

Supplementary Table 3. Functional predictions of significant SNPs using *in silico* analyses

SNP	Allele	Position	Signal sequence*	Transcriptional factor	Motif [†]	Matrix	Score
rs6682925	major T		-	-			
	minor C	5	CTAT <u>CA</u>	GATA-1			
		5	CTAT <u>C</u>	NF-E			
rs6682925	major T	2			<u>TT</u> AGTGG	SRSF5	4.042
	minor C	1			<u>C</u> AGTGGA	SRSF1	3.288
		2				<u>TC</u> AGTGG	SRSF5
rs7622183	major G	6			CAGT <u>CG</u> G	SRSF1	3.165
		1			<u>GG</u> CTCCTA	SRSF2	5.771
		7			CCAGT <u>C</u> G	SRSF5	3.692
	minor A	1			<u>A</u> GCTCCTA	SRSF2	4.019
rs6473227	major A	5			TTA <u>CAA</u> A	SRSF5	3.063
	minor C	2			<u>CC</u> AAAAG	SRSF5	3.831

The default threshold (1.956, 2.383, and 2.670 for matrix SRSF1, SRSF2, and SRSF5, respectively) is provided by the ESE Finder web site. Underlined bolds indicate major and minor alleles of each SNP.

SNP, single nucleotide polymorphism; ESE, exonic splicing enhancer.

*Putative binding site of transcriptional factor is identified using the Signal Scan program; [†]Potential ESE site is predicted using the ESE finder program.