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Table S1. NCBI sample identifier, country of origin and productive purpose of the domestic sheep and mouflon individuals analysed in the current work.

Species	**SRA**	**Biosample**	**Breed**	**Sex**	**Country**	**Continent**	**Production purpose**
Ovis aries	ERR232488	ERS154776	Local populations	F	Morocco	Africa	Unknown
Ovis aries	ERR234302	ERS154782	Timahdite	F	Morocco	Africa	Meat and wool
Ovis aries	ERR234307	ERS154764	Sardi	F	Morocco	Africa	Meat
Ovis aries	ERR266271	ERS154746	Sardi	M	Morocco	Africa	Meat
Ovis aries	ERR277075	ERS154834	Local populations	F	Morocco	Africa	Unknown
Ovis aries	ERR283420	ERS154726	Local populations	F	Morocco	Africa	Unknown
Ovis aries	ERR283425	ERS154709	Local populations	M	Morocco	Africa	Unknown
Ovis aries	ERR283428	ERS154734	D'man	M	Morocco	Africa	Meat and mannure
Ovis aries	ERR296823	ERS154724	Local populations	F	Morocco	Africa	Unknown
Ovis aries	ERR299455	ERS154805	Local populations	F	Morocco	Africa	Unknown
Ovis aries	SRR501883	SRS335688	Castellana	-	Spain	Europe	Meat, milk and wool
Ovis aries	SRS2478867	SRS2478867	Border Leicester	F	UK	Europe	Meat and wool
Ovis aries	SRS2478943	SRS2478943	Merino Horned	M	Spain	Europe	Wool
Ovis aries	SRS2479022	SRS2479022	Dorset Horned	M	UK	Europe	Meat
Ovis aries	SRS2479095	SRS2479095	Border Leicester	M	UK	Europe	Meat and wool
Ovis aries	SRS2479115	SRS2479115	Texel	M	The Nether lands	Europe	Meat
Ovis aries	SRS335707	SRS335707	Castellana	-	Spain	Europe	Meat, milk and wool
Ovis aries	SRS335729	SRS335729	Cheviot	-	UK	Europe	Meat and wool
Ovis aries	SRS335733	SRS335733	Swiss White Alpine	-	Switzer land	Europe	Meat
Ovis aries	SRS335741	SRS335741	Ojalada	-	Spain	Europe	Meat
Ovis aries	SRS2184233	SRS2184233	Barag Sheep	M	Mongolia	South and East Asia	Meat, milk and wool
Ovis aries	SRS2184234	SRS2184234	Barag Sheep	M	Mongolia	South and East Asia	Meat, milk and wool
Ovis aries	SRS335677	SRS335677	Eastern Tibetan	-	China	South and East Asia	Meat

Ovis aries	SRS335686	SRS335686	Bangladeshi	-	Bangladesh	South and East Asia	Meat
Ovis aries	SRS335689	SRS335689	Changthangi	-	China	South and East Asia	Mutton, wool, pelt, manure
Ovis aries	SRS335718	SRS335718	Garut	-	Indonesia	South and East Asia	Meat
Ovis aries	SRS335721	SRS335721	Norduz	-	Turkey	West Asia	Meat and milk
Ovis aries	SRS335727	SRS335727	Changthangi	-	China	South and East Asia	Mutton, wool, pelt, manure
Ovis aries	SRS335736	SRS335736	Indian Garole	-	India	South and East Asia	Meat
Ovis aries	ERX270550	ERS239054	Local	-	Iran	West Asia	Unknown
Ovis aries	ERX270551	ERS239053	Local	-	Iran	West Asia	Unknown
Ovis aries	ERX270553	ERS239057	Local	-	Iran	West Asia	Unknown
Ovis aries	ERX270554	ERS239047	Local	-	Iran	West Asia	Unknown
Ovis aries	ERX270555	ERS239052	Local	-	Iran	West Asia	Unknown
Ovis aries	ERX272603	ERS239055	Local	M	Iran	West Asia	Unknown
Ovis aries	ERX272605	ERS239056	Local	M	Iran	West Asia	Unknown
Ovis aries	ERX286344	ERS239049	Local	F	Iran	West Asia	Unknown
Ovis aries	ERX286349	ERS239046	Local	F	Iran	West Asia	Unknown
Ovis aries	ERX286361	ERS239050	Local	F	Iran	West Asia	Unknown
Ovis aries	SRS335723	SRS335723	Awassi	-	Turkey	West Asia	Meat, milk and wool
Ovis Orientalis	ERS154526	ERS154526	Mouflon	M	Iran-Tabriz	West Asia	Wild
Ovis orientalis	ERS154527	ERS154527	Mouflon	M	Iran-Tehran	West Asia	Wild
Ovis orientalis	ERS154528	ERS154528	Mouflon	M	Iran-Tehran	West Asia	Wild
Ovis orientalis	ERS154529	ERS154529	Mouflon	M	Iran-Tehran	West Asia	Wild
Ovis orientalis	ERS154530	ERS154530	Mouflon	M	Iran-Tehran	West Asia	Wild
Ovis orientalis	ERS154531	ERS154531	Mouflon	M	Iran-Tabriz	West Asia	Wild
Ovis orientalis	ERS154532	ERS154532	Mouflon	M	Iran-Tehran	West Asia	Wild
Ovis orientalis	ERS154533	ERS154533	Mouflon	F	Iran-Tabriz	West Asia	Wild
Ovis orientalis	ERS239022	ERS239022	Mouflon	M	Iran-Tabriz	West Asia	Wild
Ovis orientalis	ERS239058	ERS239058	Mouflon	M	Iran-Tehran	West Asia	Wild
Ovis orientalis	ERS239059	ERS239059	Mouflon	M	Iran-Tehran	West Asia	Wild

Ovis orientalis	ERS239060	ERS239060	Mouflon	F	Iran-Tabriz	West Asia	Wild
Ovis orientalis	ERS239061	ERS239061	Mouflon	M	Iran-Tabriz	West Asia	Wild
Ovis orientalis	ERS239062	ERS239062	Mouflon	M	Iran-Tabriz	West Asia	Wild
Ovis orientalis	ERS239063	ERS239063	Mouflon	F	Iran-Tabriz	West Asia	Wild
Ovis orientalis	ERS419580	ERS419580	Mouflon	F	Iran-Tabriz	West Asia	Wild
Ovis orientalis	ERS419581	ERS419581	Mouflon	M	Iran-Tabriz	West Asia	Wild

Table S2. Number of individuals per breed with available whole-genome sequences.

Continent	**Country of Origin od the Breed**	**Breed**	**Number of animals**
Africa	Morocco	Timahdite	1
Africa	Morocco	Sardi	2
Africa	Morocco	D'man	1
Africa	Morocco	Local populations	6
Europe	Spain	Castellana	2
Europe	Spain	Merino Horned	1
Europe	UK	Dorset Horned	1
Europe	Netherlands	Texel	1
Europe	UK	Cheviot	1
Europe	Switzerland	Swiss white alpine	1
Europe	Spain	Ojalada	1
Europe	UK	Border Leicester	2
South and East Asia	Mongolia	Barag Sheep	2
South and East Asia	China	Eastern Tibetan	1
South and East Asia	Bangladesh	Bangladeshi	1
South and East Asia	Indonesia	Garut	1
South and East Asia	China	Changthangi	2
South and East Asia	India	Indian Garole	1
West Asia	Iran	Unknown	10
West Asia	Saudi Arabia/Syria/Lebanon/ Israel/Jordan	Awassi	1
West Asia	Turkey	Norduz	1

Table S3. Single nucleotide polymorphisms (SNPs) identified in domestic sheep populations from North Africa, West Asia, Europe and South and East Asia and in Iranian mouflon populations from Tehran and Tabriz.

Gene	Position (bp)	A1	A2	nt Substitution	Aa Substitution	Presence*	MAF Sheep†	MAF Mouflon‡
CSN1S1	85089520	G	T	c.34G>T	p.Val12Phe	S	0.050	-
	85089563	A	T	c.51+26A>T	-	B	0.125	0.029
	85089636	C	T	c.51+99C>T	-	B	0.250	0.059
	85089637	G	A	c.51+100G>A	-	M	-	0.059
	85089648	G	A	c.51+111G>A	-	M	-	0.029
	85089673	T	A	c.51+136T>A	-	M	-	0.029
	85089725	T	C	c.51+188T>C	-	B	0.100	0.029
	85089735	G	T	c.51+198G>T	-	S	0.372	-
	85089777	C	T	c.51+240C>T	-	B	0.050	0.088
	85089940	T	G	c.51+403T>G	-	B	0.077	0
	85089962	C	T	c.51+425C>T	-	B	0.141	0.382
	85089985	A	C	c.51+448A>C	-	M	-	0.029
	85089990	C	G	c.51+453C>G	-	M	-	0.029
	85090100	G	A	c.51+563G>A	-	M	-	0.029
	85090116	G	A	c.51+579G>A	-	S	0.050	-
	85090231	G	C	c.51+694G>C	-	M	-	0.029
	85090239	T	A	c.51+702T>A	-	B	0.075	0.029
	85090311	A	T	c.51+774A>T	-	M	-	0.029
	85090392	A	C	c.52-830A>C	-	M	-	0.029
	85090417	A	G	c.52-805A>G	-	M	-	0.029
	85090540	G	A	c.52-682G>A	-	S	0.050	-
	85090565	G	A	c.52-657G>A	-	M	-	0.029
	85090591	T	G	c.52-631T>G	-	B	0.154	0.353
	85090606	C	A	c.52-616C>A	-	S	0.111	-
	85090627	A	T	c.52-595A>T	-	S	0.100	-
	85090725	G	T	c.52-497G>T	-	M	-	0.088
	85090734	G	A	c.52-488G>A	-	M	-	0.029
	85091006	C	T	c.52-216C>T	-	B	0.224	0.177
	85091074	G	A	c.52-148G>A	-	B	0.100	0.353
	85091080	C	T	c.52-142C>T	-	M	-	0.029
	85091147	T	C	c.52-75T>C	-	M	-	0.029
	85091243	G	A	c.73G>A	p.Gly25Arg	M	-	0.029
	85091277	C	T	c.84+23C>T	-	B	0.118	0.353
	85091300	A	G	c.84+46A>G	-	B	0.111	0.324
	85091414	A	C	c.84+160A>C	-	S	0.050	-

	85091466	A	G	c.84+212A>G	-	B	0.051	0
	85091514	C	A	c.84+260C>A	-	M	-	0.029
	85091568	T	C	c.84+314T>C	-	M	-	0.029
	85091736	G	A	c.85-412G>A	-	S	0.050	-
	85091742	T	A	c.85-406T>A	-	M	-	0.029
	85091788	G	T	c.85-360G>T	-	S	0.050	-
	85091889	A	G	c.85-259A>G	-	S	0.050	-
	85091924	G	T	c.85-224G>T	-	M	-	0.029
	85091968	C	T	c.85-180C>T	-	M	-	0.029
	85092039	A	G	c.85-109A>G	-	M	-	0.029
	85092091	A	G	c.85-57A>G	-	M	-	0.088
	85092186	G	A	c.123G>A	p.Ala41Ala	M	-	0.029
	85092207	T	C	c.123+21T>C	-	M	-	0.029
	85092276	C	T	c.123+90C>T	-	B	0.108	0
	85092293	T	C	c.123+107T>C	-	M	-	0.029
	85092296	C	T	c.123+110C>T	-	M	-	0.088
	85092331	A	G	c.123+145A>G	-	M	-	0.031
	85092472	T	C	c.124-161T>C	-	B	0.103	0
	85092477	C	T	c.124-156C>T	-	M	-	0.029
	85092529	C	T	c.124-104C>T	-	M	-	0.031
	85092586	C	T	c.124-47C>T	-	S	0.050	-
	85092603	G	T	c.124-30G>T	-	M	-	0.029
	85092728	A	G	c.147+72A>G	-	M	-	0.031
	85092737	A	T	c.147+81A>T	-	B	0.090	0
	85092819	C	T	c.147+163C>T	-	M	-	0.029
	85092878	T	C	c.148-203T>C	-	M	-	0.029
	85092922	A	T	c.148-159A>T	-	M	-	0.029
	85092936	G	T	c.148-145G>T	-	M	-	0.029
	85092941	C	T	c.148-140C>T	-	B	0.083	0.029
	85092942	G	A	c.148-139G>A	-	M	-	0.125
	85092987	A	G	c.148-94A>G	-	M	-	0.031
	85093004	T	C	c.148-77T>C	-	B	0.203	0.281
	85093043	C	G	c.148-38C>G	-	M	-	0.029
	85093046	T	C	c.148-35T>C	-	B	0.095	0.206
	85093144	C	T	c.171+40C>T	-	M	-	0.029
	85093157	A	T	c.171+53A>T	-	M	-	0.029
	85093185	C	A	c.171+81C>A	-	B	0.090	0
	85093200	A	G	c.171+96A>G	-	M	-	0.029
	85093228	A	G	c.171+124A>G	-	M	-	0.029
	85093259	G	T	c.171+155G>T	-	M	-	0.029
	85093266	G	A	c.171+162G>A	-	M	-	0.125
	85093287	A	G	c.171+183A>G	-	M	-	0.031
	85093331	T	C	c.171+227T>C	-	M	-	0.029

