

## Supplementary Materials

### Supplementary Text

#### Sample preparation and sequencing

We sequenced the genome of a male kiang using a whole-genome shotgun approach. DNA was isolated from muscle tissue using standard CTAB extraction and libraries were prepared following the protocols provided by Illumina. Multiple paired-end and mate-pair libraries were constructed with fragments of varying length (from 220 bp to 17 kb) (**Supplementary Table S1**). All libraries were sequenced through the Illumina HiSeq 2500 sequencing platform. In total, 400.92 Gb of raw reads ( $\sim 174 \times$  coverage of kiang genome) with an average read length of 126 bp were generated for genome assembly.

#### Genome assembly

##### Genome size estimation via K-mer

We estimated genome size and repeat content based on 21 K-mer frequency distribution of the short-insert libraries (220 bp) (Li et al., 2010). Genome size was estimated using JELLYFISH (Marçais & Kingsford, 2011) with an optimal K-mer size (<http://koke.asrc.kanazawa-u.ac.jp/HOWTO/kmer-genomesize.html>). The estimated kiang genome size was determined by the frequency distribution peak of unique K-mers. The genome size was approximately 2.30 Gb based on the K-mer method (**Supplementary Figure S1**).

##### *De novo* assembly

Prior to assembly, we excluded data resulting from poor libraries, low-quality reads, and polymerase chain reaction (PCR) artifacts. Low-quality reads were defined as: a. 'N' spanning more than 5% of read length; b. average PHRED score  $< 20$ , indicating sequencing error rate above 1%; c. after removing low-quality bases at the end of reads (PHRED score  $< 20$ ), paired-end reads whose read length was shorter than 30 bp; d. more than 10 bp of reads aligned to adapter sequences (with no more than 3 bp mismatch).

After quality control, the genome was assembled by a combination of methods using high-quality data: first, the high-quality reads were used for *de novo* assembly by ALLPATHS-LG (Gnerre et al., 2011) with default parameters. We split reads (short insert size libraries  $< 1$  kb) into K-mers to build a de Bruijn graph, regardless of pairing information. Using the sequence overlap information, the final genome generated by ALLPATHS-LG consisted of 20 678 contigs with a contig N50 of 246.4 kb and a contig length of 2.36 Gb (**Supplementary Table S2**). We then used SSPACE (Boetzer et al., 2011) to join the contigs into scaffolds with default parameters. The linkage information

supported by an unreliable weight of paired-end relationships or ambiguous connections created by repetitive sequences was discarded during scaffold construction. As a result, we constructed a total of 2 960 scaffolds with a N50 of 17.6 Mb and total length of 2.38 Gb (**Supplementary Table S2**). We polished the genome and filled the gaps using GapCloser v1.12 (for SOAPdenovo) (Luo et al., 2012). Briefly, to fill the intra-scaffold gaps, we retrieved pairs in which one read was well-aligned on the contigs, and another read was located in the gap region according to the paired-end information, and then performed local assembly for the collected reads. GapCloser with default parameters was used to align the paired-end reads to the genome and stretch gap boundaries or close gaps based on the local assemblies.

### **Accuracy assessment**

Genome assembly was evaluated from three perspectives: i.e., single base accuracy, gene region coverage, and collinearity assessment. We realigned all usable reads on the scaffold to calculate the percentage of conflicting bases. The total number of inconsistent single bases was 6 818, accounting for 0.00029% of all contigs (**Supplementary Table S3**). Given the close relationship between kiangs and horses (divergence time ~6.2–10.0 million years ago) and the high-quality horse gene annotation in the Ensembl and NCBI databases, we compared the kiang and horse genomes and annotations. Gene region completeness was first evaluated by aligning the horse coding genes to the kiang-assembled genome using BLAT (Kent, 2002). Genes with aligned lengths shorter than 100 bp were discarded. In total, 22 308 of 22 632 horse genes were aligned to the kiang genome, indicating gene region completeness of over 98.00% (**Supplementary Table S4**). Collinearity assessment can be used to assess the integrity and accuracy of genome assembly. We used Nummer (Kurtz et al., 2004) to perform collinearity assessment by aligning the kiang-assembled genome to the horse genome, which was downloaded from NCBI. Several scaffolds are shown in **Supplementary Figure S2**, demonstrating high similarity and concordance between the kiang and closely related horse. Overall, the high similarity between the two genomes indicates an accurate and complete genome assembly.

### **Gene model prediction**

We adopted three strategies to predict genes, i.e., *de novo* gene prediction, sequence homology-based prediction, and RNA-seq data prediction. All predicted gene structures were integrated into weighted consensus gene structures by GLEAN (Kieras et al., 1995).

### **Homology-based gene prediction**

For homology-based gene prediction, we used GeneBlastA (Stanke & Waack, 2003) to identify

homologous loci and GeneWise (Stanke & Waack, 2003) to predict gene structure and precise spliced alignment. The proteins used to predict the kiang gene model were from *Homo sapiens* (human) and *Equus caballus* (domestic horse) (downloaded from NCBI). Short genes (<150 bp) and premature or frame-shifted genes were removed.

### **Ab initio prediction**

We utilized AUGUSTUS (Stanke et al., 2006) for *de novo* prediction of repeat-masked sequences with model parameters trained on the horse. Short genes were discarded using the same sample filter threshold as for homology prediction.

### **Gene structure identification using unigene data**

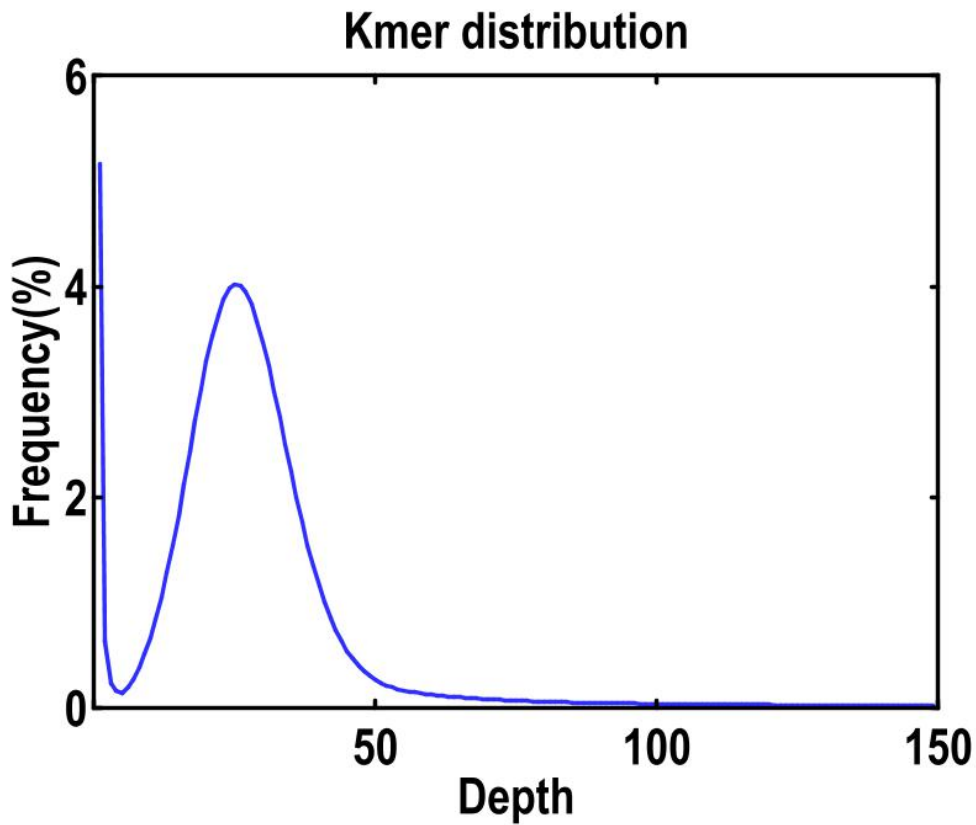
Based on downloaded horse unigene data, we used PASA (Birney et al., 2004) to predict the gene model and structures to assist in gene annotation. Unigenes were aligned to the genome assembly using BLAT (identity $\geq$ 0.95, coverage $\geq$ 0.90) and PASA was used for gene structure identification with parameters of “-I 20000 -c alignAssembly.config -C -R -g genome.fasta -t unigene.fasta.clean -T -u unigene.fasta --ALIGNERS gmap” (<http://pasapipeline.github.io/>).

The gene model sets predicted by the above methods were integrated using GLEAN with the parameters --minlen 150 --minintron 11 --maxintron 10000 (Kieras et al., 1995) to form a comprehensive and non-redundant gene set. Short genes (<150 bp) were filtered out. We identified a total of 27 178 coding genes with an average gene length of 17 204 bp and mean exon length of 157 bp (**Supplementary Tables S6-S7**). We also align-predicted coding genes to the NR (Marchler-Bauer et al., 2011), KOG (Tatusov et al., 2001), GO (Dimmer et al., 2012), KEGG (Ogata et al., 1999), and TrEMBL (Zdobnov & Apweiler, 2001) databases for functional annotation, with 66.9% of genes annotated to the databases.

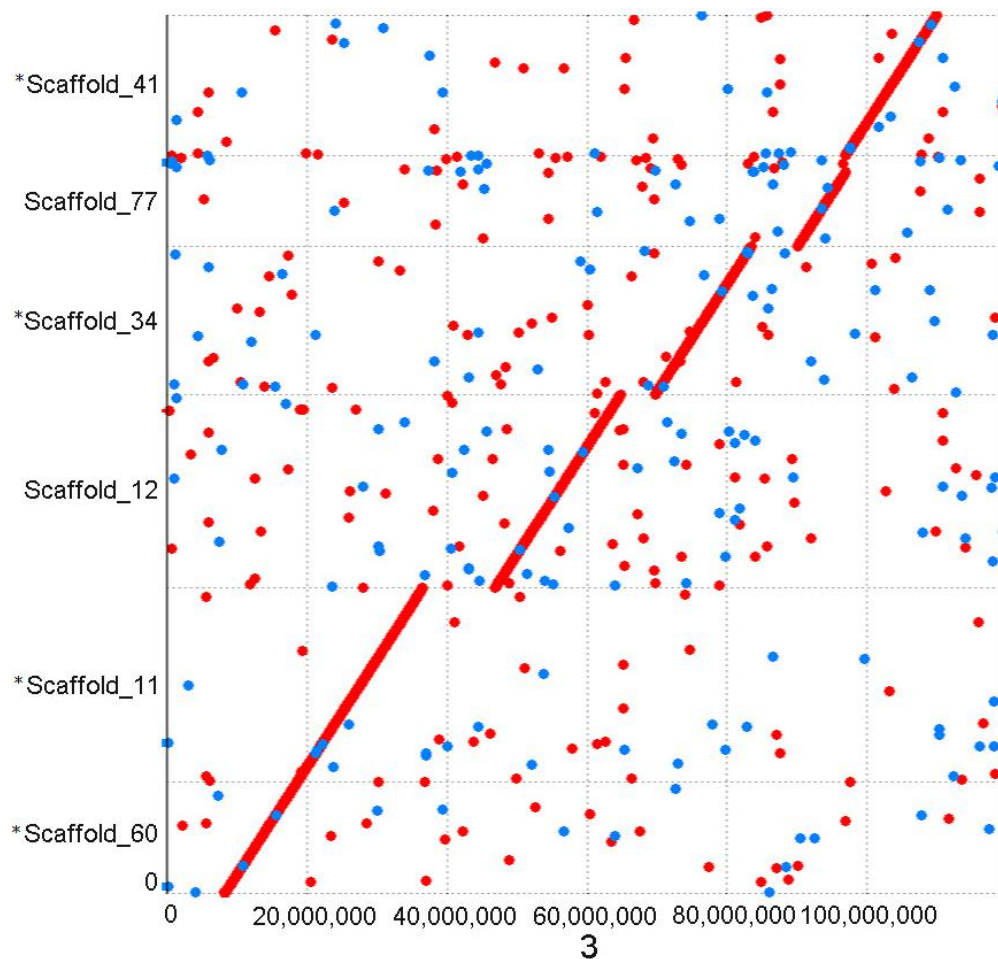
### **Repeat content annotation**

Two methods were used for repeat content identification in the kiang genome, i.e., *de novo* and homology-based strategies. A kiang-specific *de novo* repeat library was constructed using RepeatScout (Price et al., 2005), LTR-FINDER (Xu & Wang, 2007), MITE-Hunter (Han & Wessler, 2010), and PILER-DF (Edgar & Myers, 2005). The *de novo* repeat database was classified into classes, subclasses, families, and superfamilies using PASSTECClassifier (Wicker et al., 2007). We then integrated the *de novo* repeat sequence library and known repeat sequence database (Repbase) (Jurka et al., 2005) to construct a new repeat sequence database. Finally, 760.31 Mb of repeat sequences were identified by RepeatMasker (Tarailo-Graovac & Chen, 2009), accounting for

