

**Table S5.** Goat haplogroup frequencies based on modern and ancient control-region mtDNA data.<sup>a</sup>

Domestic Breeds									
	Hg A	Hg B	Hg C	Hg D	Hg F	Hg G	Other	Total	References
<b>Africa</b>	<b>574</b> <b>(95.19)</b>	<b>14 (2.32)</b>	...	...	...	<b>15</b> <b>(2.49)</b>	...	<b>603</b>	
Northern	383 (98.97)	...	...	...	...	4 (1.03)	...	387	Amills Direct subm; Benjelloun Direct subm; Daga Direct subm; [1]; [2]; [3]; This Study
Central	102 (90.27)	...	...	...	...	11 (9.73)	...	113	[4]; Amills Direct subm; Githui Direct subm; [1]; [2]; [5]
Southern	89 (86.41)	14 (13.59)	...	...	...	...	...	103	Awotunde Direct subm; [1]; [2]; Wu and Liu Direct subm
<b>America</b>	<b>64</b> <b>(100.00)</b>	...	...	...	...	...	...	<b>64</b>	
Central	34 (100.00)	...	...	...	...	...	...	34	[4]; Marcheco Direct subm
Southern	30 (100.00)	...	...	...	...	...	...	30	[4]
<b>Asia</b>	<b>2891</b> <b>(84.93)</b>	<b>392</b> <b>(11.52)</b>	<b>43</b> <b>(1.26)</b>	<b>34</b> <b>(1.00)</b>	...	<b>44</b> <b>(1.29)</b>	...	<b>3404</b>	
Middle East	876 (93.99)	6 (0.64)	2 (0.21)	8 (0.86)	...	40 (4.29)	...	932	[6]; Akis Direct subm; Mazdarani Direct subm; Kiraz Direct subm; [1]; [2]; This Study; Wu and Liu Direct subm
Southern	830 (94.10)	31 (3.51)	9 (1.02)	11 (1.25)	...	1 (0.11)	...	882	Amills Direct subm; Das Direct sub; Jimcy Direct subm; [7]; Karabasanavar Direct subm; [1]; [2]; Nomura et al Direct subm; Rana Direct subm; Sadia Direct subm; [8]; [9]; This Study
Eastern	1185 (74.53)	355 (22.33)	32 (2.01)	15 (0.94)	...	3 (0.19)	...	1590	Cai Direct subm; Chen and Wang Direct subm; [10]; Chi Direct subm; Fang Direct subm; Kim Direct subm; Li Direct subm; [11]; [12]; [13]; Liu Direct subm; [1]; [14]; Mannen Direct subm; [2]; Nomura et al Direct subm; Song and Lin Direct subm; Tang Direct subm; This Study; [15]; Wu and Liu Direct subm; Wu and Ma Direct subm; [16]; Xi Direct subm; Zhang Direct subm; [17]; Zhong and Wang Direct subm
<b>Europe</b>	<b>2148</b> <b>(97.59)</b>	<b>2 (0.09)</b>	<b>45</b> <b>(2.04)</b>	<b>3 (0.14)</b>	<b>3 (0.14)</b>	...	...	<b>2201</b>	
Continental	504 (95.27)	1 (0.19)	23 (4.35)	1 (0.19)	...	...	...	529	Amills Direct subm; Baldursdottir Direct subm; [18]; Daga Direct subm; [19]; [1]; Maudet and Taberlet Direct subm; [2]; [20]; This Study
Mediterranean	1644 (98.33)	1 (0.06)	22 (1.32)	2 (0.12)	3 (0.18)	...	...	1672	[4]; Amills Direct subm; [21]; Bigi Direct subm; Curik Direct subm; Daga Direct subm; [22]; Hughes Direct subm; [23]; [2]; [24]; [25]; [5]; [26]; This Study
<b>Total</b>	<b>5677</b> <b>(90.51)</b>	<b>408</b> <b>(6.51)</b>	<b>88</b> <b>(1.40)</b>	<b>37</b> <b>(0.59)</b>	<b>3 (0.05)</b>	<b>59</b> <b>(0.94)</b>	...	<b>6272</b>	
Wild Goats									
	Hg A	Hg B	Hg C	Hg D	Hg F	Hg G	Other	Total	References
Middle East	29 (6.35)	17 (3.72)	171 (37.42)	59 (12.91)	132 (28.88)	10 (2.19)	39 (8.53)	457	[1]; [27]; This Study
Southern Asia	...	...	14 (42.42)	...	6 (18.18)	...	13 (39.39)	33	[1]; [27]; [9]
Mediterranean Europe	4 (100.00)	...	...	...	...	...	...	4	This Study
<b>Total</b>	<b>33 (6.68)</b>	<b>17 (3.44)</b>	<b>185</b> <b>(37.45)</b>	<b>59</b> <b>(11.94)</b>	<b>138</b> <b>(27.94)</b>	<b>10</b> <b>(2.02)</b>	<b>52</b> <b>(10.53)</b>	<b>494</b>	
Ancient Goats <sup>b</sup>									
	Hg A	Hg B	Hg C	Hg D	Hg F	Hg G	Other	Total	References
<b>Asia</b>	<b>22</b> <b>(88.00)</b>	<b>2 (8.00)</b>	...	<b>1 (4.00)</b>	...	...	...	<b>25</b>	
Middle East	15 (100.00)	...	...	...	...	...	...	15	[6]; [28]; [29]; [30]; [31]
Eastern	7 (70.00)	2 (20.00)	...	1 (10.00)	...	...	...	10	[32]
<b>Europe</b>	<b>23</b> <b>(88.46)</b>	<b>1 (3.85)</b>	<b>2 (7.69)</b>	...	...	...	...	<b>26</b>	
Continental	...	1 (100.00)	...	...	...	...	...	1	[20]
Mediterranean	23 (92.00)	...	2 (8.00)	...	...	...	...	25	[19]; [33]; [34]
<b>Total</b>	<b>45</b> <b>(88.24)</b>	<b>3 (5.88)</b>	<b>2 (3.92)</b>	<b>1 (1.96)</b>	...	...	...	<b>51</b>	