	85093360	C	A	c.171+256C>A	-	M	-	0.029
	85093375	T	A	c.171+271T>A	-	B	0.053	0
	85093378	A	T	c.171+274A>T	-	B	0.067	0.029
	85093411	A	G	c.172-301A>G	-	M	-	0.029
	85093482	T	C	c.172-230T>C	-	B	0.372	0.029
	85093557	G	A	c.172-155G>A	-	M	-	0.029
	85093629	G	A	c.172-83G>A	-	M	-	0.029
	85093641	A	C	c.172-71A>C	-	M	-	0.029
	85093666	G	T	c.172-46G>T	-	M	-	0.029
	85093698	T	C	c.172-14T>C	-	M	-	0.029
	85093723	T	C	c.183T>C	p.Ser61Ser	M	-	0.029
	85093731	T	C	c.191T>C	p.Ile64Thr	M	-	0.029
	85093775	T	G	c.195+40T>G	-	M	-	0.029
	85093777	A	G	c.195+42A>G	-	M	-	0.029
	85093889	A	C	c.195+154A>C	-	M	-	0.029
	85093942	T	C	c.195+207T>C	-	M	-	0.029
	85093978	T	C	c.195+243T>C	-	M	-	0.118
	85093999	G	C	c.195+264G>C	-	M	-	0.029
	85094058	C	G	c.195+323C>G	-	M	-	0.029
	85094061	T	C	c.195+326T>C	-	M	-	0.029
	85094084	T	A	c.196-345T>A	-	M	-	0.059
	85094092	G	A	c.196-337G>A	-	M	-	0.029
	85094118	T	C	c.196-311T>C	-	M	-	0.088
	85094148	A	G	c.196-281A>G	-	M	-	0.029
	85094183	A	G	c.196-246A>G	-	M	-	0.029
	85094193	A	G	c.196-236A>G	-	M	-	0.029
	85094209	T	C	c.196-220T>C	-	M	-	0.029
	85094237	G	A	c.196-192G>A	-	M	-	0.029
	85094249	A	C	c.196-180A>C	-	M	-	0.029
	85094276	A	G	c.196-153A>G	-	B	0.066	0
	85094280	G	C	c.196-149G>C	-	M	-	0.029
	85094297	T	A	c.196-132T>A	-	S	0.056	-
	85094298	T	A	c.196-131T>A	-	B	0.039	0
	85094313	G	C	c.196-116G>C	-	M	-	0.029
	85094317	T	A	c.196-112T>A	-	M	-	0.029
	85094318	C	G	c.196-111C>G	-	S	0.050	-
	85094325	C	T	c.196-104C>T	-	M	-	0.029
	85094377	T	C	c.196-52T>C	-	M	-	0.029
	85094378	A	T	c.196-51A>T	-	B	0.050	0.353
	85094390	G	T	c.196-39G>T	-	M	-	0.088
	85094394	T	C	c.196-35T>C	-	M	-	0.029
	85094448	C	T	c.215C>T	p.Ala72Val	M	-	0.029
	85094463	T	C	c.219+11T>C	-	B	0.067	0.029

	85094465	T	A	c.219+13T>A	-	M	-	0.029
	85094490	T	G	c.219+38T>G	-	M	-	0.029
	85094497	C	T	c.219+45C>T	-	M	-	0.029
	85094511	C	T	c.219+59C>T	-	M	-	0.029
	85094530	G	A	c.219+78G>A	-	S	0.269	-
	85094533	G	C	c.219+81G>C	-	M	-	0.029
	85094594	C	T	c.219+142C>T	-	M	-	0.029
	85094598	A	G	c.219+146A>G	-	M	-	0.118
	85094874	C	T	c.219+422C>T	-	S	0.067	-
	85094876	C	T	c.219+424C>T	-	B	0.067	0.059
	85095036	C	T	c.219+584C>T	-	B	0.067	0.059
	85095255	C	T	c.220-671C>T	-	B	0.067	0.147
	85095336	A	C	c.220-590A>C	-	M	-	0.118
	85095431	T	C	c.220-495T>C	-	S	0.111	-
	85095600	G	A	c.220-326G>A	-	S	0.100	-
	85095614	T	C	c.220-312T>C	-	B	0.145	0.324
	85095648	G	A	c.220-278G>A	-	M	-	0.029
	85095664	T	G	c.220-262T>G	-	M	-	0.118
	85095758	A	T	c.220-168A>T	-	M	-	0.088
	85095774	C	A	c.220-152C>A	-	M	-	0.177
	85095964	C	T	c.252+6C>T	-	B	0.363	0.177
	85096021	C	T	c.252+63C>T	-	M	-	0.029
	85096112	A	C	c.252+154A>C	-	M	-	0.059
	85096211	T	C	c.252+253T>C	-	B	0.071	0.029
	85096282	C	T	c.252+324C>T	-	B	0.050	0.324
	85096320	C	T	c.252+362C>T	-	M	-	0.029
	85096321	G	A	c.252+363G>A	-	S	0.100	-
	85096390	G	A	c.253-319G>A	-	M	-	0.118
	85096397	C	T	c.253-312C>T	-	S	0.288	-
	85096673	A	G	c.253-36A>G	-	M	-	0.118
	85096778	C	A	c.277-45C>A	-	B	0.053	0
	85096807	T	G	c.277-16T>G	-	B	0.125	0.029
	85096949	A	G	c.330+73A>G	-	M	-	0.029
	85096960	T	C	c.330+84T>C	-	M	-	0.177
	85096975	C	T	c.330+99C>T	-	B	0.397	0.353
	85096987	C	T	c.330+111C>T	-	S	0.050	-
	85097042	T	C	c.330+166T>C	-	M	-	0.029
	85097061	T	G	c.330+185T>G	-	M	-	0.029
	85097082	T	C	c.330+206T>C	-	B	0.375	0.059
	85097138	G	T	c.330+262G>T	-	M	-	0.029
	85097187	C	T	c.330+311C>T	-	B	0.075	0.088
	85097188	G	A	c.330+312G>A	-	M	-	0.353
	85097190	C	T	c.330+314C>T	-	M	-	0.029

	85097289	A	G	c.330+413A>G	-	M	-	0.471
	85097290	C	A	c.330+414C>A	-	B	0.192	0.412
	85097394	A	G	c.330+518A>G	-	M	-	0.029
	85097611	T	C	c.331-580T>C	-	M	-	0.088
	85097743	A	T	c.331-448A>T	-	B	0.067	0.088
	85097753	G	A	c.331-438G>A	-	B	0.067	0.088
	85097769	C	T	c.331-422C>T	-	M	-	0.059
	85097796	T	C	c.331-395T>C	-	M	-	0.059
	85097893	G	T	c.331-298G>T	-	M	-	0.029
	85097997	A	C	c.331-194A>C	-	M	-	0.147
	85098007	A	C	c.331-184A>C	-	M	-	0.147
	85098139	C	A	c.331-52C>A	-	M	-	0.059
	85098331	C	T	c.372+99C>T	-	M	-	0.029
	85098357	G	A	c.372+125G>A	-	M	-	0.059
	85098411	A	C	c.372+179A>C	-	S	0.079	-
	85098734	T	A	c.373-141T>A	-	M	-	0.063
	85098735	G	A	c.373-140G>A	-	M	-	0.063
	85098760	T	A	c.373-115T>A	-	M	-	0.029
	85098789	G	A	c.373-86G>A	-	B	0.056	0.088
	85098805	A	G	c.373-70A>G	-	M	-	0.029
	85098887	A	C	c.385A>C	p.Lys129Gln	M	-	0.147
	85098951	A	G	c.396+53A>G	-	M	-	0.059
	85098984	T	C	c.396+86T>C	-	M	-	0.059
	85099015	G	A	c.396+117G>A	-	S	0.359	-
	85099136	A	G	c.396+238A>G	-	B	0.474	0.382
	85099166	A	T	c.396+268A>T	-	M	-	0.324
	85099191	A	G	c.396+293A>G	-	M	-	0.029
	85099228	G	A	c.396+330G>A	-	S	0.050	-
	85099325	T	G	c.396+427T>G	-	S	0.150	-
	85099413	T	C	c.396+515T>C	-	M	-	0.088
	85099466	A	G	c.396+568A>G	-	B	0.069	0.031
	85099518	C	T	c.397-578C>T	-	S	0.050	-
	85099664	T	C	c.397-432T>C	-	M	-	0.031
	85099722	T	A	c.397-374T>A	-	B	0.434	0.250
	85099826	T	A	c.397-270T>A	-	B	0.500	0.125
	85099867	T	C	c.397-229T>C	-	M	-	0.294
	85099884	C	T	c.397-212C>T	-	M	-	0.059
	85099917	T	A	c.397-179T>A	-	M	-	0.059
	85099985	T	G	c.397-111T>G	-	B	0.141	0.033
	85099992	G	T	c.397-104G>T	-	M	-	0.033
	85100013	T	G	c.397-83T>G	-	S	0.125	-
	85100107	T	C	c.408T>C	p.His136His	B	0.069	0.406
	85100166	T	C	c.438+29T>C	-	M	-	0.063

	85100198	C	G	c.438+61C>G	-	M	-	0.063
	85100403	T	C	c.438+266T>C	-	M	-	0.313
	85100448	C	A	c.438+311C>A	-	M	-	0.469
	85100500	A	G	c.438+363A>G	-	M	-	0.067
	85100505	A	G	c.438+368A>G	-	S	0.050	-
	85100525	C	T	c.438+388C>T	-	M	-	0.313
	85100541	C	T	c.438+404C>T	-	B	0.400	0.250
	85100634	C	G	c.439-404C>G	-	M	-	0.031
	85100719	C	T	c.439-319C>T	-	B	0.438	0.250
	85100727	T	C	c.439-311T>C	-	M	-	0.031
	85100748	T	C	c.439-290T>C	-	M	-	0.059
	85100809	C	T	c.439-229C>T	-	M	-	0.059
	85100847	C	A	c.439-191C>A	-	M	-	0.029
	85100850	A	G	c.439-188A>G	-	B	0.463	0.265
	85101085	G	T	c.465+21G>T	-	B	0.475	0.125
	85101182	C	T	c.465+118C>T	-	S	0.050	-
	85101321	A	G	c.465+257A>G	-	B	0.075	0.063
	85101325	A	G	c.465+261A>G	-	M	-	0.063
	85101353	G	A	c.465+289G>A	-	B	0.436	0.313
	85101618	C	T	c.466-392C>T	-	B	0.052	0.188
	85101636	A	T	c.466-374A>T	-	M	-	0.094
	85101647	C	T	c.466-363C>T	-	S	0.050	-
	85101779	C	T	c.466-231C>T	-	B	0.069	0.067
	85101820	A	G	c.466-190A>G	-	S	0.050	-
	85101875	T	A	c.466-135T>A	-	S	0.050	-
	85101883	T	C	c.466-127T>C	-	M	-	0.067
	85101891	A	T	c.466-119A>T	-	B	0.475	0.267
	85101968	G	T	c.466-42G>T	-	M	-	0.031
	85102013	C	T	c.469C>T	p.Leu157Leu	B	0.052	0.094
	85102070	G	C	c.489+37G>C	-	M	-	0.033
	85102103	G	A	c.489+70G>A	-	M	-	0.100
	85102281	A	G	c.489+248A>G	-	B	0.487	0.333
	85102282	T	G	c.489+249T>G	-	B	0.461	0.133
	85102297	C	T	c.489+264C>T	-	M	-	0.031
	85102426	A	T	c.489+393A>T	-	M	-	0.029
	85102550	C	A	c.490-279C>A	-	B	0.184	0.100
	85102558	G	A	c.490-271G>A	-	S	0.367	-
	85102580	A	G	c.490-249A>G	-	M	-	0.344
	85102582	T	C	c.490-247T>C	-	M	-	0.344
	85102707	A	G	c.490-122A>G	-	M	-	0.033
	85102787	T	G	c.490-42T>G	-	S	0.100	-
CSN1S2	85184193	G	A	c.34G>A	p.Val12Ile	M	-	0.059
	85184295	C	T	c.51+85C>T	-	B	0.180	0.206