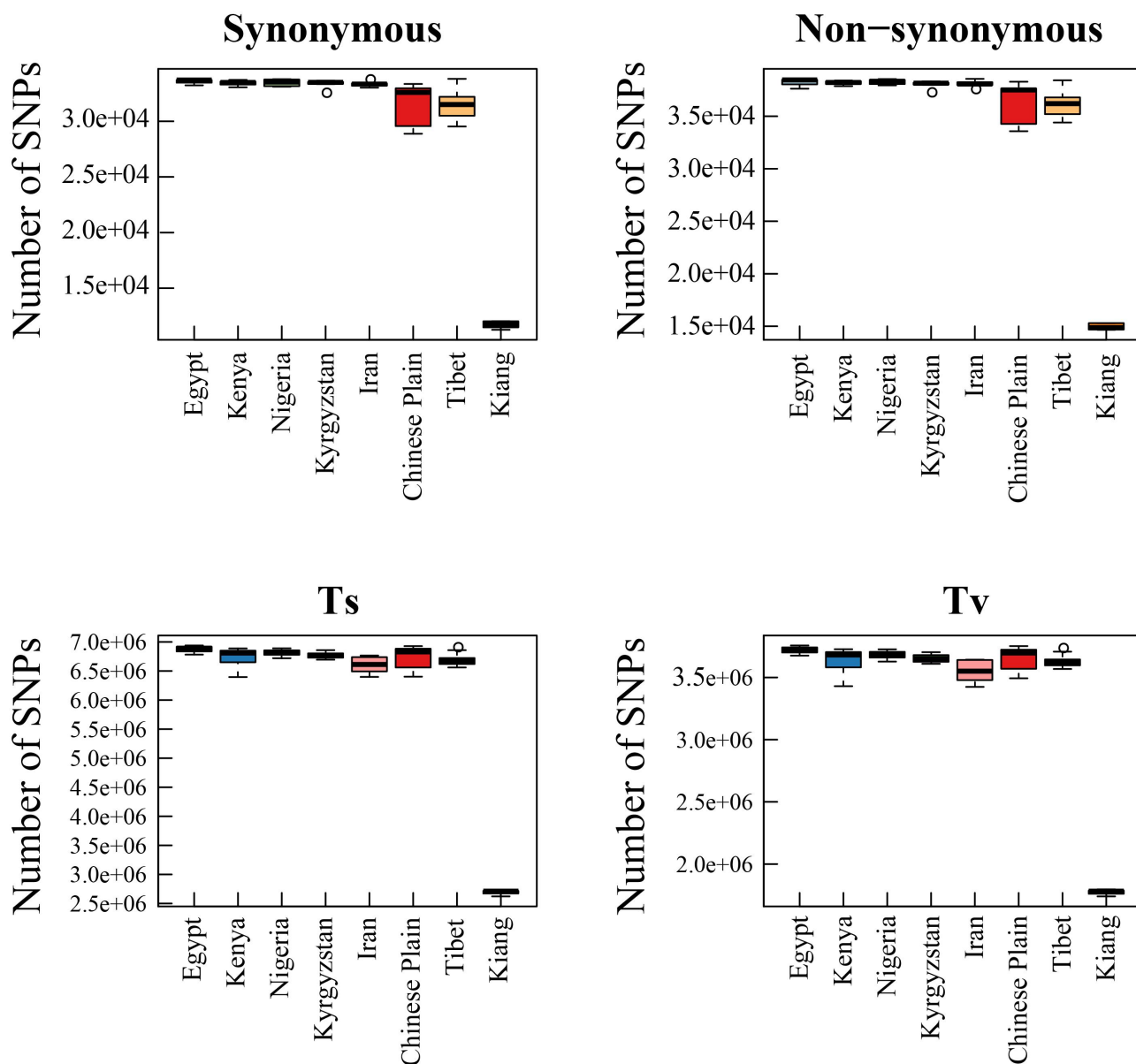
31.96% of the genome assembly (**Supplementary Table S8**).



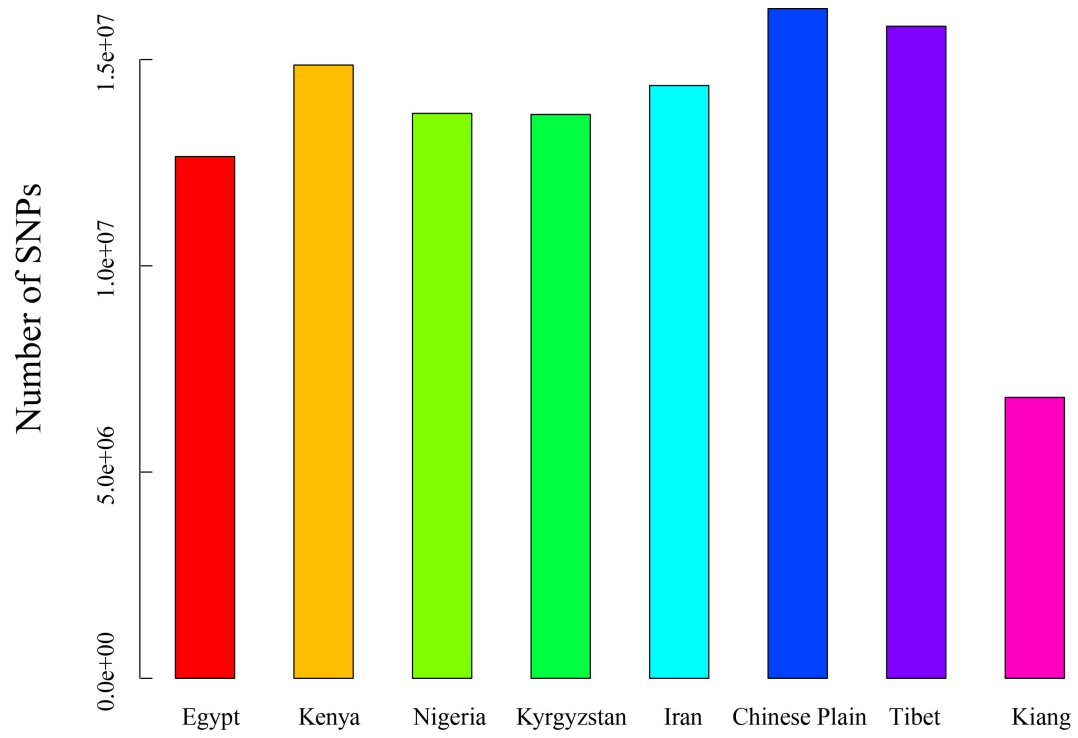
**Supplementary Figure S1:** Estimated genome size and repeat content based on 21 K-mer frequency distribution of short-insert libraries (220 bp). Estimated kiang genome size was determined by frequency distribution peak of unique K-mers. K-mer=21 was considered for kiang genome size estimation. Genome sizes were calculated as:  $\text{Genome size} = \frac{\text{21-mer number}}{\text{21-mer depth}}$ , where 21-mer number is the total counts of each unique 21-mer and 21-mer depth is the highest frequency that occurred. Estimated genome size was ~2.30 Gb, close to the total scaffold length of the assembled genome (~2.38 Gb).



**Supplementary Figure S2:** Nummer was used for collinearity assessment by aligning the kiang-assembled genome to the horse genome (downloaded from NCBI). Several scaffolds in figure show high similarity and concordance between kiang and closely related horse. Red dots indicate collinearity between kiang and horse, blue dots represent inversion.

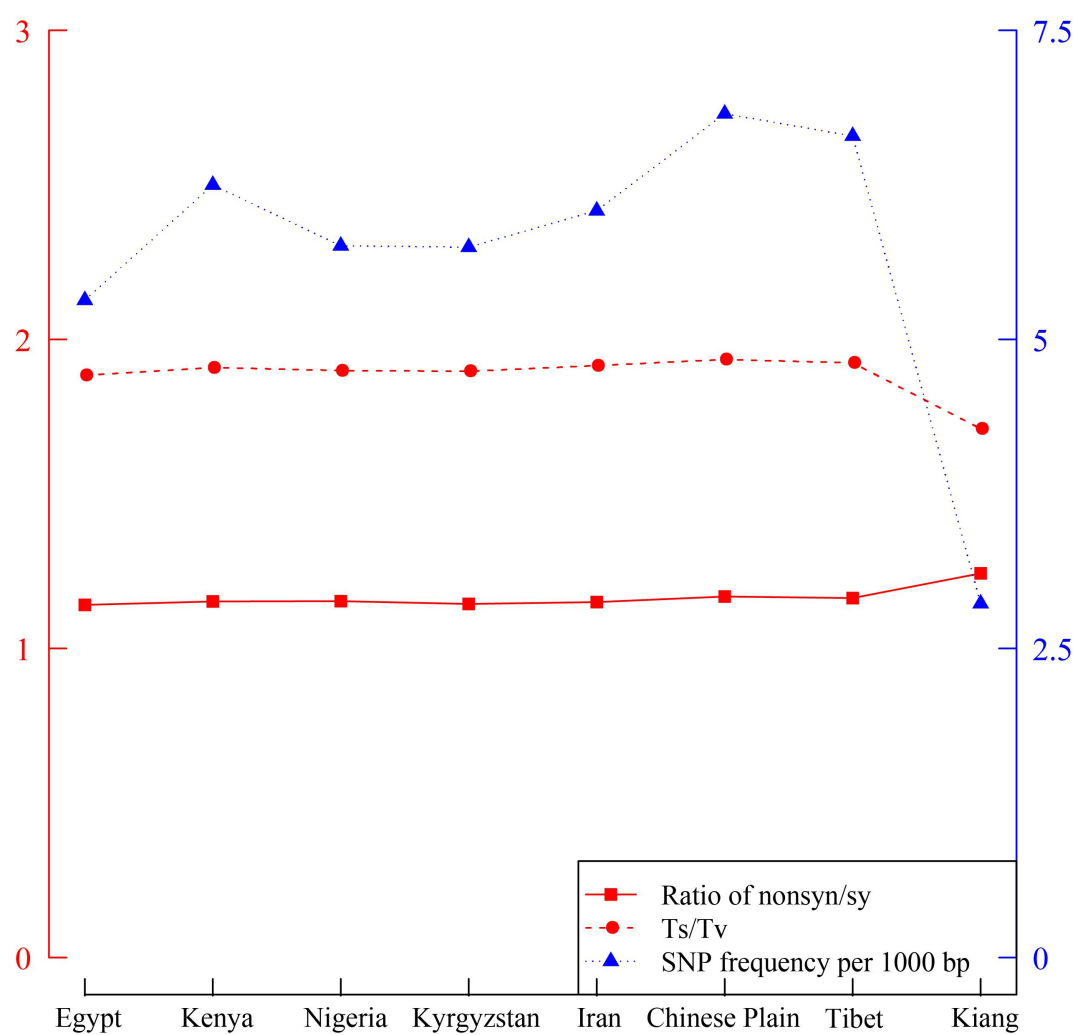


**Supplementary Figure S3:** Numbers of synonymous and non-synonymous SNPs (top) as well as transition (Ts) and transversion (Tv) (down) at individual level (details in **Supplementary Table S10**).