<sup>a</sup> Haplogroup frequencies (%) are in parentheses. Sequences with an ambiguous haplogroup affiliation and/or geographic origin were not included.

<sup>b</sup> Sequences reported by [18] were excluded due to their ambiguity: i) haplogroup affiliation was unclear, sequences did not match with known haplogroups probably because data derived from ancient parchments represent multiple individuals/species due to the complex stages of parchment manufacturing, ii) the geographic origin of the individuals may not match the location where the parchments have been stored.

**Table S6.** Diagnostic mutational motifs of goat mtDNA haplogroups and sub-haplogroups.

Clade	Diagnostic Coding Region Mutational Motif <sup>a,b</sup>
<b>A</b>	3194, 7839, 8055, <u>14746</u>
<b>A1</b>	6186
<b>A1a</b>	<u>9220</u>
<b>A2</b>	194
<b>A2a</b>	7213
<b>A2a1</b>	<u>7117</u>
<b>A3</b>	4332, 10944
<b>A4</b>	4191
<b>A5</b>	<u>6863</u>
<b>A6</b>	11127
<b>A7</b>	8279, 11913
<b>B</b>	6096, 7342, 8635, 9010, 10813, 11702, 11872, 13178, 13286, 13681, 13762
<b>B1</b>	2849, 8703, 13964, 14461, 14795
<b>C</b>	1024, <u>1112</u> , 1368, 4626, 8113, 8486, 9547, 9599, 10106, 10302, 10545, 10563, 10950, 11073, 11256, 11569, 11957, 12146, <u>12362</u> , <u>12638</u> , 13157, <u>15053</u>
<b>C1</b>	165, 3599, 4569, 4707, 6390, <u>6537</u> , 7657, 8300C, <u>8851</u> , 9111, 9205, <u>9346</u> , 11969, 12539, 12791, 14290, 14527
<b>C1a</b>	1191, 5775, <u>6324</u> , <u>7117</u> , 9061, 12386, <u>12626</u>
<b>D</b>	<u>4276</u> , 7090, 7108, 8968, 11325
<b>D1</b>	2698, 3739, 6333G, 7324, 7463, 7910, 8474, 10001, <u>12014</u> , 12242, 13293, 13894, <u>14317</u> , 14500, <u>15238</u>
<b>A'B'D'G</b>	203, 4032, 7052, 7660, 7885, 8480, 8730, 8818, 10479, <u>10686</u> , 11364, 11691, 13100T, 13280, 15220
<b>A'D'G</b>	1849, 5601, 8078, 8959, <u>9826</u> , 13741
<b>A'D</b>	2207, 3468, 10638, <u>12383</u> , 13756, 15004
<b>A'B'C'D'G</b>	211, 2885C, 3002, 3131, 3293, <u>3770</u> , 4713, 4890, 5712, 6093, 6414, 8264, 9994, 10356A, 10449, 12314, 13001, 13292, <u>13502</u> , <u>14044</u> , 14386, <u>14518</u>
<b>G</b>	<u>257</u> , 726, 797, 3197, 3949, <u>4119</u> , 8102, 8770, 9546, 11649, <u>12014</u> , 12743, 14288, <u>14587</u> , 15007, 15112
<b>A.G.M.<sup>c</sup></b>	56, 100, 227, <u>289</u> , 435, 945, 1075, 1829, 2268, 2311, 2663, 2922, 2978, 3248, 3261, 3491, 3635, 3960T, 4131, 4164, <u>4284</u> , <u>4363</u> , 4470, 4563, 4601A, 4749, 5085, 5141, <u>5312</u> , 5658, 5772, 5791, 5850, 6150, 6309, 6486, 6528, 6923, 7024, 7151, 7318, 7361, 7426, 7642, <u>7669</u> , 7842, 8456, <u>8597</u> , 8668, 8758, 8827, 9007, 9085, 9086, 9139, 9223, 9297, <u>9346</u> , 9445, 9470, 9572, 9677, 9753, 9797, 9935, 9937, 9943, 10229, 10261, <u>10374</u> , 10416, 10430, <u>10440</u> , 10473, 10557, 10776, 10842, 11001, 11052, 11163, 11797, 11849, 11912, 11915, 11973, 12044, 12218, 12257, 12260, 12369, 12651, 12683, 12762, 12776, 12987, 13146A, 13271, 13382, 13457, 13508, <u>13523</u> , 13526, 13548, 13579, 13675, 13800, 14038, 14050, 14170, 14266C, 14284, 14341, 14444, 14524, 14593, <u>14650</u> , 14674, 14686, 14720, <u>14746</u> , 14767C, 14893, <u>14968</u> , 14993, <u>15053</u> , 15076, 15348

