

**Table S1.** Oligonucleotides used for PCR amplification and sequencing of the entire *MSTN* gene. Primer pairs SHOR3737F / SHOR3737R (DNA fragment 3) and SHOR\_6F / SHOR\_6R (DNA fragment 6) were used for genotyping by sequencing the sample population.

Fragment	Primers' name	Primer sequence 5'-3'	Fragment length (bp)	Location of the primer	Annealing temperature (°C)
P	SHOR_PF	AACTTCTCTTTTAATACAGGTCTTCC	832	Promoter region	56
	SHOR_PR	GGCGCAGTTTACTGAGGATT		Exon 1	
1	SHOR_1F	AATTTTGCTTGGCATTGCTC	834	Promoter region	55
	SHOR_1R	GCAACCAAACGCAATTATGA		Intron 1	
2	SHOR_2F	AACAATCATTACCATGCCTACAGA	850	Exon 1	56
	SHOR_2R	TCCTCCCTCCCAAGAAGAAT		Intron 1	
3	SHOR3737F	TCAAAGAGGTTATAGCTCAGAGTCC	810	Intron 1	56
	SHOR3737R	GAGACACCGTGGAGGAACAT		Intron 1	
4	SHOR_4F	TCCCGAGGCTCAGTTAGTTC	779	Intron 1	56
	SHOR_4R	CAGGCTGTTGAGCCAATTT		Exon 2	
5	SHOR_5F	CATCAAACCCATGAAAGACG	805	Exon 2	56
	SHOR_5R	GCATCAACAGCCTGCAAAAT		Intron 2	
6	SHOR_6F	CCCCCAGAAGAGTGTCAAAT	849	Intron 2	56
	SHOR_6R	ACGTTACTAAGTTTACGTTAAAATGCT		Intron 2	
7	SHOR_7F	TTCAGTCTTCATGTGGTCTTGG	923	Intron 2	56
	SHOR_7R	TGACTTTTCCCTATGGCTCAA		Intron 2	
8	SHOR_8F	ACCTAGGGAATGGAGGATGG	818	Intron 2	56
	SHOR_8R	AGCACCCACAGCGATCTACT		Exon 3	
9	SHOR_9F	TGCTCTGGAGAGTGTGAATTTG	846	Exon 3	56
	SHOR_9R	TGCACCTGAAGAAAGGAGAAA		3'UTR	

**Table S2.** Levels and total numbers of horses and races according to the phenotypic fixed effects considered in the statistical models.

<b>Effect</b>	<b>levels</b>	<b>n° horses</b>	<b>n° races</b>
Sex	male	72	478
	female	108	761
Arabian blood percent	< 50	112	712
	≥ 50	68	527
Race distance (meters)	Short (1,000 - 1,400)	-	130
	Middle (1,450 - 1,800)	-	869
	Long (1,850 - 2,400)	-	240