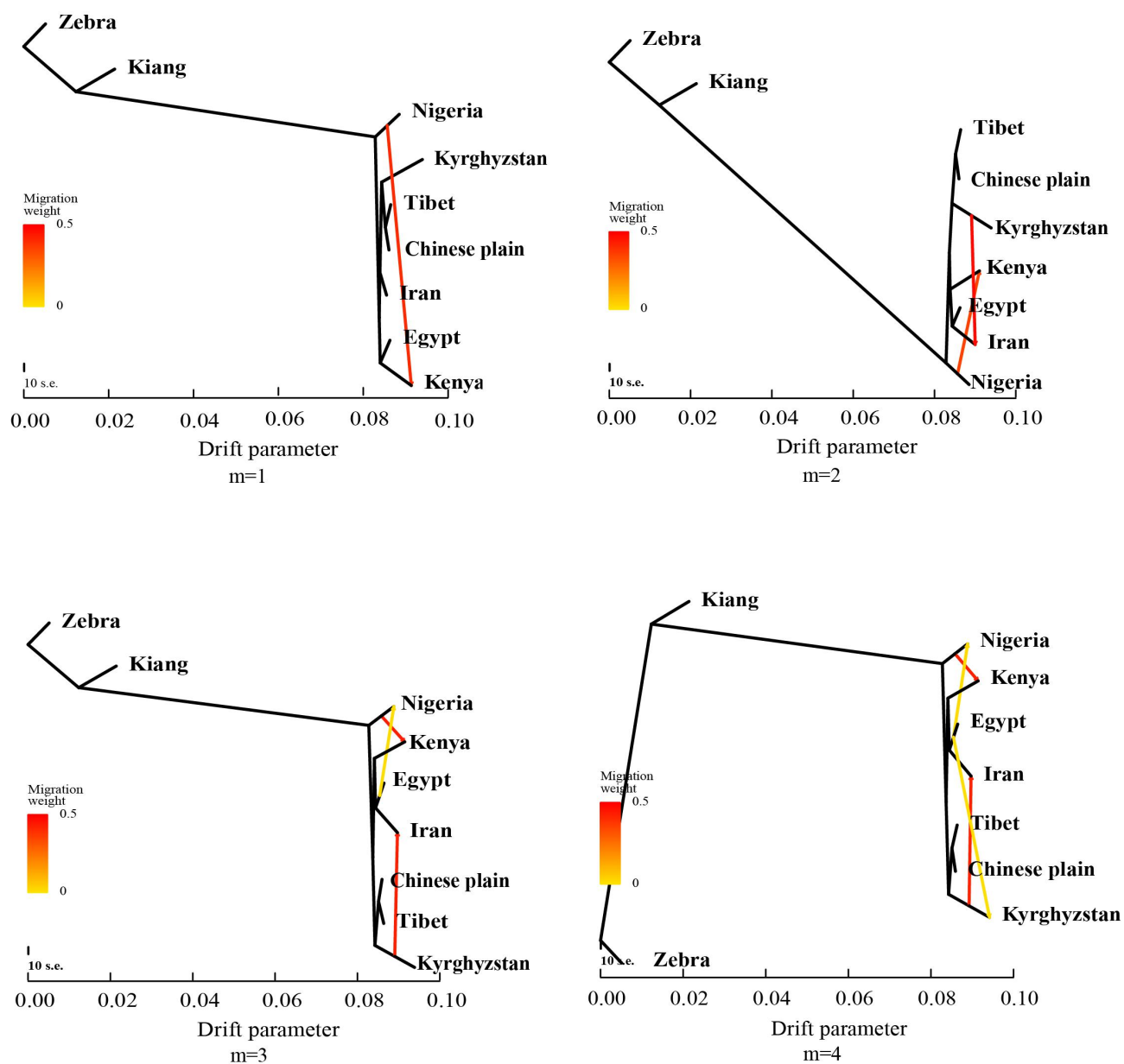


**Supplementary Figure S4:** Numbers of SNPs at population level (details in **Supplementary Table S11**).

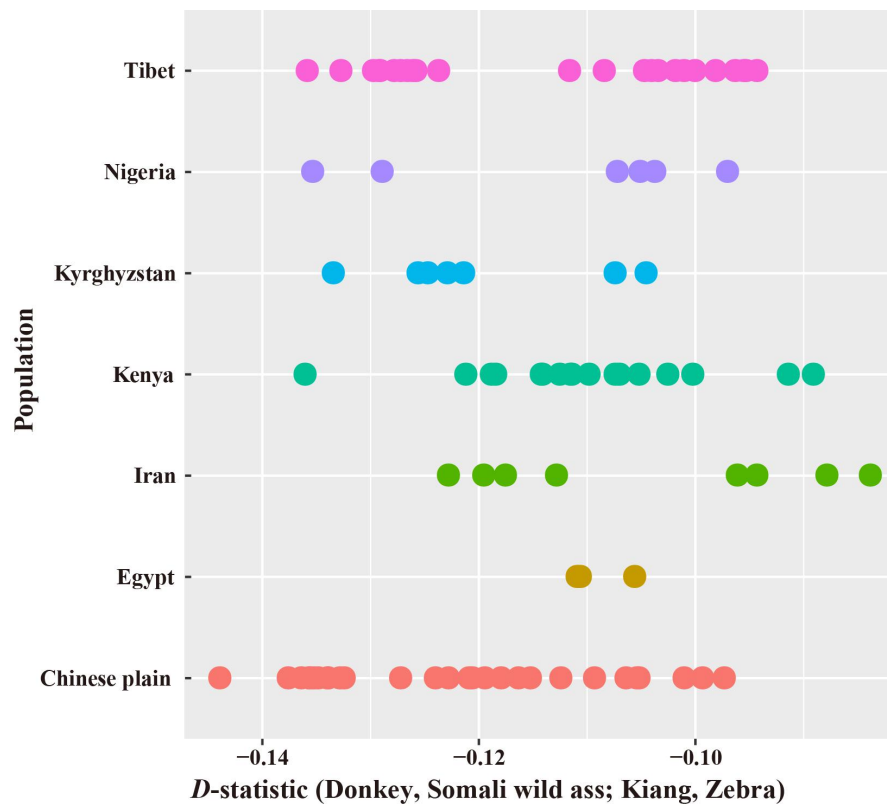




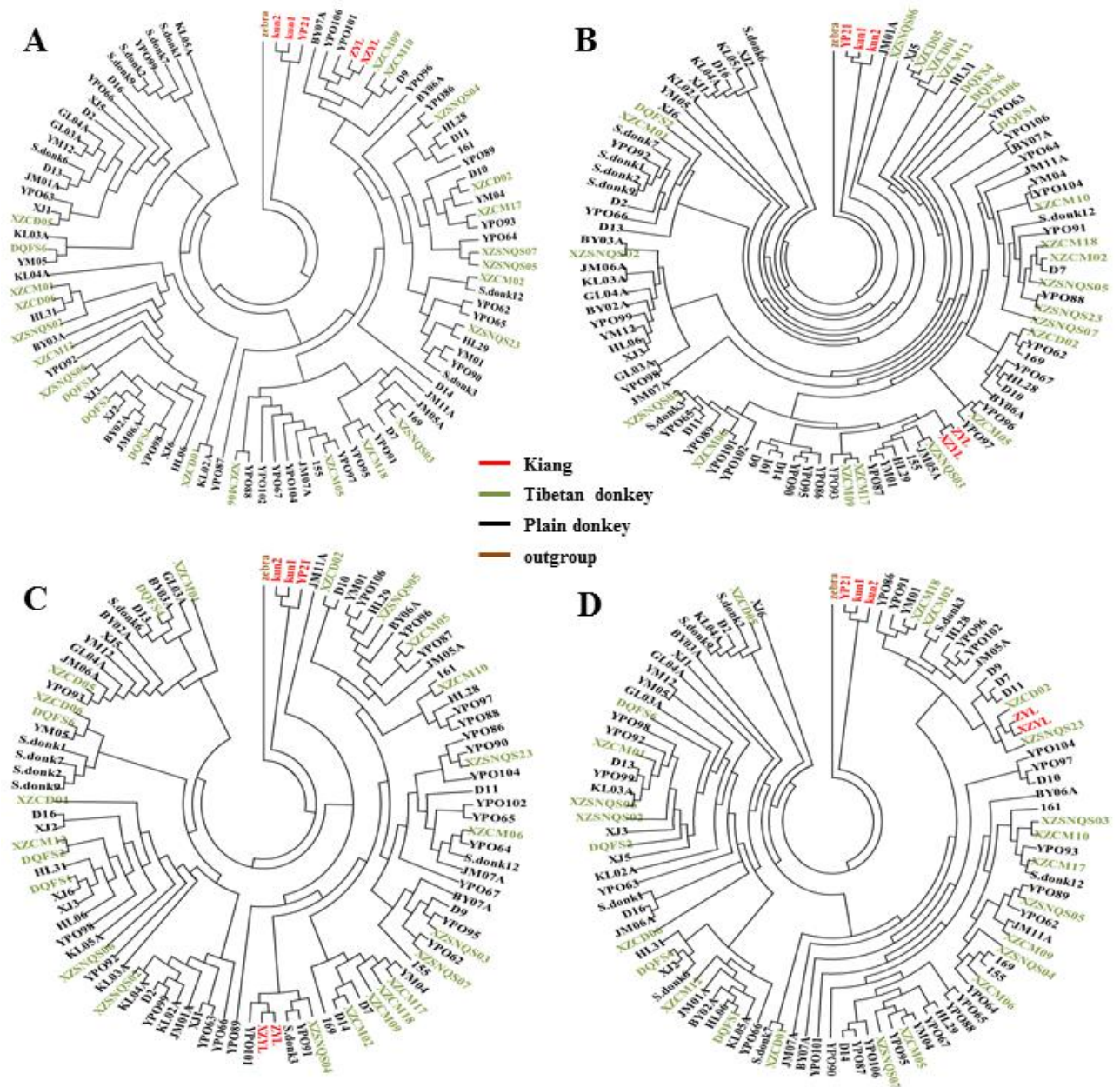
**Supplementary Figure S5:** Whole-genome SNP distribution for different populations, including ratio of non-synonymous/synonymous, transition/transversion (Ts/Tv), and SNP frequency per 1 000 bp (details in **Supplementary Table S11**).



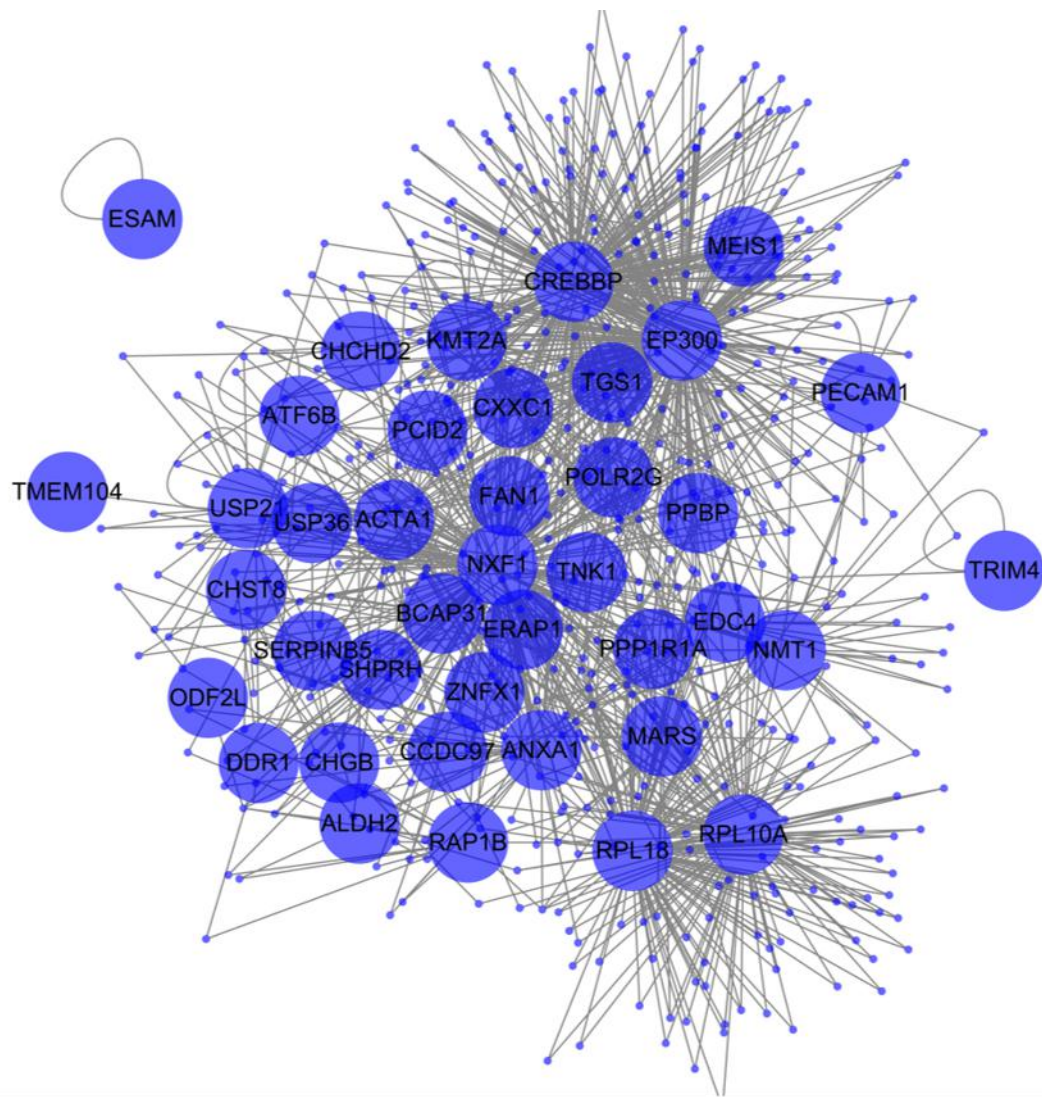
**Supplementary Figure S6:** Signals of introgression among different populations detected by TreeMix. No signals of admixture were detected between kiang and domestic donkey.



**Supplementary Figure S7:** *D*-statistic (ABBA-BABA test) of ADMIXTOOLS in (Donkey, Somali wild ass; Kiang, Zebra) in different populations.



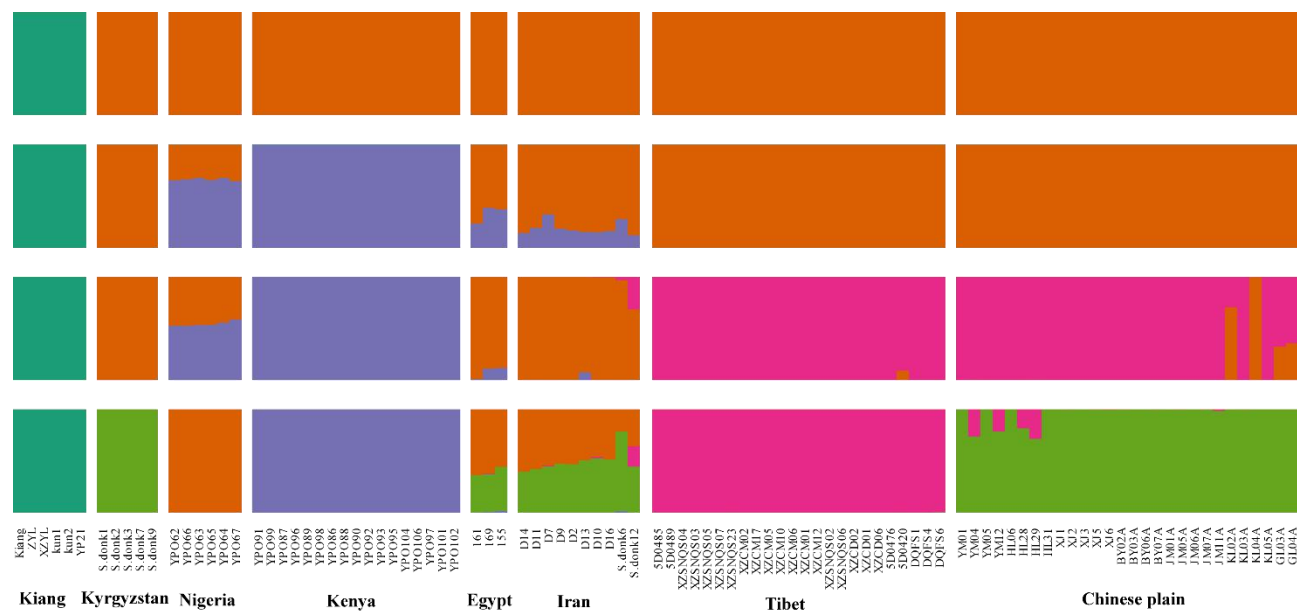
Supplementary Figure S8: Phylogenetic trees of top four windows with highest  $f_d$  values.



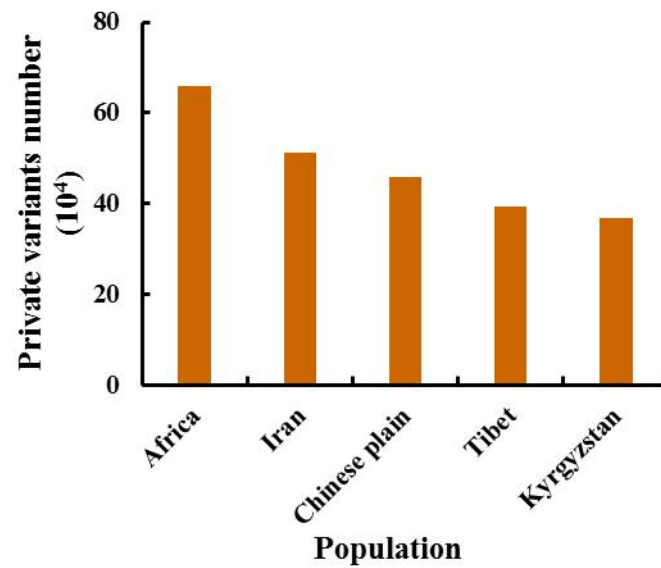
**Supplementary Figure S9:** Frequent gene-gene interactions retrieved by g:profiler (<https://biit.cs.ut.ee/gprofiler/>). Among positively selected genes, *EP300* was a hub gene.





