

Supplementary Table 1. Genotype and allele frequencies of *L-SIGN* in Chinese random controls and Caucasians of European descent (CEPH).

a

Genotypes	Chinese random controls	(%)	CEPH [#]	(%)
5/5	10	(2.6)	2	(3.4)
5/9	15	(3.9)	2	(3.4)
6/5	4	(1.0)	3	(5.2)
6/6	2	(0.5)	2	(3.4)
6/9	4	(1.0)	0	(0.0)
7/4	0	(0.0)	4	(6.9)
7/5	63	(16.6)	17	(29.3)
7/6	25	(6.6)	10	(17.2)
7/7	191	(50.3)	15	(25.9)
7/8	0	(0.0)	0	(0.0)
7/9	60	(15.8)	3	(5.2)
9/9	6	(1.6)	0	(0.0)
Total	380		58	

b

Alleles	Chinese random controls	(%)	CEPH [#]	(%)
4	0	(0.0)	4	(3.4)
5	102	(13.4)	26	(22.4)
6	37	(4.9)	17	(14.7)
7	530	(69.7)	64	(55.2)
8	0	(0.0)	0	(0.0)
9	91	(12.0)	5	(4.3)

c

Genotypes	Chinese random controls	(%)	CEPH [#]	(%)
Heterozygotes	171	(45.0)	39	(67.2)
Homozygotes	209	(55.0)	19	(32.8)

(a) *L-SIGN* genotypes were in HWE in the Chinese random controls (see Table 1 of the article) and the CEPH group (Hardy-Weinberg Exact Tests, $p=0.797$ by Markov chain method). There is significant difference in genotype frequencies between the two groups: CLUMP $T_1=59.87$, $p<0.0001$ by CLUMP.

(b) There is significant difference in allele frequencies between Chinese random controls and Caucasians of European descent (CEPH): CLUMP $T_1 = 55.96$, $p < 0.0001$ by CLUMP.

(c) There is also significant difference in the frequencies of heterozygotes and homozygotes between Chinese and Caucasians of European descent: $\chi^2_{1}=9.97$, $p=0.002$

[#]Caucasian of European descent samples analyzed were obtained from CEPH Reference Families after exclusion of genetically related individuals.