Table S1 Sequence data, alignment statistics, rate of PCR duplicates and mean genome wide coverage of each individual.

Sample[a]	Total reads	Alignment rate			% PCR duplicates	Mean coverage
		Overall	Unique concordantly	Multiple concordantly		
CR1	3,299,851,568	2,272,823,480 (68.88%)	1,612,101,578 (48.85%)	658,111,042 (19.94%)	6.18%	45.65 X
CR2	706,459,956	667,000,650 (94.42%)	475,784,910 (67.35%)	190,862,322 (27.02%)	9.54%	10.52 X
CE1	3,692,987,634	2,233,225,340 (60.47%)	1,542,953,834 (41.78%)	687,719,528 (18.62%)	9.11%	43.96 X
CE2[b]	4,890,495,549		NA		33.33%	24.69 X
TM	1,275,012,390	1,209,788,008 (94.88%)	928,246,222 (72.8%)	280,762,936 (22.02%)	8.68%	36.92 X

[a] CR1: Chinese rhesus macaque (Yunnan Province), CR2: Chinese rhesus macaque (Sichuan Province), CE1: Vietnamese cynomolgus macaque, CE2: Malaysian cynomolgus macaque, TM: Tibetan macaque

[b] The alignment statistics can be found in reference 1

[c] Reference 1: Higashino A, Sakate R, Kameoka Y, Takahashi I, Hirata M, Tanuma R, Masui T, Yasutomi Y, Osada N: Whole-genome sequencing and analysis of the Malaysian cynomolgus macaque (*Macaca fascicularis*) genome. *Genome Biology* 2012, 13:R58

Table S2 Transitions:transversions ratio for autosomes of five macaques.

Sample [a]	Ti:Tv
CR1	2.20
CR2	2.11
CE1	2.18
CE2	2.20
TM	2.17

[a] CR1: Chinese rhesus macaque (Yunnan Province), CR2: Chinese rhesus macaque (Sichuan Province), CE1: Vietnamese cynomolgus macaque, CE2: Malaysian cynomolgus macaque, TM: Tibetan macaque

Table S3 Total numbers of synonymous and non-synonymous variants in Tibetan macaque and six different GO terms. Numbers in parentheses are Tibetan macaque specific variants. Numbers of genes, which carried at least one homozygous non-synonymous variant, were listed too.

	Synonymous		Non-synonymous		Numbers of genes[#]
	Total[*]	Homozygous[*]	Total[*]	Homozygous[*]	
Total variants	52,987 (22,540)	44,878 (17,259)	33,612 (13,756)	27,348 (10,106)	—
Immune response	2,259	1,940	1,224	1,034 (397)	347 **(203)**
Response to drug	649	545	270	235 (97)	78 **(48)**
Glucose metabolic process	443	344	136	107 (29)	41 **(17)**
Insulin secretion	324	269	106	93 (40)	37 **(21)**
Insulin receptor binding	59	52	9	9 (2)	5 **(2)**
Insulin receptor signaling pathway	431	360	126	112 (48)	35 **(21)**

Numbers of genes that carry at least one Tibetan macaque specific homozygous non-synonymous variant are showed in bold.

* These numbers contain overlap hits. There are genes contain more than one transcript but we could not choose the single transcript annotation under DNA level, thus for some genomic position, we may report more than one time if there are more than one transcript cover that genomic position and these transcripts belong to same gene.

Table S4 Numbers of sites pass different filters. Percentage of the genome measured with respect to 2504762378 non-'N' bases in the autosomes of reference genome. Details of the filters can be found in Supplementary file 4.

Sample[a]	SNVs		Total useable sites	
	GF1 and SF	GF2 and SF	GF1 and SF	GF2 and SF
CR1	6,701,970	9,384,359	2,211,253,060 (88.28%)	2,264,143,011 (90.39%)
CR2	4,842,684	6,252,098	1,597,009,392 (63.76%)	1,637,370,536 (65.37%)
CE1	8,545,709	11,751,302	2,194,010,374 (87.59%)	2,245,482,535 (89.65%)
CE2	8,709,735	12,000,848	2,210,444,562 (88.25%)	2,261,105,771 (90.27%)
TM	8,720,234	11,937,445	2,229,598,137 (89.01%)	2,281,638,762 (91.09%)

[a] CR1: Chinese rhesus macaque (Yunnan Province), CR2: Chinese rhesus macaque (Sichuan Province), CE1: Vietnamese cynomolgus macaque, CE2: Malaysian cynomolgus macaque, TM: Tibetan macaque

Table S5 Single nucleotide divergence among macaques in 50 kb non-overlapping windows across the 20 autosomes. The heterozygous variants were excluded here. The divergence values were the mean values across the 20 autosomes.