<sup>a</sup> Coding Region Mutational motifs are relative to the reference sequence (GRS, GenBank NC\_005044.2), which is a member of haplogroup B.

<sup>b</sup> Recurrent mutations are underlined.

<sup>c</sup> Ancestral Goat Mitogenome.

**Table S7.** A comparison of the phylogeographic features of goat, taurine and horse mtDNA haplogroups identified by analyzing domestic breeds from Eurasia.

Goat <sup>a</sup> <i>C. hircus</i>			Taurine Cattle <sup>b</sup> <i>B. taurus</i>			Horse <sup>c</sup> <i>E. caballus</i>		
Hg	Age	Freq	Hg	Age	Freq	Hg	Age	Freq
ABCDG ( <i>A.d.G.M</i> ) <sup>d</sup>	136.7		REPQT ( <i>A.T.M.</i> ) <sup>e</sup>	135.3		A-R ( <i>A.M.M</i> ) <sup>f</sup>	152.6	
A	12.8	89.9%	Q1	15.5	0.8%(Q)	A	3.2	6.6%
B1	14.2	7.0%	Q2	0.9	n.a.	B	7.1	8.2%
C1a	9.2	1.6%	R1	3.0	0.6%(R)	C	4.6	1.4%
D1	n.a.	0.7%	R2	n.a.	n.a.	D	n.a.	3.6%
G	9.0	0.8%	T1	9.4	5.8%	E	n.a.	0.9%
			T2	10.4	5.1%	G	6.6	10.3%
			T3	11.3	85.5%	H	n.a.	1.0%
			T5	10.2	0.7%	I	10.6	7.4%
						J	11.2	2.4%(J/K)
						K	n.a.	n.a.
						L	6.4	31.9%
						M	4.1	5.9%
						N	4.3	6.3%
						O	n.a.	n.a.
						P	4.5	3.5%(O/P)
						Q	10.1	6.9%
						R	3.0	1.9%

<sup>a</sup> Percentage frequencies among Eurasian domestic goats and age estimates are from this study.

<sup>b</sup> Percentage frequencies among domestic taurine breeds in Eurasia are from [35], except for Q, R and T5 [36]. ML age estimates (based on coding-region substitutions) are from [37], except for Q1, Q2 and R1 [36].

<sup>c</sup> Percentage frequencies and ML age estimates (based on synonymous substitutions) are from [38].

<sup>d</sup> Ancestral domestic Goat Mitogenome.

<sup>e</sup> Ancestral Taurine Mitogenome.

