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Supplemental Information

Exon Definition Facilitates Reliable Control of Alternative Splicing in the *RON* Proto-Oncogene

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1 Splice site mutation effects

Mutations in splice site consensus sequences impair the recognition of the splice sites by the spliceosome. Thus, they specifically lower one of the binding probabilities $p_i, i=1,\ldots,6$, suggesting that measurements of splicing outcomes for these mutations are valuable to test our models.

1.1 Effects of splice site mutations in the intron and exon definition models

Interestingly, the binding probabilities modulate the splicing outcome differently in the intron and exon definition models, as found by comparing Eqs. (9) and (10): For example, the recognition probability of the last splice site p_6 has an effect on all splice isoforms in the exon definition model, but does not affect splicing in the intron definition model.

Fig. S2 compares the experimentally measured effects of splice site mutations in our mutagenesis screen to the effects predicted by the intron and exon definition models (and Fig. 3D shows a subset of this analysis). Plotted are changes in the frequency of each isoform with respect to wildtype for splice site mutations at the 2nd to 6th splice sites. Mutations affecting the first splice site were not present in our minigene library and were therefore excluded from this analysis. The experimentally measured changes are plotted as a median of the isoform changes among all mutations affecting the first two or last two positions of an intron (GT and AG splice site consensus sequences, respectively). For both models, qualitative simulations were performed (middle panels) and the parameters were set to $p_1=1$ and $p_i=0.9, i=2,\ldots,6$ in wildtype. The effect of a splice site mutation is qualitatively simulated by reducing the corresponding probability from 0.9 to 0.1. The rightmost panel in Fig. S2 shows the quantitative fit of the final adjusted exon definition model to the data (same data as in Fig. 3C, right). In general, the exon definition model (and in particular its best-fit version) agrees much better with the data than the intron definition model.

In fact, using analytical calculations (Section 1.2), one can show that the directionality of isoform changes upon splice site mutations, shown in the middle panels of Fig. S2, holds true for arbitrary values of the recognition parameters $p_i, i=2,\ldots,6$. Hence, the qualitative effects of splice site mutations on splice isoforms provide a unique footprint that distinguishes intron and exon definition models. The data (left panel) in Fig. S2 supports exon definition in contrast to intron definition in several points:

1. Mutations of the 6th splice site affect all isoforms (dark blue bars).
2. Mutations of the 3rd and 4th splice sites (red bars) induce comparable changes for each of the isoforms, supporting that the AE acts as module, as predicted by the exon definition model. In contrast, the intron definition model predicts that the recognition parameters p_3 and p_4 induce opposite changes in first and second intron retention.
3. Mutation effects on inclusion and skipping correspond also quantitatively to the exon definition model, while the intron definition model leads to a much smaller amplitude of changes in skipping for all splice site mutations.
4. Directionality of changes agrees to the exon definition model for 23 out of 25 effects, with exception of the changes in full intron retention at mutated AE splice sites (3rd and 4th splice sites, red bars). As shown below, a full match between exon definition model and data for all 25 effects can be achieved by additional model extensions (Sections 1.3 and 1.4).

Our data therefore strongly indicate that an exon definition mechanism controls *RON* AE 11 splicing.

1.2 Directionality of splice site mutations effects in the intron and exon definition models

Using the models in Eqs. (9) and (13) as well as Eq. (11) we can uniquely determine the directionality of changes in the splice isoform frequencies upon splice site mutations. If we denote by $\nabla p^{ID}_{isoform}$ the derivatives of the isoform frequencies in the intron definition model w.r.t. the model parameters (p_2, p_3, p_4, p_5) , we get from Eqs. (9) and (11)

$$\begin{gathered}
\nabla p^{ID}_{inclusion} = \left[p_3 p_4 p_5, p_2 p_4 p_5, p_2 p_3 p_5, p_2 p_3 p_4\right], \\
\nabla p^{ID}_{skipping} = \left[(1-p_3)(1-p_4) p_5, -p_2(1-p_4) p_5, -p_2(1-p_3) p_5, p_2(1-p_3)(1-p_4)\right], \\
\nabla p^{ID}_{firstIR} = \left[-p_3 p_4 p_5, -p_2 p_4 p_5, (1-p_2 p_3) p_5, (1-p_2 p_3) p_4\right], \\
\nabla p^{ID}_{secondIR} = \left[p_3(1-p_4 p_5), p_2(1-p_4 p_5), -p_2 p_3 p_5, -p_2 p_3 p_4\right], \\
\nabla p^{ID}_{fullIR} = \left[-p_3(1-p_5)-p_5(1-p_4), -p_2(1-p_5), -p_5(1-p_2), -p_2(1-p_3)-p_4(1-p_2)\right].
\end{gathered} \tag{14}$$

Since the splice site recognition probabilities are bounded between 0 and 1, the sign of the all derivatives with respect to the model parameters is fixed, e.g.

$$\frac{dp^{ID}_{first}}{dp_3} = -p_2 p_4 p_5 < 0, \textit{for all}\ 0 < p_i < 1, i = 2,4,5. \qquad (15)$$

Similarly, for the exon definition model we can denote by $\nabla p^{ED}_{isoform}$ the derivatives of the single isoform frequencies w.r.t. to the exon definition probabilities (p_{12}, p_{34}, p_{56}). Using Eqs. (11) and (13) we find

$$\begin{gathered}
\nabla p^{ED}_{inclusion} = \left[p_{34} p_{56}, p_{12} p_{56}, p_{12} p_{34}\right], \\
\nabla p^{ED}_{skipping} = \left[(1-p_{34}) p_{56}, -p_{12} p_{56}, p_{12}(1-p_{34})\right], \\
\nabla p^{ED}_{firstIR} = \left[-p_{34} p_{56}, (1-p_{12}) p_{56}, (1-p_{12}) p_{34}\right], \\
\nabla p^{ED}_{secondIR} = \left[p_{34}(1-p_{56}), p_{12}(1-p_{56}), -p_{12} p_{34}\right], \\
\nabla p^{ED}_{fullIR} = -\left[p_{34}(1-p_{56})+p_{56}(1-p_{34}), p_{12}(1-p_{56})+p_{56}(1-p_{12}), p_{12}(1-p_{34})+p_{34}(1-p_{12})\right].
\end{gathered} \tag{16}$$

Also for the exon definition model, all derivatives have fixed sign, e.g.

$$\frac{dp^{ED}_{first}}{dp_{34}} = (1-p_{12}) p_{56} > 0, \textit{for all}\ 0 < p_i < 1, i = 12,56. \qquad (17)$$

By comparing the signs of the single terms in Eqs. (14) and (16) we can find differences in the directionality of predicted changes for splice site mutations in the two models, and thereby discriminate both models based on experimental data (see Section 1.3). For instance, a mutation in the 3rd splice site decreases the recognition probabilities p_3 and p_{34} in the intron and exon definition models, respectively p_{34}. By comparing Eqs. (15) and (17) we find that for such a mutation, first intron retention is predicted to increase in the intron definition model, but to decrease in the exon definition model. The latter is observed experimentally (Fig. S2), which supports the exon definition model.

The analytically calculated directionalities of isoform changes in response to splice site mutations for intron and exon definition mechanisms are indicated by ‘+’ and ‘-‘ signs in the bottom of Fig. 3D.

1.3 Adjusted exon definition model with isoform-specific degradation rates

The exon definition model reproduces almost completely the directionality of splice isoform changes upon splice site mutations (see Fig. S2, first and third columns). However, it fails to reproduce the measured changes in full IR, overestimates mutation effects on first and second intron retention, and slightly underestimates the effects on skipping. As detailed below, these quantitative differences between model and data can be counterbalanced by assuming that different splice products degrade at different rates (see Fig. S2, right panel).

In the adjusted exon definition model, the measured splice isoforms are assumed to be produced at a rate proportional to the individual splice isoform probabilities derived in Eqs. (13), but are degraded at individual rates. This leads to the following kinetic model

$$\begin{gathered}
\frac{d}{dt} inclusion = s\, p^{ED}_{inclusion}\, premRNA - d_1\, inclusion, \\
\frac{d}{dt} skipping = s\, p^{ED}_{skipping}\, premRNA - d_2\, skipping, \\
\frac{d}{dt} fullIRtot = \frac{d}{dt} premRNA + \frac{d}{dt} fullIR = trans - (s + d_0)\, premRNA \\
+ s\left(1 - p^{ED}_{inclusion} - p^{ED}_{skipping} - p^{ED}_{firstIR} - p^{ED}_{secondIR}\right) premRNA - d_3 (fullIRtot - premRNA), \\
\frac{d}{dt} first = s\, p^{ED}_{firstIR}\, premRNA - d_4\, firstIR, \\
\frac{d}{dt} secondIR = s\, p^{ED}_{secondIR}\, premRNA - d_5\, secondIR.
\end{gathered} \tag{18}$$

Here, *fullIRtot* is the sum of the two unspliced species, nascent pre-mRNA and mature unspliced mRNA (*fullIR*), which cannot be distinguished experimentally. The nascent pre-mRNA is produced by transcription at a rate *trans*, spliced at total rate s and degraded at rate d_0.

The steady state found by inserting Eqs. (13) in (18) is given by

$$\begin{gathered}
premRNA = \frac{trans}{s + d_0}, inclusion = premRNA \frac{s}{d_1} p_{12} p_{34} p_{56}, \\
skipping = premRNA \frac{s}{d_2} p_{12} (1 - p_{34}) p_{56}, \\
fullIRtot = premRNA \left[1 + \frac{s}{d_3} \left(1 - p_{12} p_{34} - p_{12} p_{56} - p_{34} p_{56} + 2 p_{12} p_{34} p_{56}\right) \right], \\
firstIR = premRNA \frac{s}{d_4} (1 - p_{12}) p_{34} p_{56}, secondIR = premRNA \frac{s}{d_5} p_{12} p_{34} (1 - p_{56}).
\end{gathered} \tag{19}$$

In these steady state equations, synthesis and degradation terms always occur as ratios (e.g., s and d_1 for inclusion). This implies that the model also accommodates that each isoform may be generated with its own splicing rate s_i from the pre-mRNA precursor, as this would ultimately lead to an isoform-specific value for the ratio (s_i/d_i), much like an isoform-specific degradation rate. Likewise, length biases in RNA sequencing – which may disfavor the detection of long isoforms such as full intron retention – are expected to scale this ratio and are therefore effectively considered in the model. Hence, the exon definition model with isoform-specific degradation takes into account various technical and biological effects leading to isoform biases and thereby allows for a more realistic description of splicing decisions.

Finally, we can connect the steady state to the measured isoform *frequencies* by normalizing Eqs. (19) with the total number of measured RNA transcripts:

$$total = inclusion + skipping + fullIRtot + firstIR + secondIR, \quad (20)$$

and find

$$\begin{aligned} p_{inclusion} &= \frac{s\, p_{12}\, p_{34}\, p_{56}}{d_1 R},\; p_{skipping} = \frac{s\, p_{12}(1-p_{34})\, p_{56}}{d_2 R}, \\ p_{fullIR} &= \frac{\left[d_3 + s(1-p_{12}p_{34} - p_{12}p_{56} - p_{34}p_{56} + 2p_{12}p_{34}p_{56})\right]}{d_3 R}, \quad (21) \\ p_{firstIR} &= \frac{s(1-p_{12})\, p_{34}\, p_{56}}{d_4 R},\; p_{secondIR} = \frac{s\, p_{12}\, p_{34}(1-p_{56})}{d_5 R}. \end{aligned}$$

Here, the factor R in Eqs. (21) equals the total quantified RNA to pre-mRNA ratio

$$R = \frac{total}{premRNA} = \frac{mRNA + premRNA}{premRNA} \quad (22)$$

and is equal to $(1+s/d)$ if all degradation rates are the same ($d_i = d, i = 1,\ldots,5$). In this case, the simple model given in Eqs. (13) is recovered. For variable degradation rates, R reads

$$\begin{aligned} R = 1 &+ \frac{s\, p_{12}\, p_{34}\, p_{56}}{d_1} + \frac{s\, p_{12}(1-p_{34})\, p_{56}}{d_2} + \frac{s(1-p_{12}p_{34} - p_{12}p_{56} - p_{34}p_{56} + 2p_{12}p_{34}p_{56})}{d_3} \\ &\frac{+s(1-p_{12})\, p_{34}\, p_{56}}{d_4} + \frac{s\, p_{12}\, p_{34}(1-p_{56})}{d_5}. \end{aligned} \quad (23)$$

1.4 Effect of variable degradation rates on the directionality of changes upon splice site mutations

The inclusion of isoform-specific degradation rates leads to a better quantitative model fit of the exon definition to the mutagenesis data (Fig. 3C). Furthermore, on a qualitative level, this model extension can fix the disagreement between the exon definition model and the experimental data with respect to the directionality of splice site mutation effects on the full IR isoform (Fig. S2). In fact, this will be proven below by showing that the consideration of variable degradation rates does not switch the directionality of splice isoform changes compared to a model with common degradation rates, except for the isoform full IR.

The proof of this claim can be done by looking at the structure of the adjusted model derived in Eqs. (21). When computing the derivative of the splice isoforms inclusion, skipping, first or second IR with respect to a certain exon definition probability p_i we find either

$$\frac{\partial p_{isoform}}{\partial p_i} = \frac{p_{isoform}}{p_i R}\left(R - p_i \frac{\partial R}{\partial p_i}\right), \quad (24)$$

if the particular isoform $p_{isoform}$ increases with p_i ($p_{isoform} \sim p_i$) in the basic exon definition model derived in Eqs. (13), or

$$\frac{\partial p_{isoform}}{\partial p_i} = -\frac{p_{isoform}}{(1-p_i)R}\left(R + (1-p_i)\frac{\partial R}{\partial p_i}\right), \tag{25}$$

if the particular isoform decreases with p_i ($p_{isoform} \sim (1-p_i)$) in the unadjusted model of Eqs. (13). For example, for the skipping isoform $p_{skipping} = \frac{p_{12}(1-p_{34})p_{56}}{d_2 R}$ we get:

$$\begin{aligned}
\frac{\partial p_{skipping}}{\partial p_{12}} &= \frac{p_{skipping}}{p_{12} R}\left(R - p_{12}\frac{\partial R}{\partial p_{12}}\right), \\
\frac{\partial p_{skipping}}{\partial p_{34}} &= -\frac{p_{skipping}}{(1-p_{34})R}\left(R + (1-p_{34})\frac{\partial R}{\partial p_{34}}\right), \\
\frac{\partial p_{skipping}}{\partial p_{56}} &= \frac{p_{skipping}}{p_{56} R}\left(R - p_{56}\frac{\partial R}{\partial p_{56}}\right).
\end{aligned} \tag{26}$$

The normalization factor R depends on the exon definition probabilities $p_i, i = 12, 34, 56$ like a first order polynomial, as given in Eq. (23). We thus have

$$\begin{aligned}
R - p_{12}\frac{\partial R}{\partial p_{12}} &= 1 + \frac{s}{d_3}(1 - p_{34}p_{56}) + \frac{p_{34}p_{56}}{d_4} > 1, \\
R - p_{34}\frac{\partial R}{\partial p_{34}} &= 1 + \frac{s}{d_3}(1 - p_{12}p_{56}) + \frac{p_{12}p_{56}}{d_2} > 1, \\
R - p_{56}\frac{\partial R}{\partial p_{56}} &= 1 + \frac{s}{d_3}(1 - p_{12}p_{34}) + \frac{p_{12}p_{34}}{d_5} > 1.
\end{aligned} \tag{27}$$

Furthermore, from Eq. (23) we can calculate

$$\begin{aligned}
R + (1-p_{12})\frac{\partial R}{\partial p_{12}} &= 1 + \frac{s\,p_{34}p_{56}}{d_1} + \frac{s(1-p_{34})p_{56}}{d_2} + \frac{s(1-p_{34})(1-p_{56})}{d_3} + \frac{s\,p_{34}(1-p_{56})}{d_5} > 1, \\
R + (1-p_{34})\frac{\partial R}{\partial p_{34}} &= 1 + \frac{s\,p_{12}p_{56}}{d_1} + \frac{s(1-p_{12})(1-p_{56})}{d_3} + \frac{s(1-p_{12})p_{56}}{d_4} + \frac{s\,p_{12}(1-p_{56})}{d_5} > 1, \\
R + (1-p_{56})\frac{\partial R}{\partial p_{56}} &= 1 + \frac{s\,p_{12}p_{34}}{d_1} + \frac{s\,p_{12}(1-p_{34})}{d_2} + \frac{s(1-p_{12})(1-p_{34})}{d_3} + \frac{s(1-p_{12})p_{34}}{d_4} > 1.
\end{aligned} \tag{28}$$

Note that we have used the fact that all probabilities $p_i, i = 12, 34, 56$ are positive numbers smaller than 1. By combining Eqs. (24) and (27) we thus find

$$\frac{\partial p_{isoform}}{\partial p_i} = \frac{p_{isoform}}{p_i R}\left(R - p_i\frac{\partial R}{\partial p_i}\right) > 0, \tag{28}$$

for all isoforms $p_{isoform}$ that increase with p_i in the basic exon definition model derived in Eqs. (13). By combining Eqs. (25) and (28) we further find

$$\frac{\partial p_{isoform}}{\partial p_i} = -\frac{p_{isoform}}{(1-p_i)R}\left(R + (1-p_i)\frac{\partial R}{\partial p_i}\right) < 0, \tag{30}$$

for all isoforms $p_{isoform}$ that decrease with p_i in the unadjusted exon definition model derived in Eqs.

(13). Therefore, the introduction of individual degradation rates cannot induce a switch in the directionality of changes with respect to the exon definition probabilities, but can adjust only the amplitude of changes for inclusion, skipping, first and second intron retention.

In contrast, numeric simulations show that variable degradation rates can induce a switch of the directionality in the changes of full intron retention, and thus correct the difference between the basic exon definition model and data (see Fig. S2).

2 Quantitative estimation of mutations effects on splice site definition

Both intron and exon definition models as well as the adjusted exon definition model were fitted to the single mutation effects on the isoforms frequencies inferred from our RNA-seq data (see Methods). Since our microscopic model does not handle non-standard isoforms (e.g., those using cryptic splice sites or those including insertion/deletion mutations), mutations that have a significant effect on the measured non-standard isoforms ('others') were filtered out from the dataset. More precisely, we keep mutations with $p_{others} < 2\, p_{others}^{wt}$, where p_{others} denotes the frequency of non-standard isoforms in the mutated gene and p_{others}^{wt} denotes the corresponding mean frequency in the wildtype minigenes. Furthermore, the frequencies of the five canonical isoforms (inclusion, skipping, full IR, first IR and second IR) were re-normalized, such that their total summed up frequency is one, like expected in the model.

In total, 1854 single point mutation effects and the wildtype values of five canonical splice isoforms were fitted. We assume that each mutation may affect spliceosome binding to splice sites, and thus allowed all recognition probabilities to be fitted independently for each mutation and the wildtype. For the intron definition model in Eqs. (9), we have four unknown parameters per mutation, namely the recognition probabilities of the 3’ and 5’ ends of each intron $p_{2,}\, p_{3,}\, p_{4\,,}\, p_5$. The recognition probability p_6 does not affect splicing outcomes in this model. For the exon definition model in Eqs. (13), there are only three parameters per mutation, that correspond to the joint recognition probabilities of the three exons p_{12}, p_{34}, p_{56}. The adjusted definition model in Eqs. (21) includes five additional parameters, i.e., the ratios of the degradation to splicing rates of the five splice products $d_1/s, \ldots, d_5/s$. These five parameters are assumed to have the same values for all mutations and the wildtype (i.e., mutations effects on degradation rates are neglected), and were thus fitted globally to all mutation and wildtype measurements.

The total number of parameters was therefore 7420, 5565 and 5570 for the intron, exon and adjusted exon definition models, respectively. Fitting was done by minimizing the squared norm of the difference vector between model (Eqs. (9), (13) and (21), respectively) and measured values using Matlab subroutine lsqnonlin. Starting parameter values were sampled using latin hypercube sampling. Minimization was repeated for 100 sets of starting parameters, which led to stable results for the optimal parameter values.

Optimization was done while restricting parameter values to [0,1] for all recognition probabilities. For the adjusted exon definition model, the degradation rates d_1, d_2, d_4, d_5 of the isoforms inclusion, skipping, first and second intron retention were constrained to be between 0.3 and 3.33 times the degradation rate d_3 of the full intron retention isoform. The ratio d_3/s was at its turn constrained between 0 and 3.33. The best-fit values of the global parameters were

$d_1/s=0.059, d_2/s=0.079, d_3/s=0.197, d_4/s=0.562, d_5/s=0.648$. Thus, inclusion and skipping isoforms were more stable compared to retention isoforms as expected based on the literature (*26*). The best-fit values of the recognition probabilities were $p_{12}^{wt}=0.60, p_{34}^{wt}=0.79, p_{56}^{wt}=0.73$ for the wildtype. The corresponding values for all single mutation effects are summarized in Table S1.

3 Analysis of alternative exon modularity

In the exon definition model, exons function as modules as the recognition parameters corresponding to the surrounding splice sites enter the overall exon recognition parameter in a multiplicative fashion (Eqs. (12)). Hence, mutations should have identical effects on splice isoforms, irrespective of whether they target the 3' and 5' splice sites of the exon, which would not be the case for the intron definition model in Eqs. (9). To confirm the predicted modularity, we analyzed mutations nearby splice sites, sorted them according to mutation strength and compared their effects on splice isoforms (Fig. 4B and Fig. S5). In line with the exon definition hypothesis, we found that 3' and 5' mutations in the alternative exon have almost identical effects on splicing outcomes.

For the plots in Fig. 4B, mutations in a +/- 30-nt window around the 5' and 3' splice sites of the AE 11 were selected (164 mutations at positions 266-325 and 157 mutations at positions 415-474, respectively). The best-fit parameters of the adjusted exon definition model in Eqs. (21) were used to sort these mutations according to their effect on the recognition probability of the alternative exon p_{34} (reflecting the mutation strength), and classified the mutations into 10 uniform bins between $p_{34}=0$ and $p_{34}=1$ (e.g. the 5th bin contains mutations that lead to an exon recognition probability p_{34} between 0.4 and 0.5). The top plots in Fig. 4B show the experimentally measured splice isoform frequencies as the mean in each bin vs. bin center value of p_{34}. Mutations in the vicinity of the left and right AE splice sites induce similar effects, supporting the concept that the alternative exon is recognized as a module. The plots below show simulations of the adjusted exon definition model (middle) as well as intron definition model (bottom). For the exon definition model, the degradation to splice rates $d_1/s, \ldots, d_5/s$ are fixed to the best-fit values. For both models, the recognition probabilities p_{12}, p_{56} and $p_{2,} p_5$ respectively, take the best-fit values obtained for the wildtype minigenes. To mimic 5' regulation of the alternative exon, the parameter p_3 is varied from 0 to 1 in the left plots, while keeping $p_4=0.9$. In the right column, 3' regulation is simulated by varying p_4 from 0 to 1 while keeping $p_3=0.9$.

