



**Supplementary Table S2. Read alignment to the *Canis lupus familiaris* genome**

Sample	Total reads	Total mapped reads	Mapping rate (%)
NI R1	85606752	81804853	95.56
NI R2	84356860	80920542	95.93
NI R3	93253244	89230524	95.69
BCN R1	89101392	70090761	78.66
BCN R2	93735740	73992850	78.94
BCN R3	82088190	64195954	78.20
BOS R1	86499804	68713256	79.44
BOS R2	80736160	64485975	79.87
BOS R3	81701352	64312991	78.72