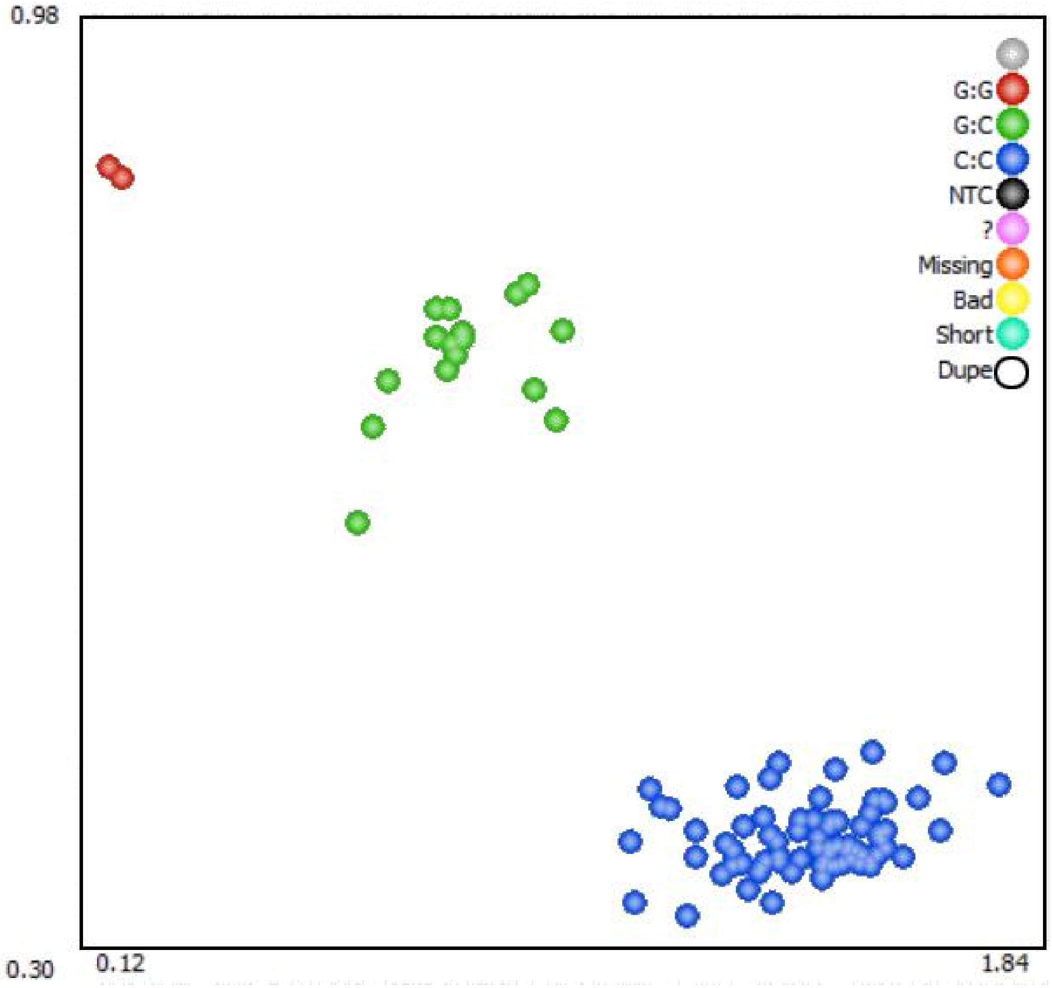
Supplementary Materials

Supplementary Figure S1 Genotyping of ovine *IFI44* c. 54413058 C>G SNP with KASPar technology.



Supplementary Table S1 Overview of sample information and sequencing statistics.

Breed	Sample ID	Clean Reads (bp)	Clean Bases (bp)	Mapped Bases (bp)	Duplication Rate (%)	Clean Q30 Bases Rate (%)	Mapping Rate (%)	Uniq Rate (%)	Mean Depth	Coverage Rate (%) (>=1X)
Australian white	Australian white1	170,843,842	25,626,576,300	25,088,588,783	23.55	91.89	97.9	91.8	9.69	96.87
	Australian white2	167,784,918	25,167,737,700	24,643,604,271	24.82	92.4	97.92	91.88	9.52	96.79
	Australian white3	148,357,830	22,253,674,500	21,811,775,405	21.45	93.53	98.01	92.1	8.43	96.52
	Australian white4	161,541,914	24,231,287,100	23,762,659,613	23.17	93.67	98.07	91.73	9.18	96.71
	Australian white5	189,630,354	28,444,553,100	27,874,284,808	24.78	92.61	98	92	10.77	97.24
	Australian white6	166,080,390	24,912,058,500	24,457,755,395	24.16	92.96	98.18	92	9.45	96.98
	Australian white7	157,996,064	23,699,409,600	23,250,434,171	23.66	92.47	98.11	91.88	8.98	96.84
	Australian white8	160,178,196	24,026,729,400	23,574,539,258	23.47	92.61	98.12	91.86	9.11	96.89
	Australian white9	141,141,420	21,171,213,000	20,756,441,040	24.68	92.42	98.04	91.71	8.02	96.23
	Australian white10	172,400,354	25,860,053,100	25,347,340,908	25.12	92.49	98.02	91.97	9.79	97.12
Black suffolk	Black suffolk1	183,963,938	27,594,590,700	27,006,495,365	27.14	92.87	97.87	91.85	10.43	96.98
	Black suffolk2	188,745,728	28,311,859,200	27,720,003,740	28.45	92.99	97.91	91.94	10.71	97.03
	Black suffolk3	224,806,694	33,721,004,100	32,994,112,402	29.9	92.59	97.84	91.59	12.75	97.37
	Black suffolk4	173,790,860	26,068,629,000	25,381,767,722	27.13	92.63	97.37	91.44	9.81	96.74
	Black suffolk5	198,792,578	29,818,886,700	29,195,173,065	25.08	92.7	97.91	91.58	11.28	97.3
	Black suffolk6	174,061,254	26,109,188,100	25,590,276,957	24.85	92.61	98.01	92.08	9.89	97.2
	Black suffolk7	169,695,926	25,454,388,900	24,964,050,259	23.96	92.36	98.07	92.09	9.65	97.14
	Black suffolk8	203,506,608	30,525,991,200	29,921,355,419	25.61	92.54	98.02	91.76	11.56	97.42
	Black suffolk9	172,753,056	25,912,958,400	25,416,559,867	23.79	92.52	98.08	92.01	9.82	97.2
	Black suffolk10	213,173,416	31,976,012,400	31,355,323,480	24.73	92.73	98.06	92.15	12.11	97.56
Dorper	Dorper1	175,399,374	26,309,906,100	25,795,577,070	22.04	93.17	98.05	92.02	9.97	97.05
	Dorper2	148,801,556	22,320,233,400	21,861,945,791	21.37	93.62	97.95	91.6	8.45	96.27
	Dorper3	189,462,300	28,419,345,000	24,612,029,099	26.68	92.73	86.6	91.89	9.51	96.74

	Dorper4	146,634,164	21,995,124,600	16,647,941,754	26.06	92.31	75.69	91.31	6.43	94.23
	Dorper5	175,354,424	26,303,163,600	25,748,029,603	25.98	92.39	97.89	92.13	9.95	96.95
	Dorper6	168,686,112	25,302,916,800	24,822,383,758	25.36	92.62	98.1	91.86	9.59	96.96
	Dorper7	157,307,748	23,596,162,200	23,162,603,842	26.28	92.59	98.16	92.09	8.95	96.8
	Dorper8	184,296,488	27,644,473,200	27,145,028,506	26.81	92.73	98.19	92.18	10.49	97.23
	Dorper9	158,289,944	23,743,491,600	23,266,034,643	26.8	92.45	97.99	91.71	8.99	96.75
	Dorper10	141,347,354	21,202,103,100	20,808,168,581	25.23	91.85	98.14	92.01	8.04	96.46
East friensian milk sheep	East friensian milk sheep1	199,290,496	29,893,574,400	26,499,770,923	25.03	92.62	88.65	92.16	10.24	97.2
	East friensian milk sheep2	219,231,118	32,884,667,700	31,052,493,174	25.73	93.05	94.43	92.23	12	97.42
	East friensian milk sheep3	213,763,206	32,064,480,900	31,365,250,611	25.86	92.7	97.82	91.68	12.12	97.36
	East friensian milk sheep4	180,719,156	27,107,873,400	26,550,780,191	24.32	92.7	97.94	92.08	10.26	97.13
	East friensian milk sheep5	144,850,188	21,727,528,200	21,274,962,993	24.54	92.7	97.92	91.59	8.22	96.05
	East friensian milk sheep6	195,915,076	29,387,261,400	28,833,003,158	24.62	92.5	98.11	92.6	11.14	97.52
	East friensian milk sheep7	169,093,576	25,364,036,400	24,867,091,971	24.84	92.64	98.04	91.77	9.61	97.06
	East friensian milk sheep8	167,405,574	25,110,836,100	24,628,815,296	25.39	92.55	98.08	91.8	9.52	96.98
	East friensian milk sheep9	177,587,610	26,638,141,500	26,095,632,074	25.59	92.61	97.96	91.8	10.08	97.13
	East friensian milk	183,739,602	27,560,940,300	26,964,640,897	25.32	92.63	97.84	91.7	10.42	97.25

	sheep10									
SA mutton merino	SA mutton merino1	182,223,690	27,333,553,500	26,265,258,696	26.11	92.92	96.09	89.04	10.15	94.81
	SA mutton merino2	201,863,290	30,279,493,500	29,697,170,384	24.21	93.56	98.08	92.3	11.47	97.4
	SA mutton merino3	184,045,326	27,606,798,900	27,068,223,304	24.19	93.35	98.05	92.14	10.46	97.13
	SA mutton merino4	152,043,786	22,806,567,900	22,353,779,824	22.72	93.47	98.01	92.14	8.64	96.62
	SA mutton merino5	184,612,594	27,691,889,100	27,124,925,503	24.18	93.21	97.95	91.98	10.48	97.14
	SA mutton merino6	145,010,808	21,751,621,200	21,342,622,299	22.25	93.08	98.12	91.98	8.25	96.66
	SA mutton merino7	160,777,276	24,116,591,400	23,683,214,983	22.97	93.41	98.2	92.24	9.15	96.95
	SA mutton merino8	218,093,632	32,714,044,800	32,079,163,887	28.89	92.7	98.06	92.03	12.39	97.51
	SA mutton merino9	218,694,608	32,804,191,200	31,791,029,849	28.1	92.57	96.91	92.07	12.28	97.48
	SA mutton merino10	187,654,078	28,148,111,700	27,583,183,299	26.72	92.5	97.99	91.94	10.66	97.28
Texel	Texel1	167,130,040	25,069,506,000	24,576,603,806	24.37	93.43	98.03	91.26	9.5	96.82
	Texel2	177,846,500	26,676,975,000	26,123,346,781	25.42	93.65	97.92	91.16	10.09	96.92
	Texel3	159,450,640	23,917,596,000	23,428,160,781	23.79	93.7	97.95	91.32	9.05	96.66
	Texel4	152,728,018	22,909,202,700	22,371,670,143	25.14	93.33	97.65	90.53	8.64	96.1
	Texel5	168,775,980	25,316,397,000	23,131,910,284	26.86	92.55	91.37	90.77	8.94	96.07
	Texel6	178,317,864	26,747,679,600	26,205,402,178	28.03	92.84	97.97	91.34	10.12	96.94
	Texel7	189,422,096	28,413,314,400	27,827,516,946	27.57	92.28	97.94	91.21	10.75	97.16
	Texel8	192,492,344	28,873,851,600	28,313,698,690	27.12	92.58	98.06	91.27	10.94	97.27
	Texel9	203,324,162	30,498,624,300	29,935,990,901	25.92	93.67	98.16	91.46	11.57	97.4
	Texel10	190,542,876	28,581,431,400	28,038,450,420	25.11	93.74	98.1	91.33	10.83	97.07
Altay sheep	Altay sheep1	116,347,000	17,452,050,000	17,001,957,946	23.72	93.08	97.42	90.34	6.57	93.69
	Altay sheep2	143,254,582	21,488,187,300	20,704,029,414	25.52	92.67	96.35	88.49	8	94.47
	Altay sheep3	138,503,136	20,775,470,400	20,250,938,726	27.5	92.73	97.48	89.39	7.82	94.47
	Altay sheep4	136,219,934	20,432,990,100	19,908,945,736	27.27	92.85	97.44	89.49	7.69	94.14

	Altay sheep5	181,272,490	27,190,873,500	26,492,721,793	27.1	92.99	97.43	90.98	10.24	96.81
	Altay sheep6	167,917,268	25,187,590,200	24,614,129,374	26.96	92.68	97.72	90.72	9.51	96.58
	Altay sheep7	159,395,222	23,909,283,300	23,379,844,614	25.57	92.95	97.79	90.92	9.03	96.56
	Altay sheep8	185,938,110	27,890,716,500	27,260,508,999	25.98	92.94	97.74	90.9	10.53	97.02
	Altay sheep9	204,932,778	30,739,916,700	30,080,331,099	27.44	93.37	97.85	90.34	11.62	97.18
	Altay sheep10	156,789,190	23,518,378,500	22,994,007,035	28.08	93.05	97.77	90.3	8.88	96.12
Lanzhou Large-tailed sheep	Large-tailed Han sheep1	213,957,826	32,093,673,900	31,386,958,700	28.55	92.6	97.8	91.06	12.13	97.22
	Large-tailed Han sheep2	181,924,490	27,288,673,500	26,654,541,494	26.75	92.54	97.68	90.99	10.3	96.31
	Large-tailed Han sheep3	141,103,772	21,165,565,800	20,733,806,945	22.61	93.56	97.96	91.7	8.01	96.03
	Large-tailed Han sheep4	147,524,302	22,128,645,300	21,680,810,563	24.7	93.29	97.98	91.79	8.38	96.31
	Large-tailed Han sheep5	150,539,826	22,580,973,900	21,792,868,825	21.88	93.29	96.51	91.23	8.42	95.69
	Large-tailed Han sheep6	139,450,274	20,917,541,100	20,444,943,456	22.14	93.21	97.74	91.33	7.9	96.14
	Large-tailed Han sheep7	151,910,370	22,786,555,500	22,357,606,327	22.94	93.56	98.12	91.25	8.64	96.58
	Large-tailed Han sheep8	132,241,788	19,836,268,200	19,457,518,106	20.56	93.28	98.09	91.64	7.52	96.01
	Large-tailed Han sheep9	129,884,244	19,482,636,600	19,101,440,919	21.16	93.7	98.04	91.31	7.38	95.62
	Large-tailed Han sheep10	157,281,466	23,592,219,900	23,064,959,033	23.49	93.44	97.77	91.45	8.91	96.69

Lanzhou Large-tailed sheep	Lanzhou Large-tailed sheep1	163,113,178	24,466,976,700	23,968,138,579	25.66	92.19	97.96	91.51	9.26	96.68
	Lanzhou Large-tailed sheep2	159,352,520	23,902,878,000	23,413,799,704	26.36	92.61	97.95	91.67	9.05	96.49
	Lanzhou Large-tailed sheep3	148,928,386	22,339,257,900	21,845,880,545	26.19	92.17	97.79	90.82	8.44	95.59
	Lanzhou Large-tailed sheep4	168,357,324	25,253,598,600	24,708,217,220	26.59	92.34	97.84	91.46	9.55	96.75
	Lanzhou Large-tailed sheep5	170,179,522	25,526,928,300	24,861,367,986	26.1	92.56	97.39	91.18	9.6	96.53
	Lanzhou Large-tailed sheep6	199,360,210	29,904,031,500	29,338,269,540	26.99	92.54	98.11	92.06	11.34	97.43
	Lanzhou Large-tailed sheep7	149,534,110	22,430,116,500	22,029,966,437	25.92	92.61	98.22	91.17	8.51	96.48
	Lanzhou Large-tailed sheep8	191,879,902	28,781,985,300	28,255,689,289	28.16	92.39	98.17	91.8	10.92	97.22
	Lanzhou Large-tailed sheep9	171,114,548	25,667,182,200	25,186,282,640	27.61	92.87	98.13	91.53	9.73	96.86
	Lanzhou Large-tailed sheep10	163,412,116	24,511,817,400	24,045,492,611	26.13	91.95	98.1	91.67	9.29	96.89
Mongolian sheep	Mongolian sheep1	147,980,646	22,197,096,900	21,697,854,748	21.83	93.1	97.75	91.47	8.38	96.24
	Mongolian sheep2	170,308,256	25,546,238,400	25,022,790,538	20.45	93.58	97.95	92.51	9.67	97.02
	Mongolian sheep3	152,357,538	22,853,630,700	22,341,573,260	22.45	92.8	97.76	91.54	8.63	96.37
	Mongolian sheep4	135,750,848	20,362,627,200	19,892,886,850	22.29	93.27	97.69	91.72	7.69	95.69
	Mongolian sheep5	135,465,506	20,319,825,900	19,864,085,995	23.76	93.33	97.76	91.26	7.67	95.59

Mongolian sheep6	149,229,398	22,384,409,700	21,909,655,014	23.01	93.11	97.88	91.71	8.47	96.43
Mongolian sheep7	173,867,568	26,080,135,200	25,535,695,553	24.22	91.56	97.91	92.23	9.87	97.23
Mongolian sheep8	141,539,512	21,230,926,800	20,776,160,508	23.4	92.02	97.86	92.02	8.03	96.17
Mongolian sheep9	158,899,756	23,834,963,400	23,360,050,335	23.12	92.94	98.01	92.32	9.03	97.01
Mongolian sheep10	132,518,432	19,877,764,800	19,498,051,283	22.92	93.41	98.09	92.64	7.53	96.15

Supplementary Table S2 Overview of publicly available whole-genome sequencing data used for analyses.

