

Table S2. SNPs highly associated with Familial Shar-Pei Fever on Chromosome 13.

A summary of 7 SNPs on chromosome 13 that together formed a peak of association to the susceptibility of Familial Shar-Pei Fever (FSF). 41 Shar-Pei classified as affected ($n=24$, FSF+ and FSF+A) and unaffected ($n=17$, H+) by FSF were genotyped with an 18 K SNPs and analyzed based on 100,000 permutations. After correcting for stratification two outliers (affected by FSF) were removed and the association remained (best SNP, $p = 0.01$).

Position (bp)	Before removing outliers (24 cases + 17 controls)		After removing outliers (22 cases + 17 controls)	
	p raw (not permuted)	p genome (permuted)	p raw (not permuted)	p genome (permuted)
chr13:27,913,803	7.0e-07	0.005	2.3e-06	0.014
chr13:28,879,708	1.3e-06	0.010	3.5e-06	0.023
chr13:30,775,049	2.5e-06	0.019	8.0e-06	0.052
chr13:29,058,515	2.9e-06	0.023	7.3e-06	0.049
chr13:22,467,679	7.0e-06	0.049	2.1e-05	0.12
chr13:23,430,873	7.0e-06	0.051	2e-05	0.12
chr13:29,629,329	1.0e-05	0.077	2.6e-05	0.15