

Table S4. Genotypic, allelic frequencies and diversity parameters of three mutations of *LEPR* in eight sheep populations.

Locus/Breed	Genotype frequency			Allele frequency		Diversity parameter				
						Ho	He	n _e	PIC	χ ² (HWE)
c.185G>A (Arg62His)	GG	GA	AA	G	A					
UM	0.766	0.218	0.015	0.875	0.125	0.782	0.218	1.279	0.195	0.001
DBU	0.819	0.181	0.000	0.910	0.090	0.835	0.165	1.197	0.150	3.007
SFKU	0.530	0.379	0.091	0.720	0.280	0.597	0.403	1.676	0.322	0.247
SN	0.661	0.311	0.028	0.816	0.184	0.700	0.300	1.428	0.255	0.235
MG	0.972	0.000	0.028	0.972	0.028	0.946	0.054	1.058	0.053	250.000
Tan	0.833	0.167	0.000	0.917	0.083	0.847	0.153	1.180	0.141	0.248
Hu	0.667	0.300	0.033	0.817	0.183	0.701	0.299	1.427	0.254	0.000
STH	0.767	0.200	0.033	0.867	0.133	0.769	0.231	1.301	0.204	0.544
c.240C>T (80Asn)	CC	CT	TT	C	T					
UM	0.185	0.452	0.363	0.411	0.589	0.516	0.484	1.938	0.367	1.400
DBU	0.053	0.398	0.549	0.252	0.748	0.623	0.377	1.604	0.306	0.980
SFKU	0.076	0.530	0.394	0.341	0.659	0.551	0.449	1.816	0.348	2.140
SN	0.120	0.495	0.386	0.367	0.633	0.535	0.465	1.868	0.357	0.769
MG	0.128	0.460	0.412	0.358	0.642	0.540	0.460	1.851	0.354	0.000
Tan	0.267	0.567	0.167	0.550	0.450	0.505	0.495	1.980	0.372	0.629
Hu	0.200	0.500	0.300	0.450	0.550	0.505	0.495	1.980	0.372	0.003
STH	0.300	0.400	0.300	0.500	0.500	0.500	0.500	2.000	0.375	1.200
c.279C>T (93Ser)	CC	CT	TT	C	T					
UM	0.185	0.452	0.363	0.411	0.589	0.516	0.484	1.938	0.367	1.400
DBU	0.053	0.398	0.549	0.252	0.748	0.623	0.377	1.604	0.306	0.980
SFKU	0.076	0.530	0.394	0.341	0.659	0.551	0.449	1.816	0.348	2.140
SN	0.121	0.468	0.410	0.355	0.645	0.542	0.458	1.846	0.353	0.082

MG	0.128	0.460	0.412	0.358	0.642	0.540	0.460	1.851	0.354	0.000
Tan	0.267	0.567	0.167	0.550	0.450	0.505	0.495	1.980	0.372	0.629
Hu	0.200	0.500	0.300	0.450	0.550	0.505	0.495	1.980	0.372	0.003
STH	0.300	0.400	0.300	0.500	0.500	0.500	0.500	2.000	0.375	1.200

*UM: Ujimqin; DPU: Dorper × Ujimqin; SFKU: Suffolk × Ujimqin; SN: Sonid; MG: Mongolia; STH: Small-tailed Han; H_o : observed heterozygosity; H_e : expected heterozygosity; n_e : effective allele numbers; PIC : polymorphism information content; HWE : Hardy-Weinberg equilibrium; ¹The classification was conducted according to the PIC values (PIC value < 0.25, low polymorphism; 0.25 < PIC value < 0.5, moderate polymorphism; and PIC value > 0.5, high polymorphism); ²No Hardy-Weinberg departure was detected from the obtained genotype frequencies.