Breed	Biosample	Accession number	Bases	Size	Sex
Asian Mouflon1	SAMEA2012638	ERR157930	40.5G	25.9G	male
Asian Mouflon2	SAMEA2012641	ERR157931	40.1G	24.9G	male
Asian Mouflon3	SAMEA2012642	ERR157932	39.5G	24.9G	male
Asian Mouflon4	SAMEA2012643	ERR157935	40G	25.3G	male
Asian Mouflon5	SAMEA2012637	ERR157938	42.1G	27.6G	male
Asian Mouflon6	SAMEA2012639	ERR157939	37.9G	24.2G	male
Asian Mouflon7	SAMEA2012640	ERR157942	40.1G	25.1G	male
Asian Mouflon8	SAMEA1967031	ERR157944	40G	25.1G	male
Asian Mouflon9	SAMEA2065604	ERR315509	37.7G	25.4G	female
Asian Mouflon10	SAMEA1972234	ERR332573	44.2G	28.9G	male
Asian Mouflon11	SAMEA2065601	ERR332575	42.2G	27G	male
Asian Mouflon12	SAMEA2065603	ERR332582	44.3G	28.6G	male
Asian Mouflon13	SAMEA2065602	ERR332587	38.5G	23.5G	female
Asian Mouflon14	SAMEA2065600	ERR332589	39.8G	24.6G	male
Asian Mouflon15	SAMEA1964491	ERR340346	37.7G	25.1G	male
Asian Mouflon16	SAMEA2395411	ERR466544	36.9G	23.7G	male
Asian Mouflon17	SAMEA2395410	ERR466546	38.7G	25.6G	female

Sardi1	SAMEA2012858	ERR299293	40G	27.4G	female
Sardi2	SAMEA2012337	ERR332591	37.1G	24.5G	female
Sardi3	SAMEA2012244	ERR318906	39.5G	24.6G	female
Sardi4	SAMEA1973547	ERR299458	37.8G	23.4G	female
Sardi5	SAMEA2012249	ERR299454	34.2G	21.1G	female
Sardi6	SAMEA2012242	ERR318902	37.7G	23.2G	male
D'man1	SAMEA2012440	ERR318900	38.1G	23.6G	male
D'man2	SAMEA2012525	ERR277069	44.6G	29.1G	male
D'man3	SAMEA2012334	ERR318899	39G	23.9G	male
D'man4	SAMEA2012526	ERR318760	37.6G	25G	male
D'man5	SAMEA2012324	ERR283428	40.4G	25.3G	male
D'man6	SAMEA2012435	ERR318916	36.1G	22G	female
D'man7	SAMEA2012247	ERR283423	43.3G	27.5G	female
D'man8	SAMEA2012528	ERR318762	33.5G	20.4G	female
D'man9	SAMEA2012233	ERR299278	33.4G	20.4G	female
Beni Guil1	SAMEA2012918	ERR318758	37G	25.7G	female
Beni Guil2	SAMEA2012855	ERR315499	30.3G	18G	female
Beni Guil3	SAMEA2012853	ERR299462	31.7G	19.5G	female
Beni Guil4	SAMEA2012114	ERR299276	33.4G	20.9G	male
Beni Guil5	SAMEA2012162	ERR299288	45.7G	30.4G	female
Beni Guil6	SAMEA2012859	ERR299281	38.3G	24.5G	female
Timahdite1	SAMEA2012593	ERR332590	35G	21.7G	female
Timahdite2	SAMEA2012535	ERR319042	36.8G	24.2G	female
Timahdite3	SAMEA2012605	ERR319037	36.7G	23.8G	female
Timahdite4	SAMEA2012844	ERR319038	38G	24.8G	female
Timahdite5	SAMEA2042062	ERR345984	33.4G	20.6G	female

Timahdite6	SAMEA2012537	ERR234303	45.2G	30.7G	male
Timahdite7	SAMEA2012606	ERR318777	34.2G	21G	male
Ouled Djellal1	SAMEA2012913	ERR319040	39G	27.1G	male
Ouled Djellal2	SAMEA2012117	ERR318896	32.1G	19.4G	female
Ouled Djellal3	SAMEA2012919	ERR318770	36.5G	25.2G	female
Ouled Djellal4	SAMEA2012925	ERR299284	38.8G	24.6G	female
Ouled Djellal5	SAMEA2012920	ERR299280	31.1G	18.8G	female
Ouled Djellal6	SAMEA2012923	ERR299275	39.8G	26.5G	female
Bayinbuluke sheep1	SAMN04306062	SRR2980596	9.8G	3.5G	female
Bayinbuluke sheep2	SAMN04306061	SRR2976723	13.1G	4.7G	female
Bayinbuluke sheep3	SAMN04306059	SRR2976711	15.4G	5.4G	female
Bayinbuluke sheep4	SAMN04306058	SRR2976708	19.1G	6.6G	female
Bayinbuluke sheep5	SAMN04306057	SRR2976545	18.5G	8.7G	male
Bayinbuluke sheep6	SAMN04306056	SRR2976544	17.6G	8.2G	male
Bayinbuluke sheep7	SAMN04306055	SRR2976542	14.8G	5.3G	male
Bayinbuluke sheep8	SAMN04306054	SRR2976539	11.3G	4G	male
Bayinbuluke sheep9	SAMN04306053	SRR2976535	11.9G	4.1G	male
Qira Black sheep1	SAMN04306072	SRR2992575	19.7G	9.7G	female
Qira Black sheep2	SAMN04306071	SRR2992573	16.2G	7.9G	female
Qira Black sheep3	SAMN04306070	SRR2984620	8.5G	2.8G	female
Qira Black sheep4	SAMN04306069	SRR2984619	11.5G	3.9G	female
Qira Black sheep5	SAMN04306068	SRR2984616	18.7G	6.4G	female
Qira Black sheep6	SAMN04306067	SRR2982588	17.5G	5.9G	male
Qira Black sheep7	SAMN04306066	SRR2982564	18.9G	6.4G	male
Qira Black sheep8	SAMN04306065	SRR2982559	18.7G	6.4G	male
Qira Black sheep9	SAMN04306064	SRR2980624	18.8G	6.5G	male

Qira Black sheep10	SAMN04306063	SRR2980606	9.9G	3.4G	male
Tibetan sheep1（Valley）	SAMN04306082	SRR3023068	10.5G	3.7G	female
Tibetan sheep2（Valley）	SAMN04306081	SRR3022928	16.3G	5.7G	female
Tibetan sheep3（Valley）	SAMN04306080	SRR2997425	17.4G	6.1G	female
Tibetan sheep4（Valley）	SAMN04306079	SRR2997424	20.1G	6.9G	female
Tibetan sheep5（Valley）	SAMN04306078	SRR2997390	18.8G	6.5G	female
Tibetan sheep6（Valley）	SAMN04306077	SRR2997388	17G	5.8G	male
Tibetan sheep7（Valley）	SAMN04306076	SRR2997142	16.9G	5.9G	male
Tibetan sheep8（Valley）	SAMN04306075	SRR2992820	9.4G	3.2G	male
Tibetan sheep9（Valley）	SAMN04306074	SRR2992761	18.4G	6.2G	male
Tibetan sheep10（Valley）	SAMN04306073	SRR2992628	17.5G	5.9G	male
Tibetan sheep11（Valley）	SAMN06161578	SRR5149616	31G	12.9G	female
Tibetan sheep12（Valley）	SAMN03565385	SRR1999380	36.1G	21.3G	female
Tibetan sheep13（Valley）	SAMN03565384	SRR1999378	29.5G	18.1G	female
Tibetan sheep14（Valley）	SAMN03565379	SRR1999369	37.2G	23G	female
Tibetan sheep15（Valley）	SAMN03565378	SRR1999366	31.1G	19.1G	female
Tibetan sheep16（Valley）	SAMN03565377	SRR1999363	34.7G	21.2G	female
Tibetan sheep1（Oula）	SAMN04306102	SRR3055051	11.2G	3.8G	female
Tibetan sheep2（Oula）	SAMN04306101	SRR3055050	17.8G	6.1G	female
Tibetan sheep3（Oula）	SAMN04306100	SRR3055048	13.6G	4.6G	female
Tibetan sheep4（Oula）	SAMN04306099	SRR3054976	17.8G	6.1G	female
Tibetan sheep5（Oula）	SAMN04306098	SRR3054905	18.4G	8.7G	female
Tibetan sheep6（Oula）	SAMN04306097	SRR3054904	17.3G	6G	male
Tibetan sheep7（Oula）	SAMN04306096	SRR3043360	13.5G	4.7G	male
Tibetan sheep8（Oula）	SAMN04306095	SRR3043358	15.9G	5.6G	male
Tibetan sheep9（Oula）	SAMN04306093	SRR3043353	14.3G	5.2G	male

Tibetan sheep1 （Prairie）	SAMN04306139	SRR3471450	16.8G	6.1G	female
Tibetan sheep2 （Prairie）	SAMN04306141	SRR3471455	16.0G	5.9G	female
Tibetan sheep3 （Prairie）	SAMN04306140	SRR3471451	10.7G	4.1G	female
Tibetan sheep4 （Prairie）	SAMN04306138	SRR3471448	20.2G	6.9G	female
Tibetan sheep5 （Prairie）	SAMN04306137	SRR3471444	17.3G	6G	female
Tibetan sheep6 （Prairie）	SAMN04306136	SRR3193955	15.5G	5.5G	male
Tibetan sheep7 （Prairie）	SAMN04306135	SRR3193949	7.1G	2.4G	male
Tibetan sheep8 （Prairie）	SAMN04306134	SRR3193947	19G	6.4G	male
Tibetan sheep9 （Prairie）	SAMN04306133	SRR3193937	16.1G	5.5G	male
Tibetan sheep10 （Prairie）	SAMN04306132	SRR3193935	18.7G	6.3G	male
Tibetan sheep11 （Prairie）	SAMN03565383	SRR1999376	30.6G	18.8G	male
Tibetan sheep12 （Prairie）	SAMN03565382	SRR1999375	44.6G	27.4G	male
Tibetan sheep13 （Prairie）	SAMN03565381	SRR1999373	38.7G	23.5G	male
Tibetan sheep14 （Prairie）	SAMN03565380	SRR1999372	31.7G	19.3G	male
Small-tailed Han sheep1	SAMN06161577	SRR5149614	36.3G	15.2G	female
Small-tailed Han sheep2	SAMN04306131	SRR3184750	15.1G	5.1G	female
Small-tailed Han sheep3	SAMN04306129	SRR3184733	14.3G	4.7G	female
Small-tailed Han sheep4	SAMN04306128	SRR3184728	18.4G	6.3G	female
Small-tailed Han sheep5	SAMN04306127	SRR3180891	15.7G	7G	male
Small-tailed Han sheep6	SAMN04306126	SRR3180889	16.1G	7.3G	male
Small-tailed Han sheep7	SAMN04306125	SRR3180887	14.3G	6.6G	male
Small-tailed Han sheep8	SAMN04306124	SRR3180874	12.5G	5.6G	male
Small-tailed Han sheep9	SAMN04306123	SRR3180871	13.2G	4.7G	male
Tan sheep1	SAMN04521026	SRR5337772	57.5G	21.0G	male
Tan sheep2	SAMN04521029	SRR5337769	81.3G	30.4G	male
Tan sheep3	SAMN04521031	SRR5337767	84.2G	31.8G	male

Tan sheep4	SAMN04521032	SRR5337766	86.0G	32.8G	male
Tan sheep5	SAMN04521028	SRR5337770	81.3G	30.8G	male
Tan sheep6	SAMN04306110	SRR3065081	17.0G	6.5G	female
Tan sheep7	SAMN04306111	SRR3065082	18.0G	6.8G	female
Tan sheep8	SAMN04306108	SRR3065079	17.4G	6.7G	female
Tan sheep9	SAMN04521027	SRR5337771	97.8G	37.2G	female
Tan sheep10	SAMN04521030	SRR5337768	81.2G	31.3G	female
Ujimqin sheep1	SAMN04306122	SRR3087388	13.6G	4.9G	female
Ujimqin sheep2	SAMN04306121	SRR3087381	15.1G	5.4G	female
Ujimqin sheep3	SAMN04306120	SRR3087377	17.6G	8.5G	female
Ujimqin sheep4	SAMN04306118	SRR3087354	17.4G	5.7G	female
Ujimqin sheep5	SAMN04306117	SRR3068478	17.9G	5.9G	male
Ujimqin sheep6	SAMN04306116	SRR3068471	18.5G	6.1G	male
Ujimqin sheep7	SAMN04306115	SRR3068467	17.3G	5.7G	male
Ujimqin sheep8	SAMN04306114	SRR3068457	17.8G	5.9G	male
Ujimqin sheep9	SAMN04306113	SRR3068438	18.7G	6.2G	male
Hu sheep 1	SAMN04306092	SRR3043352	18.3G	9G	female
Hu sheep 2	SAMN04306091	SRR3043125	19.9G	6.7G	female
Hu sheep 3	SAMN04306090	SRR3036496	18.1G	8.9G	female
Hu sheep 4	SAMN04306089	SRR3036494	14.5G	5.6G	female
Hu sheep 5	SAMN04306088	SRR3036477	19.2G	8.1G	female
Hu sheep 6	SAMN04306087	SRR3036476	17.7G	6.3G	male
Hu sheep 7	SAMN04306086	SRR3036475	18.4G	6.4G	male
Hu sheep 8	SAMN04306085	SRR3023153	19.2G	8.2G	male
Hu sheep 9	SAMN04306084	SRR3023084	19.8G	8.3G	male
Hu sheep 10	SAMN04306083	SRR3023075	15.9G	6.5G	male

Barag sheep1	SAMN06947432	SRR5534414	14.5G	5.6G	male
Barag sheep2	SAMN06947431	SRR5534403	15.7G	6.1G	male
Barag sheep3	SAMN06947430	SRR5534400	13.5G	5.3G	male
Barag sheep4	SAMN06947429	SRR5534398	14.2G	5.6G	male
Barag sheep5	SAMN06947428	SRR5534378	15.1G	6G	female
Barag sheep6	SAMN06947427	SRR5534377	16.1G	5.7G	female
Barag sheep7	SAMN06947426	SRR5534376	14.9G	5.9G	female
Barag sheep8	SAMN06947425	SRR5534375	14.3G	5.5G	female
Barag sheep9	SAMN06947140	SRR5533820	14.9G	5.9G	female
Barag sheep10	SAMN06947141	SRR5533814	14.3G	5.5G	female
Short tail sheep1	SAMN06947440	SRR5534686	14.2G	5.6G	male
Short tail sheep2	SAMN06947439	SRR5534612	13.7G	5.4G	male
Short tail sheep3	SAMN06947438	SRR5534607	13.2G	5.3G	male
Short tail sheep4	SAMN06947437	SRR5534552	13.2G	5.3G	male
Short tail sheep5	SAMN06947435	SRR5534535	14.2G	5.6G	female
Short tail sheep6	SAMN06947434	SRR5534495	15.5G	6.1G	female
Short tail sheep7	SAMN06947433	SRR5534489	14.6G	5.8G	female
White suffolk1	SAMN07344251	SRR5991196	27.4G	11.5G	male
White suffolk2	SAMN07344015	SRR5991292	47.8G	20.2G	male
White suffolk3	SAMN07344162	SRR5991293	15.1G	6.5G	male
White suffolk4	SAMN07344178	SRR5991294	36.8G	14.1G	male
White suffolk5	SAMN07344029	SRR5991295	34G	13.8G	male
White suffolk6	SAMN07344019	SRR5991296	18.7G	7.8G	male
White suffolk7	SAMN07344018	SRR5991297	64.7G	27.2G	male
White suffolk8	SAMN07344017	SRR5991298	54.8G	23.1G	male
White suffolk9	SAMN07344016	SRR5991299	63.7G	27.1G	male

White suffolk10	SAMN07344347	SRR5991300	44.2G	19.4G	male
White suffolk11	SAMN07344125	SRR5991301	72.5G	32.2G	male
White suffolk12	SAMN07344030	SRR5991302	37.9G	15.4G	male
White suffolk13	SAMN07344346	SRR5991433	42.8G	18.5G	male
Australian Merino1	SAMN04302872	SRR2968869	16.2G	7.9G	male
Australian Merino2	SAMN04302873	SRR2970522	14G	6.8G	male
Australian Merino3	SAMN04302874	SRR2970524	16.7G	8.1G	male
Australian Merino4	SAMN04306052	SRR2976383	3.8G	1.5G	female
Australian Merino5	SAMN04306051	SRR2976380	10.3G	5.3G	female
Australian Merino6	SAMN04306050	SRR2976378	15.2G	7.8G	female
Australian Merino7	SAMN04306049	SRR2973635	16.7G	8.6G	female
Australian Merino8	SAMN04306048	SRR2973610	13.4G	6.5G	female
Australian Merino9	SAMN04306047	SRR2970619	18.2G	8.8G	male
Australian Merino10	SAMN04306046	SRR2970616	17.4G	8.4G	male
Australian Merino11	SAMN07343995	SRR5991165	105.7G	47.8G	male
Australian Merino12	SAMN07344003	SRR5991323	69.4G	29.2G	male
Australian Merino13	SAMN07344008	SRR5991500	46.2G	19.4G	male
Australian Merino14	SAMN07344011	SRR5991496	64G	27G	male
Australian Merino15	SAMN07344023	SRR5991273	40.5G	16.5G	male
Australian Merino16	SAMN07344143	SRR5991324	44.6G	19.4G	male
Australian Merino17	SAMN07344174	SRR5991370	41G	15.4G	male
Australian Merino18	SAMN07344191	SRR5991162	46G	19.2G	male
Australian Merino19	SAMN07344204	SRR5991345	28.7G	11.9G	male
Australian Merino20	SAMN07344213	SRR5991366	29.3G	12.7G	male
Australian Merino21	SAMN07344226	SRR5991160	48.5G	22.2G	male
Australian Merino22	SAMN07344233	SRR5991367	29.9G	12.5G	male

Australian Merino23	SAMN07344234	SRR5991405	32.1G	14G	male
Australian Merino24	SAMN07344245	SRR5991161	30.2G	13G	male
Australian Merino25	SAMN07344326	SRR5991369	40.1G	17.3G	male
Australian Merino26	SAMN07344337	SRR5991346	38.2G	16.7G	male
Australian Merino27	SAMN07344232	SRR5991368	49.3G	20.7G	male
Australian Merino28	SAMN07344344	SRR5991235	41.3G	18G	male
Border leicester1	SAMN07343973	SRR5991214	44.6G	18.9G	male
Border leicester2	SAMN07343974	SRR5991215	21.7G	9.1G	male
Border leicester3	SAMN07344129	SRR5991216	37.5G	16.5G	male
Border leicester4	SAMN07344269	SRR5991217	39.2G	17.1G	male
Border leicester5	SAMN07344037	SRR5991334	34.6G	15.5G	male
Border leicester6	SAMN07344164	SRR5991447	36.4G	13.9G	male
Border leicester7	SAMN07344268	SRR5991451	40.5G	17.4G	male
Border leicester8	SAMN07343972	SRR5991455	89.7G	37.8G	male
Border leicester9	SAMN07344127	SRR5991453	34.2G	14.9G	male
Border leicester10	SAMN07344128	SRR5991454	37.1G	16.2G	male
Poll Dorset1	SAMN07344185	SRR5991225	53.4G	22.9G	male
Poll Dorset2	SAMN07344119	SRR5991226	37.5G	16.8G	male
Poll Dorset3	SAMN07344211	SRR5991227	41.8G	17.9G	male
Poll Dorset4	SAMN07344319	SRR5991276	37.6G	16.2G	male
Poll Dorset5	SAMN07344137	SRR5991394	51.8G	22.9G	male
Poll Dorset6	SAMN07343989	SRR5991395	59.8G	25G	male
Poll Dorset7	SAMN07344020	SRR5991396	35G	14.3G	male
Poll Dorset8	SAMN07344168	SRR5991397	36.6G	14G	male
Poll Dorset9	SAMN07344154	SRR5991492	34.3G	15.1G	male
Poll Dorset10	SAMN07344246	SRR5991493	41.6G	17.5G	male

Supplementary Table S3 Primers used for KASPar detection.

Primer's purpose	Primer name	Primer sequence
KAspar	*IFI44*_AlleleX	GAAGGTGACCAAGTTCATGCTCCACACAATGGATTCTGTCCTTG
	*IFI44*_AlleleY	GAAGGTCGGAGTCAACGGATTCCACACAATGGATTCTGTCCTTC
	*IFI44*_Common	AAGGCATTGGTAACCATACAGGCTG

Supplementary Table S4 Distribution of SNPs within different genomic regions.

Category	Number of SNPs
Intergenic	21661272
Upstream	273106
Downstream	320038
NcRNA_exonic	276728
NcRNA_intronic	1184564
NcRNA_splicing	527
UTR5	207156
UTR3	268918
Intronic	14611625
Exonic	535578
Splicing	1263
Total SNP	39331475

Supplementary Table S5 Statistics on allele frequency changes in 30 sheep breeds.

Group	Breed	Name	(0,25]	(25,50]	(50,75]	(75,100]
African	Timahdite	TI	79.758	16.960	2.995	0.287
	Ouled Djellal	OD	80.218	16.381	3.122	0.278
	Beni Guil	BG	80.201	16.382	3.139	0.278
	Sardi	SA	80.097	16.454	3.172	0.278
	D'man	DM	80.580	16.262	2.922	0.236
Chinese	Altay sheep	AL	78.117	17.259	4.075	0.548
	Tibetan sheep (Oula)	OU	77.717	17.748	4.028	0.507
	Barag sheep	BAR	78.487	17.224	3.810	0.479
	Tibetan sheep (Prairie)	PT	78.411	17.221	3.909	0.460
	Qira Black sheep	CB	78.143	17.546	3.859	0.452
	Short tail sheep	ST	78.815	17.150	3.587	0.448
	Small tailed han sheep	STH	78.372	17.442	3.756	0.430
	Valley Tibetan	VT	78.920	16.920	3.743	0.416
	Large-tailed Han sheep	LH	78.839	17.046	3.698	0.416
	Hu sheep	HU	78.735	17.191	3.666	0.408
	Tan sheep	TAN	78.656	17.285	3.660	0.399
	Lanzhou large-tailed sheep	LL	79.322	16.744	3.547	0.387
	Bayinbuluke sheep	BAY	79.135	17.045	3.467	0.354
	Ujimqin sheep	UJ	79.136	17.075	3.439	0.350
	Mongolian sheep	MG	79.866	16.462	3.334	0.338
Improved breeds	Border leicester	BL	73.588	19.100	5.984	1.328
	East Friesian milk sheep	EF	74.346	18.573	5.819	1.262
	Texel sheep	TE	75.612	18.257	5.191	0.941
	South African mutton merino sheep	NM	76.296	18.064	4.786	0.854
	Dorper sheep	DP	75.952	18.258	4.963	0.827

Black Suffolk sheep	BS	77.198	17.795	4.359	0.649
Australian white sheep	AW	76.848	18.035	4.468	0.648
Dorset polled	PD	77.115	17.862	4.445	0.578
White suffolk	WS	78.769	17.268	3.576	0.387
Australian merino	AM	79.352	16.877	3.411	0.360

Supplementary Table S6 Putatively selected regions in domestic sheep.