	85184324	T	C	c.51+114T>C	-	B	0.176	0.118
	85184355	C	T	c.51+145C>T	-	S	0.050	-
	85184418	A	G	c.51+208A>G	-	B	0.462	0.059
	85184432	T	A	c.51+222T>A	-	S	0.050	-
	85184452	G	A	c.51+242G>A	-	S	0.050	-
	85184483	C	T	c.51+273C>T	-	S	0.050	-
	85184498	C	T	c.51+288C>T	-	M	-	0.118
	85184549	C	T	c.51+339C>T	-	S	0.050	-
	85184550	T	G	c.51+340T>G	-	S	0.075	-
	85184552	C	A	c.51+342C>A	-	B	0.150	0.177
	85184565	G	A	c.51+355G>A	-	B	0.175	0.177
	85184566	G	A	c.51+356G>A	-	M	-	0.059
	85184591	C	A	c.51+381C>A	-	S	0.050	-
	85184593	C	A	c.51+383C>A	-	S	0.050	-
	85184607	A	G	c.51+397A>G	-	B	0.263	0.265
	85184657	C	A	c.51+447C>A	-	B	0.275	0.265
	85184662	T	A,G	c.51+452T>A	-	B	0.283	0.233
	85184677	G	A	c.51+467G>A	-	M	-	0.088
	85184687	A	G	c.51+477A>G	-	M	-	0.029
	85184689	G	T	c.51+479G>T	-	B	0.288	0.235
	85184787	T	C	c.51+577T>C	-	B	0.225	0.265
	85184788	T	C	c.51+578T>C	-	B	0.317	0.324
	85184795	A	G	c.51+585A>G	-	M	-	0.059
	85184811	C	T	c.51+601C>T	-	M	-	0.324
	85184855	G	A	c.51+645G>A	-	B	0.050	0.059
	85184872	A	G	c.51+662A>G	-	B	0.463	0.471
	85184884	G	C	c.51+674G>C	-	B	0.200	0.206
	85184935	C	T	c.51+725C>T	-	B	0.050	0.059
	85184945	T	C	c.51+735T>C	-	B	0.050	0.059
	85184948	G	T	c.51+738G>T	-	B	0.450	0.118
	85185100	G	A	c.51+890G>A	-	B	0.425	0.235
	85185118	C	T	c.51+908C>T	-	S	0.125	-
	85185122	G	A	c.51+912G>A	-	S	0.083	-
	85185123	C	A	c.51+913C>A	-	S	0.083	-
	85185182	C	T	c.52-859C>T	-	M	-	0.059
	85185186	T	C	c.52-855T>C	-	B	0.413	0.471
	85185202	A	T	c.52-839A>T	-	M	-	0.029
	85185203	A	G	c.52-838A>G	-	B	0.267	0.382
	85185206	C	A	c.52-835C>A	-	S	0.083	-
	85185228	G	T	c.52-813G>T	-	M	-	0.118
	85185332	T	A	c.52-709T>A	-	S	0.050	-
	85185378	T	C	c.52-663T>C	-	B	0.167	0.441
	85185417	A	G	c.52-624A>G	-	M	-	0.118

	85185552	T	C	c.52-489T>C	-	M	-	0.029
	85185569	T	G	c.52-472T>G	-	M	-	0.029
	85185641	G	A	c.52-400G>A	-	S	0.075	-
	85185686	A	G	c.52-355A>G	-	B	0.205	0.206
	85185690	T	C	c.52-351T>C	-	B	0.231	0.059
	85185728	C	T	c.52-313C>T	-	M	-	0.059
	85185734	T	C	c.52-307T>C	-	B	0.224	0.382
	85185735	A	C	c.52-306A>C	-	B	0.224	0.206
	85185749	G	A	c.52-292G>A	-	M	-	0.029
	85185755	A	C	c.52-286A>C	-	M	-	0.029
	85185825	T	C	c.52-216T>C	-	B	0.375	0.382
	85185877	T	G	c.52-164T>G	-	S	0.050	-
	85185950	G	A	c.52-91G>A	-	M	-	0.118
	85186016	A	G	c.52-25A>G	-	B	0.282	0.353
	85186160	A	G	c.78+93A>G	-	B	0.163	0.118
	85186169	A	G	c.78+102A>G	-	B	0.375	0.118
	85186215	A	G	c.78+148A>G	-	M	-	0.059
	85186218	T	G	c.78+151T>G	-	B	0.359	0.118
	85186382	G	C	c.78+315G>C	-	S	0.111	-
	85186396	G	A	c.78+329G>A	-	M	-	0.029
	85186427	C	A	c.78+360C>A	-	S	0.050	-
	85186428	A	G	c.78+361A>G	-	B	0.154	0.406
	85186430	C	T	c.78+363C>T	-	B	0.213	0.219
	85186466	G	A	c.79-385G>A	-	M	-	0.063
	85186531	G	A	c.79-320G>A	-	B	0.205	0.406
	85186564	A	C	c.79-287A>C	-	B	0.133	0.059
	85186582	A	G	c.79-269A>G	-	B	0.231	0.471
	85186706	G	A	c.79-145G>A	-	B	0.125	0.059
	85186789	A	G	c.79-62A>G	-	M	-	0.029
	85186812	G	A	c.79-39G>A	-	B	0.154	0.438
	85186902	T	C	c.102+28T>C	-	B	0.132	0.059
	85187019	C	T	c.144+15C>T	-	S	0.075	-
	85187172	C	T	c.144+168C>T	-	B	0.197	0.188
	85187249	T	C	c.145-140T>C	-	B	0.180	0.200
	85187326	C	G	c.145-63C>G	-	B	0.194	0.206
	85187329	C	A	c.145-60C>A	-	M	-	0.029
	85187339	A	T	c.145-50A>T	-	S	0.079	-
	85187340	T	C	c.145-49T>C	-	M	-	0.029
	85187352	G	A	c.145-37G>A	-	B	0.216	0.177
	85187376	T	A	c.145-13T>A	-	M	-	0.029
	85187436	T	A	c.171+21T>A	-	B	0.132	0.059
	85187437	A	G	c.171+22A>G	-	B	0.500	0.118
	85187471	G	C	c.171+56G>C	-	B	0.203	0.188

	85187479	C	T	c.171+64C>T	-	B	0.392	0.177
	85187712	A	G	c.171+297A>G	-	B	0.200	0.147
	85187732	A	G	c.171+317A>G	-	B	0.171	0.188
	85187752	C	G	c.171+337C>G	-	B	0.050	0.059
	85187761	T	G	c.171+346T>G	-	M	-	0.029
	85187813	A	G	c.171+398A>G	-	B	0.141	0.059
	85187843	C	T	c.172-370C>T	-	S	0.050	-
	85187915	T	C	c.172-298T>C	-	S	0.275	-
	85187997	T	C	c.172-216T>C	-	B	0.213	0.188
	85188009	C	A	c.172-204C>A	-	M	-	0.029
	85188038	C	T	c.172-175C>T	-	B	0.300	0.265
	85188219	G	A	c.178G>A	p.Val60Ile	S	0.050	-
	85188228	G	T	c.187G>T	p.Ala63Ser	S	0.050	-
	85188321	A	G	c.198+82A>G	-	S	0.275	-
	85188341	A	T	c.198+102A>T	-	B	0.410	0.265
	85188404	A	C	c.198+165A>C	-	B	0.207	0.029
	85188447	G	A	c.198+208G>A	-	B	0.487	0.118
	85188557	G	T	c.199-123G>T	-	B	0.449	0.412
	85188723	C	T	c.225+17C>T	-	B	0.269	0.471
	85188731	T	C	c.225+25T>C	-	B	0.263	0.471
	85188822	C	T	c.225+116C>T	-	B	0.100	0.353
	85188831	T	G	c.225+125T>G	-	B	0.188	0.118
	85188933	G	T	c.225+227G>T	-	B	0.450	0.147
	85189014	G	C	c.225+308G>C	-	M	-	0.118
	85189027	G	A	c.225+321G>A	-	B	0.400	0.471
	85189040	G	A	c.225+334G>A	-	M	-	0.118
	85189081	C	T	c.225+375C>T	-	B	0.188	0.088
	85189082	T	C	c.225+376T>C	-	B	0.475	0.088
	85189116	C	G	c.225+410C>G	-	S	0.050	-
	85189155	A	G	c.225+449A>G	-	M	-	0.029
	85189233	C	T	c.226-470C>T	-	M	-	0.265
	85189341	T	C	c.226-362T>C	-	B	0.217	0.088
	85189347	C	T	c.226-356C>T	-	B	0.413	0.500
	85189405	G	A	c.226-298G>A	-	S	0	-
	85189459	T	G	c.226-244T>G	-	S	0.250	-
	85189501	C	T	c.226-202C>T	-	S	0.050	-
	85189514	A	G	c.226-189A>G	-	S	0.050	-
	85189589	T	C	c.226-114T>C	-	B	0.425	0.500
	85189595	G	T	c.226-108G>T	-	S	0.050	-
	85189601	G	T	c.226-102G>T	-	S	0.050	-
	85189633	C	T	c.226-70C>T	-	M	-	0.118
	85189680	A	T	c.226-23A>T	-	M	-	0.029
	85189688	T	C	c.226-15T>C	-	B	0.400	0.500

	85189771	C	T	c.249+45C>T	-	B	0.487	0.118
	85189841	G	T	c.268G>T	p.Asp90Tyr	B	0.488	0.118
	85189843	C	T	c.270C>T	p.Asp90Asp	B	0.050	0.412
	85189864	A	C	c.291A>C	p.Ala97Ala	B	0.463	0.500
	85189890	A	T	c.294+23A>T	-	B	0.488	0.500
	85189978	C	T	c.294+111C>T	-	S	0.075	-
	85189988	C	G	c.294+121C>G	-	S	0.167	-
	85190019	C	T	c.295-110C>T	-	B	0.461	0.500
	85190074	C	T	c.295-55C>T	-	M	-	0.059
	85190109	G	C	c.295-20G>C	-	S	0.050	-
	85190117	C	G	c.295-12C>G	-	M	-	0.088
	85190123	A	C	c.295-6A>C	-	B	0.392	0.412
	85190124	T	G	c.295-5T>G	-	B	0.125	0.088
	85190178	T	C	c.344T>C	p.Leu115Pro	B	0.050	0.177
	85190187	G	A	c.353G>A	p.Gly118Asp	S	0.050	-
	85190188	C	T	c.354C>T	p.Gly118Gly	B	0.050	0.118
	85190192	A	G	c.358A>G	p.Ile120Val	B	0.447	0.059
	85190241	C	T	c.407C>T	p.Thr136Ile	M	-	0.118
	85190344	T	C	c.417+93T>C	-	B	0.474	0.063
	85190367	C	T	c.417+116C>T	-	B	0.125	0.088
	85190397	A	G	c.417+146A>G	-	S	0.050	-
	85190431	A	G	c.417+180A>G	-	M	-	0.029
	85190466	A	G	c.417+215A>G	-	B	0.117	0.324
	85190555	A	G	c.418-218A>G	-	M	-	0.059
	85190559	G	A	c.418-214G>A	-	B	0.488	0.118
	85190576	C	G	c.418-197C>G	-	B	0.488	0.059
	85190583	A	G	c.418-190A>G	-	M	-	0.118
	85190599	G	A	c.418-174G>A	-	B	0.488	0.059
	85190639	A	C	c.418-134A>C	-	B	0.488	0.059
	85190699	C	T	c.418-74C>T	-	M	-	0.059
	85190700	A	G	c.418-73A>G	-	B	0.375	0.206
	85190705	G	A	c.418-68G>A	-	S	0.188	-
	85190717	G	A	c.418-56G>A	-	S	0.050	-
	85190765	T	G	c.418-8T>G	-	B	0.474	0.059
	85190839	G	A	c.444+40G>A	-	M	-	0.118
	85190917	A	G	c.444+118A>G	-	B	0.475	0.177
	85190941	A	G	c.444+142A>G	-	M	-	0.059
	85190942	T	C	c.444+143T>C	-	M	-	0.324
	85190985	G	A	c.444+186G>A	-	M	-	0.088
	85191000	T	C	c.444+201T>C	-	M	-	0.265
	85191115	T	G	c.444+316T>G	-	B	0.397	0.324
	85191178	T	C	c.444+379T>C	-	B	0.475	0.059
	85191179	G	A	c.444+380G>A	-	B	0.375	0.324

