1=1.00000 w2=144.45238	791, 1051*	2 > 0.50, 1 > 0.95, 0 > 0.99					IPT/TIG 2
Nef1	Passed	-6738.969644	p0=0.86960 p1=0.12200 p2=0.00737 p3=0.00103 w0=0.06396 w1=1.00000 w2=998.99896	43**, 304, 323, 414	4 > 0.50, 1 > 0.95, 1 > 0.99					PX
Nos2	Passed	-34686.44064	p0=0.78681 p1=0.19467 p2=0.01485 p3=0.00367 w0=0.10331 w1=1.00000 w2=15.76793	133, 251, 372*, 678, 692, 924, 978	7 > 0.50, 1 > 0.95, 0 > 0.99					Flavodoxin-like and FAD-binding FR-type
Rel	Passed	-14041.33044	p0=0.57332 p1=0.41987 p2=0.00393 p3=0.00288 w0=0.06109 w1=1.00000 w2=999.00000	474	1 > 0.50, 0 > 0.95, 0 > 0.99					
Rnf31	Passed	-22413.29401	p0=0.76809 p1=0.22861 p2=0.00254 p3=0.00076 w0=0.06200 w1=1.00000 w2=999.00000	104, 135, 276, 824, 872	5 > 0.50, 0 > 0.95, 0 > 0.99					Removed (R)
Vdr	Passed	-9510.441834	p0=0.77452 p1=0.21870 p2=0.00528 p3=0.00149 w0=0.04005 w1=1.00000 w2=998.99997	183*, 325	2 > 0.50, 1 > 0.95, 0 > 0.99					
Tyro3	Removed (R)	-24732.93757	p0=0.78088 p1=0.21180 p2=0.00575 p3=0.00156 w0=0.08847 w1=1.00000 w2=709.23987	155*	1 > 0.50, 1 > 0.95, 0 > 0.99					Ig-like C2-type 1
<i>Genes under positive selection specifically in the murinae lineage</i>										
Bear1	Passed	-16655.2351	p0=0.83519 p1=0.14510 p2=0.01679 p3=0.00292 w0=0.03568 w1=1.00000 w2=999.00000	208, 666	2 > 0.50, 0 > 0.95, 0 > 0.99					
C11nh	Passed	-8300.143711	p0=0.55879 p1=0.43149 p2=0.00548 p3=0.00423 w0=0.10625 w1=1.00000 w2=114.24086	268, 378	2 > 0.50, 0 > 0.95, 0 > 0.99					
C9	Passed	-12947.08599	p0=0.58215 p1=0.40568 p2=0.00717 p3=0.00500 w0=0.10479 w1=1.00000 w2=43.19163	483, 486*	2 > 0.50, 1 > 0.95, 0 > 0.99					MACPF
Ccdc88a	Passed	-40782.06554	p0=0.91943 p1=0.07955 p2=0.00094 p3=0.00008 w0=0.04403 w1=1.00000 w2=281.60012	197, 223, 487, 712, 724, 746, 749, 786, 1126, 1153, 1169, 1175, 1406, 1417, 1422, 1947, 1976, 2085, 2087, 2090, 2255, 2280	22 > 0.50, 0 > 0.95, 0 > 0.99					
Ctsd	Passed	-11909.81464	p0=0.77032 p1=0.16135 p2=0.05649 p3=0.01183 w0=0.09928 w1=1.00000 w2=408.50878	12, 50, 286, 378, 381	5 > 0.50, 0 > 0.95, 0 > 0.99					
Dhx9	Passed	-21536.77297	p0=0.87452 p1=0.11497 p2=0.00929 p3=0.00122 w0=0.03548 w1=1.00000 w2=9.54713	91, 289*, 381, 685*	4 > 0.50, 2 > 0.95, 0 > 0.99					MTAD
Ltb4r	Passed	-5599.364798	p0=0.69273 p1=0.28326 p2=0.01704 p3=0.00697 w0=0.06121 w1=1.00000 w2=742.27852	19, 258	2 > 0.50, 0 > 0.95, 0 > 0.99					
Nup153	Passed	-39350.55592	p0=0.70761 p1=0.28476 p2=0.00544 p3=0.00219 w0=0.13305 w1=1.00000 w2=13.02906	723, 769, 940, 1136, 1463	5 > 0.50, 0 > 0.95, 0 > 0.99					
Olfm4	Passed	-4759.933388	p0=0.58661 p1=0.34625 p2=0.04222 p3=0.02492 w0=0.04244 w1=1.00000 w2=34.87299	17, 58, 186, 211, 233, 234, 237, 289, 319, 354, 455	11 > 0.50, 0 > 0.95, 0 > 0.99					Olfactomedin-like