Similar plots for mutations within a +/- 30-nt window around the 2nd, 5th and 6th splice sites are shown in Fig. S5. For these plots, 168 mutations within positions 180-240 (left column), 132 mutations within positions 490-550 (middle column) and 127 mutations within positions 660-720 (right column) were selected. The best-fit parameters of the adjusted exon definition model in Eqs. (21) were used to sort these mutations according to their effect on the recognition probability of the constitutive exons (p_{12} in the left column and p_{56} in the middle and right columns) . For the data plots (top row), mutations were classified as already described in uniform bins according to the values of p_{12} and p_{56}, respectively. For the adjusted exon definition model (middle row) the parameters p_{34}, p_{56} (left column) or p_{12}, p_{34} (middle and right columns) were fixed at their best-fit values. For the intron definition model (bottom row) the parameters $p_{3,} p_{4,} p_5$ (left column) or $p_{2,} p_{3,} p_4$ (middle and right columns) were fixed at their best fit values. To mimic the regulation of the constitutive exon 10, the parameter p_2 is varied between 0 and 1 in the left column. To mimic the regulation of the constitutive exon 12, p_5 (middle column) or p_6 (right column) are varied between 0 and 1, while keeping $p_6 = 0.9$ or $p_5 = 0.9$, respectively. The available data shows similar isoform distribution for mutations on both sites of the constitutive exon 12 (top, middle and right), supporting again the modular character of splicing reflected by the exon definition model in contrast to the intron definition model. Note that data on mutated 5th splice site is partially missing (top, middle), since these mutations lead to the activation of a cryptic splice site and formation of non-canonical isoforms, that are not currently described by the model.

4 Prediction of combined mutation effects

To further support modular exon regulation, we assessed whether the adjusted exon definition model trained on single mutation effects (Fig. 3B, right) could successfully predict combined mutation effects. For the plots in Fig. 4C, we focused on predicting a subset of 908 minigenes in our mutagenesis data that contained only two point mutations. However, most of these individual mutations do not have a strong effect on *RON* splicing, so that the prediction of their combined effect would be trivial. We therefore further filtered for those single point mutations that induce more than 20% change with respect to wildtype taken as a sum of all absolute isoform changes $(\sum |p_i - p_i^{wt}| > 0.2)$ and ended up with 45 double mutation minigenes that could be used to test the exon definition model.

The combined effect of two mutations was calculated based on the assumption that mutations multiplicatively affect the k^{on}/k^{off} ratio of the spliceosome binding to the single exons. Thus, in similarity to Eqs. (3), we assume for each exon recognition probability in a double mutation minigene:

$$p_{combined} = \frac{k^{on}_{combined}/k^{off}_{combined}}{1 + k^{on}_{combined}/k^{off}_{combined}}, \quad (31)$$

with

$$\frac{k^{on}_{combined}}{k^{off}_{combined}} = \left(\frac{k^{on}_{wt}}{k^{off}_{wt}}\right)^{-1} \frac{k^{on}_{1}}{k^{off}_{1}} \cdot \frac{k^{on}_{2}}{k^{off}_{2}} \quad (32)$$

and

$$\frac{k^{on}_{i}}{k^{off}_{i}} = \frac{p_i}{1 - p_i}, i = wt, 1, 2. \quad (33)$$

In (32) and (33) $p_{wt}, k^{on}_{wt}, k^{off}_{wt}$ are the exon definition probabilities and binding/unbinding rates fitted to the wildtype and $p_i, k^{on}_i, k^{off}_i, i = 1,2$ are the corresponding values associated with the single mutation effects. Thus, Eqs. (31-33) allow us to calculate the exon recognition probabilities in the double mutation minigene from the estimated exon recognition probabilities in the single mutation minigenes. Finally, predictions of the five isoform frequencies in minigenes containing two mutations are made using the models in Eqs. (9) and (21). These predictions (in total 225 isoform values for each model) are compared to the experimental measurements in Fig. 4C (right panel).

For the left panel in Fig. 4, the analysis was further restricted based on the positions of mutations: specifically, only mutations in a +/- 30 nt window around the 3' and 5' sites of the AE were considered (positions 275-330 and 415-475). This leads to a subset of 3 double mutation minigenes (in total 15 isoform value predictions for each model).

5 Simulation of mutation effects on PSI and total intron retention

We used the model to investigate how alternative splicing regulation relates to intron retention. For simplicity, we did not distinguish intron retention isoforms but considered only total intron retention, i.e., the sum of all retention products. Considering that all isoform frequencies sum up to 1, we derive an analytical expression for *totalIR* from Eqs. (13)

$$totalIR = 1 - p_{inclusion} - p_{skipping} = 1 - p_{12}\, p_{56}\,, \qquad (34)$$

For the PSI of the middle exon as a measure of alternative splicing, we obtain

$$PSI = \frac{p_{inclusion}}{p_{inclusion} + p_{skipping}} = p_{34}. \qquad (35)$$

Hence, alternative splicing and the degree of intron retention are controlled independently in the exon definition model (if all splice isoforms are degraded turned over with the same rates), and alternative splicing regulation occurs without the accumulation of retention products.

For the intron definition model *totalIR* and *PSI* cannot be uncoupled in the same way. Specifically, we obtain from Eq. (11):

$$totalIR = 1 - 2\, p_2 p_3 p_4 p_5 - p_2 p_5 + p_2 p_3 p_5 + p_2 p_4 p_5\,,$$
$$PSI = \frac{p_3 p_4}{2\, p_3 p_4 + 1 - p_3 - p_4}. \qquad (36)$$

If both splice sites flanking the alternative exon are jointly recognized ($p_3 = p_4 = 0$), or jointly not recognized ($p_3 = p_4 = 1$), we have

$$totalIR = 1 - p_2 p_5\,, \qquad (37)$$

which resembles Eq. (34). In contrast to the exon definition model, *totalIR* approaches 1 if only one of the splice sites is recognized ($(p_3 = 1 \wedge p_4 = 0) \vee (p_3 = 0 \wedge p_4 = 1)$). Hence, both splice sites need to be regulated jointly to prevent retention in the intron definition model.

However, even in this scenario of joint regulation ($p_3 = \alpha\, p_4$), intron retention isoforms accumulate at intermediate PSI values, i.e., during the switch from exon skipping to inclusion. Plugging $p_3 = \alpha\, p_4$ into Eqs. (36) yields

$$totalIR = 1 - \frac{2\alpha}{(1+\alpha)^2} \qquad (38)$$

for $PSI = 0.5$ and $p_2 = p_5 = 1$. Hence, even if the splice sites of the outer exons are perfectly recognized ($p_2 = p_5 = 1$) *totalIR* will accumulate to at least 50% of all splice products at intermediate inclusion levels (PSI=0.5). Less complete recognition of the outer exons results in even higher retention (not shown), implying alternative splicing regulation in the intron definition model inevitably results in the accumulation of retention products.

To visualize the distinct accumulation of retention products in the intron and exon definition models, Monte-Carlo simulations mimicking point mutation effects were performed (Fig. 4D, middle and right). To this end, 2000 sets of binding probabilities ($p_1, \dots, p_6$) were used. In all runs, five of the six binding probabilities ($p_2 - p_6$) are drawn from a Gauss distribution (standard deviation 5%). In 45 of the runs, one of the constitutive exons splice sites (2,5,6) is randomly chosen and its binding probability additionally perturbed (standard deviation 50%). In other 300 of the runs, one of the alternative exons splice sites (3 or 4) is randomly chosen and the corresponding binding probability is additionally perturbed (standard deviation 50%). The distributions for $p_2 - p_6$ are centered around (0.95,0.7,0.7,0.95,0.95) and (0.9, 0.9, 0.9, 0.9, 0.9) for the intron and exon definition models, respectively. These values were chosen to mimic the experimentally measured wildtype PSI and intron retention values. The value of p_1 is set to 1 in both models since the minigene used in the experiment does not include the 1st splice site.

6 Analysis of splicing for a pre-mRNA containing four exons

In this section, we theoretically analyze splicing of a four-exon gene to show that the same principles we derived above also hold for longer sequences and more complex splicing scenarios.

Consider a gene with four exons in which the recognition is denoted in a binary fashion, e.g., (1111) and (0000) for the fully bound (all exons or recognized) and empty states (no exon recognized), respectively. We define the sum of the states (1111), (1011), (1101) and (1001) as the *productive states*, as only for these cases no intron will be retained after splicing (following the same splicing rules as in Section 1).

With p_i being the individual recognition probability of each exon, we obtain for the frequency of total intron retention, i.e., the sum of all retention isoforms

$$totalIR = 1 - productive\,states = 1 - p_1 p_4 \qquad (39)$$

and

$$productive\,states = p_1 p_4 . \qquad (40)$$

This expression resembles Eq. (34) and shows that *totalIR* solely depends on the recognition of the outer exons.

The percent spliced-in (*PSI*) for the second and third (i.e., the inner) exons is given by

$$\begin{aligned} PSI_2 &= \frac{p_{1111} + p_{1101}}{productive\,states} = p_2 , \\ PSI_3 &= \frac{p_{1111} + p_{1011}}{productive\,states} = p_3 . \end{aligned} \qquad (41)$$

Thus, as for the three-exon case (Eq. (35)), alternative splicing is controlled independently of *totalIR*. Furthermore, alternative splicing regulation is modularized in two ways: (i) By assigning a total recognition probability to each exon (p_i), we implicitly assumed that splice signals acting on the two splice sites of this exon are integrated into a net outcome (within-exon modularity); (ii) According to Eqs. (41), the inclusion level of exon is controlled only by its own recognition probability independent of its neighboring exons. This gives rise to an additional cross-exon modularity that was not present in the three-exon case (Section 1).

Similar conclusions also hold for more complex scenarios involving more than four exons (as long as we assume that exon skipping can also occur across long sequences comprising multiple introns and exons). Taken together, these calculations support that exon definition is generally beneficial for the alternative splicing regulation, also for long pre-mRNAs with complex exon structure.

7 Analysis of the *HNRNPH* knockdown response and synergistic effects

In order to analyze how *HNRNPH* affects *RON* splicing, we quantitatively analyzed *HNRNP* knockdown data in HEK293T cells using our model. The distribution of the exon recognition probabilities in wildtype minigenes and the mutation effects on these probabilities were calculated by fitting the adjusted exon definition model to the *HNRNPH* knockdown data as described in Section 2. Here, the global parameters $d_1/s,\dots,d_5/s$ were kept at the values determined for control conditions.

The distribution of the exon recognition probabilities p_{12}, p_{34}, p_{56} for the wildtype minigenes is shown in Fig. S4C. The knockdown mainly increases the recognition probability of the alternative exon p_{34}, while the recognition probabilities of the constitutive exons p_{12}, p_{56} are comparable to control values.

In order to identify which sites are most relevant for HNRNPH-dependent regulation, we inferred the splicing response of single point mutation variants upon *HNRNPH* knockdown using our model. We hypothesized that mutations that either weaken or reinforce an HNRNPH binding site would display positive or negative synergy with the *HNRNPH* knockdown. For instance, a reduced knockdown response compared to the wildtype minigene would be expected if an important HNRNPH binding site is compromised by a mutation (negative synergy). For the exon recognition probabilities $p_i, i=12,34,56$ in mutated minigenes, a z-score was calculated based on the mean and standard deviation in wildtype minigenes:

$$z_i=\frac{\log\left(p_i^{KD}/p_i^{control}\right)-wtmean}{wtstd}, \quad (42)$$

where *wtmean* and *wtstd* are the mean and standard deviation of $\log\left(p_i^{KD}/p_i^{control}\right)$ in wildtype minigenes. Mutations with $|z_i|>5$ indicate a highly distinct knockdown response in wildtype and mutant background and were considered as a synergistic interaction which hints to the presence of a cis-regulated element targeted by HNRNPH. The density of such interactions in a 5-nt sliding window is plotted in Fig. S4D. The most reliable synergistic interactions are found for the recognition probability p_{34} of the alternative exon with corresponding mutations located in the alternative exon or flanking introns. For a similar analysis in MCF7 cells see also Fig. 5 in (*19*).

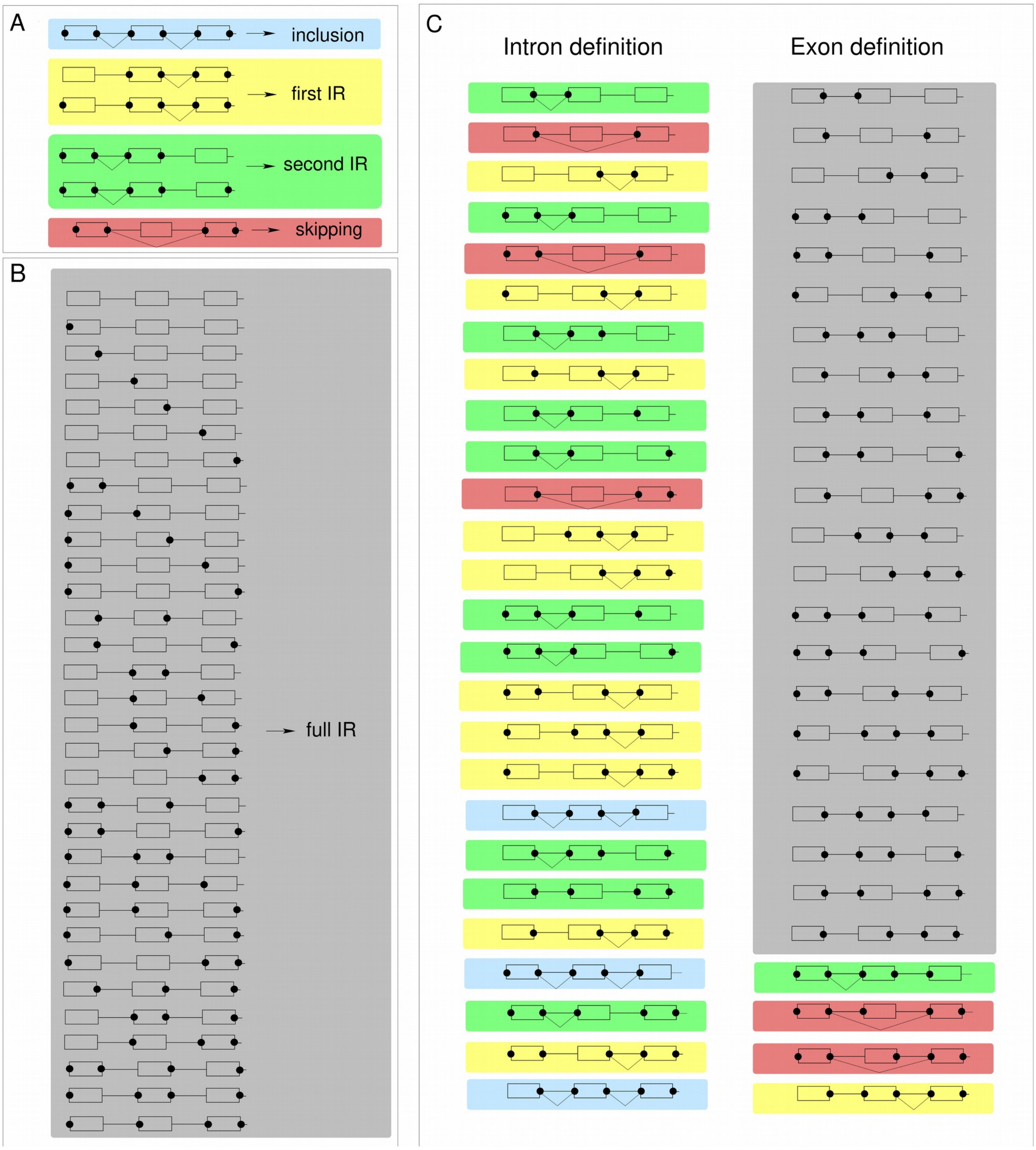

Fig. S1. Common and distinct splicing decisions in intron vs. exon definition models. A Spliceosomal binding states leading to identical splicing outcomes in both models. **B** Binding states with no matching 3' and 5' splice sites across introns. Since no splicing reaction can take place, these binding states lead to the full intron retention isoform in both models. **C** Binding states that lead to different splice outcomes in the intron (left column) and exon definition (right column) model. Black dots indicate U1 and U2 binding to splice sites. Splicing reactions are indicated by triangular black lines. The background color reflects the splice outcome (blue: inclusion, red: skipping, yellow: first IR, green: second IR, gray: full IR).

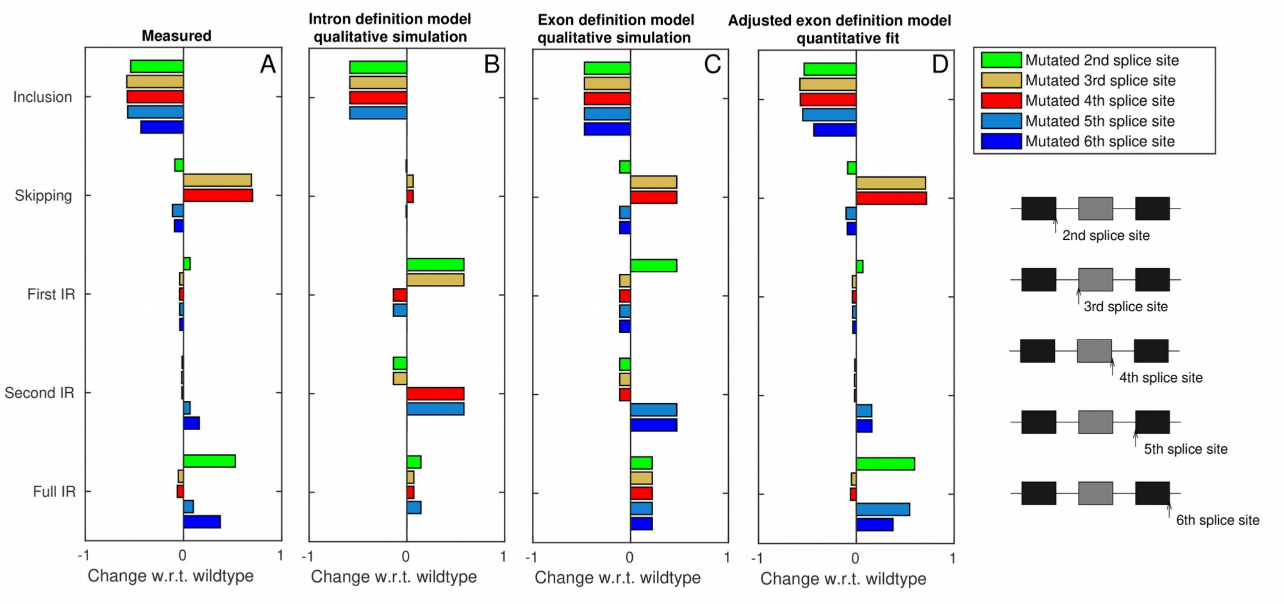

Fig. S2. Splice site mutation effects on splice isoforms support the exon definition model. A Bar plots showing the median isoform differences w.r.t. wildtype for directly measured minigenes containing single point mutations at different splice sites. Splice sites are defined as the first and last two positions within an intron (sites 211-212,296-297,445-446,523-524,691-692). Mutations at these positions have the strongest effect on splicing outcomes within the library. A subset of this data is shown in Fig. 3D. **B,C** Predictions of splice site mutation effects based on qualitative simulations of the intron and exon definition models, respectively. Importantly, the directionality of the simulated isoform changes hold true for arbitrary sets of splice recognition parameters (see Sections 1.1 and 1.2 for details). The exon definition (but not the intron definition) model reproduces 23 out of 25 splice mutation effects, and only fails to describe AE splice site effects on full IR. **D** The adjusted exon definition model with isoform-specific degradation and fitted parameters (Fig. 3B, right) qualitatively and quantitatively reproduces all measured splice site effects.

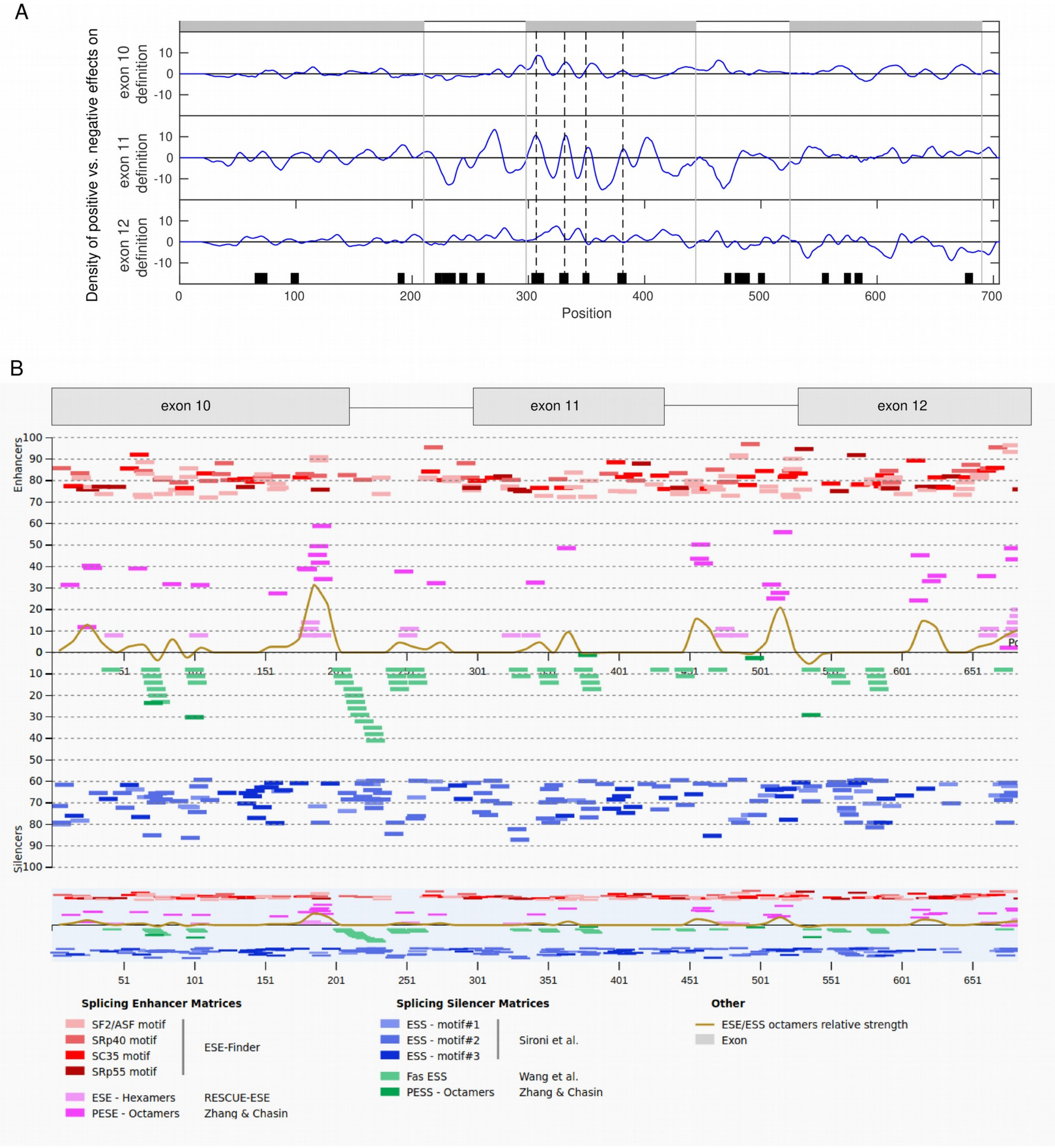

Fig. S3 Strong point mutation effects partially overlap with known RBP motifs. A Maps showing the densities of positive vs. negative point mutation effects on the recognition probabilities of the three exons. The difference in the number of positive effects (z-score >2) and the number of negative effects (z-score < -2) on each exon recognition probability was calculated for adjacent 8-nt windows along the minigene. The mean value of this difference over a sliding 8-nt window is plotted. Effects within 2-nt distance from the splice sites were excluded. Exons and splice sites are marked by grey boxes and grey vertical lines, respectively. HNRNPH splice-regulatory binding sites (SRBS) predicted in (*19*) are shown as black boxes. Four of the positions with enhanced positive effects on exon 11 recognition correspond to HNRNPH SRBS within the alternative exon (dashed vertical lines). **B** Summary of exonic splicing enhancers (ESE) and exonic splicing silencers (ESS) predicted for the wildtype minigene sequence. The plot was generated with the Human Splicing Finder, Version 3.1. Results are also summarized in Table S2.