Comparison [a]	Divergence
IR/CR1	0.00115
IR/CR2	0.00105
IR/CE1	0.00179
IR/CE2	0.00191
CR1/CR2	0.00042
CE1/CE2	0.00086
CR1/CE1	0.00108
CR1/CE2	0.00121
CR2/CE1	0.00109
CR2/CE2	0.00122
TM/IR	0.00384
TM/CR1	0.00300
TM/CR2	0.00301
TM/CE1	0.00289
TM/CE2	0.00280

[a] IR: the reference genome, Indian rhesus macaque, CR1: Chinese rhesus macaque (Yunnan Province), CR2: Chinese rhesus macaque (Sichuan Province), CE1: Vietnamese cynomolgus macaque, CE2: Malaysian cynomolgus macaque, TM: Tibetan macaque

Table S6 Total sizes of possible putative introgression regions (PIRs) in Tibetan macaque genome with different window sizes under different control sets. The numbers are without statistical criteria.

Comparisons [a]	Total sizes of possible PIRs at different window sizes (kb)											
	10kb	20kb	30kb	40kb	50kb	60kb	80kb	100kb	200kb	400kb	600kb	1000kb
TM/CR1 - CR1/CR2	87,700	41,460	23,670	16,240	11,900	9,720	7,760	6,600	4,400	4,800	3,600	2,000
TM/CR1 - CR1/CE1	409,370	290,080	218,100	171,000	141,200	119,160	82,720	63,300	24,200	13,600	11,400	7,000
TM/CR1 - CR1/CE2	557,890	431,660	354,180	299,480	258,600	224,580	172,880	143,000	64,600	28,000	22,800	16,000
TM/CR2 - CR1/CR2	76,110	33,220	18,870	12,200	8,000	6,660	5,040	4,700	2,800	3,200	3,000	4,000
TM/CR2 - CR2/CE1	403,710	283,820	215,490	168,160	136,550	113,520	78,720	60,300	21,800	14,000	12,600	8,000
TM/CR2 - CR2/CE2	546,640	418,360	336,060	278,840	239,300	203,940	155,600	125,100	54,200	22,400	15,600	13,000

[a] CR1: Chinese rhesus macaque (Yunnan Province), CR2: Chinese rhesus macaque (Sichuan Province), CE1: Vietnamese cynomolgus macaque, CE2: Malaysian cynomolgus macaque, TM: Tibetan macaque

Table S7 Total sizes of possible putative introgression regions (PIRs) in Tibetan macaque genome with different window sizes under different control sets. The possible PIRs here are all detected in both Chinese rhesus macaques. The numbers are without statistical criteria.

Comparisons [a]	Total sizes of possible PIRs at different window sizes (kb)											
	10kb	20kb	30kb	40kb	50kb	60kb	80kb	100kb	200kb	400kb	600kb	1000kb
TM/CRs - CR1/CR2	32,750	13,220	6,780	4,480	2,950	2,400	1,760	1,800	1,600	2,000	1,800	1,000
TM/CRs - CRs/CE1	303,970	206,040	150,330	115,680	93,250	76,200	52,160	39,800	15,800	10,400	9,000	5,000
TM/CRs - CRs/CE2	437,000	321,860	253,020	206,880	176,050	148,320	109,600	88,900	39,600	19,200	14,400	12,000

[a] CR1: Chinese rhesus macaque (Yunnan Province), CR2: Chinese rhesus macaque (Sichuan Province), CE1: Vietnamese cynomolgus macaque, CE2: Malaysian cynomolgus macaque, TM: Tibetan macaque

Table S8 Numbers of specific SNVs in macaques. Numbers of specific SNVs for different groups mean all the samples in that groups have that SNV whereas other samples do not.