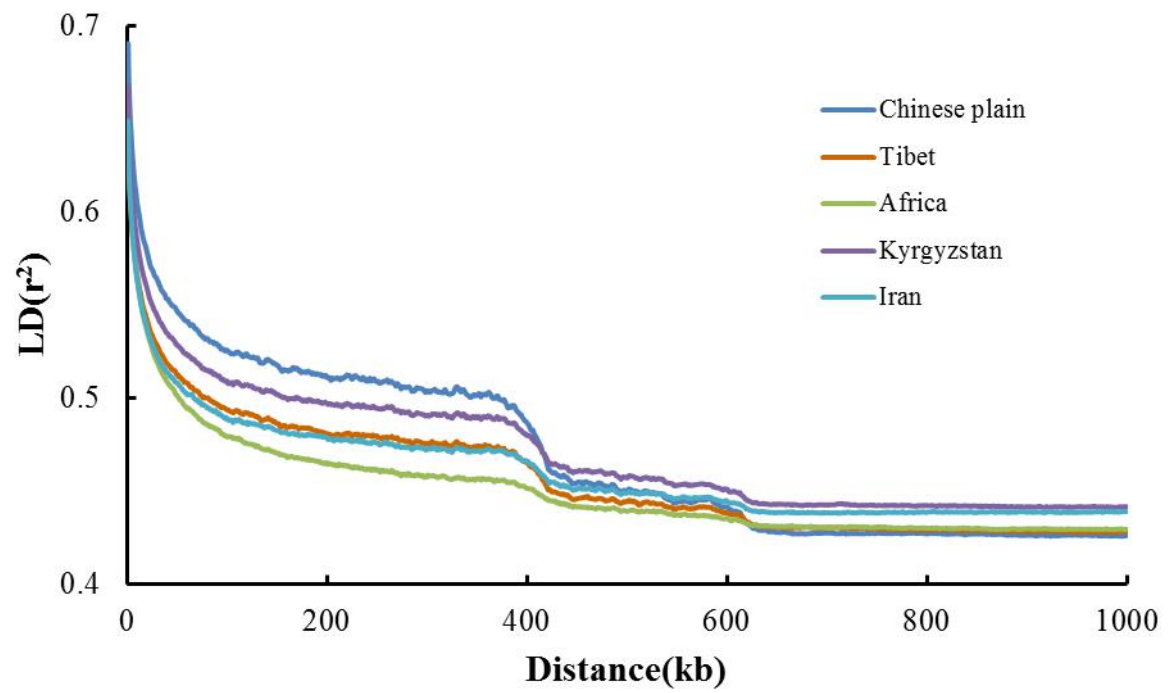


**Supplementary Figure S11:** Population structure analysis by ADMIXTURE with K from 2 to 5. Analysis clearly separated kiangs from donkeys, and no signature of admixture was found between them.

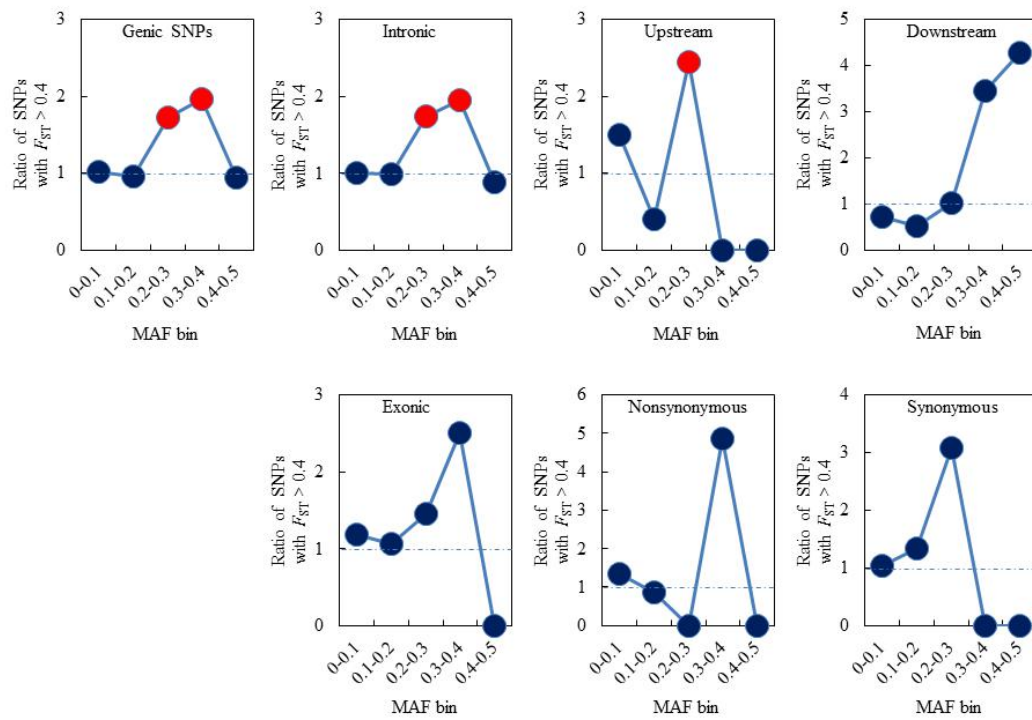


**Supplementary Figure S12:** Number of private variants in each population (choosing randomly the same number of individuals  $n=7$  within each population), showing African donkey population has the largest number of private variants, thus supporting an out-of-Africa theory for domestic donkeys.

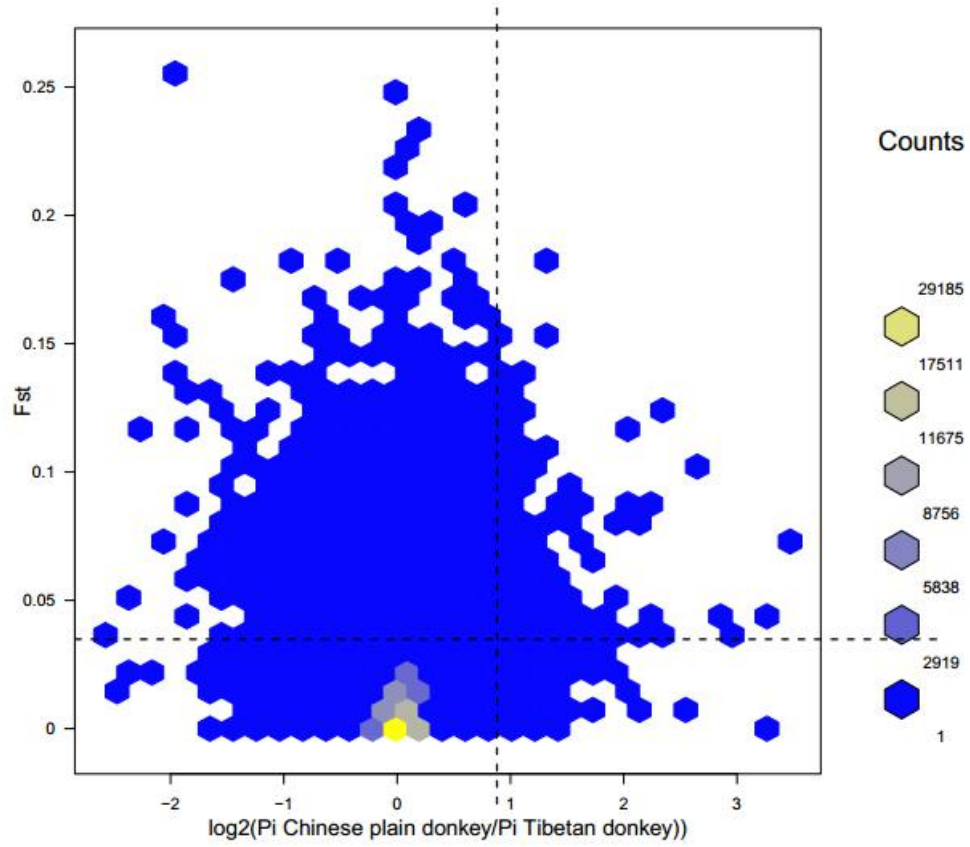




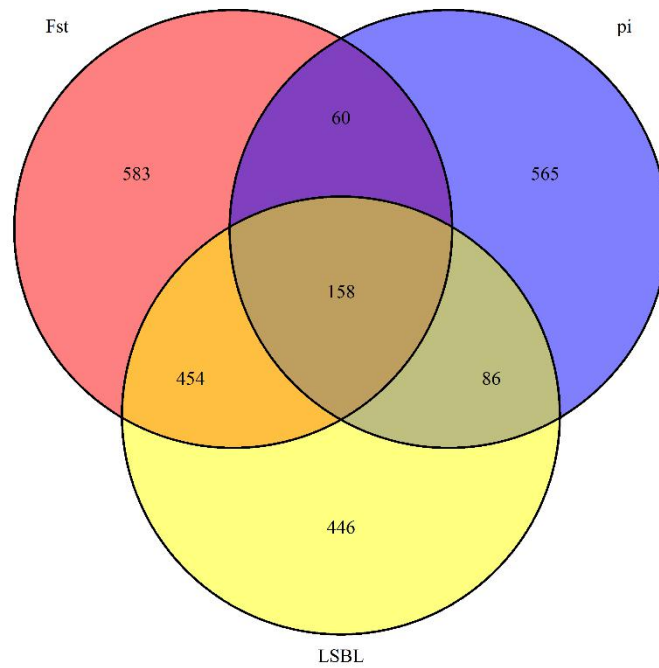
**Supplementary Figure S13:** Linkage disequilibrium (LD) decay in each population. Same number of individuals ( $n=7$ ) was chosen randomly for each population to calculate  $r^2$ . African donkey exhibited fastest LD decay.



**Supplementary Figure S14:** Enrichment of genic SNPs with high  $F_{ST}$  values ( $>0.4$ ) when matching different minor allele frequency (MAF) bins. Excess high  $F_{ST}$  values ( $>0.4$ ) among genic SNPs, with respect to non-genic SNPs, were observed when constraining analyses to SNPs presenting the same MAF. Red circles indicate statistical significance ( $P < 0.05$ ).



**Supplementary Figure S15:** Distribution of  $\log_2(\theta\pi \text{ ratios}) = \theta\pi(\text{Chinese plain donkey}) / \theta\pi(\text{Tibetan donkey})$  and  $F_{ST}$  values calculated between Tibetan and Chinese plain donkeys.



**Supplementary Figure S16:** Identified candidate genes (158) in Tibetan donkey lineage based on  $F_{ST}$ ,  $LSBL$ , and nucleotide diversity ratio ( $\Delta\pi$ ) between Tibetan and Chinese plain donkeys (FDR-corrected  $P < 0.01$ ) in sliding windows across donkey genomes.

## REFERENCE

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## **Supplementary Tables**

Supplementary Table S1. Library information.

Supplementary Table S2. Scaffold information.

Supplementary Table S3. Single base error.

Supplementary Table S4. Gene region coverage.

Supplementary Table S5. Genome completeness assessment for kiang using BUSCO.

Supplementary Table S6. Gene model prediction.

Supplementary Table S7. Gene model statistics.

Supplementary Table S8. Repeat sequence annotation.

Supplementary Table S9. Genome re-sequencing data used in this study.

Supplementary Table S10. Number and distribution of SNPs for each individual.

Supplementary Table S11. Summary of whole-genome SNP distribution for different groups.

Supplementary Table S12. D-statistic (ABBA-BABA test) of (Donkey, Somali wild ass; Kiang; Zebra)

Supplementary Table S13. Sliding window (50 kb) analysis of  $f_d$  statistics.

Supplementary Table S14. Positively selected genes in kiang detected by PAML.

Supplementary Table S15. Functional enrichment of positively selected genes in kiang.

Supplementary Table S16. McDonald-Kreitman (MK) test to identify genes with evidence of amino acid substitutions fixed by positive selection in kiang.

Supplementary Table S17. Overlapping genes (34) located in top 1% of highest CLR values, and top 1% of lowest nucleotide diversity windows.

Supplementary Table S18. Average polymorphism in different groups.

Supplementary Table S19. Candidate protein-coding genes (158) evolving under positive selection detected by three statistical methods.

Supplementary Table S20. Genes (22) overlapping in top 1% of CLR regions between kiang and Tibetan donkey populations.

Supplementary Table S21. Comparison of demographic models for Chinese plain, Tibetan, and foreign plain donkeys using  $\partial a \partial i$ .

**Supplementary Table S1.** Library information

Library	Data (Gb)	Depth (X)	Q20 (%)	Q30 (%)
220 bp_1	35.04	15.26	93.38	88.43
220 bp_2	38.86	16.92	93.52	88.71
220 bp_3	57.94	25.19	95.06	91.35
3 K_1	13.54	5.89	96.56	89.02
3 K_2	36.18	15.73	97.38	91.02
4 K-1	14.54	6.32	96.66	89.23
4 K-2	32.37	14.08	97.42	91.01
5 K-1	17.01	7.4	97.14	90.57
5 K-2	26.86	11.68	97.97	92.81
8 K-1	15.85	6.89	97.33	91.33
8 K-2	18.16	7.89	97.26	91.25
10 K_1	14.07	6.12	92.52	87
10 K_2	15.98	6.95	93.1	87.9
15 K_1	9.87	4.29	97.22	91.15
15 K_2	10.17	4.42	92.47	86.96
15 K_3	9.63	4.18	97.04	90.57
17 K_1	12.31	5.35	92.68	87.25
17 K_2	12.83	5.58	92.86	87.57
17 K_3	9.71	4.22	96.89	90.2
Total	400.92	174.36	--	--



**Supplementary Table S2.** Scaffold information

Scaffold number	Scaffold length (bp)	Scaffold N50 (bp)	Scaffold N90 (bp)	Scaffold max (bp)	Gap total length (bp)
2,960	2,378,791,009	17,604,317	3,241,824	57,891,938	18,366,217
Contig number	Contig length (bp)	Contig N50 (bp)	Contig N90 (bp)	Contig max (bp)	GC content (%)
20,678	2,360,424,792	264,601	68,805	2,410,919	41.28

**Supplementary Table S3.** Single base error

Contig length (bp)	Correct base number (bp)	Error base number (bp)	Error base percentage (%)
2,360,424.79	2,336,434,365	6,818	0.00029

**Supplementary Table S4.** Gene region coverage

Length of unigenes	Total number	Aligned number	Percentage (%)
All	22,632	22,308	98.57%
$\geq 1,000$	19,838	19,593	98.76%
$\geq 2,000$	13,084	12,926	98.79%

**Supplementary Table S5.** Genome completeness assement for kiang using BUSCO

Categories	Number	Percent (%)
Complete BUSCOs	3953	0.963
Complete and single-copy BUSCOs	3921	0.955
Complete and duplicated BUSCOs	32	0.008
Fragmented BUSCOs	81	0.02
Missing BUSCOs	70	0.017
Total BUSCO groups searched	4104	1

**Supplementary Table S6.** Gene model prediction

Method	Software	Gene number
Ab initio	Augustus	36,459
Homology-based	GeneWise	1,662
EST/Unigene	PASA	5,429
Integration	GLEAN	27,178
Integration		

