**Table S4. Position weight scores for all predicted splice acceptor sites within the *Anopheles stephensi* genome. Scores are additive for each position.**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Position\* |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Base | -21 | -20 | -19 | -18 | -17 | -16 | -15 | -14 | -13 | -12 | -11 | -10 | -9 | -8 | -7 | -6 | -5 | -4 | -3 | -2 | -1 |
| A | .0174 | .0178 | .0187 | .0199 | .0212 | .0221 | .0216 | .0238 | .0243 | .0250 | .0274 | .0287 | .0258 | .0219 | .0207 | .0358 | .0414 | .0041 | .0462 | 1.9023 | .0063 |
| C | .0214 | .0230 | .0273 | .0307 | .0365 | .0408 | .0422 | .0463 | .0522 | .0534 | .0601 | .0669 | .0618 | .0423 | .0376 | .0978 | .0884 | .0030 | .5811 | .0038 | .0110 |
| G | .0122 | .0132 | .0157 | .0169 | .0197 | .0207 | .0216 | .0213 | .0225 | .0231 | .0219 | .0206 | .0209 | .0155 | .0165 | .0308 | .0316 | .0042 | .0082 | .0051 | 1.8645 |
| N | .0001 | .0001 | .0001 | .0001 | .0001 | .0002 | .0001 | .0002 | .0002 | .0002 | .0002 | .0002 | .0001 | .0001 | .0001 | .0002 | .0002 | .0000 | .0004 | .0007 | .0006 |
| T | .0336 | .0364 | .0438 | .0490 | .0589 | .0642 | .0656 | .0710 | .0771 | .0814 | .0858 | .0850 | .0764 | .0479 | .0496 | .1866 | .2020 | .0030 | .2024 | .0059 | .0046 |

\*Nucleotide positon 5’-upstream of the splice junction