

Table S3

Comparison using the Fisher's exact test, of the number of patients having had a severe bacterial infection at least once in their follow-up, in the presence and in the absence of the genotype.

	Genotype	Number of cases having had severe bacterial infections		OR (95% CI)	Fisher's exact test ¹ p-value
		Presence	Absence		
Individual loci					
-196 to -174del					
	Ins/Ins	5	45		
	Ins/Del	3	36		1
	Del/Del	1	5		1
Del	Presence	4	41		
	Absence	5	45		1
Ins	Presence	8	81		
	Absence	1	5		1
rs4696480					
	TT	4	29		
	TA	5	38		1
	AA	0	19		0.2836
A	Presence	5	57		

	Absence	4	29	0.7145
T	Presence	9	67	
	Absence	0	19	0.1966
GTn (2 nd intron) ²				
	[Other than S]/[Other than S]	7	68	
	[Other than S/S]	2	15	1
	S/S	0	3	1
S	Presence	2	18	
	Absence	7	68	1
[Other than S]	Presence	9	83	
	Absence	0	3	1
Haplotypes ^{3,4}				
Hap1 as an allele				
	Hap1/Hap1	0	5	
	Hap1/[Other than Hap1]	1	18	1
	[Other than Hap1]/[Other than Hap1]	8	63	1
Hap1	Presence	1	23	
	Absence	8	63	0.4409
[Other than Hap1]	Presence	9	81	
	Absence	0	5	1
Hap2 as an allele				

Hap2/Hap2		0	0	
Hap2/[Other than Hap2]		1	4	1
[Other than Hap2]/[Other than Hap2]		8	82	1
Hap2	Presence	1	4	
	Absence	8	82	0.3989
[Other than Hap2]	Presence	9	86	
	Absence	0	0	1
Hap3 as an allele				
Hap3/Hap3		3	23	
Hap3/[Other than Hap3]		5	42	1
[Other than Hap3]/[Other than Hap3]		1	21	0.6142
Hap3	Presence	8	65	
	Absence	1	21	0.4593
[Other than Hap3]	Presence	6	63	
	Absence	3	23	0.7016
Hap4 as an allele				
Hap4/Hap4		0	0	
Hap4/[Other than Hap4]		0	5	1
[Other than Hap4]/[Other than Hap4]		9	81	1
Hap4	Presence	0	5	
	Absence	9	81	1
[Other than Hap4]	Presence	9	86	

	Absence	0	0	1
Hap5 as an allele				
	Hap5/Hap5	0	3	
	Hap5/[Other than Hap5]	2	28	1
	[Other than Hap5]/[Other than Hap5]	7	55	1
Hap5				
	Presence	2	31	
	Absence	7	55	0.4892
[Other than Hap5]				
	Presence	9	83	
	Absence	0	3	1
Hap6 as an allele				
	Hap6/Hap6	0	1	
	Hap6/[Other than Hap6]	1	8	1
	[Other than Hap6]/[Other than Hap6]	8	77	1
Hap6				
	Presence	1	9	
	Absence	8	77	1
[Other than Hap6]				
	Presence	9	85	
	Absence	0	1	1
Hap7 as an allele				
	Hap7/Hap7	0	0	
	Hap7/[Other than Hap7]	2	1	1
	[Other than Hap7]/[Other than Hap7]	7	85	1
Hap7				
	Presence	2	1	

	Absence	7	85	24.29 [1.95-302.20]	0.0230
[Other than Hap7]	Presence	9	86		
	Absence	0	0		1
Hap8 as an allele					
Hap8/Hap8		0	0		
Hap8/ [Other than Hap8]		0	2		1
[Other than Hap8]/[Other than Hap8]		9	84		1
Hap8	Presence	0	2		
	Absence	9	84		1
[Other than Hap8]	Presence	9	86		
	Absence	0	0		1

¹The Fisher's exact test refers to the two-tailed Fisher's exact test

²For the *TLR2* locus GTn (2nd intron), the following subdivision based on the number of GT copies (n) was used: Allele S, $n \leq 16$; Allele M, $17 \leq n \leq 22$, and Allele L, $n \geq 23$, (Yim et al., 2006).

³For 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]). For the *TLR2* (GT)n (intron 2) STR, the following subdivision based on the number of repeats (n) was used: Allele S, $n \leq 16$; Allele M, $17 \leq n \leq 22$, and Allele L, $n \geq 23$, which was further simplified as a binary variable S versus others (M or L) (Yim et al., 2006).

⁴For descriptive statistics the haplotypes were considered as alleles.

Abbreviations: SCA, sickle cell anemia; SNP, single nucleotide polymorphism; Hap, haplotype; CI, Confidence interval; OR, odds ration; NA, not applicable; ND, not done; Indel, insertion or deletion variation; Del, deletion; Ins, insertion.