**Supplementary Table S7.** Gene model statistics

Software	GeneNum	Genelen	AveGenlen	ExonLen	AveExonlen	IntronLen	aveIntronLen
augustus	36,459	919,260,297	25,213.54	35,040,469	154.16	884,219,828	3,890.25
genewise	1,662	17,524,131	10,544.00	1,841,879	228.72	15,678,325	1,947.13
pasa	5,429	153,763,432	28,322.61	7,701,561	169.92	145,250,758	3,204.79
Glean	27,178	467,591,186	17,204.77	21,989,376	157.23	445,601,810	3,186.28

**Supplementary Table S8.** Repeat sequence annotation

Type	Number	Length	Rate(%)
ClassI/?/?	2,447	626,645	0.03
ClassI/?/Sola	5	203	0
ClassI/DIRS/?	1,571	517,250	0.02
ClassI/DIRS/DIRS	1,229	78,851	0
ClassI/DIRS/Ngaro	74	5,107	0
ClassI/LARD/?	186,211	48,446,230	2.04
ClassI/LINE/?	201	57,226	0
ClassI/LINE/I	1,316	441,030	0.02
ClassI/LINE/Jockey	145,603	32,648,556	1.37
ClassI/LINE/L1	1,401,325	525,357,281	22.08
ClassI/LINE/R2	422	52,221	0
ClassI/LINE/RTE	12,397	4,273,744	0.18
ClassI/LTR/?	2,738	541,534	0.02
ClassI/LTR/Bel-Pao	1,705	96,412	0
ClassI/LTR/Copia	743	53,608	0
ClassI/LTR/ERV	575,190	165,819,885	6.97
ClassI/LTR/Gypsy	15,205	1,766,926	0.07
ClassI/LTR/Retrovirus	6,898	2,465,635	0.1
ClassI/PLE/?	4,392	3,127,278	0.13
ClassI/PLE/Penelope	2,450	215,549	0.01
ClassI/SINE/5S	78	5,805	0
ClassI/SINE/7SL	10	2,826	0
ClassI/SINE/?	22,544	4,347,611	0.18
ClassI/SINE/Alu	3	303	0
ClassI/TRIM/?	1,066	531,164	0.02
ClassII/?/?	36,474	5,048,771	0.21
ClassII/?/Academ	455	28,177	0
ClassII/?/Chapaev	1,741	123,558	0.01
ClassII/?/Ginger1	4,043	314,762	0.01
ClassII/?/Ginger2/TDD	114	15,322	0
ClassII/?/ISL2EU	971	66,689	0
ClassII/?/Kolobok	4,038	328,053	0.01
ClassII/?/Mirage	3	171	0
ClassII/?/MuDR	1,441	178,299	0.01
ClassII/?/Sola	4,657	504,132	0.02
ClassII/?/Zator	34	1,864	0
ClassII/Crypton/Crypton	734	48,282	0
ClassII/Helitron/?	14	4,979	0
ClassII/Helitron/Helitron	12,101	1,747,846	0.07
ClassII/MITE/?	5,913	1,469,066	0.06

ClassII/Maverick/Maverick	3,973	285,054	0.01
ClassII/TIR/?	2,677	1,253,291	0.05
ClassII/TIR/CACTA	13,945	1,014,150	0.04
ClassII/TIR/Merlin	23	4,101	0
ClassII/TIR/P	1,805	147,006	0.01
ClassII/TIR/PIF-Harbinger	5,797	743,037	0.03
ClassII/TIR/PiggyBac	304	19,853	0
ClassII/TIR/Tc1-Mariner	183,891	49,559,643	2.08
ClassII/TIR/Transib	1,203	103,154	0
ClassII/TIR/hAT	407,912	80,673,281	3.39
PotentialHostGene	3,767	1,410,225	0.06
SSR	56,975	4,442,847	0.19
Unknown	83,563	14,063,951	0.59
Total:	3,224,391	760,313,906	31.96

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**Supplementary Table S9.** Genome Resequencing data used in this study.

Population	ID	Average Sequencing depth (X)	Coverage to the assembled genome(%)	
<i>Equus kiang</i>	ZYL	5.70	96.70	this study
	XZYL	5.63	96.20	this study
	kun1	5.80	97.14	this study
	kun2	5.81	96.77	this study
	YP21	5.57	96.62	this study
<i>Equus asinus asinus</i>	Kyrgyzstan	S.donk1	7.88	this study
		S.donk2	7.36	this study
		S.donk3	6.04	this study
		S.donk6	8.79	this study
		S.donk7	8.31	this study
		S.donk9	8.82	this study
		S.donk12	7.65	this study
	Nigeria	YPO62	7.70	this study
		YPO63	10.16	this study
		YPO64	8.35	this study
		YPO65	8.88	this study
		YPO66	8.64	this study
		YPO67	11.94	this study
	Kenya	YPO86	9.80	this study
		YPO87	8.26	this study

	YPO88	8.94	97.32	this study	
	YPO89	11.10	98.20	this study	
	YPO90	9.93	97.85	this study	
	YPO91	9.17	97.45	this study	
	YPO92	8.67	97.48	this study	
	YPO93	10.12	98.45	this study	
	YPO95	8.61	97.46	this study	
	YPO96	10.43	98.01	this study	
	YPO97	7.65	92.85	this study	
	YPO98	7.66	95.50	this study	
	YPO99	7.98	94.47	this study	
	YPO101	6.58	91.42	this study	
	YPO102	7.70	91.63	this study	
	YPO104	8.15	97.40	this study	
	YPO106	9.62	98.03	this study	
<b>Egypt</b>	161	8.04	97.93	Wang et al (2020)	provided by Changfa Wang
	169	8.13	97.86	Wang et al (2020)	provided by Changfa Wang
	155	11.52	98.48	Wang et al (2020)	provided by Changfa Wang
<b>Iran</b>	D2	8.54	95.11	this study	
	D7	6.65	91.81	this study	
	D9	6.75	93.16	this study	
	D11	6.48	91.08	this study	

	D14	10.07	97.64	this study
	D13	7.78	94.04	this study
	D10	8.86	95.91	this study
	D16	8.80	96.43	this study
<b>Tibet Plateau</b>	XZSNQS02	5.67	96.05	this study
	XZSNQS03	5.21	96.78	this study
	XZSNQS04	5.16	96.69	this study
	XZSNQS05	5.17	96.54	this study
	XZSNQS06	5.00	96.44	this study
	XZSNQS07	5.62	96.89	this study
	XZSNQS23	6.07	97.25	this study
	XZCM02	5.40	96.60	this study
	XZCM09	7.92	97.65	this study
	XZCM18	9.21	98.08	this study
	XZCM17	5.50	97.01	this study
	XZCM05	5.53	96.38	this study
	XZCM10	6.18	96.56	this study
	XZCM06	5.67	95.78	this study
	XZCM01	5.84	97.29	this study
	XZCM12	5.31	97.13	this study
	XZCD02	5.35	96.51	this study
	XZCD01	6.30	96.77	this study
	XZCD05	7.87	97.98	this study
	XZCD06	5.56	96.56	this study

	DQFS1	5.81	96.31	this study	
	DQFS2	8.59	97.63	this study	
	DQFS4	6.17	96.40	this study	
	DQFS6	6.10	96.61	this study	
<b>Chinese plain</b>	YM01	5.53	96.93	this study	
	YM04	5.48	96.79	this study	
	YM05	5.14	96.00	this study	
	YM12	5.04	95.69	this study	
	HL06	5.40	95.62	this study	
	HL28	5.85	95.80	this study	
	HL29	5.71	95.55	this study	
	HL31	5.44	95.48	this study	
	XJ1	5.28	95.54	this study	
	XJ2	5.34	95.66	this study	
	XJ3	5.23	95.62	this study	
	XJ5	6.79	97.42	this study	
	XJ6	5.87	96.91	this study	
	BY02A	9.83	98.38	Wang et al (2020) Wang	provided by Changfa
	BY03A	8.61	98.29	Wang et al (2020) Wang	provided by Changfa
	BY06A	10.43	98.48	Wang et al (2020) Wang	provided by Changfa
	BY07A	7.75	97.93	Wang et al (2020) Wang	provided by Changfa

JM01A	9.53	98.46	Wang et al (2020) Wang	provided by Changfa
JM05A	8.69	98.26	Wang et al (2020) Wang	provided by Changfa
JM06A	9.40	98.44	Wang et al (2020) Wang	provided by Changfa
JM07A	8.89	98.31	Wang et al (2020) Wang	provided by Changfa
JM11A	8.17	98.18	Wang et al (2020) Wang	provided by Changfa
KL02A	8.26	98.22	Wang et al (2020) Wang	provided by Changfa
KL03A	10.10	98.46	Wang et al (2020) Wang	provided by Changfa
KL04A	9.67	98.49	Wang et al (2020) Wang	provided by Changfa
KL05A	7.96	98.23	Wang et al (2020) Wang	provided by Changfa
GL03A	9.43	98.37	Wang et al (2020) Wang	provided by Changfa
GL04A	9.09	98.37	Wang et al (2020) Wang	provided by Changfa

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**Supplementary Table S10.** Number and distribution of SNPs for each individual.

**Supplementary Table S11.** Summary of whole genome SNPs distribution for different groups.

**Supplementary Table S10, S11 are listed as a separate excel file due to their large size.**

**Supplementary Table S12.** D-statistic (ABBA-BABA test) of (Donkey, Somali wild ass; Kiang; Zebra)

					D stat	Z
	155	somali wilad ass	:	Kiang zebra	-0.1059	-19
	161	somali wilad ass	:	Kiang zebra	-0.1112	-18.531
	169	somali wilad ass	:	Kiang zebra	-0.1109	-16.67
5D0420		somali wilad ass	:	Kiang zebra	-0.133	-22.53
5D0476		somali wilad ass	:	Kiang zebra	-0.1281	-16.574
5D0485		somali wilad ass	:	Kiang zebra	-0.1087	-17.605
5D0489		somali wilad ass	:	Kiang zebra	-0.1119	-17.677
BY02A		somali wilad ass	:	Kiang zebra	-0.1359	-26.669
BY03A		somali wilad ass	:	Kiang zebra	-0.1055	-18.919
BY06A		somali wilad ass	:	Kiang zebra	-0.1155	-17.291
BY07A		somali wilad ass	:	Kiang zebra	-0.1197	-19.57
D10		somali wilad ass	:	Kiang zebra	-0.0964	-16.542
D11		somali wilad ass	:	Kiang zebra	-0.0841	-15.61
D13		somali wilad ass	:	Kiang zebra	-0.1178	-21.538
D14		somali wilad ass	:	Kiang zebra	-0.1131	-20.645
D16		somali wilad ass	:	Kiang zebra	-0.1198	-17.097
D2		somali wilad ass	:	Kiang zebra	-0.1231	-21.631
D7		somali wilad ass	:	Kiang zebra	-0.0881	-11.822
D9		somali wilad ass	:	Kiang zebra	-0.0946	-17.65
DQFS1		somali wilad ass	:	Kiang zebra	-0.1294	-16.267
DQFS4		somali wilad ass	:	Kiang zebra	-0.13	-17.66
DQFS6		somali wilad ass	:	Kiang zebra	-0.1269	-19.685
GL03A		somali wilad ass	:	Kiang zebra	-0.1359	-20.909
GL04A		somali wilad ass	:	Kiang zebra	-0.1367	-16.512
HL06		somali wilad ass	:	Kiang zebra	-0.1331	-14.952
HL28		somali wilad ass	:	Kiang zebra	-0.0976	-11.712
HL29		somali wilad ass	:	Kiang zebra	-0.0996	-14.209
HL31		somali wilad ass	:	Kiang zebra	-0.1212	-16.559
JM01A		somali wilad ass	:	Kiang zebra	-0.1355	-22.218
JM05A		somali wilad ass	:	Kiang zebra	-0.1067	-15.061
JM06A		somali wilad ass	:	Kiang zebra	-0.1342	-30.834
JM07A		somali wilad ass	:	Kiang zebra	-0.1127	-17.877
JM11A		somali wilad ass	:	Kiang zebra	-0.1096	-15.037
KL02A		somali wilad ass	:	Kiang zebra	-0.1351	-30.499
KL03A		somali wilad ass	:	Kiang zebra	-0.1379	-18.247
KL04A		somali wilad ass	:	Kiang zebra	-0.1231	-19.736
KL05A		somali wilad ass	:	Kiang zebra	-0.1442	-24.87
S.donk1		somali wilad ass	:	Kiang zebra	-0.1337	-18.297
S.donk12		somali wilad ass	:	Kiang zebra	-0.1077	-14.86
S.donk2		somali wilad ass	:	Kiang zebra	-0.1259	-18.185

S.donk3	somali wilad ass	:	Kiang	zebra	-0.1048	-14.097
S.donk6	somali wilad ass	:	Kiang	zebra	-0.1217	-16.274
S.donk7	somali wilad ass	:	Kiang	zebra	-0.1232	-20.203
S.donk9	somali wilad ass	:	Kiang	zebra	-0.125	-23.577
XJ1	somali wilad ass	:	Kiang	zebra	-0.1243	-17.269
XJ2	somali wilad ass	:	Kiang	zebra	-0.1166	-16.886
XJ3	somali wilad ass	:	Kiang	zebra	-0.1182	-16.372
XJ5	somali wilad ass	:	Kiang	zebra	-0.1342	-23.494
XJ6	somali wilad ass	:	Kiang	zebra	-0.1327	-15.41
XZCD01	somali wilad ass	:	Kiang	zebra	-0.1295	-19.872
XZCD02	somali wilad ass	:	Kiang	zebra	-0.0958	-16.058
XZCD06	somali wilad ass	:	Kiang	zebra	-0.1261	-20.522
XZCM01	somali wilad ass	:	Kiang	zebra	-0.1361	-20.868
XZCM02	somali wilad ass	:	Kiang	zebra	-0.105	-13.798
XZCM05	somali wilad ass	:	Kiang	zebra	-0.1003	-15.029
XZCM06	somali wilad ass	:	Kiang	zebra	-0.0984	-12.648
XZCM10	somali wilad ass	:	Kiang	zebra	-0.1037	-16.652
XZCM12	somali wilad ass	:	Kiang	zebra	-0.1264	-16.317
XZCM17	somali wilad ass	:	Kiang	zebra	-0.1043	-14.852
XZSNQS02	somali wilad ass	:	Kiang	zebra	-0.124	-19.154
XZSNQS03	somali wilad ass	:	Kiang	zebra	-0.0956	-21.313
XZSNQS04	somali wilad ass	:	Kiang	zebra	-0.1021	-20.948
XZSNQS05	somali wilad ass	:	Kiang	zebra	-0.1013	-15.116
XZSNQS06	somali wilad ass	:	Kiang	zebra	-0.1275	-19.111
XZSNQS07	somali wilad ass	:	Kiang	zebra	-0.0966	-18.802
XZSNQS23	somali wilad ass	:	Kiang	zebra	-0.0946	-14.774
YM01	somali wilad ass	:	Kiang	zebra	-0.1013	-16.193
YM04	somali wilad ass	:	Kiang	zebra	-0.1057	-14.831
YM05	somali wilad ass	:	Kiang	zebra	-0.1209	-17.037
YM12	somali wilad ass	:	Kiang	zebra	-0.1275	-15.784
YPO101	somali wilad ass	:	Kiang	zebra	-0.0894	-13.992
YPO102	somali wilad ass	:	Kiang	zebra	-0.0917	-18.762
YPO104	somali wilad ass	:	Kiang	zebra	-0.1028	-18.657
YPO106	somali wilad ass	:	Kiang	zebra	-0.1187	-21.447
YPO62	somali wilad ass	:	Kiang	zebra	-0.0973	-14.222
YPO63	somali wilad ass	:	Kiang	zebra	-0.1356	-27.767
YPO64	somali wilad ass	:	Kiang	zebra	-0.1075	-18.21
YPO65	somali wilad ass	:	Kiang	zebra	-0.1054	-23.084
YPO66	somali wilad ass	:	Kiang	zebra	-0.1292	-22.751
YPO67	somali wilad ass	:	Kiang	zebra	-0.104	-14.842
YPO86	somali wilad ass	:	Kiang	zebra	-0.1117	-19.789
YPO87	somali wilad ass	:	Kiang	zebra	-0.1128	-14.84
YPO88	somali wilad ass	:	Kiang	zebra	-0.1055	-14.823