Samples/Groups [a]	Total	Heterozygous	Homozygous
CR1	2,038,702	1,866,243	172,459
CR2	2,005,637	1,835,136	170,501
CE1	2,876,161	2,450,466	425,695
CE2	3,452,073	3,009,976	442,097
TM	3,936,546	1,075,356	2,861,190
CR1 + CR2	468,065	413,082	54,983
CE1 + CE2	521,403	387,696	133,707

[a] CR1: Chinese rhesus macaque (Yunnan Province), CR2: Chinese rhesus macaque (Sichuan Province), CE1: Vietnamese cynomolgus macaque, CE2: Malaysian cynomolgus macaque, TM: Tibetan macaque

Table S10 gProfiler functional enrichment analysis for genes carried at least one Tibetan macaque specific homozygous non-synonymous variant, which were probably, or possibly damaging from the estimation of PolyPhen-2.

Term name	Category	*P*-value	Total genes in category	Total genes in input[#]	Input genes in category
Sensory perception	GO:0007600	0.00151	598	892	52
Sensory perception of chemical stimulus	GO:0007606	0.05000	391	892	35
Diabetes mellitus	HP:0000819	0.03140	168	881	14
Type II diabetes mellitus	HP:0005978	0.01700	82	881	9
Ectopic calcification	HP:0010766	0.00778	113	881	12
Cerebral calcification	HP:0002514	0.01800	56	881	7
Scarring	HP:0100699	0.02370	101	881	10
Atypical scarring of skin	HP:0000987	0.01950	98	881	10
Abnormality of the face	HP:0000271	0.02450	1096	881	64
Abnormal cortical gyration	HP:0002536	0.02780	61	881	7
Thickened skin	HP:0001072	0.01130	210	881	18
Epidermal thickening	HP:0011368	0.00959	191	881	17
Abnormality of the conjunctiva	HP:0000502	0.04000	52	881	6
Inflammatory abnormality of the eye	HP:0100533	0.04240	81	881	8
Glaucoma	HP:0000501	0.03000	167	881	14
Cleft upper lip	HP:0000204	0.03160	91	881	9
Non-midline cleft lip	HP:0100335	0.04430	40	881	5
Wide nasal bridge	HP:0000431	0.02730	181	881	15
Abnormality of the morphology of the rib cage	HP:0001547	0.03040	76	881	8
Abnormality of circulating hormone level	HP:0003117	0.01170	119	881	12
Hyperinsulinemia	HP:0000842	0.01060	76	881	9
Abnormality of the choroid	HP:0000610	0.01100	90	881	10
Chorioretinal abnormality	HP:0000532	0.03730	79	881	8
Lymphadenopathy	HP:0002716	0.04670	68	881	7
Aplasia/Hypoplasia affecting the eye	HP:0008056	0.03140	168	881	14
Abnormality of globe size	HP:0100887	0.01940	70	881	8
Microphthalmos	HP:0000568	0.00957	62	881	8
Abnormality of the vasculature	HP:0002597	0.01330	382	881	28
Arteriovenous malformation	HP:0100026	0.03650	38	881	5
Abnormality of the vasculature of the eye	HP:0008047	0.03370	92	881	9
Pigmentary retinopathy	HP:0000580	0.00985	50	881	7
Abnormality of skin physiology	HP:0011122	0.02170	176	881	15
Inflammatory abnormality of the skin	HP:0011123	0.02100	144	881	13

Numbers of input genes can be identified in each database (GO and HP).

Table S11 gProfiler functional enrichment analysis for genes carried at least one Tibetan macaque specific homozygous non-synonymous variant, which were probably or possibly damaging from the estimation of PolyPhen-2 and also 'deleterious' from the estimation of SIFT.

