Table S1. *ICAM4* genotypes observed in 60 Ethiopian individuals, 57 from Gambela and 3 from Addis Ababa

	Genotype*		
Genotype number	rs3093030	rs5030384	Total
NG_007728.1	C/C	G/G	54†
01	C/T	G/G	3
02	C/C	G/A	2
03	T/T	G/G	1†

*   The nucleotides at the 2 SNP positions are shown in 5'- to 3'- orientation (see Table 2). The remaining 1,918 nucleotide positions that we determined had no variation relative to the reference sequence NG_007728.1. The genotypes in red show homozygous and heterozygous variations with respect to the reference sequence NG_007728.1.

†   3 samples drawn in Addis Ababa:[3] 2 samples with genotype NG_007728.1 and 1 sample with genotype number 03.

Table S2. Genetic variations detected in *ICAM4* gene in 60 Ethiopian individuals, 57 from Gambela and 3 from Addis Ababa

Location	Nucleotide change*	dbSNP reference no.	Homozygote reference	Heterozygote variant	Homozygote variant	VAF	HWE (p)	Caucasian VAF[2]	African American VAF[2]	Global VAF†
			Observations in present study (n=60)						African	
Promoter	c.-286C>T	rs3093030	56	3	1	0.042	0.004‡	0.361	0.143	0.320
Intron 1	c.394+7G>A	rs5030384	58	2	0	0.017	0.896	0.000	0.000	0.004

*   Nucleotide substitutions are shown relative to the reference sequence (NG_007728.1). Nucleotide positions are defined using the first nucleotide of the coding sequence (CDs) of NM_001544.5 isoform 1 as nucleotide position 1

†   Global VAF from 1000Genome, TOPMed (nhlbiwgs.org) and gnomAD (http://gnomad.broadinstitute.org/) databases

‡   A p value of <0.05 indicates a deviation from the Hardy Weinberg Equilibrium (HWE), see main text for explanation.

VAF − variant allele frequency

HWE – Hardy-Weinberg equilibrium