

Table S2

Comparison of the average rates of respiratory infections for all the patients (number of respiratory infections/ time at risk in person*years), in the presence and in the absence of the *TLR2* variants.

	Genotype	The average rates of respiratory infections (in person*years) for all the patients	
		Presence	Absence
Individual loci			
-196 to -174 indel			
	Ins/Ins*	0,25	0,21
	Ins/Del	0,2	0,26
	Del/Del*	0,32	0,23
	Del	0,21	0,25
	Ins	0,23	0,32
rs4696480			
	TT*	0,27	0,21
	TA	0,23	0,24
	AA	0,18	0,25
	A	0,21	0,27
	T*	0,25	0,18
(GT)n (intron 2) ¹			
	[Other than S]/[Other than S]*	0,24	0,21
	[Other than S]/S	0,17	0,28
	S/S*	0,37	0,23

	S	0,21	0,24
	[Other than S]	0,23	0,37
Haplotypes ^{2,3}			
Hap1**			
[Ins]-A-[M or L]	Hap1/Hap1*	0,39	0,23
	Hap1/[Other than Hap1]	0,09	0,27
	[Other than Hap1]/[Other than Hap1]*	0,26	0,15
	Hap1	0,15	0,26
	[Other than Hap1]	0,23	0,39
Hap2			
[Ins]-A-[S]	Hap2/Hap2	NA	0,23
	Hap2/[Other than Hap2]	0,06	0,24
	[Other than Hap2]/[Other than Hap2]*	0,24	0,06
	Hap2	0,06	0,24
	[Other than Hap2]	0,23	NA
Hap3**			
[Ins]-T-[M or L]	Hap3/Hap3*	0,28	0,21
	Hap3/[Other than Hap3]*	0,23	0,24
	[Other than Hap3]/[Other than Hap3]	0,18	0,25
	Hap3*	0,25	0,18
	[Other than Hap3]	0,21	0,28
Hap4			
[Ins]-T-[S]	Hap4/Hap4	NA	0,23
	Hap4/[Other than Hap4]	0,12	0,24
	[Other than Hap4]/[Other than Hap4]*	0,24	0,12
	Hap4	0,12	0,24

	[Other than Hap4]	0,23	NA
Hap5**			
[Del]-A-[M or L]	Hap5/Hap5	0,12	0,24
	Hap5/[Other than Hap5]	0,21	0,25
	[Other than Hap5]/[Other than Hap5]*	0,26	0,2
	Hap5	0,2	0,26
	[Other than Hap5]*	0,24	0,12
Hap6			
[Del]-A-[S]	Hap6/Hap6	NA	0,22
	Hap6/[Other than Hap6]	0,14	0,24
	[Other than Hap6]/[Other than Hap6]	0,23	0,26
	Hap6*	0,26	0,22
	[Other than Hap6]	0,22	NA
Hap7			
[Del]-T-[M or L]	Hap7/Hap7	NA	0,23
	Hap7/[Other than Hap7]*	0,31	0,23
	[Other than Hap7]/[Other than Hap7]	0,23	0,31
	Hap7*	0,31	0,23
	[Other than Hap7]	0,23	NA
Hap8			
[Del]-T-[S]	Hap8/Hap8	NA	0,23
	Hap8/[Other than Hap8]*	0,32	0,23
	[Other than Hap8]/[Other than Hap8]	0,23	0,32
	Hap8*	0,32	0,23
	[Other than Hap8]	0,23	NA

¹For the *TLR2* microsatellite (GT)_n STR (intron 2) STR, the following subdivision based on the number of repeats (n) was used: Allele S, n ≤ 16; Allele M, 17 ≤ n ≤ 22, and Allele L, n ≥ 23 (Yim et al., 2006).

²For haplotype designation allele annotations are in the following order 5' – 196 to 174 a 22 bp nucleotide indel (untranslated exon 1) – SNP rs4696480, c.-16934A>T (promotor) – the (GT)_n STR polymorphism (intron 2) – 3': Hap1, 101 ([Ins]-A-[M or L]); Hap2, 100 ([Ins]-A-[S]); Hap3, 111 ([Ins]-T-[M or L]); Hap4, 110 ([Ins]-T-[S]); Hap5, 001 ([Del]-A-[M or L]); Hap6, 000 ([Del]-A-[S]); Hap7, 011 ([Del]-T-[M or L]); Hap8, 010 ([Del]-T-[S]). In this study “Time at risk” is equal to “Time under observation”. For the *TLR2* (GT)_n (intron 2) STR, the following subdivision based on the number of repeats (n) was used: Allele S, n ≤ 16; Allele M, 17 ≤ n ≤ 22, and Allele L, n ≥ 23, which was further simplified as a binary variable S versus others (M or L) (Yim et al., 2006).

³For descriptive statistics the haplotypes were considered as alleles.

Notes:

*Possibly deleterious genotype, i.e. the presence of the genotype is associated with an increase in incidence (positive statistical effect) corresponding to an unfavorable clinical effect.

**Haplotypes with a frequency ≥ 5% in the study population.

Abbreviations: SCA, sickle cell anemia; SNP, single nucleotide polymorphism; Hap, haplotype; NA, not applicable; Indel, insertion or deletion variation; Del, deletion; Ins, insertion.