YPO89	somali wilad ass	:	Kiang	zebra	-0.1144	-21.212
YPO90	somali wilad ass	:	Kiang	zebra	-0.1073	-15.328
YPO91	somali wilad ass	:	Kiang	zebra	-0.1077	-13.304
YPO92	somali wilad ass	:	Kiang	zebra	-0.1363	-23.099
YPO93	somali wilad ass	:	Kiang	zebra	-0.1118	-16.337
YPO95	somali wilad ass	:	Kiang	zebra	-0.1101	-15.333
YPO96	somali wilad ass	:	Kiang	zebra	-0.1145	-17.798
YPO97	somali wilad ass	:	Kiang	zebra	-0.1005	-15.905
YPO98	somali wilad ass	:	Kiang	zebra	-0.1191	-15.938
YPO99	somali wilad ass	:	Kiang	zebra	-0.1215	-17.572

**Supplemental Table S13.** 50kb sliding window analysis of fd statistics

**Supplementary Table S13 are listed as a separate excel file due to its large size.**

**Supplementary Table S14.** Positively selected genes of kiang detected by paml.

Gene ID	Gene name	2ΔlnL	P value
Gglean008826	PPBP	8.877084	2.89E-03
Gglean006837	PEAR1	8.892396	2.86E-03
Gglean008906	TRIM4	5.554974	1.84E-02
Gglean014553	USP21	7.778842	5.29E-03
Gglean024813	FAM172A	10.631922	1.11E-03
Gglean022165	RPS29	7.906882	4.93E-03
Gglean017647	PPT1	19.303496	1.12E-05
Gglean017115	LEPREL1	20.74889	5.24E-06
Gglean001422	TMEM176A	9.236646	2.37E-03
Gglean015376	MCTP2	6.325472	1.19E-02
Gglean016957	ADPRH	14.438572	1.45E-04
Gglean013337	CHGB	9.257682	2.35E-03
Gglean004766	CMTR2	19.177866	1.19E-05
Gglean023183	PHACTR3	24.008218	9.59E-07
Gglean019151	LOC100057424	5.35738	2.06E-02
Gglean000799	C11H17orf75	8.559028	3.44E-03
Gglean026826	HELB	6.16882	1.30E-02
Gglean008940	TFR2	6.239054	1.25E-02
Gglean008571	LOC103565413	82.269368	0.00E+00
Gglean009717	PCDH17	26.147642	3.16E-07
Gglean014157	CXXC1	6.889654	8.67E-03
Gglean018005	RPL10A	9.407932	2.16E-03
Gglean007484	KMT2A	6.65637	9.88E-03
Gglean016932	ZBTB20	4.373422	3.65E-02
Gglean014969	LOC103553733	9.426078	2.14E-03
Gglean014943	LOC103553540	15.930694	6.57E-05
Gglean015041	LOC103553829	35.719926	2.28E-09
Gglean017908	LRRC73	11.389716	7.39E-04
Gglean006535	MRPL19	8.620134	3.33E-03
Gglean015771	TTC21B	9.99009	1.57E-03
Gglean007466	DPAGT1	19.415402	1.05E-05
Gglean012702	TMX1	16.857212	4.03E-05
Gglean015218	LOC101408193	5.753226	1.65E-02
Gglean003926	FIBP	12.774124	3.51E-04
Gglean007421	ESAM	12.677402	3.70E-04
Gglean022509	APPL2	4.387916	3.62E-02
Gglean018650	ACP1	6.687316	9.71E-03
Gglean024828	ERAP1	5.77009	1.63E-02
Gglean014642	MARCH10	23.40482	1.31E-06
Gglean024463	ODF2L	19.115906	1.23E-05

Gglean023915	UPK3A	16.044662	6.19E-05
Gglean011274	RIMS2	4.803328	2.84E-02
Gglean013912	RIBC1	27.058024	1.97E-07
Gglean013284	SPTLC3	20.156138	7.14E-06
Gglean020349	PPP1R1A	18.273926	1.91E-05
Gglean024276	SGCA	8.26624	4.04E-03
Gglean011240	LOC103561237	12.105822	5.03E-04
Gglean011109	GNL3L	11.02918	8.97E-04
Gglean026170	LOH12CR1	5.698356	1.70E-02
Gglean018821	RNF207	12.006276	5.30E-04
Gglean010554	LOC103546284	5.604842	1.79E-02
Gglean014935	PRKCDBP	11.959796	5.44E-04
Gglean015279	FAN1	12.02708	5.24E-04
Gglean008302	EMC3	9.873672	1.68E-03
Gglean026751	AVIL	12.911382	3.27E-04
Gglean002123	CREBBP	11.983108	5.37E-04
Gglean023957	EP300	30.18345	3.93E-08
Gglean010385	LOC100069277	6.680608	9.75E-03
Gglean025183	ZC3H6	10.339476	1.30E-03
Gglean017461	LOC100067335	7.056968	7.90E-03
Gglean012386	DDR1	5.273256	2.17E-02
Gglean006328	RAP1B	23.520364	1.24E-06
Gglean025409	GPKOW	11.42746	7.24E-04
Gglean011323	ANKRD46	29.476348	5.66E-08
Gglean014616	NMT1	9.167532	2.46E-03
Gglean010402	ZNFX1	6.484674	1.09E-02
Gglean005209	ZFYVE1	10.547026	1.16E-03
Gglean009369	EFCAB9	20.515734	5.91E-06
Gglean019605	ICA1	10.359284	1.29E-03
Gglean006967	PFKP	22.733482	1.86E-06
Gglean011161	LOC103540879	10.65277	1.10E-03
Gglean020779	ADCK2	11.053596	8.85E-04
Gglean019522	PCLO	9.55373	2.00E-03
Gglean002412	TGS1	8.77504	3.05E-03
Gglean026073	LOC103548196	4.000884	4.55E-02
Gglean004019	TSPAN33	11.090788	8.68E-04
Gglean000016	FAM3D	14.260332	1.59E-04
Gglean003125	TTC28	8.129502	4.36E-03
Gglean013474	AAR2	10.635032	1.11E-03
Gglean013003	LOC103562505	8.695324	3.19E-03
Gglean001514	DNAJC8	15.344422	8.96E-05
Gglean018259	ANP32B	10.579012	1.14E-03
Gglean008591	CCDC97	12.23621	4.69E-04

Gglean013378	DDR GK1	8.594258	3.37E-03
Gglean011891	PCID2	9.884998	1.67E-03
Gglean014663	PECAM1	8.849794	2.93E-03
Gglean024343	SASH3	9.041584	2.64E-03
Gglean015152	ANKRD42	8.464568	3.62E-03
Gglean011569	POLR2G	10.77421	1.03E-03
Gglean014979	LOC103553518	3.884092	4.88E-02
Gglean025584	SMS	10.986478	9.18E-04
Gglean012797	LOC100066639	4.76473	2.91E-02
Gglean005641	MEIS1	11.243602	7.99E-04
Gglean009018	ITGB2	13.2012	2.80E-04
Gglean025308	NR1H3	13.686066	2.16E-04
Gglean013695	P2RX3	7.021958	8.05E-03
Gglean023678	PTPN5	31.985952	1.55E-08
Gglean000192	PRSS46	11.077538	8.74E-04
Gglean008636	LOC100147106	9.899558	1.65E-03
Gglean005561	SFXN5	26.6538	2.43E-07
Gglean003756	TAF1D	23.59529	1.19E-06
Gglean014821	USP36	10.058172	1.52E-03
Gglean020934	LOC100271875	5.462688	1.94E-02
Gglean019475	PITX3	16.804734	4.14E-05
Gglean010592	ANXA1	4.354536	3.69E-02
Gglean015757	TBR1	9.27757	2.32E-03
Gglean000974	TNK1	19.578292	9.66E-06
Gglean026738	MARS	4.074694	4.35E-02
Gglean021430	PRRC2C	11.41654	7.28E-04
Gglean002106	LOC103553966	16.878506	3.99E-05
Gglean007214	CPLX1	15.330042	9.03E-05
Gglean020532	SHPRH	13.065644	3.01E-04
Gglean009735	KBTBD7	5.084554	2.41E-02
Gglean007049	PIKFYVE	3.934424	4.73E-02
Gglean001914	CHST8	6.245764	1.25E-02
Gglean018368	RHOB	9.010988	2.68E-03
Gglean003941	EHBP1L1	8.254658	4.07E-03
Gglean002300	CHCHD2	18.40588	1.79E-05
Gglean026211	GDF3	23.246776	1.43E-06
Gglean000108	NT5DC2	15.030216	1.06E-04
Gglean005619	BMP10	18.232008	1.96E-05
Gglean017946	TFEB	13.79036	2.04E-04
Gglean014788	EVPL	10.072378	1.51E-03
Gglean016766	IGFBP-1	11.13306	8.48E-04
Gglean023806	SYT9	27.628336	1.47E-07
Gglean014272	SERPINB5	36.432528	1.58E-09

Gglean011823	ATF6B	11.76543	6.03E-04
Gglean021906	NCOA4	11.879432	5.68E-04
Gglean014755	TMEM104	11.326076	7.64E-04
Gglean004757	COG4	17.097332	3.55E-05
Gglean003093	DUSP18	5.75436	1.65E-02
Gglean008944	SLC12A9	4.413394	3.57E-02
Gglean013943	ESCO1	39.000234	4.24E-10
Gglean006882	PBXIP1	17.876896	2.36E-05
Gglean005800	SLC3A1	4.16936	4.12E-02
Gglean020727	FAM131B	7.731244	5.43E-03
Gglean012256	BCAP31	13.776332	2.06E-04
Gglean010128	MTERF4	8.389762	3.77E-03
Gglean022874	N4BP2L2	22.86515	1.74E-06
Gglean007461	RNF26	10.204466	1.40E-03
Gglean008670	EIF4E	9.868486	1.68E-03
Gglean004582	ZCCHC14	7.937292	4.84E-03
Gglean019061	LOC103566074	7.263468	7.04E-03
Gglean009598	MMAB	18.930966	1.36E-05
Gglean023566	RBM34	30.187094	3.92E-08
Gglean026566	AMELX	10.98715	9.18E-04
Gglean018166	ACTL7B	20.551324	5.81E-06
Gglean002032	KIAA0141	9.853746	1.70E-03
Gglean004825	EDC4	9.504348	2.05E-03
Gglean001570	SRSF10	9.070712	2.60E-03
Gglean014756	GRIN2C	9.075292	2.59E-03
Gglean024118	KLC1	40.482554	1.98E-10
Gglean009041	ACTA1	16.36793	5.22E-05
Gglean011574	NXF1	4.191882	4.06E-02
Gglean004501	RPL18	5.768314	1.63E-02
Gglean006871	HCN3	12.99471	3.12E-04
Gglean006372	SPTA1	6.887622	8.68E-03
Gglean025656	CPPED1	7.92818	4.87E-03
Gglean003047	TAF7L	23.503186	1.25E-06
Gglean020450	WNT10B	4.213802	4.01E-02
Gglean013314	LAMP5	11.144688	8.43E-04
Gglean000262	SS18L2	8.722758	3.14E-03
Gglean025607	ALDH2	8.480402	3.59E-03
Gglean003934	AP5B1	26.939266	2.10E-07

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**Supplementary Table S15.** Functional enrichment of positively selected genes of kiang.