	85191213	T	C	c.444+414T>C	-	B	0.125	0.118
	85191248	C	A,T	c.444+449C>A	-	M	-	0.133
	85191249	A	G	c.444+450A>G	-	B	0.150	0.147
	85191316	A	G	c.445-460A>G	-	B	0.363	0.324
	85191319	A	G	c.445-457A>G	-	M	-	0.118
	85191374	G	A	c.445-402G>A	-	B	0.363	0.324
	85191377	A	C	c.445-399A>C	-	B	0.488	0.300
	85191407	C	T	c.445-369C>T	-	S	0.075	-
	85191408	A	G	c.445-368A>G	-	S	0.075	-
	85191412	G	C	c.445-364G>C	-	M	-	0.118
	85191430	A	G	c.445-346A>G	-	B	0.200	0.147
	85191533	G	A	c.445-243G>A	-	M	-	0.029
	85191580	T	G	c.445-196T>G	-	S	0.050	-
	85191622	G	A	c.445-154G>A	-	B	0.363	0.265
	85191772	C	T	c.445-4C>T	-	B	0.132	0.147
	85191773	G	A	c.445-3G>A	-	B	0.180	0.233
	85191900	G	A	c.471+98G>A	-	B	0.487	0.059
	85191935	C	A	c.471+133C>A	-	M	-	0.118
	85191937	G	C	c.471+135G>C	-	B	0.405	0.324
	85191956	C	T	c.471+154C>T	-	M	-	0.118
	85191962	A	G	c.471+160A>G	-	M	-	0.118
	85191997	C	T	c.471+195C>T	-	B	0.388	0.235
	85192039	C	T	c.471+237C>T	-	B	0.385	0.324
	85192123	G	A	c.471+321G>A	-	B	0.421	0.324
	85192173	C	T	c.471+371C>T	-	S	0.050	-
	85192192	C	T	c.471+390C>T	-	M	-	0.029
	85192193	T	C	c.471+391T>C	-	M	-	0.147
	85192221	T	A	c.471+419T>A	-	B	0.117	0.088
	85192408	G	A	c.471+606G>A	-	B	0.385	0.324
	85192451	A	G	c.471+649A>G	-	M	-	0.029
	85192635	G	A	c.471+833G>A	-	B	0.125	0.118
	85192639	A	T	c.471+837A>T	-	B	0.413	0.324
	85192790	C	T	c.472-709C>T	-	B	0.475	0.059
	85192805	G	A	c.472-694G>A	-	S	0.050	-
	85192826	C	A	c.472-673C>A	-	B	0.500	0.059
	85192837	T	C	c.472-662T>C	-	B	0.487	0.177
	85192840	T	A	c.472-659T>A	-	B	0.125	0.059
	85192853	G	A	c.472-646G>A	-	B	0.200	0.088
	85192904	A	G	c.472-595A>G	-	S	0.275	-
	85192932	T	A	c.472-567T>A	-	B	0.125	0.059
	85192971	A	C	c.472-528A>C	-	B	0.388	0.265
	85192972	G	A	c.472-527G>A	-	B	0.388	0.265
	85192977	C	T	c.472-522C>T	-	M	-	0.118

	85192988	C	T	c.472-511C>T	-	M	-	0.059
	85192998	A	T	c.472-501A>T	-	S	0.075	-
	85193026	T	C	c.472-473T>C	-	B	0.200	0.059
	85193036	A	G	c.472-463A>G	-	B	0.487	0.177
	85193068	G	A	c.472-431G>A	-	S	0.050	-
	85193123	C	T	c.472-376C>T	-	B	0.488	0.059
	85193139	A	C	c.472-360A>C	-	B	0.475	0.177
	85193186	G	C	c.472-313G>C	-	B	0.372	0.353
	85193197	C	T	c.472-302C>T	-	M	-	0.029
	85193245	T	C	c.472-254T>C	-	S	0.050	-
	85193248	G	A	c.472-251G>A	-	B	0.400	0.353
	85193293	T	C	c.472-206T>C	-	M	-	0.029
	85193310	C	T	c.472-189C>T	-	B	0.474	0.059
	85193388	C	A	c.472-111C>A	-	B	0.500	0.059
	85193436	T	C	c.472-63T>C	-	S	0.050	-
	85193438	T	C	c.472-61T>C	-	B	0.145	0
	85193443	A	G	c.472-56A>G	-	M	-	0.029
	85193455	A	G	c.472-44A>G	-	B	0.405	0.265
	85193481	A	T	c.472-18A>T	-	S	0.444	-
	85193514	T	G	c.487T>G	p.Phe163Val	M	-	0.059
	85193587	T	C	c.496-26T>C	-	M	-	0.029
	85193604	C	T	c.496-9C>T	-	B	0.375	0.441
	85193644	G	A	c.527G>A	p.Arg176His	B	0.238	0.059
	85193790	T	G	c.540+133T>G	-	M	-	0.118
	85193812	A	G	c.540+155A>G	-	B	0.487	0.500
	85193837	C	T	c.540+180C>T	-	S	0.050	-
	85193862	C	T	c.540+205C>T	-	S	0.050	-
	85193882	A	C	c.540+225A>C	-	B	0.180	0.088
	85194005	G	A	c.540+348G>A	-	M	-	0.294
	85194044	T	G	c.540+387T>G	-	B	0.270	0.344
	85194089	T	C	c.541-375T>C	-	S	0.063	-
	85194102	G	T	c.541-362G>T	-	M	-	0.088
	85194144	G	A	c.541-320G>A	-	B	0.338	0.235
	85194162	C	T	c.541-302C>T	-	M	-	0.059
	85194163	G	T	c.541-301G>T	-	B	0.075	0.029
	85194251	A	G	c.541-213A>G	-	B	0.308	0.438
	85194568	C	T,G	c.645C>G	p.Asn215Lys	M	-	0.063
	85194597	T	A	c.660+14T>A	-	M	-	0.313
	85194618	A	G	c.660+35A>G	-	B	0.205	0.324
	85194697	T	C	c.660+114T>C	-	B	0.218	0.324
	85194811	A	G	c.660+228A>G	-	S	0.275	-
	85194905	A	G	c.660+322A>G	-	B	0.158	0
	85194980	T	C	c.661-365T>C	-	S	0.079	-

	85195006	A	G	c.661-339A>G	-	M	-	0.059
	85195033	T	C	c.661-312T>C	-	M	-	0.029
	85195142	T	A	c.661-203T>A	-	M	-	0.059
	85195214	A	G	c.661-131A>G	-	B	0.474	0.059
	85195225	C	T	c.661-120C>T	-	B	0.218	0.324
	85195226	G	A	c.661-119G>A	-	S	0.125	-
	85195250	A	T	c.661-95A>T	-	M	-	0.029
	85195305	A	G	c.661-40A>G	-	M	-	0.029
CSN2	85116838	T	C	c.679A>G	p.Thr227Ala	M	-	0.029
	85117013	C	T	c.667-163G>A	-	B	0.163	0.500
	85117090	G	C	c.666+172C>G	-	M	-	0.088
	85117091	A	G	c.666+171T>C	-	S	0.050	-
	85117166	A	G	c.666+96T>C	-	M	-	0.118
	85117168	C	A	c.666+94G>T	-	B	0.100	0.118
	85117207	A	G	c.666+55T>C	-	B	0.163	0.500
	85117294	G	T	c.634C>A	p.Leu212Ile	B	0.175	0.500
	85117313	C	A	c.615G>T	p.Leu205Leu	M	-	0.029
	85117333	T	C	c.595A>G	p.Met199Val	S	0.117	-
	85117756	G	A	c.175-3C>T	-	B	0.103	0.118
	85117808	T	C	c.175-55A>G	-	B	0.163	0.471
	85118048	G	C	c.175-295C>G	-	B	0.163	0.471
	85118121	G	A	c.175-368C>T	-	B	0.117	0.382
	85118191	G	A	c.175-438C>T	-	B	0.125	0.088
	85118306	T	C	c.175-553A>G	-	M	-	0.029
	85118469	A	T	c.174+611T>A	-	M	-	0.088
	85118557	T	A	c.174+523A>T	-	B	0.100	0.118
	85118559	A	T	c.174+521T>A	-	B	0.100	0.118
	85118572	T	C	c.174+508A>G	-	M	-	0.029
	85118618	T	C	c.174+462A>G	-	M	-	0.029
	85118680	T	C	c.174+400A>G	-	B	0.163	0.471
	85118691	G	T	c.174+389C>A	-	M	-	0.177
	85118716	A	G	c.174+364T>C	-	S	0.050	-
	85118759	T	C	c.174+321A>G	-	B	0.150	0.500
	85118765	C	T	c.174+315G>A	-	M	-	0.118
	85118794	T	C	c.174+286A>G	-	M	-	0.177
	85118921	T	G	c.174+159A>C	-	B	0.103	0.118
	85118931	C	T	c.174+149G>A	-	B	0.167	0.471
	85118966	T	C	c.174+114A>G	-	B	0.103	0.118
	85119048	T	C	c.174+32A>G	-	M	-	0.029
	85119140	G	C	c.130-16C>G	-	B	0.342	0.353
	85119174	C	T	c.129+41G>A	-	M	-	0.029
	85119178	G	A	c.129+37C>T	-	B	0.150	0.471
	85119194	G	A	c.129+21C>T	-	M	-	0.029

	85119270	G	A	c.106-32C>T	-	S	0.050	-
	85119288	T	C	c.106-50A>G	-	M	-	0.088
	85119299	G	A	c.106-61C>T	-	B	0.368	0.324
	85119353	A	T	c.106-115T>A	-	B	0.163	0.500
	85119387	A	G	c.106-149T>C	-	M	-	0.029
	85119403	C	A	c.106-165G>T	-	B	0.167	0.469
	85119452	A	C	c.106-214T>G	-	B	0.167	0.500
	85119551	A	G	c.106-313T>C	-	M	-	0.029
	85119695	A	T	c.106-457T>A	-	B	0.150	0.500
	85119731	A	T	c.106-493T>A	-	B	0.163	0.500
	85119761	T	C	c.106-523A>G	-	B	0.163	0.500
	85119835	G	C	c.106-597C>G	-	B	0.117	0.382
	85119861	G	A	c.106-623C>T	-	S	0.050	-
	85119872	T	C	c.106-634A>G	-	B	0.086	0.118
	85119877	A	G	c.106-639T>C	-	B	0.154	0.441
	85119897	A	G	c.106-659T>C	-	B	0.115	0.412
	85119946	G	A	c.106-708C>T	-	S	0.133	-
	85120010	T	C	c.106-772A>G	-	S	0.155	-
	85120029	A	G	c.106-791T>C	-	S	0.150	-
	85120048	A	C	c.106-810T>G	-	B	0.086	0.029
	85120061	A	G	c.106-823T>C	-	S	0.138	-
	85120081	T	C	c.106-843A>G	-	M	-	0.029
	85120102	T	A,G	c.106-864A>T	-	S	0.056	-
	85120135	A	C	c.106-897T>G	-	S	0.050	-
	85120137	C	T	c.106-899G>A	-	S	0.103	-
	85120161	G	T	c.106-923C>A	-	S	0.086	-
	85120206	C	T	c.106-968G>A	-	M	-	0.029
	85120226	G	C	c.106-988C>G	-	S	0.100	-
	85120232	T	C	c.106-994A>G	-	S	0.050	-
	85120240	C	G	c.106-1002G>C	-	B	0.100	0.029
	85120245	T	G	c.106-1007A>C	-	M	-	0.031
	85120260	T	A	c.106-1022A>T	-	B	0.125	0.219
	85120264	T	C	c.106-1026A>G	-	S	0.125	-
	85120267	T	A	c.106-1029A>T	-	S	0.125	-
	85120270	G	A	c.106-1032C>T	-	S	0.117	-
	85120271	A	G	c.106-1033T>C	-	B	0.125	0.219
	85120292	C	T	c.106-1054G>A	-	B	0.438	0.094
	85120297	C	G	c.106-1059G>C	-	M	-	0.063
	85120329	A	G	c.106-1091T>C	-	S	0.075	-
	85120336	G	A	c.106-1098C>T	-	B	0.163	0.324
	85120343	T	A	c.106-1105A>T	-	S	0.100	-
	85120350	T	C	c.106-1112A>G	-	B	0.100	0.118
	85120373	C	T	c.106-1135G>A	-	B	0.100	0.500