No.	Combined region (Mb)	Chromosome	Position		Gene name
			Start	End	
1	Chr1: 20.4-20.55	1	20400001	20550000	*PIK3R3, TSPAN1, POMGNT1, TRNAC-ACA, PIK3R3-TSPAN1*
2	Chr1: 50.77-50.92	1	50775001	50925000	*LHX8, SLC44A5, TYW3-LHX8, LHX8-SLC44A5*
3	Chr1: 54.375-54.525	1	54300001	54450000	*PTGFR, LOC105613526, LOC101110201, LOC101103103, IFI44L, IFI44, LOC105613526-LOC101103103, LOC101110201-IFI44L, IFI44L-IFI44, IFI44-ADGRL4*
		1	54375001	54525000	*IFI44L, IFI44, IFI44L-IFI44, IFI44-ADGRL4*
4	Chr1: 63.075-63.225	1	63075001	63225000	*LOC101116267, LOC105609232, LOC106990167, SH3GLB1, LOC106990167-LOC101116267, LOC105609232-SH3GLB1, SH3GLB1-LOC105614834*
5	Chr1: 119.4-199.65	1	119400001	119550000	*MRPS6, SLC5A3, KCNE2-MRPS6, MRPS6-ATP5O*
		1	199425001	199575000	*IGF2BP2, TRA2B-IGF2BP2*
		1	199500001	199650000	*IGF2BP2, SENP2, IGF2BP2-SENP2*
6	Chr2: 37.275-37.425	2	37275001	37425000	*UBAP2, UBE2R2, DCAF12-UBAP2*

7	Chr2: 71.1-71.325	2	71100001	71250000	*RFX3*
		2	71175001	71325000	*RFX3*
8	Chr2: 72.075-72.225	2	72075001	72225000	*GLIS3, GLIS3-LOC106990941*
9	Chr2: 114.975-115.35	2	114975001	115125000	*LOC101106660-LOC101117569*
		2	115050001	115200000	*LOC101106660-LOC101117569*
		2	115125001	115275000	*LOC101117569, LOC101106660-LOC101117569*
		2	115200001	115350000	*LOC101117569, LOC101106660-LOC101117569, LOC101117569-LOC105608719*
10	Chr2: 122.25-122.475	2	122250001	122400000	*LOC101122056, LOC101120641-LOC101122056, LOC101122056-FSIP2*
		2	122325001	122475000	*FSIP2, LOC101122056, LOC101120641-LOC101122056, LOC101122056-FSIP2*
11	Chr2: 122.625-122.85	2	122625001	122775000	*LOC105608888, LOC105608888-LOC101121406*
		2	122700001	122850000	*LOC105608888-LOC101121406*
12	Chr2: 123-123.15	2	123000001	123150000	*LOC105608888-LOC101121406*
13	Chr2: 184.95-185.1	2	184950001	185100000	*LOC105609957-TRNAW-CCA, TRNAW-CCA, TRNAW-CCA-GLI2*
14	Chr2: 213.75-213.9	2	213750001	213900000	*IKZF2, LOC105610530, LOC105611887-LOC105610530, LOC105610530-IKZF2*
15	Chr2: 214.275-214.425	2	214275001	214425000	*SPAG16*
16	Chr2: 219.375-219.525	2	219375001	219525000	*CTDSP1, rna8716, RQCD1, SLC11A1, USP37, VIL1*
17	Chr3: 1.65-1.8	3	1650001	1800000	*ANAPC2, LOC101109608, LOC106990978, NDOR1, RNF224, SSNA1, TMEM203, TPRN, LOC105607205-TMEM210*

18	Chr3: 18.075-18.3	3	18075001	18225000	*KIDINS220, MBOAT2, KIDINS220-MBOAT2, MBOAT2-LOC101102303*
		3	18150001	18300000	*LOC101102303, MBOAT2, MBOAT2-LOC101102303, LOC101102303-ASAP2*
19	Chr3: 94.425-94.65	3	94425001	94575000	*EXOC6B, LOC105614905, LOC106991063*
		3	94500001	94650000	*LOC105614905, EXOC6B-SPR, EXOC6B*
20	Chr3: 97.725-97.875	3	97725001	97875000	*LOC105612338-TMEM182*
21	Chr3: 124.575-124.875	3	124575001	124725000	*KITLG, KITLG-TRNAG-CCC, TRNAG-CCC*
		3	124650001	124800000	*TRNAG-CCC, KITLG-TRNAG-CCC, TRNAG-CCC-LOC101105320*
		3	124725001	124875000	*TRNAG-CCC, TRNAG-CCC-LOC101105320*
22	Chr3: 129.6-129.75	3	129600001	129750000	*SOCS2-CRADD, CRADD*
23	Chr3: 153.525-153.675	3	153525001	153675000	*HMGA2-LOC105609945, HMGA2*
24	Chr3: 162.075-162.3	3	162075001	162225000	*GPR182, TAC3-ZBTB39, LOC105612238-LOC101104222, LOC101104222, LOC105612238, LOC105612239, MYO1A, NEMP1, SDR9C7, TAC3, ZBTB39*
		3	162150001	162300000	*LOC105612238-LOC101104222, LOC101104897-LOC101105146, LOC101104222, LOC101104897, LOC105612238, LOC105612239, SDR9C7, SDR9C7-LOC101104897*
25	Chr3: 213.6-213.75	3	213600001	213750000	*BAIAP2L2, MAFF, PLA2G6, PLA2G6-MAFF, SLC16A8, TMEM184B*
26	Chr4: 23.7-23.85	4	23700001	23850000	*AGMO*

27	Chr4: 63-63.225	4	63000001	63150000	*BMPER-LOC105612117, LOC105612117-BBS9, LOC105612117*
		4	63075001	63225000	*BBS9, BMPER-LOC105612117, LOC105612117-BBS9, LOC105612117*
28	Chr4: 78.825-78.975	4	78825001	78975000	*GLI3*
29	Chr4: 101.625-101.85	4	101625001	101775000	*AKR1D1-TRIM24*
		4	101700001	101850000	*AKR1D1-TRIM24*
30	Chr4: 111.75-111.9	4	111750001	111900000	*ZNF777-ZNF746, ZNF746-TRNAC-GCA, LOC106991146, TRNAC-GCA, TRNAC-GCA-LOC106991146, ZNF746, ZNF777*
31	Chr5: 7.5-7.725	5	7500001	7650000	*AKAP8, AKAP8L, EPHX3, AKAP8-LOC101123297, EPHX3-NOTCH3, LOC101123297, LOC105615346, NOTCH3*
		5	7575001	7725000	*AKAP8-LOC101123297, LOC101123297, LOC105615346, EPHX3, EPHX3-NOTCH3, LOC101101981, LOC101120324, LOC101120324-LOC101101981, NOTCH3*
32	Chr5: 106.875-107.475	5	106875001	107025000	*SLC25A46-LOC105615337, SLC25A46*
		5	106950001	107100000	*LOC105615337-WDR36, LOC105615337, SLC25A46-LOC105615337*
		5	107025001	107175000	*SLC25A46-LOC105615337, LOC105615337, LOC105615337-WDR36*
		5	107100001	107250000	*LOC105615337-WDR36*

		5	107175001	107325000	*LOC105615337-WDR36, WDR36*
		5	107250001	107400000	*LOC105615337-WDR36, WDR36, LOC106991207, LOC106991207-LOC105615338, WDR36-LOC106991207*
		5	107325001	107475000	*CAMK4, WDR36-LOC106991207, LOC106991207-LOC105615338, LOC105615338-CAMK4, LOC106991207, WDR36*
33	Chr6: 24.6-24.975	6	24600001	24750000	*H2AFZ, LOC106990491-H2AFZ, LOC106990491, TRNAC-GCA-LOC106990491*
		6	24675001	24825000	*DAPP1, DNAJB14, H2AFZ, LOC106990491-H2AFZ, LAMTOR3, LOC106990491, TRNAC-GCA-LOC106990491*
		6	24750001	24900000	*LAMTOR3, DAPP1-LOC105612764, H2AFZ, DNAJB14, DAPP1*
		6	24825001	24975000	*DAPP1, DAPP1-LOC105612764*
34	Chr6: 44.625-44.775	6	44625001	44775000	*ANAPC4, PI4K2B-ZCCHC4, ANAPC4-SLC34A2, PI4K2B, ZCCHC4*
35	Chr6: 53.55-53.775	6	53550001	53700000	*LOC101109539-TRNAC-GCA*
		6	53625001	53775000	*LOC101109539-TRNAC-GCA*
36	Chr6: 80.025-81.75	6	80025001	80175000	*LOC106991226-LOC101119727*
		6	81525001	81675000	*LOC101120245-TRNAW-CCA*
		6	81600001	81750000	*LOC101120245-TRNAW-CCA*
37	Chr6: 115.875-116.1	6	115875001	116025000	*WHSC1-LETM1, LETM1, LOC106991222, WHSC1*

		6	115950001	116100000	*TMEM129, SLBP, LOC106991222, LOC106990166, LETM1, SLBP-CTBP1, WHSC1-LETM1*
38	Chr6: 116.4-116.55	6	116400001	116550000	*CPLX1, DGKQ, GAK, TMEM175-GAK, GAK-CPLX1, CPLX1-LOC105615565, TMEM175*
39	Chr7: 43.425-43.575	7	43425001	43575000	*FBXL22, USP3*
40	Chr7: 72.525-72.675	7	72525001	72675000	*LOC105615745, PPP2R5E*
41	Chr8: 89.4-89.625	8	89400001	89550000	*SMOC2-THBS2*
		8	89475001	89625000	*SMOC2-THBS2*
42	Chr9: 25.35-25.5	9	25350001	25500000	*LOC106990507, LOC106990507-MYC, LOC105616004-LOC106990507*
43	Chr9: 30.825-30.975	9	30825001	30975000	*LOC101110341-LOC101110602, LOC101110602-TRNAM-CAU, LOC101110068-LOC101110341, LOC101110341, LOC101110602*
44	Chr9: 36-36.225	9	36000001	36150000	*CHCHD7, RPS20-MOS, MOS-PLAG1, CHCHD7-SDR16C5, MOS, PLAG1, RPS20*
		9	36075001	36225000	*CHCHD7, CHCHD7-SDR16C5, SDR16C5-LOC101116323, LOC101116323, PLAG1, SDR16C5*
45	Chr9: 37.735-37.95	9	37725001	37875000	*TOX*
		9	37800001	37950000	*TRNAC-GCA, TOX*
46	Chr10: 7.425-7.65	10	7425001	7575000	*LOC101105926-LOC101121613*
		10	7500001	7650000	*LOC101105926-LOC101121613*
47	Chr10: 31.875-32.025	10	31875001	32025000	*PAN3, FLT1*
48	Chr10: 37.5-38.025	10	37500001	37650000	*ATP12A-LOC105614068*

		10	37575001	37725000	*LOC105614068-LOC101120586, LOC105614068, ATP12A-LOC105614068*
		10	37650001	37800000	*LOC105614068-LOC101120586, LOC105614068, ATP12A-LOC105614068*
		10	37725001	37875000	*LOC105614068-LOC101120586*
		10	37800001	37950000	*LOC105614068-LOC101120586*
		10	37875001	38025000	*LOC105614068-LOC101120586, LOC101120586-LOC101120503, LOC101120586*
49	Chr10: 41.775-41.925	10	41775001	41925000	*LOC101121273-LOC101121526*
50	Chr10: 42.6-42.75	10	42600001	42750000	*LOC101121526-TRNAW-CCA*
51	Chr10: 43.35-43.5	10	43350001	43500000	*LOC101121526-TRNAW-CCA*
52	Chr10: 75.15-75.3	10	75150001	75300000	*LOC105616225, LOC105616225-UBAC2, DOCK9*
53	Chr11: 10.725-10.875	11	10725001	10875000	*BRIP1, INTS2*
54	Chr11: 24.6-24.75	11	24600001	24750000	*XAF1, TEKT1, SMTNL2, MYBBP1A, LOC105610748, LOC105610740, LOC101112994, XAF1-LOC101112994, TEKT1-SMTNL2, GGT6, FBXO39*
55	Chr12: 78.75-78.9	12	78750001	78900000	*SHISA4, NAV1, LOC105610031, IPO9, LOC105610030-LOC105610031, SHISA4-LOC105610030*
56	Chr13: 49.2-49.35	13	49200001	49350000	*LOC101110166-LOC101110438*
57	Chr13: 49.5-49.95	13	49500001	49650000	*LOC101110166-LOC101110438*
		13	49575001	49725000	*LOC101110166-LOC101110438, LOC101110438, LOC101110438-HAO1*

		13	49650001	49800000	*LOC101110438-HAO1, LOC101110166-LOC101110438, LOC101110438*
		13	49725001	49875000	*LOC101110438-HAO1*
		13	49800001	49950000	*HAO1, LOC101110438-HAO1*
58	Chr13: 50.175-50.625	13	50175001	50325000	*SMOX, SMOX-LOC105606258, ADRA1D-SMOX, ADRA1D*
		13	50250001	50400000	*LOC105606258-RNF24, LOC105606258, SMOX-LOC105606258*
		13	50325001	50475000	*SMOX-LOC105606258, LOC105606258, LOC105606258-RNF24, RNF24*
		13	50400001	50550000	*PANK2, LOC105606258-RNF24, RNF24*
		13	50475001	50625000	*AP5S1, PANK2-MAVS, LOC105606256-AP5S1, MAVS, PANK2, RNF24*
59	Chr13: 53.175-53.325	13	53175001	53325000	*ABHD16B, ARFRP1, ABHD16B-ZBTB46, LIME1, RTEL1, STMN3, TNFRSF6B, TPD52L2, ZBTB46, ZGPAT*
60	Chr13: 63-63.15	13	63000001	63150000	*LOC101112245-ASIP, ASIP, ASIP-AHCY*
61	Chr14: 34.275-34.575	14	34275001	34425000	*AGRP, ATP6V0D1, CTCF, FAM65A, HSD11B2, FAM65A-LOC106991595, LOC105606370, LOC105606370-FAM65A, LOC106991595, ZDHHC1*
		14	34350001	34500000	*ACD, ACTB, C14H16orf86, CTCF, FAM65A, GFOD2, FAM65A-LOC106991595, LOC105606370-FAM65A, LOC106991595, PARD6A, RLTPR*

		14	34425001	34575000	*ACD, ACTB, C14H16orf86, CTCF, GFOD2, PARD6A, RANBP10, RLTPR, TRNAG-CCC, TSNAXIP1*
62	Chr15: 21.825-21.975	15	21825001	21975000	*BCO2, IL18, LOC101112255, LOC105602162, PTS, TEX12*
63	Chr15: 47.55-47.7	15	47550001	47700000	*LOC101104933-LOC101105186, LOC101105186-LOC101105439, LOC101105686-LOC101105946, LOC101106712, LOC101104177, LOC101104177-LOC101104426, LOC101104426, LOC101104685, LOC101104933, LOC101105186, LOC101105439, LOC101105686, LOC101105946, LOC101106201, LOC101106459, LOC101106459-LOC101106712*
64	Chr16: 70.8-70.95	16	70800001	70950000	*TRIP13, TPPP, LOC105602658, LOC105602658-LOC101110873, TRIP13-LOC105602658, CEP72, BRD9*
65	Chr17: 33-33.15	17	33000001	33150000	*LOC101101922-LOC105608293, ANKRD50-LOC101101922, LOC101101922*
66	Chr17: 45.45-45.6	17	45450001	45600000	*ADGRD1, LOC106990371-ADGRD1*
67	Chr17: 52.125-52.275	17	52125001	52275000	*ABCB9, ARL6IP4, CCDC62, HIP1R, OGFOD2, VPS37B*
68	Chr17: 52.425-52.575	17	52425001	52575000	*ZCCHC8, RSRC2, KNTC1, CLIP1*
69	Chr17: 53.475-53.7	17	53475001	53625000	*CAMKK2, P2RX4-P2RX7, P2RX7-IFT81, IFT81, P2RX4, P2RX7*
		17	53550001	53700000	*P2RX7-IFT81, IFT81, P2RX7*
70	Chr17: 59.4-59.55	17	59400001	59550000	*LOC105602894-TBX3*

71	Chr17: 64.95-65.1	17	64950001	65100000	*ADRBK2, CRYBB2, CRYBB2-ADRBK2, CRYBB3, KIAA1671*
72	Chr18: 23.625-23.85	18	23625001	23775000	*MEX3B-MORF4L1*
		18	23700001	23850000	*MEX3B-MORF4L1*
73	Chr18: 29.325-29.475	18	29325001	29475000	*TRNAS-CGA, TBC1D2B, LOC101113889, ADAMTS7*
74	Chr18: 32.1-32.475	18	32100001	32250000	*SNUPN-PTPN9, IMP3, PTPN9, SNUPN, SNX33*
		18	32175001	32325000	*SIN3A, PTPN9, MAN2C1*
		18	32250001	32400000	*COMMD4, COMMD4-LOC105603152, LOC105603152, LOC105603296, MAN2C1, NEIL1, PTPN9, SIN3A*
		18	32325001	32475000	*C18H15orf39, COMMD4, LOC105603152, LOC105603154, LOC105603296, MAN2C1, NEIL1, SIN3A*
75	Chr18: 45.075-45.6	18	45075001	45225000	*BRMS1L-LOC101104531, LOC101104787-LOC106991743, LOC101104531, LOC101104531-LOC101104787, LOC101104787, LOC106991743*
		18	45150001	45300000	*LOC101104787-LOC106991743, LOC101104787, LOC106991743*
		18	45225001	45375000	*MBIP-LOC106991744, LOC106991743, MBIP*
		18	45375001	45525000	*MBIP-LOC106991744, LOC106991743, LOC106991745*

		18	45450001	45600000	*NKX2-1, LOC106991745, LOC106991744*
76	Chr18: 65.85-66.15	18	65850001	66000000	*ANKRD9-RCOR1, ANKRD9*
		18	65925001	66075000	*RCOR1, RCOR1-TRAF3, ANKRD9-RCOR1*
		18	66000001	66150000	*TRAF3, RCOR1, RCOR1-TRAF3, ANKRD9-RCOR1*
77	Chr19: 60.375-60.525	19	60375001	60525000	*LOC106990579, KLF15, KLF15-CFAP100, CFAP100*
78	Chr20: 10.8-10.95	20	10800001	10950000	*PPIL1, PI16, MTCH1-LOC105603679, MTCH1, LOC105603679-FGD2, LOC105603679, FGD2, CPNE5-PPIL1, C20H6orf89-PI16*
79	Chr20: 15-15.225	20	15000001	15150000	*TRNAG-UCC, TREML2-TREM1, TREML2, TREML1, TREM2-TREML2, TREM2, OARD1, NFYA, LOC101108001, APOBEC2*
		20	15075001	15225000	*LOC101108001, TREM1, TREM1-LOC105603703, TREM2, TREM2-TREML2, TRNAG-UCC, TREML1, TREML2, TREML2-TREM1*
80	Chr20: 49.95-50.4	20	49950001	50100000	*LOC105603912, GMDS*
		20	50025001	50175000	*LOC105603912, GMDS*
		20	50100001	50250000	*LOC105603912, GMDS*
		20	50175001	50325000	*LOC105603912, GMDS, FOXC1-TRNAS-GGA, FOXC1*
		20	50250001	50400000	*TRNAS-GGA-LOC106990336, GMDS, FOXC1*
81	Chr20: 50.7-51.15	20	50700001	50850000	*IRF4, EXOC2*
		20	50775001	50925000	*DUSP22, EXOC2, EXOC2-IRF4, IRF4, IRF4-DUSP22*

		20	50850001	51000000	*DUSP22, IRF4, IRF4-DUSP22, LOC105603919*
		20	50925001	51075000	*DUSP22, LOC105603919, LOC105603919-CHR_END*
		20	51000001	51150000	*LOC105603919-CHR_END*
82	Chr21: 39.15-39.3	21	39150001	39300000	*CPSF7, DDB1, LOC101106637, LOC105604096, LRRC10B, PPP1R32, PPP1R32-LRRC10B, SDHAF2, SDHAF2-PPP1R32, SYT7, TKFC, TMEM138, TMEM216*
83	Chr21: 49.35-49.5	21	49350001	49500000	*RNH1, RASSF7, PTDSS2, PHRF1, LRRC56, LOC106991826, LMNTD2, IRF7, HRAS, CDHR5*
84	Chr21: 49.575-49.8	21	49575001	49725000	*PSMD13, NLRP6-PSMD13, NLRP6, LOC105604159-LOC101105867, LOC105604159, LOC101105867, IFITM5, IFITM3, B4GALNT4, ATHL1*
		21	49650001	49800000	*SIRT3, SCGB1C1, RIC8A, PSMD13, ODF3, NLRP6-PSMD13, NLRP6, IFITM5, BET1L, ATHL1*
85	Chr24: 10.35-10.5	24	10350001	10500000	*ZC3H7A, TXNDC11, SNN, LOC105604663, LITAF-SNN*
	Chr24: 32.625-32.775	24	32625001	32775000	*GTF2I, LOC101112784, NCF1, TRNAC-ACA*
86	Chr24: 34.575-34.8	24	34575001	34725000	*TRNAG-CCC, TRNAE-UUC, LOC106991890, LOC105604781, LOC105604780, CUX1*
		24	34650001	34800000	*CUX1, LOC105604780*
87	Chr24: 41.55-42.075	24	41550001	41700000	*LOC106991921, LOC105604883, DNAAF5*

		24	41625001	41775000	*LOC106991898, FAM20C*
		24	41700001	41850000	*LOC106991898, FAM20C*
		24	41850001	42000000	*LOC105604839, LOC105604839*
		24	41925001	42075000	*LOC105604839*
88	Chr27: 76.275-76.5	X	76275001	76425000	*LOC101106825*
		X	76350001	76500000	*LOC101116810*
89	Chr27: 135.075-135.5	X	135075001	135225000	*PABPC5*
		X	135150001	135300000	*PABPC5*

Supplementary Table S7 Kyoto Encyclopedia of Genes and Genomes (KEGG) enrichment analysis of candidate genes during domestication.

