Table S4. Summary statistics of the targeted resequencing.
Data is reported for the full or repeat-masked target sequence (CamFam 2.0 Chr13: 22,937,592-24,414,650). Three control breeds (Pug, Neapolitan Mastiff, Standard Poodle) and two of each type of Shar-Pei (M= Meatmouth type and T= traditional type) were sequenced. The two traditional type Shar-Pei were sequenced at different read lengths but were aligned using the same strict criteria (allowing two mismatches per read) and therefore vary in the percentage of mapped reads as well as coverage when compared to the other individuals. Individual 7 was sequenced from whole genome amplified material and this may have impacted the ability to map reads and detect SNP.

Nr	Breed	No of reads	Full Reference Sequence in Target Region			Repeat-masked Reference Sequence in Target Region		
			% mapped[1]	Coverage (x)[2]	No of SNPs[3]	% mapped[1]	Coverage (x)[2]	No of SNPs[3]
1	Pug	9,868,613	74	178	3381	45	171	1630
2	N. Mastiff	11,011,789	92	246	2773	60	256	1380
3	Poodle	8,672,727	79	165	2646	48	161	1356
4	Shar-Pei (M)	10,789,354	90	236	3399	58	245	1791
5	Shar-Pei (M)	9,715,905	75	176	3343	47	176	1666
6	Shar-Pei (T)	26,710,494	41	547	4363	24	513	1978
7	Shar-Pei (T)	23,132,652	30	214	7942	18	204	3952

[1]Proportion of reads aligned the dog reference sequence (CanFam 2.0)
[2]Average number of sequences covering each base position
[3]Number of SNPs identified in each resequenced individual compared to the reference genome (CanFam 2.0)