	85120427	G	C	c.106-1189C>G	-	B	0.167	0.500
	85120428	G	A	c.106-1190C>T	-	S	0.103	-
	85120457	T	C	c.106-1219A>G	-	B	0.163	0.500
	85120461	C	T	c.106-1223G>A	-	B	0.308	0.353
	85120474	C	T	c.106-1236G>A	-	B	0.163	0.471
	85120521	C	T	c.105+1204G>A	-	B	0.100	0.118
	85120548	C	T	c.105+1177G>A	-	M	-	0.059
	85120557	G	C	c.105+1168C>G	-	B	0.163	0.500
	85120574	A	G	c.105+1151T>C	-	M	-	0.029
	85120595	T	G	c.105+1130A>C	-	B	0.117	0.382
	85120598	C	A	c.105+1127G>T	-	B	0.163	0.471
	85120600	T	A	c.105+1125A>T	-	M	-	0.029
	85120619	G	A	c.105+1106C>T	-	B	0.163	0.500
	85120693	G	A	c.105+1032C>T	-	B	0.183	0.441
	85120708	T	C	c.105+1017A>G	-	B	0.150	0.441
	85120730	A	G	c.105+995T>C	-	B	0.138	0.412
	85120785	G	A	c.105+940C>T	-	M	-	0.029
	85120837	C	T	c.105+888G>A	-	B	0.150	0.500
	85120838	A	G	c.105+887T>C	-	B	0.150	0.500
	85120845	T	A	c.105+880A>T	-	B	0.150	0.500
	85120846	A	C	c.105+879T>G	-	B	0.150	0.500
	85120895	A	C	c.105+830T>G	-	B	0.163	0.500
	85120924	A	G	c.105+801T>C	-	S	0.133	-
	85121058	A	T	c.105+667T>A	-	B	0.163	0.500
	85121065	G	A	c.105+660C>T	-	M	-	0.029
	85121072	T	C	c.105+653A>G	-	B	0.163	0.500
	85121095	A	T	c.105+630T>A	-	B	0.163	0.500
	85121128	T	C	c.105+597A>G	-	B	0.150	0.471
	85121169	G	A	c.105+556C>T	-	B	0.163	0.471
	85121240	G	A	c.105+485C>T	-	B	0.150	0.471
	85121271	G	A	c.105+454C>T	-	B	0.150	0.471
	85121328	G	T	c.105+397C>A	-	B	0.163	0.471
	85121374	A	G	c.105+351T>C	-	B	0.333	0.417
	85121379	T	G	c.105+346A>C	-	B	0.143	0.364
	85121386	C	T	c.105+339G>A	-	M	-	0.029
	85121399	A	G	c.105+326T>C	-	B	0.125	0.364
	85121426	C	A,*	c.105+299G>T	-	S	0.019	-
	85121446	T	C	c.105+279A>G	-	B	0.100	0.308
	85121658	A	G	c.105+67T>C	-	M	-	0.029
	85121679	G	A	c.105+46C>T	-	B	0.163	0.471
	85121798	A	G	c.79-47T>C	-	B	0.175	0.471
	85121812	G	A	c.78+52C>T	-	M	-	0.059
	85121917	C	A	c.52-27G>T	-	B	0.154	0.471

	85121918	G	T	c.52-28C>A	-	B	0.154	0.471
	85121923	C	T	c.52-33G>A	-	B	0.158	0.471
	85121965	A	G	c.52-75T>C	-	B	0.100	0.059
	85122020	C	T	c.52-130G>A	-	B	0.154	0.471
	85122023	T	C	c.52-133A>G	-	B	0.154	0.471
	85122036	T	C	c.52-146A>G	-	B	0.154	0.500
	85122048	A	G	c.52-158T>C	-	B	0.500	0.029
	85122230	C	T	c.52-340G>A	-	B	0.163	0.471
	85122265	G	A	c.51+357C>T	-	B	0.163	0.471
	85122287	T	A	c.51+335A>T	-	B	0.100	0.059
	85122288	G	T	c.51+334C>A	-	B	0.100	0.059
	85122296	A	G	c.51+326T>C	-	B	0.138	0.500
	85122298	G	A	c.51+324C>T	-	B	0.100	0.088
	85122312	G	A	c.51+310C>T	-	B	0.163	0.471
	85122315	C	A	c.51+307G>T	-	B	0.088	0.471
	85122341	G	A	c.51+281C>T	-	M	-	0.029
	85122356	T	G	c.51+266A>C	-	B	0.163	0.471
	85122401	A	T	c.51+221T>A	-	B	0.163	0.471
	85122499	G	C	c.51+123C>G	-	M	-	0.029
	85122502	T	C	c.51+120A>G	-	B	0.100	0.118
	85122679	C	T	c.-7G>A	-	B	0.163	0.471
	85122721	C	G	c.-49G>C	-	B	0.150	0.469
	85122723	C	A	c.-51G>T	-	B	0.100	0.063
	85122762	C	A	c.-90G>T	-	B	0.154	0.471
	85122769	C	A	c.-97G>T	-	B	0.158	0.471
CSN3	85309593	A	G	c.42A>G	p.Leu14Leu	B	0.050	0.147
	85309623	T	C	c.57+15T>C	-	S	0.100	-
	85309654	C	T	c.57+46C>T	-	B	0.128	0.147
	85309805	C	G	c.57+197C>G	-	B	0.167	0.147
	85310101	G	T	c.57+493G>T	-	S	0.050	-
	85310112	C	T	c.57+504C>T	-	B	0.372	0.324
	85310116	A	G	c.57+508A>G	-	M	-	0.059
	85310125	C	T	c.57+517C>T	-	M	-	0.059
	85310141	C	T	c.57+533C>T	-	B	0.385	0.294
	85310217	C	T	c.57+609C>T	-	B	0.359	0.206
	85310258	T	C	c.57+650T>C	-	B	0.197	0.294
	85310343	G	A	c.57+735G>A	-	S	0.056	-
	85310384	G	T	c.57+776G>T	-	B	0.200	0.029
	85310452	A	T	c.57+844A>T	-	S	0.233	-
	85310455	T	A	c.57+847T>A	-	B	0.225	0.088
	85310473	C	A	c.57+865C>A	-	B	0.138	0.147
	85310499	T	G	c.57+891T>G	-	B	0.133	0.235
	85310507	G	A	c.57+899G>A	-	M	-	0.147

	85310848	C	T	c.57+1240C>T	-	M	-	0.029
	85310868	G	C	c.57+1260G>C	-	B	0.125	0.147
	85310922	T	G	c.57+1314T>G	-	B	0.325	0.147
	85310946	G	A	c.57+1338G>A	-	B	0.138	0.147
	85310988	A	G,*	c.57+1380A>G	-	S	0.273	-
	85311018	G	A	c.57+1410G>A	-	S	0.050	-
	85311134	A	G	c.57+1526A>G	-	B	0.154	0
	85311362	T	C	c.57+1754T>C	-	B	0.138	0
	85311385	T	C	c.57+1777T>C	-	B	0.138	0.147
	85311408	G	A	c.57+1800G>A	-	B	0.175	0.147
	85311464	G	A	c.57+1856G>A	-	S	0.100	-
	85311465	C	T	c.57+1857C>T	-	S	0.050	-
	85311477	A	C	c.57+1869A>C	-	S	0.100	-
	85311487	T	A	c.57+1879T>A	-	S	0.050	-
	85311488	C	T	c.57+1880C>T	-	S	0.050	-
	85311508	T	C	c.57+1900T>C	-	S	0.163	-
	85311515	G	T	c.57+1907G>T	-	B	0.175	0.088
	85311524	T	G	c.57+1916T>G	-	B	0.188	0.118
	85311544	T	G	c.57+1936T>G	-	S	0.150	-
	85311547	C	A	c.57+1939C>A	-	S	0.100	-
	85311548	A	T	c.57+1940A>T	-	S	0.050	-
	85311550	A	T,C	c.57+1942A>C	-	S	0.079	-
	85311553	T	C	c.57+1945T>C	-	S	0.050	-
	85311565	G	A	c.57+1957G>A	-	S	0.050	-
	85311566	A	C	c.57+1958A>C	-	S	0.050	-
	85311580	C	A	c.57+1972C>A	-	B	0.213	0.324
	85311585	G	A	c.57+1977G>A	-	S	0.050	-
	85311588	G	A	c.57+1980G>A	-	S	0.050	-
	85311664	G	C,A	c.57+2056G>A	-	S	0.026	-
	85311666	T	A	c.57+2058T>A	-	S	0.050	-
	85311708	A	C	c.57+2100A>C	-	S	0.150	-
	85311711	C	G	c.57+2103C>G	-	S	0.050	-
	85311712	C	A	c.57+2104C>A	-	S	0.050	-
	85311730	A	G	c.57+2122A>G	-	B	0.375	0.353
	85311815	T	C	c.57+2207T>C	-	B	0.225	0.206
	85311926	C	T	c.58-2315C>T	-	B	0.013	0.029
	85311929	G	C	c.58-2312G>C	-	B	0.200	0.029
	85311990	G	C	c.58-2251G>C	-	M	-	0.029
	85312140	A	C	c.58-2101A>C	-	B	0.200	0.324
	85312182	T	C	c.58-2059T>C	-	B	0.050	0.029
	85312230	G	A	c.58-2011G>A	-	B	0.244	0.206
	85312285	A	G	c.58-1956A>G	-	S	0.218	-
	85312314	T	C	c.58-1927T>C	-	M	-	0.059

	85312318	T	A	c.58-1923T>A	-	S	0.050	-
	85312414	G	A	c.58-1827G>A	-	B	0.133	0.206
	85312436	A	G	c.58-1805A>G	-	B	0.158	0.147
	85312467	G	A	c.58-1774G>A	-	B	0.150	0.177
	85312571	C	G	c.58-1670C>G	-	B	0.141	0.147
	85312764	T	C	c.58-1477T>C	-	M	-	0.059
	85312811	C	A	c.58-1430C>A	-	S	0.269	-
	85312812	C	A	c.58-1429C>A	-	B	0.487	0.471
	85313047	G	A	c.58-1194G>A	-	M	-	0.029
	85313055	G	A	c.58-1186G>A	-	B	0.175	0.324
	85313119	A	G	c.58-1122A>G	-	B	0.050	0.059
	85313121	T	C	c.58-1120T>C	-	B	0.050	0.059
	85313178	A	G	c.58-1063A>G	-	B	0.141	0.118
	85313463	T	C	c.58-778T>C	-	B	0.050	0.059
	85313715	T	A	c.58-526T>A	-	B	0.013	0.029
	85313865	T	C	c.58-376T>C	-	B	0.145	0.147
	85314041	G	A	c.58-200G>A	-	B	0.066	0.088
	85314053	T	C	c.58-188T>C	-	S	0.050	-
	85314123	C	A	c.58-118C>A	-	M	-	0.029
	85314152	A	C	c.58-89A>C	-	B	0.083	0.088
	85314571	G	A	c.90+298G>A	-	B	0.141	0.147
	85314642	C	T	c.90+369C>T	-	S	0.192	-
	85314727	G	T	c.90+454G>T	-	M	-	0.029
	85314739	T	C	c.90+466T>C	-	B	0.231	0.324
	85314831	T	A	c.90+558T>A	-	B	0.172	0.147
	85314859	A	T	c.90+586A>T	-	M	-	0.059
	85314865	C	T	c.90+592C>T	-	B	0.173	0.147
	85314975	T	C	c.90+702T>C	-	B	0.080	0.133
	85315042	A	T	c.90+769A>T	-	S	0.100	-
	85315043	T	G	c.90+770T>G	-	S	0.050	-
	85315064	T	C	c.90+791T>C	-	B	0.460	0.267
	85315199	G	C	c.90+926G>C	-	B	0.177	0
	85315343	T	G	c.91-1003T>G	-	B	0.200	0.177
	85315411	C	A	c.91-935C>A	-	S	0.167	-
	85315637	C	T	c.91-709C>T	-	M	-	0.177
	85315758	G	A	c.91-588G>A	-	B	0.176	0
	85315838	G	A	c.91-508G>A	-	S	0.056	-
	85315845	A	G	c.91-501A>G	-	S	0.056	-
	85315859	T	C	c.91-487T>C	-	B	0.200	0.206
	85315882	A	G	c.91-464A>G	-	M	-	0.059
	85315916	C	T	c.91-430C>T	-	B	0.194	0.406
	85315918	C	T	c.91-428C>T	-	M	-	0.235
	85315949	G	C	c.91-397G>C	-	M	-	0.029

	85315979	T	C	c.91-367T>C	-	S	0.050	-
	85315983	A	G	c.91-363A>G	-	B	0.175	0.206
	85316130	T	G	c.91-216T>G	-	B	0.288	0.147
	85316304	C	G	c.91-42C>G	-	S	0.218	-
	85316328	A	T	c.91-18A>T	-	S	0.050	-
	85316423	C	T	c.168C>T	p.Tyr56Tyr	B	0.141	0
	85316562	G	A	c.307G>A	p.Ala103Thr	M	-	0.147
	85316665	A	G	c.410A>G	p.Lys137Arg	M	-	0.029

*Presence, S= Sheep, M= Mouflon, B= Both; †MAF Sheep, minor allele frequency in domestic sheep; ‡MAF Mouflon, minor allele frequency in mouflon.

Table S4. Classification and number of SNPs mapping to the casein genes in domestic sheep populations from North Africa, West Asia, Europe and South and East Asia.