Term	Input number	Background number	*P*-Value	Input
Thyroid hormone signaling pathway	5	121	0.0037528	*HRAS, SIN3A, PIK3R3, ACTB, NOTCH3*
Hepatitis B	6	183	0.00461858	*DDB1, IRF7, HRAS, TRAF3, PIK3R3, MAVS*
NOD-like receptor signaling pathway	6	187	0.00510821	*IL18, NLRP6, IRF7, TRAF3, MAVS, P2RX7*
Influenza A	6	198	0.0066506	*IL18, TRAF3, IRF7, PIK3R3, ACTB, MAVS*
Longevity regulating pathway	4	90	0.00735024	*CAMKK2, HRAS, PIK3R3, CAMK4*
Progesterone-mediated oocyte maturation	4	91	0.00762542	*MOS, ANAPC2, PIK3R3, ANAPC4*
Phospholipase D signaling pathway	5	148	0.00843512	*PTGFR, DGKQ, PIK3R3, HRAS, KITLG*
Rap1 signaling pathway	6	215	0.00966168	*HRAS, PARD6A, PIK3R3, KITLG, ACTB, FLT1*
Choline metabolism in cancer	4	101	0.01075578	*HRAS, DGKQ, PIK3R3, SLC44A5*
Glycerophospholipid metabolism	4	102	0.01110801	*PLA2G6, MBOAT2, PTDSS2, DGKQ*
Glycerolipid metabolism	3	63	0.01669877	*MBOAT2, DGKQ, TKFC*
Viral carcinogenesis	6	244	0.01685566	*TRAF3, IRF7, HRAS, PIK3R3, ATP6V0D1, DDB1*
Epstein-Barr virus infection	6	245	0.01715522	*TRAF3, IRF7, PSMD13, PIK3R3, MAVS, SIN3A*
Hepatitis C	5	178	0.0172026	*PIK3R3, HRAS, MAVS, IRF7, TRAF3*

RIG-I-like receptor signaling pathway	4	118	0.01777726	*TRAF3, MAVS, IRF7, TKFC*
Oocyte meiosis	4	121	0.01925289	*MOS, PPP2R5E, ANAPC2, ANAPC4*
Central carbon metabolism in cancer	3	68	0.0202525	*SIRT3, HRAS, PIK3R3*
Neurotrophin signaling pathway	4	125	0.02133512	*HRAS, PIK3R3, CAMK4, KIDINS220*
Cytosolic DNA-sensing pathway	3	74	0.02502338	*IL18, MAVS, IRF7*
Autophagy - animal	4	133	0.02590012	*CAMKK2, HRAS, PIK3R3, SH3GLB1*
Osteoclast differentiation	4	134	0.0265088	*NCF1, PIK3R3, CAMK4, TREM2*
Glioma	3	76	0.02673646	*HRAS, PIK3R3, CAMK4*
Calcium signaling pathway	5	203	0.02798658	*P2RX4, PTGFR, CAMK4, P2RX7, ADRA1D*
B cell receptor signaling pathway	3	78	0.02851078	*HRAS, DAPP1, PIK3R3*
Fructose and mannose metabolism	2	35	0.03642411	*GMDS, TKFC*
Ubiquitin mediated proteolysis	4	149	0.03667167	*DDB1, UBE2R2, ANAPC4, ANAPC2*
Human papillomavirus infection	7	376	0.03790055	*TRAF3, HRAS, PARD6A, NOTCH3, PIK3R3, PPP2R5E, ATP6V0D1*
Oxytocin signaling pathway	4	154	0.04049353	*CAMKK2, HRAS, CAMK4, ACTB*
Aldosterone-regulated sodium reabsorption	2	38	0.04199087	*HSD11B2, PIK3R3*
Fc gamma R-mediated phagocytosis	3	94	0.04488055	*PLA2G6, NCF1, PIK3R3*
mTOR signaling pathway	4	160	0.04536774	*HRAS, PIK3R3, CLIP1, LAMTOR3*
Endocrine resistance	3	96	0.0471933	*HRAS, PIK3R3, NOTCH3*
mRNA surveillance pathway	3	99	0.05077046	*CPSF7, PPP2R5E, PABPC5*
Ras signaling pathway	5	242	0.05196266	*PLA2G6, HRAS, PIK3R3, KITLG, FLT1*
Measles	4	168	0.05235431	*PIK3R3, MAVS, IRF7, TRAF3*
Rheumatoid arthritis	3	101	0.05322645	*IL18, ATP6V0D1, FLT1*
Phosphatidylinositol signaling system	3	101	0.05322645	*PI4K2B, DGKQ, PIK3R3*
Melanogenesis	3	103	0.05573872	*HRAS, KITLG, ASIP*

Cholinergic synapse	3	111	0.06633804	*HRAS, PIK3R3, CAMK4*
Leukocyte transendothelial migration	3	117	0.07484619	*NCF1, PIK3R3, ACTB*
Toll-like receptor signaling pathway	3	119	0.07778479	*PIK3R3, TRAF3, IRF7*
AMPK signaling pathway	3	125	0.08689739	*CAMKK2, PIK3R3, PPP2R5E*
Endometrial cancer	2	59	0.08829447	*HRAS, PIK3R3*
Lysosome	3	126	0.0884584	*ABCB9, ATP6V0D1, SLC11A1*
Sphingolipid signaling pathway	3	126	0.0884584	*PPP2R5E, HRAS, PIK3R3*
VEGF signaling pathway	2	60	0.0907666	*HRAS, PIK3R3*
Focal adhesion	4	208	0.09539122	*HRAS, PIK3R3, ACTB, FLT1*
Longevity regulating pathway - multiple species	2	63	0.09830238	*HRAS, PIK3R3*
Non-small cell lung cancer	2	66	0.10600717	*HRAS, PIK3R3*
Kaposi sarcoma-associated herpesvirus infection	4	217	0.1068284	*PIK3R3, HRAS, TRAF3, IRF7*
Apelin signaling pathway	3	138	0.1080807	*HRAS, CAMK4, NOTCH3*
Taurine and hypotaurine metabolism	1	13	0.10810641	*GGT6*
Fc epsilon RI signaling pathway	2	67	0.10861081	*HRAS, PIK3R3*
Acute myeloid leukemia	2	67	0.10861081	*HRAS, PIK3R3*
Regulation of actin cytoskeleton	4	219	0.10945108	*MOS, HRAS, PIK3R3, ACTB*
Alcoholism	4	219	0.10945108	*CAMKK2, HRAS, CAMK4, H2AFZ*
Yersinia infection	3	141	0.11323028	*IL18, ACTB, PIK3R3*
Long-term potentiation	2	69	0.11386846	*HRAS, CAMK4*
Melanoma	2	72	0.12187425	*HRAS, PIK3R3*
Renal cell carcinoma	2	73	0.12457295	*HRAS, PIK3R3*
Adipocytokine signaling pathway	2	73	0.12457295	*CAMKK2, AGRP*
Fluid shear stress and atherosclerosis	3	149	0.1274029	*NCF1, PIK3R3, ACTB*

Bacterial invasion of epithelial cells	2	77	0.13550725	*ACTB, PIK3R3*
Apoptosis	3	154	0.13656686	*HRAS, PIK3R3, ACTB*
Breast cancer	3	155	0.13842634	*HRAS, PIK3R3, NOTCH3*
Chronic myeloid leukemia	2	79	0.1410525	*HRAS, PIK3R3*
Synaptic vesicle cycle	2	80	0.14384329	*ATP6V0D1, CPLX1*
Human T-cell leukemia virus 1 infection	4	246	0.14753046	*HRAS, ANAPC2, PIK3R3, ANAPC4*
Pantothenate and CoA biosynthesis	1	19	0.15079871	*PANK2*
EGFR tyrosine kinase inhibitor resistance	2	83	0.15228383	*HRAS, PIK3R3*
RNA degradation	2	83	0.15228383	*PAN3, PABPC5*
Salmonella infection	2	88	0.16655695	*IL18, ACTB*
ErbB signaling pathway	2	89	0.16943927	*HRAS, PIK3R3*
Other glycan degradation	1	22	0.17137573	*MAN2C1*
Ribosome biogenesis in eukaryotes	2	90	0.17233004	*IMP3, WDR36*
Prolactin signaling pathway	2	90	0.17233004	*HRAS, PIK3R3*
Herpes simplex virus 1 infection	6	457	0.17731106	*ZNF746, TRAF3, IRF7, PIK3R3, ZNF777, MAVS*
Mannose type O-glycan biosynthesis	1	23	0.17812384	*POMGNT1*
Colorectal cancer	2	92	0.17813564	*HRAS, PIK3R3*
PD-L1 expression and PD-1 checkpoint pathway in cancer	2	92	0.17813564	*HRAS, PIK3R3*
RNA transport	3	178	0.1833528	*SNUPN, SENP2, PABPC5*
Endocytosis	4	269	0.18342252	*HRAS, VPS37B, PARD6A, SH3GLB1*
Phagosome	3	180	0.18743102	*NCF1, ATP6V0D1, ACTB*
Prostate cancer	2	97	0.19277525	*HRAS, PIK3R3*
Neuroactive ligand-receptor	5	372	0.19440404	*PTGFR, TAC3, ADRA1D, P2RX7, P2RX4*

interaction				
Hepatocellular carcinoma	3	184	0.19565718	*HRAS, PIK3R3, ACTB*
Metabolic pathways	16	1540	0.20044239	*B4GALNT4, PTDSS2, PANK2, SMOX, POMGNT1, HSD11B2, DGKQ, PI4K2B, PLA2G6, MBOAT2, GMDS, GGT6, TKFC, HAO1, ATP6V0D1, PTS*
Small cell lung cancer	2	100	0.20163305	*TRAF3, PIK3R3*
Chemokine signaling pathway	3	188	0.20397066	*NCF1, PIK3R3, HRAS*
Transcriptional misregulation in cancer	3	189	0.20606188	*SIN3A, HMGA2, FLT1*
Axon guidance	3	191	0.21025901	*HRAS, PIK3R3, PARD6A*
Collecting duct acid secretion	1	28	0.21105258	*ATP6V0D1*
alpha-Linolenic acid metabolism	1	28	0.21105258	*PLA2G6*
Inflammatory mediator regulation of TRP channels	2	106	0.21947937	*PLA2G6, PIK3R3*
Folate biosynthesis	1	30	0.22385333	*PTS*
MicroRNAs in cancer	3	198	0.22509247	*HRAS, HMGA2, NOTCH3*
PI3K-Akt signaling pathway	5	398	0.23206245	*PPP2R5E, HRAS, PIK3R3, KITLG, FLT1*
AGE-RAGE signaling pathway in diabetic complications	2	111	0.23445038	*HRAS, PIK3R3*
T cell receptor signaling pathway	2	112	0.23745238	*HRAS, PIK3R3*
C-type lectin receptor signaling pathway	2	112	0.23745238	*HRAS, PIK3R3*
HIF-1 signaling pathway	2	113	0.24045644	*PIK3R3, FLT1*
Base excision repair	1	33	0.24266783	*NEIL1*
MAPK signaling pathway	4	305	0.24442798	*HRAS, LAMTOR3, KITLG, FLT1*
Glyoxylate and dicarboxylate	1	35	0.25495791	*HAO1*

metabolism				
SNARE interactions in vesicular transport	1	35	0.25495791	*BET1L*
Tuberculosis	3	212	0.25531633	*IL18, ATP6V0D1, NFYA*
Linoleic acid metabolism	1	36	0.26102829	*PLA2G6*
Proteoglycans in cancer	3	215	0.26186973	*HRAS, PIK3R3, ACTB*
beta-Alanine metabolism	1	38	0.27302175	*SMOX*
African trypanosomiasis	1	39	0.27894562	*IL18*
Platelet activation	2	127	0.282605	*ACTB, PIK3R3*
Carbon metabolism	2	127	0.282605	*HAO1, TKFC*
Bladder cancer	1	40	0.28482144	*HRAS*
TNF signaling pathway	2	128	0.28561397	*TRAF3, PIK3R3*
Cell cycle	2	129	0.28862169	*ANAPC2, ANAPC4*
Thyroid cancer	1	41	0.29064959	*HRAS*
Pathways in cancer	6	551	0.30137468	*TRAF3, HRAS, NOTCH3, GLI3, PIK3R3, KITLG*
Carbohydrate digestion and absorption	1	43	0.30216444	*PIK3R3*
Homologous recombination	1	43	0.30216444	*BRIP1*
Vascular smooth muscle contraction	2	134	0.30363557	*PLA2G6, ADRA1D*
Relaxin signaling pathway	2	135	0.30663221	*HRAS, PIK3R3*
Proteasome	1	45	0.31349322	*PSMD13*
Estrogen signaling pathway	2	138	0.31560693	*HRAS, PIK3R3*
FoxO signaling pathway	2	138	0.31560693	*HRAS, PIK3R3*
Nucleotide excision repair	1	46	0.31908876	*DDB1*
cAMP signaling pathway	3	242	0.32153683	*GLI3, PIK3R3, CAMK4*
Type II diabetes mellitus	1	47	0.32463891	*PIK3R3*

Arginine and proline metabolism	1	48	0.33014402	*SMOX*
Basal transcription factors	1	48	0.33014402	*GTF2I*
Signaling pathways regulating pluripotency of stem cells	2	143	0.33050496	*HRAS, PIK3R3*
Hedgehog signaling pathway	1	49	0.33560446	*GLI3*
Human immunodeficiency virus 1 infection	3	249	0.33708644	*HRAS, DDB1, PIK3R3*
Insulin signaling pathway	2	146	0.33940149	*HRAS, PIK3R3*
Natural killer cell mediated cytotoxicity	2	147	0.34235913	*HRAS, PIK3R3*
Notch signaling pathway	1	51	0.34639278	*NOTCH3*
Ether lipid metabolism	1	51	0.34639278	*PLA2G6*
Fanconi anemia pathway	1	52	0.35172136	*BRIP1*
Amino sugar and nucleotide sugar metabolism	1	54	0.36224915	*GMDS*
Adrenergic signaling in cardiomyocytes	2	154	0.3629392	*PPP2R5E, ADRA1D*
Malaria	1	56	0.37260674	*IL18*
Regulation of lipolysis in adipocytes	1	56	0.37260674	*PIK3R3*
Hippo signaling pathway	2	158	0.3745918	*ACTB, PARD6A*
Long-term depression	1	58	0.38279688	*HRAS*
Gastric cancer	2	163	0.38903446	*HRAS, PIK3R3*
Cellular senescence	2	169	0.40616881	*HRAS, PIK3R3*
cGMP-PKG signaling pathway	2	171	0.4118294	*GTF2I, ADRA1D*
Glutathione metabolism	1	64	0.41238928	*GGT6*
Basal cell carcinoma	1	66	0.42193611	*GLI3*

Mitophagy - animal	1	67	0.42665147	*HRAS*
Legionellosis	1	68	0.43132854	*IL18*
Amphetamine addiction	1	68	0.43132854	*CAMK4*
Steroid hormone biosynthesis	1	69	0.43596763	*HSD11B2*
Tight junction	2	181	0.43972199	*ACTB, PARD6A*
Adherens junction	1	72	0.44966008	*ACTB*
Retinol metabolism	1	74	0.45860404	*SDR16C5*
Arachidonic acid metabolism	1	75	0.46302162	*PLA2G6*
Pancreatic cancer	1	75	0.46302162	*PIK3R3*
Inflammatory bowel disease (IBD)	1	75	0.46302162	*IL18*
Inositol phosphate metabolism	1	76	0.46740331	*PI4K2B*
ABC transporters	1	76	0.46740331	*ABCB9*
Arrhythmogenic right ventricular cardiomyopathy (ARVC)	1	76	0.46740331	*ACTB*
Leishmaniasis	1	77	0.47174941	*NCF1*
Viral myocarditis	1	81	0.48878362	*ACTB*
Peroxisome	1	85	0.50527097	*HAO1*
Platinum drug resistance	1	88	0.51728815	*PIK3R3*
Huntington disease	2	212	0.52128644	*RCOR1, SIN3A*
Gap junction	1	91	0.52901473	*HRAS*
Hypertrophic cardiomyopathy (HCM)	1	92	0.53286023	*ACTB*
IL-17 signaling pathway	1	92	0.53286023	*TRAF3*
GnRH signaling pathway	1	93	0.53667447	*HRAS*
Viral protein interaction with cytokine and cytokine receptor	1	94	0.54045771	*IL18*
Dilated cardiomyopathy (DCM)	1	95	0.5442102	*ACTB*

Antigen processing and presentation	1	96	0.54793219	*NFYA*
Amoebiasis	1	96	0.54793219	*PIK3R3*
Aldosterone synthesis and secretion	1	99	0.5589176	*CAMK4*
Salivary secretion	1	100	0.56252002	*ADRA1D*
Jak-STAT signaling pathway	2	234	0.57418367	*HRAS, PIK3R3*
NF-kappa B signaling pathway	1	104	0.57663921	*TRAF3*
Th1 and Th2 cell differentiation	1	104	0.57663921	*NOTCH3*
Insulin resistance	1	111	0.60026492	*PIK3R3*
Serotonergic synapse	1	113	0.60677075	*HRAS*
Thermogenesis	2	251	0.61207369	*HRAS, ACTB*
Hematopoietic cell lineage	1	117	0.6194679	*KITLG*
Human cytomegalovirus infection	2	255	0.62060814	*HRAS, PIK3R3*
Chagas disease (American trypanosomiasis)	1	118	0.6225779	*PIK3R3*
Ribosome	2	258	0.626914	*MRPS6, RPS20*
Th17 cell differentiation	1	120	0.62872219	*IRF4*
Dopaminergic synapse	1	132	0.66355217	*PPP2R5E*
Oxidative phosphorylation	1	151	0.71216662	*ATP6V0D1*
Spliceosome	1	155	0.72147369	*PPIL1*
Non-alcoholic fatty liver disease (NAFLD)	1	164	0.74133376	*PIK3R3*
Wnt signaling pathway	1	168	0.74970175	*SENP2*
Systemic lupus erythematosus	1	175	0.76370244	*H2AFZ*
Necroptosis	1	190	0.79113357	*H2AFZ*
Cytokine-cytokine receptor interaction	2	358	0.79329466	*IL18, TNFRSF6B*

Supplementary Table S8 Human Phenotype Ontology (HPO) analysis of candidate genes during domestication.

