

**Table S1. Primers information used for qPCR investigated in this study**

Gene	Accession number	Primer sequences (5'-3')	Amplification efficiency
<i>GAPDH</i>	XM_006065800	F: ATGGAGAAGGCTGGGGCTCA R: GCAGGAGGCATTGCTGACAA	2.058
<i>RPS23</i>	XM_006059350	F: ACCGACGAGACCAGAAGT R: CTCCAGGAATGTCACCAA	2.012
<i>ACTB</i>	NM_001290932	F: TGGGCATGGAATCCTG R: GCGCGATGATCTTGAT	2.032
<i>AGPAT6</i>	NM_001290846	F: CTTTGCGTGGGCTACCTTG R: TCTTGGTCACCTCGTCGTC	2.032
<i>PPARG</i>	XM_006077448	F: GCTCCAAGAGTACCAAAGTG R: GTCCTCCTGAAGAAACCCTT	2.096
<i>SREBF1</i>	KU517672	F: GCACCGAGGCCAAGTTGAATAA R: CAGGTCCTTCAGCGATTTGCTT	2.041
<i>SREBF2</i>	XM_006068914	F: GCCAAGATGCACAAGTCTGGTGTT R: TGCCCTTCAGGAGCTTGCTCT	2.099
<i>INSIG1</i>	JX853922	F: ACGTTCAGCTCTCCTTGACATT R: CTGTCGTCCTATGTTTCCCAC	2.091
<i>INSIG2</i>	NM_001290944	F: AGCCAGGGAGGGAAATGACCAT R: GCCTCTGCCTGTGGGTTACTCA	2.067
<i>PPARGC1A</i>	NM_177945	F: CCACCGAGAATGAGGCTAGTCCTT R: TTGACAAATGCTCTTCGCTTTATTGCTCCA	2.089
<i>FASN</i>	XM_006061793	F: GGGCTCCACCACCGTGTTCCTCA R: GCTCTGCTGGGCCTGCAGCTG	2.053
<i>ACC</i>	XM_025281121	F: CCTCTTCAGACAGGTTCAAGC R: TTCACCGCACACTGTTCC A	1.968
<i>SCAP</i>	XM_025272558	F: CCATGTGCACTTCAAGGAGGA R: TGTCGATCTTGCGTGTGGAG	1.972
<i>ABCG2</i>	XM_006042277	F: AGCAAATATCAATGGAGTCA R: CGACATCATCTTGTACCACATA	2.062

**Table S2. Primer information for polymorphism identification**

	Primer sequence (5'-3')	Product length (bp)	Annealing temperature (°C)
Exon 2	F: TTTACCTGGACTATCAAC R: ATGTCAATGAACCTACTTA	512	50.0
Exon 3	F: TTGTGCTTTTTTTTCTATC R: CCAAATGTCAAATCTCTAT	304	45.0
Exon 4	F: GCTAAGAGGTAAAGCCTG R: GCGGGTATAAAGAAAAGTTG	307	48.5
Exon 5	F: AGATATACTACAGAGTGATG R: CTTGACCATACATATTATAG	325	47.0
Exon 6	F: GCTGGAACATTTTAGGAG R: CTTACTGATGAATCCCTTGC	330	51.0
Exon 7	F: CAAGTTGAATGAGGAATAA R: AGTGCTCCAAGTGACTC	344	49.0
Exon 8	F: CACCTCCCTCACTCTCTAA R: CTAGTACAACCCATATCAGA	315	49.0
Exon 9	F: AATGAAGGTGCTAGAGTA R: GGAATGGGGATAAATAAA	455	48.9
Exon 10	F: TAATAATAAAGGGTGTG R: TAAGAATATGAAAACCTCTC	304	44.0
Exon 11	F: GGAAGAAAAATGACCTGTAAATGT R: TCTCAGTCAACACTGGTAAC	264	52.0
Exon 12	F: CTGTATAGCAGGGAGTACATCTG R: ACTTGATTTATAGTTTTGAGAA	310	47.0
Exon 13	F: CCCTGATAGACAGTGTTGGATTA R: CCTTAAAGCAGAGTCTGATGTA	315	49.5
Exon 14	F: GTCCTTAGCAGTATTCACGAGAC R: ACTCTCCTTCATTGTCCTAAA	301	49.5
Exon 15	F: AATTCTTTGGAAACTTTTGTC R: CCTCAGCCCAGTAGTATT	221	51.0
Exon 16	F: TCTTTAAGGAACAGTGAAT R: CAAGTGAAAAGAAGACAACC	381	47.8

**Table S3. Information of shRNA used for knockdown of *ABCG2***

Name of shRNA	Sequences (5'-3')
ABCG2_sh1_F	CCGGGTATTGCAATGGAGCTTATTACTCGAGTAATAAGCTCCATTGCAATACTTTTG
ABCG2_sh1_R	AATTCAAAAAGTATTGCAATGGAGCTTATTACTCGAGTAATAAGCTCCATTGCAATAC
ABCG2_sh2_F	CCGGGAGGATGTTACCAAGTATTATCTCGAGATAATACTTGGTAACATCCTCTTTTG
ABCG2_sh2_R	AATTCAAAAAGAGGATGTTACCAAGTATTATCTCGAGATAATACTTGGTAACATCCTC
ABCG2_sh3_F	CCGGGGAAGAATCACGTAGCCTTGGCTCGAGCCAAGGCTACGTGATTCTTCCTTTTG
ABCG2_sh3_R	AATTCAAAAAGGAAGAATCACGTAGCCTTGGCTCGAGCCAAGGCTACGTGATTCTTCC

**Table S4. Haplotype information of buffalo *ABCG2* gene**

Haplotype	Accession number	Alleles	Actual frequency	Expected frequency
Buffalo_hap1	ON515705	CTCGC	0.892	0.892
Buffalo_hap2	ON515706	CTCGT	0.010	0.010
Buffalo_hap3	ON515707	CTCAC	0.024	0.024
Buffalo_hap4	ON515708	CTTGC	0.049	0.049
Buffalo_hap5	ON515709	CCCGC	0.010	0.010
Buffalo_hap6	ON515710	CCTGC	0.005	0.005
Buffalo_hap7	ON515711	TTCGC	0.010	0.010