Otub2	Passed	-3903.653786	p0=0.86336 p1=0.07916 p2=0.05266 p3=0.00483 w0=0.03434 w1=1.00000 w2=373.90617	267	1 > 0.50, 0 > 0.95, 0 > 0.99					OTU
Plec2	Passed	-33334.996	p0=0.95797 p1=0.03820 p2=0.00369 p3=0.00015 w0=0.04905 w1=1.00000 w2=998.65099	222, 407*, 544, 636, 1150, 1401*	6 > 0.50, 2 > 0.95, 0 > 0.99					PI-PLC X-box, SH2 1, PI-PLC Y-box
Pml	Passed	-17023.9819	p0=0.75786 p1=0.21644 p2=0.01999 p3=0.00571 w0=0.12529 w1=1.00000 w2=20.00909	120, 276, 394, 576, 722, 750, 838, 971, 1008	9 > 0.50, 0 > 0.95, 0 > 0.99					
Ptk2b	Passed	-25172.43122	p0=0.95569 p1=0.03864 p2=0.00545 p3=0.00022 w0=0.03450 w1=1.00000 w2=6.89029	345*, 1222*, 1225	3 > 0.50, 2 > 0.95, 0 > 0.99					FERM and Focal adhesion targeting (FAT)
Rasgef1b	Passed	-10514.23732	p0=0.96525 p1=0.03208 p2=0.00258 p3=0.00009 w0=0.03518 w1=1.00000 w2=43.56554	126*	1 > 0.50, 1 > 0.95, 0 > 0.99					N-terminal Ras-GEF
Rsad2	Passed	-7521.535098	p0=0.75983 p1=0.23385 p2=0.00483 p3=0.00149 w0=0.03778 w1=1.00000 w2=10.15840	40	1 > 0.50, 0 > 0.95, 0 > 0.99					
Rumx3	Passed	-6980.76136	p0=0.86575 p1=0.12481 p2=0.00825 p3=0.00119 w0=0.03573 w1=1.00000 w2=130.19437	371, 436*, 471	3 > 0.50, 1 > 0.95, 0 > 0.99					
Traf6	Passed	-15379.32643	p0=0.82256 p1=0.16704 p2=0.00865 p3=0.00176 w0=0.07399 w1=1.00000 w2=102.21019	16*	1 > 0.50, 1 > 0.95, 0 > 0.99					
Tyk2	Passed	-34832.07016	p0=0.80527 p1=0.18559 p2=0.00742 p3=0.00171 w0=0.10243 w1=1.00000 w2=249.63150	124, 158, 618, 628, 749, 1202	6 > 0.50, 0 > 0.95, 0 > 0.99					FERM and Protein kinase 1
Igf1r	Removed (R)	-32712.18489	p0=0.92792 p1=0.07105 p2=0.00096 p3=0.00007 w0=0.04690 w1=1.00000 w2=315.18544	161, 264**	2 > 0.50, 1 > 0.95, 1 > 0.99					Insulin-like growth factor 1 receptor alpha chain
Ilgam	Removed (R)	-24779.57551	p0=0.70311 p1=0.28691 p2=0.00709 p3=0.00289 w0=0.14745 w1=1.00000 w2=998.99906	99, 133, 215, 227, 473, 799	6 > 0.50, 0 > 0.95, 0 > 0.99					FG-GAP 2 and VWFA
Mst1r	Removed (R)	-46802.09026	p0=0.63555 p1=0.35503 p2=0.00604 p3=0.00337 w0=0.12131 w1=1.00000 w2=33.79659	110, 289, 312, 585, 824, 1184	6 > 0.50, 0 > 0.95, 0 > 0.99					Macrophage-stimulating protein receptor alpha & beta chains
Nup214	Removed (R)	-44322.0221	p0=0.72051 p1=0.27112 p2=0.00608 p3=0.00229 w0=0.12311 w1=1.00000 w2=37.36046	118, 449, 466, 1334, 1565	5 > 0.50, 0 > 0.95, 0 > 0.99					
Tyro3	Removed (R)	-24734.57377	p0=0.77965 p1=0.21212 p2=0.00647 p3=0.00176 w0=0.08839 w1=1.00000 w2=46.83218	165, 169, 191, 267, 287, 305, 474*, 513	8 > 0.50, 1 > 0.95, 0 > 0.99					Ig-like C2-type 1, 2, Fibronectin type-III 1, and 2

<sup>1</sup>Positions given in ancestral lineages are human for primates and mouse for rodent and murinae.

<sup>2</sup>The posterior probability of each positively selected site is indicated as follows: \* >0.95, \*\* >0.99 and no asterisk indicates >0.50