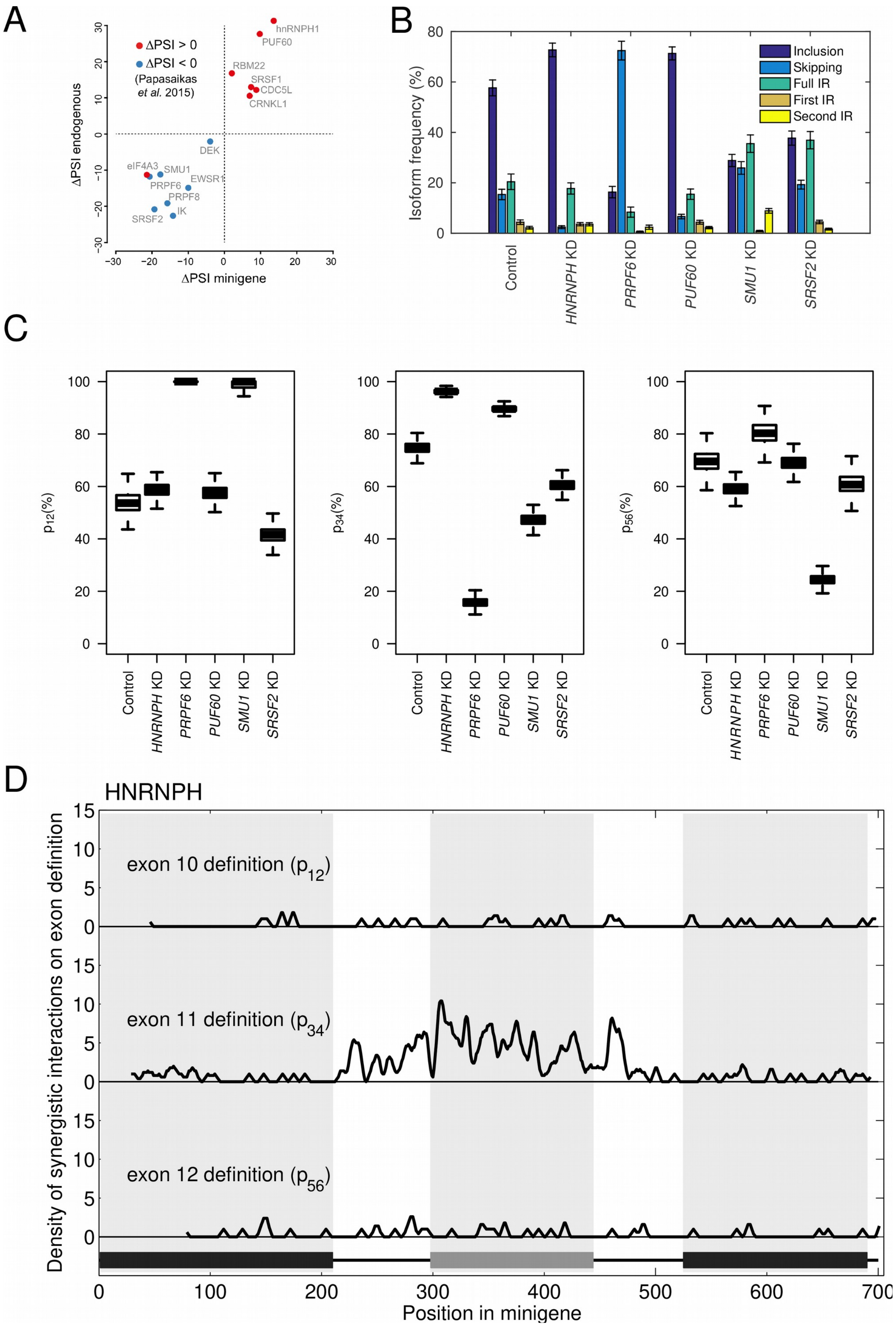
A
ΔPSI > 0
ΔPSI < 0
(Papasaikas et al. 2015)
hnRNPH1
PUF60
RBM22
SRSF1
CDC5L
CRNKL1
DEK
eIF4A3
SMU1
EWSR1
PRPF6
PRPF8
IK
SRSF2
ΔPSI endogenous
ΔPSI minigene
−30
−20
−10
0
10
20
30
B
Isoform frequency (%)
0
20
40
60
80
Inclusion
Skipping
Full IR
First IR
Second IR
Control
HNRNPH KD
PRPF6 KD
PUF60 KD
SMU1 KD
SRSF2 KD
C
p12(%)
p34(%)
p56(%)
0
20
40
60
80
100
Control
HNRNPH KD
PRPF6 KD
PUF60 KD
SMU1 KD
SRSF2 KD
D
HNRNPH
Density of synergistic interactions on exon definition
exon 10 definition (p12)
exon 11 definition (p34)
exon 12 definition (p56)
0
5
10
15
0
100
200
300
400
500
600
700
Position in minigene

Fig. S4. Knockdowns of RNA-binding proteins most prominently affect the recognition probability of the alternative exon. A The change in the percent spliced-in metric relative to scrambled control (ΔPSI) upon RBP knockdown for the minigene construct (x-axis) and for the endogeneous exon 11 (y-axis). Semi-quantitative RT-PCR of exon 11 splicing in the minigene and the endogeneous *RON* gene was performed as described in (*19)*. Data points are coloured based on their regulation in a previous study (*28*). **B** Measured isoform frequencies for wildtype minigenes in control and *HNRNPH, PRPF6, PUF60, SMU1* or *SRSF2* knockdown conditions. Error bars indicate the standard deviation of all 586 wildtype plasmids in the mutagenesis library. Targeted RNA sequencing and data analysis was performed as described in (*19*). **C** Model-based quantification of knockdown effects. Boxplots show the distribution of the best-fit recognition probabilities p_{12}, p_{34}, p_{56} of the three exons in wildtype minigenes under control and knockdown conditions. The fit was generated using the adjusted exon definition model by separately fitting all wildtype minigenes (see Section 7 for details). **D** HNRNPH may target cis-regulatory elements in the alternative exon, as evidenced by a synergistic interaction of *HNRNPH* knockdown with point mutations in this region. Maps show the density of synergistic mutation-knockdown effects on the three exon recognition probabilities. Single mutation effects on the exon recognition were determined separately for control and *HNRNPH* knockdown conditions. The difference (in logarithmic space) between control and *HNRNPH* knockdown values for single point mutations was compared to the knockdown response of wildtype minigenes and expressed as a z-score relative to the within-wildtype-variation (see Section 7 and (*19*)). Large z-scores indicate a synergistic interaction with the *HNRNPH* knockdown. The density of mutations with a | z-score | >5 in a 5-nt sliding window is plotted.

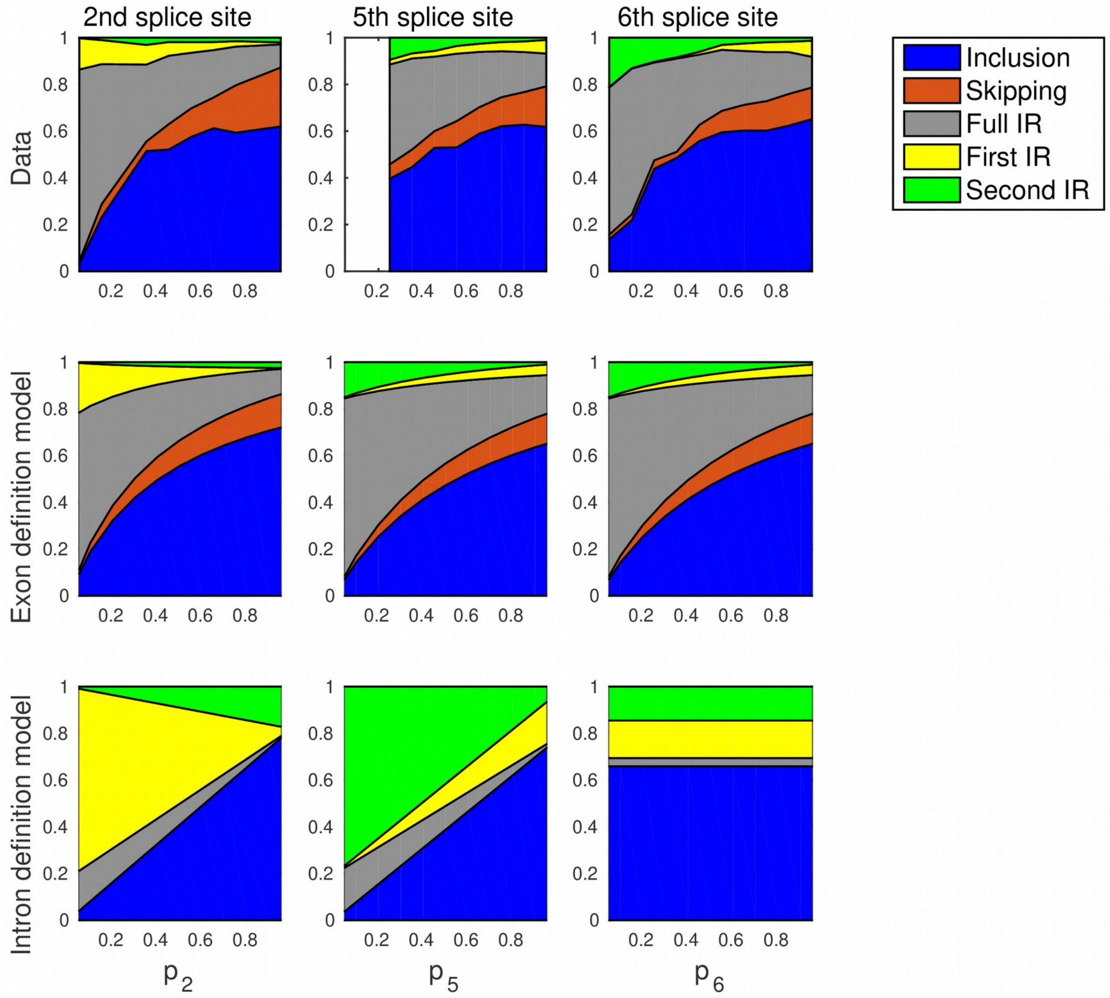

Fig. S5. Position-dependent mutation effects on splice isoforms support the exon definition model (related to Fig. 4B). Plots show a similar analysis as in Fig. 4B for the other splice sites. Mutations at positions in a +/- 30-nt window around the 2nd, 5th and 6th splice sites were selected. The mutations were sorted according to their effect on the recognition probability p_{12}(left) or p_{56} (middle and right) in the best-fit model (adjusted exon definition model; Fig. 3B, right). The measured changes in the splice isoform fractions with varying mutation strength (1st row) are similar for the 5th and 6th splice splice sites, and agree with simulations of the exon definition model in which p_{56} is systematically varied (2nd row), but disagree with the intron definition model (3rd row). Furthermore, mutations at the 2nd splice site induce similar changes as mutations at the 5th and 6th splice sites for the inclusion, skipping and full intron retention isoforms, as reflected by the exon definition model in contrast to the intron definition model. The vertical white line is located at the best-fit parameter values corresponding to wildtype minigenes.

Best Fit Values of Model Parameters

	Exon Definition Model			Intron Definition Model			
	p_{12}	p_{34}	p_{56}	p_2	p_3	p_4	p_5
wildtype	0.60	0.79	0.73	0.80	1.00	0.97	0.85
A26T	0.58	0.79	0.71	0.80	0.99	1.00	0.81
A26G	0.58	0.79	0.61	0.77	0.99	0.99	0.78
G27T	0.67	0.71	0.77	0.95	0.84	0.88	0.92
G27C	0.69	0.76	0.66	0.82	0.99	0.99	0.82
G27A	0.53	0.78	0.67	0.76	0.99	0.99	0.77
C28T	0.58	0.82	0.70	0.81	1.00	1.00	0.82
C28G	0.40	0.64	0.97	0.85	0.79	0.82	0.88
C28A	0.66	0.75	0.63	0.80	1.00	0.99	0.80
T29G	0.61	0.76	0.75	0.83	0.97	0.98	0.83
T29C	0.63	0.79	0.70	0.81	0.99	0.99	0.83
T29A	0.54	0.78	0.66	0.76	0.99	1.00	0.78
G30A	0.56	0.79	0.73	0.80	0.99	1.00	0.81
T31G	0.61	0.79	0.73	0.81	1.00	0.99	0.83
T31C	0.61	0.81	0.71	0.81	1.00	0.99	0.83
T31A	0.61	0.79	0.67	0.81	0.98	1.00	0.81
G32T	0.60	0.80	0.68	0.80	1.00	0.99	0.81
G32C	0.44	0.61	0.75	0.71	0.80	0.80	0.73
G32A	0.60	0.76	0.67	0.78	0.99	0.99	0.79
C33T	0.62	0.78	0.77	0.83	0.99	0.98	0.85
C33G	0.78	0.65	0.60	0.90	0.86	0.84	0.90
C33A	0.68	0.88	0.78	0.87	1.00	0.99	0.89
C34T	0.56	0.78	0.63	0.76	0.99	0.99	0.77
C34A	0.51	0.85	0.73	0.79	1.00	0.96	0.86
G35T	0.49	0.80	0.73	0.76	0.99	1.00	0.79
G35A	0.57	0.81	0.71	0.81	0.99	1.00	0.82
C36T	0.61	0.84	0.77	0.84	1.00	1.00	0.86
C36G	0.54	0.73	0.69	0.74	0.99	0.98	0.77
C36A	0.66	0.77	0.79	0.89	0.93	0.97	0.87
C37T	0.61	0.79	0.71	0.82	0.98	0.99	0.83
C37A	0.53	0.79	0.71	0.77	1.00	0.98	0.81
CT38C	0.54	0.79	0.79	0.80	0.99	0.98	0.83
T38G	0.65	0.73	0.71	0.79	1.00	0.99	0.81
T38C	0.57	0.79	0.70	0.79	0.99	0.99	0.81
T38A	0.62	0.80	0.74	0.82	1.00	0.99	0.84
T39C	0.59	0.78	0.72	0.80	0.99	0.98	0.83
T39A	0.64	0.73	0.70	0.81	0.97	0.98	0.82
TC40T	0.59	0.75	0.72	0.78	1.00	0.96	0.82
C40T	0.49	0.74	0.64	0.71	0.97	0.98	0.72
C40A	0.58	0.56	0.81	0.90	0.72	0.71	0.94
C41T	0.55	0.77	0.79	0.80	0.99	0.99	0.82
C41G	0.69	0.77	0.68	0.84	0.98	1.00	0.82
C41A	0.59	0.79	0.72	0.80	0.99	0.99	0.81
T42G	0.65	0.81	0.68	0.82	1.00	0.97	0.85
T42C	0.64	0.82	0.67	0.82	1.00	0.98	0.84
T42A	0.57	0.82	0.77	0.82	1.00	0.99	0.85
G43T	0.55	0.76	0.46	0.70	0.79	0.98	0.56
G43C	0.55	0.78	0.72	0.77	1.00	0.99	0.80
G43A	0.57	0.78	0.73	0.79	0.99	0.98	0.82
A44T	0.47	0.80	0.71	0.80	0.92	1.00	0.77
A44G	0.53	0.77	0.74	0.77	0.99	0.98	0.80

A44C	0.51	0.73	0.68	0.72	1.00	0.98	0.76
A45T	0.59	0.82	0.72	0.83	0.98	1.00	0.83
A45G	0.60	0.82	0.66	0.81	1.00	0.99	0.82
T46G	0.68	0.76	0.82	0.95	0.88	0.90	0.94
T46C	0.62	0.76	0.68	0.82	0.95	1.00	0.79
T46A	0.58	0.80	0.77	0.82	0.99	0.99	0.84
A47T	0.56	0.71	0.79	0.83	0.92	0.96	0.82
A47G	0.54	0.74	0.82	0.80	0.97	0.96	0.84
T48G	0.62	0.97	0.82	0.91	0.98	1.00	0.92
T48C	0.59	0.75	0.78	0.82	0.97	0.97	0.83
T48A	0.61	0.78	0.61	0.78	0.99	1.00	0.78
G49C	0.73	0.88	0.76	0.89	1.00	1.00	0.90
G49A	0.68	0.82	0.76	0.86	0.99	0.99	0.88
T50G	0.57	0.87	0.65	0.82	1.00	1.00	0.83
T50C	0.60	0.79	0.75	0.81	0.99	0.99	0.83
T50A	0.59	0.80	0.79	0.82	1.00	0.99	0.85
TG51T	0.56	0.80	0.60	0.75	1.00	0.99	0.77
G51T	0.52	0.85	0.74	0.80	1.00	1.00	0.83
G51A	0.63	0.83	0.68	0.83	1.00	1.00	0.84
G52T	0.58	0.82	0.77	0.82	1.00	1.00	0.84
G52C	0.62	0.78	0.71	0.81	0.99	1.00	0.82
G52A	0.65	0.75	0.74	0.82	0.99	0.98	0.84
T53G	0.49	0.82	0.74	0.77	0.99	1.00	0.81
T53C	0.58	0.79	0.73	0.81	0.99	0.98	0.84
T53A	0.58	0.81	0.83	0.83	0.99	0.99	0.85
C54T	0.59	0.80	0.73	0.81	0.99	0.99	0.83
C54G	0.63	0.64	0.87	0.98	0.78	0.79	0.99
C54A	0.51	0.86	0.68	0.79	1.00	1.00	0.81
C55T	0.55	0.79	0.74	0.78	1.00	0.98	0.82
C55G	0.54	0.82	0.84	0.83	0.98	1.00	0.85
C55A	0.52	0.81	0.72	0.78	0.99	0.99	0.80
G56T	0.54	0.66	0.96	0.97	0.78	0.80	0.98
G56C	0.36	0.79	0.91	0.73	0.99	1.00	0.78
G56A	0.60	0.78	0.70	0.80	0.99	0.99	0.81
GA57G	0.65	0.78	0.80	0.83	1.00	0.95	0.89
A57T	0.56	0.81	0.81	0.82	1.00	0.97	0.86
A57G	0.55	0.87	0.70	0.81	1.00	1.00	0.83
G58T	0.52	0.68	0.80	0.81	0.89	0.88	0.85
G58A	0.61	0.76	0.68	0.78	1.00	0.99	0.80
A59T	0.67	0.75	0.60	0.79	0.99	1.00	0.78
A59G	0.64	0.80	0.70	0.82	1.00	0.99	0.84
AC60A	0.54	0.73	0.70	0.77	0.96	0.98	0.77
C60T	0.71	0.83	0.65	0.85	1.00	1.00	0.85
C60A	0.57	0.75	0.68	0.76	1.00	0.98	0.79
C61T	0.59	0.78	0.76	0.82	0.98	1.00	0.83
C61G	0.61	0.94	0.77	0.87	1.00	1.00	0.89
C61A	0.62	0.74	0.80	0.86	0.94	0.93	0.88
C62T	0.68	0.77	0.77	0.89	0.94	0.99	0.85
C62A	0.61	0.80	0.68	0.80	1.00	0.99	0.82
C63T	0.64	0.78	0.71	0.82	0.99	0.99	0.83
C63G	0.45	0.73	1.00	0.97	0.76	0.83	0.98
C63A	0.62	0.86	0.62	0.82	1.00	1.00	0.82
C63CT	0.55	0.83	0.73	0.83	0.96	1.00	0.83

C64T	0.48	0.79	0.88	0.79	1.00	0.99	0.84
C64A	0.58	0.82	0.69	0.80	1.00	0.99	0.82
C64CA	0.66	0.74	0.78	0.90	0.90	0.91	0.91
CA65C	0.50	0.67	0.89	0.88	0.84	0.87	0.88
A65T	0.61	0.79	0.75	0.82	0.99	0.99	0.83
A65G	0.61	0.84	0.73	0.84	0.98	1.00	0.84
A65C	0.58	0.81	0.73	0.81	1.00	0.99	0.83
AG66A	0.57	0.77	0.67	0.77	0.99	0.99	0.77
G66T	0.68	0.75	0.78	0.92	0.90	0.93	0.90
G66A	0.63	0.79	0.73	0.82	1.00	0.98	0.84
G67T	0.67	0.77	0.79	0.90	0.92	0.97	0.87
G67C	0.82	0.61	0.79	1.00	0.78	0.78	1.00
G67A	0.69	0.79	0.76	0.86	0.98	0.97	0.87
G68A	0.70	0.81	0.78	0.86	0.99	0.98	0.88
A69T	0.59	0.85	0.70	0.82	1.00	1.00	0.84
A69G	0.57	0.82	0.67	0.80	0.99	1.00	0.81
A69C	0.68	0.89	0.77	0.88	1.00	0.99	0.90
A69AT	0.47	0.80	0.87	0.81	0.97	1.00	0.82
T70G	0.69	0.86	0.74	0.87	1.00	1.00	0.87
T70C	0.60	0.81	0.73	0.82	0.99	0.99	0.84
T70A	0.57	0.86	0.68	0.81	1.00	1.00	0.82
TG71T	0.62	0.83	0.75	0.84	1.00	0.99	0.86
G71C	0.68	0.81	0.90	0.95	0.91	0.93	0.96
G71A	0.58	0.81	0.74	0.81	1.00	0.99	0.84
G72T	0.67	0.78	0.67	0.82	0.99	0.99	0.82
G72C	0.71	0.81	0.73	0.86	0.99	0.99	0.86
G72A	0.63	0.79	0.69	0.81	0.99	0.99	0.82
G73T	0.70	0.78	0.81	0.91	0.93	0.93	0.92
G73C	0.67	0.89	0.80	0.89	0.99	1.00	0.89
G73A	0.70	0.78	0.80	0.93	0.91	0.91	0.93
T74G	0.43	0.70	0.99	0.85	0.87	0.83	0.96
T74C	0.63	0.77	0.72	0.82	0.99	0.97	0.83
T74A	0.61	0.79	0.68	0.81	0.98	0.99	0.82
T74TG	0.66	0.76	0.73	0.82	0.99	0.98	0.84
G75T	0.55	0.81	0.79	0.81	1.00	1.00	0.84
G75A	0.63	0.79	0.75	0.89	0.92	1.00	0.84
G76T	0.64	0.78	0.68	0.80	1.00	0.96	0.84
G76C	0.66	0.80	0.72	0.83	1.00	0.98	0.85
G76A	0.66	0.77	0.76	0.83	0.99	0.98	0.86
C77T	0.60	0.83	0.66	0.81	1.00	1.00	0.82
C77G	0.56	0.89	0.44	0.74	0.97	0.99	0.71
C77A	0.62	0.83	0.70	0.83	1.00	0.99	0.84
CA78C	0.56	0.76	0.76	0.78	1.00	0.98	0.81
A78T	0.58	0.81	0.75	0.81	1.00	0.99	0.83
A78G	0.59	0.80	0.73	0.81	0.99	1.00	0.83
A78C	0.65	0.68	0.75	0.91	0.84	0.86	0.90
AG79A	0.72	0.82	0.72	0.85	1.00	0.97	0.88
G79T	0.69	0.77	0.75	0.85	0.97	0.97	0.86
G79C	0.53	0.76	0.67	0.74	0.99	1.00	0.76
G79A	0.70	0.79	0.71	0.84	0.99	0.99	0.85
G80T	0.70	0.79	0.78	0.87	0.97	0.97	0.88
G80C	0.60	0.71	0.84	0.92	0.86	0.86	0.93
G80A	0.71	0.81	0.74	0.86	0.99	0.97	0.88

