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Cloning and expression of caprine *KIT* gene and associations of polymorphisms with litter size

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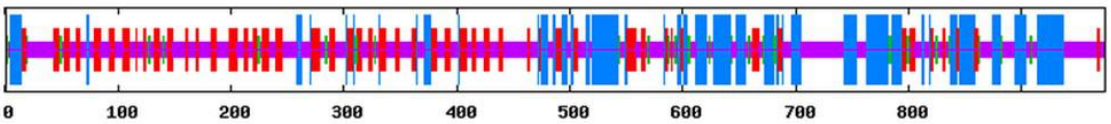

Fig. S1. Predicted secondary structure of KIT protein. Alpha helix, extended strands, β-turns and random coils are indicated, respectively, with blue, red, green and purple vertical lines

Table S1. Primer information of *KIT* and *β-actin* genes for cloning CDS and qRT-PCR

Primer	Sequence (5'→3')	Product size (bp)	Tm (℃)
CF1	ATAGATCCGGTCCCAGCGCAG	590	65.3
CR1	TGAGCAGTGCAGACAGAGCCG		
CF2	AACTGTCTCTACCATCTATCC	1080	57.5
CR2	ATGTGTAAGTGCCTCCTTC		
CF3	ACAGAACCTCCACTGATAAG	820	53
CR3	AGCATCTTGACAGCAACA		
CF4	ACATAGACCCAACACAACTT	858	53
CR4	CATAGGACCAGACATCACTT		
CF5	GCCAGAGACATCAAGAATG	501	50
CR5	CAGACTGCTTCAGACATCT		
RT-KF	TGACCAATTACTCTCTCACGGG	341	58
RT-KR	TGCTTTACTCTGCTGGCTGTTT		
β-actin-F	CCACACCTTCTACAACGAGC	105	58
β-actin-R	ATCTGGGTCATCTTCTCACG		

Note: The primer pairs RT-KF/RT-KR and β-actin-F/β-actin-R were used for qRT-PCR.

Table S2. Primer information of *KIT* gene for screening polymorphisms

Primer	Sequence (5'→3')	Gene region	Product size (bp)	Tm (℃)
F1	GGAACGTGGAACAGAGCT	Exon 1 and partial	406	57
R1	AAAGCAGCCCTAAACTCAC	intron 1		
F2	GGAACTGTCTCTACCATCTAT	Exon 2	325	54
R2	CTCAGCTATCTGTATGTCATC			
F3	CCTGATTGACCTTCCCTTG	Exon 3	366	60
R3	GCCTGAGTGACCAACATAC			
F4	ATTCTAGCCATCAAAGCTGT	Exon 4	304	52.7
R4	ACTGAATCACTTTGCCGTAT			
F5	GCACAGATGAAGAAGAATAGC	Exon 5 and partial	421	60
R5	GGTTAAGCAGAGAATGACATG	intron 5		
F6	TCATTCTGCTGTGGTTAGAT	Exon 6	431	57
R6	CAGGAGATGGGATTTCAATC			
F7	GGTAGGTGATCCACAGGT	Exon 7	362	56
R7	TGGTCAGCGAATTGTAGG			
F8	TTCCAGCAGTCTGACATAC	Exon 8 and partial	364	50
R8	CGTCGTTCAGTAATCATGTT	intron 8		
F9	TTCTCTGAGAGTAAGTCTGG	Exon 9	365	56
R9	TGACAATCACATGCGTAATG			
F10	CAGCTAATAGGTTGTGATTCC	Exon 10-11	423	52
R10	AAGGCAATGCGATGTGAA			
F11	CCTTGTCTTCCTTCCTACAG	Exon 12-13	460	51
R11	GGAAATCCAGCAAGAGGTT			
F12	GGTGGTCTGTATATCTTACCT	Exon 14	306	56
R12	CCTCAAAGTACCTCAGTTCA			
F13	ATAGCCTGCCTCTCACAT	Exon 15	327	54
R13	GATGCTCAGATACAGTAACAC			
F14	GCAAGTTCACATCAGTTCC	Exon 16	308	56
R14	TGGCTCTAAATACTCCTTGG			
F15	GCAGCATTCTAGCATTCAAT	Exon 17	326	54
R15	GCATGATATCGCAAAGGTAG			
F16	CATAATTCTCAGAGGCAATCAG	Exon 18	353	55
R16	AAGGAGAGCACTGGTAGC			
F17	AAGGCATTGAGGAGTGATAA	Exon 20	300	53
R17	ACTTGCTTCCATTGCTTCA			
F18	TACTGGCGTATTGACTGTG	Exon 21 and partial	408	57
R18	CACCCTCCCTTTCTCCAA	3′UTR		
F19	CACTTCACCTTGCTGTATAG	3′UTR	364	57.2
R19	GCCACAGTTCTCTAAATGAA			

Table S3. Genotype frequencies of two SNP loci in the *KIT* gene for each breed

Locus	Restriction enzyme			Breed		
				SN	GZ	BG
g.88430T>A	*Hinc*II	Genotype	AA	60	37	32
			TA	125	88	77
			TT	121	106	89
		Allele	A	0.40	0.35	0.36
			T	0.60	0.65	0.64
		He		0.41	0.38	0.39
		PIC		0.36	0.35	0.35
		Equilibrium χ^2 test		$P<0.01$	$P=0.01$	$P=0.03$
g.120466G>A	*Hinf*I	Genotype	AA	29	22	23
			GA	117	83	84
			GG	160	126	91
		Allele	A	0.29	0.27	0.33
			G	0.71	0.73	0.67
		He		0.38	0.36	0.42
		PIC		0.33	0.32	0.34
		Equilibrium χ^2 test		$P=0.27$	$P=0.13$	$P=0.59$
LD of g.88430T>A and g.120466G>A				$r^2=0.02$	$r^2=0.01$	$r^2=0.02$

Note: LD = linkage disequilibrium