

Table S1. Sequence data generated, rate of PCR duplicates, alignment statistics, and mean depth of coverage per sample.

	Basenji	Dingo	Israeli wolf	Chinese wolf	Croatian wolf	Golden jackal
Total reads ^a	969.0	2194.5	1803.5	694.0	2180.8	3365.8
Reads aligned ^a	816.6	1602.2	1249.5	652.7	1464.5	2437.8
% Reads aligned	84.3	73.0	69.3	94.0	67.2	72.4
% PCR duplicates	28.5	28.5	20.2	3.2	16.0	51.5
Uniquely aligned reads ^a	581.3	1145.5	997.3	632.0	1229.8	1181.8
Uniquely aligned bases (Gb)	28.1	70.7	52.7	61.3	62.4	59.5
Mean coverage	12.6x	25.75x	21.6x	24.6x	25.3x	23.8x

^a Millions of reads