G81T	0.64	0.72	0.63	0.77	1.00	0.99	0.78
G81A	0.66	0.79	0.78	0.86	0.97	0.98	0.86
A82T	0.56	0.80	0.75	0.80	1.00	0.99	0.82
A82G	0.64	0.80	0.71	0.82	1.00	0.99	0.84
A82C	0.58	0.80	0.74	0.80	1.00	0.99	0.83
A83T	0.56	0.79	0.81	0.81	0.99	0.99	0.84
A83G	0.61	0.79	0.75	0.82	0.99	0.99	0.84
T84G	0.69	0.83	0.71	0.85	1.00	1.00	0.86
T84C	0.63	0.80	0.72	0.82	0.99	0.99	0.83
T84A	0.69	0.78	0.70	0.83	1.00	0.99	0.84
C85T	0.59	0.67	0.69	0.82	0.88	0.91	0.80
C85A	0.48	0.75	0.79	0.78	0.95	0.99	0.78
T86G	0.72	0.70	0.52	0.79	0.94	0.96	0.76
T86C	0.56	0.72	0.73	0.78	0.97	0.97	0.79
T86A	0.52	0.71	0.75	0.75	0.98	0.93	0.81
G87T	0.54	0.72	0.70	0.75	0.97	0.97	0.77
G87A	0.58	0.79	0.73	0.81	0.98	0.99	0.82
A88T	0.51	0.72	0.77	0.76	0.98	0.97	0.79
A88G	0.50	0.76	0.76	0.75	0.99	1.00	0.78
A88C	0.64	0.75	1.00	1.00	0.83	0.86	1.00
G89T	0.61	0.73	0.74	0.80	0.97	0.93	0.85
G89A	0.62	0.83	0.66	0.82	1.00	1.00	0.83
T90G	0.48	0.76	0.71	0.73	0.99	0.99	0.76
T90C	0.60	0.76	0.79	0.89	0.90	1.00	0.83
T90A	0.58	0.77	0.77	0.81	0.99	0.99	0.83
G91C	0.50	0.76	0.86	0.80	0.97	0.99	0.82
G91A	0.58	0.79	0.70	0.80	0.99	0.99	0.81
GC92G	0.69	0.77	0.74	0.86	0.96	0.97	0.86
C92T	0.61	0.77	0.68	0.79	0.99	1.00	0.80
C92A	0.72	0.81	0.75	0.86	1.00	0.97	0.89
C93T	0.58	0.78	0.71	0.79	0.99	0.99	0.81
C93A	0.48	0.80	0.83	0.80	0.98	1.00	0.83
C94T	0.59	0.78	0.73	0.80	0.99	0.97	0.83
C94G	0.52	0.75	0.82	0.79	0.97	0.97	0.82
C94A	0.68	0.84	0.73	0.86	1.00	1.00	0.87
G95T	0.60	0.81	0.71	0.82	1.00	1.00	0.83
G95C	0.85	0.84	0.76	0.93	0.96	0.98	0.91
G95A	0.58	0.81	0.69	0.80	1.00	1.00	0.82
G95GA	0.55	0.81	0.75	0.81	0.99	1.00	0.83
GA96G	0.44	0.66	0.83	0.71	0.95	0.90	0.78
A96T	0.60	0.75	0.68	0.78	0.99	0.98	0.80
A96G	0.58	0.81	0.72	0.81	1.00	1.00	0.82
A96C	0.64	0.82	0.69	0.83	1.00	1.00	0.84
AG97A	0.64	0.81	0.70	0.82	1.00	0.99	0.84
G97T	0.66	0.78	0.73	0.83	0.99	0.99	0.84
G97C	0.63	0.70	0.75	0.83	0.93	0.87	0.91
G97A	0.61	0.80	0.74	0.82	1.00	1.00	0.84
G98T	0.66	0.77	0.76	0.85	0.97	0.96	0.87
G98C	0.77	0.89	0.92	0.91	1.00	0.98	0.95
G98A	0.64	0.80	0.77	0.85	0.97	1.00	0.85
G99T	0.62	0.82	0.78	0.83	1.00	0.98	0.86
G99C	0.57	0.79	0.79	0.81	0.99	0.98	0.84
G99A	0.64	0.77	0.78	0.86	0.95	0.96	0.86

G100T	0.56	0.81	0.70	0.79	1.00	1.00	0.81
G100C	0.61	0.78	0.71	0.80	1.00	0.99	0.82
G100A	0.66	0.82	0.68	0.83	1.00	1.00	0.84
A101T	0.59	0.77	0.78	0.81	0.99	0.98	0.84
A101G	0.59	0.78	0.73	0.80	0.99	0.99	0.82
T102C	0.57	0.81	0.77	0.81	1.00	0.99	0.84
T102A	0.55	0.79	0.78	0.81	0.99	0.99	0.83
TG103T	0.68	0.85	0.77	0.87	0.99	1.00	0.88
G103T	0.67	0.77	0.59	0.79	0.99	1.00	0.78
G103A	0.58	0.84	0.66	0.80	1.00	0.99	0.82
G104A	0.59	0.80	0.73	0.84	0.96	1.00	0.83
GA105G	0.58	0.85	0.67	0.81	0.99	1.00	0.82
A105T	0.63	0.81	0.71	0.83	0.99	0.99	0.84
A105G	0.57	0.82	0.69	0.80	1.00	0.99	0.82
A105C	0.61	0.76	0.53	0.73	1.00	0.97	0.75
G106T	0.65	0.78	0.77	0.83	1.00	0.98	0.86
G106C	0.53	0.73	0.97	0.98	0.82	0.88	0.95
G106A	0.59	0.79	0.73	0.80	1.00	0.98	0.84
C107T	0.64	0.79	0.65	0.81	0.99	1.00	0.81
C107G	0.51	0.83	0.81	0.80	1.00	0.97	0.86
C107A	0.60	0.78	0.74	0.80	1.00	1.00	0.82
T108G	0.67	0.83	0.71	0.84	1.00	1.00	0.85
T108C	0.62	0.84	0.74	0.84	1.00	0.99	0.86
T108A	0.62	0.79	0.69	0.82	0.98	0.99	0.82
G109T	0.55	0.74	0.67	0.75	0.99	1.00	0.77
G109C	0.64	0.77	0.74	0.83	0.98	0.97	0.85
G109A	0.56	0.77	0.78	0.81	0.98	0.99	0.82
C110T	0.62	0.87	0.76	0.91	0.93	1.00	0.87
C110A	0.59	0.84	0.66	0.81	0.99	1.00	0.82
T111G	0.59	0.79	0.81	0.82	0.99	0.98	0.85
T111C	0.57	0.81	0.73	0.81	1.00	0.99	0.83
T111A	0.60	0.82	0.75	0.82	0.99	1.00	0.84
TG112T	0.61	0.78	0.77	0.83	0.97	1.00	0.83
G112T	0.65	0.79	0.65	0.80	1.00	0.99	0.82
G112C	0.71	0.85	0.80	0.88	1.00	0.99	0.89
G112A	0.55	0.76	0.86	0.82	0.98	0.95	0.87
G113T	0.65	0.75	0.76	0.84	0.96	0.94	0.87
G113C	0.78	0.78	0.75	0.94	0.91	0.90	0.95
G113A	0.62	0.80	0.79	0.83	0.99	0.99	0.86
C114T	0.68	0.81	0.70	0.86	0.97	1.00	0.84
C114G	0.61	0.79	0.81	0.83	0.99	0.98	0.86
C114A	0.73	0.77	0.79	0.97	0.87	0.88	0.96
CT115C	0.66	0.83	0.68	0.83	1.00	0.99	0.85
T115G	0.75	0.63	0.63	0.92	0.81	0.83	0.89
T115C	0.62	0.82	0.78	0.84	1.00	0.99	0.86
T115A	0.57	0.80	0.75	0.81	0.99	1.00	0.82
T116C	0.58	0.82	0.74	0.82	0.99	1.00	0.83
T116A	0.64	0.81	0.71	0.83	1.00	1.00	0.84
T117C	0.64	0.77	0.76	0.85	0.96	1.00	0.83
T117A	0.59	0.72	0.75	0.79	0.98	1.00	0.79
TA118T	0.57	0.84	0.76	0.83	0.98	1.00	0.85
A118T	0.51	0.79	0.81	0.79	0.99	0.99	0.82
A118G	0.65	0.82	0.73	0.84	1.00	0.99	0.85

A118C	0.66	0.74	0.74	0.86	0.93	0.95	0.86
C119T	0.60	0.82	0.70	0.81	1.00	0.96	0.86
C119G	0.52	0.75	0.84	0.81	0.96	0.98	0.82
C119A	0.56	0.81	0.54	0.74	0.99	1.00	0.73
A120T	0.59	0.80	0.70	0.80	0.99	0.99	0.82
A120G	0.57	0.81	0.72	0.81	0.99	1.00	0.82
A120C	0.52	0.81	0.89	0.85	0.96	1.00	0.86
C121T	0.56	0.78	0.74	0.79	0.99	0.99	0.82
C121G	0.48	0.81	0.87	0.80	0.99	1.00	0.83
C121A	0.56	0.79	0.71	0.79	0.99	0.98	0.81
T122G	0.62	0.82	0.77	0.84	1.00	0.99	0.86
T122C	0.62	0.77	0.80	0.83	0.98	0.97	0.86
T122A	0.64	0.78	0.71	0.82	0.99	0.98	0.85
G123T	0.62	0.81	0.77	0.84	0.99	0.99	0.86
G123C	0.58	0.83	0.71	0.81	1.00	1.00	0.82
G123A	0.58	0.82	0.69	0.80	1.00	1.00	0.82
C124T	0.60	0.83	0.78	0.87	0.95	1.00	0.85
C124G	0.53	0.75	0.81	0.80	0.97	0.99	0.81
C124A	0.64	0.79	0.69	0.82	0.99	0.99	0.83
C125T	0.59	0.77	0.79	0.82	0.99	0.98	0.84
C125A	0.62	0.82	0.70	0.83	0.99	1.00	0.83
T126G	0.83	0.75	0.56	0.85	0.94	0.92	0.85
T126C	0.62	0.76	0.70	0.80	0.99	0.99	0.81
T126A	0.46	0.80	0.75	0.75	0.99	0.99	0.79
G127T	0.57	0.78	0.70	0.79	0.99	0.99	0.81
G127A	0.59	0.88	0.86	0.88	0.97	1.00	0.89
G128T	0.62	0.87	0.68	0.87	0.97	1.00	0.85
G128C	0.67	0.81	0.78	0.86	0.98	1.00	0.87
G128A	0.65	0.84	0.71	0.84	1.00	0.99	0.86
C129T	0.59	0.82	0.76	0.82	0.99	0.99	0.84
C129G	0.64	0.74	0.82	0.91	0.89	0.92	0.91
C129A	0.63	0.76	0.77	0.83	0.98	0.97	0.85
CT130C	0.69	0.90	0.81	0.89	1.00	0.98	0.92
T130G	0.65	0.75	0.77	0.89	0.91	0.99	0.83
T130C	0.64	0.75	0.81	0.89	0.91	0.93	0.89
T130A	0.56	0.80	0.72	0.79	1.00	1.00	0.82
T131G	0.44	0.79	0.82	0.76	0.99	0.99	0.79
T131C	0.59	0.77	0.67	0.78	0.99	0.99	0.79
T131A	0.61	0.75	0.72	0.78	1.00	0.94	0.85
T132C	0.62	0.79	0.74	0.82	1.00	0.99	0.84
T132A	0.58	0.84	0.67	0.80	0.99	1.00	0.81
TC133T	0.75	0.89	0.65	0.88	1.00	1.00	0.87
C133T	0.58	0.79	0.69	0.79	0.99	1.00	0.80
C133G	0.67	0.65	0.97	1.00	0.79	0.81	1.00
C133A	0.64	0.74	0.85	0.96	0.85	0.88	0.95
G134T	0.66	0.86	0.68	0.85	1.00	1.00	0.86
G134C	0.64	0.82	0.69	0.83	0.99	1.00	0.83
G134A	0.59	0.80	0.72	0.80	1.00	0.99	0.83
C135T	0.59	0.72	0.71	0.78	0.98	0.94	0.82
C135G	0.36	0.43	1.00	0.82	0.20	0.32	0.72
C135A	0.52	0.92	0.95	0.86	0.99	0.99	0.92
T136C	0.59	0.78	0.80	0.81	1.00	0.98	0.85
T136A	0.55	0.78	0.72	0.78	1.00	0.99	0.80

T137G	0.62	0.78	0.76	0.81	1.00	0.97	0.85
T137C	0.60	0.80	0.70	0.80	1.00	1.00	0.82
T137A	0.58	0.82	0.75	0.82	1.00	0.99	0.84
TC138T	0.63	0.78	0.68	0.81	0.98	0.99	0.81
C138T	0.58	0.77	0.69	0.78	1.00	0.93	0.85
C139T	0.56	0.78	0.70	0.78	0.99	1.00	0.80
C139A	0.58	0.79	0.72	0.80	0.99	0.98	0.83
T140C	0.60	0.78	0.73	0.81	0.99	1.00	0.82
T140A	0.59	0.78	0.74	0.80	0.99	0.99	0.82
A141T	0.56	0.80	0.74	0.80	0.99	1.00	0.82
A141G	0.61	0.79	0.77	0.82	0.99	0.98	0.85
A141C	0.60	0.73	0.79	0.82	0.96	0.93	0.87
A141AC	0.56	0.81	0.73	0.80	1.00	0.99	0.83
AC142A	0.65	0.81	0.70	0.83	1.00	1.00	0.84
C142T	0.60	0.80	0.73	0.82	0.99	1.00	0.82
C142G	0.57	0.77	0.78	0.79	1.00	0.98	0.83
C142A	0.64	0.67	0.77	0.90	0.85	0.84	0.93
C143T	0.62	0.73	0.64	0.77	0.99	0.99	0.78
C143G	0.55	0.76	0.76	0.79	0.98	0.98	0.81
C143A	0.65	0.77	0.74	0.83	0.98	1.00	0.83
C144T	0.61	0.74	0.78	0.80	0.99	0.97	0.84
C144G	0.81	0.82	0.61	0.86	0.99	1.00	0.84
C144A	0.70	0.82	0.80	0.87	0.98	0.99	0.87
C145T	0.63	0.80	0.68	0.81	1.00	0.99	0.83
C145G	0.62	0.77	0.75	0.82	0.98	0.98	0.83
C145A	0.67	0.77	0.62	0.80	1.00	0.99	0.80
C146T	0.62	0.82	0.72	0.82	1.00	1.00	0.84
C146A	0.60	0.84	0.75	0.83	1.00	0.99	0.86
CA147C	0.62	0.62	0.66	0.79	0.89	0.85	0.84
A147T	0.60	0.81	0.73	0.82	0.99	1.00	0.83
A147G	0.59	0.80	0.76	0.82	0.99	0.99	0.84
A147C	0.62	0.80	0.74	0.82	1.00	0.98	0.85
A147AC	0.58	0.83	0.77	0.82	1.00	0.99	0.85
AC148A	0.64	0.80	0.75	0.83	1.00	1.00	0.84
C148T	0.66	0.79	0.74	0.84	0.98	0.99	0.85
C148G	0.62	0.82	0.74	0.83	0.99	0.99	0.85
C148A	0.73	0.88	0.70	0.89	1.00	1.00	0.89
C149T	0.62	0.79	0.76	0.82	1.00	0.99	0.84
C149G	0.49	0.79	0.80	0.77	1.00	0.99	0.81
C149A	0.58	0.76	0.71	0.79	0.99	0.98	0.81
C150T	0.60	0.74	0.79	0.89	0.89	0.98	0.83
C150G	0.78	0.79	0.61	0.85	0.98	0.99	0.83
C150A	0.65	0.78	0.73	0.88	0.93	1.00	0.83
C151T	0.55	0.74	0.77	0.78	0.98	0.98	0.80
C151CT	0.58	0.87	0.64	0.81	1.00	0.96	0.86
A152T	0.59	0.77	0.73	0.80	0.99	0.99	0.82
A152G	0.58	0.78	0.76	0.80	1.00	0.99	0.83
A152C	0.68	0.81	0.81	0.86	0.99	0.99	0.88
AT153A	0.68	0.86	0.76	0.86	1.00	0.99	0.88
T153C	0.61	0.77	0.70	0.80	0.99	0.99	0.81
T153A	0.61	0.75	0.78	0.81	0.99	0.99	0.83
C154T	0.58	0.83	0.70	0.81	0.99	1.00	0.83
C154G	0.59	0.75	0.68	0.78	0.98	0.98	0.79

C154A	0.56	0.81	0.72	0.80	1.00	0.99	0.82
C155T	0.57	0.81	0.72	0.81	0.99	0.99	0.83
C155G	0.62	0.82	0.75	0.83	1.00	0.99	0.85
C155A	0.61	0.76	0.73	0.80	0.99	0.98	0.83
CA156C	0.60	0.86	0.67	0.82	1.00	1.00	0.84
A156T	0.60	0.82	0.70	0.81	1.00	0.99	0.83
A156G	0.58	0.78	0.73	0.79	1.00	0.99	0.82
A156C	0.69	0.81	0.78	0.87	0.98	0.98	0.88
AC157A	0.60	0.81	0.71	0.81	1.00	0.99	0.83
C157T	0.65	0.82	0.73	0.85	0.98	1.00	0.85
C157G	0.62	0.81	0.67	0.81	1.00	0.99	0.82
C157A	0.62	0.73	0.56	0.71	1.00	0.90	0.79
C158T	0.57	0.79	0.72	0.80	1.00	1.00	0.81
C158G	0.56	0.76	0.71	0.77	0.99	0.98	0.79
C158A	0.62	0.77	0.71	0.82	0.97	0.99	0.82
C159T	0.61	0.80	0.64	0.80	0.99	1.00	0.80
C159G	0.67	0.81	0.57	0.80	1.00	0.99	0.80
C159A	0.72	0.92	0.76	0.89	1.00	1.00	0.91
CA160C	0.61	0.86	0.77	0.85	1.00	0.99	0.87
A160T	0.67	0.77	0.71	0.85	0.96	1.00	0.82
A160G	0.70	0.75	0.75	0.90	0.92	0.94	0.88
A160C	0.60	0.84	0.71	0.83	1.00	0.99	0.85
G161T	0.56	0.83	0.72	0.81	1.00	0.98	0.84
G161C	0.50	0.75	0.84	0.79	0.97	0.98	0.81
G161A	0.54	0.79	0.77	0.79	0.99	0.99	0.82
T162G	0.60	0.84	0.66	0.82	0.99	1.00	0.82
T162C	0.64	0.80	0.73	0.82	1.00	0.99	0.84
T162A	0.60	0.79	0.73	0.82	0.98	0.99	0.83
G163T	0.52	0.84	0.67	0.78	1.00	1.00	0.80
G163C	0.60	0.69	0.67	0.77	0.95	0.97	0.77
G163A	0.59	0.80	0.75	0.81	1.00	1.00	0.84
C164T	0.60	0.79	0.73	0.82	0.98	1.00	0.82
C164G	0.55	0.92	0.73	0.84	1.00	1.00	0.86
C164A	0.78	0.78	0.71	0.89	0.96	0.94	0.90
C165T	0.54	0.76	0.73	0.77	0.99	1.00	0.79
C165G	0.77	0.88	0.57	0.87	1.00	1.00	0.85
C165A	0.66	0.77	0.92	0.99	0.85	0.87	0.99
CA166C	0.47	0.76	1.00	0.90	0.87	0.91	0.93
A166T	0.66	0.80	0.68	0.83	0.99	1.00	0.83
A166G	0.64	0.79	0.74	0.83	0.99	0.99	0.84
A166C	0.58	0.82	0.70	0.80	1.00	0.99	0.82
A167T	0.59	0.75	0.78	0.83	0.95	0.99	0.81
A167G	0.58	0.83	0.65	0.80	1.00	1.00	0.81
AC168A	0.46	0.72	0.76	0.72	0.98	0.98	0.75
C168T	0.63	0.82	0.66	0.82	1.00	1.00	0.83
C168G	0.65	0.82	0.68	0.83	1.00	1.00	0.83
C168A	0.61	0.85	0.69	0.90	0.93	1.00	0.85
C169T	0.62	0.82	0.69	0.82	1.00	1.00	0.83
C169G	0.55	0.72	0.83	0.79	0.98	0.93	0.86
C169A	0.64	0.80	0.76	0.84	0.99	1.00	0.85
T170G	0.71	0.79	0.79	0.91	0.93	0.98	0.88
T170C	0.61	0.77	0.73	0.82	0.97	0.99	0.82
T170A	0.61	0.79	0.71	0.81	1.00	0.97	0.84

A171T	0.65	0.78	0.74	0.82	1.00	0.99	0.84
A171G	0.60	0.76	0.84	0.85	0.96	0.95	0.88
A171C	0.71	0.64	0.77	0.99	0.77	0.78	0.98
G172T	0.59	0.78	0.93	0.95	0.87	0.92	0.94
G172A	0.61	0.77	0.75	0.83	0.97	0.98	0.83
GT173G	0.90	0.94	0.93	0.97	0.98	1.00	0.96
T173G	0.61	0.82	0.71	0.82	1.00	0.99	0.84
T173C	0.62	0.80	0.71	0.81	1.00	0.99	0.83
T173A	0.60	0.79	0.79	0.82	0.99	0.99	0.85
T174G	0.57	0.67	0.52	0.63	0.78	0.69	0.71
T174C	0.55	0.77	0.70	0.76	1.00	0.94	0.83
T174A	0.65	0.82	0.75	0.84	1.00	0.99	0.86
C175T	0.60	0.82	0.63	0.79	1.00	1.00	0.80
C175G	0.52	0.75	0.87	0.82	0.95	0.95	0.86
C175A	0.69	0.97	0.72	0.90	1.00	1.00	0.91
C176T	0.69	0.79	0.70	0.84	0.99	0.97	0.86
C176A	0.67	0.80	0.63	0.81	1.00	0.99	0.82
A177T	0.55	0.81	0.64	0.77	0.99	1.00	0.79
A177G	0.65	0.80	0.63	0.81	0.99	1.00	0.81
A177C	0.62	0.63	0.73	0.89	0.82	0.83	0.88
C178T	0.71	0.78	0.74	0.86	0.98	0.98	0.87
C178G	0.73	0.82	0.82	0.88	0.99	0.97	0.91
C178A	0.58	0.83	0.70	0.81	1.00	0.99	0.84
T179G	0.62	0.74	0.77	0.81	0.99	0.96	0.85
T179C	0.60	0.80	0.77	0.82	1.00	0.94	0.89
T179A	0.57	0.83	0.73	0.81	1.00	1.00	0.83
G180T	0.48	0.82	0.68	0.74	1.00	0.99	0.78
G180A	0.48	0.75	0.69	0.73	0.98	1.00	0.73
A181T	0.55	0.79	0.65	0.76	1.00	0.96	0.81
A181G	0.68	0.79	0.68	0.83	0.99	0.99	0.84
A181C	0.53	0.77	1.00	0.96	0.85	0.89	0.96
A182T	0.45	0.78	0.92	0.79	0.99	0.99	0.84
A182G	0.59	0.84	0.67	0.81	0.99	0.99	0.83
A182C	0.57	0.84	0.52	0.75	0.99	0.98	0.75
G183T	0.53	0.85	0.89	0.84	0.99	0.99	0.87
G183C	0.48	0.88	0.63	0.75	1.00	0.99	0.78
G183A	0.58	0.77	0.72	0.80	0.98	1.00	0.80
C184T	0.67	0.80	0.88	0.96	0.89	0.95	0.92
C184A	0.94	0.70	0.70	1.00	0.85	0.83	1.00
C185T	0.77	0.77	0.79	0.95	0.91	0.89	0.97
C185A	0.70	0.72	0.66	0.82	0.98	0.97	0.82
T186G	0.35	0.96	0.84	0.77	1.00	1.00	0.82
T186C	0.62	0.78	0.73	0.82	0.99	0.99	0.83
T186A	0.63	0.80	0.71	0.82	0.99	0.98	0.84
G187T	0.69	0.85	0.58	0.84	1.00	0.99	0.84
G187A	0.50	0.72	0.84	0.78	0.97	0.95	0.82
A188T	0.55	0.80	0.72	0.83	0.94	1.00	0.81
A188G	0.59	0.81	0.66	0.80	1.00	1.00	0.82
A188C	0.62	0.80	0.72	0.83	0.98	1.00	0.83
AG189A	0.58	0.82	0.62	0.79	1.00	1.00	0.80
G189T	0.56	0.85	0.66	0.80	1.00	1.00	0.82
G189C	0.60	0.80	0.67	0.80	0.99	1.00	0.81
G189A	0.55	0.78	0.80	0.80	0.99	0.99	0.83