Term	Id	*P*-value	Gene name
Iris coloboma	HP:0000612	0.00000	*ACTB, CPLX1, CRYBB2, HRAS, LETM1, NOTCH3, POMGNT1, SIN3A, TMEM138, TMEM216*
Abnormality iris morphology	HP:0000525	0.00000	*ACTB, BRIP1, CPLX1, CRYBB2, FOXC1, GTF2I, HRAS, KITLG, LETM1, NOTCH3, POMGNT1, SIN3A, TMEM138, TMEM216, TRIP13*
Coloboma	HP:0000589	0.00600	*ACTB, CPLX1, CRYBB2, HRAS, LETM1, NOTCH3, POMGNT1, SIN3A, TMEM138, TMEM216*
Ocular anterior segment dysgenesis	HP:0007700	0.01700	*BRIP1, CPLX1, CRYBB2, CRYBB3, FOXC1, GLIS3, GTF2I, LETM1, POMGNT1, TMEM216, TRIP13*
Abnormality of the eye	HP:0000478	0.02000	*ACD, ACTB, BBS9, BRIP1, CLIP1, CPLX1, CRADD, CRYBB2, CRYBB3, CTCF, CUX1, DNAAF5, EXOC6B, FAM20C, FLT1, FOXC1, GLI3, GLIS3, GTF2I, HRAS, HSD11B2, IFITM5, IFT81, KIDINS220, KITLG, LETM1, NCF1, NOTCH3, PANK2, PLA2G6, POMGNT1, PTS, RTEL1, SIN3A, SLC25A46, TAC3, TKFC, TMEM138, TMEM216, TREM2, TRIP13, WDR36*
Aplasia/Hypoplasia affecting the eye	HP:0008056	0.02000	*ACTB, BRIP1, CPLX1, FOXC1, GLI3, GTF2I, HRAS, LETM1, POMGNT1, SIN3A, TKFC, TMEM216, TRIP13*
Aplasia/Hypoplasia affecting the uvea	HP:0008055	0.03300	*BRIP1, CPLX1, FOXC1, GTF2I, LETM1, TMEM216, TRIP13*
Abnormal uvea morphology	HP:0000553	0.00800	*ACTB, BRIP1, CPLX1, CRYBB2, FOXC1, GTF2I, HRAS, KITLG, LETM1, NOTCH3, POMGNT1, SIN3A, TMEM138, TMEM216, TRIP13*
Aplasia/Hypoplasia of the iris	HP:0008053	0.03300	*BRIP1, CPLX1, FOXC1, GTF2I, LETM1, TMEM216, TRIP13*
Posteriorly rotated ears	HP:0000358	0.03800	*BBS9, CTCF, FAM20C, GLI3, GTF2I, HRAS, LETM1, NOTCH3, POMGNT1, TMEM138, TMEM216, TRIP13*

Ventriculomegaly	HP:0002119	0.00200	*ACD, ACTB, BRIP1, CPLX1, CTCF, CUX1, DNAAF5, GLI3, HRAS, KIDINS220, LETM1, POMGNT1, RTEL1, SIN3A, TMEM138, TMEM216, TREM2, TRIP13*
Abnormality of body weight	HP:0004323	0.01600	*ACD, ACTB, AGRP, BBS9, BRIP1, CPLX1, CTCF, EXOC6B, FLT1, GLI3, GTF2I, HRAS, HSD11B2, IGF2BP2, KIDINS220, LETM1, NKX2-1, PANK2, PLA2G6, PLAG1, POMGNT1, PTS, RTEL1, SIN3A, SLC11A1, TAC3, TKFC, TMEM216, TRIP13*
Abnormality of the cerebral ventricles	HP:0002118	0.01800	*ACD, ACTB, BRIP1, CPLX1, CTCF, CUX1, DNAAF5, FAM20C, GLI3, HRAS, KIDINS220, LETM1, POMGNT1, RTEL1, SIN3A, TMEM138, TMEM216, TREM2, TRIP13*
Spina bifida	HP:0002414	0.02600	*ACTB, BRIP1, GLI3, GTF2I, NOTCH3, POMGNT1, SIN3A, TMEM216*
Abnormality of the calvaria	HP:0002683	0.03100	*ACTB, BRIP1, CPLX1, CTCF, EXOC6B, FAM20C, GLI3, GLIS3, HRAS, IFITM5, IFT81, KIDINS220, LETM1, NKX2-1, NOTCH3, PLA2G6, PLAG1, TMEM138, TMEM216, TRIP13*
Global developmental delay	HP:0001263	0.03800	*ACD, ACTB, BRIP1, CLIP1, CPLX1, CRADD, CTCF, CUX1, EXOC6B, FAM20C, GLI3, GLIS3, HRAS, KIDINS220, LETM1, NKX2-1, NOTCH3, PANK2, PLA2G6, PLAG1, POMGNT1, PTS, RTEL1, SIN3A, SLC25A46, TKFC, TMEM138, TMEM216, TRIP13*
Meningocele	HP:0002435	0.04500	*GLI3, NOTCH3, POMGNT1, SIN3A, TMEM216*
Spinal dysraphism	HP:0010301	0.04800	*ACTB, BRIP1, GLI3, GTF2I, NOTCH3, POMGNT1, SIN3A, TMEM216*

Supplementary Table S9 Putatively selected regions in Asiatic mouflon-to-indigenous breed comparison.

No.	Combined region (Mb)	Chromosome	Position		Gene name
			Start	End	
1	Chr1: 27.75-27.9	1	27750001	27900000	*GLIS1, GLIS1-NDC1*

2	Chr1: 54.3-54.525	1	54300001	54450000	*PTGFR, LOC105613526, LOC105613526-LOC101103103, LOC101110201, LOC101110201-IFI44L, IFI44L, IFI44, IFI44L-IFI44, IFI44-ADGRL4*
		1	54375001	54525000	*IFI44L, IFI44L-IFI44, IFI44, IFI44-ADGRL4*
3	Chr1: 119.4-119.55	1	119400001	1.2E+08	*KCNE2-MRPS6, MRPS6, SLC5A3, MRPS6-ATP5O,*
4	Chr2: 71.175-71.325	2	71175001	71325000	*RFX3*
5	Chr2: 114.975-115.425	2	114975001	1.15E+08	*LOC101106660-LOC101117569*
		2	115050001	1.15E+08	*LOC101106660-LOC101117569*
		2	115125001	1.15E+08	*LOC101106660-LOC101117569, LOC101117569*
		2	115200001	1.15E+08	*LOC101106660-LOC101117569, LOC101117569, LOC101117569-LOC105608719*
		2	115275001	1.15E+08	*LOC101117569, LOC101117569-LOC105608719, LOC105608719*
6	Chr2: 122.325-122.775	2	122325001	1.22E+08	*LOC101120641-LOC101122056, LOC101122056, LOC101122056-FSIP2, FSIP2*
		2	122625001	1.23E+08	*LOC105608888, LOC105608888-LOC101121406*
7	Chr2: 123-123.15	2	123000001	1.23E+08	*LOC105608888-LOC101121406*
8	Chr2: 209.55-209.7	2	209550001	2.1E+08	*PTH2R-LOC101107339*
9	Chr2: 213.75-213.9	2	213750001	2.14E+08	*LOC105611887-LOC105610530, LOC105610530, LOC105610530-IKZF2,*
10	Chr2: 214.275-214.425	2	214275001	2.14E+08	*SPAG16*
11	Chr2: 219.375-219.6	2	219375001	2.2E+08	*SLC11A1, SLC11A1-CTDSP1, CTDSP1, CTDSP1-VIL1, VIL1, USP37, USP37-RQCD1, RQCD1*
		2	219450001	2.2E+08	*USP37, USP37-RQCD1, RQCD1, RQCD1-PLCD4, PLCD4, PLCD4-ZNF142, ZNF142*

12	Chr2: 234.375-234.6	2	234375001	2.35E+08	*LCK, FAM167B, FAM167B-LOC101115435, LOC101115435, EIF3I, TMEM234, DCDC2B, LOC106990972, IQCC, DCDC2B-IQCC, DCDC2B-TXLNA, TXLNA, TXLNA-KPNA6, KPNA6, KPNA6-TMEM39B, TMEM39B*
		2	234450001	2.35E+08	*KPNA6, KPNA6-TMEM39B, TMEM39B, TMEM39B-KHDRBS1, KHDRBS1, KHDRBS1-PTP4A2*
13	Chr3: 18.15-18.3	3	18150001	18300000	*MBOAT2, MBOAT2-LOC101102303, LOC101102303, LOC101102303-ASAP2*
14	Chr3: 94.425-94.65	3	94425001	94575000	*EXOC6B, LOC106991063*
		3	94500001	94650000	*EXOC6B, LOC105614905, EXOC6B-SPR*
15	Chr3: 97.725-97.95	3	97725001	97875000	*LOC105612338-TMEM182*
		3	97800001	97950000	*LOC105612338-TMEM182*
16	Chr3: 111.3-111.45	3	111300001	1.11E+08	*LOC105611140-LOC105611141*
17	Chr3: 124.425-124.875	3	124425001	1.25E+08	*TMTC3-KITLG, KITLG*
		3	124575001	1.25E+08	*KITLG, KITLG-TRNAG-CCC-31*
		3	124650001	1.25E+08	*KITLG-TRNAG-CCC-31, TRNAG-CCC-31, TRNAG-CCC-31-LOC101105320*
		3	124725001	1.25E+08	*TRNAG-CCC-31, TRNAG-CCC-31-LOC101105320*
18	Chr3: 213.15-213.375	3	213150001	2.13E+08	*TUBA8-CDC42EP1, CDC42EP1, CDC42EP1-LGALS2, LGALS2, LGALS2-LOC105609489, LOC105609489, GGA1-LOC105609489, LOC105609489, GGA1, GGA1-LOC105609488, LOC105609488, SH3BP1, PDXP, PDXP-LGALS1, LGALS1, LGALS1-NOL12, NOL12, LOC105609492, TRNAG-CCC-36, LOC101119130*

		3	213225001	2.13E+08	*LOC105609488, SH3BP1, PDXP, PDXP-LGALS1, LGALS1, LGALS1-NOL12, NOL12, LOC105609492, TRNAG-CCC-36, LOC101119130, LOC101119130-LOC101102223, LOC101102223, GCAT, GCAT-GALR3, GALR3*
19	Chr4: 23.7-23.85	4	23700001	23850000	*AGMO*
20	Chr4: 47.475-47.625	4	47475001	47625000	*NAMPT-LOC101102639*
21	Chr4: 63-63.15	4	63000001	63150000	*BMPER-LOC105612117, LOC105612117, LOC105612117-BBS9*
22	Chr4: 78.825-78.975	4	78825001	78975000	*GLI3*
23	Chr4: 101.625-101.925	4	101625001	1.02E+08	*AKR1D1-TRIM24*
		4	101700001	1.02E+08	*AKR1D1-TRIM24*
		4	101775001	1.02E+08	*AKR1D1-TRIM24, TRIM24*
24	Chr4: 111.75-111.9	4	111750001	1.12E+08	*TRNAC-GCA-108-TRNAC-GCA-109, TRNAC-GCA-109, TRNAC-GCA-109-TRNAC-GCA-110, TRNAC-GCA-110, TRNAC-GCA-110-LOC106991146, LOC106991146, LOC106991146-ZNF777, ZNF777, ZNF777-ZNF746, ZNF746, ZNF746-TRNAC-GCA-111, TRNAC-GCA-111, TRNAC-GCA-111-TRNAC-GCA-112, TRNAC-GCA-112, TRNAC-GCA-112-TRNAC-GCA-113, TRNAC-GCA-113, TRNAC-GCA-113-TRNAC-GCA-114, TRNAC-GCA-114, TRNAC-GCA-114-TRNAC-GCA-115, TRNAC-GCA-115, TRNAC-GCA-115-TRNAC-GCA-116, TRNAC-GCA-116, TRNAC-GCA-116-TRNAC-GCA-117, TRNAC-GCA-117, TRNAC-GCA-117-TRNAC-GCA-118, TRNAC-GCA-118, TRNAC-GCA-118-TRNAC-GCA-119*

25	Chr5: 7.5-7.725	5	7500001	7650000	*AKAP8L, AKAP8-LOC101123297, LOC101123297, LOC105615346-LOC101123297, LOC105615346, EPHX3, EPHX3-NOTCH3*
		5	7575001	7725000	*AKAP8-LOC101123297, LOC101123297, LOC105615346-LOC101123297, LOC105615346, EPHX3, EPHX3-NOTCH3, NOTCH3, NOTCH3-LOC101120324, LOC101120324, LOC101120324-LOC101101981, LOC101101981*
26	Chr5: 106.875-107.1	5	106875001	1.07E+08	*SLC25A46, SLC25A46-LOC105615337*
		5	106950001	1.07E+08	*SLC25A46-LOC105615337, LOC105615337, LOC105615337-WDR36*
27	Chr6: 19.875-20.025	6	19875001	20025000	*PPA2, LOC105611776, PPA2-TET2, TET2*
28	Chr6: 24.6-24.9	6	24600001	24750000	*TRNAC-GCA-141-LOC106990491, LOC106990491, LOC106990491-H2AFZ*
		6	24675001	24825000	*TRNAC-GCA-141-LOC106990491, LOC106990491, LOC106990491-H2AFZ, H2AFZ, DNAJB14, DNAJB14-LAMTOR3, LAMTOR3, LAMTOR3-DAPP1, DAPP1*
		6	24750001	24900000	*LOC106990491-H2AFZ, H2AFZ, DNAJB14-H2AFZ, DNAJB14, DNAJB14-LAMTOR3, LAMTOR3, LAMTOR3-DAPP1, DAPP1, DAPP1-LOC105612764*
29	Chr6: 30.9-31.125	6	30900001	31050000	*GRID2*
		6	30975001	31125000	*GRID2*
30	Chr6: 36.15-36.3	6	36150001	36300000	*HERC5, HERC5-HERC6, HERC6, HERC6-PPM1K*
31	Chr6: 37.275-37.425	6	37275001	37425000	*LCORL, LOC105615456*

32	Chr6: 44.625-44.775	6	44625001	44775000	*PI4K2B, PI4K2B-ZCCHC4, ZCCHC4, ZCCHC4-ANAPC4, ANAPC4, ANAPC4-SLC34A2*
33	Chr6: 53.55-53.775	6	53550001	53700000	*LOC101109539-TRNAC-GCA-144*
		6	53625001	53775000	*LOC101109539-TRNAC-GCA-144*
34	Chr6: 70.425-70.575	6	70425001	70575000	*LOC101116147-KDR, KDR, KDR-SRD5A3*
35	Chr6: 79.875-80.25	6	79875001	80025000	*TECRL-LOC106991226, LOC106991226, LOC106991226-LOC101119727*
		6	79950001	80100000	*TECRL-LOC106991226, LOC106991226, LOC106991226-LOC101119727*
		6	80025001	80175000	*LOC106991226-LOC101119727*
		6	80100001	80250000	*LOC106991226-LOC101119727*
36	Chr6: 81.525-81.75	6	81525001	81675000	*LOC101120245-TRNAW-CCA-57*
		6	81600001	81750000	*LOC101120245-TRNAW-CCA-57*
37	Chr6: 115.875-116.025	6	115875001	1.16E+08	*WHSC1, WHSC1-LETM1, LETM1, FGFR3, LOC106991222*
38	Chr6: 116.325-117	6	116325001	1.16E+08	*LOC105615563-FGFRL1, FGFRL1, FGFRL1-IDUA, IDUA, LOC105613208, LOC105613208-DGKQ, TMEM175, TMEM175-GAK, GAK*
		6	116400001	1.17E+08	*TMEM175, TMEM175-GAK, GAK, GAK-CPLX1, CPLX1, CPLX1-LOC105615565*
		6	116475001	1.17E+08	*GAK, GAK-CPLX1, CPLX1, CPLX1-LOC105615565, LOC105615565, LOC105615565-UVSSA*
		6	116700001	1.17E+08	*PCGF3, PCGF3-MFSD7, MFSD7, MFSD7-ATP5I, ATP5I, PDE6B, LOC101108751, LOC101108751-LOC105613214, LOC105613214, LOC105613214-PIGG, PIGG*
		6	116775001	1.17E+08	*PDE6B, LOC101108751, LOC101108751-LOC105613214, LOC105613214, LOC105613214-PIGG, PIGG*

		6	116850001	1.17E+08	*PIGG*
39	Chr7: 72.525-72.675	7	72525001	72675000	*PPP2R5E, PPP2R5E-WDR89*
40	Chr8: 67.2-67.35	8	67200001	67350000	*HIVEP2, HIVEP2-AIG1*
41	Chr8: 89.4-89.55	8	89400001	89550000	*SMOC2-THBS2*
42	Chr9: 30.825-30.975	9	30825001	30975000	*LOC101110068-LOC101110341, LOC101110341, LOC101110341-LOC101110602, LOC101110602, LOC101110602-TRNAM-CAU-10*
43	Chr9: 36-36.225	9	36000001	36150000	*LYN-RPS20, RPS20, RPS20-MOS, MOS, MOS-PLAG1, PLAG1, CHCHD7, CHCHD7-SDR16C5*
		9	36075001	36225000	*PLAG1, CHCHD7, CHCHD7-SDR16C5, SDR16C5, SDR16C5-LOC101116323, LOC101116323*
44	Chr9: 37.8-37.95	9	37800001	37950000	*TOX, TRNAC-GCA-170*
45	Chr10: 7.425-7.575	10	7425001	7575000	*LOC101105926-LOC101121613*
46	Chr10: 31.875-32.025	10	31875001	32025000	*FLT1, FLT1-PAN3*
47	Chr10: 35.4-35.625	10	35400001	35550000	*LOC105609559-FGF9*
		10	35475001	35625000	*LOC105609559-FGF9, FGF9, FGF9-MICU2*
48	Chr10: 37.5-37.95	10	37500001	37650000	*ATP12A-LOC105614068*
		10	37650001	37800000	*ATP12A-LOC105614068, LOC105614068, LOC105614068-LOC101120586*
		10	37725001	37875000	*LOC105614068-LOC101120586*
		10	37800001	37950000	*LOC105614068-LOC101120586*
49	Chr10: 41.775-41.925	10	41775001	41925000	*LOC101121273-LOC101121526*
50	Chr10: 43.35-43.5	10	43350001	43500000	*LOC101121526-TRNAW-CCA-83*
51	Chr10: 75.15-75.3	10	75150001	75300000	*DOCK9, LOC105616225, LOC105616225-UBAC2*
52	Chr11: 10.725-10.875	11	10725001	10875000	*INTS2, BRIP1*

53	Chr11: 24.6-24.75	11	24600001	24750000	*MYBBP1A, GGT6, TEKT1, SMTNL2, LOC105610740, LOC105610748, LOC105610748-FBXO39, FBXO39, XAF1, LOC101112994*
54	Chr12: 42.675-42.825	12	42675001	42825000	*ENO1-RERE, RERE*
55	Chr12: 78.675-79.05	12	78675001	78825000	*LOC106991464-NAV1, NAV1, NAV1-IPO9, IPO9*
		12	78750001	78900000	*NAV1, NAV1-IPO9, IPO9, IPO9-SHISA4, SHISA4, SHISA4-LOC105610030, LOC105610030, LOC105610030-LOC105610031*
		12	78825001	78975000	*IPO9, IPO9-SHISA4, SHISA4, IPO9-SHISA4, SHISA4, SHISA4-LOC105610030, LOC105610030, LOC105610030-LOC105610031, LOC105610031, TIMM17A, TIMM17A-RNPEP, RNPEP, ELF3, ELF3-LOC105610032, LOC105610032*
		12	78900001	79050000	*LOC105610031, TIMM17A, TIMM17A-RNPEP, RNPEP, ELF3, ELF3-LOC105610032, LOC105610032, LOC105610032-GPR37L1, GPR37L1, ARL8A, ARL8A-LOC101114718, LOC101114718*
56	Chr13: 49.2-49.35	13	49200001	49350000	*LOC101110166-LOC101110438*
57	Chr13: 49.575-49.95	13	49575001	49725000	*LOC101110166-LOC101110438, LOC101110438-HAO1*
		13	49650001	49800000	*LOC101110166-LOC101110438, LOC101110438-HAO1*
		13	49725001	49875000	*LOC101110438-HAO1*
		13	49800001	49950000	*LOC101110438-HAO1, HAO1*
58	Chr13: 50.175-50.625	13	50175001	50325000	*ADRA1D, ADRA1D-SMOX, SMOX, SMOX-LOC105606258*
		13	50250001	50400000	*SMOX-LOC105606258, LOC105606258, LOC105606258-RNF24*
		13	50325001	50475000	*SMOX-LOC105606258, LOC105606258,*

