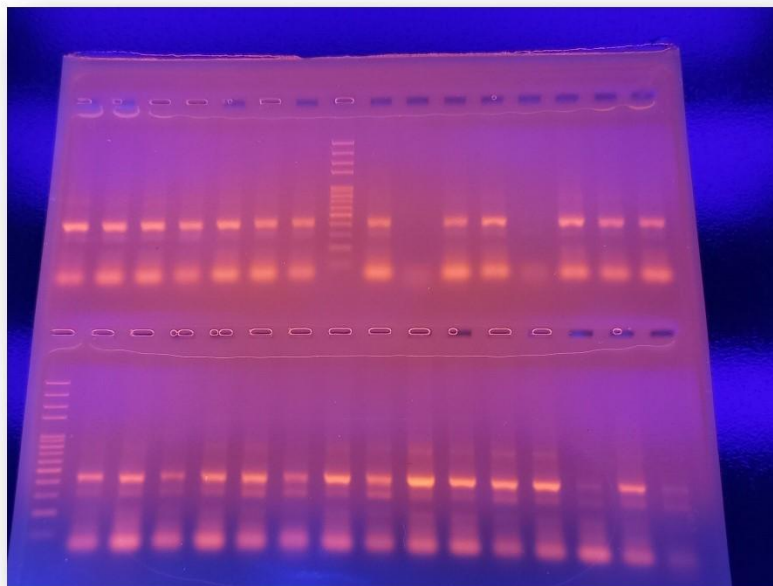**Supplementary Table 1:**

S1. Genetic features of studied SNPs according to National Center for Biotechnology Information (NCBI).

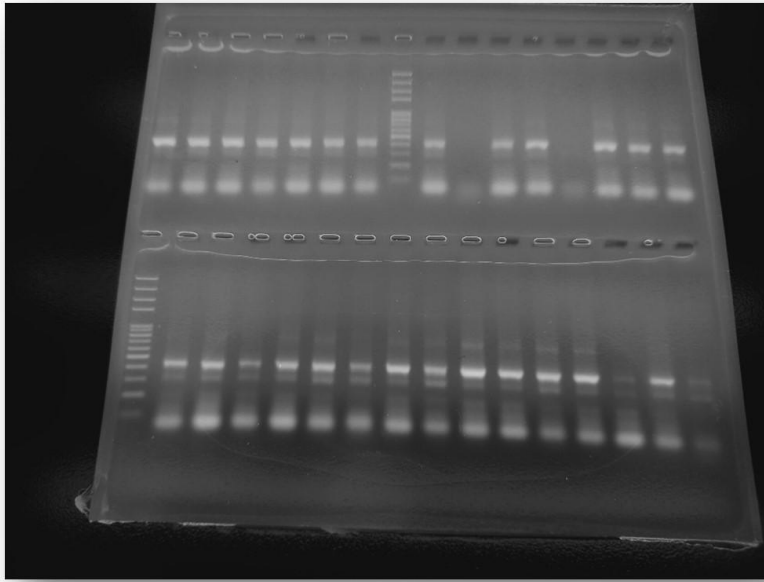| ID	*IL10* −1082 A/G
	rs1800896
Alleles	AG
Reference Allele	A
Alternative allele	G
Gene	IL10
Chromosome	1
Reference	*https://www.ncbi.nlm.nih.gov/snp/rs1800896*

The studied SNP, **rs1800896** is composed of A and G alleles, A is the reference and G is the alternative allele, it is located within *IL10* gene, on chromosome 1.

Supplementary Figures 1,2, Full Agarose gel electrophoresis for *IL10* genotypes from different exposures: ladder size marker (M) 50-1000 bp. Where **G** allele at 288bp and **A** allele at 197 bp. 430 bp as internal control. **(Supplementary)**

Supplementary Figure 1: S1

Supplementary Figure 2: S2

Supplementary Table 2:

S2. Association between IL10 −1082 A/G (rs1800896) with clinical presentation among ALL patients.

	IL10 −1082 A/G (rs1800896)						X^2	p
	AA n = 13		AG n = 40		GG n = 47			
Fever								
Absent	0	0.0%	14	35.0%	10	21.3%	9.766	**0.008**
Present	13	100.0%	26	65.0%	37	78.7%		
Pallor								
Absent	1	7.7%	17	42.5%	18	38.3%	6.527	**0.038**
Present	12	92.3%	23	57.5%	29	61.7%		
Fatigue								
Absent	2	15.4%	14	35.0%	15	31.9%	1.997	0.368
Present	11	84.6%	26	65.0%	32	68.1%		
Bleeding Tendency								
Absent	12	92.3%	31	77.5%	36	76.6%	1.940	0.379
Present	1	7.7%	9	22.5%	11	23.4%		

X2, chi square test.

Fever and pallor differed significantly between rs1800896 genotypes, with the highest incidence associated with AA genotype, followed by GG, and AG genotypes (p=0.008, 0.038 respectively). Fatigue and bleeding tendency were not affected by rs1800896 genotypes (p>0.05 for each).

Supplementary Table 3:

S3. Association between IL10 −1082 A/G (rs1800896) with organomegaly among ALL patients.