Gene	**Exon**	**Intron**	**Splice site**	**Upstream**	**Downstream**	**5'UTR**	**3'UTR**	**# SNPs North Africa**	**# SNPs West Asia**	**# SNPs South and East Asia**	**# SNPs Europe**	**Total**
CSN1S1	4	90	1	0	0	0	0	64	67	63	74	95
CSN1S2	10	182	4	0	0	0	0	185	143	122	159	196
CSN2	2	107	1	0	0	5	0	97	102	83	108	115
CSN3	2	93	0	0	0	0	0	64	61	62	73	95

Table S5. Classification and number of SNPs mapping to the casein genes in mouflons.

Gene	Exon	Intron	Splice site	Upstream	Downstream	5'UTR	3'UTR	Mouflon Tabriz	Mouflon Tehran	Total
CSN1S1	8	205	2	0	0	0	0	201	40	215
CSN1S2	11	197	5	0	0	0	0	195	103	213
CSN2	3	114	1	0	0	5	0	122	79	123
CSN3	4	69	0	0	0	0	0	73	28	73

Table S6. Description and frequencies of the missense variants identified in each sheep and mouflon population.

Gene	**SNP**	**Nucleotide substitution**	**Effect***	**South and East Asia**	**Europe**	**West Asia**	**North-Africa**	**Mouflon from Tabriz**	**Mouflon from Tehran**	**Associated allele**	**Study reporting the allele**
CSN1S1	rs593739642	c.34G>T	p.Val12Phe **DEL**	0	0	0	0.05	0	0		
	Oar_3.1:6:85091243:G>A	c.73G>A	p.Gly25Arg	0	0	0	0	0.05	0		
	Oar_3.1:6:85093731:T>C	c.191T>C	p.Ile64Thr	0	0	0	0	0.05	0		
	Oar_3.1:6:85094448:C>T	c.215C>T	p.Ala72Val	0	0	0	0	0.05	0		
	Oar_3.1:6:85098887:A>C	c.385A>C	p.Lys129Gln	0	0	0	0	0.05	0.29		
CSN1S2	Oar_3.1:6:85184193:G>A	c.34G>A	p.Val12Ile	0	0	0	0	0.11	0		
	rs588453493	c.178G>A	P.Val60Ile	0	0	0.05	0.05	0	0	**C**	Giambra & Erhardt, (2012)
	rs596411552	c.187G>T	p.Ala63Ser	0	0	0.05	0.05	0		**C**	Giambra & Erhardt, (2012)
	rs430397133	c.268G>T	p.Asp90Tyr **DEL**	0.75	0.2	0.67	0.35	0.22	0	**B**	Giambra & Erhardt, (2012)
	rs591309828	c.344T>C	p.Leu115Pro	0	0	0.05	0.05	0.11	0.286		
	rs424657035	C.358A>G	p.Ile120Val	0.83	0.4	0.67	0.4	0.11	0	**B**	Giambra & Erhardt, (2012)
	Oar_3.1:6:85190241:C>T	c.407C>T	c.407C>T	0	0	0	0	0	0.29		
	Oar_3.1:6:85193514:T>C	c.487T>G	p.Phe163Val	0	0	0	0	0.11	0		
	rs399378277	c.527G>A	p.Arg176His	0	0.35	0.25	0.3	0.11	0	**G**	Giambra & Erhardt,

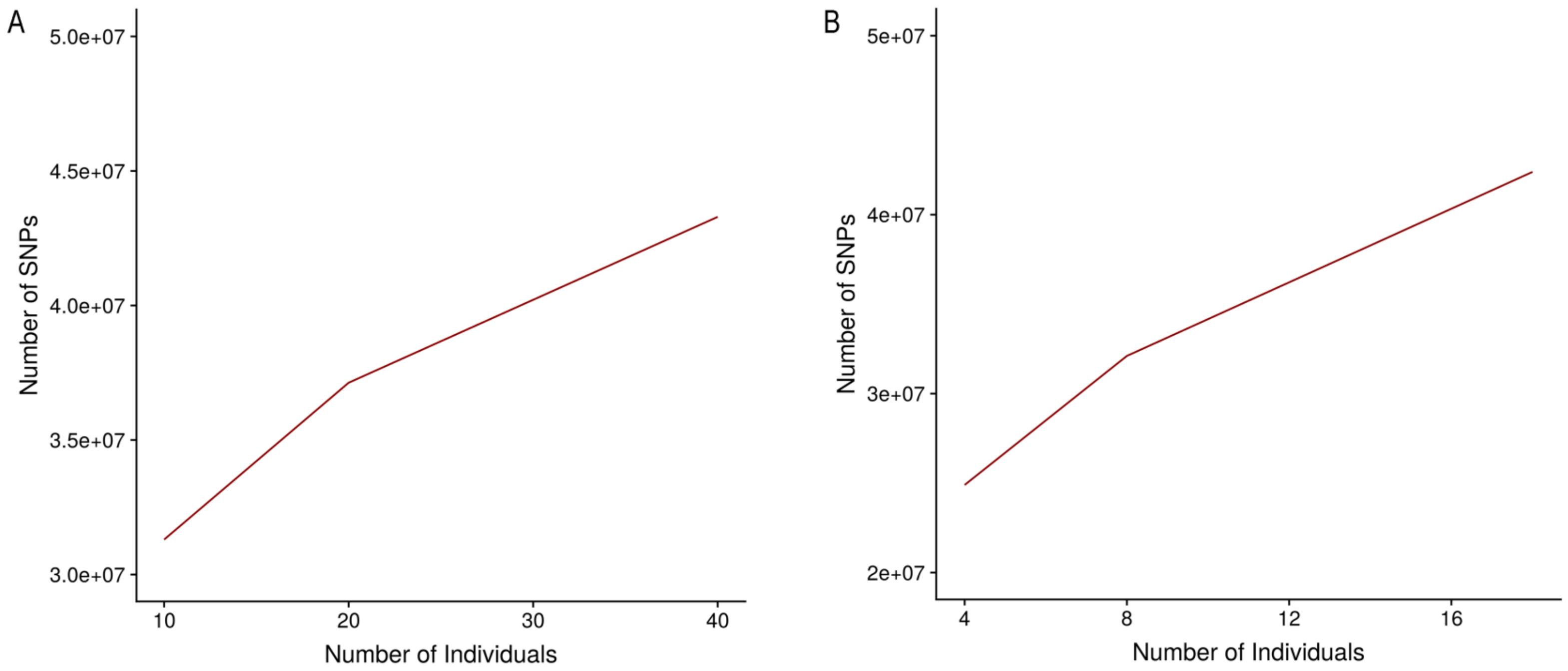
											(2012)
CSN2	Oar_3.1:6:85116838:A>G	c.679A>G	p.Thr227Ala	0	0	0	0	0.05	0		
	rs416941267	c.634C>A	p.Leu212Ile	0.06	0.3	0.16	0.15	0.61	0		
	rs430298704	c.595A>G	p.Met199Val	0	0.15	0.5	0.1	0	0	**G**	Giambra & Erhardt, (2012), Bastos et al., (2001), Corral et al., (2010) and Suárez-Vega et al., (2017)
CSN3	rs420470202	c.307G>A	p.Ala103Thr	0	0	0	0	0.28	0		
	Oar_3.1:6:85316665:A>G	c.410A>G	p.Lys137Arg **DEL**	0	0	0	0	0.05	0		

***DEL**, mutation predicted by SIFT to be deleterious (SIFT score lower than 0.05).

Table S7. Nucleotide diversity estimates (π) ± Standard Error in two Iranian mouflon populations and in 4 domestic sheep populations from North Africa, West Asia, Europe and South and East Asia by using the *per-site* and *per-window* (1,000 bp) analyses implemented in VCFtools.

Genomic region	**Mouflon**		**Mouflon from Tabriz**		**Mouflon from Tehran**		**Domestic Sheep**		**European Sheep**		**Nor-African Sheep**		**West Asian Sheep**		**South and East Asian Sheep**	
Nucleotide diversity	**Per-site**	**Window**	**Per-site**	**Window**	**Per-site**	**Window**	**Per-site**	**Window**	**Per-site**	**Window**	**Per-site**	**Window**	**Per-site**	**Window**	**Per-site**	**Window**
Whole Genome	0.24± $2.4x10^{-5}$	0.0038 $2.2x10^{-06}$	0.25± $2.6x10^{-5}$	0.0042± $1.8x10^{-06}$	0.16 ± $8.7x10^{-5}$	0.0029± $3.45x10^{-06}$	0.28 ± $3.2x10^{-5}$	0.003± $1.69x10^{-06}$	-	-	-	-	-	-	-	-
Casein cluster	0.23 ±0.007	0.0034 ± 0.00036	0.25± 0.006	0.0036± 0.0003	0.17±0.009	0.0026± 0.0003	0.27± 0.006	0.0025± 0.0003	0.31± 0.0068	0.0037± 0.00037	0.3± 0.0066	0.0036± 0.00036	0.28± 0.0075	0.0026± 0.00031	0.25± 0.0069	0.0018± 0.0002
CSN1S1	0.14 ±0.009	0.0021± 0.00018	0.17± 0.009	0.0025 ± $2x10^{-5}$	0.071± 0.011	0.0011± 0.0002	0.22± 0.015	0.0011±0.0001	-	-	-	-	-	-	-	-
CSN1S2	0.25 ± 0.010	0.0044 ± 0.00044	0.19± 0.01	0.0044± 0.0004	0.21± 0.015	0.0036± 0.0004	0.32± 0.011	0.0041±0.0004	-	-	-	-	-	-	-	-
CSN2	0.34 ± 0.017	0.0059 ± 0.0013	0.36± 0.015	0.0061± 0.0013	0.28± 0.020	0.0057± 0.001	0.24± 0.007	0.0037±0.0008	-	-	-	-	-	-	-	-
CSN3	0.22 ± 0.016	0.002 ± 0.00038	0.25± 0.017	0.0022± 0.0003	0.13± 0.04	0.0013± 0.0003	0.234± 0.012	0.0019±0.0005	-	-	-	-	-	-	-	-

Fig. S1. Number of SNPs discovered in **(A)** sheep and **(B)** Iranian mouflon by using whole-genome sequence data sets with varying sizes. Individuals comprised in the reduced data sets (N < 40 in sheep and N < 17 in mouflon) were chosen at random.



Sheep (N=10)	Sheep (N=20)	Sheep (N=40)
31,301,016 SNPs	37,129,602 SNPs	43,293,496 SNPs

Mouflon (N=4)	Mouflon (N=8)	Mouflon (N=17)
24,897,916 SNPs	32,106,197 SNPs	42,388,204 SNPs

Fig. S2. Histogram showing the proportion of the total SNP dataset (*y*-axis) belonging to each one of the minimum allele frequency intervals defined in the *x*-axis. In total, we have considered 58,626,591 SNPs detected in sheep and Iranian mouflons. It can be seen that 50% of these SNPs display frequencies below 0.10.

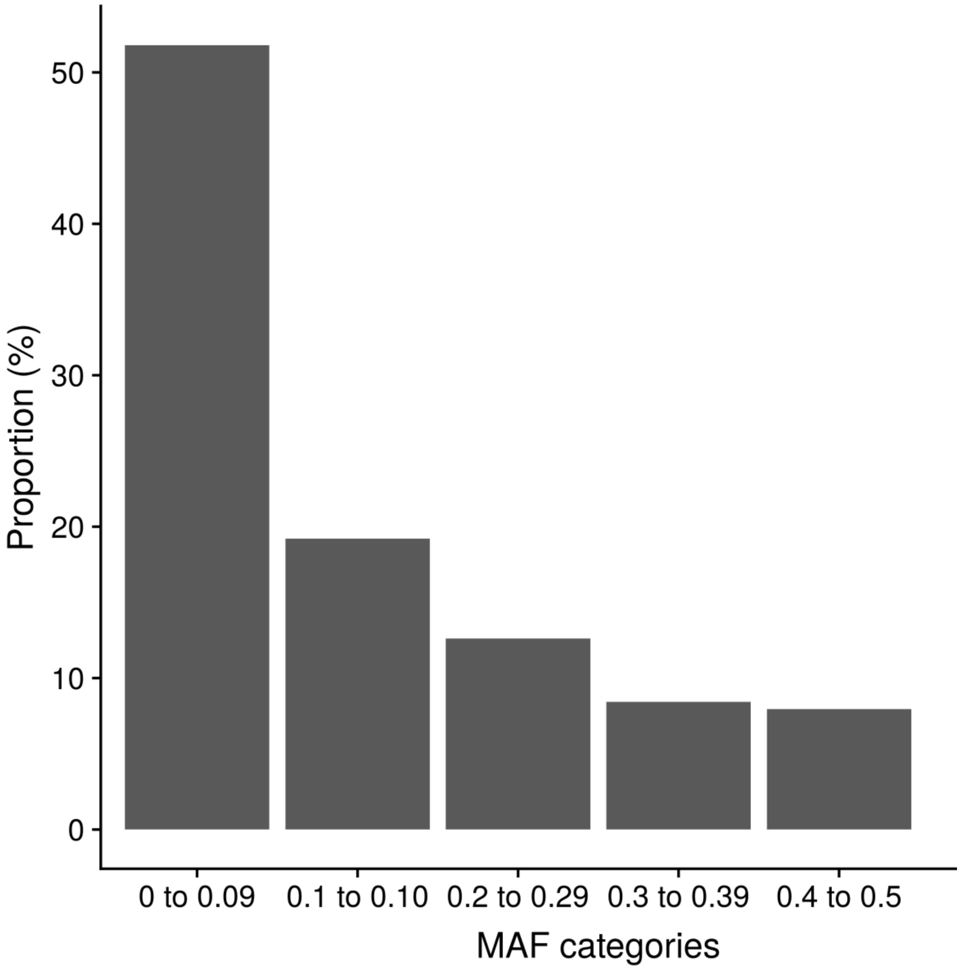


Fig. S3. Cross-validation error values for each K- value obtained in the Admixture analysis based on a dataset of 55,352,935 autosomal SNPs.