					LOC105606258-RNF24, RNF24
		13	50400001	50550000	*LOC105606258-RNF24, RNF24, RNF24-PANK2, PANK2, PANK2-MAVS*
		13	50475001	50625000	*RNF24, RNF24-PANK2, PANK2, PANK2-MAVS, MAVS, LOC105606256, LOC105606256-AP5S1, AP5S1*
59	Chr13: 53.1-53.55	13	53100001	53250000	*PRPF6, SAMD10, ZNF512B, UCKL1, DNAJC5, TPD52L2, ABHD16B, ZBTB46*
		13	53175001	53325000	*TPD52L2, ABHD16B, ZBTB46, ZGPAT, ARFRP1, TNFRSF6B, RTEL1, STMN3*
		13	53250001	53400000	*ZBTB46, ZGPAT, ARFRP1, TNFRSF6B, RTEL1, STMN3, GMEB2, C13H20orf195, SRMS, PTK6, PPDPF, EEF1A2*
		13	53325001	53475000	*STMN3, GMEB2, C13H20orf195, SRMS, PTK6, PPDPF, EEF1A2, KCNQ2*
		13	53400001	53550000	*EEF1A2, KCNQ2, CHRNA4, COL20A1, ARFGAP1, BIRC7*
60	Chr13: 56.25-56.4	13	56250001	56400000	*EDN3, LOC105616728, ZNF831*
61	Chr13: 63-63.15	13	63000001	63150000	*ASIP*
62	Chr14: 34.275-34.575	14	34275001	34425000	*ZDHHC1, HSD11B2, ATP6V0D1, AGRP, LOC105606370, FAM65A, LOC106991595, CTCF*
		14	34350001	34500000	*FAM65A, LOC106991595, CTCF, RLTPR, ACD, PARD6A, ACTB, ENKD1, C14H16orf86, GFOD2*
		14	34425001	34575000	*CTCF, RLTPR, ACD, PARD6A, ACTB, ENKD1, C14H16orf86, GFOD2, RANBP10, TSNAXIP1*
63	Chr15: 21.825-21.975	15	21825001	21975000	*LOC105602162, IL18, TEX12, BCO2*
64	Chr15: 47.55-47.775	15	47550001	47700000	*LOC101104177, LOC101104426, LOC101104685, LOC101104933, LOC101105186, LOC101105439, LOC101105686, LOC101105946, LOC101106201,*

					LOC101106712
		15	47625001	47775000	*LOC101105439, LOC101105686, LOC101105946, LOC101106201, LOC101106459, LOC101106712, LOC101106966, LOC101107221, LOC101107469, LOC101107731*
65	Chr16: 70.8-70.95	16	70800001	70950000	*CEP72, TPPP, BRD9, TRIP13, LOC105602658*
66	Chr17: 33-33.15	17	33000001	33150000	*ANKRD50-LOC101101922, LOC101101922*
67	Chr17: 52.125-52.575	17	52125001	52275000	*OGFOD2, ABCB9, VPS37B, HIP1R, CCDC62*
		17	52200001	52350000	*VPS37B, HIP1R, CCDC62, DENR, HCAR1*
		17	52425001	52575000	*KNTC1, RSRC2, ZCCHC8, CLIP1*
68	Chr17: 53.475-53.7	17	53475001	53625000	*CAMKK2, P2RX4, P2RX7, IFT81*
		17	53550001	53700000	*P2RX7, IFT81*
69	Chr17: 59.4-59.55	17	59400001	59550000	*LOC105602894-TBX3*
70	Chr17: 64.95-65.1	17	64950001	65100000	*KIAA1671, CRYBB3, CRYBB2, ADRBK2*
71	Chr18: 22.65-22.8	18	22650001	22800000	*BNC1*
72	Chr18: 23.55-23.85	18	23550001	23700000	*EFTUD1-MEX3B, MEX3B-MORF4L1*
		18	23625001	23775000	*MEX3B-MORF4L1*
		18	23700001	23850000	*MEX3B-MORF4L1*
73	Chr18: 32.175-32.475	18	32175001	32325000	*PTPN9, SIN3A*
		18	32250001	32400000	*PTPN9, SIN3A, MAN2C1, NEIL1, COMMD4, LOC105603152, LOC105603296, LOC105603153*
		18	32325001	32475000	*MAN2C1, NEIL1, COMMD4, LOC105603152, LOC105603296, LOC105603153, C18H15orf39, LOC105603154*
74	Chr18: 45.15-45.6	18	45150001	45300000	*LOC106991743*

		18	45375001	45525000	*LOC106991744, LOC106991745*
		18	45450001	45600000	*LOC106991744, LOC106991745, NKX2-1*
75	Chr18: 65.85-66.15	18	65850001	66000000	*ANKRD9, ANKRD9-RCOR1*
		18	65925001	66075000	*RCOR1, RCOR1-TRAF3*
		18	66000001	66150000	*RCOR1, RCOR1-TRAF3, TRAF3*
76	Chr19: 60.375-60.525	19	60375001	60525000	*KLF15, CFAP100, LOC106990579*
77	Chr20: 10.8-10.95	20	10800001	10950000	*PPIL1, C20H6orf89, PI16, MTCH1, LOC105603679, FGD2*
78	Chr20: 15-15.225	20	15000001	15150000	*APOBEC2, OARD1, NFYA, LOC101108001, TREML1, TREM2*
		20	15075001	15225000	*LOC101108001, TREML1, TREM2*
79	Chr20: 49.875-50.4	20	49875001	50025000	*GMDS*
		20	49950001	50100000	*GMDS, LOC105603912*
		20	50025001	50175000	*GMDS, LOC105603912*
		20	50100001	50250000	*GMDS*
		20	50175001	50325000	*GMDS, FOXC1, FOXC1-TRNAS-GGA-94*
		20	50250001	50400000	*GMDS, FOXC1-TRNAS-GGA-94, TRNAS-GGA-94*
80	Chr20: 50.85-51.15	20	50850001	51000000	*IRF4, DUSP22, LOC105603919*
		20	50925001	51075000	*DUSP22, LOC105603919*
		20	51000001	51150000	-
81	Chr21: 49.65-49.8	21	49650001	49800000	*IFITM5, LOC105604160, ATHL1, NLRP6, PSMD13, SIRT3, RIC8A, BET1L*
82	Chr22: 41.1-41.25	22	41100001	41250000	*PLEKHA1, HTRA1*
83	Chr24: 10.35-10.5	24	10350001	10500000	*SNN, TXNDC11, ZC3H7A, LOC105604663*
84	Chr24: 32.625-32.775	24	32625001	32775000	*LOC101112784, TRNAC-ACA-78, NCF1, GTF2I, GTF2I-GTF2IRD1*

85	Chr24: 34.575-34.8	24	34575001	34725000	*LOC106991890-CUX1, CUX1, LOC105604781, TRNAE-UUC-101, LOC105604780*
		24	34650001	34800000	*CUX1, LOC105604780*
86	Chr24: 41.625-42.075	24	41625001	41775000	*LOC106991898, FAM20C*
		24	41700001	41850000	*LOC106991898, FAM20C*
		24	41850001	42000000	*FAM20C-LOC105604839, LOC105604839*
		24	41925001	42075000	*LOC105604839*
87	Chr25: 18.825-18.975	25	18825001	18975000	*LOC101121824, LOC101121824-NRBF2*
88	ChrX: 19.95-20.1	X	19950001	20100000	*PHEX-LOC106991986*
89	ChrX: 76.275-76.5	X	76275001	76425000	*LOC101116546-LOC101116810*
		X	76350001	76500000	*LOC101116810*
90	ChrX: 135.075-135.225	X	135075001	1.35E+08	*PABPC5*

Supplementary Table S10 Putatively selected regions in indigenous breed-to-improved breed comparison.

No.	Combined region (Mb)	Chromosome	Position		Gene name
			Start	End	
1	Chr1:27.45-27.9	1	27450001	27600000	*C1H1orf123, MAGOH, MAGOH-LRP8, LRP8, LRP8-LOC101119086*
		1	27675001	27825000	*DMRTB1, GLIS1, GLIS1-NDC1*
		1	27750001	27900000	*GLIS1, GLIS1-NDC1*
2	Chr1:68.775-69.15	1	68775001	68925000	*RPAP2, GFI1, EVI5*
		1	68850001	69000000	*EVI5*
		1	68925001	69075000	*EVI5*
		1	69000001	69150000	*EVI5, RPL5*

3	Chr1:89.025-89.175	1	89025001	89175000	*CAPZA1, MOV10, RHOC, PPM1J, FAM19A3, TRNAL-UAA, TRNAL-UAA-LOC101108016*
4	Chr1:109.425-109.575	1	1.09E+08	1.1E+08	*LOC105612162, PEA15, DCAF8, COPA, NCSTN*
5	Chr1:119.025-119.475	1	1.19E+08	1.19E+08	*LOC101118835-RCAN1, RCAN1, RCAN1-KCNE1, KCNE1, SMIM11A, C1H21orf140,*
		1	1.19E+08	1.19E+08	*KCNE1-SMIM11A, SMIM11A, C1H21orf140, SMIM11A, KCNE2, KCNE2-MRPS6*
		1	1.19E+08	1.19E+08	*SMIM11A-KCNE2, KCNE2, KCNE2-MRPS6*
		1	1.19E+08	1.19E+08	*KCNE2-MRPS6*
		1	1.19E+08	1.19E+08	*KCNE2-MRPS6, MRPS6, SLC5A3*
6	Chr1:161.1-161.325	1	1.61E+08	1.61E+08	*GPR15, GPR15-CPOX, CPOX, LOC105609869*
		1	1.61E+08	1.61E+08	*CPOX-LOC105609869, LOC105609869, ST3GAL6*
7	Chr1:164.625-164.775	1	1.65E+08	1.65E+08	*LOC105616787-LOC105616785, LOC105616785, LOC105616785-ZPLD1*
8	Chr1:234.6-234.825	1	2.35E+08	2.35E+08	*MED12L, P2RY13, GPR87, P2RY14, P2RY12*

		1	2.35E+08	2.35E+08	*MED12L, P2RY13, GPR87, P2RY14, GPR171*
9	Chr1:236.925-237.075	1	2.37E+08	2.37E+08	*HPS3, LOC101122652, HPS3-HLTF, HLTF, HLTF-GYG1, GYG1*
10	Chr1:275.1-275.325	1	2.75E+08	2.75E+08	*RAB5A, PP2D1, PP2D1-KAT2B, KAT2B, KAT2B-SGOL1*
		1	2.75E+08	2.75E+08	*KAT2B, KAT2B-SGOL1, SGOL1, LOC101116279, LOC101116279-ZNF596*
11	Chr2:0.225-0.45	2	225001	375000	*FAM150B-LOC105606464, LOC105606464, LOC105606464-LOC105606460*
		2	300001	450000	*FAM150B-LOC105606464, LOC105606464, LOC105606464-LOC105606460, LOC105606460, LOC105606458, LOC105606458-TMEM18*
12	Chr2:30.075-30.3	2	30075001	30225000	*ERCC6L2*
		2	30150001	30300000	*ERCC6L2, ERCC6L2-LOC101111936*
13	Chr2:58.575-58.8	2	58575001	58725000	*GNAQ, GNAQ-GNA14*
		2	58650001	58800000	*GNAQ, GNAQ-GNA14, GNA14*
14	Chr2:121.2-121.35	2	1.21E+08	1.21E+08	*CALCRL-LOC105608872, LOC105608872, LOC105608872-ZSWIM2*
15	Chr2:197.925-198.075	2	1.98E+08	1.98E+08	*CCDC150, CCDC150-GTF3C3, GTF3C3*

16	Chr3:166.425-166.575	3	1.66E+08	1.67E+08	*LOC105609279-LOC105609280, LOC105609280*
17	Chr3:212.7-213.225	3	2.13E+08	2.13E+08	*CECR1-CECR2, CECR2, CECR2-ATP6V1E1, ATP6V1E1, BCL2L13*
		3	2.13E+08	2.13E+08	*CECR2, CECR2-ATP6V1E1, ATP6V1E1, BCL2L13, TRNAE-UUC-43, LOC105614865, BID, MICAL3*
		3	2.13E+08	2.13E+08	*BCL2L13, LOC105614865, BID, MICAL3*
		3	2.13E+08	2.13E+08	*MICAL3, MICAL3-LOC105614866*
		3	2.13E+08	2.13E+08	*MICAL3, MICAL3-LOC105614866, LOC105614866, PEX26, LOC105610007, TUBA8, TUBA8-CDC42EP1*
		3	2.13E+08	2.13E+08	*MICAL3-LOC105614866, LOC105614866, PEX26, PEX26-LOC105610007, TUBA8, TUBA8-CDC42EP1, CDC42EP1, LGALS2, LOC105609489, GGA1, LOC105609488*

18	Chr3:214.2-214.425	3	2.14E+08	2.14E+08	*CBX6, CBX6-APOBEC3Z1, APOBEC3Z1, LOC105609481, APOBEC3F, APOBEC3F-CBX7, CBX7, CBX7-PDGFB*
		3	2.14E+08	2.14E+08	*APOBEC3Z1-LOC105609481, LOC105609481, APOBEC3F, CBX7, PDGFB, LOC106991092*
	Chr4:28.425-28.575	4	28425001	28575000	*TWISTNB, LOC105611892, TMEM196*
19	Chr4:46.65-47.1	4	46650001	46800000	*RINT1, LOC101122944, ATXN7L1,*
		4	46725001	46875000	*ATXN7L1*
		4	46950001	47100000	*ATXN7L1, ATXN7L1-CDHR3, CDHR3, LOC105609617*
20	Chr4:74.625-74.85	4	74625001	74775000	*HUS1-TNS3, TNS3*
		4	74700001	74850000	*HUS1-TNS3, TNS3*
21	Chr4:75.675-75.9	4	75675001	75825000	*LOC105615056-IGFBP3*
		4	75750001	75900000	*LOC105615056-IGFBP3*
22	Chr5:19.35-19.5	5	19350001	19500000	*RAD50, IL5, RAD50-IRF1, IRF1, LOC105615229*
23	Chr5:43.35-43.875	5	43350001	43500000	*LOC105607068-JADE2, JADE2, LOC105607066, SAR1B, SEC24A*
		5	43425001	43575000	*LOC105607066, SAR1B, SEC24A, CAMLG, DDX46*

		5	43725001	43875000	*CATSPER3, PITX1, LOC106991192*
24	Chr5:70.8-71.025	5	70800001	70950000	*TRNAF-GAA-5-GABRA1, GABRA1, GABRA1-GABRG2*
		5	70875001	71025000	*GABRA1-GABRG2, GABRG2*
25	Chr6:22.05-22.2	6	22050001	22200000	*LOC106991231-UBE2D3, UBE2D3, UBE2D3-MANBA, MANBA*
26	Chr6:32.1-32.325	6	32100001	32250000	*GRID2*
		6	32175001	32325000	*GRID2*
27	Chr6:36.3-36.45	6	36300001	36450000	*HERC6-PPM1K, PPM1K, ABCG2*
28	Chr6:36.975-37.35	6	36975001	37125000	*LOC101103815-TRNAA-CGC-2, TRNAA-CGC-2, TRNAA-CGC-2-LAP3, LAP3, MED28, FAM184B, LOC105615455*
		6	37125001	37275000	*FAM184B, NCAPG, LOC105608051, DCAF16, LCORL, NCAPG*
		6	37200001	37350000	*DCAF16, NCAPG, LCORL, LOC105615456*
29	Chr6:69.75-70.05	6	69750001	69900000	*PDGFRA-LOC106990548, LOC106990548, LOC106990548-LOC105613064, LOC105613064, LOC105613064-KIT*
		6	69825001	69975000	*LOC106990548-LOC105613064, LOC105613064, LOC105613064-KIT*

		6	69900001	70050000	*LOC105613064-KIT*
30	Chr6:79.35-79.725	6	79350001	79500000	*LOC101119476-TECRL*
		6	79575001	79725000	*TECRL, TECRL-LOC106991226*
31	Chr6:116.4-117	6	1.16E+08	1.17E+08	*TMEM175, TMEM175-GAK, GAK, CPLX1, CPLX1-LOC105615565*
		6	1.17E+08	1.17E+08	*PCGF3, PCGF3-MFSD7, MFSD7, ATP5I, PDE6B, LOC101108751, LOC105613214, PIGG*
		6	1.17E+08	1.17E+08	*PDE6B, LOC101108751, LOC105613214, PIGG*
		6	1.17E+08	1.17E+08	*PIGG*
32	Chr7:33.975-34.2	7	33975001	34125000	*TYRO3, TYRO3-LOC105608920, LOC105608920, MGA, LOC101116404, LOC106991249*
		7	34050001	34200000	*MGA, LOC106991249, MAPKBP1*
33	Chr7:34.725-34.95	7	34725001	34875000	*GANC, CAPN3, ZNF106, SNAP23*
		7	34800001	34950000	*ZNF106, SNAP23, LRRC57, HAUS2, LOC101117673, STARD9*
34	Chr7:42.075-42.225	7	42075001	42225000	*NID2-LOC101107359*
35	Chr7:57.375-57.6	7	57375001	57525000	*LOC105607291, ATP8B4*
		7	57450001	57600000	*LOC105607291, LOC105607291-DTWD1*
36	Chr8:10.575-10.8	8	10575001	10725000	*PRSS35, SNAP91, LOC105613508*
		8	10650001	10800000	*SNAP91, SNAP91-C8H6orf58*

37	Chr8:31.575-32.175	8	31575001	31725000	*LOC101110517-PREP, PREP*
		8	31650001	31800000	*PREP, PREP-POPDC3*
		8	31875001	32025000	*PREP-POPDC3, POPDC3, BVES, LIN28B*
		8	31950001	32100000	*BVES, LIN28B*
		8	32025001	32175000	*LIN28B, HACE1*
38	Chr8:62.55-62.85	8	62550001	62700000	*OLIG3-LOC105608892, LOC105608892, TNFAIP3*
		8	62625001	62775000	*TNFAIP3, TNFAIP3-LOC101113418*
		8	62700001	62850000	*TNFAIP3, TNFAIP3-LOC101113418, LOC101113418, LOC101113418-PERP*
39	Chr8:90.225-90.525	8	90225001	90375000	*LOC106991326-DLL1*
		8	90300001	90450000	*LOC106991326-DLL1, DLL1, FAM120B*
		8	90375001	90525000	*LOC106991326-DLL1, DLL1, FAM120B, FAM120B-PSMB1*
40	Chr9:60.225-60.375	9	60225001	60375000	*LOC106991339-UTP23, UTP23, UTP23-EIF3H, EIF3H*
41	Chr10:25.95-26.1	10	25950001	26100000	*DCLK1-NBEA, NBEA*
42	Chr10:26.7-26.85	10	26700001	26850000	*LOC105611533, TRNAC-GCA-174*
43	Chr10:35.475-35.625	10	35475001	35625000	*LOC105609559-FGF9, FGF9, FGF9-MICU2*

44	Chr11:22.65-22.875	11	22650001	22800000	*OVCA2-HIC1, HIC1, SMG6, TRNAG-UCC-21*
		11	22725001	22875000	*SMG6, TRNAG-UCC-21, SRR*
45	Chr11:26.175-26.475	11	26175001	26325000	*TM4SF5-ZMYND15, ZMYND15, CXCL16, MED11, PELP1, ARRB2, LOC105616328, LOC105607815, LOC101116587, LOC101113251*
		11	26250001	26400000	*PELP1, LOC105607815, LOC101116587, LOC101113251, LOC105607814, ALOX12, RNASEK, LOC106991418, C11H17orf49, BCL6B*
		11	26325001	26475000	*LOC105607815, LOC105607814, ALOX12, RNASEK, LOC106991418, C11H17orf49, BCL6B, SLC16A13, LOC101117600, ASGR2*
46	Chr11:27.6-27.75	11	27600001	27750000	*LOC105607815, LOC105607814, ALOX12, RNASEK, LOC106991418, C11H17orf49, BCL6B, SLC16A13, LOC101117600, ASGR2*
47	Chr12:42-42.3	12	42000001	42150000	*SLC25A33, LOC101113870, LOC105606443, LOC105606444*
		12	42075001	42225000	*LOC101113870, LOC105606443, LOC105606444, SPSB1*
		12	42150001	42300000	*SPSB1, LOC105616528, H6PD*

