Supplementary Information

Whole-genome sequencing of eight goat populations for the detection of selection signatures underlying production and adaptive traits

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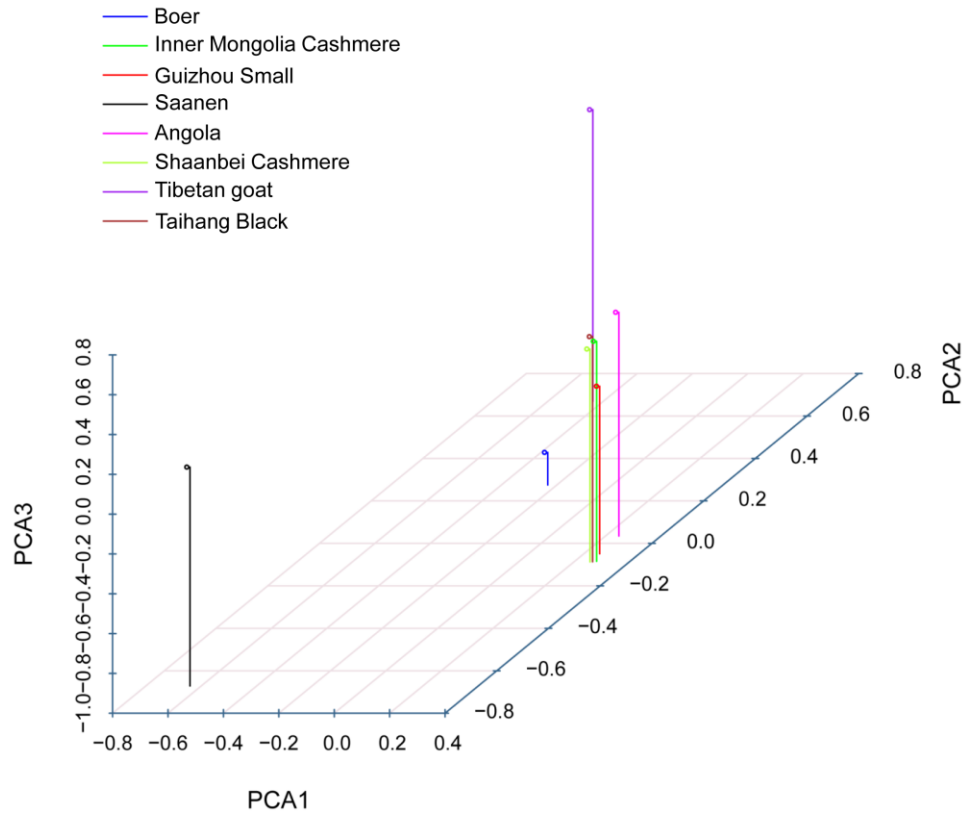
Supplementary Fig. S1 Principal components analysis (PCA) of eight goat breeds using components PC1, PC2, and PC3.
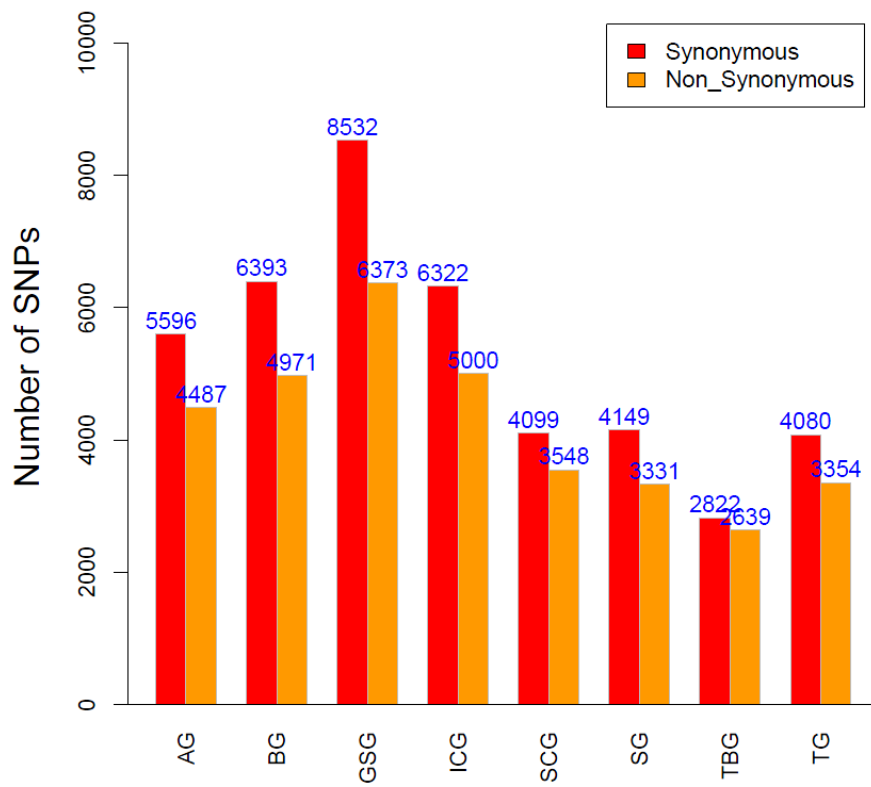
Supplementary Fig. S2 The number of synonymous and non-synonymous mutations in each goat breed. Angora (AG), Boer (BG), Guizhou Small (GSG), Inner Mongolia Cashmere (ICG), Shaanbei Cashmere (SCG), Saanen (SG), Taihang Black (TBG), Tibetan (TG).
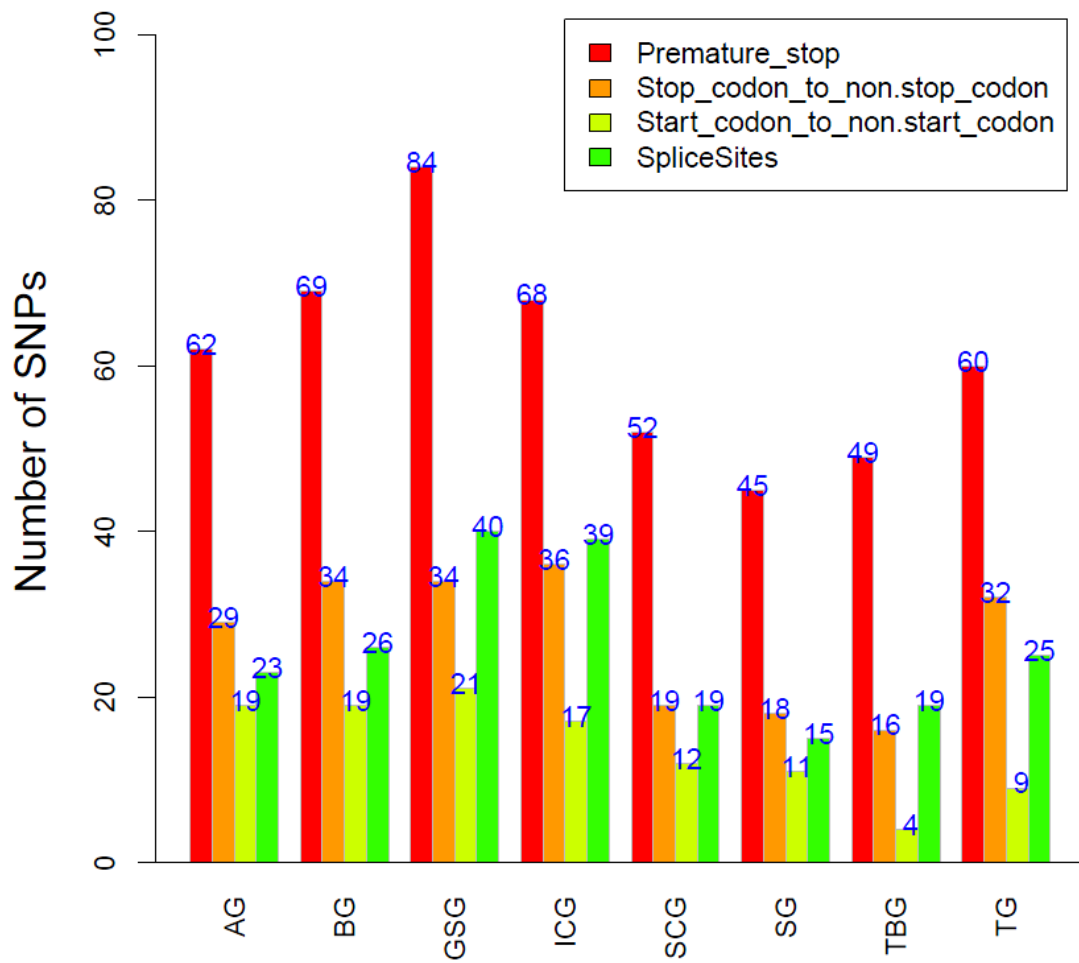
Supplementary Fig. S3 The number of SNPs with large effects (premature stop, stop codon to nonstop codon, start codon to nonstart codon, and splicing sites) in each goat breed. Angora (AG), Boer (BG), Guizhou Small (GSG), Inner Mongolia Cashmere (ICG), Shaanbei Cashmere (SCG), Saanen (SG), Taihang Black (TBG), Tibetan (TG).

Supplementary Table S1. Pooled samples information for resequencing data from goats. Goat DNA pools represent eight separate breeds respectively. The number of individuals from each breed (n) and the number of males and females, the average sequence and assembly coverage per

Breed	No. of samples	Sequence coverage (x)	Phenotype/Feature
Taihang Black	(M=10, F=11)	9.35	Meat, black coated
Tibetan goat	(F=25)	13.95	Highland adaption
Inner Mongolia Cashmere	(M=8, F=20)	9.67	Fiber (cashmere)
Shaanbei Cashmere	(M=9, F=20)	9.13	Fiber (cashmere)
Angora	(M=10, F=10)	10.65	Fiber (mohair)
Saanen	(M=6, F=15)	10.86	Dairy
Boer	(M=7, F=15)	13.95	Meat, higher body weight
Guizhou Small	(M=3, F=18)	10.00	Meat, lower body weight

pool are indicated.

Supplementary Table S2. The number of candidate regions and genes identified by ZH_p and di in different breeds.

Breed	ZH_p	di	Overlapped regions	Overlapped genes
Taihang Black	48	54	6	6
Guizhou Small	49	56	4	4
Inner Mongolia Cashmere	40	37	5	5
Tibetan goat	49	53	7	6
Total	182	200	22	21