|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| g.DNA-position | c.DNA | Protein effect | spliceAI-G delta score§ - acceptor gain (position\*) | spliceAI-G delta score§ - acceptor loss (position\*) | spliceAI-G delta score§ -donor gain (position\*) | spliceAI-G delta score§ -donor loss (position\*) |
| Chr3:g.18435955T>C | c.1205A>G | p.Q402R¥ | 0 (-1) | 0 (45) | 0.0099 (32) | 0.2482 (-1) |
| Chr3:g.18419663T>C | c.1574A>G | p.Q525R£ | 0 (-1) | 0 (19) | 0 (20) | 0 (-1) |
| Chr3:g.18393687C>T | c.1576G>A | p.G526R# | 0.6666 (-2) | 0.0937 (0) | 0 (-2) | 0 (-17) |

**Table S2. Splice-AI predictions for missense variants at intron-exon or exon-intron junctions.**

\*a negative nucleotide position represents positions upstream of the variant, a positive nucleotide position represents positions downstream of the variant.

§cut offs for splice-AI delta score: 0.2 (high recall), 0.5 (recommended), and 0.8 (high precision)

¥p.Q402R:

* Although the variant affects the last amino acid of exon 7, none of the Splice-AI delta scores exceeds the recommended cut-off of >0.5, specifically not the scores for loss or gain of splice donor sites.

£p.Q525R

* Although the variant affects the last amino acid of exon 9, none of the Splice-AI delta scores exceeds the recommended cut-off of >0.5, specifically not the scores for loss or gain of splice donor sites.

#p.G526R:

* The variant affects the first amino acid of exon 10. Splice-AI predicts splice acceptor site gain 2 nucleotides upstream of the variant, resulting in a frameshift.