

## Supporting Information

### Phenotypic diversity in domestic mammals does not result from an increased recombination rate

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This section contains: **Supporting Figures**  
**Supporting Tables**

#### Supporting Figure Legends

**Figure S1. MLH1 foci counts for all samples.** Graphs display MLH1 counts for all individuals analyzed: 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 represent the average found in each sample (A-C).

**Figure S2. LD patterns in dogs and wolves for each of the regions studied.** Values of  $r^2$  as a measure of pairwise LD between SNPs. Wolf genotype data was thinned to match the dog data by selecting the SNP with the same or the closest coordinates to each dog SNP. LDhat maps, based on the inference of population recombination rate ( $\rho$ ), 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  $\rho = 4N_e r$  estimates along each fragment (penalty 5). Each dot represents the value of  $\rho$  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 represents the location of the locus associated with the phenotypic character (see Table 1). The dashed line is the average recombination rate for the region.

## **Supporting Table Legends**

**Table S1** Approaches and samples used in this study to compare recombination between wild and domestic species.

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

## Supporting Tables

**Table S1** Approaches and samples used in this study to compare recombination between wild and domestic species

<b>Approach</b>	<b>Species</b>	<b>Common name</b>	<b>Origin</b>	<b>Sample ID</b>	
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	
	Population genomics on 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)	465B1	
<i>Canis lupus</i>		Wolf	United States (captive)	475B1	

<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

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

chr	Dogs		Spain + Italy wolves		Sweden+Finland wolves		North American wolves	
	Segr. Sites	Breakpoints	Segr. Sites	Breakpoints	Segr. Sites	Breakpoints	Segr. Sites	Breakpoints
<b>1</b>	247	9	268	7	324	0	353	17
<b>9</b>	198	9	392	16	402	11	388	10
<b>10</b>	46	2	72	2	92	1	290	4
<b>12</b>	485	25	563	23	642	19	854	33
<b>13</b>	494	11	481	11	606	31	748	31
<b>15</b>	196	9	262	15	285	9	447	18
<b>16a</b>	283	13	474	15	396	12	471	20
<b>16b</b>	928	51	907	42	1181	66	1255	71
<b>17</b>	435	28	485	28	503	17	598	38
<b>18a</b>	313	10	462	17	544	26	531	30
<b>18b</b>	937	44	1197	59	1212	66	1246	54
<b>20</b>	459	20	745	51	723	38	744	39
<b>22</b>	349	19	441	18	553	29	640	33
<b>25</b>	613	37	830	36	858	34	1144	55
<b>27</b>	770	40	1084	48	1159	61	1445	87
<b>32</b>	286	16	471	19	395	15	572	32



















