Figure S1.

Clade	Median	Mean
Asian Spitz	0	1575000
Mediterranean	516900	1318000
Asian Toy	1766000	2824000
UK Rural	2128000	3061000
European Mastiff	2256000	3319000
Continental Herder	2277000	3163000
Scent Hound	2325000	3058000
American Toy	2417000	3406000
Poodle	2485000	3380000
Nordic Spitz	2525000	3593000
Alpine	2590000	3839000
Pointer Setter	2627000	3455000
New World	2704000	4466000
Drover	2794000	4051000
Retriever	2888000	3888000
Spaniel	2958000	3951000
Small Spitz	3011000	4141000
Schnauzer	3017000	4101000
Toy Spitz	3159000	4282000
American Terrier	3356000	4565000
Pinscher	3459000	4507000

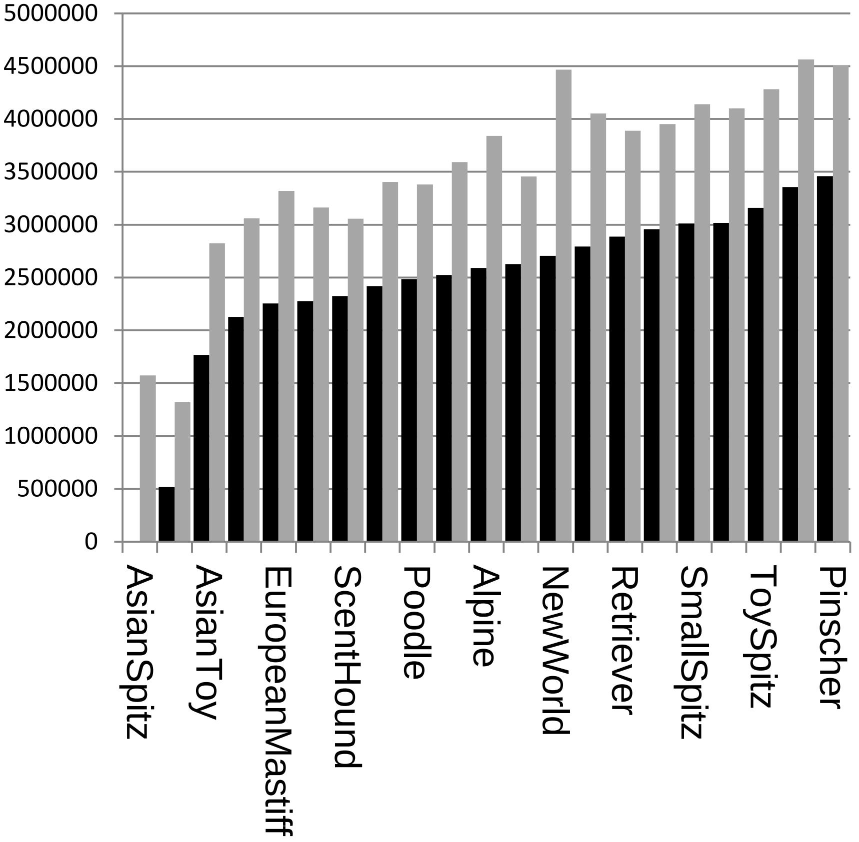

Figure S1. The mean and median haplotype sharing of the individual dogs from each clade with dogs from all other clades, Related to Figure 4. The table and graph are both ordered from lowest to highest median haplotype sharing.

Figure S2.