G190T	0.53	0.86	0.65	0.78	1.00	0.97	0.83
G190A	0.64	0.84	0.80	0.85	1.00	0.99	0.88
A191T	0.52	0.80	0.71	0.78	0.99	0.99	0.80
A191G	0.56	0.84	0.65	0.79	0.99	0.99	0.81
A191C	0.57	0.87	0.65	0.81	1.00	1.00	0.82
G192T	0.66	0.84	0.75	0.85	1.00	0.99	0.87
G192C	0.62	0.79	0.65	0.80	1.00	1.00	0.80
G192A	0.59	0.76	0.75	0.80	0.99	0.99	0.81
C193T	0.66	0.81	0.71	0.84	0.99	1.00	0.84
C193G	0.58	0.83	0.73	0.82	0.99	1.00	0.84
C193A	0.65	0.82	0.64	0.85	0.96	1.00	0.82
A194T	0.59	0.77	0.69	0.78	1.00	0.97	0.81
A194G	0.60	0.81	0.73	0.82	0.99	0.99	0.83
T195G	0.61	0.81	0.68	0.81	1.00	1.00	0.83
T195C	0.59	0.79	0.75	0.82	0.99	0.99	0.83
T195A	0.65	0.78	0.77	0.83	0.99	1.00	0.84
G196T	0.61	0.79	0.76	0.84	0.97	1.00	0.84
G196C	0.63	0.84	0.69	0.83	0.99	1.00	0.84
G196A	0.63	0.82	0.74	0.83	1.00	0.98	0.86
C197T	0.52	0.79	0.80	0.79	0.99	0.99	0.82
C197G	0.45	0.82	0.80	0.77	0.99	1.00	0.80
C197A	0.63	0.79	0.69	0.82	0.98	0.99	0.83
C198T	0.56	0.78	0.70	0.78	0.99	1.00	0.80
C198G	0.75	0.80	0.84	0.98	0.89	0.93	0.95
C198A	0.54	0.73	0.73	0.77	0.97	0.98	0.79
A199T	0.61	0.83	0.72	0.82	1.00	1.00	0.84
A199G	0.65	0.81	0.66	0.82	1.00	1.00	0.82
A199C	0.61	0.83	0.75	0.83	0.99	1.00	0.85
AT200A	0.41	0.87	0.97	0.81	0.99	0.99	0.87
T200C	0.65	0.81	0.74	0.83	1.00	0.99	0.85
T200A	0.63	0.79	0.71	0.82	0.99	0.99	0.83
T201G	0.68	0.72	0.85	0.99	0.83	0.84	0.99
T201C	0.53	0.78	0.88	0.82	0.98	0.97	0.86
T201A	0.63	0.79	0.79	0.83	0.99	0.98	0.86
A202T	0.65	0.79	0.74	0.83	0.99	1.00	0.84
A202G	0.60	0.77	0.74	0.81	0.98	0.98	0.83
A202C	0.63	0.74	0.72	0.83	0.96	0.99	0.82
A203T	0.54	0.78	0.83	0.82	0.97	0.98	0.84
A203G	0.57	0.78	0.63	0.76	1.00	0.99	0.78
G204T	0.55	0.93	0.64	0.83	1.00	1.00	0.85
G204C	0.52	0.82	0.81	0.80	1.00	1.00	0.83
G204A	0.62	0.77	0.93	0.98	0.85	0.89	0.96
T205G	0.68	0.76	0.86	0.97	0.87	0.88	0.98
T205C	0.62	0.82	0.79	0.84	0.99	0.98	0.87
T205A	0.66	0.80	0.68	0.83	1.00	0.99	0.84
T206G	0.57	0.80	0.65	0.78	1.00	1.00	0.79
T206C	0.61	0.77	0.77	0.82	0.99	0.99	0.83
T206A	0.57	0.80	0.73	0.80	0.99	1.00	0.82
T207G	0.57	0.79	0.73	0.80	1.00	1.00	0.81
T207C	0.63	0.84	0.77	0.84	1.00	0.99	0.87
T207A	0.64	0.85	0.67	0.84	1.00	0.99	0.86
G208T	0.57	0.75	0.72	0.79	0.99	0.99	0.81
G208A	0.65	0.79	0.75	0.83	1.00	0.93	0.90

A209T	0.61	0.79	0.68	0.82	0.97	1.00	0.81
A209G	0.53	0.81	0.63	0.76	1.00	0.99	0.78
A209C	0.65	0.85	0.69	0.85	1.00	1.00	0.86
G210T	0.47	0.82	0.51	0.64	0.95	0.95	0.65
G210C	0.60	0.84	0.63	0.81	1.00	1.00	0.83
G210A	0.49	0.79	0.64	0.73	0.98	0.99	0.75
G211T	0.03	0.73	0.49	0.07	0.23	0.37	0.35
T212C	0.19	0.76	0.56	0.37	0.34	0.37	0.52
T212A	0.02	0.66	0.63	0.07	0.26	0.31	0.51
A213T	0.40	0.82	0.49	0.53	0.65	0.79	0.46
A213G	0.58	0.79	0.66	0.78	1.00	0.99	0.80
A214T	0.53	0.85	0.67	0.79	1.00	1.00	0.81
A214G	0.53	0.79	0.64	0.75	0.99	1.00	0.77
A214C	0.57	0.90	0.72	0.84	1.00	1.00	0.87
G215C	0.41	0.82	0.54	0.56	0.99	0.93	0.62
G215A	0.46	0.85	0.51	0.93	0.69	1.00	0.66
T216G	0.48	0.89	0.48	0.71	0.95	0.98	0.69
T216C	0.59	0.80	0.66	0.83	0.96	1.00	0.81
T216A	0.53	0.79	0.64	0.75	0.99	0.99	0.77
G217T	0.60	0.72	0.68	0.78	0.97	0.96	0.79
G217C	0.59	0.75	0.87	0.92	0.87	0.88	0.93
G217A	0.63	0.84	0.68	0.83	1.00	1.00	0.84
GT218G	1.00	0.59	0.92	1.00	0.81	0.80	1.00
T218G	0.52	0.93	0.74	0.83	1.00	1.00	0.88
T218C	0.54	0.80	0.73	0.78	1.00	0.99	0.81
T218A	0.65	0.78	0.70	0.82	1.00	0.99	0.83
TA219T	0.64	0.77	0.64	0.80	0.98	0.99	0.80
A219T	0.60	0.80	0.66	0.81	0.99	1.00	0.81
A219G	0.65	0.84	0.72	0.84	1.00	1.00	0.85
A220T	0.62	0.68	0.83	0.95	0.82	0.83	0.95
A220G	0.55	0.81	0.74	0.81	0.98	1.00	0.82
A220C	0.69	0.80	0.77	0.87	0.97	1.00	0.85
AG221A	0.63	0.66	0.69	0.81	0.92	0.85	0.89
G221T	0.62	0.73	0.70	0.78	0.99	0.99	0.79
G221A	0.57	0.79	0.60	0.76	1.00	0.97	0.79
G222T	0.57	0.83	0.67	0.80	1.00	0.99	0.81
G222A	0.50	0.83	0.64	0.76	1.00	1.00	0.78
G223T	0.71	0.77	0.81	0.94	0.90	0.91	0.94
G223A	0.56	0.76	0.70	0.77	1.00	0.98	0.80
A224T	0.59	0.73	0.74	0.79	0.98	0.97	0.82
A224G	0.57	0.73	0.86	0.88	0.89	0.90	0.90
T225C	0.65	0.77	0.80	0.84	0.98	0.95	0.89
TA226T	0.76	0.50	0.83	1.00	0.64	0.65	1.00
A226T	0.51	0.73	0.81	0.78	0.97	0.96	0.81
A226G	0.65	0.77	0.82	0.90	0.92	0.93	0.90
A226C	0.73	0.59	0.65	0.94	0.76	0.78	0.91
A226AT	0.47	0.85	0.74	0.77	1.00	1.00	0.81
A226AG	0.59	0.85	0.72	0.82	1.00	1.00	0.85
AG227A	0.59	0.79	0.50	0.73	0.98	0.99	0.72
G227T	0.52	0.78	0.80	0.78	1.00	0.99	0.81
G227C	0.50	0.34	0.51	0.64	0.16	0.16	0.65
G227A	0.47	0.73	0.81	0.75	0.98	0.98	0.78
G228T	0.65	0.59	0.53	0.68	0.45	0.39	0.78

G228A	0.49	0.62	0.74	0.75	0.80	0.74	0.84
G228GT	0.68	0.72	0.66	0.82	0.96	0.97	0.81
G229T	0.60	0.62	0.67	0.83	0.82	0.90	0.77
G229A	0.47	0.63	0.71	0.85	0.58	0.75	0.68
G230T	0.55	0.61	0.79	0.88	0.77	0.80	0.87
G230C	0.51	0.68	0.67	0.73	0.91	0.95	0.72
G230A	0.57	0.71	0.70	0.77	0.96	0.95	0.79
C231T	0.55	0.80	0.74	0.79	1.00	1.00	0.82
C231A	0.58	0.81	0.82	0.86	0.96	1.00	0.84
CA232C	0.54	0.83	0.96	0.86	0.98	0.98	0.89
A232T	0.59	0.77	0.79	0.83	0.97	0.99	0.83
A232G	0.59	0.83	0.74	0.82	0.99	1.00	0.84
A232C	0.62	0.71	0.77	0.88	0.89	0.90	0.88
AG233A	0.64	0.70	0.68	0.78	0.98	0.99	0.78
G233T	0.49	0.65	0.88	0.91	0.79	0.84	0.88
G233C	0.58	0.69	0.70	0.78	0.94	0.94	0.79
G233A	0.58	0.64	0.85	0.96	0.77	0.82	0.92
G234T	0.62	0.58	0.81	0.97	0.73	0.76	0.94
G234C	0.67	0.69	0.79	0.96	0.83	0.87	0.93
G234A	0.56	0.58	0.85	0.91	0.76	0.72	0.98
G235T	0.64	0.65	0.73	0.86	0.87	0.83	0.92
G235A	0.58	0.70	0.75	0.81	0.93	0.97	0.80
A236T	0.61	0.79	0.81	0.83	0.99	0.97	0.87
A236G	0.57	0.80	0.87	0.83	1.00	0.97	0.87
A236C	0.57	0.73	0.55	0.75	0.90	0.92	0.74
C237T	0.65	0.79	0.70	0.82	0.99	0.99	0.83
C237G	0.55	0.83	0.70	0.79	0.99	1.00	0.81
A238T	0.58	0.80	0.77	0.82	0.98	1.00	0.83
A238G	0.62	0.80	0.77	0.83	0.99	0.97	0.86
A238C	0.50	0.83	0.89	0.84	0.96	1.00	0.84
G239T	0.57	0.70	0.80	0.82	0.93	0.89	0.88
G239C	0.55	0.76	0.75	0.78	0.99	0.99	0.80
G239A	0.61	0.75	0.73	0.81	0.98	0.97	0.83
T240C	0.62	0.76	0.74	0.80	1.00	0.95	0.86
T240A	0.61	0.78	0.70	0.80	0.99	0.99	0.82
T241G	0.67	0.82	0.83	0.87	0.99	0.99	0.88
T241C	0.64	0.82	0.72	0.83	1.00	0.96	0.88
T241A	0.60	0.72	0.74	0.79	0.98	0.98	0.81
TG242T	0.58	0.84	0.77	0.83	1.00	1.00	0.86
G242T	0.49	0.76	0.87	0.81	0.96	0.98	0.83
G242C	0.51	0.84	0.74	0.79	1.00	1.00	0.82
G242A	0.54	0.83	0.59	0.77	0.98	1.00	0.77
G243T	0.57	0.87	0.63	0.80	1.00	1.00	0.82
G243A	0.63	0.84	0.61	0.82	1.00	1.00	0.82
G244T	0.57	0.90	0.70	0.85	0.97	1.00	0.86
G244A	0.58	0.86	0.67	0.82	1.00	1.00	0.84
G245T	0.62	0.83	0.75	0.85	0.98	1.00	0.85
G245C	0.44	0.68	0.78	0.69	0.98	0.91	0.77
G245A	0.60	0.80	0.68	0.80	1.00	1.00	0.81
G245GT	1.00	0.02	1.00	0.99	0.01	0.02	0.99
GA246G	0.61	0.56	0.73	0.80	0.62	0.55	0.91
A246T	0.63	0.77	0.73	0.82	0.98	0.98	0.84
A246G	0.56	0.48	0.89	0.84	0.32	0.35	0.81

T247G	0.62	0.77	0.71	0.80	1.00	0.98	0.83
T247C	0.52	0.74	0.89	0.81	0.96	0.97	0.84
T247A	0.53	0.81	0.76	0.80	1.00	1.00	0.82
C248T	0.58	0.79	0.77	0.82	0.99	0.99	0.83
C248G	0.31	0.68	1.00	0.86	0.68	0.74	0.88
C248A	0.59	0.77	0.84	0.85	0.96	0.96	0.87
T249G	0.56	0.73	0.81	0.83	0.94	0.97	0.83
T249C	0.59	0.73	0.73	0.79	0.98	0.97	0.81
T249A	0.59	0.76	0.75	0.80	0.99	0.99	0.81
G250T	0.52	0.81	0.73	0.78	0.99	0.99	0.81
G250C	0.57	0.81	0.71	0.80	1.00	1.00	0.82
G250A	0.57	0.80	0.74	0.80	1.00	0.99	0.82
GA251G	0.60	0.69	0.64	0.76	0.95	0.96	0.76
A251T	0.57	0.78	0.69	0.78	0.99	0.99	0.80
A251G	0.59	0.76	0.72	0.80	0.97	1.00	0.80
A251C	0.54	0.78	0.66	0.76	1.00	0.99	0.79
A252T	0.56	0.72	0.74	0.82	0.92	1.00	0.78
A252G	0.56	0.62	0.88	0.94	0.77	0.78	0.96
A252C	0.42	0.83	0.82	0.76	1.00	1.00	0.81
A253T	0.60	0.80	0.72	0.81	1.00	0.99	0.83
A253G	0.61	0.73	0.72	0.81	0.96	0.98	0.81
A253C	0.71	0.78	0.78	0.88	0.95	0.91	0.93
G254T	0.55	0.68	0.57	0.75	0.85	0.97	0.66
G254C	0.61	0.77	0.64	0.79	0.99	0.99	0.80
G254A	0.60	0.84	0.64	0.81	1.00	1.00	0.82
T255G	0.49	0.61	0.85	0.91	0.73	0.81	0.84
T255C	0.57	0.85	0.73	0.82	1.00	1.00	0.84
T255A	0.67	0.85	0.68	0.86	0.99	1.00	0.85
A256T	0.61	0.83	0.75	0.83	1.00	0.99	0.86
A256G	0.57	0.87	0.78	0.84	1.00	1.00	0.87
AG257A	0.53	0.81	0.72	0.78	1.00	1.00	0.81
G257T	0.69	0.83	0.77	0.86	0.99	1.00	0.87
G257A	0.61	0.84	0.68	0.82	1.00	1.00	0.83
G258T	0.53	0.82	0.79	0.80	1.00	0.99	0.84
G258A	0.58	0.70	0.76	0.79	0.96	0.94	0.83
G259T	0.60	0.94	0.75	0.87	1.00	1.00	0.88
G259C	0.40	0.90	0.99	0.82	0.98	0.99	0.89
G259A	0.65	0.81	0.68	0.83	0.99	1.00	0.83
G260C	0.73	0.72	0.63	0.83	0.96	0.97	0.82
G260A	0.63	0.73	0.72	0.81	0.97	0.97	0.82
GC261G	0.43	0.84	0.82	0.77	1.00	0.99	0.82
C261T	0.59	0.78	0.73	0.80	0.99	0.99	0.81
C261G	0.54	0.73	0.77	0.82	0.93	0.99	0.79
C261A	0.79	0.10	0.94	0.83	0.04	0.07	0.96
C262T	0.59	0.83	0.77	0.83	1.00	0.99	0.85
C262G	0.72	0.84	1.00	1.00	0.88	0.91	1.00
C262A	0.63	0.76	0.70	0.80	1.00	0.99	0.82
A263T	0.64	0.82	0.72	0.83	1.00	0.94	0.89
A263G	0.64	0.78	0.69	0.81	0.99	1.00	0.81
A263C	0.64	0.88	0.86	0.87	1.00	0.99	0.89
G264T	0.69	0.91	0.77	0.89	1.00	1.00	0.90
G264C	0.61	0.94	0.76	0.87	1.00	1.00	0.89
G264A	0.65	0.87	0.71	0.85	1.00	1.00	0.86

C265T	0.53	0.81	0.78	0.80	1.00	0.99	0.83
C265G	0.45	0.92	0.77	0.80	1.00	1.00	0.84
C265A	0.64	0.82	0.74	0.84	0.98	1.00	0.84
C266T	0.70	0.94	0.75	0.90	1.00	1.00	0.91
C266G	0.23	0.63	1.00	0.97	0.34	0.67	0.68
C266A	0.36	0.81	0.81	0.71	0.99	0.99	0.76
T267C	0.51	0.84	0.85	0.81	1.00	0.95	0.89
T267A	0.71	0.93	0.67	0.89	1.00	1.00	0.89
TA268T	0.47	0.91	0.80	0.81	1.00	1.00	0.86
A268T	0.54	0.90	0.84	0.85	1.00	1.00	0.89
A268G	0.47	0.87	0.82	0.80	1.00	1.00	0.84
A268C	0.82	0.74	0.83	1.00	0.86	0.86	1.00
C269T	0.55	0.88	0.73	0.82	1.00	1.00	0.85
C269G	0.50	0.78	0.83	0.79	0.98	1.00	0.81
C269A	0.87	0.96	0.64	0.93	1.00	1.00	0.90
T270G	0.56	0.89	0.71	0.82	1.00	1.00	0.85
T270C	0.61	0.81	0.67	0.81	0.99	0.99	0.83
T270A	0.70	0.87	0.75	0.87	1.00	0.99	0.89
TG271T	0.40	0.84	0.81	0.75	0.99	1.00	0.79
G271T	0.59	0.93	0.77	0.86	1.00	1.00	0.89
G271C	0.65	0.87	0.64	0.87	0.96	1.00	0.84
G271A	0.75	0.93	0.72	0.90	1.00	0.99	0.91
G272T	0.63	0.94	0.80	0.88	1.00	1.00	0.90
G272C	0.50	0.73	1.00	0.97	0.81	0.85	0.99
G272A	0.77	0.96	0.68	0.90	1.00	1.00	0.90
C273T	0.64	0.84	0.67	0.83	1.00	1.00	0.83
C273G	0.57	0.73	0.77	0.80	0.97	0.96	0.82
C273A	0.74	0.92	0.69	0.89	1.00	1.00	0.89
T274G	0.79	0.94	0.57	0.90	1.00	1.00	0.87
T274C	0.64	0.83	0.72	0.85	0.98	1.00	0.85
T274A	0.63	0.80	0.71	0.82	1.00	0.98	0.85
TG275T	0.41	0.64	0.86	0.69	0.93	0.78	0.88
G275T	0.62	0.84	0.72	0.84	0.99	1.00	0.84
G275C	0.71	0.90	0.65	0.88	1.00	1.00	0.87
G275A	0.61	0.81	0.83	0.84	1.00	0.98	0.88
G276T	0.56	0.85	0.80	0.83	1.00	0.99	0.86
G276C	0.54	0.76	0.65	0.75	0.98	0.99	0.76
G276A	0.64	0.94	0.84	0.89	1.00	0.99	0.91
T277C	0.46	0.72	0.88	0.77	0.96	0.98	0.79
T277A	0.53	0.72	0.76	0.77	0.96	0.97	0.79
C278T	0.53	0.85	0.84	0.82	1.00	0.99	0.86
C278G	0.51	0.58	0.97	0.96	0.72	0.75	0.96
C278A	0.53	0.76	0.84	0.83	0.94	1.00	0.82
C279T	0.63	0.67	0.69	0.80	0.93	0.88	0.86
C279A	0.59	0.77	0.72	0.79	0.99	0.99	0.80
CT280C	0.47	0.12	0.96	0.85	0.03	0.14	0.74
T280G	0.77	0.03	0.69	0.91	0.01	0.03	0.74
T280C	0.40	0.21	0.95	0.80	0.07	0.12	0.69
T280A	0.52	0.19	0.96	0.76	0.07	0.09	0.84
C281T	0.53	0.75	0.81	0.79	0.98	0.99	0.81
C281A	0.53	0.83	0.82	0.85	0.96	1.00	0.84
A282T	0.57	0.46	0.68	0.63	0.24	0.19	0.86
A282G	0.62	0.10	0.75	0.91	0.03	0.05	0.67