48	Chr12:52.575-52.8	12	52575001	52725000	*LOC101114795-LOC101115051, LOC101115051, LOC105601896, LOC105601879, LOC106990612, C12H1orf158*
		12	52650001	52800000	*LOC106990612, C12H1orf158, AADACL3*
49	Chr13:48.6-49.125	13	48600001	48750000	*BMP2-LOC101117953*
		13	48675001	48825000	*BMP2-LOC101117953*
		13	48750001	48900000	*BMP2-LOC101117953*
		13	48825001	48975000	*BMP2-LOC101117953, LOC101117953, LOC101117953-LOC101118207*
		13	48900001	49050000	*BMP2-LOC101117953, LOC101117953, LOC101117953-LOC101118207*
		13	48975001	49125000	*LOC101117953-LOC101118207, LOC101118207, LOC101110166*
50	Chr13:52.875-53.55	13	52875001	53025000	*GINS1-TRNAC-GCA-202, TRNAC-GCA-202, PCMTD2, LOC105606235, MYT1, LOC105616721, NPBWR2, OPRL1*

		13	52950001	53100000	*LOC105616721, LOC105616721-NPBWR2, NPBWR2, OPRL1, LKAAEAR1, RGS19, TCEA2, SOX18, LOC105616788, PRPF6*
		13	53175001	53325000	*DNAJC5-TPD52L2, TPD52L2, ABHD16B, ZBTB46, ZGPAT, ARFRP1, TNFRSF6B, RTEL1, STMN3*
		13	53250001	53400000	*ZBTB46, ZGPAT, ARFRP1, TNFRSF6B, RTEL1, STMN3, GMEB2, C13H20orf195, SRMS, PTK6, PPDPF, EEF1A2*
		13	53325001	53475000	*STMN3, GMEB2, C13H20orf195, SRMS, PTK6, PPDPF, EEF1A2, KCNQ2, KCNQ2-CHRNA4*
		13	53400001	53550000	*EEF1A2, KCNQ2, CHRNA4, COL20A1, ARFGAP1, BIRC7, BIRC7-YTHDF1*
51	Chr13:56.175-56.4	13	56175001	56325000	*PHACTR3-EDN3, EDN3, LOC105616728*
		13	56250001	56400000	*PHACTR3-EDN3, EDN3, LOC105616728, ZNF831*
52	Chr13:59.475-59.625	13	59475001	59625000	*FAM110A-SLC52A3, SLC52A3, SLC52A3-SCRT2, SCRT2, SRXN1, SRXN1-TCF15*
53	Chr13:62.475-62.775	13	62475001	62625000	*PXMP4, ZNF341, LOC105606908, CHMP4B, CHMP4B-TRNAG-UCC-29*

		13	62550001	62700000	*LOC105606908, CHMP4B, TRNAG-UCC-29, TRNAG-UCC-29-RALY*
		13	62625001	62775000	*CHMP4B-TRNAG-UCC-29, TRNAG-UCC-29, TRNAG-UCC-29-RALY, RALY*
54	Chr13:63.075-63.225	13	63075001	63225000	*ASIP, ASIP-AHCY, AHCY-ITCH*
56	Chr14:35.325-35.625	14	35325001	35475000	*CDH1, TANGO6*
		14	35400001	35550000	*TANGO6, LOC105606375*
		14	35475001	35625000	*TANGO6, LOC105606375, HAS3, CHTF8, UTP4, UTP4-SNTB2*
57	Chr14:51.3-51.525	14	51300001	51450000	*CEACAM20-LOC101110442, LOC101110442, IGSF23, LOC101110963, CEACAM19, CEACAM16*
		14	51375001	51525000	*IGSF23-LOC101110963, LOC101110963, CEACAM19, CEACAM16, BCL3, CBLC, BCAM*
58	Chr14:62.55-62.7	14	62550001	62700000	*LOC105602113, LOC101121964*
59	Chr15:3.525-3.825	15	3525001	3675000	*LOC106991615-PDGFD*
		15	3600001	3750000	*LOC106991615-PDGFD*
		15	3675001	3825000	*LOC106991615-PDGFD*
60	Chr15:28.125-28.275	15	28125001	28275000	*IL10RA, IL10RA-TMPRSS4, TMPRSS4, TMPRSS4-SCN4B*
61	Chr16:3.225-3.45	16	3225001	3375000	*TLX3-NPM1, NPM1, FGF18, FGF18-LOC106991647*

		16	3300001	3450000	*FGF18, FGF18-LOC106991647*
62	Chr16:40.725-40.95	16	40725001	40875000	*TARS-NPR3, NPR3*
		16	40800001	40950000	*TARS-NPR3, NPR3, LOC106990644, LOC106990644-SUB1*
63	Chr17:13.125-13.275	17	13125001	13275000	*ANAPC10-HHIP, HHIP*
64	Chr17:53.25-53.4	17	53250001	53400000	*KDM2B, RNF34, ANAPC5, LOC105602972*
65	Chr17:58.2-58.5	17	58200001	58350000	*LOC105602892-MED13L, MED13L*
		17	58275001	58425000	*MED13L*
		17	58350001	58500000	*MED13L, MED13L-TRNAC-GCA-229*
66	Chr17:72-72.375	17	72000001	72150000	*TXNRD2, TXNRD2-ARVCF, ARVCF, TANGO2, DGCR8, RANBP1, ZDHHC8*
		17	72075001	72225000	*ARVCF, TANGO2, DGCR8, RANBP1, ZDHHC8, LOC105612806-RTN4R, RTN4R*
		17	72150001	72300000	*LOC105612806-RTN4R, RTN4R*
		17	72225001	72375000	*RTN4R*
67	Chr18:19.2-19.425	18	19200001	19350000	*LOC101120869-LOC105603084, LOC105603084, LOC101121378, LOC105603293, LOC101121632, LOC101121887, LOC101122139, LOC101122387*
		18	19275001	19425000	*LOC101121887, LOC101122139, LOC101122387, LOC101122633,*

					LOC101122633-ACAN
68	Chr18:38.4-38.55	18	38400001	38550000	*LOC106991725-PRKD1*
69	Chr19:31.725-31.95	19	31725001	31875000	*MITF, MITF-LOC105603450*
		19	31800001	31950000	*MITF, MITF-LOC105603450*
70	Chr20:40.425-40.65	20	40425001	40575000	*JARID2, LOC106991812, JARID2-LOC105603854*
		20	40500001	40650000	*JARID2, LOC106991812, JARID2-LOC105603854*
71	Chr20:49.275-49.425	20	49275001	49425000	*LOC101122475, LOC101122475-LOC101122734, LOC101122734, BPHL, RIPK1, LOC106991816, NQO2, NQO2-LOC101110458*
72	Chr20:49.875-50.175	20	49875001	50025000	*MYLK4-GMDS, GMDS*
		20	49950001	50100000	*GMDS, LOC105603912*
		20	50025001	50175000	*GMDS, LOC105603912*
73	Chr21:44.25-44.475	21	44250001	44400000	*RHOD-LOC105604121, LOC105604121, KDM2A, ADRBK1, LOC101108527*
		21	44325001	44475000	*KDM2A, ADRBK1, LOC101108527, LOC106991824, SSH3, POLD4, CLCF1, RAD9A, PPP1CA-RAD9A*
74	Chr24:1.275-1.425	24	1275001	1425000	*HN1L, MAPK8IP3, EME2, SPSB3, NUBP2, IGFALS, HAGH, FAHD1, MEIOB*

75	Chr25:7.2-7.5	25	7200001	7350000	*LOC101113195, TARBP1, TARBP1-LOC105604914*
		25	7275001	7425000	*TARBP1-LOC105604914, LOC105604914, LOC101113650, IRF2BP2, IRF2BP2-LOC105604916*
		25	7350001	7500000	*TARBP1-LOC105604914, LOC105604914, LOC101113650, IRF2BP2, IRF2BP2-LOC105604916*
76	ChrX:42.3-42.525	X	42300001	42450000	*LOC101108192-LOC105605445*
		X	42375001	42525000	*LOC101108192-LOC105605445*
77	ChrX:56.25-56.475	X	56250001	56400000	*LOC101119962-AR*
		X	56325001	56475000	*LOC101119962-AR*

Supplementary Table S11 KEGG enrichment analysis of candidate genes during domestication.

Term	Input number	Background number	*P*-value	Input
Rap1 signaling pathway	7	215	0.00196	*KITLG, PARD6A, FGF9, ACTB, FGFR3, KDR, FLT1*
Lysosome	5	126	0.00386	*GGA1, ABCB9, ATP6V0D1, IDUA, SLC11A1*
Neuroactive ligand-receptor interaction	8	372	0.01083	*CHRNA4, PTGFR, ADRA1D, GRID2, GALR3, EDN3, P2RX4, P2RX7*
Thyroid hormone signaling pathway	4	121	0.01732	*PLCD4, SIN3A, ACTB, NOTCH3*
NOD-like receptor signaling pathway	5	187	0.01828	*MAVS, IL18, NLRP6, TRAF3, P2RX7*
Calcium signaling pathway	5	203	0.0248	*PTGFR, PLCD4, ADRA1D, P2RX7, P2RX4*

MAPK signaling pathway	6	305	0.03718	*FGF9, KITLG, FLT1, FGFR3, KDR, LAMTOR3*
Ras signaling pathway	5	242	0.04639	*FGF9, KITLG, FGFR3, KDR, FLT1*
Rheumatoid arthritis	3	101	0.0492	*IL18, ATP6V0D1, FLT1*
Vitamin B6 metabolism	1	8	0.06871	*PDXP*
Oocyte meiosis	3	121	0.07493	*MOS, PPP2R5E, ANAPC4*
Influenza A	4	198	0.07612	*IL18, ACTB, MAVS, TRAF3*
Osteoclast differentiation	3	134	0.09424	*NCF1, LCK, TREM2*
Regulation of actin cytoskeleton	4	219	0.10027	*MOS, ACTB, FGFR3, FGF9*
PI3K-Akt signaling pathway	6	398	0.10105	*FGF9, PPP2R5E, KITLG, FGFR3, KDR, FLT1*
Taurine and hypotaurine metabolism	1	13	0.10484	*GGT6*
Yersinia infection	3	141	0.1054	*IL18, ACTB, LCK*
Central carbon metabolism in cancer	2	68	0.10542	*SIRT3, FGFR3*
Legionellosis	2	68	0.10542	*IL18, EEF1A2*
Adipocytokine signaling pathway	2	73	0.11816	*CAMKK2, AGRP*
Fluid shear stress and atherosclerosis	3	149	0.11876	*NCF1, ACTB, KDR*
Cytosolic DNA-sensing pathway	2	74	0.12075	*IL18, MAVS*
Inositol phosphate metabolism	2	76	0.12598	*PLCD4, PI4K2B*
Epstein-Barr virus infection	4	245	0.1344	*TRAF3, MAVS, PSMD13, SIN3A*
Synaptic vesicle cycle	2	80	0.13659	*ATP6V0D1, CPLX1*
EGFR tyrosine kinase inhibitor resistance	2	83	0.14467	*FGFR3, KDR*
Pantothenate and CoA biosynthesis	1	19	0.14635	*PANK2*
Pathways in cancer	7	551	0.15293	*TRAF3, BIRC7, NOTCH3, GLI3, FGF9, KITLG, FGFR3*
Salmonella infection	2	88	0.15835	*IL18, ACTB*
Other glycan degradation	1	22	0.16638	*MAN2C1*
Progesterone-mediated oocyte maturation	2	91	0.16667	*MOS, ANAPC4*

Endocytosis	4	269	0.16951	*ARFGAP1, FGFR3, PARD6A, VPS37B*
RNA transport	3	178	0.17174	*EIF3I, EEF1A2, PABPC5*
Phagosome	3	180	0.17561	*NCF1, ATP6V0D1, ACTB*
Glycosaminoglycan degradation	1	24	0.17947	*IDUA*
Human papillomavirus infection	5	376	0.18308	*PPP2R5E, ATP6V0D1, TRAF3, PARD6A, NOTCH3*
mRNA surveillance pathway	2	99	0.1892	*PPP2R5E, PABPC5*
Small cell lung cancer	2	100	0.19205	*BIRC7, TRAF3*
Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	1	26	0.19236	*PIGG*
Phosphatidylinositol signaling system	2	101	0.1949	*PLCD4, PI4K2B*
Melanogenesis	2	103	0.20062	*KITLG, ASIP*
NF-kappa B signaling pathway	2	104	0.20348	*TRAF3, LCK*
Th1 and Th2 cell differentiation	2	104	0.20348	*LCK, NOTCH3*
Collecting duct acid secretion	1	28	0.20505	*ATP6V0D1*
Phototransduction	1	28	0.20505	*PDE6B*
Cholinergic synapse	2	111	0.22367	*CHRNA4, KCNQ2*
Focal adhesion	3	208	0.23211	*ACTB, KDR, FLT1*
Base excision repair	1	33	0.23591	*NEIL1*
Tuberculosis	3	212	0.24045	*IL18, ATP6V0D1, NFYA*
Leukocyte transendothelial migration	2	117	0.24109	*NCF1, ACTB*
Primary immunodeficiency	1	34	0.24193	*LCK*
RIG-I-like receptor signaling pathway	2	118	0.244	*MAVS, TRAF3*
Metabolic pathways	15	1540	0.24531	*PANK2, SMOX, UCKL1, PLCD4, PDE6B, MBOAT2, GGT6, GMDS, PI4K2B, GCAT, PDXP, HAO1, ATP6V0D1, HSD11B2, IDUA*

Glyoxylate and dicarboxylate metabolism	1	35	0.24791	*HAO1*
SNARE interactions in vesicular transport	1	35	0.24791	*BET1L*
Fructose and mannose metabolism	1	35	0.24791	*GMDS*
Th17 cell differentiation	2	120	0.24982	*LCK, IRF4*
AMPK signaling pathway	2	125	0.2644	*CAMKK2, PPP2R5E*
beta-Alanine metabolism	1	38	0.26557	*SMOX*
Apoptosis - multiple species	1	38	0.26557	*BIRC7*
Aldosterone-regulated sodium reabsorption	1	38	0.26557	*HSD11B2*
African trypanosomiasis	1	39	0.27136	*IL18*
Bladder cancer	1	40	0.27711	*FGFR3*
Nicotine addiction	1	41	0.28282	*CHRNA4*
Vascular smooth muscle contraction	2	134	0.29063	*EDN3, ADRA1D*
Homologous recombination	1	43	0.29409	*BRIP1*
cAMP signaling pathway	3	242	0.30421	*GLI3, EDN3, HCAR1*
Proteasome	1	45	0.30518	*PSMD13*
Signaling pathways regulating pluripotency of stem cells	2	143	0.31674	*PCGF3, FGFR3*
Glycine, serine and threonine metabolism	1	48	0.3215	*GCAT*
Arginine and proline metabolism	1	48	0.3215	*SMOX*
Basal transcription factors	1	48	0.3215	*GTF2I*
Hedgehog signaling pathway	1	49	0.32686	*GLI3*
Phospholipase D signaling pathway	2	148	0.33116	*PTGFR, KITLG*
Ubiquitin mediated proteolysis	2	149	0.33403	*BIRC7, ANAPC4*
Notch signaling pathway	1	51	0.33744	*NOTCH3*
Oxidative phosphorylation	2	151	0.33977	*ATP6V0D1, PPA2*
Fanconi anemia pathway	1	52	0.34267	*BRIP1*

Oxytocin signaling pathway	2	154	0.34835	*CAMKK2, ACTB*
Adrenergic signaling in cardiomyocytes	2	154	0.34835	*PPP2R5E, ADRA1D*
Spliceosome	2	155	0.3512	*PPIL1, PRPF6*
Breast cancer	2	155	0.3512	*FGF9, NOTCH3*
Amino sugar and nucleotide sugar metabolism	1	54	0.35301	*GMDS*
Hippo signaling pathway	2	158	0.35973	*ACTB, PARD6A*
Malaria	1	56	0.36318	*IL18*
mTOR signaling pathway	2	160	0.36539	*CLIP1, LAMTOR3*
Pyrimidine metabolism	1	57	0.36821	*UCKL1*
Long-term depression	1	58	0.3732	*GRID2*
VEGF signaling pathway	1	60	0.38306	*KDR*
Measles	2	168	0.38784	*MAVS, TRAF3*
cGMP-PKG signaling pathway	2	171	0.39617	*GTF2I, ADRA1D*
Glycerolipid metabolism	1	63	0.39755	*MBOAT2*
Glutathione metabolism	1	64	0.40231	*GGT6*
Basal cell carcinoma	1	66	0.41171	*GLI3*
Hepatitis C	2	178	0.41539	*MAVS, TRAF3*
Tight junction	2	181	0.42354	*ACTB, PARD6A*
Steroid hormone biosynthesis	1	69	0.42554	*HSD11B2*
Hepatitis B	2	183	0.42894	*MAVS, TRAF3*
Renin secretion	1	71	0.43458	*EDN3*
Melanoma	1	72	0.43905	*FGF9*
Adherens junction	1	72	0.43905	*ACTB*
Transcriptional misregulation in cancer	2	189	0.44498	*SIN3A, FLT1*
Retinol metabolism	1	74	0.44787	*SDR16C5*
Inflammatory bowel disease (IBD)	1	75	0.45224	*IL18*

ABC transporters	1	76	0.45656	*ABCB9*
Arrhythmogenic right ventricular cardiomyopathy (ARVC)	1	76	0.45656	*ACTB*
Leishmaniasis	1	77	0.46086	*NCF1*
Bacterial invasion of epithelial cells	1	77	0.46086	*ACTB*
B cell receptor signaling pathway	1	78	0.46512	*DAPP1*
MicroRNAs in cancer	2	198	0.46856	*FGFR3, NOTCH3*
Viral myocarditis	1	81	0.47769	*ACTB*
RNA degradation	1	83	0.48592	*PABPC5*
Herpes simplex virus 1 infection	4	457	0.49315	*ZNF777, MAVS, TRAF3, ZNF746*
Peroxisome	1	85	0.49401	*HAO1*
Huntington disease	2	212	0.50403	*RCOR1, SIN3A*
Proteoglycans in cancer	2	215	0.51143	*ACTB, KDR*
Longevity regulating pathway	1	90	0.51369	*CAMKK2*
Drug metabolism - other enzymes	1	90	0.51369	*UCKL1*
Alcoholism	2	219	0.52119	*CAMKK2, H2AFZ*
Hypertrophic cardiomyopathy (HCM)	1	92	0.52135	*ACTB*
PD-L1 expression and PD-1 checkpoint pathway in cancer	1	92	0.52135	*LCK*
IL-17 signaling pathway	1	92	0.52135	*TRAF3*
Viral protein interaction with cytokine and cytokine receptor	1	94	0.52889	*IL18*
Fc gamma R-mediated phagocytosis	1	94	0.52889	*NCF1*
Dilated cardiomyopathy (DCM)	1	95	0.53261	*ACTB*
Antigen processing and presentation	1	96	0.53631	*NFYA*
Endocrine resistance	1	96	0.53631	*NOTCH3*

Salivary secretion	1	100	0.5508	*ADRA1D*
Glycerophospholipid metabolism	1	102	0.55787	*MBOAT2*
Viral carcinogenesis	2	244	0.57916	*ATP6V0D1, TRAF3*
Human T-cell leukemia virus 1 infection	2	246	0.58357	*LCK, ANAPC4*
AGE-RAGE signaling pathway in diabetic complications	1	111	0.58837	*PLCD4*
T cell receptor signaling pathway	1	112	0.59162	*LCK*
HIF-1 signaling pathway	1	113	0.59486	*FLT1*
Hematopoietic cell lineage	1	117	0.60753	*KITLG*
Ribosome	2	258	0.60931	*MRPS6, RPS20*
Toll-like receptor signaling pathway	1	119	0.61371	*TRAF3*
Sphingolipid signaling pathway	1	126	0.63461	*PPP2R5E*
Toxoplasmosis	1	127	0.6375	*BIRC7*
Platelet activation	1	127	0.6375	*ACTB*
Carbon metabolism	1	127	0.6375	*HAO1*
TNF signaling pathway	1	128	0.64037	*TRAF3*
Cell cycle	1	129	0.64322	*ANAPC4*
Dopaminergic synapse	1	132	0.65162	*PPP2R5E*
Autophagy - animal	1	133	0.65438	*CAMKK2*
Apelin signaling pathway	1	138	0.66785	*NOTCH3*
Purine metabolism	1	141	0.67568	*PDE6B*
Natural killer cell mediated cytotoxicity	1	147	0.69079	*LCK*
Apoptosis	1	154	0.70753	*ACTB*
Gastric cancer	1	163	0.72774	*FGF9*
Protein processing in endoplasmic reticulum	1	172	0.74656	*DNAJC5*
Systemic lupus erythematosus	1	175	0.75254	*H2AFZ*

Hepatocellular carcinoma	1	184	0.76966	*ACTB*
Chemokine signaling pathway	1	188	0.77688	*NCF1*
Cytokine-cytokine receptor interaction	2	358	0.77823	*IL18, TNFRSF6B*
Necroptosis	1	190	0.78041	*H2AFZ*
Axon guidance	1	191	0.78215	*PARD6A*
Kaposi sarcoma-associated herpesvirus infection	1	217	0.82292	*TRAF3*
Thermogenesis	1	251	0.86499	*ACTB*

Supplementary Table S12 KEGG enrichment analysis of candidate genes during breeding.

