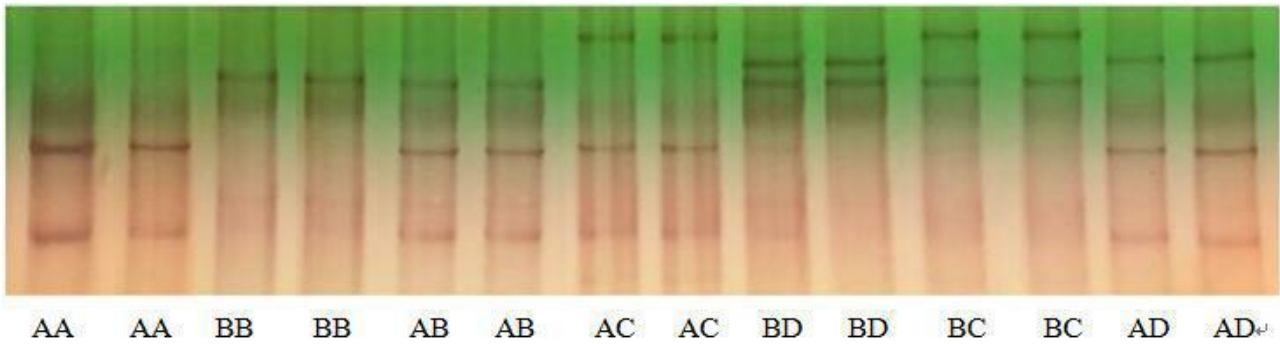


Variation in the yak lipin-1 gene and its association with milk traits

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SUPPLEMENTARY FILE



Supplementary Figure S1. PCR SSCP banding patterns for a yak *LPIN1* amplicon spanning part of the 5' untranslated region (UTR). Four unique banding patterns representing four different variant sequences (A to D) are shown in either homozygous or heterozygous forms.

Supplementary Table S1. Genotype and variant frequencies in the 5' untranslated region (UTR) of yak *LPIN1*.

Population	Genotype frequencies (%)							Variant frequencies (%)			
	<i>AA</i>	<i>BB</i>	<i>AB</i>	<i>AC</i>	<i>BC</i>	<i>AD</i>	<i>BD</i>	<i>A</i>	<i>B</i>	<i>C</i>	<i>D</i>
Gannan yaks (n = 260)	12.7	20.4	46.6	6.1	6.1	5.0	3.1	41.6	48.3	6.1	4.0
Tianzhu white yaks (n = 111)	19.8	18.9	53.2	0	0	3.6	4.5	48.2	44.8	0	4.1
Qinghai yaks (n = 91)	5.5	20.9	63.7	0	0	5.5	4.4	40.1	55.0	0	5.0
Wild yaks (n = 38)	18.4	5.3	71.1	0	0	2.6	2.6	55.3	42.1	0	2.6