<sup>f</sup> Ancestral Mare Mitogenome.

**Table S8.** Oligonucleotides used to amplify and sequence (Sanger method) the goat mitochondrial genome.

PCR ID Number	Fragment Length (bps)	Oligonucleotide for PCR			Oligonucleotide for sequencing		
		Name <sup>a</sup>	Sequence (5'→3')	T <sub>m</sub> (°C)	Name <sup>a</sup>	Sequence (5'→3')	T <sub>m</sub> (°C)
1	1884	16539F	GCTCCCTCCTAGATATTAGTGCAA	59.47	16614F	TAAGTGCCTGGGTCTTTTAC	54.97
		1779R	GACTTAAACTTGTGCAGGGAGAAA	59.42	486F	CTGGGATTAGATACCCCACT	55.37
2	1891	1601F	AGGCCTAAAAGCAGCCATC	57.80	1777R	CTTAAACTTGTGCAGGGAGA	55.28
		3491R	ATAGGGGCTGTGAAATGCTC	57.64	1685F	CCTAGACCTAATACTGGACCAC	56.79
3	1868	3128F	CATTGGAGCCTTACGAGCAG	58.71	2073F	CACGAGGGTTTTACTGTCTC	55.82
		4995R	CTTGCTTAGGGCTTTGAAGG	56.69	2633F	TACAAACAAAACCTGCCCTA	54.76
4	1907	4670F	CCCCACTATCAGGATTTGTACC	57.91	3217F	CCTTCGCCCTCTCTACACTA	57.95
		6576R	AATTGCGAAGTGGATTTTGG	55.13	3793F	AAGAACCFAAACTCTTCGT	55.11
5	1858	6221F	ACGTCGATACACGGGCTTAC	59.90	4261F	ACACAAGGTATCCCCTATC	55.68
		8078R	GAGTGCCCATTTGTGGAGAG	58.54	4736F	TCTTACCCACCTTATAGCA	54.94
6	1765	7772F	TGCCACAACCTAGACACATCG	57.92	5253F	CAGGACTTGGTAAAAAGAGG	53.51
		9536R	GGGGAGTCAAAATGCGATAG	56.29	5776F	CTACACCTAGCAGGCATCTC	57.19
7	1834	9208F	CACAGGATTCCACGGTCTTC	58.27	6313F	GGAGGCAATATCAAATGGT	52.58
		11041R	TGACGGAAGAATATGCGATG	55.74	6840F	ATTTGAAGAACCACATACG	53.60
8	1769	10725F	ACCCAACCTCTGATCCAATG	57.19	7401F	AACCTGGAGAACTACGACTG	56.60
		12493R	GAGTGGAGTAATGCTGAAACGG	59.33	7864F	GACTTCTACCACAACCCAGA	56.48
9	1923	12123F	ATCACAATACTCATCTCGTCACC	60.20	8334F	CCACTAATCCCAATGCTAGT	54.50
		14045R	TCTTTGTAATAGGTTTTGTGGGGT	58.29	8806F	CTTCCAAGGTCATCATACTCC	55.47
10	1871	13797F	TAACAAACGCCCTAGAACAA	57.51	9288F	TCACCTCTAATCATCACTTCG	54.88
		15667R	GTAGGCGAGCGGTGTAATGTA	59.93	9773F	CGAATGAACCTCAAAAAGGAC	52.83
11	1634	15177F	CAGTCGAACATCCCTACATTATTATTGG	60.12	10332F	CTTCTTCTCCGACTCCCTAT	55.46
		00167R	TTAGTCTTATTGATTTGGAGGGCGTTA	60.58	10814F	TACCTAAAGCCACGTAGAA	55.59
					11258F	TAACCTAATCTGGCCCTACCC	55.69
					11826F	TACAAATCCACCAACTACCC	54.64
					12215F	ATGGTGATATGGACGAACAG	54.94
					12709F	AACCTACCTAGCATTCTC	56.00
					13252F	TAGAAACCGCTAACATAACTCA	54.96
					13852F	AGTAGCCATAGCCGTCGTATAACC	61.87
					14221F	CCCATCAAACATCTCATCAT	52.99
					14779F	AGGAATTCCATCAGACGCAG	57.68
					15306F	TACAATCAATACACTGGTCTT	52.18
					15935F	ATTAAACGATCTCCCCCAT	53.07

<sup>a</sup>Primer names correspond to the (5') nucleotide position in GRS.

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