Term name	Category	*P*-value	Total genes in category	Total genes in input#	Input genes in category
G-protein coupled receptor signaling pathwaya	GO:0007186	0.03320	947	348	32
detection of stimulus	GO:0051606	0.00000	448	348	27
detection of chemical stimulus	GO:0009593	0.00000	368	348	25
neurological system process	GO:0050877	0.01410	986	348	34
sensory perception	GO:0007600	0.00000	604	348	34
sensory perception of chemical stimulus	GO:0007606	0.00000	397	348	26
sensory perception of smell	GO:0007608	0.00001	350	348	23
detection of stimulus involved in sensory perception	GO:0050906	0.00001	380	348	24
detection of chemical stimulus involved in sensory perception	GO:0050907	0.00001	346	348	23
detection of chemical stimulus involved in sensory perception of smell	GO:0050911	0.00001	334	348	22
visual perception	GO:0007601	0.03590	71	348	7
receptor activity	GO:0004872	0.02720	1368	348	42
signaling receptor activity	GO:0038023	0.00815	1000	348	35
transmembrane signaling receptor activity	GO:0004888	0.00303	913	348	34
G-protein coupled receptor activity	GO:0004930	0.00826	606	348	25
olfactory receptor activity	GO:0004984	0.00001	334	348	22
Aplasia/Hypoplasia of the cerebrum	HP:0007364	0.05000	480	345	16
Abnormality of globe size	HP:0100887	0.01550	86	345	6
Microphthalmos	HP:0000568	0.00842	76	345	6
Abnormal cortical gyration	HP:0002536	0.03520	74	345	5

Numbers of input genes can be identified in each database (GO and HP).

Table S12 Numbers of transcripts contain loss-of-function variants in Tibetan macaque. We examined the following categories: lose start codon, lose stop codon, and gain stop codon (premature stop codon). All of the examinations are based on the annotation of reference genome, and excluding the transcripts contain loss-of function variants in the reference genome. Tibetan macaque specific means these transcripts only contain loss-of-function variants in Tibetan macaque, whereas there are none loss-of-function variants in all the rest macaques (including reference).

Failed Category	Tibetan Macaque		Tibetan Macaque specific	
	Homozygous	Heterozygous	Homozygous	Heterozygous
Lose start codon	89*	14	49#	8
Lose stop codon	31	9	10	3
Gain stop codon	183*	95	100#	57
Total	300	118	158	68

* Three transcripts contain both lose start codon variant and gain stop codon variant.

\# One transcript contains both lose start codon variant and gain stop codon variant.

Table S13 Information of Tibetan macaque specific transcripts, which containing homozygous loss-of-function variants. We examined the following categories: lose start codon, lose stop codon, and gain stop codon (premature stop codon). All of the examinations are based on the annotation of reference genome, and excluding the transcripts contain loss-of function variants in the reference genome. Tibetan macaque specific means these transcripts only contain loss-of-function variants in Tibetan macaque, whereas there are none loss-of-function variants in all the rest macaques (including reference). "1" is loss-of-function variant, "0" is normal. GO terms are the six GO terms we scanned in the main text.

Transcripts	Lose start codon	Lose stop codon	Gain stop codon	Gene symbol	GO terms
XM_001106842.2	1	0	0	ADAMDEC1	Immune response
XM_001098401.1	1	0	0	ARCN1	None
XM_001098236.2	1	0	0	ASAH1	None
XM_001087415.2	0	0	1	ATP13A2	None
XM_001105143.2	0	0	1	ATP5J	None
XM_002803160.1	0	0	1	ATP5J	None
XM_001095529.2	0	0	1	BCAS4	None
XM_001111612.2	1	0	0	BNC1	None
XM_001083792.2	0	0	1	C11H12orf72	None
XM_001084019.2	0	0	1	C11H12orf72	None
XM_001110274.2	1	0	0	C5AR1	Immune response
XM_001116077.2	0	0	1	CACNG6	None
XM_001092440.2	0	0	1	CLYBL	None
XM_001093299.2	0	0	1	CYPIA1	None
XM_001097922.2	0	0	1	FLNB	None
XM_001103527.2	0	0	1	GPR116	None
XM_001089205.2	0	0	1	GPR124	None
XM_001110531.2	1	0	0	HSD11B1	None
XM_001096630.2	1	0	0	IFITM1	Immune response
XM_001084639.2	0	0	1	LECT1	None
XM_002804572.1	1	0	0	LOC100423271	None
XM_002802688.1	0	0	1	LOC100423442	None
XM_002804499.1	0	0	1	LOC100423633	None
XM_002800116.1	0	0	1	LOC100423856	None
XM_002803928.1	0	0	1	LOC100423945	None
XM_002798118.1	0	0	1	LOC100424089	None
XM_002802573.1	0	0	1	LOC100424182	None
XM_002803741.1	0	1	0	LOC100424317	None
XM_002798052.1	0	0	1	LOC100424641	None
XM_002799261.1	0	0	1	LOC100424682	None
XM_002800992.1	0	1	0	LOC100425114	None
XM_002800691.1	0	1	0	LOC100425402	None