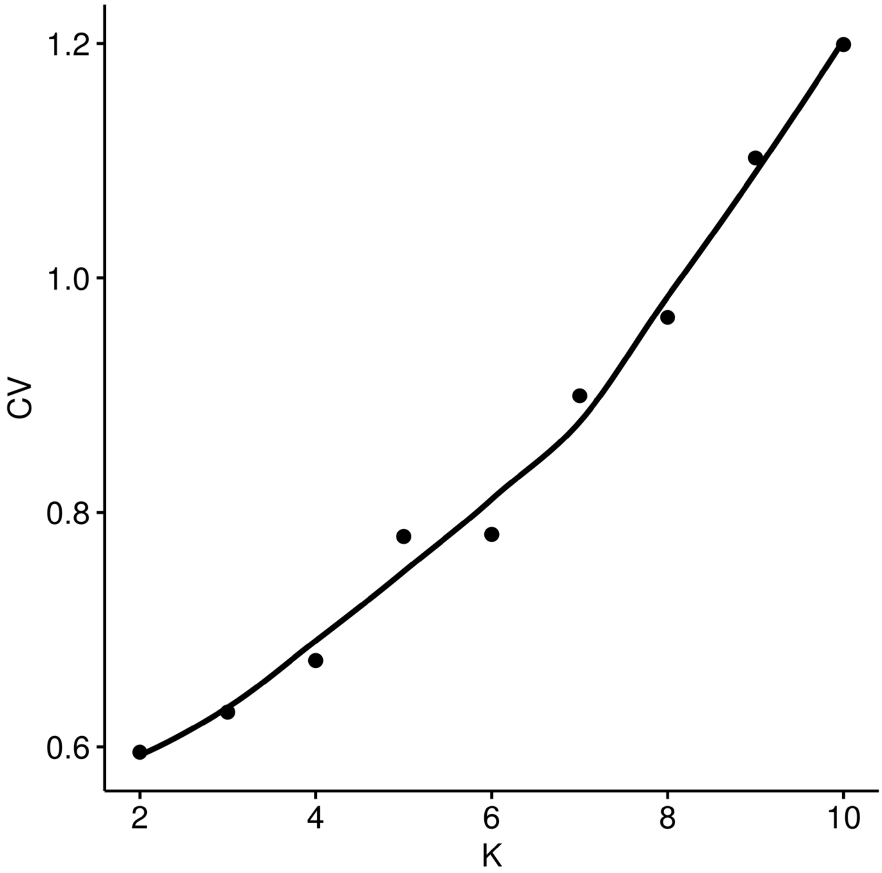


Fig. S4. Principal component analysis (PCA) based on 774 SNPs mapping to the casein genes and comprising two Iranian mouflon populations as well as four domestic sheep populations from North Africa, West Asia, Europe and South and East Asia. **B** Admixture analysis (K=2-10) encompassing the same number of markers and populations defined in **A**.

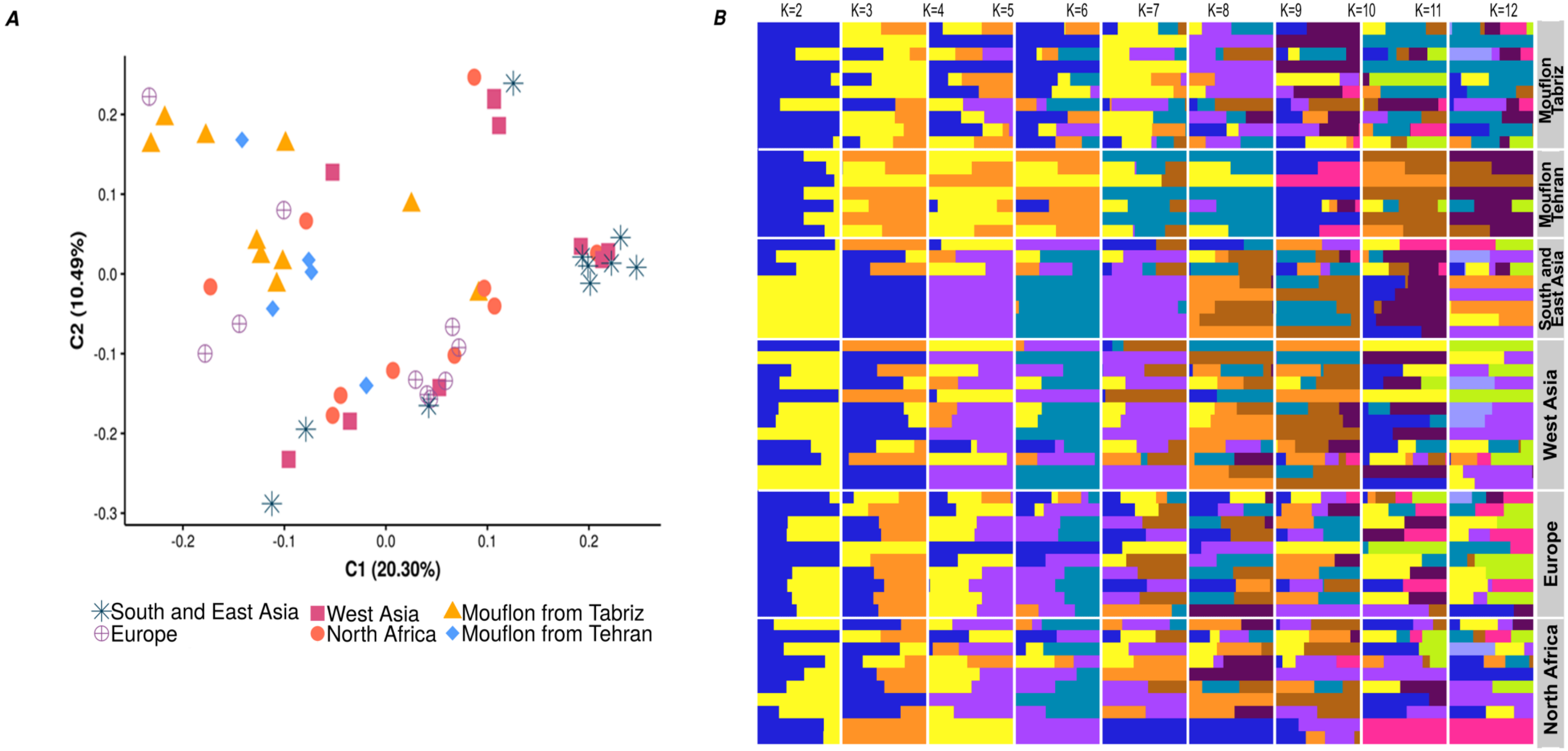


Fig. S5. Cross-validation error values for each K- value obtained in the Admixture analysis based on 774 SNPs mapping to the casein genes.

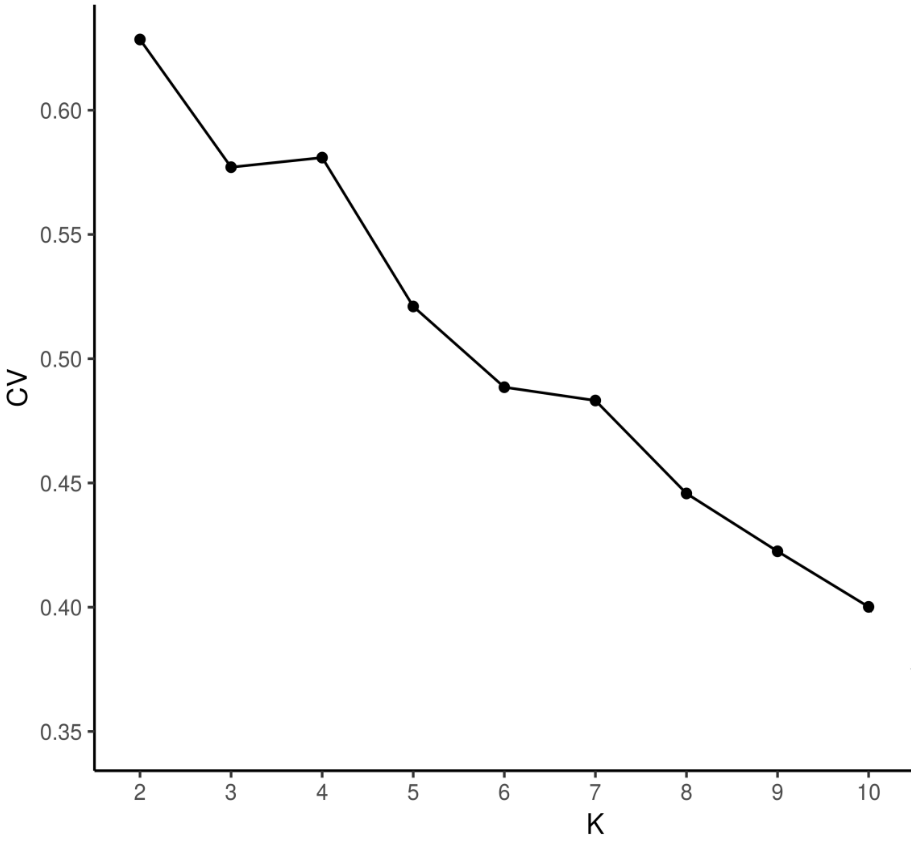


Fig. S6. Principal component analysis of domestic sheep and Iranian mouflon populations based on **(A)** 248 SNPs mapping to the *CSN1S1* gene; **(B)** 268 SNPs mapping to the *CSN1S2* gene; **(C)** 146 SNPs mapping to the *CSN2* gene; and **(D)** 112 SNPs mapping to the *CSN3* gene.

