

Supporting Information

Strong artificial selection in domestic mammals did not result in an increased recombination rate

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Supporting Figure Legends

Figure S1. MLH1 foci counts per cell. Each dot represents the number of MLH1 foci found per cell in dogs and wolves (green and red, respectively, A), goats and ibexes (green and red, respectively, B) and sheep and mouflons (green and red, respectively, C). Black lines designate the average number of MLH1 foci found per individual.

Figure S2. Linkage disequilibrium (LD) patterns in dogs and wolves for each of the 16 genomic regions studied. Values of r^2 as a measure of pair wise LD between SNPs. The number of SNPs in wolves were thinned to match those found in dogs by selecting the wolf SNP with the same or the closest coordinates to each dog SNP. Genetic maps, based on the inference of population recombination rate (ρ), for the same markers, are plotted above each LD plot.

Figure S3. Genetic maps for the 16 genomic regions studied for dogs and wolves. Mean $\rho = 4Ner$ estimates along each fragment (penalty 5). Each dot represents the value of ρ between each pair of SNPs. The colour of the dot indicates whether the SNP is found in an intergenic region (green), an intron (pink) or an exon (blue, synonymous change; red, non-synonymous change). The red line above the x-axis represents the location of the locus associated with the phenotypic character (see Table 1). The dashed horizontal line represents the average recombination rate for the region. The vertical dashed lines designate three windows, two of 70 kb in size at the two ends of the region, and a central window of size between 60 and 160 kb (see Results and Methods for details).

Supporting Table Legends

Table S1 Methods and samples used in this study to infer recombination rates in wild and domestic species.

Table S2 Number of observed segregating sites and estimated number of recombination breakpoints found in the 16 genomic regions studied in dogs and wolves.

Supplementary Tables

Table S1 Methods and samples used in this study to infer recombination rates in wild and domestic species.

Method	Species	Common name	Origin	Sample ID
MLH1 mapping	<i>Canis familiaris</i>	Dog	Veterinary clinic	CaFa31
	<i>Canis familiaris</i>	Dog	Veterinary clinic	CaFa32
	<i>Canis familiaris</i>	Dog	Veterinary clinic	CaFa33
	<i>Canis familiaris</i>	Dog	Veterinary clinic	CaFa34
	<i>Canis familiaris</i>	Dog	Veterinary clinic	CaFa38
	<i>Canis familiaris</i>	Dog	Veterinary clinic	CaFa39
	<i>Canis lupus</i>	Wolf	Madrid Zoo	Z/LG8
	<i>Canis lupus</i>	Wolf	Madrid Zoo	Z/LG7
	<i>Capra hircus</i>	Goat	Pilas	CaHir1
	<i>Capra hircus</i>	Goat	Pilas	CaHir2
	<i>Capra hircus</i>	Goat	Pilas	CaHir3
	<i>Capra hircus</i>	Goat	Pilas	CaHir4
	<i>Capra hircus</i>	Goat	Pilas	CaHir5
	<i>Capra hircus</i>	Goat	Pilas	CaHir6
	<i>Capra pyrenaica</i>	Spanish ibex	Cazorla	CaPyr1
	<i>Capra pyrenaica</i>	Spanish ibex	Cazorla	CaPyr4
	<i>Capra pyrenaica</i>	Spanish ibex	Cazorla	CaPyr5
	<i>Capra pyrenaica</i>	Spanish ibex	Cazorla	CaPyr6
	<i>Capra pyrenaica</i>	Spanish ibex	Cazorla	CaPyr7
	<i>Capra pyrenaica</i>	Spanish ibex	Cazorla	CaPyr8
	<i>Ovis aries</i>	Sheep	Los Corrales	OvAri1
	<i>Ovis aries</i>	Sheep	Los Corrales	OvAri3
	<i>Ovis aries</i>	Sheep	Los Corrales	OvAri4
	<i>Ovis aries</i>	Sheep	Los Corrales	OvAri5
	<i>Ovis aries</i>	Sheep	Los Corrales	OvAri6
	<i>Ovis aries</i>	Sheep	Pilas	OvAri8
	<i>Ovis musimon</i>	Mouflon	Cazorla	OvMus6
	<i>Ovis musimon</i>	Mouflon	Cazalla de la Sierra	OvMus11
	<i>Ovis musimon</i>	Mouflon	Cazalla de la Sierra	OvMus13
	<i>Ovis musimon</i>	Mouflon	Cazalla de la Sierra	OvMus14
	<i>Ovis musimon</i>	Mouflon	Cazalla de la Sierra	OvMus15
Sequence data	<i>Canis familiaris</i>	Dog	Veterinary clinic	CaFa1Sp
	<i>Canis familiaris</i>	Dog	Veterinary clinic	CaFa2Sp
	<i>Canis familiaris</i>	Dog	Veterinary clinic	CaFa5Sp
	<i>Canis familiaris</i>	Dog	Veterinary clinic	CaFa8Sp
	<i>Canis familiaris</i>	Dog	Veterinary clinic	CaFa9Sp
	<i>Canis lupus</i>	Wolf	United States (captive)	465Bl
	<i>Canis lupus</i>	Wolf	United States (captive)	475Bl
	<i>Canis lupus</i>	Wolf	Spain	CaLu3M
	<i>Canis lupus</i>	Wolf	Spain	CaLu8M
	<i>Canis lupus</i>	Wolf	Spain	CaLu9M
	<i>Canis lupus</i>	Wolf	Spain	CaLu10M
	<i>Canis lupus</i>	Wolf	Sweden	CaLu4M
	<i>Canis lupus</i>	Wolf	Sweden	CaLu5M
	<i>Canis lupus</i>	Wolf	Sweden	CaLu6M

<i>Canis lupus</i>	Wolf	Sweden	CaLu7M
<i>Canis lupus</i>	Wolf	Finland	FIN7462
<i>Canis lupus</i>	Wolf	Finland	FIN7760
<i>Canis lupus</i>	Wolf	Finland	FIN8174
<i>Canis lupus</i>	Wolf	Italy	IT001
<i>Canis lupus</i>	Wolf	Italy	IT050
<i>Canis lupus</i>	Wolf	Italy	IT973
<i>Canis lupus</i>	Wolf	North Western Territories	NRS2010.005
<i>Canis lupus</i>	Wolf	North Western Territories	NRS2010.016
<i>Canis lupus</i>	Wolf	North Western Territories	NRS2010.021
<i>Canis lupus</i>	Wolf	British Columbia	ex111
<i>Canis lupus</i>	Wolf	British Columbia	ex112

Table S2 Number of observed segregating sites and estimated number of recombination breakpoints in the 16 genomic regions studied in dogs and wolves.

Dogs		Spain + Italy wolves		Sweden+Finland wolves		North American wolves	
chr	Segr. Sites	Breakpoints	Segr. Sites	Breakpoints	Segr. Sites	Breakpoints	Breakpoints
1	247	9	268	7	324	0	353
9	198	9	392	16	402	11	388
10	46	2	72	2	92	1	290
12	485	25	563	23	642	19	854
13	494	11	481	11	606	31	748
15	196	9	262	15	285	9	447
16a	283	13	474	15	396	12	471
16b	928	51	907	42	1181	66	1255
17	435	28	485	28	503	17	598
18a	313	10	462	17	544	26	531
18b	937	44	1197	59	1212	66	1246
20	459	20	745	51	723	38	744
22	349	19	441	18	553	29	640
25	613	37	830	36	858	34	1144
27	770	40	1084	48	1159	61	1445
32	286	16	471	19	395	15	572

