Term	Input number	Background number	*P*-value	Input
Melanoma	5	72	0.00041	*MITF, CDH1, PDGFB, FGF18, FGF9*
Pathways in cancer	12	551	0.00226	*PDGFB, GNAQ, CDH1, BIRC7, BID, DLL1, IL5, FGF9, MITF, FGF18, TXNRD2, HHIP*
Neuroactive ligand-receptor interaction	9	372	0.00406	*GRID2, P2RY14, GABRG2, P2RY13, CHRNA4, NPBWR2, EDN3, GABRA1, OPRL1*
Nicotine addiction	3	41	0.00544	*CHRNA4, GABRG2, GABRA1*
Notch signaling pathway	3	51	0.0096	*DLL1, KAT2B, NCSTN*
Thyroid hormone signaling pathway	4	121	0.01897	*RCAN1, MED13L, KAT2B, MED12L*
Legionellosis	3	68	0.02001	*EEF1A2, SAR1B, BCL2L13*
TNF signaling pathway	4	128	0.02265	*RIPK1, IRF1, BCL3, TNFAIP3*
Endocytosis	6	269	0.02499	*CBLC, CAPZA1, RAB5A, CHMP4B, ARRB2, ARFGAP1*
Starch and sucrose metabolism	2	33	0.03261	*GANC, GYG1*
Rap1 signaling pathway	5	215	0.03384	*CDH1, PDGFB, FGF18, GNAQ, FGF9*
Ubiquitin mediated proteolysis	4	149	0.03616	*CBLC, BIRC7, ANAPC5, UBE2D3*
Gap junction	3	91	0.04105	*PDGFB, TUBA8, GNAQ*
Apoptosis - multiple species	2	38	0.04165	*BIRC7, BID*

IL-17 signaling pathway	3	92	0.04215	*IL5, ANAPC5, TNFAIP3*
Morphine addiction	3	94	0.04438	*ARRB2, GABRA1, GABRG2*
Amoebiasis	3	96	0.04667	*GNA14, RAB5A, GNAQ*
Homologous recombination	2	43	0.0515	*POLD4, RAD50*
Melanogenesis	3	103	0.05513	*MITF, GNAQ, ASIP*
Human immunodeficiency virus 1 infection	5	249	0.05634	*RIPK1, BID, APOBEC3F, GNAQ, APOBEC3Z1*
Hedgehog signaling pathway	2	49	0.06428	*ARRB2, HHIP*
Cholinergic synapse	3	111	0.06563	*CHRNA4, KCNQ2, GNAQ*
Antifolate resistance	2	52	0.07104	*ABCG2, ALOX12*
Necroptosis	4	190	0.07343	*RIPK1, BID, CHMP4B, TNFAIP3*
Amyotrophic lateral sclerosis (ALS)	2	56	0.08037	*BID, RAB5A*
Long-term depression	2	58	0.08518	*GNAQ, GRID2*
Platelet activation	3	127	0.0891	*GNAQ, P2RY12, SNAP23*
Non-homologous end-joining	1	13	0.10764	*RAD50*
Mitophagy - animal	2	67	0.10779	*MITF, BCL2L13*
Regulation of actin cytoskeleton	4	219	0.10812	*PDGFB, FGF18, SSH3, FGF9*
MAPK signaling pathway	5	305	0.1083	*PDGFB, FGF18, ARRB2, FGF9, MAPK8IP3*
Renin secretion	2	71	0.1183	*EDN3, GNAQ*
Gastric acid secretion	2	75	0.12906	*KCNE2, GNAQ*
Retrograde endocannabinoid signaling	3	152	0.13158	*GABRG2, GABRA1, GNAQ*
Apoptosis	3	154	0.13524	*RIPK1, BID, TUBA8*
Spliceosome	3	155	0.13709	*PRPF6, MAGOH, DDX46*
Breast cancer	3	155	0.13709	*DLL1, FGF18, FGF9*
Ras signaling pathway	4	242	0.13995	*PDGFB, FGF18, RAB5A, FGF9*
Synaptic vesicle cycle	2	80	0.1428	*CPLX1, ATP6V1E1*
Gastric cancer	3	163	0.15215	*CDH1, FGF18, FGF9*

Peroxisome	2	85	0.15684	*PXMP4, PEX26*
Selenocompound metabolism	1	20	0.15705	*TXNRD2*
Human cytomegalovirus infection	4	255	0.15941	*RIPK1, BID, IL10RA, GNAQ*
Measles	3	168	0.16182	*EIF3H, BID, TNFAIP3*
GABAergic synapse	2	87	0.16252	*GABRG2, GABRA1*
Protein processing in endoplasmic reticulum	3	172	0.16968	*SAR1B, SEC24A, UBE2D3*
Other glycan degradation	1	22	0.17066	*MANBA*
Cytokine-cytokine receptor interaction	5	358	0.17287	*CXCL16, CLCF1, IL5, IL10RA, TNFRSF6B*
Mismatch repair	1	23	0.17739	*POLD4*
RNA transport	3	178	0.18168	*EIF3H, EEF1A2, MAGOH*
Vitamin digestion and absorption	1	24	0.18406	*SLC52A3*
Phagosome	3	180	0.18573	*ATP6V1E1, TUBA8, RAB5A*
Renin-angiotensin system	1	26	0.19723	*PREP*
Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	1	26	0.19723	*PIGG*
mRNA surveillance pathway	2	99	0.19732	*SMG6, MAGOH*
Alzheimer disease	3	187	0.20009	*BID, GNAQ, NCSTN*
Collecting duct acid secretion	1	28	0.2102	*ATP6V1E1*
Phototransduction	1	28	0.2102	*PDE6B*
NF-kappa B signaling pathway	2	104	0.21208	*RIPK1, TNFAIP3*
Th1 and Th2 cell differentiation	2	104	0.21208	*DLL1, IL5*
Glycosphingolipid biosynthesis - lacto and neolacto series	1	29	0.2166	*ST3GAL6*
RNA polymerase	1	29	0.2166	*TWISTNB*
Inflammatory mediator regulation of TRP channels	2	106	0.21801	*GNAQ, ALOX12*

Parathyroid hormone synthesis, secretion and action	2	106	0.21801	*ARRB2, GNAQ*
Pentose phosphate pathway	1	32	0.23551	*H6PD*
Galactose metabolism	1	32	0.23551	*GANC*
C-type lectin receptor signaling pathway	2	112	0.2359	*IRF1, BCL3*
Serotonergic synapse	2	113	0.23888	*GNAQ, ALOX12*
Base excision repair	1	33	0.24171	*POLD4*
Tuberculosis	3	212	0.25318	*BID, RAB5A, IL10RA*
Chagas disease (American trypanosomiasis)	2	118	0.25386	*GNA14, GNAQ*
Asthma	1	35	0.25396	*IL5*
SNARE interactions in vesicular transport	1	35	0.25396	*SNAP23*
Fructose and mannose metabolism	1	35	0.25396	*GMDS*
DNA replication	1	36	0.26001	*POLD4*
Kaposi sarcoma-associated herpesvirus infection	3	217	0.26406	*RCAN1, BID, PDGFB*
Lysosome	2	126	0.27784	*GGA1, MANBA*
Sphingolipid signaling pathway	2	126	0.27784	*BID, GNAQ*
African trypanosomiasis	1	39	0.27787	*GNAQ*
Toxoplasmosis	2	127	0.28084	*BIRC7, IL10RA*
Bladder cancer	1	40	0.28373	*CDH1*
Thyroid cancer	1	41	0.28954	*CDH1*
Pyruvate metabolism	1	41	0.28954	*HAGH*
Tyrosine metabolism	1	43	0.30102	*FAHD1*
Jak-STAT signaling pathway	3	234	0.30138	*PDGFB, IL5, IL10RA*
Vascular smooth muscle contraction	2	134	0.30178	*EDN3, GNAQ*
Apelin signaling pathway	2	138	0.3137	*CDH1, GNAQ*

Nucleotide excision repair	1	46	0.31789	*POLD4*
Vasopressin-regulated water reabsorption	1	47	0.32343	*RAB5A*
Epstein-Barr virus infection	3	245	0.32569	*RIPK1, BID, TNFAIP3*
Human T-cell leukemia virus 1 infection	3	246	0.32791	*ANAPC5, RANBP1, KAT2B*
Signaling pathways regulating pluripotency of stem cells	2	143	0.32854	*PCGF3, JARID2*
Arginine and proline metabolism	1	48	0.32892	*LAP3*
Endocrine and other factor-regulated calcium reabsorption	1	48	0.32892	*GNAQ*
Porphyrin and chlorophyll metabolism	1	48	0.32892	*CPOX*
Fanconi anemia pathway	1	52	0.35044	*EME2*
Oxytocin signaling pathway	2	154	0.36086	*RCAN1, GNAQ*
Adrenergic signaling in cardiomyocytes	2	154	0.36086	*KCNE1, GNAQ*
Amino sugar and nucleotide sugar metabolism	1	54	0.36094	*GMDS*
Intestinal immune network for IgA production	1	55	0.36612	*IL5*
Endometrial cancer	1	59	0.38646	*CDH1*
Allograft rejection	1	60	0.39144	*IL5*
Cellular senescence	2	169	0.40396	*RAD9A, RAD50*
Glutathione metabolism	1	64	0.41096	*LAP3*
Basal cell carcinoma	1	66	0.42049	*HHIP*
Fc epsilon RI signaling pathway	1	67	0.42519	*IL5*
Hepatitis C	2	178	0.42915	*RIPK1, BID*
Cortisol synthesis and secretion	1	68	0.42986	*GNAQ*
Long-term potentiation	1	69	0.43449	*GNAQ*

Tight junction	2	181	0.43743	*BVES, TUBA8*
Adherens junction	1	72	0.44816	*CDH1*
Thyroid hormone synthesis	1	73	0.45264	*GNAQ*
Renal cell carcinoma	1	73	0.45264	*PDGFB*
NOD-like receptor signaling pathway	2	187	0.45378	*RIPK1, TNFAIP3*
Chemokine signaling pathway	2	188	0.45648	*ARRB2, CXCL16*
Cytosolic DNA-sensing pathway	1	74	0.45708	*RIPK1*
Arachidonic acid metabolism	1	75	0.46149	*ALOX12*
Inflammatory bowel disease (IBD)	1	75	0.46149	*IL5*
Glioma	1	76	0.46587	*PDGFB*
ABC transporters	1	76	0.46587	*ABCG2*
Autoimmune thyroid disease	1	76	0.46587	*IL5*
Bacterial invasion of epithelial cells	1	77	0.47021	*CDH1*
Taste transduction	1	78	0.47451	*GABRA1*
Influenza A	2	198	0.48303	*BID, TMPRSS4*
Viral myocarditis	1	81	0.48721	*BID*
Pertussis	1	82	0.49138	*IRF1*
EGFR tyrosine kinase inhibitor resistance	1	83	0.49551	*PDGFB*
p53 signaling pathway	1	83	0.49551	*BID*
Calcium signaling pathway	2	203	0.49601	*GNA14, GNAQ*
Insulin secretion	1	86	0.50771	*GNAQ*
Platinum drug resistance	1	88	0.51568	*BID*
Ribosome biogenesis in eukaryotes	1	90	0.52352	*UTP4*
Prolactin signaling pathway	1	90	0.52352	*IRF1*
Progesterone-mediated oocyte maturation	1	91	0.52739	*ANAPC5*
GnRH signaling pathway	1	93	0.53504	*GNAQ*

Viral protein interaction with cytokine and cytokine receptor	1	94	0.53882	*IL10RA*
Endocrine resistance	1	96	0.54629	*DLL1*
Circadian entrainment	1	96	0.54629	*GNAQ*
Prostate cancer	1	97	0.54998	*PDGFB*
Aldosterone synthesis and secretion	1	99	0.55727	*GNAQ*
Salivary secretion	1	100	0.56086	*GNAQ*
Small cell lung cancer	1	100	0.56086	*BIRC7*
Bile secretion	1	100	0.56086	*ABCG2*
Choline metabolism in cancer	1	101	0.56443	*PDGFB*
Rheumatoid arthritis	1	101	0.56443	*ATP6V1E1*
Pancreatic secretion	1	105	0.57843	*GNAQ*
Glucagon signaling pathway	1	108	0.58863	*GNAQ*
cAMP signaling pathway	2	242	0.58986	*EDN3, HHIP*
Glutamatergic synapse	1	109	0.59198	*GNAQ*
Viral carcinogenesis	2	244	0.5943	*RANBP1, KAT2B*
T cell receptor signaling pathway	1	112	0.60185	*IL5*
Metabolic pathways	12	1540	0.60766	*PDE6B, ST3GAL6, GANC, HAGH, LAP3, ATP6V1E1, H6PD, CPOX, FAHD1, GMDS, ALOX12, GYG1*
Hematopoietic cell lineage	1	117	0.61778	*IL5*
RIG-I-like receptor signaling pathway	1	118	0.62089	*RIPK1*
Toll-like receptor signaling pathway	1	119	0.62398	*RIPK1*
Ribosome	2	258	0.62444	*MRPS6, RPL5*
Oocyte meiosis	1	121	0.63007	*ANAPC5*
PI3K-Akt signaling pathway	3	398	0.63299	*PDGFB, FGF18, FGF9*
Carbon metabolism	1	127	0.64777	*H6PD*

Cell cycle	1	129	0.65348	*ANAPC5*
Dopaminergic synapse	1	132	0.66187	*GNAQ*
Osteoclast differentiation	1	134	0.66736	*MITF*
Relaxin signaling pathway	1	135	0.67006	*ARRB2*
Estrogen signaling pathway	1	138	0.67806	*GNAQ*
Purine metabolism	1	141	0.68586	*PDE6B*
Natural killer cell mediated cytotoxicity	1	147	0.7009	*BID*
Phospholipase D signaling pathway	1	148	0.70333	*PDGFB*
Fluid shear stress and atherosclerosis	1	149	0.70575	*PDGFB*
Oxidative phosphorylation	1	151	0.71052	*ATP6V1E1*
Hippo signaling pathway	1	158	0.72663	*CDH1*
mTOR signaling pathway	1	160	0.73107	*ATP6V1E1*
Cushing syndrome	1	161	0.73326	*GNAQ*
Non-alcoholic fatty liver disease (NAFLD)	1	164	0.73973	*BID*
cGMP-PKG signaling pathway	1	171	0.75422	*GNAQ*
Cell adhesion molecules (CAMs)	1	173	0.75821	*CDH1*
Hepatitis B	1	183	0.77722	*BID*
Hepatocellular carcinoma	1	184	0.77904	*TXNRD2*
Transcriptional misregulation in cancer	1	189	0.7879	*MITF*
Axon guidance	1	191	0.79135	*SSH3*
MicroRNAs in cancer	1	198	0.80298	*PDGFB*
Human papillomavirus infection	2	376	0.81317	*IRF1, ATP6V1E1*
Focal adhesion	1	208	0.81848	*PDGFB*
Huntington disease	1	212	0.82434	*GNAQ*
Herpes simplex virus 1 infection	1	457	0.97665	*BID*
Olfactory transduction	1	1127	0.99992	*ARRB2*

Supplementary Table S13 Overlapping regions during domestication and breeding.

No.	Combined Region (Mb)	Chr	Position		Gene Name
			Start	End	
1	Chr1: 27.75-27.9	1	27750001	27900000	*GLIS1*
2	Chr6:116.4-116.55	6	1.16E+08	116550000	*TMEM175, GAK, CPLX1*
3	Chr6:116.7-117	6	1.17E+08	116850000	*PCGF3, MFSD7, ATP5I, PDE6B, LOC101108751, LOC105613214, PIGG*
		6	1.17E+08	116925000	*PDE6B, LOC101108751, LOC105613214, PIGG*
		6	1.17E+08	117000000	*PIGG*
4	Chr10:35.475-35.625	10	35475001	35625000	*FGF9*
5	Chr13:53.175-53.55	13	53175001	53325000	*TPD52L2, ABHD16B, ZBTB46, ZGPAT, ARFRP1, TNFRSF6B, RTEL1, STMN3*
		13	53250001	53400000	*ZBTB46, ZGPAT, ARFRP1, TNFRSF6B, RTEL1, STMN3, GMEB2, C13H20orf195, SRMS, PTK6, PPDPF, EEF1A2*
		13	53325001	53475000	*STMN3, GMEB2, C13H20orf195, SRMS, PTK6, PPDPF, EEF1A2, KCNQ2*
		13	53400001	53550000	*EEF1A2, KCNQ2, CHRNA4, COL20A1, ARFGAP1, BIRC7*
6	Chr13:56.25-56.4	13	56250001	56400000	*EDN3, LOC105616728, ZNF831*
7	Chr20:49.875-50.175	20	49875001	50025000	*GMDS*
		20	49950001	50100000	*GMDS, LOC105603912*
		20	50025001	50175000	*GMDS, LOC105603912*

Supplementary Table S14 KEGG enrichment analysis of candidate genes from overlapping regions during domestication and breeding.

Term	Input number	Background number	*P*-value	Input
Cholinergic synapse	2	111	0.00673673	*CHRNA4, KCNQ2*

Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	1	26	0.02903342	*PIGG*
Phototransduction	1	28	0.03115136	*PDE6B*
Fructose and mannose metabolism	1	35	0.03852909	*GMDS*
Apoptosis - multiple species	1	38	0.04167434	*BIRC7*
Nicotine addiction	1	41	0.04480965	*CHRNA4*
Amino sugar and nucleotide sugar metabolism	1	54	0.05828194	*GMDS*
Neuroactive ligand-receptor interaction	2	372	0.06238825	*CHRNA4, EDN3*
Legionellosis	1	68	0.07258535	*EEF1A2*
Renin secretion	1	71	0.07562296	*EDN3*
Melanoma	1	72	0.07663336	*FGF9*
Synaptic vesicle cycle	1	80	0.08467826	*CPLX1*
Small cell lung cancer	1	100	0.10449556	*BIRC7*
Pathways in cancer	2	551	0.12135438	*BIRC7, FGF9*
Toxoplasmosis	1	127	0.13059285	*BIRC7*
Vascular smooth muscle contraction	1	134	0.13723801	*EDN3*
Purine metabolism	1	141	0.14383412	*PDE6B*
Signaling pathways regulating pluripotency of stem cells	1	143	0.14570976	*PCGF3*
Ubiquitin mediated proteolysis	1	149	0.15131291	*BIRC7*
Breast cancer	1	155	0.15688057	*FGF9*
Gastric cancer	1	163	0.16424928	*FGF9*
RNA transport	1	178	0.17789837	*EEF1A2*
Rap1 signaling pathway	1	215	0.21065224	*FGF9*
Regulation of actin cytoskeleton	1	219	0.21411677	*FGF9*
cAMP signaling pathway	1	242	0.23375473	*EDN3*

Ras signaling pathway	1	242	0.23375473	*FGF9*
Endocytosis	1	269	0.25620371	*ARFGAP1*
MAPK signaling pathway	1	305	0.2851499	*FGF9*
Cytokine-cytokine receptor interaction	1	358	0.3257945	*TNFRSF6B*
PI3K-Akt signaling pathway	1	398	0.35498277	*FGF9*
Metabolic pathways	2	1540	0.50728578	*PDE6B, GMDS*