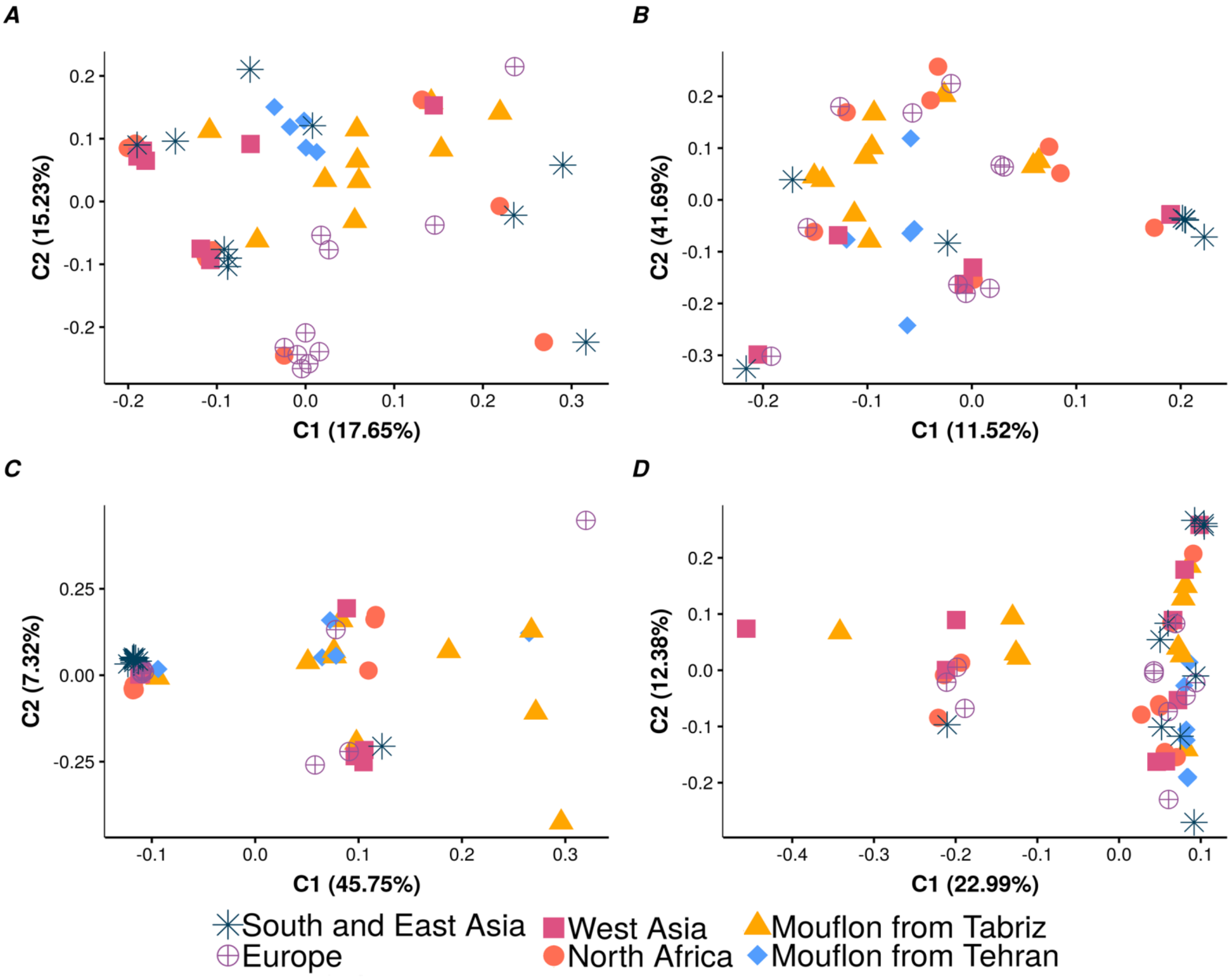


Fig. S7. Neighbor-joining tree of sheep from North Africa, West Asia, Europe and South and East Asia and Iranian mouflons (Tabriz and Tehran) based on 774 SNPs mapping to the casein genes.

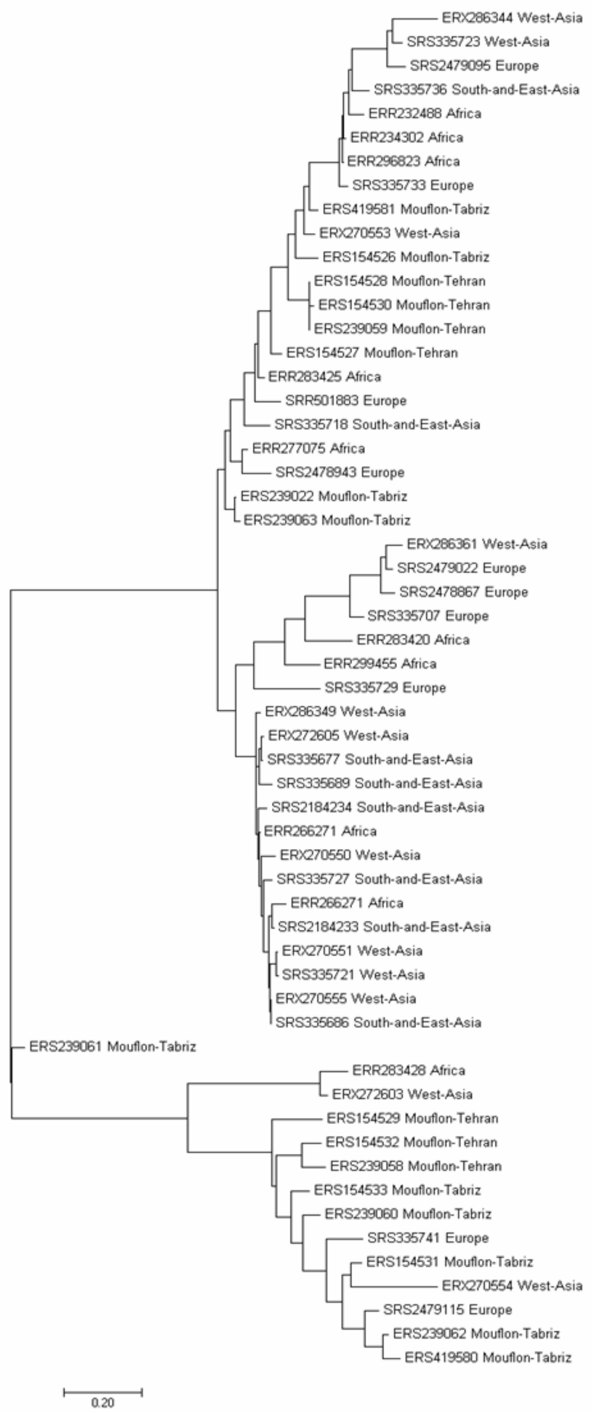
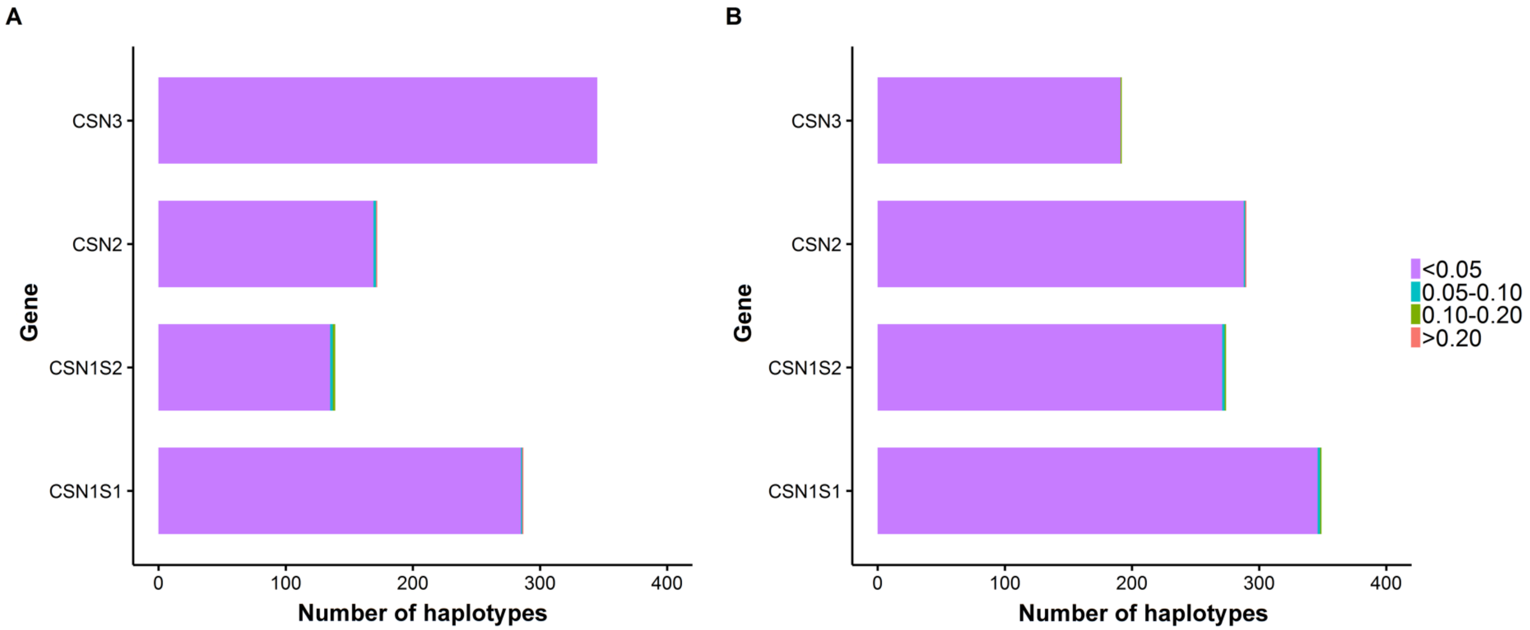


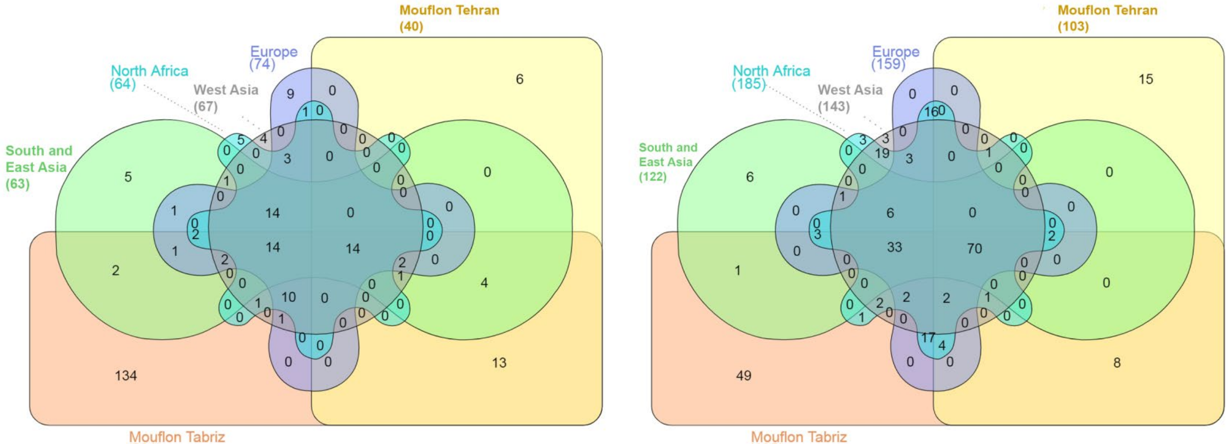
Fig. S8. Number of reconstructed casein haplotypes and proportion of haplotypes corresponding to each frequency interval in **(A)** domestic sheep and **(B)** mouflon populations. It can be seen that the vast majority of casein haplotypes have very low frequencies.



Frequency interval	*CSN1S1*	*CSN1S2*	*CSN2*	*CSN3*
< 0.05	99.30%	97.12%	98.25%	100%
0.05- 0.10	0.3%	1.4%	1.16%	0%
0.10 -0.20	0%	1.4%	0%	0%
> 0.20	0.3%	0%	0.5%	0%

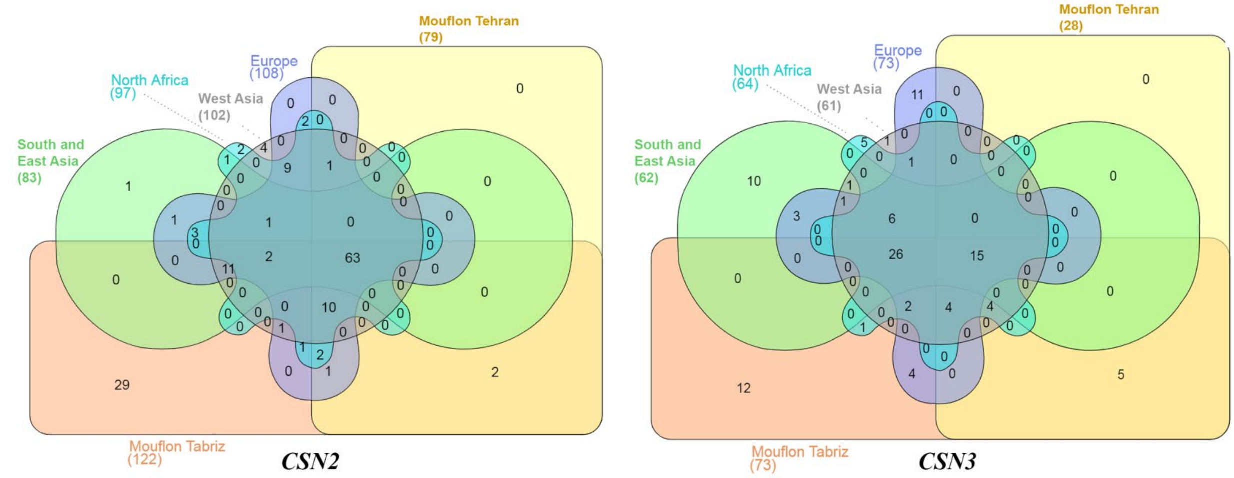
Frequency interval	*CSN1S1*	*CSN1S2*	*CSN2*	*CSN3*
< 0.05	99.14%	98.9%	99.3%	99%
0.05- 0.10	0.57%	0.7%	0.3%	0%
0.10 -0.20	0.28%	0.3%	0%	1%
> 0.20	0 %	0%	0.3%	0%

Fig. S9. Venn diagrams depicting the sharing of casein SNPs between domestic sheep populations from North-Africa, West Asia, Europe and South and East Asia, and two Iranian mouflon populations (Tabriz and Tehran).



CSN1S1

CSN1S2



CSN2

CSN3