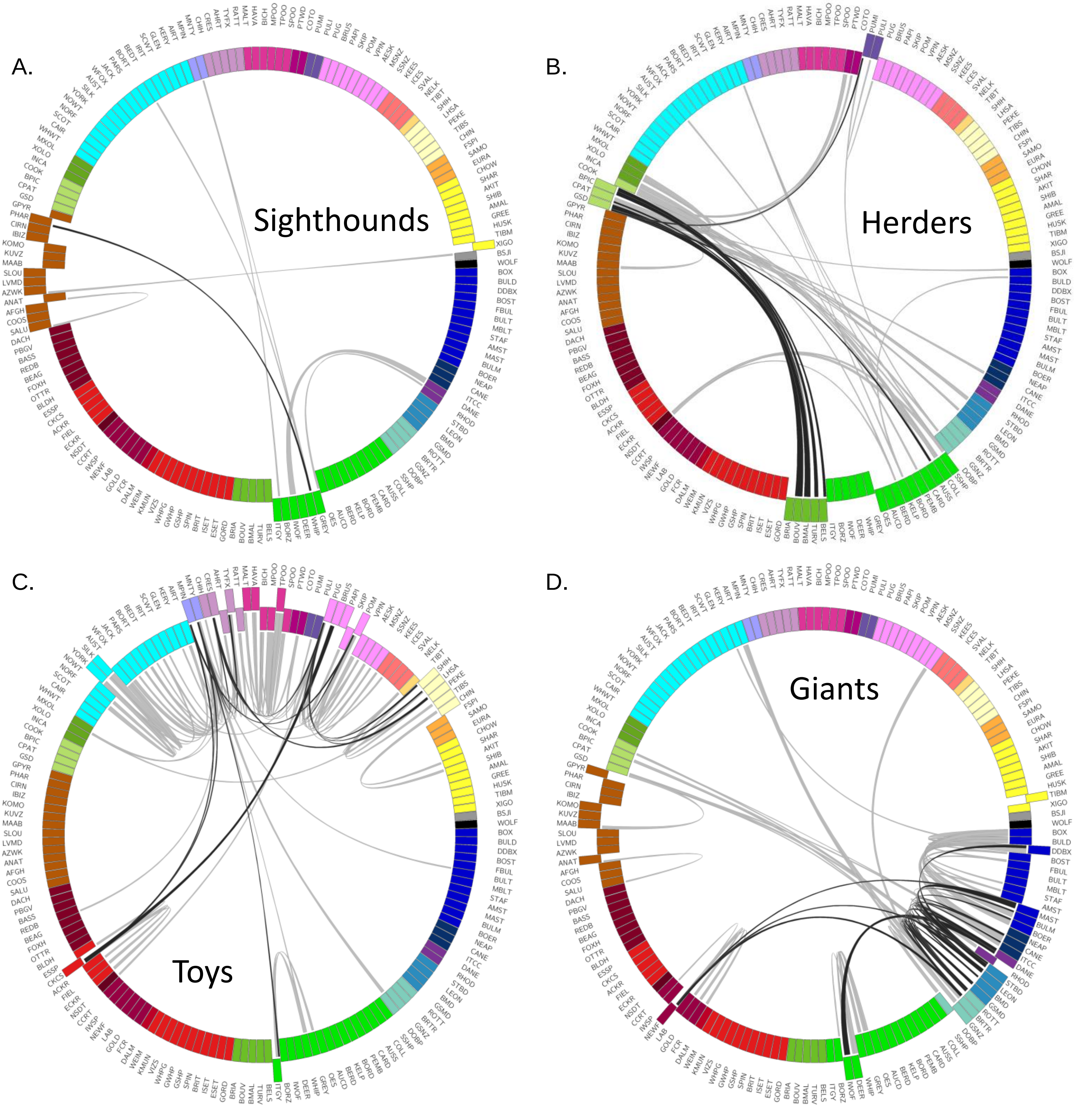

Figure S2. Circos plots showing haplotype sharing among unrelated breeds with similar traits, Related to Figure 7. Links between breeds are shown if the median paired haplotype sharing exceeds the 95%threshold. Sharing between breeds with similar traits is shown in black, sharing with other breeds is shown in grey. Haplotype sharing among the breeds in the same clade with the same phenotype is not shown but can be found in Figure S1. Breeds sharing the trait are shown in the outer circle. A) Haplotype sharing among breeds that display the sighthound build and behavior. B) Breeds that work as sheep herders or are included in the Herding group by the AKC. C) Haplotype sharing among toy breeds as determined by AKC or FCI standards. D) Haplotype sharing among giant breeds, average breed weight greater than the average weight of the Grey Wolf.

Data File S1. Bar graphs of haplotype sharing distributions, Related to Figure 3. Distributions are shown as the total sharing between individual dogs of each breed for all 161 dog breeds, three varieties, three country of origin populations and two wild canid species. Breeds are colored and ordered according to clade position in Figure 1. Graphs are presented in alphabetical order by breed name.

Data File S2. Nexus style tree file for breed cladogram, Related to Figure1. File produces a bootstrapped consensus cladogram of 161 breeds and the Grey Wolf, rooted with the Golden Jackal.

Table S1. List of all dog breed samples used in the analyses and their respective data repositories or sources, Related to Figure 1.

Legend:

* - Breeds included in the clade with <50% bootstrap support

1 - Vaysse A, et al. (2011) Identification of genomic regions associated with phenotypic variation between dog breeds using lelection mapping, PLoS Genet. 7(10): e1002316

2 - Hayward JJ, et al. (2016) Complex disease and phenotype mapping in the domestic dog, Nature Commun. 7:10460

3 - Mizzou Comparative Canine Resequencing: BioProject PRJNA263947; samples 86405, 88986, 91180

COO = dogs collected in the country from which the breed originated, other than the United States

Table S2. Mean haplotype sharing totals that reach the 95% significance level between all pairs of breeds, Related to Figure 4.

Legend:

* Breeds that are included in a clade with <50% bootstrap support