

Table S1. Genetic variations identified in the *ICAM4* gene

Pattern	Nucleotide substitution (position) *						Number of samples observed (n)		
	5'UTR	Exon 1		Intron 1 (IVS1)		Exon 2	Exon 3	Caucasian	African American
	-286C>T	c.188A>G	c.299A>G	IVS1+49A>C	IVS1+124C>T	c.545G>C	c.773A>C		
1	C	A	A	A	C	G	A	36	60
2	T	A	A	A	C	G	A	13	1
3	C/T	A	A	A	C	G	A	44	22
4	C	A/G	A	A	C	G	A	0	1
5	C	A	A	A/C	C	G	A	1	0
6	C	A	A	A	C/T	G	A	2	0
7	C	A	A	A	C	G/C	A	0	5
8	C	A	A	A	C	G	A/C	1	0
9	C/T	A	A/G	A	C	G	A	0	1
10	C/T	A	A	A	C	G/C	A	0	1
Total								97	91

* within 1920 nucleotides of the *ICAM4* gene relative to NCBI Reference Sequence NG_007728.1. Numbering is according to ICAM4 Isoform 3 (NM_001039132.2, NP_001034221.1). Variant nucleotides and heterozygous nucleotide positions are in bold.

Table S2. Positions of the non-synonymous genetic variations in the 3 isoforms of the *ICAM4* gene

Allele*	dbSNP reference no.	<i>ICAM4</i> cDNA (isoform)		
		Isoform Long (1) NM_001544.4	Isoform Short (2) NM_022377.3	Isoform 3 NM_001039132.2
KF725836	rs150654072	c.188A>G (p.Lys63Arg)	c.188A>G (p.Lys63Arg)	c.188A>G (p.Lys63Arg)
KF725831	rs77493670	c.299A>G (p.Gln100Arg)	c.299A>G (p.Gln100Arg)	c.299A>G (p.Gln100Arg)
KF725832	rs36023325	c.622G>C (p.Val208Leu)	c.622G>C (p.Val208Leu)	c.545G>C (p.Arg182Pro)
KF725833	rs201399464	Not present	Not present	c.773A>C (p.Lys258Thr)

* GenBank nucleotide database accession number

Table S3. Variant allele frequencies (VAF) in the populations

dbSNP reference no.	Donors observed (n) *		VAF observed				NHLBI ESP VAF (%)
	Caucasians	African Americans	Caucasians		African Americans		
			Mean †	95% CI ‡	Mean †	95% CI ‡	
rs3093030	57	25	36%	25.2-49.8%	14%	7.6 - 23.5%	NA
rs34385135	1	0	1%	0.2 - 5.6%	0%	0 - 3.7%	1%
rs35165411	2	0	1%	0.2 - 5.6%	0%	0 - 3.7%	1%
rs201399464	1	0	1%	0.2 - 5.6%	0%	0 - 3.7%	NA
rs150654072	0	1	0%	0 - 3.7%	1%	0.2 - 5.6%	0.4%
rs77493670	0	1	0%	0 - 3.7%	1%	0.2 - 5.6%	0.04%
rs36023325	0	7	0%	0 - 3.7%	4%	1.1 - 9.2%	2%

* All observations were heterozygous with the exception of 13 and 1 homozygous observations for rs3093030 in Caucasians and African Americans, respectively

† (2 x homozygous + 1 x heterozygous)/total number of alleles

‡ 95% confidence interval (CI), Poisson distribution, two sided

NHLBI ESP – NHLBI Exome Sequencing Project (<http://evs.gs.washington.edu/EVS>). Total number of samples in Caucasians = 4300; and total number of samples in African Americans = 2203