**Supplementary Table S15** are listed as a separate excel file due to its large size.

**Supplementary Table S16.** McDonald-Kreitman (MK) test to identify genes with evidence for amino acid substitutions fixed by positive selection in kiang

Gene ID	Gene name	P_nonsyn	P_syn	D_nonsyn	D_syn	neutrality.index	alpha	fisher.P.value
ENSECAG00000011724	ADCY10	0	5	5	1	0.0125	0.9875	0.001020337
ENSECAG00000010780	BICD2	0	4	4	0	0	1	0.006302521
ENSECAG00000010229	CRMP1	0	7	2	0	0	1	0.00952381
ENSECAG00000016564	RPRML	17	12	13	1	0.103448276	0.896551724	0.013772697
ENSECAG00000007153	HUNK	2	3	4	0	0	1	0.019230769
ENSECAG00000008023	B3GAT1	0	6	2	0	0	1	0.022222222
ENSECAG00000020743	RINL	0	3	2	0	0	1	0.022222222
ENSECAG00000019234	UNC13B	0	5	3	1	0.027777778	0.972222222	0.022268908
ENSECAG00000013024		4	2	7	0	0	1	0.022681666
ENSECAG00000021545	MTSS1	1	7	3	0	0	1	0.022727273
ENSECAG00000013760	TTI1	2	2	6	0	0	1	0.023871437
ENSECAG00000016765		0	5	5	1	0.028571429	0.971428571	0.025641026
ENSECAG00000020919	C17orf53	3	1	6	0	0	1	0.027543832
ENSECAG00000020928	TEKT5	0	2	3	0	0	1	0.028571429
ENSECAG00000020656	CLDND1	0	3	4	0	0	1	0.028571429
ENSECAG00000020562	AXDND1	2	2	3	0	0	1	0.030701754
ENSECAG00000012693	LONRF1	3	6	4	0	0	1	0.031055901
ENSECAG00000022405	NOTCH1	5	22	7	7	0.24	0.76	0.035190268
ENSECAG00000003869	ZC3H7A	1	0	4	1	0.055555556	0.944444444	0.035714286
ENSECAG00000019301	CFAP58	0	5	2	0	0	1	0.038461538
ENSECAG00000016566	TEK	0	6	2	0	0	1	0.038461538
ENSECAG00000016746	ATP13A2	4	6	3	0	0	1	0.040056022

ENSECAG00000000361	HEATR3	6	8	8	1	0.096153846	0.903846154	0.04429366
ENSECAG00000022609	CHRNA2	0	2	3	2	0	1	0.045454545
ENSECAG00000008506	HMMR	0	1	3	0	0	1	0.045454545
ENSECAG00000014657	MYT1L	0	5	4	2	0.090909091	0.909090909	0.046034203
ENSECAG00000021288	IMPG2	3	4	10	1	0.1	0.9	0.047216106
ENSECAG00000015796	LIAS	0	4	2	0	0	1	0.047619048
ENSECAG00000021295	SHMT2	0	3	3	0	0	1	0.047619048
ENSECAG00000015538		0	2	2	0	0	1	0.047619048

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**Supplementary Table S17.** 34 overlaped genes located at the top 1% highest CLR values, and top 1% lowest nucleotide diversity windows

Gene ID	Gene name
ENSECAG000000021999	GNB1
ENSECAG000000002115	
ENSECAG000000014796	MIB2
ENSECAG000000018423	CCNL2
ENSECAG000000024877	RNF4
ENSECAG000000024955	ZFYVE28
ENSECAG000000011661	NSD2
ENSECAG000000026946	
ENSECAG000000008326	SCAMP4
ENSECAG000000014371	CSNK1G2
ENSECAG000000017108	FLT4
ENSECAG000000009303	GFPT2
ENSECAG000000015254	RASGEF1C
ENSECAG000000007222	RNF130
ENSECAG000000017830	TBC1D9B
ENSECAG000000003079	CANX
ENSECAG000000023719	RUFY1
ENSECAG000000014530	SEPTIN10
ENSECAG000000019446	SH3RF3
ENSECAG000000016174	
ENSECAG000000009529	IMP4
ENSECAG000000018043	
ENSECAG000000018073	
ENSECAG000000023095	AMMECR1L
ENSECAG000000000691	WDR33
ENSECAG000000009694	IWS1
ENSECAG000000006957	BIN1
ENSECAG000000008016	GLI2
ENSECAG000000014701	RALB
ENSECAG000000016637	EPB41L5
ENSECAG000000010919	MYO9B
ENSECAG000000021961	IL12RB1
ENSECAG000000012875	GATAD2A
ENSECAG000000000250	CILP2

**Supplementary Table S18.** The average polymorphism in different groups.

Category	Geographic distrubution	Sample Size	Diversity Index	
			polymorphism $\pi$ (10-3)	polymorphism $\theta_w$ (10-3)
<b>Foreign Plain</b>	Egypt	3	0.936	2.337
	Kenya	17	0.898	1.534
	Nigeria	6	0.910	1.913
	Kyrgyzstan	7	0.888	1.813
	Iran	8	0.935	1.827
	total	41	0.948	1.457
<b>Chinese Plain</b>	-	28	0.925	1.491
<b>Plain</b>	Foreign Plain+Chinese Plain	69	0.949	1.401
<b>Tibetan</b>	Domesticated	24	0.920	1.503
	Kiang	5	0.793	1.020
	total	29	1.723	1.756

**Supplementary Table S19.** A total of 158 candidate protein coding genes evolving under positive selection detected by the three statistics

GeneID	FST	FST_PVALUE	FST_FDR	log2(PI_ratio)	PI_PVALUE	PI_FDR	LSBL	LSBL_Pvalue	LSBL_FDR
Gglean000098	0.056125	0.000299985	0.009220819	0.440996195	0.000149993	0.006354757	0.05688	0.000180766	0.0065
Gglean000119	0.0570165	0.000299985	0.009220819	0.473550949	1.00E-04	0.004442351	0.06141	9.04E-05	0.00436
Gglean000120	0.0570165	0.000299985	0.009220819	0.473550949	1.00E-04	0.004442351	0.06141	9.04E-05	0.00436
Gglean000654	0.0709475	0.000149993	0.008361886	0.624973053	5.00E-05	0.003983369	0.04872	0.000361533	0.00809
Gglean000680	0.0607669	0.000299985	0.009220819	0.795685717	5.00E-05	0.003983369	0.05001	0.000361533	0.00809
Gglean000920	0.0610026	0.000299985	0.009220819	0.554501948	1.00E-04	0.004442351	0.06924	9.04E-05	0.00436
Gglean000921	0.0610026	0.000299985	0.009220819	0.554501948	1.00E-04	0.004442351	0.06924	9.04E-05	0.00436
Gglean000922	0.0610026	0.000299985	0.009220819	0.554501948	1.00E-04	0.004442351	0.06924	9.04E-05	0.00436
Gglean000923	0.0610026	0.000299985	0.009220819	0.554501948	1.00E-04	0.004442351	0.06924	9.04E-05	0.00436
Gglean000924	0.0789982	0.000149993	0.008361886	0.740633206	5.00E-05	0.003983369	0.09493	9.04E-05	0.00436
Gglean000925	0.0789982	0.000149993	0.008361886	0.740633206	5.00E-05	0.003983369	0.09493	9.04E-05	0.00436
Gglean000926	0.0702792	0.000149993	0.008361886	0.707909131	5.00E-05	0.003983369	0.08476	9.04E-05	0.00436
Gglean001528	0.113919	5.00E-05	0.007821677	0.49067698	1.00E-04	0.004442351	0.07776	9.04E-05	0.00436
Gglean001529	0.111208	5.00E-05	0.007821677	1.111144353	5.00E-05	0.003983369	0.08662	9.04E-05	0.00436
Gglean001530	0.111208	5.00E-05	0.007821677	1.111144353	5.00E-05	0.003983369	0.08662	9.04E-05	0.00436
Gglean001531	0.13878	5.00E-05	0.007821677	0.998074514	5.00E-05	0.003983369	0.10311	9.04E-05	0.00436
Gglean001532	0.119378	5.00E-05	0.007821677	0.970183197	5.00E-05	0.003983369	0.08771	9.04E-05	0.00436
Gglean001533	0.0921951	5.00E-05	0.007821677	0.854040839	5.00E-05	0.003983369	0.06668	9.04E-05	0.00436
Gglean001534	0.0767923	0.000149993	0.008361886	0.565151037	5.00E-05	0.003983369	0.06265	9.04E-05	0.00436
Gglean002563	0.0676736	0.000149993	0.008361886	0.919204821	5.00E-05	0.003983369	0.04541	0.000451916	0.00913
Gglean002564	0.0582558	0.000299985	0.009220819	0.784206664	5.00E-05	0.003983369	0.04911	0.000361533	0.00809
Gglean002753	0.0576453	0.000299985	0.009220819	0.485847974	1.00E-04	0.004442351	0.06119	9.04E-05	0.00436
Gglean004174	0.0867716	5.00E-05	0.007821677	0.628548875	5.00E-05	0.003983369	0.11185	9.04E-05	0.00436

Gglean004175	0.0867716	5.00E-05	0.007821677	0.628548875	5.00E-05	0.003983369	0.11185	9.04E-05	0.00436
Gglean004176	0.135515	5.00E-05	0.007821677	0.492881114	1.00E-04	0.004442351	0.18529	9.04E-05	0.00436
Gglean004177	0.0657349	0.000149993	0.008361886	0.594606492	5.00E-05	0.003983369	0.09793	9.04E-05	0.00436
Gglean004178	0.0549311	0.000299985	0.009220819	0.581592699	5.00E-05	0.003983369	0.08089	9.04E-05	0.00436
Gglean004179	0.0657285	0.000149993	0.008361886	0.492536468	1.00E-04	0.004442351	0.10277	9.04E-05	0.00436
Gglean004181	0.0612786	0.000299985	0.009220819	0.448575841	1.00E-04	0.004442351	0.08216	9.04E-05	0.00436
Gglean004183	0.0719952	0.000149993	0.008361886	0.511623171	1.00E-04	0.004442351	0.052	0.000361533	0.00809
Gglean004184	0.0719952	0.000149993	0.008361886	0.923383742	5.00E-05	0.003983369	0.08697	9.04E-05	0.00436
Gglean004185	0.108654	5.00E-05	0.007821677	1.27261999	5.00E-05	0.003983369	0.13446	9.04E-05	0.00436
Gglean004186	0.115998	5.00E-05	0.007821677	0.923578896	5.00E-05	0.003983369	0.14483	9.04E-05	0.00436
Gglean005679	0.0707191	0.000149993	0.008361886	0.444407541	0.000149993	0.006354757	0.05075	0.000361533	0.00809
Gglean005680	0.09025	5.00E-05	0.007821677	0.50806835	1.00E-04	0.004442351	0.0523	0.000361533	0.00809
Gglean006101	0.0575498	0.000299985	0.009220819	0.433144746	0.00019999	0.007986622	0.05643	0.000180766	0.0065
Gglean006657	0.0741944	0.000149993	0.008361886	0.475163991	1.00E-04	0.004442351	0.05938	0.000180766	0.0065
Gglean007028	0.0606744	0.000299985	0.009220819	0.491509885	1.00E-04	0.004442351	0.076	9.04E-05	0.00436
Gglean007035	0.0548249	0.000299985	0.009220819	0.793466563	5.00E-05	0.003983369	0.06067	9.04E-05	0.00436
Gglean007036	0.0655535	0.00019999	0.009220819	0.675117534	5.00E-05	0.003983369	0.049	0.000361533	0.00809
Gglean007037	0.0722692	0.000149993	0.008361886	0.622258965	5.00E-05	0.003983369	0.05511	0.000180766	0.0065
Gglean007038	0.0671706	0.000149993	0.008361886	0.55620754	1.00E-04	0.004442351	0.04952	0.000361533	0.00809
Gglean007615	0.0717487	0.000149993	0.008361886	0.804031552	5.00E-05	0.003983369	0.0853	9.04E-05	0.00436
Gglean007672	0.0694065	0.000149993	0.008361886	0.811853366	5.00E-05	0.003983369	0.07109	9.04E-05	0.00436
Gglean007870	0.0882252	5.00E-05	0.007821677	0.796749264	5.00E-05	0.003983369	0.06201	9.04E-05	0.00436
Gglean008210	0.0564744	0.000299985	0.009220819	0.509376435	1.00E-04	0.004442351	0.07019	9.04E-05	0.00436
Gglean008543	0.114061	5.00E-05	0.007821677	0.854263864	5.00E-05	0.003983369	0.05056	0.000361533	0.00809
Gglean008544	0.0589496	0.000299985	0.009220819	0.453829198	1.00E-04	0.004442351	0.04901	0.000361533	0.00809

Gglean008779	0.0543717	0.000299985	0.009220819	0.604150418	5.00E-05	0.003983369	0.06854	9.04E-05	0.00436
Gglean008795	0.0670848	0.000149993	0.008361886	1.394641703	5.00E-05	0.003983369	0.04546	0.000451916	0.00913
Gglean008796	0.0670848	0.000149993	0.008361886	1.394641703	5.00E-05	0.003983369	0.04546	0.000451916	0.00913
Gglean008922	0.0624812	0.000249988	0.009220819	0.478151586	1.00E-04	0.004442351	0.0543	0.00027115	0.00809
Gglean008923	0.0772753	0.000149993	0.008361886	0.52314824	1.00E-04	0.004442351	0.06605	9.04E-05	0.00436
Gglean008924	0.0764396	0.000149993	0.008361886	0.574960906	5.00E-05	0.003983369	0.07102	9.04E-05	0.00436
Gglean008925	0.0764396	0.000149993	0.008361886	0.574960906	5.00E-05	0.003983369	0.07102	9.04E-05	0.00436
Gglean008926	0.121273	5.00E-05	0.007821677	0.806412902	5.00E-05	0.003983369	0.05196	0.000361533	0.00809
Gglean008927	0.121273	5.00E-05	0.007821677	0.806412902	5.00E-05	0.003983369	0.11061	9.04E-05	0.00436
Gglean008928	0.112075	5.00E-05	0.007821677	0.850510129	5.00E-05	0.003983369	0.10538	9.04E-05	0.00436
Gglean008929	0.107446	5.00E-05	0.007821677	0.738132688	5.00E-05	0.003983369	0.09305	9.04E-05	0.00436
Gglean008930	0.0811216	0.000149993	0.008361886	0.44771458	0.000149993	0.006354757	0.05783	0.000180766	0.0065
Gglean008931	0.080098	0.000149993	0.008361886	0.477047777	1.00E-04	0.004442351	0.06281	9.04E-05	0.00436
Gglean008932	0.080098	0.000149993	0.008361886	0.477047777	1.00E-04	0.004442351	0.06281	9.04E-05	0.00436
Gglean008933	0.080098	0.000149993	0.008361886	0.477047777	1.00E-04	0.004442351	0.06281	9.04E-05	0.00436
Gglean008935	0.121463	5.00E-05	0.007821677	0.848582563	5.00E-05	0.003983369	0.09948	9.04E-05	0.00436
Gglean008936	0.103452	5.00E-05	0.007821677	0.826005714	5.00E-05	0.003983369	0.09125	9.04E-05	0.00436
Gglean008937	0.0678751	0.000149993	0.008361886	0.770852339	5.00E-05	0.003983369	0.09428	9.04E-05	0.00436
Gglean008938	0.0678751	0.000149993	0.008361886	0.770852339	5.00E-05	0.003983369	0.09428	9.04E-05	0.00436
Gglean008939	0.0607521	0.000299985	0.009220819	0.871780881	5.00E-05	0.003983369	0.08888	9.04E-05	0.00436
Gglean008940	0.0609983	0.000299985	0.009220819	0.857652715	5.00E-05	0.003983369	0.08064	9.04E-05	0.00436
Gglean008941	0.0609983	0.000299985	0.009220819	0.856358115	5.00E-05	0.003983369	0.07616	9.04E-05	0.00436
Gglean008942	0.0609983	0.000299985	0.009220819	0.856358115	5.00E-05	0.003983369	0.07616	9.04E-05	0.00436
Gglean008943	0.127616	5.00E-05	0.007821677	0.837077395	5.00E-05	0.003983369	0.12946	9.04E-05	0.00436
Gglean008944	0.127616	5.00E-05	0.007821677	0.837077395	5.00E-05	0.003983369	0.12946	9.04E-05	0.00436

