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

<table>
<thead>
<tr>
<th>SNP</th>
<th>Allele</th>
<th>Position</th>
<th>Signal sequence*</th>
<th>Transcriptional factor</th>
<th>Motif†</th>
<th>Matrix</th>
<th>Score</th>
</tr>
</thead>
<tbody>
<tr>
<td>rs6682925</td>
<td>major T</td>
<td>5</td>
<td>CTATCA</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>minor C</td>
<td>5</td>
<td>CTATC</td>
<td>GATA-1</td>
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<td>-</td>
<td>-</td>
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<tr>
<td></td>
<td></td>
<td>2</td>
<td>TAAGTG</td>
<td>SRSF5</td>
<td>4.042</td>
<td></td>
<td></td>
</tr>
<tr>
<td>rs6682925</td>
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<td>CAGTGGA</td>
<td>SRSF1</td>
<td>3.288</td>
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<td></td>
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<tr>
<td></td>
<td>minor C</td>
<td>2</td>
<td>TCAGTG</td>
<td>SRSF5</td>
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<tr>
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<tr>
<td></td>
<td></td>
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<td>SRSF2</td>
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<td>SRSF5</td>
<td>3.692</td>
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<tr>
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<tr>
<td>rs6473227</td>
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<td>TTACAAA</td>
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<tr>
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<td>CAAAAG</td>
<td>SRSF5</td>
<td>3.831</td>
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</tr>
</tbody>
</table>

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.