**Supplemental Table S1. Possible consequences of splice site variants predicted by MaxEntScan.**

|  |  |  |  |
| --- | --- | --- | --- |
| **Consensus score** | **Splicing?** | **Score difference between wild type and mutant sequences** | **Consequences** |
| Above 3 | Donor or acceptor splice site | Increase | Splice site is retained |
| Decrease > 30% (-30%) | Splice site is broken |
| Below 3 | No splicing | Increase > 30% (+30%) | New splice site is created |
| Decrease | No splicing |