XM_002804059.1	1	0	0	LOC100425512	None
XM_002803769.1	0	0	1	LOC100425582	None
XM_002805112.1	1	0	0	LOC100426007	None
XM_002799795.1	0	0	1	LOC100426356	None
XM_002799223.1	0	0	1	LOC100426488	None
XM_002800121.1	1	0	0	LOC100426559	None
XM_002805767.1	0	0	1	LOC100426789	None
XM_002801560.1	0	0	1	LOC100426914	None
XM_002799798.1	0	0	1	LOC100427074	None
XM_002800058.1	0	0	1	LOC100427457	None
XM_002798577.1	0	0	1	LOC100427895	None
XM_002802943.1	0	0	1	LOC100427922	None
XM_002804155.1	0	0	1	LOC100428052	None
XM_002804951.1	0	0	1	LOC100428104	None
XM_002805720.1	1	0	0	LOC100428135	None
XM_002805632.1	1	0	0	LOC100428212	None
XM_002800243.1	1	0	0	LOC100428281	None
XM_002802208.1	0	0	1	LOC100428293	None
XM_002803708.1	0	0	1	LOC100428305	None
XM_002801310.1	0	0	1	LOC100428395	None
XM_002804691.1	0	0	1	LOC100428442	None
XM_002798717.1	0	0	1	LOC100428676	None
XM_002798509.1	0	0	1	LOC100428805	None
XM_002798841.1	0	0	1	LOC100428808	None
XM_002800348.1	0	0	1	LOC100428972	None
XM_002801753.1	1	0	0	LOC100429230	None
XM_002804971.1	0	0	1	LOC100429418	None
XM_002801719.1	0	0	1	LOC100429545	None
XM_002803845.1	0	1	0	LOC100429558	None
XM_002802033.1	1	0	0	LOC100429613	None
XM_002798976.1	0	0	1	LOC100429750	None
XM_002798155.1	1	0	0	LOC100430211	None
XM_002800940.1	1	0	0	LOC100430263	None
XM_002799316.1	1	0	0	LOC100430329	None
XM_002800808.1	1	0	0	LOC100430372	None
XM_002800179.1	1	0	0	LOC100430447	None
XM_002798511.1	0	0	1	LOC100430610	None
XM_002804571.1	0	0	1	LOC100430648	None
XM_002804529.1	1	0	0	LOC100430673	None
XM_002804191.1	0	0	1	LOC100430934	None
XM_002803377.1	0	1	0	LOC100430997	None
XM_001082317.2	1	0	0	LOC693603	None
XM_001082159.2	0	0	1	LOC693699	None