A282C	0.38	0.27	0.78	0.91	0.06	0.16	0.51
T283C	0.45	0.75	0.79	0.75	0.97	0.99	0.77
T283A	0.73	0.06	0.71	0.89	0.02	0.04	0.74
G284T	0.78	0.94	0.79	0.92	1.00	0.99	0.93
G284A	0.59	0.87	0.72	0.83	1.00	1.00	0.85
A285T	0.51	0.82	0.80	0.80	1.00	1.00	0.83
A285G	0.63	0.52	0.82	0.93	0.68	0.65	0.99
AC286A	0.43	0.68	0.54	0.61	0.39	0.41	0.62
C286T	0.63	0.55	0.73	0.88	0.68	0.67	0.91
C286G	0.59	0.46	0.70	0.75	0.22	0.23	0.75
C286A	0.60	0.80	0.67	0.80	1.00	0.99	0.81
C287T	0.59	0.97	0.86	0.89	1.00	1.00	0.92
C287G	0.64	0.76	0.77	0.89	0.92	0.99	0.84
C287A	0.56	0.87	0.74	0.82	1.00	0.99	0.85
C288T	0.63	0.91	0.75	0.86	1.00	1.00	0.88
C288A	0.59	0.65	0.68	0.81	0.86	0.84	0.84
T289C	0.66	0.15	0.91	0.76	0.06	0.06	0.93
T289A	0.60	0.22	0.79	0.76	0.08	0.09	0.80
C290T	0.72	0.80	0.63	0.83	0.99	0.99	0.83
C290A	0.62	0.37	0.83	0.76	0.19	0.18	0.86
T291C	0.62	0.18	0.82	0.94	0.06	0.10	0.69
T291A	0.80	0.06	0.77	0.98	0.02	0.03	0.73
C292T	0.76	0.93	0.65	0.89	1.00	1.00	0.88
C292G	0.71	0.11	0.75	0.81	0.04	0.04	0.81
C292A	0.68	0.10	0.81	0.82	0.03	0.04	0.82
T293G	0.98	0.03	1.00	0.95	0.01	0.04	0.98
T293C	0.61	0.87	0.73	0.84	1.00	1.00	0.86
G294T	0.59	0.49	0.80	0.81	0.30	0.32	0.79
G294C	0.67	0.64	0.65	0.87	0.84	0.89	0.82
G294A	0.65	0.86	0.80	0.87	1.00	1.00	0.88
C295T	0.63	0.41	0.92	0.94	0.20	0.27	0.75
C295G	0.92	0.01	0.96	0.90	0.01	0.00	0.97
C295A	0.90	0.01	0.93	0.92	0.01	0.01	0.92
CA296C	0.95	0.01	0.90	0.91	0.01	0.00	0.95
A296T	0.96	0.01	0.94	0.92	0.00	0.00	0.96
A296G	0.95	0.01	0.94	1.00	0.00	0.01	0.88
A296C	0.96	0.01	0.89	0.92	0.00	0.00	0.93
G297T	0.95	0.01	0.99	0.95	0.01	0.00	0.94
G297C	0.95	0.01	0.96	0.99	0.00	0.01	0.90
G297A	0.92	0.01	0.96	0.93	0.01	0.00	0.94
G298T	0.92	0.03	0.79	0.89	0.01	0.01	0.88
G298C	0.88	0.05	0.75	0.80	0.02	0.02	0.93
G298A	0.73	0.12	0.79	0.79	0.05	0.05	0.88
A299T	0.66	0.87	0.68	0.84	1.00	1.00	0.85
A299G	0.90	0.07	0.84	0.86	0.03	0.03	0.93
T300C	0.82	0.89	0.80	0.91	1.00	0.99	0.92
T300A	0.59	0.90	0.63	0.83	1.00	1.00	0.84
A301T	0.69	0.81	0.70	0.84	0.99	1.00	0.85
A301G	0.57	0.77	0.70	0.79	0.98	0.99	0.80
T302C	0.60	0.87	0.75	0.84	1.00	1.00	0.86
T302A	0.59	0.75	0.81	0.82	0.97	0.96	0.85
T303C	0.71	0.95	0.78	0.91	0.99	1.00	0.91
T303A	0.65	0.90	0.70	0.86	0.99	1.00	0.86

TG304T	0.62	0.91	0.75	0.86	1.00	1.00	0.87
G304T	0.69	0.97	0.88	0.92	1.00	1.00	0.94
G304A	0.66	0.94	0.68	0.88	1.00	1.00	0.88
G305T	0.73	0.97	0.71	0.91	0.99	1.00	0.90
G305C	0.55	0.97	0.80	0.86	1.00	1.00	0.88
G305A	0.72	0.98	0.74	0.91	1.00	1.00	0.92
G306T	0.76	0.97	0.80	0.92	1.00	1.00	0.93
G306C	0.75	0.98	0.79	0.92	1.00	1.00	0.93
G306A	0.71	0.98	0.78	0.91	1.00	1.00	0.92
C307T	0.56	0.26	0.95	0.91	0.09	0.14	0.73
C307G	0.96	0.04	0.74	0.88	0.01	0.01	0.89
C307A	0.57	0.64	0.76	0.89	0.81	0.90	0.82
T308G	0.58	0.56	0.80	0.90	0.73	0.72	0.94
T308C	0.70	0.95	0.76	0.91	0.99	1.00	0.90
T308A	0.58	0.82	0.69	0.80	0.99	1.00	0.82
TG309T	0.58	0.93	0.74	0.88	0.97	1.00	0.87
G309T	0.71	0.97	0.51	0.87	1.00	1.00	0.84
G309C	0.79	0.99	0.78	0.94	1.00	1.00	0.94
G309A	0.59	0.89	0.64	0.82	1.00	1.00	0.83
G310T	0.74	0.97	0.73	0.91	1.00	0.96	0.95
G310A	0.70	0.97	0.83	0.91	1.00	0.98	0.94
G311T	0.83	0.92	0.96	0.94	0.99	0.99	0.96
G311A	0.83	0.98	0.74	0.93	1.00	1.00	0.92
C312T	0.53	0.45	0.94	0.81	0.28	0.29	0.82
C312A	0.59	0.79	0.72	0.80	1.00	0.99	0.82
G313T	0.60	0.37	0.85	0.89	0.15	0.20	0.73
G313C	0.49	0.83	0.85	0.80	1.00	0.99	0.84
G313A	0.55	0.46	0.85	0.84	0.24	0.29	0.75
C314A	0.54	0.63	0.80	0.83	0.84	0.77	0.93
T315G	0.57	0.58	0.78	0.88	0.76	0.74	0.92
T315C	0.65	0.89	0.75	0.86	1.00	1.00	0.88
T315A	0.55	0.65	0.78	0.85	0.85	0.87	0.84
G316T	0.62	0.56	0.80	0.97	0.69	0.75	0.92
G316C	0.84	0.52	0.69	0.98	0.66	0.66	0.97
G316A	0.67	0.64	0.66	0.84	0.87	0.85	0.87
T317C	0.62	0.93	0.79	0.87	1.00	0.92	0.96
T317A	0.51	0.72	0.73	0.72	1.00	0.96	0.77
G318T	0.63	0.90	0.66	0.85	1.00	1.00	0.86
G318C	0.69	0.93	0.69	0.89	0.99	1.00	0.89
G318A	0.65	0.68	0.67	0.78	0.97	0.92	0.83
G319T	0.60	0.69	0.73	0.81	0.94	0.93	0.83
G319C	0.42	0.76	0.91	0.77	0.98	0.98	0.81
G319A	0.69	0.85	0.74	0.86	1.00	0.99	0.87
C320T	0.59	0.36	0.91	0.78	0.19	0.19	0.86
C320G	0.88	0.03	0.95	0.92	0.01	0.02	0.92
C320A	0.50	0.69	0.72	0.73	0.96	0.98	0.73
T321G	0.53	0.75	0.76	0.77	0.98	0.99	0.79
T321C	0.63	0.89	0.75	0.86	1.00	1.00	0.87
T321A	0.53	0.62	0.82	0.85	0.81	0.77	0.92
G322T	0.51	0.36	0.99	0.85	0.17	0.23	0.78
G322C	0.54	0.63	0.79	0.97	0.72	0.89	0.80
G322A	0.53	0.37	0.99	0.88	0.17	0.22	0.76
A323T	0.58	0.70	0.80	0.85	0.90	0.90	0.88

A323G	0.61	0.48	0.84	0.79	0.34	0.32	0.87
A323C	0.66	0.82	0.73	0.84	1.00	0.98	0.87
C324T	0.60	0.55	0.82	0.93	0.71	0.71	0.95
C324A	0.62	0.60	0.94	1.00	0.75	0.76	1.00
T325G	0.30	0.98	1.00	0.78	0.97	1.00	0.91
T325C	0.70	0.94	0.86	0.91	1.00	0.99	0.94
T325A	0.58	0.63	0.73	0.81	0.87	0.82	0.87
TG326T	0.54	0.72	0.89	0.89	0.88	0.89	0.92
G326T	0.52	0.74	0.80	0.79	0.97	0.98	0.81
G326C	0.61	0.86	0.69	0.84	1.00	1.00	0.85
G326A	0.60	0.70	0.75	0.82	0.93	0.93	0.84
T327C	0.72	0.96	0.74	0.91	1.00	1.00	0.91
T327A	0.59	0.85	0.73	0.83	0.99	1.00	0.84
G328T	0.66	0.85	0.67	0.86	0.99	1.00	0.85
G328C	0.77	0.92	0.71	0.90	1.00	1.00	0.90
G328A	0.65	0.78	0.74	0.83	0.99	0.99	0.84
T329G	0.53	0.52	0.92	0.81	0.56	0.49	0.96
T329C	0.69	0.96	0.77	0.90	1.00	1.00	0.91
T329A	0.66	0.92	0.74	0.88	1.00	1.00	0.89
TG330T	0.65	0.96	0.86	0.90	1.00	1.00	0.92
G330T	0.77	0.97	0.65	0.92	0.99	1.00	0.90
G330C	0.86	0.97	0.63	0.94	0.97	1.00	0.90
G330A	0.52	0.86	0.57	0.75	1.00	0.99	0.77
G331T	0.66	0.96	0.78	0.89	1.00	1.00	0.91
G331C	0.76	0.97	0.75	0.92	1.00	1.00	0.91
G331A	0.71	0.97	0.60	0.88	1.00	1.00	0.88
G332C	0.58	0.93	0.86	0.87	1.00	1.00	0.90
G332A	0.78	0.98	0.80	0.93	0.99	1.00	0.93
T333C	0.67	0.94	0.73	0.88	1.00	0.99	0.90
T333A	0.68	0.93	0.72	0.88	1.00	1.00	0.89
A334T	0.56	0.79	0.66	0.77	0.99	0.99	0.79
A334G	0.58	0.82	0.79	0.83	1.00	0.99	0.86
T335C	0.60	0.83	0.77	0.83	1.00	1.00	0.85
T335A	0.56	0.69	0.72	0.74	0.99	0.96	0.78
C336T	0.68	0.19	0.91	0.83	0.07	0.09	0.86
C336A	0.89	0.83	0.64	0.90	0.97	0.97	0.89
A337T	0.58	0.74	0.80	0.82	0.97	0.97	0.84
A337G	0.64	0.90	0.72	0.86	1.00	1.00	0.88
A337C	0.59	0.75	0.67	0.79	0.97	1.00	0.78
A338T	0.57	0.79	0.72	0.80	0.99	0.99	0.81
A338G	0.61	0.67	0.73	0.85	0.88	0.89	0.85
A338C	0.59	0.79	0.78	0.82	1.00	0.99	0.84
C339T	0.61	0.20	0.94	0.84	0.08	0.09	0.82
C339A	0.70	0.17	0.83	0.79	0.07	0.07	0.88
G340T	0.44	0.64	1.00	0.93	0.76	0.80	0.94
G340C	0.60	0.62	0.64	0.76	0.73	0.68	0.82
G340A	0.55	0.58	0.81	0.90	0.72	0.76	0.88
T341G	0.74	0.12	0.87	0.83	0.05	0.05	0.88
T341C	0.63	0.89	0.74	0.86	1.00	1.00	0.88
T341A	0.65	0.77	0.75	0.83	0.98	0.98	0.85
G342T	0.63	0.71	0.72	0.79	0.98	0.98	0.81
G342A	0.49	0.48	0.95	0.78	0.33	0.33	0.85
A343T	0.57	0.60	0.81	0.92	0.76	0.78	0.92

A343G	0.56	0.71	0.85	0.91	0.86	0.90	0.89
A343C	0.48	0.60	0.98	0.96	0.72	0.77	0.95
AC344A	0.47	0.91	0.88	0.84	0.99	1.00	0.88
C344T	0.60	0.74	0.70	0.79	0.98	0.99	0.80
C344A	0.64	0.18	0.90	0.91	0.06	0.09	0.76
C345T	0.57	0.53	0.74	0.74	0.55	0.46	0.90
C345G	0.69	0.53	0.83	0.99	0.69	0.70	0.99
C345A	0.58	0.48	0.83	0.85	0.27	0.32	0.76
G346T	0.60	0.83	0.80	0.84	1.00	0.98	0.87
G346C	0.63	0.73	0.80	0.88	0.91	0.88	0.92
G346A	0.65	0.88	0.69	0.86	1.00	1.00	0.86
T347G	0.55	0.48	0.91	0.87	0.33	0.38	0.81
T347C	0.65	0.91	0.75	0.87	1.00	0.99	0.88
T347A	0.69	0.90	0.68	0.87	1.00	1.00	0.87
TG348T	0.66	0.92	0.53	0.84	1.00	1.00	0.82
G348T	0.58	0.91	0.62	0.82	1.00	0.99	0.84
G348C	0.55	0.99	0.99	0.89	1.00	0.99	0.95
G349T	0.58	0.86	0.63	0.80	1.00	1.00	0.81
G349C	0.51	0.53	0.76	0.75	0.31	0.33	0.76
G349A	0.72	0.98	0.74	0.91	0.99	1.00	0.91
G350C	0.49	0.67	0.54	0.55	0.51	0.39	0.75
G350A	0.78	0.99	0.80	0.93	1.00	0.96	0.96
G35G1	0.99	0.91	0.11	0.68	0.96	0.95	0.50
GT351G	0.53	0.93	0.68	0.82	1.00	1.00	0.85
T351C	0.59	0.89	0.67	0.83	1.00	1.00	0.85
T351A	0.72	0.96	0.74	0.90	1.00	0.98	0.92
TG352T	0.59	0.82	0.62	0.79	0.99	1.00	0.79
G352T	0.62	0.89	0.75	0.86	1.00	0.99	0.88
G352C	0.65	0.95	0.83	0.89	1.00	0.99	0.91
G352A	0.58	0.77	0.70	0.79	0.98	0.99	0.81
G353T	0.86	0.95	0.68	0.93	1.00	1.00	0.91
G353C	0.59	0.94	0.68	0.85	1.00	0.97	0.89
G353A	0.62	0.97	0.83	0.89	1.00	1.00	0.91
GT354G	0.95	0.09	0.91	0.90	0.05	0.04	0.95
T354G	0.66	0.76	0.69	0.79	1.00	0.94	0.85
T354C	0.56	0.71	0.67	0.75	0.96	0.97	0.76
T354A	0.66	0.92	0.75	0.88	1.00	1.00	0.89
G355T	0.74	0.26	0.64	0.78	0.10	0.09	0.77
G355C	0.33	0.62	0.99	0.90	0.61	0.78	0.80
G355A	0.62	0.53	0.70	0.85	0.38	0.43	0.75
GA356G	0.53	0.69	0.67	0.70	0.99	0.90	0.79
A356T	0.56	0.69	0.80	0.87	0.86	0.92	0.84
A356G	0.79	0.06	0.97	0.87	0.02	0.03	0.93
G357T	0.58	0.44	0.91	0.72	0.27	0.23	0.94
G357A	0.57	0.74	0.70	0.77	0.98	1.00	0.77
A358T	0.78	0.45	0.58	0.74	0.26	0.22	0.82
A358G	0.89	0.04	0.88	0.91	0.01	0.02	0.90
A358C	0.54	0.70	0.77	0.79	0.94	0.93	0.82
G359T	0.65	0.83	0.72	0.84	1.00	0.96	0.88
G359C	0.64	0.85	0.56	0.81	1.00	1.00	0.80
G359A	0.53	0.75	0.74	0.79	0.96	0.99	0.79
C360T	0.53	0.52	0.87	0.74	0.55	0.42	1.00
C360A	0.60	0.74	0.79	0.85	0.94	0.96	0.85

T361G	0.62	0.87	0.60	0.84	0.99	1.00	0.84
T361C	0.56	0.73	0.77	0.79	0.98	0.93	0.84
T361A	0.60	0.64	0.79	0.90	0.82	0.81	0.93
G362C	0.63	0.28	0.98	0.80	0.14	0.15	0.91
G362A	0.60	0.69	0.77	0.87	0.88	0.90	0.87
GC363G	0.51	0.65	0.83	0.84	0.85	0.86	0.86
C363T	0.61	0.59	0.78	0.90	0.78	0.75	0.95
C363G	0.56	0.57	0.63	0.75	0.38	0.41	0.71
C363A	0.53	0.74	0.80	0.81	0.95	0.99	0.81
C364T	0.66	0.46	0.77	0.77	0.28	0.26	0.85
C364G	0.33	0.64	1.00	0.82	0.70	0.72	0.91
C364A	0.65	0.83	0.62	0.82	0.99	1.00	0.82
A365T	0.56	0.59	0.80	0.91	0.75	0.79	0.90
A365G	0.60	0.83	0.74	0.83	1.00	1.00	0.85
A365C	0.51	0.53	0.63	0.76	0.23	0.30	0.63
G366T	0.60	0.73	0.75	0.81	0.97	0.98	0.82
G366C	0.47	0.48	0.85	0.69	0.29	0.27	0.85
G366A	0.63	0.66	0.76	0.91	0.83	0.83	0.92
C367T	0.63	0.64	0.82	0.96	0.79	0.79	0.97
C367G	0.64	0.71	0.79	0.92	0.86	0.89	0.91
C367A	0.62	0.87	0.79	0.86	0.99	1.00	0.87
C367CA	0.69	0.90	0.65	0.86	1.00	0.99	0.87
A368T	0.58	0.60	0.76	0.87	0.78	0.77	0.89
A368G	0.60	0.83	0.72	0.84	0.97	1.00	0.83
A368C	0.55	0.59	0.86	0.92	0.76	0.75	0.96
C369T	0.62	0.59	0.71	0.89	0.71	0.75	0.86
C369G	0.56	0.79	0.77	0.80	1.00	0.99	0.83
C369A	0.59	0.89	0.71	0.83	1.00	1.00	0.85
G370T	0.64	0.31	0.85	0.83	0.13	0.15	0.80
G370A	0.60	0.71	0.73	0.80	0.96	0.95	0.83
A371T	0.60	0.69	0.70	0.81	0.92	0.95	0.79
A371G	0.49	0.24	0.93	0.94	0.08	0.14	0.65
G372A	0.73	0.68	0.65	0.84	0.93	0.78	0.99
GT373G	0.32	0.64	0.96	0.73	0.80	0.83	0.76
T373C	0.52	0.72	0.78	0.78	0.96	0.97	0.80
T373A	0.66	0.88	0.71	0.86	1.00	1.00	0.87
T374G	0.50	0.78	0.62	0.71	1.00	0.99	0.73
T374C	0.54	0.53	0.81	0.83	0.52	0.54	0.84
T374A	0.61	0.78	0.75	0.81	1.00	0.99	0.83
C375T	0.60	0.63	0.70	0.82	0.84	0.81	0.87
C375G	0.68	0.66	0.67	0.86	0.87	0.85	0.88
C376T	0.55	0.59	0.81	0.88	0.77	0.76	0.92
C376G	0.71	0.46	0.87	0.89	0.31	0.33	0.86
C376A	0.63	0.69	0.68	0.80	0.94	0.94	0.80
C376CG	0.60	0.51	0.80	0.95	0.37	0.49	0.74
CG377C	0.52	0.88	0.75	0.81	1.00	0.99	0.85
G377T	0.61	0.89	0.79	0.86	1.00	1.00	0.88
G377C	0.44	0.82	0.86	0.78	1.00	0.99	0.84
G377A	0.62	0.89	0.63	0.83	1.00	1.00	0.84
G378A	0.63	0.93	0.71	0.87	1.00	1.00	0.88
G379T	0.62	0.94	0.72	0.87	1.00	1.00	0.88
G379A	0.65	0.97	0.83	0.90	1.00	1.00	0.92
G380T	0.51	0.92	0.70	0.81	1.00	1.00	0.84

G380C	0.87	0.92	0.75	0.93	1.00	0.99	0.92
G380A	0.71	0.95	0.74	0.90	1.00	1.00	0.90
G38G4	0.63	0.83	0.71	0.83	1.00	1.00	0.84
G381C	0.56	0.94	0.70	0.84	1.00	1.00	0.87
G381A	0.63	0.95	0.68	0.88	0.99	1.00	0.88
G382A	0.61	0.84	0.62	0.80	1.00	1.00	0.81
A383G	0.59	0.79	0.72	0.80	1.00	0.95	0.86
A383C	0.57	0.82	0.62	0.78	0.99	1.00	0.79
C384T	0.56	0.41	0.93	0.76	0.23	0.21	0.88
C384G	1.00	0.45	0.51	0.80	0.33	0.28	0.87
C384A	0.59	0.45	0.89	0.85	0.26	0.29	0.81
A385T	0.60	0.73	0.65	0.76	0.99	0.98	0.77
A385G	0.59	0.78	0.78	0.82	0.98	0.98	0.85
A385C	0.46	0.76	0.82	0.77	0.97	0.99	0.80
T386G	0.37	0.83	0.95	0.76	0.99	1.00	0.82
T386C	0.64	0.85	0.70	0.84	1.00	1.00	0.85
T386A	0.65	0.80	0.73	0.83	0.99	0.99	0.85
TG387T	0.61	0.81	0.72	0.82	1.00	0.99	0.84
G387T	0.54	0.71	0.78	0.78	0.96	0.93	0.83
G387A	0.58	0.51	0.81	0.77	0.35	0.34	0.84
G388T	0.51	0.78	0.75	0.77	0.99	1.00	0.80
G388C	0.59	0.76	0.74	0.79	0.99	0.99	0.81
GT389G	0.61	0.80	0.68	0.80	1.00	1.00	0.81
T389G	0.56	0.69	0.85	0.92	0.83	0.89	0.89
T389C	0.56	0.92	0.73	0.84	1.00	1.00	0.87
T389A	0.67	0.96	0.76	0.89	1.00	1.00	0.91
T390G	0.59	0.77	0.73	0.80	0.99	1.00	0.81
T390C	0.60	0.94	0.76	0.86	1.00	1.00	0.89
T390A	0.60	0.49	0.81	0.77	0.33	0.31	0.86
G391T	0.61	0.52	0.85	0.96	0.66	0.68	0.95
G391C	0.55	0.63	0.79	0.91	0.77	0.85	0.84
G391A	0.60	0.63	0.82	0.92	0.80	0.79	0.96
T392C	0.63	0.78	0.75	0.84	0.97	0.98	0.84
C393T	0.60	0.49	0.84	0.90	0.31	0.38	0.77
C393G	0.50	0.71	0.79	0.83	0.88	0.99	0.77
C393A	0.70	0.65	0.80	0.99	0.79	0.80	0.98
T394G	0.66	0.82	0.73	0.84	0.99	0.99	0.86
T394C	0.64	0.93	0.68	0.86	1.00	0.97	0.90
T394A	0.57	0.72	0.80	0.82	0.96	0.92	0.87
G395T	0.54	0.81	0.67	0.78	0.99	0.99	0.79
G395C	0.59	0.79	0.77	0.81	1.00	0.99	0.83
G395A	0.62	0.79	0.70	0.81	0.99	0.99	0.83
G395GC	0.61	0.84	0.72	0.83	1.00	1.00	0.85
GC396G	0.57	0.86	0.70	0.82	1.00	1.00	0.84
C396T	0.58	0.85	0.69	0.82	1.00	1.00	0.83
C396G	0.56	0.73	0.86	0.85	0.93	0.92	0.89
C397T	0.55	0.87	0.71	0.82	0.99	1.00	0.84
C397G	0.60	0.93	0.83	0.87	1.00	1.00	0.90
C397A	0.65	0.93	0.77	0.88	1.00	0.99	0.91
C398T	0.64	0.92	0.69	0.87	1.00	1.00	0.88
C398A	0.60	0.90	0.70	0.84	1.00	1.00	0.86
C399T	0.66	0.78	0.75	0.83	0.99	0.99	0.85
C399A	0.60	0.87	0.72	0.83	1.00	1.00	0.85

