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Supplement of

A novel 17 bp indel in the *SMAD3* gene alters transcription level, contributing to phenotypic traits in Chinese cattle

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Supplementary Material

Table S1 Primers in bovine *SMAD3* for variations detection

Name ^a	Primer sequences (5'to3')	Position of amplicon in NC_007308 ^b	Size (bp)	T _a (°C)	Location within gene
P1	F: CAAAGTTTGGCTGGGGGTTG R:GAGGTGAAAAGCCAATGCGG	nt- 409 to 750	847	67.3	5'UTR,Exon 1, partial Intron 1
P2	F:TCACTGTCCGTTTCTGCTCC R: GCCTTGCTATTTCCGCTTC	nt 100225 to101019	795	61.4	Exon 2, 3 and partial Intron 1, 2, 3
P3	F: CCTTTCGGAGCCATCTAC R: TCTTCCATCAGGGCATAACA	nt 101364 to 102434	1071	57.0	Exon 4 and partial Intron 3, 4
P4	F:TGCGGGCTTGATTAGACG R: GCCCACTTGTCAGCCGTA	nt 105182 to 106585	1404	62.5	Exon 5 and partial Intron 4, 5
P5	F:CTTGAAGATGGCTCTGACCT R: AAGGGTCTTCTCTACTGCT	nt 114439 to 115116	696	61.4	Exon 6 and partial Intron 5, 6
P6	F:GCTGCTAGAGACCAGTCACC R:TGAGACAGCAAGGCACAGAG	nt 117001 to 1177415	415	61.4	Exon 7 and partial Intron 6, 7
P7	F: CCTCCCTATTGAAGTGGCG R: ACTGCTGGCATCTCCTCC	nt 119469 to 120312	861	61.4	Exon 8 and partial Intron 7, 8
P8	F: ACCTCCTTTCCTTCCTG R: CTCTGGGTTTGCTTTCGT	nt 122029 to 122531	503	57.0	Exon 9 and partial Intron 8, 9, 3'UTR

Note: ^a P1, P2, P3, P4, P5, P6, P7, P8 were primer pairs for sequencing, covering all of exons and partial introns of *SMAD3* gene.

^b Nucleotide + 1 is the transcription initiation site; the nucleotide 5' to +1 is numbered