XM_001082718.2	1	0	0	LOC694009	None
XM_001082966.2	1	0	0	LOC694262	None
XM_001083089.2	0	0	1	LOC694395	None
XM_001083320.1	0	0	1	LOC694656	None
XM_001088636.2	0	0	1	LOC695115	None
XM_001083764.2	0	0	1	LOC695131	None
XM_001084343.1	0	0	1	LOC695700	None
XM_001086742.2	0	0	1	LOC695873	None
XM_001088982.2	1	0	0	LOC696151	None
XM_001086586.2	1	0	0	LOC697070	None
XM_001090938.2	1	0	1	LOC698002	None
XM_002799710.1	1	0	0	LOC699328	None
XM_001088432.2	0	0	1	LOC700024	None
XM_001088760.1	1	0	0	LOC700405	None
XM_001096561.2	0	0	1	LOC701327	None
XM_001089687.1	0	0	1	LOC701396	None
XM_001094673.2	0	0	1	LOC701840	None
XM_001090152.2	1	0	0	LOC701870	None
XM_001099612.2	0	1	0	LOC702143	None
XM_001090733.1	0	0	1	LOC702427	None
XM_001091570.2	0	0	1	LOC703272	None
XM_001104264.2	0	0	1	LOC703645	None
XM_001092960.1	1	0	0	LOC704594	None
XM_001093190.2	0	0	1	LOC704829	None
XM_001099141.2	0	0	1	LOC705360	None
XM_001100470.1	0	0	1	LOC705678	None
XM_001096487.2	0	0	1	LOC708042	None
XM_001104416.2	0	0	1	LOC708085	None
XM_001104842.2	0	0	1	LOC708539	None
XM_001104915.2	0	0	1	LOC708539	None
XM_001097383.2	0	0	1	LOC708887	None
XM_001109550.2	1	0	0	LOC709014	None
XM_001106570.2	0	1	0	LOC709560	None
XM_002800155.1	0	1	0	LOC709560	None
XM_001094140.2	0	0	1	LOC709652	None
XM_001098646.2	0	0	1	LOC710063	None
XM_001098747.2	0	0	1	LOC710159	None
XM_001099165.2	1	0	0	LOC710528	None
XM_001110734.2	0	0	1	LOC711432	None
XM_001110773.2	0	0	1	LOC711432	None
XM_001110816.2	0	0	1	LOC711432	None
XM_001100246.2	0	0	1	LOC711444	None
XM_001111484.2	0	0	1	LOC711991	None

XM_001111004.2	1	0	0	LOC712160	None
XM_001112828.2	1	0	0	LOC713986	None
XM_001104157.2	0	0	1	LOC714417	None
XM_001111884.2	1	0	0	LOC715124	None
XM_001105303.2	1	0	0	LOC715195	None
XM_001105373.2	0	0	1	LOC715243	None
XM_001116547.2	0	0	1	LOC716163	None
XM_001107106.2	0	0	1	LOC716398	None
XM_001107484.1	0	0	1	LOC716640	None
XM_001108092.2	1	0	0	LOC716986	None
XM_001110670.2	1	0	0	LOC718263	None
XM_001110906.2	0	0	1	LOC718353	None
XM_001111234.2	0	0	1	LOC718483	None
XM_002801818.1	0	0	1	LOC719152	None
XM_001113842.2	0	0	1	LOC719516	None
XM_001113864.2	0	0	1	LOC719519	None
XM_001114397.2	1	0	0	LOC719750	None
XM_001115954.2	0	1	0	LOC720477	None
XM_001116180.2	1	0	0	LOC720596	None
XM_001116567.2	0	0	1	LOC720768	None
XM_001118014.2	0	1	0	LOC721815	None
XM_001118456.2	1	0	0	LOC722292	None
XM_001085216.2	1	0	0	MS4A10	None
XM_001103964.2	1	0	0	PRMT5	None
XM_002804980.1	1	0	0	PRMT5	None
XM_001107427.2	0	0	1	RHPN2	None
XM_001110408.2	0	0	1	S100A9	Immune response
XM_002803380.1	0	0	1	SAMD9	None
XM_001093788.2	1	0	0	SFRS2IP	None
XM_001086434.1	0	0	1	SKI	None
XM_001090485.2	0	0	1	SLC24A3	None
XM_001090491.2	0	0	1	SPINK4	None
XM_001102219.2	0	0	1	SPTLC1	None
XM_002803240.1	0	0	1	SRCRB4D	None
XM_001092105.1	0	0	1	TAS2R60	None
XM_001096255.2	0	0	1	TNFRSF13B	None
XM_001118873.2	0	0	1	TNFRSF8	None
XM_001083155.2	1	0	0	UBE2C	None
XM_001083272.2	1	0	0	UBE2C	None
XM_001108117.2	0	0	1	ZNF222	None

Table S14 Information of Tibetan macaque specific transcripts, which containing heterozygous loss-of-function variants. We examined the following categories: lose start codon, lose stop codon, and gain stop codon (premature stop codon). All of the examinations are based on the annotation of reference genome, and excluding the transcripts contain loss-of function variants in the reference genome. Tibetan macaque specific means these transcripts only contain loss-of-function variants in Tibetan macaque, whereas there are none loss-of-function variants in all the rest macaques (including reference). “1” is loss-of-function variant, “0” is normal. GO terms are the six GO terms we scanned in the main text.

