

Table S1. Primer sequences and position used for AS-PCR.

CSN2- Amplified Fragment	Position	Primer Sequence (5'-3')	Primer Name
Partial intron 6 - partial exon 7	8470-8495 *	F: AGGAGGATAATTCATCATGAATAACA	CSN2
	Complementary to 8914 - 8932 **	R: CAGGCAGAACTTTGGGCT <u>A</u>	CSN201
	Complementary to 8915- 8932 *	R: AGGCAGAACTTTGGGCT <u>G</u>	CSN2N

* Numbering of primers was according to the goat *CSN2* sequence (AJ011018.3)

** Numbering of primer is according to the goat *CSN2* sequence (AJ011019.3)

Table S2. Comparison of the allele frequencies for the *CSN1S1* locus in different Italian goat breeds.

Goat Breed	<i>CSN1S1</i>						References
	F	N	B*	A*	E	01	
Capestrina	0.5700	- ¹	0.2600	0.170	-	-	Present work
Bianca Monticellana	0.4260	0.004	0.2800	0.2800	-	-	Present work
Ciociara	0.3800	-	0.3900	0.2400	-	-	Present work
Napoletana	0.3680	0.227	0.1800	0.1420	0.0830	-	[2]
Saanen	0.1400	-	0.0600	0.3500	0.4300	0.0200	[49]
Camosciata Alpina	0.1100	-	0.1500	0.5600	0.1800	-	[49]
Girgentana	0.2900	0.047	0.0650	0.5900	0.008	-	[63]
Sarda	0.2420	0.006	0.5200	0.2020	0.0300	0.0010	[25]
Argentata dell'Etna	0.3690	-	0.6310		-	-	[41]
Rossa Mediterranea	0.480	-	0.5200		-	-	[64]
Vallesana	0.3860	-	0.1270	0.0300	0.2830	0.1750	[42]
Roccaverano	0.3770	0.0190	0.1170	0.2270	0.2140	0.0450	[42]
Jonica	0.2820	-	0.3050	0.3500	0.0640	-	[42]
Garganica	0.2281	0.0088	0.2807	0.4298	0.0175	0.0351	[56]
Maltese	0.3710	-	0.1570	0.4140	0.0570	-	[42]
Frisa	0.5570	-	0.0070	0.1290	0.2000	0.1070	[46]
Orobica	0.9620	-	0.0080	-	0.0080	0.0230	[46]
Verzasca	0.7540	-	0.0370	-	0.2010	0.0070	[46]

¹:- allele frequency = 0.



Figure S1. (a) flock of Bianca Monticellana goat breed that goes to pasture; (b) Capestrina goat at the recovery; (c) Ciociara Grigia goat breed at the pasture.

aggaggataattcatcatgaataacaattataactggattatggactcaaagatttttttcttctttccag

D E L Q D K I H P F A Q A Q S L V Y P F T G P I P N S
GATGAACTCCAGGATAAAATCCACCCCTTTGCCCAGGCACAGTCTCTAGTCTATCCCTTCACTGGGCCCATCCCTAACAG

L P Q N I L P L T Q T P V V V P P F L Q P E I M G V
CCTCCACAAAACATCCTGCCTCTTACTCAAACCCCTGTGGTGGTGCCGCCTTTCCTTCAGCCTGAAATAATGGGAGTCC

P K V K E T M V P K H K E M P F P K Y P V E P F T E S
CCAAAGTGAAGGAGACTATGGTTCCTAAGCACAAAGAAATGCCCTTCCCTAAATATCCAGTTGAGCCCTTTACTGAAAGC

Q S L T L T D V E K L H L P L P L V Q S W M H Q P P Q
CAGAGCCTGACTCTCACTGATGTTGAAAAGCTGCACCTTCTGCTCTGGTCCAGTCTTGGATGCACCAGCCTCCCCA

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P L S P T V M F P P Q S V L S L S Q P K V L P V P Q
GCCTCTTCTCCAACCGTCATGTTTCCTCCTCAGTCCGTGCTGTCCCTTTCTCAGCCCAAAGTTCTGCCTGTTCCTCCAGA

A T
Y *

K A V P Q R D M P I Q A F L L Y Q E P V L G P V R G P
AAGCAGTGCCCCAGAGAGATATGCCCATCCAGGCCTTTCTGCTGTACCAGGAGCCTGTACTTGGTCCTGTCCGGGGACCC

F P I L
TTCCCTATTCTTgtaagtctaaatttactaactgtgctgtttaacttctgatgtttgtatgatatttgagtaattaagag

ccctacaaaaaatcaataatgaatggttccaaaataagcatagctgagattaatgattctcagcattagttataaaataga

ataagctggaaaac

Figure S2. The goat CSN2 exon 7 nucleotide sequence (capital letters) plus the partial intron flanking region (small letters). Primer sequences for AS-PCR reported by Ramunno *et al.* (1995) are double underlined. Amino acid sequence is in uppercase and bold letters. Primer sequences for AS-PCR reported in this work are boxed. Transversion AJ011018.3:g.8913C>T responsible for the amino acid exchange p.Ser166>Tyr in the mature protein encoded by CSN2^E allele is highlighted in gray. CSN2⁰¹ premature stop codon is symbolized by *.

References

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