	IL10 −1082 A/G (rs1800896)						X^2	p
	AA n = 13		AG n = 40		GG n = 47			
Splenomegaly								
Absent	11	84.6%	20	50.0%	32	68.1%	6.312	0.043
Present	2	15.4%	20	50.0%	15	31.9%		
Hepatomegaly								
Absent	3	23.1%	17	42.5%	21	44.7%	2.155	0.340
Present	10	76.9%	23	57.5%	26	55.3%		
Lymphadenopathy								
Absent	1	7.7%	17	42.5%	20	42.6%	7.104	0.029
Present	12	92.3%	23	57.5%	27	57.4%		

X^2, chi square test.

Splenomegaly differed significantly between rs1800896 genotypes, with the highest incidence associated with AG genotype, followed by GG, and AA genotypes (p=0.043). Moreover, lymphadenopathy differed significantly between rs1800896 genotypes, with the highest incidence associated with AA genotype, followed by AG, and GG genotypes (p= 0.038). Hepatomegaly was not affected by rs1800896 genotypes (p>0.05).

Supplementary Table 4:

S4. Serologic data among patients with ALL.

	ALL n = 100	
	Number	%
CRP		
Negative	61	61.0
Positive	39	39.0

Among all studied ALL cases, 39% had positive CRP and 61% had negative CRP.

Supplementary Table 5:

S5. Association between IL10 −1082 A/G (rs1800896) with CRP among ALL patients.

	IL10 −1082 A/G (rs1800896)			Test (p1)	Post hoc test		
	AA n = 13	AG n = 40	GG n = 47		P2	P3	P4
CRP							

						
Negative	12 (92.3%)	17 (42.5%)	32 (68.1%)	X2= 12.1, p=0.002	0.002	0.153	0.016
Positive	1 (7.7%)	23 (57.5%)	15 (31.9%)			

X2, chi square test.

P1: comparison between AA, AG and GG

P2: comparison between AA, AG

P3: comparison between AA, GG

P4: comparison between AG, GG

CRP differed significantly between rs1800896 genotypes (p1=0.002). This was attributed to significant association of positive CRP with AG when compared to AA (p2=0.002), as well as when compared to GG (p4=0.016).
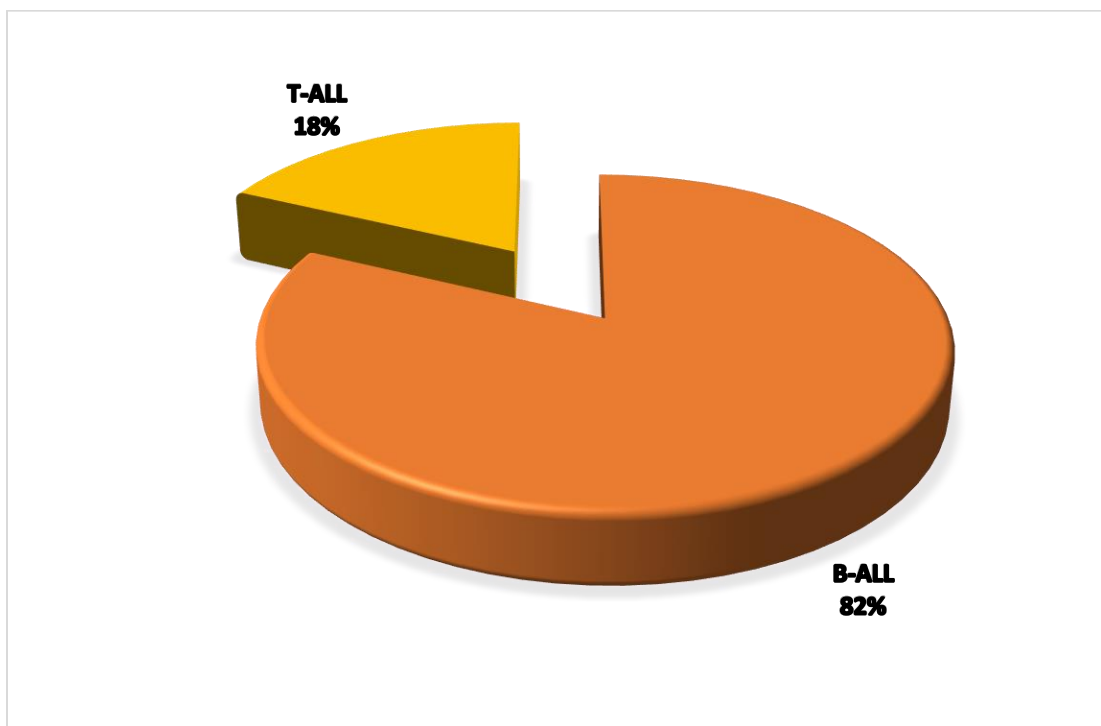
Supplementary Figure 3: S3. Immunophenotyping among patients with ALL

Supplementary Table 6:

S6. Association between IL10 −1082 A/G (rs1800896) with FAB among ALL patients.

	IL10 −1082 A/G (rs1800896)			Test (p1)	Post hoc test		
	AA n = 13	AG n = 40	GG n = 47		P2	P3	P4
FAB							
L1	9 (69.2%)	31 (77.5%)	23 (48.9%)		0.712	0.194	0.006

				X2= 7.812,			
L2	4 (30.8%)	9 (22.5%)	24 (51.1%)	p=0.020			

X2, chi square test.

P1: comparison between AA, AG and GG

P2: comparison between AA, AG

P3: comparison between AA, GG

P4: comparison between AG, GG

FAB classification differed significantly between rs1800896 genotypes (p1=0.020). This was attributed to significant association of L1 with AG when compared to GG, as well as L2 with GG when compared to AG (p4=0.006).