Transcripts	Lose start codon	Lose stop codon	Gain stop codon	Gene symbol	GO terms
XM_001101072.1	0	0	1	ANXA13	None
XM_001101163.2	0	0	1	ANXA13	None
XM_001081983.2	0	0	1	C13H2orf79	None
XM_001107677.2	0	0	1	CAPZA1	Immune response
XM_001097284.2	0	0	1	CST2	None
XM_001105622.2	0	0	1	DUSP11	None
XM_001094642.2	0	1	0	FHIT	None
XM_001099955.2	0	0	1	HNRPH1	None
XM_001089749.2	0	0	1	KCNE2	None
XM_001099641.2	0	0	1	KRTAP15-1	None
XM_002803609.1	0	0	1	LOC100423209	None
XM_002805610.1	0	0	1	LOC100423320	None
XM_002803267.1	0	0	1	LOC100423547	None
XM_002800813.1	0	0	1	LOC100423926	None
XM_002803507.1	1	0	0	LOC100424055	None
XM_002804006.1	0	0	1	LOC100424970	None
XM_002804503.1	0	0	1	LOC100425139	None
XM_002800650.1	0	0	1	LOC100425805	None
XM_002805551.1	0	0	1	LOC100426145	None
XM_002801806.1	1	0	0	LOC100426716	None
XM_002802220.1	0	0	1	LOC100426943	None
XM_002799112.1	0	0	1	LOC100426954	None
XM_002802716.1	0	0	1	LOC100427061	None
XM_002798655.1	0	0	1	LOC100427518	None
XM_002800346.1	0	0	1	LOC100428062	None
XM_002803312.1	0	0	1	LOC100428263	None
XM_002802253.1	0	0	1	LOC100429165	None
XM_002800923.1	1	0	0	LOC100430041	None
XM_002798953.1	0	0	1	LOC100430325	None
XM_001082844.2	0	0	1	LOC694141	None
XM_001083923.2	0	1	0	LOC694712	None
XM_001084233.2	0	0	1	LOC695597	None

XM_001086104.2	0	0	1	LOC697534	None
XM_001088444.2	0	0	1	LOC700038	None
XM_001090940.2	0	0	1	LOC700257	None
XM_002805571.1	0	0	1	LOC700257	None
XM_001099502.2	0	0	1	LOC701418	None
XM_001099697.2	0	0	1	LOC701418	None
XM_001089802.2	1	0	0	LOC701506	None
XM_001090262.2	0	0	1	LOC701982	None
XM_001090390.2	0	0	1	LOC702107	None
XM_001091566.2	0	0	1	LOC703267	None
XM_001093514.2	0	0	1	LOC705133	None
XM_001097061.1	1	0	0	LOC708585	None
XM_001097172.2	0	0	1	LOC708687	None
XM_001106627.2	0	0	1	LOC708726	None
XM_001104102.2	0	1	0	LOC709203	None
XM_001097871.2	0	0	1	LOC709347	None
XM_001108568.2	0	0	1	LOC710595	None
XM_001104811.2	0	0	1	LOC712404	None
XM_001101814.2	0	0	1	LOC712728	None
XM_002799392.1	0	0	1	LOC712728	None
XM_002799393.1	0	0	1	LOC712728	None
XM_001102637.2	1	0	0	LOC713322	None
XM_001102724.2	0	0	1	LOC713381	None
XM_001105162.2	0	0	1	LOC715088	None
XM_001105243.2	0	0	1	LOC715160	None
XM_001107850.2	0	0	1	LOC716859	None
XM_001110595.2	0	0	1	LOC718221	None
XM_001114435.2	1	0	0	LOC719766	None
XM_001118627.2	0	0	1	LOC722485	None
XM_002805543.1	0	0	1	LOC722485	None
XM_001099855.2	0	0	1	NR3C2	None
XM_001111014.2	0	0	1	RNF11	None
XM_001090497.2	0	0	1	SAMD9	None
XM_001106157.2	1	0	0	SLC44A4	None
XM_001092064.2	0	0	1	SYCP3	None
XM_001091775.2	0	0	1	SYNJ2BP	None