C400T	0.60	0.80	0.71	0.81	1.00	0.99	0.82
C400G	0.62	0.84	0.68	0.82	1.00	0.99	0.84
C400A	0.60	0.82	0.71	0.82	1.00	0.99	0.84
T401G	0.75	0.84	0.56	0.85	0.99	1.00	0.83
T401C	0.58	0.88	0.71	0.86	0.97	1.00	0.85
T401A	0.58	0.85	0.70	0.82	1.00	1.00	0.84
G402T	0.49	0.70	0.77	0.76	0.94	0.99	0.75
G402C	0.57	0.80	0.74	0.80	1.00	0.97	0.83
G402A	0.54	0.78	0.73	0.78	1.00	0.99	0.80
GC403G	0.59	0.79	0.67	0.79	0.99	1.00	0.80
C403T	0.58	0.85	0.64	0.80	1.00	1.00	0.82
C403G	0.47	0.76	0.93	0.80	0.97	0.98	0.83
C403A	0.54	0.83	0.81	0.81	1.00	0.99	0.85
C404T	0.63	0.77	0.72	0.81	0.99	0.99	0.82
C404A	0.62	0.91	0.70	0.86	0.99	1.00	0.87
C405T	0.61	0.87	0.68	0.84	0.99	1.00	0.85
C405A	0.64	0.89	0.68	0.88	0.97	1.00	0.86
C406T	0.57	0.86	0.72	0.82	1.00	0.95	0.88
C406G	0.35	0.97	1.00	0.82	0.97	1.00	0.91
C406A	0.54	0.88	0.73	0.82	1.00	0.99	0.86
C407T	0.67	0.64	0.71	0.87	0.86	0.79	0.95
C407G	0.65	0.93	0.71	0.87	1.00	1.00	0.89
C407A	0.65	0.65	0.80	0.97	0.78	0.81	0.95
A408T	0.57	0.71	0.72	0.77	0.97	0.94	0.81
A408G	0.61	0.87	0.69	0.84	0.99	1.00	0.85
A408C	0.62	0.74	0.71	0.80	0.98	0.96	0.82
T409G	0.65	0.82	0.76	0.84	1.00	0.99	0.87
T409C	0.62	0.84	0.71	0.83	1.00	1.00	0.85
T409A	0.63	0.85	0.75	0.84	1.00	0.95	0.90
TC410T	0.66	0.71	0.71	0.90	0.88	0.96	0.83
C410T	0.50	0.79	0.78	0.78	0.99	1.00	0.81
C410A	0.56	0.79	0.79	0.81	0.99	0.99	0.84
C411T	0.61	0.92	0.77	0.87	1.00	1.00	0.89
C411A	0.55	0.94	0.71	0.84	1.00	1.00	0.87
C412T	0.48	0.60	0.88	0.88	0.76	0.78	0.89
C412A	0.83	0.75	0.69	0.95	0.89	0.89	0.95
CT413C	0.58	0.84	0.76	0.83	0.99	1.00	0.85
T413G	0.64	0.43	1.00	0.91	0.26	0.30	0.84
T413C	0.65	0.73	0.74	0.84	0.96	0.94	0.86
T413A	0.65	0.73	0.71	0.80	0.99	0.98	0.81
G414T	0.55	0.70	0.84	0.86	0.88	0.89	0.88
G414C	0.61	0.81	0.69	0.80	1.00	1.00	0.81
G414A	0.47	0.62	0.88	0.85	0.80	0.80	0.88
C415T	0.68	0.26	0.91	0.84	0.11	0.12	0.85
C415G	0.67	0.54	0.91	1.00	0.69	0.70	1.00
C415A	0.64	0.87	0.76	0.86	1.00	1.00	0.88
A416T	0.61	0.82	0.68	0.81	1.00	0.99	0.83
A416G	0.63	0.70	0.73	0.86	0.90	0.92	0.85
A416C	0.74	0.37	0.78	0.77	0.19	0.17	0.89
G417T	0.60	0.82	0.78	0.83	0.99	0.99	0.86
G417C	0.54	0.83	0.72	0.79	1.00	1.00	0.82
G417A	0.56	0.80	0.75	0.80	0.99	0.99	0.83
C418T	0.62	0.56	0.80	0.93	0.73	0.72	0.95

C418A	0.44	0.59	0.85	0.93	0.61	0.80	0.75
CT419C	0.42	0.81	0.66	0.69	0.99	0.98	0.74
T419G	0.59	0.77	0.71	0.80	0.98	1.00	0.80
T419C	0.60	0.87	0.76	0.84	1.00	1.00	0.87
T419A	0.62	0.85	0.72	0.84	1.00	1.00	0.85
T420G	0.73	0.65	0.77	0.99	0.79	0.80	0.99
T420C	0.63	0.87	0.69	0.84	1.00	1.00	0.85
T420A	0.78	0.28	0.91	0.85	0.14	0.13	0.90
G421T	0.61	0.68	0.68	0.78	0.96	0.95	0.79
G422T	0.58	0.81	0.82	0.82	1.00	0.97	0.88
G422C	0.49	0.77	0.78	0.76	0.99	0.99	0.80
GC423G	0.69	0.56	0.71	0.91	0.73	0.71	0.94
C423T	0.65	0.61	0.71	0.97	0.74	0.85	0.85
C423G	0.62	0.40	0.80	0.67	0.22	0.17	0.95
C424T	0.65	0.42	0.86	0.76	0.25	0.22	0.91
A425G	0.63	0.43	0.78	0.75	0.23	0.22	0.84
A425C	0.61	0.82	0.73	0.82	1.00	0.97	0.86
G427T	0.67	0.37	0.88	0.80	0.19	0.18	0.87
G427C	0.49	0.60	0.88	0.86	0.79	0.77	0.92
G427A	0.75	0.50	0.62	0.79	0.33	0.32	0.81
GA428G	0.68	0.53	0.80	0.98	0.69	0.69	0.98
A428G	0.73	0.25	0.87	0.88	0.10	0.12	0.82
A428C	0.72	0.36	0.84	0.77	0.21	0.17	0.94
T429C	0.64	0.85	0.71	0.84	1.00	1.00	0.85
T429A	0.64	0.72	0.71	0.82	0.96	0.96	0.82
G430A	0.64	0.46	0.73	0.87	0.23	0.29	0.72
G431T	0.64	0.80	0.70	0.83	0.98	0.99	0.84
G431C	0.66	0.81	0.65	0.82	0.99	1.00	0.82
G431A	0.64	0.91	0.76	0.87	1.00	1.00	0.89
T432G	0.83	0.61	0.72	1.00	0.77	0.77	1.00
T432C	0.62	0.86	0.73	0.84	1.00	0.97	0.88
T432A	0.62	0.93	0.73	0.86	1.00	1.00	0.88
G433C	0.62	0.78	0.66	0.81	0.98	0.99	0.80
G433A	0.62	0.75	0.67	0.79	0.99	0.99	0.79
GC434G	0.62	0.75	0.72	0.82	0.97	0.98	0.82
C434G	0.77	0.48	0.55	0.83	0.25	0.28	0.71
C434A	0.67	0.89	0.76	0.87	1.00	0.99	0.90
C435A	0.53	0.90	0.82	0.86	0.98	1.00	0.87
C436A	0.61	0.87	0.70	0.84	1.00	1.00	0.85
C437T	0.61	0.74	0.75	0.79	1.00	0.92	0.88
C437G	0.58	0.87	0.71	0.83	1.00	1.00	0.84
C437A	0.62	0.79	0.62	0.79	1.00	1.00	0.79
CA438C	0.77	0.31	0.52	0.79	0.13	0.13	0.70
A438T	0.68	0.71	0.71	0.94	0.85	0.97	0.82
A438G	0.61	0.73	0.73	0.81	0.96	0.96	0.83
A438C	0.52	0.63	0.88	0.92	0.77	0.81	0.91
A438AT	0.65	0.67	0.61	0.77	0.94	0.95	0.77
AT439A	0.64	0.70	0.67	0.79	0.97	0.96	0.80
T439C	0.64	0.69	0.76	0.89	0.88	0.85	0.93
T439A	0.67	0.88	0.76	0.87	1.00	1.00	0.88
T440G	0.70	0.77	0.76	0.84	1.00	0.97	0.88
T440C	0.71	0.84	0.72	0.92	0.93	1.00	0.86
T440A	0.64	0.73	0.64	0.78	0.99	0.97	0.79

G441T	0.63	0.80	0.63	0.79	1.00	1.00	0.80
G441C	0.66	0.75	0.64	0.79	0.99	0.99	0.80
G441A	0.63	0.83	0.66	0.82	1.00	0.94	0.88
C442T	0.68	0.18	0.95	0.93	0.07	0.09	0.79
C442G	0.82	0.26	0.88	0.87	0.11	0.11	0.88
C442A	0.67	0.87	0.76	0.87	1.00	1.00	0.88
A443T	0.91	0.05	0.97	0.93	0.02	0.02	0.93
A443G	0.96	0.03	0.96	0.95	0.01	0.01	0.93
A443C	0.99	0.04	0.99	0.98	0.02	0.01	0.92
AG444A	0.99	0.01	0.98	0.92	0.00	0.00	0.99
G444T	0.91	0.01	0.97	0.96	0.01	0.01	0.91
G444C	1.00	0.00	1.00	1.00	0.00	0.00	0.96
G444A	0.95	0.02	0.99	0.94	0.01	0.01	0.95
G445C	0.94	0.02	0.86	0.97	0.01	0.01	0.86
G445A	0.96	0.01	0.95	0.95	0.00	0.00	0.94
T446C	0.95	0.01	0.94	0.88	0.01	0.00	1.00
T446A	0.96	0.02	0.79	0.90	0.01	0.01	0.90
A447T	0.96	0.02	0.97	0.96	0.01	0.01	0.93
A447G	0.97	0.03	0.92	0.90	0.01	0.01	0.96
G448A	0.68	0.97	0.78	0.90	1.00	1.00	0.92
G449T	0.76	0.10	0.98	0.87	0.04	0.04	0.91
G449A	0.90	0.08	0.84	0.85	0.04	0.03	0.94
C450T	0.62	0.89	0.81	0.86	1.00	0.96	0.92
C450A	0.64	0.85	0.72	0.84	1.00	1.00	0.86
A451T	0.60	0.85	0.70	0.83	1.00	1.00	0.84
A451G	0.60	0.67	0.81	0.90	0.84	0.83	0.93
A451C	0.68	0.84	0.76	0.85	1.00	0.98	0.87
G452T	0.58	0.82	0.70	0.80	1.00	1.00	0.81
G452A	0.65	0.85	0.70	0.85	1.00	1.00	0.86
GC453G	0.67	0.60	0.53	0.73	0.80	0.71	0.81
C453T	0.65	0.74	0.72	0.83	0.96	0.97	0.83
C453G	0.59	0.72	0.69	0.79	0.96	0.97	0.79
C453A	0.69	0.72	0.64	0.82	0.95	0.98	0.80
C454T	0.53	0.66	0.83	0.87	0.84	0.86	0.88
C454G	0.65	0.61	0.80	0.97	0.76	0.78	0.96
C454A	0.63	0.75	0.70	0.80	0.99	0.98	0.82
C455T	0.62	0.68	0.72	0.82	0.92	0.90	0.85
C455CA	0.53	0.84	0.76	0.80	1.00	0.98	0.85
CA456C	0.51	0.77	0.42	0.60	0.49	0.55	0.52
A456T	0.64	0.80	0.76	0.84	0.99	0.98	0.86
A456G	0.62	0.81	0.67	0.81	1.00	1.00	0.82
A456C	0.61	0.88	0.72	0.84	1.00	1.00	0.85
G457T	0.61	0.84	0.74	0.83	1.00	1.00	0.85
G457C	0.58	0.63	0.84	0.92	0.80	0.78	0.96
G457A	0.64	0.84	0.71	0.84	1.00	0.99	0.85
C458T	0.63	0.84	0.75	0.84	1.00	0.97	0.88
C458G	0.62	0.79	0.71	0.81	0.98	1.00	0.81
C458A	0.61	0.85	0.67	0.82	1.00	1.00	0.83
T459G	0.53	0.87	0.82	0.83	1.00	0.99	0.87
T459C	0.58	0.78	0.72	0.80	0.99	0.99	0.82
T459A	0.67	0.64	0.80	0.98	0.78	0.79	0.98
TG460T	0.77	0.30	0.87	0.89	0.13	0.14	0.83
G460T	0.72	0.55	0.70	0.94	0.72	0.71	0.96

G460C	0.76	0.14	0.60	0.90	0.06	0.07	0.67
G460A	0.69	0.20	0.93	0.89	0.08	0.09	0.82
G461T	0.62	0.54	0.85	0.96	0.70	0.69	0.99
G461C	0.85	0.08	0.98	0.93	0.03	0.08	0.93
G461A	0.60	0.50	0.90	0.93	0.50	0.54	0.89
A462T	0.60	0.75	0.84	0.90	0.90	0.97	0.86
A462G	0.59	0.68	0.75	0.83	0.90	0.89	0.86
A462C	0.88	0.51	0.95	1.00	0.72	0.73	1.00
AC463A	0.72	0.63	0.76	0.98	0.78	0.77	1.00
C463T	0.56	0.83	0.73	0.81	0.99	1.00	0.83
C464T	0.57	0.83	0.75	0.81	1.00	0.99	0.84
C464A	0.62	0.82	0.72	0.82	1.00	0.98	0.85
CT465C	0.69	0.60	0.69	0.90	0.79	0.75	0.96
T465G	0.66	0.82	0.68	0.83	1.00	0.99	0.84
T465C	0.64	0.69	0.76	0.91	0.85	0.89	0.88
T465A	0.57	0.73	0.71	0.78	0.97	0.98	0.78
TC466T	0.63	0.63	0.65	0.80	0.89	0.87	0.82
C466T	0.57	0.54	0.90	0.97	0.69	0.70	0.97
C466G	0.92	0.15	0.76	0.85	0.06	0.06	0.90
C466A	0.71	0.25	0.79	0.77	0.11	0.10	0.87
C467T	0.80	0.32	0.79	0.83	0.15	0.15	0.86
C467G	0.99	0.17	0.51	0.82	0.09	0.08	0.79
C467A	0.66	0.27	0.74	0.78	0.11	0.11	0.79
C468T	0.63	0.75	0.76	0.82	0.98	0.99	0.83
CT469C	0.58	0.82	0.61	0.78	1.00	1.00	0.78
T469G	0.62	0.82	0.62	0.80	0.99	1.00	0.81
T469C	0.55	0.75	0.77	0.79	0.98	0.97	0.82
T469A	0.66	0.70	0.69	0.85	0.91	0.93	0.84
T469TG	0.68	0.70	0.84	0.98	0.82	0.83	0.99
G470A	0.61	0.60	0.56	0.67	0.50	0.42	0.80
G471T	0.64	0.52	0.66	0.69	0.36	0.30	0.87
G471C	0.59	0.53	0.69	0.73	0.34	0.32	0.80
G471A	0.61	0.59	0.63	0.83	0.69	0.74	0.78
G472A	0.59	0.66	0.55	0.69	0.89	0.87	0.71
GA473G	0.45	0.71	0.86	0.75	0.97	0.91	0.84
A473T	0.58	0.79	0.64	0.78	0.99	0.99	0.80
A473G	0.61	0.74	0.78	0.83	0.96	0.98	0.84
A473C	0.65	0.51	0.69	0.74	0.35	0.31	0.85
A474T	0.61	0.78	0.76	0.82	0.98	1.00	0.83
A474G	0.56	0.78	0.73	0.79	0.99	1.00	0.81
A474C	0.50	0.70	0.88	0.83	0.91	0.89	0.88
A475T	0.56	0.77	0.67	0.77	0.99	1.00	0.77
A475G	0.59	0.80	0.70	0.80	1.00	0.99	0.82
C476T	0.61	0.84	0.70	0.82	1.00	1.00	0.84
C476G	0.58	0.82	0.79	0.82	1.00	0.99	0.85
C476A	0.67	0.78	0.85	0.98	0.85	0.88	0.96
C476CA	0.72	0.76	0.77	0.92	0.91	0.91	0.93
A477T	0.59	0.79	0.69	0.80	1.00	1.00	0.81
A477G	0.57	0.81	0.78	0.81	1.00	1.00	0.83
AC478A	0.71	0.75	0.75	0.95	0.87	0.94	0.88
C478T	0.60	0.80	0.71	0.81	0.99	1.00	0.83
C478G	0.65	0.70	0.92	1.00	0.82	0.84	0.99
C478A	0.64	0.82	0.79	0.88	0.95	1.00	0.86

G479A	0.61	0.61	0.63	0.82	0.73	0.76	0.79
G481C	0.57	0.83	0.43	0.67	0.94	0.92	0.66
C482T	0.68	0.82	0.73	0.85	1.00	1.00	0.86
C482G	0.48	0.74	0.63	0.66	0.99	1.00	0.67
C482A	0.74	0.84	0.87	0.92	0.96	0.91	0.98
A483T	0.59	0.88	0.69	0.83	1.00	1.00	0.85
A483G	0.57	0.86	0.85	0.86	0.97	1.00	0.87
A483C	0.88	0.98	0.44	0.89	1.00	1.00	0.85
G484T	0.62	0.82	0.63	0.81	0.99	1.00	0.81
G484C	0.67	0.87	0.44	0.85	0.93	1.00	0.75
G484A	0.57	0.81	0.75	0.80	1.00	0.99	0.83
A485T	0.63	0.77	0.78	0.83	0.99	0.98	0.85
A485G	0.60	0.78	0.90	0.92	0.91	0.90	0.95
A485C	0.57	0.82	0.63	0.78	1.00	1.00	0.79
G486T	0.61	0.73	0.87	0.95	0.85	0.87	0.96
G486A	0.55	0.80	0.63	0.76	1.00	1.00	0.78
G487T	0.54	0.85	0.63	0.78	1.00	1.00	0.80
G487A	0.51	0.81	0.52	0.71	0.96	1.00	0.69
G488T	0.49	0.82	0.79	0.78	1.00	1.00	0.81
G488C	0.54	0.79	0.58	0.73	0.99	0.98	0.74
C489T	0.64	0.76	0.84	0.92	0.90	0.92	0.92
C490T	0.64	0.75	0.87	0.98	0.85	0.90	0.94
C490A	0.60	0.80	0.79	0.83	0.99	0.98	0.85
T491C	0.63	0.77	0.66	0.80	0.99	0.99	0.80
T491A	0.67	0.79	0.68	0.82	1.00	1.00	0.83
A492T	0.62	0.76	0.76	0.81	0.99	0.97	0.84
A492G	0.60	0.81	0.68	0.80	0.99	0.99	0.82
A492C	0.66	0.82	0.77	0.85	0.99	1.00	0.86
C493T	0.62	0.79	0.71	0.81	1.00	0.95	0.86
C493G	0.66	0.80	0.73	0.84	0.99	0.98	0.85
C493A	0.65	0.78	0.79	0.87	0.96	0.97	0.87
A494T	0.64	0.81	0.64	0.81	1.00	0.99	0.82
A494G	0.58	0.81	0.79	0.82	1.00	0.99	0.85
A494C	0.63	0.75	0.76	0.81	1.00	0.95	0.86
G495T	0.59	0.77	0.69	0.79	0.99	0.99	0.80
G495A	0.70	0.80	0.74	0.85	1.00	0.98	0.87
G496T	0.60	0.77	0.62	0.77	1.00	0.99	0.78
G496A	0.56	0.78	0.82	0.81	0.99	0.98	0.85
C497T	0.70	0.84	0.44	0.77	1.00	0.99	0.75
C497G	0.78	0.81	0.36	0.75	0.98	1.00	0.70
C497A	0.61	0.84	0.71	0.83	0.99	1.00	0.83
T498G	0.59	0.85	0.64	0.80	1.00	0.99	0.82
T498C	0.57	0.75	0.55	0.73	0.97	0.97	0.72
T498A	0.62	0.82	0.73	0.83	0.99	1.00	0.84
G499T	0.54	0.80	0.64	0.79	0.96	1.00	0.77
G499A	0.58	0.71	0.74	0.80	0.95	0.96	0.81
G500T	0.63	0.75	0.83	0.88	0.93	0.93	0.90
G500C	0.60	0.84	0.68	0.82	1.00	0.99	0.83
G500A	0.60	0.63	0.92	0.99	0.77	0.78	0.99
G501T	0.56	0.76	0.94	0.93	0.87	0.89	0.95
G501A	0.62	0.75	0.83	0.89	0.92	0.91	0.92
C502T	0.60	0.79	0.97	0.97	0.86	0.89	0.98
C502A	0.60	0.80	0.99	0.96	0.88	0.89	0.99

G505T	0.59	0.84	0.56	0.78	0.99	1.00	0.78
G505A	0.54	0.78	0.85	0.80	1.00	0.99	0.84
G507T	0.65	0.75	0.98	1.00	0.84	0.87	1.00
G507C	0.70	0.68	0.98	1.00	0.82	0.84	1.00
G507A	0.57	0.69	0.94	0.98	0.80	0.83	0.98
T508C	0.65	0.81	0.62	0.81	0.99	0.99	0.81
T508A	0.64	0.77	0.61	0.78	1.00	0.99	0.79
T509C	0.60	0.75	0.67	0.80	0.97	1.00	0.78
T509A	0.63	0.80	0.60	0.79	1.00	0.99	0.80
G510T	0.64	0.83	1.00	1.00	0.86	0.91	1.00
G510C	0.64	0.82	0.56	0.78	1.00	0.99	0.78
G510A	0.64	0.79	0.76	0.85	0.97	1.00	0.84
GC511G	0.61	0.87	0.61	0.82	1.00	1.00	0.83
C511T	0.61	0.79	0.95	0.97	0.87	0.91	0.96
C511G	0.65	0.79	0.55	0.77	0.99	0.99	0.77
C511A	0.63	0.80	0.81	0.84	0.99	0.98	0.87
C512T	0.67	0.81	0.79	0.86	0.98	0.99	0.87
C512A	0.59	0.79	0.78	0.82	1.00	0.99	0.84
A513T	0.60	0.75	0.88	0.91	0.89	0.90	0.93
A513G	0.64	0.80	0.64	0.80	1.00	1.00	0.80
C514T	0.63	0.76	0.94	0.99	0.84	0.87	0.99
C514A	0.58	0.70	0.63	0.78	0.92	0.91	0.80
C515T	0.66	0.70	0.98	1.00	0.82	0.84	1.00
C515G	0.92	0.12	0.54	0.92	0.04	0.05	0.69
C515A	0.59	0.74	0.72	0.79	0.98	0.97	0.81
T516C	0.60	0.80	0.67	0.79	0.99	1.00	0.80
G517T	0.63	0.67	1.00	1.00	0.77	0.83	1.00
G517C	0.61	0.69	0.97	1.00	0.80	0.83	1.00
G517A	0.60	0.77	0.82	0.84	0.97	0.99	0.84
G517GC	0.62	0.74	0.92	0.97	0.84	0.86	0.99
C518T	0.57	0.75	0.90	0.93	0.87	0.93	0.90
C519T	0.51	0.82	0.60	0.73	1.00	0.99	0.75
C520T	0.56	0.78	0.78	0.80	0.99	0.98	0.83
C520A	0.57	0.79	0.53	0.72	0.99	1.00	0.72
C521T	0.61	0.82	0.71	0.83	0.98	1.00	0.83
C521G	0.57	0.77	0.87	0.90	0.90	0.96	0.86
C521A	0.60	0.73	0.99	1.00	0.81	0.85	1.00
C522T	0.58	0.78	0.88	0.85	0.96	0.97	0.87
C527T	0.56	0.82	0.56	0.75	0.99	0.99	0.75
C527G	0.66	0.83	0.28	0.46	0.98	0.75	0.54
C527A	0.63	0.87	0.50	0.79	1.00	1.00	0.77
T528G	0.60	0.71	0.64	0.78	0.95	0.99	0.75
T528C	0.60	0.79	0.70	0.80	1.00	0.99	0.82
T528A	0.51	0.80	0.48	0.63	0.92	0.93	0.63
G529T	0.63	0.79	0.73	0.82	1.00	0.94	0.89
G529C	0.74	0.84	0.86	0.93	0.96	0.98	0.92
G529A	0.57	0.74	0.68	0.76	0.99	0.99	0.78
C530T	0.59	0.83	0.54	0.76	0.99	1.00	0.76
G531T	0.68	0.71	0.39	0.79	0.64	0.89	0.53
G531C	0.40	0.83	1.00	0.97	0.77	0.89	0.98
G531A	0.68	0.77	0.68	0.82	1.00	0.99	0.83
T532C	0.62	0.70	0.93	0.99	0.81	0.83	1.00
T532A	0.51	0.70	0.92	0.91	0.84	0.88	0.91