Gglean008945	0.119771	5.00E-05	0.007821677	0.979796437	5.00E-05	0.003983369	0.12445	9.04E-05	0.00436
Gglean008946	0.119771	5.00E-05	0.007821677	0.979796437	5.00E-05	0.003983369	0.12445	9.04E-05	0.00436
Gglean008947	0.0947819	5.00E-05	0.007821677	0.875311987	5.00E-05	0.003983369	0.09694	9.04E-05	0.00436
Gglean009159	0.0599173	0.000299985	0.009220819	1.051974182	5.00E-05	0.003983369	0.05125	0.000361533	0.00809
Gglean009160	0.0599173	0.000299985	0.009220819	1.11484802	5.00E-05	0.003983369	0.05125	0.000361533	0.00809
Gglean009163	0.0712988	0.000149993	0.008361886	0.879867442	5.00E-05	0.003983369	0.08628	9.04E-05	0.00436
Gglean009164	0.0746006	0.000149993	0.008361886	0.750749631	5.00E-05	0.003983369	0.11902	9.04E-05	0.00436
Gglean009165	0.0746006	0.000149993	0.008361886	0.750749631	5.00E-05	0.003983369	0.11902	9.04E-05	0.00436
Gglean009166	0.0746006	0.000149993	0.008361886	0.750749631	5.00E-05	0.003983369	0.11902	9.04E-05	0.00436
Gglean009167	0.0820296	1.00E-04	0.008361886	0.79777995	5.00E-05	0.003983369	0.12626	9.04E-05	0.00436
Gglean010182	0.0581254	0.000299985	0.009220819	0.49137051	1.00E-04	0.004442351	0.05092	0.000361533	0.00809
Gglean011979	0.0679082	0.000149993	0.008361886	0.75586228	5.00E-05	0.003983369	0.08085	9.04E-05	0.00436
Gglean011981	0.0575583	0.000299985	0.009220819	0.425859308	0.000249988	0.00986023	0.07873	9.04E-05	0.00436
Gglean012281	0.0641958	0.000249988	0.009220819	0.452048484	1.00E-04	0.004442351	0.06	9.04E-05	0.00436
Gglean012282	0.0575944	0.000299985	0.009220819	0.452048484	1.00E-04	0.004442351	0.06813	9.04E-05	0.00436
Gglean013070	0.0546745	0.000299985	0.009220819	0.741328633	5.00E-05	0.003983369	0.04701	0.000361533	0.00809
Gglean013071	0.0552634	0.000299985	0.009220819	0.791858641	5.00E-05	0.003983369	0.04787	0.000361533	0.00809
Gglean013072	0.0552634	0.000299985	0.009220819	0.791858641	5.00E-05	0.003983369	0.04787	0.000361533	0.00809
Gglean013073	0.0541812	0.000299985	0.009220819	0.625261792	5.00E-05	0.003983369	0.0604	9.04E-05	0.00436
Gglean013339	0.060681	0.000299985	0.009220819	0.430564902	0.00019999	0.007986622	0.05992	9.04E-05	0.00436
Gglean013992	0.0700633	0.000149993	0.008361886	0.57075007	5.00E-05	0.003983369	0.05384	0.00027115	0.00809
Gglean014805	0.0833427	1.00E-04	0.008361886	0.496537714	1.00E-04	0.004442351	0.0467	0.000361533	0.00809
Gglean015222	0.0588482	0.000299985	0.009220819	0.484392776	1.00E-04	0.004442351	0.06137	9.04E-05	0.00436
Gglean015974	0.069237	0.000149993	0.008361886	0.513887751	1.00E-04	0.004442351	0.05889	0.000180766	0.0065
Gglean016191	0.12318	5.00E-05	0.007821677	0.810789412	5.00E-05	0.003983369	0.05052	0.000361533	0.00809

Gglean016224	0.0688696	0.000149993	0.008361886	0.566150324	5.00E-05	0.003983369	0.07897	9.04E-05	0.00436
Gglean016906	0.0582837	0.000299985	0.009220819	0.584402861	5.00E-05	0.003983369	0.07176	9.04E-05	0.00436
Gglean016912	0.055149	0.000299985	0.009220819	0.572381911	5.00E-05	0.003983369	0.05499	0.000180766	0.0065
Gglean016913	0.0588153	0.000299985	0.009220819	0.572381911	5.00E-05	0.003983369	0.05499	0.000180766	0.0065
Gglean017336	0.123506	5.00E-05	0.007821677	0.430384969	0.00019999	0.007986622	0.10775	9.04E-05	0.00436
Gglean017337	0.133604	5.00E-05	0.007821677	0.430384969	0.00019999	0.007986622	0.12727	9.04E-05	0.00436
Gglean017338	0.133604	5.00E-05	0.007821677	0.430384969	0.00019999	0.007986622	0.12727	9.04E-05	0.00436
Gglean017417	0.0756855	0.000149993	0.008361886	0.539613828	1.00E-04	0.004442351	0.06893	9.04E-05	0.00436
Gglean018173	0.0626394	0.000249988	0.009220819	0.432940526	0.00019999	0.007986622	0.06304	9.04E-05	0.00436
Gglean018220	0.054088	0.000299985	0.009220819	1.041962449	5.00E-05	0.003983369	0.07175	9.04E-05	0.00436
Gglean019139	0.0613554	0.000299985	0.009220819	0.450827781	1.00E-04	0.004442351	0.0572	0.000180766	0.0065
Gglean019237	0.0712266	0.000149993	0.008361886	0.489051768	1.00E-04	0.004442351	0.07133	9.04E-05	0.00436
Gglean019404	0.0824115	1.00E-04	0.008361886	2.129706271	5.00E-05	0.003983369	0.09486	9.04E-05	0.00436
Gglean019405	0.0801369	0.000149993	0.008361886	1.878737819	5.00E-05	0.003983369	0.09411	9.04E-05	0.00436
Gglean019406	0.0801369	0.000149993	0.008361886	1.878737819	5.00E-05	0.003983369	0.09411	9.04E-05	0.00436
Gglean019407	0.0655194	0.00019999	0.009220819	0.667199154	5.00E-05	0.003983369	0.05084	0.000361533	0.00809
Gglean019436	0.0822818	1.00E-04	0.008361886	0.60279833	5.00E-05	0.003983369	0.04611	0.000451916	0.00913
Gglean019584	0.0781697	0.000149993	0.008361886	0.474481187	1.00E-04	0.004442351	0.04537	0.000451916	0.00913
Gglean019817	0.0567066	0.000299985	0.009220819	0.850305142	5.00E-05	0.003983369	0.05845	0.000180766	0.0065
Gglean019953	0.124143	5.00E-05	0.007821677	0.480845698	1.00E-04	0.004442351	0.12414	9.04E-05	0.00436
Gglean020014	0.0795812	0.000149993	0.008361886	0.679609295	5.00E-05	0.003983369	0.06788	9.04E-05	0.00436
Gglean020015	0.0795812	0.000149993	0.008361886	0.679609295	5.00E-05	0.003983369	0.06788	9.04E-05	0.00436
Gglean020016	0.139893	5.00E-05	0.007821677	0.964944601	5.00E-05	0.003983369	0.13946	9.04E-05	0.00436
Gglean020017	0.153609	5.00E-05	0.007821677	0.855523225	5.00E-05	0.003983369	0.14304	9.04E-05	0.00436
Gglean020018	0.128786	5.00E-05	0.007821677	0.925092872	5.00E-05	0.003983369	0.11771	9.04E-05	0.00436

Gglean020019	0.0748662	0.000149993	0.008361886	0.863592389	5.00E-05	0.003983369	0.06772	9.04E-05	0.00436
Gglean020020	0.0799481	0.000149993	0.008361886	0.824544341	5.00E-05	0.003983369	0.07029	9.04E-05	0.00436
Gglean020516	0.0636337	0.000249988	0.009220819	0.494659706	1.00E-04	0.004442351	0.05727	0.000180766	0.0065
Gglean020517	0.0599521	0.000299985	0.009220819	0.463566703	1.00E-04	0.004442351	0.05603	0.000180766	0.0065
Gglean020519	0.0712629	0.000149993	0.008361886	0.492295359	1.00E-04	0.004442351	0.0717	9.04E-05	0.00436
Gglean020520	0.0712629	0.000149993	0.008361886	0.492295359	1.00E-04	0.004442351	0.0717	9.04E-05	0.00436
Gglean020537	0.0766481	0.000149993	0.008361886	1.128699203	5.00E-05	0.003983369	0.08031	9.04E-05	0.00436
Gglean020759	0.0949852	5.00E-05	0.007821677	0.780193054	5.00E-05	0.003983369	0.05325	0.00027115	0.00809
Gglean020760	0.0949852	5.00E-05	0.007821677	0.780193054	5.00E-05	0.003983369	0.05325	0.00027115	0.00809
Gglean020788	0.0748486	0.000149993	0.008361886	0.887638915	5.00E-05	0.003983369	0.06682	9.04E-05	0.00436
Gglean021277	0.0637957	0.000249988	0.009220819	0.480947205	1.00E-04	0.004442351	0.05927	0.000180766	0.0065
Gglean021278	0.0654522	0.00019999	0.009220819	0.480947205	1.00E-04	0.004442351	0.05927	0.000180766	0.0065
Gglean021868	0.0829385	1.00E-04	0.008361886	0.454611496	1.00E-04	0.004442351	0.0584	0.000180766	0.0065
Gglean021928	0.0917278	5.00E-05	0.007821677	0.750194401	5.00E-05	0.003983369	0.05223	0.000361533	0.00809
Gglean021975	0.0596719	0.000299985	0.009220819	0.527124759	1.00E-04	0.004442351	0.0493	0.000361533	0.00809
Gglean022194	0.0584242	0.000299985	0.009220819	0.543587808	1.00E-04	0.004442351	0.0553	0.000180766	0.0065
Gglean022719	0.0749062	0.000149993	0.008361886	0.443406492	0.000149993	0.006354757	0.07357	9.04E-05	0.00436
Gglean022720	0.103623	5.00E-05	0.007821677	0.443406492	0.000149993	0.006354757	0.10731	9.04E-05	0.00436
Gglean022721	0.162352	5.00E-05	0.007821677	0.784712347	5.00E-05	0.003983369	0.15944	9.04E-05	0.00436
Gglean022722	0.133954	5.00E-05	0.007821677	0.597358449	5.00E-05	0.003983369	0.14055	9.04E-05	0.00436
Gglean022723	0.133954	5.00E-05	0.007821677	0.597358449	5.00E-05	0.003983369	0.14055	9.04E-05	0.00436
Gglean022724	0.0815522	0.000149993	0.008361886	0.597358449	5.00E-05	0.003983369	0.10529	9.04E-05	0.00436
Gglean022949	0.0614702	0.000299985	0.009220819	0.548367434	1.00E-04	0.004442351	0.05009	0.000361533	0.00809
Gglean022951	0.0800476	0.000149993	0.008361886	0.536355033	1.00E-04	0.004442351	0.06413	9.04E-05	0.00436
Gglean023090	0.0583231	0.000299985	0.009220819	0.650293609	5.00E-05	0.003983369	0.04862	0.000361533	0.00809



Gglean023091	0.078831	0.000149993	0.008361886	1.26430756	5.00E-05	0.003983369	0.04862	0.000361533	0.00809
Gglean023614	0.057326	0.000299985	0.009220819	0.527746337	1.00E-04	0.004442351	0.06499	9.04E-05	0.00436
Gglean023615	0.126888	5.00E-05	0.007821677	0.463196245	1.00E-04	0.004442351	0.09358	9.04E-05	0.00436
Gglean024356	0.0544389	0.000299985	0.009220819	0.796567747	5.00E-05	0.003983369	0.05688	0.000180766	0.0065
Gglean024357	0.0544389	0.000299985	0.009220819	0.796567747	5.00E-05	0.003983369	0.05688	0.000180766	0.0065
Gglean024366	0.0936329	5.00E-05	0.007821677	0.817483508	5.00E-05	0.003983369	0.06896	9.04E-05	0.00436
Gglean024568	0.0954005	5.00E-05	0.007821677	0.709754803	5.00E-05	0.003983369	0.05538	0.000180766	0.0065
Gglean024824	0.0558467	0.000299985	0.009220819	0.557802918	1.00E-04	0.004442351	0.04772	0.000361533	0.00809
Gglean026872	0.0813396	0.000149993	0.008361886	0.625073952	5.00E-05	0.003983369	0.08718	9.04E-05	0.00436
Gglean027163	0.0821316	1.00E-04	0.008361886	1.029371854	5.00E-05	0.003983369	0.04943	0.000361533	0.00809

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**Supplementary Table S20.** 22 genes that overlapped at the top 1% CLR regions between Kiang and Tibetan population

Gene ID	Gene name
ENSECAG00000014796	MIB2
ENSECAG00000007315	ACAP3
ENSECAG00000009215	SLC7A5
ENSECAG00000000420	BANP
ENSECAG00000008732	GALNS
ENSECAG00000003668	CBFA2T3
ENSECAG00000015121	ACSF3
ENSECAG00000014825	LRPAP1
ENSECAG00000000623	TCF3
ENSECAG00000012857	JSRP1
ENSECAG00000007272	NCOR2
ENSECAG00000016328	ADAMTS2
ENSECAG00000024626	FAM193B
ENSECAG00000021191	UGGT1
ENSECAG00000016753	LIMS2
ENSECAG00000020054	MYO7B
ENSECAG00000008016	GLI2
ENSECAG00000014273	ANO8
ENSECAG00000017720	SSBP4
ENSECAG00000000336	COMP
ENSECAG00000013871	SUGP1
ENSECAG00000026946	

**Supplementary Table S21.** Comparison of demographic models for the three groups of Chinese plain, Tibetan and foreign plain donkey using  $\partial a \partial i$

**Supplementary Table S21 are listed as a separate excel file due to its large size.**