Supplementary Table S2 Primers and results for CNV validations by qPCR

GENE	Forward Pri	Reverse Pri	CN_qPCR	CN_PennCNV	ADAPTmap code	Goat Group	Breed name	Validation result
AHCY	ACACATGAC	GACTCAAGC	2		control			
			1	cn=2	MG_AND0006	MAD	Androy	0
			0	cn=2	KE_GAL0011	SEA	Galla	0
			2	cn=2	ML_GUE0024	NWA	Guera	1
			28	state5,cn=3	MG_SOF0023	MAD	Sofia	1
			42	state5,cn=3	ET_ABR0027	SEA	Abergelle	1
			2	state5,cn=3	CM_WAD0026	NWA	WAD	0
ASIP	TCTCTCCCGA	GTGGTCTGG	2		control			
			0	cn=2	MG_AND0006	MAD	Androy	0
			1	cn=2	ML_GUE0011	NWA	Guera	0
			7	state5,cn=3	TZ_SNJ0016	SEA	Sonjo	1
ITCH	AGCCAGTA	GTGGTACTT	2		control			
			1	cn=2	MG_AND0006	MAD	Androy	0
			2	cn=2	ET_GUM0023	SEA	Gumez	1
			1	cn=2	TZ_MAA0005	SEA	Maasai	0
			10	state5,cn=3	TZ_SNJ0016	SEA	Sonjo	1
			3	state5,cn=3	KE_SEA0015	SEA	SEA	1
			5	state5,cn=3	ZW_MSH0018	SEA	Mashona	1
			17	state2,cn=1	ML_SDN0006	NWA	Soundanaise	0
EDNRA	ACGCTCTC	GTGGAGAAA	2		control			
			4	cn=2	MG_SOF0021	MAD	Sofia	0
			2	cn=2	ML_GUE0011	NWA	Guera	1
			3	cn=2	ET_ABR0011	SEA	Abergelle	0
			18	state5,cn=3	MG_AND0006	MAD	Androy	1
			24	state5,cn=3	KE_GAL0011	SEA	Galla	1
			33	state5,cn=3	ET_GUM0023	SEA	Gumez	1
NR3C2	CGACTTGT	GAAACTTAA	2		control			
			1	cn=2	TZ_SNJ0016	SEA	Sonjo	0
			2	cn=2	ET_ABR0027	SEA	Abergelle	1
			2	cn=2	KE_GAL0011	SEA	Galla	1
			22	state5,cn=3	MG_SOF0021	MAD	Sofia	1
			13	state5,cn=3	ML_GUE0011	NWA	Guera	1
			1	state5,cn=3	ET_ABR0011	SEA	Abergelle	0
DGAT1	CCAAATTG	GTCCTGCTC	2		control			
			2	cn=2	MG_AND0006	MAD	Androy	1
			1	cn=2	ML_GUE0011	NWA	Guera	0
			2	cn=2	KE_GAL0011	SEA	Galla	1
			1	state2,cn=1	MG_SOF0024	MAD	Sofia	1
			1	state2,cn=1	TZ_MAA0005	SEA	Maasai	1
			2	state2,cn=1	ML_SDN0006	NWA	Soundanaise	0
			2	state1,cn=0	ML_GUE0024	NWA	Guera	0

Comment:

Gene: Primers for MC1R(reference gene): Forward Primer Seq: CTCGTTGGCCTCTTCATAGC; Reverse Primer Seq: GAAGTTCTTGAAGATGCAGCC

CN_qPCR: Copy number was caculated by the 2X2-ΔΔCT method using qPCR. Control mean the reference samples selected from outgroup, which included three Saanen and three Alpine goats.

CN_PENCNV: CNV call results by PennCNV. cn=2 mean copy number normal; state1,cn=0 and state2,cn=1 mean copy number loss; state5,cn=3 mean copy number gain.

Validation result: 1 mean the gene copy number status caculated by two methods were consistant in terms of CNV direction, while 0 mean they were not consistant. The accuracy percent (57%)=Number of consistan (20)/Number of total tests (35)