Supplemental Table 2 Genotypic and allelic frequencies of ANXA11 polymorphisms in the controls and patients with sarcoidosis

Variable	**Controls** (n=418)		**Sarcoidosis** (n=412)		***P*-value**[a]	**OR, 95% CI**
	No.	%	No.	%		
rs2245168					0.920	
CC	156	37.3	150	36.4	0.791	1.04, 0.74-1.38
CT	200	47.9	197	47.8	0.955	0.99, 0.76-1.30
TT	62	14.8	65	15.8	0.781	0.95, 0.65-1.39
Per T allele	324	38.8	327	39.7	0.698	1.04, 0.85-1.27
rs2236558					0.172	
GG	118	28.2	104	25.2	0.72	1.06, 0.77-1.45
TG	190	45.5	214	51.9	0.060	0.77, 0.59-1.01
TT	110	26.3	94	22.8	0.073	1.33, 0.97-1.82
Per T allele	410	49.0	402	48.8	0.917	0.99, 0.82-1.20
rs7067644					0.173	
AA	152	36.4	176	42.7	0.059	0.76, 0.58-1.01
GA	206	49.3	182	44.2	0.137	1.23, 0.94-1.68
GG	60	14.4	54	13.1	0.597	1.11, 0.75-1.65
Per G allele	326	38.0	290	35.2	0.109	0.85, 0.70-1.04
rs12763624					0.118	
TT	126	75.6	150	36.4	0.008	0.68, 0.51-0.91
CT	216	51.7	186	45.2	0.059	1.30, 0.99-1.71
CC	76	18.2	76	18.5	0.411	1.16, 0.81-1.67
Per C allele	368	44.0	338	41.0	0.216	0.88, 0.73-1.08
rs2573351					0.437	

TT	120	28.7	104	25.2	0.263	1.19, 0.88-1.62
CT	202	48.3	216	52.4	0.238	0.85, 0.65-1.12
CC	96	23.0	92	22.3	0.826	1.04, 0.75-1.44
Per C allele	394	47.1	400	48.5	0.564	1.06, 0.87-1.28
rs10887581					0.290	
TT	114	27.3	96	23.3	0.190	1.23, 0.90-1.69
TC	190	45.5	208	50.5	0.148	0.82, 0.62-1.07
CC	114	27.3	108	26.2	0.729	1.06, 0.78-1.44
Per C allele	418	50.0	424	51.5	0.583	1.06,0.87-1.29
rs11201989					0.144	
GG	130	31.1	128	31.1	0.995	1.00, 0.75-1.34
GC	218	52.2	194	47.1	0.141	1.23, 0.93-1.62
CC	70	16.8	90	21.9	0.060	0.71, 0.50-1.01
Per C allele	358	42.8	374	45.4	0.29	1.11, 0.91-1.35
rs2573353					0.918	
CC	178	42.6	176	42.7	0.957	0.99, 0.75-1.31
CA	196	46.9	192	46.6	0.921	1.01, 0.77-1.33
AA	44	10.5	44	10.7	0.941	0.98, 0.63-1.53
Per A allele	284	34.0	280	34.0	0.997	1.00, 0.82-1.23
rs2789695					0.918	
TT	178	42.6	180	34.0	0.740	0.95, 0.73-1.26
CT	188	45.0	184	44.7	0.920	1.01, 0.77-1.33
CC	52	12.4	48	11.7	0.73	1.08, 0.71-1.64
Per C allele	292	34.9	280	34.0	0.69	0.96, 0.78-1.17
rs2573356					0.892	
CC	118	28.2	112	27.2	0.742	1.05, 0.78-1.43

CT	190	45.5	194	47.1	0.639	0.94, 0.71-1.23
TT	110	26.3	106	25.7	0.843	1.03, 0.76-1.41
Per T allele	410	49.0	406	49.3	0.926	0.99, 0.82-1.20
rs2819945					0.101	
GG	119	28.5	130	31.6	0.294	0.85, 0.63-1.15
GA	221	52.9	188	45.6	0.030	1.35, 1.03-1.78
AA	78	18.7	94	22.8	0.138	0.78, 0.55-1.09
Per A allele	377	45.1	376	45.6	0.827	1.02, 0.84-1.24
rs11202059					0.064	
GG	106	25.4	128	31.1	0.067	0.75, 0.56-1.02
GA	226	54.1	190	46.1	0.021	1.38, 1.05-1.81
AA	86	20.6	94	22.8	0.429	0.88, 0.63-1.22
Per A allele	398	47.6	378	45.9	0.479	0.93, 0.77-1.13

[a] *P*-value was calculated by 2×3 and 2×2 chi-squared tests based on codominant, dominant for the rare allele, heterosis and recessive for the rare allele models of inheritance.

Alpha value is adjusted by Bonferroni correction and statistically significant results ($P<0.003$)