A533T	0.63	0.72	0.85	0.93	0.87	0.83	0.99
A533G	0.55	0.70	0.91	0.94	0.83	0.86	0.94
G534T	0.68	0.82	0.61	0.83	1.00	1.00	0.83
G534C	0.62	0.76	0.68	0.80	0.98	0.98	0.80
G534A	0.66	0.83	0.63	0.82	1.00	1.00	0.82
A535T	0.57	0.80	0.51	0.74	0.95	0.97	0.72
A535G	0.60	0.83	0.72	0.82	1.00	0.99	0.85
T536C	0.66	0.77	0.72	0.83	0.98	0.98	0.84
T536A	0.65	0.85	0.59	0.82	1.00	1.00	0.82
TG537T	0.77	0.80	0.77	0.93	0.93	0.93	0.93
G537T	0.59	0.82	0.49	0.75	0.98	0.99	0.74
G537C	0.55	0.78	0.83	0.81	0.99	0.98	0.85
G537A	0.49	0.90	0.35	0.39	1.00	0.79	0.47
G538T	0.64	0.84	0.60	0.81	1.00	1.00	0.81
G538C	0.60	0.76	0.76	0.82	0.97	0.99	0.83
G538A	0.59	0.80	0.63	0.80	0.97	1.00	0.79
T539G	0.79	0.89	0.40	0.82	1.00	1.00	0.78
T539C	0.57	0.77	0.82	0.81	0.99	1.00	0.83
T539A	0.68	0.77	0.65	0.86	0.94	1.00	0.81
G540T	0.60	0.89	0.40	0.72	0.99	0.99	0.69
G540A	0.56	0.87	0.35	0.56	0.94	0.97	0.52
A541T	0.59	0.82	0.60	0.78	1.00	0.99	0.80
A541G	0.59	0.77	0.77	0.82	0.98	0.97	0.84
A541C	0.64	0.83	0.68	0.83	1.00	1.00	0.84
A542G	0.61	0.81	0.55	0.77	0.99	0.99	0.77
T543G	0.49	0.54	1.00	0.96	0.62	0.67	0.96
T543C	0.54	0.75	0.96	0.91	0.89	0.88	0.96
T543A	0.61	0.79	0.66	0.80	0.99	0.99	0.82
G544T	0.60	0.88	0.57	0.81	1.00	1.00	0.81
G544C	0.58	0.78	0.70	0.80	0.99	1.00	0.81
G544A	0.55	0.82	0.69	0.78	1.00	1.00	0.81
T545G	0.56	0.83	0.83	0.84	0.99	1.00	0.86
T545C	0.63	0.81	0.70	0.82	0.99	1.00	0.83
T545A	0.54	0.76	0.82	0.80	0.99	0.97	0.83
C546T	0.60	0.86	0.55	0.78	1.00	1.00	0.78
C546A	0.55	0.84	0.50	0.72	1.00	0.97	0.74
A547T	0.62	0.83	0.65	0.81	1.00	1.00	0.82
A547G	0.54	0.76	0.92	0.92	0.87	0.94	0.90
A547C	0.69	0.73	0.86	0.99	0.84	0.85	0.99
T548C	0.58	0.72	0.87	0.93	0.85	0.89	0.91
T548A	0.60	0.77	0.75	0.81	0.99	0.98	0.84
A549G	0.63	0.77	0.74	0.82	0.99	0.99	0.83
A549C	0.59	0.86	0.64	0.80	1.00	1.00	0.81
AT550A	0.73	0.75	0.63	0.82	0.99	0.98	0.82
T550C	0.63	0.80	0.69	0.82	0.99	0.99	0.83
T550A	0.58	0.84	0.59	0.79	1.00	1.00	0.79
TC551T	0.68	0.84	0.57	0.82	0.99	1.00	0.80
C551T	0.64	0.85	0.56	0.81	1.00	1.00	0.81
C551G	0.40	0.73	0.64	0.61	0.79	0.84	0.60
C551A	0.75	0.90	0.55	0.87	1.00	0.98	0.86
C552G	0.65	0.82	0.76	0.84	1.00	0.99	0.86
C552A	0.54	0.83	0.59	0.77	0.99	1.00	0.77
T553G	0.60	0.83	0.71	0.82	1.00	0.99	0.83

T553C	0.60	0.82	0.78	0.85	0.97	1.00	0.85
T553A	0.59	0.82	0.64	0.79	1.00	0.99	0.81
TG554T	0.70	0.73	0.92	1.00	0.84	0.85	1.00
G555C	0.56	0.76	0.95	0.96	0.84	0.88	0.96
G555A	0.57	0.76	0.90	0.91	0.89	0.93	0.91
G556C	0.62	0.79	0.89	0.89	0.94	0.95	0.91
G556A	0.58	0.69	0.97	0.99	0.80	0.83	0.99
T557C	0.60	0.75	0.87	0.89	0.91	0.89	0.94
T557A	0.61	0.69	0.96	1.00	0.80	0.83	1.00
A558T	0.67	0.76	0.73	0.83	0.98	0.97	0.85
A558G	0.62	0.75	0.72	0.80	0.99	0.99	0.80
G559T	0.67	0.84	0.61	0.83	1.00	0.99	0.83
G559A	0.61	0.79	0.74	0.81	1.00	0.99	0.84
A560T	0.60	0.83	0.68	0.81	1.00	1.00	0.82
A560C	0.52	0.89	0.73	0.81	1.00	1.00	0.84
G561C	0.63	0.77	0.70	0.80	1.00	0.99	0.82
G561A	0.59	0.85	0.67	0.81	1.00	0.99	0.83
T562C	0.61	0.75	0.83	0.86	0.94	0.93	0.89
T562A	0.63	0.82	0.75	0.83	1.00	0.99	0.86
TG563T	0.81	0.85	0.75	0.90	0.99	0.99	0.89
G563T	0.52	0.80	0.74	0.78	0.99	0.99	0.81
G563C	0.78	0.73	0.85	1.00	0.85	0.86	1.00
G563A	0.56	0.88	0.54	0.78	1.00	1.00	0.78
G564C	0.69	0.71	0.81	0.99	0.83	0.85	0.97
G564A	0.56	0.68	0.92	0.97	0.80	0.83	0.96
T565G	0.73	0.94	0.23	0.65	1.00	0.98	0.58
T565C	0.59	0.75	0.82	0.84	0.96	0.92	0.89
T565A	0.57	0.85	0.74	0.82	1.00	1.00	0.84
G566T	0.59	0.43	0.88	0.88	0.21	0.27	0.75
G566A	0.63	0.77	0.66	0.81	0.97	1.00	0.80
GC567G	0.75	0.89	0.48	0.85	1.00	1.00	0.81
C567T	0.61	0.81	0.63	0.79	1.00	1.00	0.80
C567G	0.63	0.92	0.25	0.51	0.81	0.92	0.43
C567A	0.61	0.54	0.70	0.79	0.64	0.57	0.90
G568T	0.61	0.87	0.75	0.84	1.00	1.00	0.87
G568A	0.63	0.80	0.70	0.82	0.99	0.99	0.83
G569T	0.60	0.78	0.83	0.84	0.98	0.97	0.87
G569C	0.55	0.68	0.81	0.84	0.89	0.88	0.87
G569A	0.55	0.72	0.85	0.86	0.90	0.91	0.88
GC570G	0.74	0.78	0.82	0.97	0.88	0.90	0.96
C570T	0.54	0.83	0.48	0.71	0.96	0.97	0.70
C570G	0.64	0.91	0.27	0.52	0.97	0.88	0.51
C570A	0.51	0.80	0.75	0.78	1.00	0.99	0.81
C571T	0.58	0.88	0.60	0.80	1.00	1.00	0.81
C571G	0.69	0.73	0.88	0.99	0.83	0.84	1.00
C571A	0.63	0.85	0.87	0.88	0.98	0.99	0.89
CA572C	0.68	0.66	0.97	1.00	0.80	0.81	1.00
A572T	0.57	0.81	0.81	0.81	1.00	0.99	0.84
A572G	0.63	0.82	0.61	0.80	1.00	1.00	0.80
A572C	0.56	0.69	0.90	0.95	0.81	0.85	0.94
A572AG	0.83	0.79	0.90	1.00	0.88	0.88	1.00
G573T	0.63	0.80	0.88	0.89	0.95	0.95	0.91
G573A	0.53	0.77	0.87	0.80	1.00	0.98	0.84

G574T	0.70	0.83	0.77	0.87	0.99	0.99	0.88
G574C	0.61	0.80	0.82	0.84	0.99	0.99	0.86
G574A	0.56	0.70	0.96	0.99	0.79	0.83	0.98
G575T	0.51	0.69	0.98	0.97	0.79	0.82	0.98
G575C	0.62	0.74	0.84	0.92	0.88	0.89	0.93
G575A	0.62	0.75	0.85	0.88	0.93	0.86	0.98
GC576G	0.86	0.90	0.49	0.87	1.00	1.00	0.84
C576T	0.61	0.82	0.62	0.80	1.00	0.99	0.81
C576G	0.66	0.86	0.62	0.83	1.00	0.99	0.84
C576A	0.60	0.86	0.63	0.82	1.00	1.00	0.82
C577T	0.56	0.87	0.47	0.73	1.00	0.99	0.72
C577G	0.45	0.51	1.00	0.90	0.50	0.56	0.89
C577A	0.54	0.85	0.68	0.82	0.97	1.00	0.81
A578T	0.64	0.78	0.70	0.81	1.00	0.99	0.82
A578G	0.62	0.75	0.86	0.92	0.89	0.89	0.95
A578C	0.67	0.61	0.80	0.98	0.76	0.77	0.98
G579T	0.67	0.83	0.66	0.84	1.00	1.00	0.84
G579C	0.64	0.79	0.78	0.84	0.99	0.98	0.86
G579A	0.62	0.71	0.61	0.76	0.97	0.97	0.76
A580T	0.61	0.81	0.65	0.80	0.99	0.99	0.82
A580G	0.62	0.85	0.49	0.77	0.99	0.99	0.76
T581G	0.67	0.95	0.68	0.88	1.00	1.00	0.88
T581C	0.55	0.76	0.79	0.81	0.97	0.99	0.82
T581A	0.60	0.77	0.80	0.83	0.97	0.97	0.85
T581TC	0.47	0.79	0.69	0.73	1.00	1.00	0.75
T581TA	0.59	0.90	0.58	0.82	1.00	1.00	0.82
TG582T	0.74	0.83	0.88	0.97	0.91	0.94	0.95
G582T	0.65	0.79	0.65	0.81	0.99	0.97	0.84
G582A	0.52	0.83	0.44	0.59	0.91	0.91	0.58
G583T	0.43	0.78	0.76	0.72	0.99	0.98	0.77
G583A	0.55	0.72	0.84	0.85	0.92	0.93	0.87
G584T	0.72	0.73	0.73	0.87	0.93	0.83	0.99
G584C	0.43	0.70	1.00	0.92	0.79	0.81	0.95
G584A	0.58	0.71	0.99	1.00	0.80	0.84	1.00
G585T	0.47	0.80	0.77	0.77	0.99	0.99	0.81
G585C	0.54	0.78	0.64	0.75	1.00	0.99	0.78
G585A	0.62	0.74	0.79	0.82	0.97	0.97	0.84
T586G	0.58	0.75	0.76	0.79	0.98	0.94	0.85
T586C	0.60	0.77	0.77	0.84	0.96	0.98	0.83
T586A	0.57	0.74	0.92	0.93	0.87	0.88	0.95
TC587T	0.71	0.77	0.80	0.95	0.89	0.91	0.94
C587T	0.61	0.78	0.68	0.80	0.99	1.00	0.81
C587G	0.43	1.00	1.00	0.86	0.97	0.99	0.97
C587A	0.62	0.86	0.65	0.82	1.00	1.00	0.83
C588T	0.62	0.85	0.70	0.83	1.00	1.00	0.85
C588A	0.50	0.77	0.79	0.77	0.99	1.00	0.80
C589T	0.57	0.82	0.73	0.82	0.98	1.00	0.83
C589G	0.58	0.69	0.75	0.84	0.89	0.97	0.78
C589A	0.57	0.78	0.74	0.80	0.99	0.99	0.82
A590T	0.60	0.77	0.66	0.78	0.99	0.99	0.79
A590G	0.59	0.79	0.74	0.80	1.00	0.98	0.84
A590C	0.48	0.60	0.74	0.86	0.67	0.81	0.72
C591T	0.59	0.85	0.62	0.80	1.00	1.00	0.81

C591G	0.58	0.78	0.72	0.81	0.98	1.00	0.81
C591A	0.59	0.85	0.63	0.81	1.00	1.00	0.81
A592T	0.53	0.82	0.78	0.80	1.00	1.00	0.83
A592G	0.59	0.84	0.56	0.77	1.00	1.00	0.77
A592C	0.49	0.74	0.84	0.78	0.98	1.00	0.80
G593T	0.58	0.77	0.64	0.76	1.00	0.99	0.78
G593A	0.63	0.79	0.75	0.83	0.99	0.99	0.84
A594T	0.56	0.78	0.65	0.77	0.99	0.99	0.78
A594G	0.51	0.85	0.42	0.56	0.94	0.93	0.56
A594C	0.46	0.75	0.81	0.75	0.98	0.99	0.78
G595T	0.59	0.78	0.77	0.82	0.98	0.99	0.83
G595C	0.55	0.67	0.77	0.85	0.85	0.84	0.86
G595A	0.53	0.73	0.93	0.97	0.81	0.91	0.90
C596T	0.62	0.79	0.68	0.80	1.00	0.99	0.82
C596A	0.64	0.76	0.79	0.86	0.95	0.91	0.91
A597T	0.63	0.81	0.78	0.84	0.99	0.98	0.87
A597G	0.58	0.76	0.76	0.81	0.97	0.98	0.82
A597C	0.65	0.70	0.64	0.77	0.99	0.96	0.80
C598T	0.65	0.83	0.68	0.83	1.00	1.00	0.84
C598G	0.59	0.86	0.51	0.77	0.99	1.00	0.76
C598A	0.62	0.80	0.55	0.77	1.00	0.99	0.78
G599A	0.61	0.80	0.72	0.81	1.00	0.98	0.84
C600T	0.41	0.77	0.95	0.77	0.98	0.97	0.83
C600A	0.61	0.79	0.70	0.81	0.99	1.00	0.82
T601C	0.55	0.81	0.64	0.77	0.99	1.00	0.78
T601A	0.62	0.85	0.59	0.81	1.00	1.00	0.81
TC602T	0.77	0.79	0.79	0.96	0.89	0.90	0.96
C602T	0.63	0.82	0.82	0.84	1.00	0.96	0.90
C602G	0.69	0.78	0.68	0.83	0.98	1.00	0.82
C603T	0.52	0.81	0.58	0.73	0.98	0.99	0.73
C603G	0.61	0.79	0.77	0.82	0.99	0.99	0.84
C603A	0.57	0.79	0.66	0.78	0.99	1.00	0.79
CT604C	0.72	0.68	0.90	1.00	0.82	0.83	1.00
T604G	0.63	0.87	0.59	0.82	1.00	1.00	0.82
T604C	0.55	0.78	0.75	0.79	0.99	0.99	0.80
T604A	0.58	0.79	0.74	0.81	0.99	1.00	0.83
T605G	0.61	0.84	0.63	0.81	1.00	1.00	0.81
T605C	0.59	0.80	0.81	0.82	1.00	1.00	0.85
T605A	0.65	0.84	0.56	0.81	1.00	1.00	0.80
TG606T	0.73	0.71	0.80	0.99	0.83	0.83	0.99
G606T	0.63	0.76	0.68	0.81	0.98	0.99	0.82
G606A	0.56	0.83	0.56	0.75	1.00	1.00	0.76
G607T	0.68	0.65	0.56	0.75	0.92	0.86	0.80
G607C	0.60	0.82	0.60	0.78	0.99	0.99	0.78
G607A	0.58	0.79	0.71	0.79	1.00	0.98	0.82
T608C	0.58	0.74	0.70	0.77	0.99	0.99	0.79
T608A	0.63	0.71	0.87	0.98	0.82	0.84	0.98
A609T	0.70	0.85	0.75	0.87	0.99	1.00	0.87
A609G	0.64	0.79	0.75	0.83	0.99	0.98	0.85
T610G	0.71	0.80	0.63	0.83	0.99	0.99	0.82
T610C	0.59	0.83	0.55	0.77	1.00	1.00	0.77
T610A	0.58	0.82	0.69	0.81	0.99	1.00	0.82
C611T	0.61	0.77	0.72	0.80	1.00	0.99	0.82

C611G	0.65	0.87	0.63	0.83	1.00	1.00	0.83
C611A	0.58	0.81	0.64	0.79	1.00	1.00	0.80
C612T	0.59	0.85	0.60	0.79	1.00	1.00	0.80
C612G	0.57	0.83	0.54	0.76	0.99	0.99	0.76
C612A	0.62	0.84	0.61	0.80	1.00	1.00	0.81
CT613C	0.87	0.79	0.91	1.00	0.89	0.90	1.00
T613C	0.65	0.82	0.70	0.83	1.00	0.99	0.84
T613A	0.63	0.78	0.67	0.80	0.99	0.97	0.83
G614T	0.61	0.84	0.59	0.80	1.00	1.00	0.81
G614C	0.72	0.80	0.66	0.84	0.99	1.00	0.83
G614A	0.58	0.83	0.59	0.79	0.99	1.00	0.79
C615T	0.58	0.83	0.60	0.78	0.99	0.99	0.79
C615G	0.64	0.77	0.63	0.79	0.99	0.99	0.80
C615A	0.62	0.78	0.68	0.80	0.99	0.99	0.81
T616C	0.64	0.82	0.69	0.83	1.00	0.99	0.84
G617T	0.76	0.75	0.61	0.83	0.97	0.96	0.84
G617C	0.58	0.81	0.71	0.80	1.00	0.99	0.83
G617A	0.60	0.80	0.71	0.80	1.00	0.97	0.84
GC618G	0.71	0.73	0.97	1.00	0.84	0.85	1.00
C618T	0.59	0.75	0.86	0.89	0.91	0.93	0.89
C618G	0.43	0.77	1.00	0.88	0.86	0.88	0.94
C618A	0.63	0.76	1.00	1.00	0.84	0.86	1.00
C619T	0.66	0.83	0.79	0.85	0.99	0.98	0.88
C619G	0.60	0.77	0.88	0.88	0.94	0.93	0.91
C619A	0.59	0.80	0.86	0.90	0.92	1.00	0.86
C619CT	0.74	0.78	0.96	1.00	0.87	0.89	1.00
CT620C	0.77	0.65	0.86	1.00	0.80	0.81	1.00
T620G	0.65	0.77	0.81	0.87	0.95	0.98	0.87
T620C	0.52	0.74	0.82	0.78	0.99	0.94	0.84
T620A	0.57	0.78	0.73	0.79	0.99	0.98	0.82
T621G	0.61	0.69	0.70	0.80	0.93	0.95	0.80
T621C	0.69	0.81	0.72	0.86	0.98	0.99	0.86
T621A	0.55	0.78	0.83	0.82	0.98	0.98	0.85
T622C	0.70	0.82	0.77	0.86	1.00	0.99	0.88
T622A	0.60	0.81	0.67	0.80	1.00	1.00	0.81
G623T	0.49	0.89	0.31	0.36	1.00	0.84	0.41
G623A	0.60	0.78	0.85	0.83	0.99	0.95	0.89
C624T	0.61	0.79	0.80	0.83	0.98	0.98	0.85
C624G	0.54	0.81	0.65	0.77	0.99	1.00	0.78
C624A	0.67	0.70	0.83	0.98	0.82	0.83	0.98
T625G	0.55	0.78	0.72	0.80	0.98	0.99	0.80
T625C	0.62	0.83	0.68	0.82	1.00	1.00	0.83
T625A	0.53	0.76	0.56	0.71	0.95	0.96	0.71
G626T	0.65	0.66	0.82	0.97	0.80	0.81	0.97
G626A	0.62	0.79	0.69	0.80	1.00	0.99	0.82
C627T	0.59	0.78	0.72	0.80	0.99	0.99	0.82
C627G	0.60	0.82	0.66	0.80	0.99	0.99	0.81
C627A	0.50	0.73	0.92	0.83	0.93	0.89	0.91
T628G	0.51	0.76	0.75	0.75	1.00	0.98	0.78
T628C	0.62	0.84	0.71	0.83	1.00	1.00	0.85
T628A	0.57	0.83	0.63	0.78	1.00	1.00	0.80
TG629T	0.68	0.84	0.74	0.86	0.99	1.00	0.86
G629T	0.60	0.77	0.70	0.79	1.00	0.99	0.81

G629C	0.60	0.78	0.67	0.80	0.99	0.99	0.81
G629A	0.57	0.78	0.65	0.77	0.99	0.99	0.79
C630T	0.58	0.77	0.71	0.82	0.95	1.00	0.80
C630G	0.58	0.83	0.77	0.82	0.99	1.00	0.84
C630A	0.55	0.79	0.75	0.79	0.99	0.99	0.82
T631G	0.49	0.74	0.95	0.86	0.91	0.89	0.92
T631C	0.68	0.81	0.72	0.84	1.00	0.99	0.85
T631A	0.54	0.79	0.78	0.79	0.99	0.99	0.82
T632C	0.62	0.80	0.75	0.82	1.00	0.99	0.84
T632A	0.65	0.83	0.63	0.82	1.00	1.00	0.82
G633T	0.56	0.85	0.61	0.79	1.00	1.00	0.80
G633C	0.62	0.75	0.92	0.98	0.84	0.87	0.97
G633A	0.62	0.79	0.65	0.79	1.00	0.99	0.80
T634C	0.54	0.74	0.75	0.78	0.98	0.98	0.79
T634A	0.53	0.76	0.79	0.78	0.99	0.98	0.82
TG635T	0.74	0.76	0.91	1.00	0.86	0.87	1.00
G635T	0.59	0.72	0.80	0.84	0.94	0.93	0.86
G635C	0.57	0.86	0.52	0.77	0.99	1.00	0.76
G635A	0.62	0.85	0.68	0.83	1.00	1.00	0.84
G636C	0.66	0.80	0.75	0.90	0.92	1.00	0.84
G636A	0.50	0.75	0.93	0.86	0.92	0.92	0.90
C637T	0.59	0.80	0.67	0.79	1.00	1.00	0.80
C637G	0.59	0.74	1.00	1.00	0.81	0.86	1.00
C637A	0.65	0.71	0.91	0.99	0.82	0.84	0.99
T638C	0.62	0.83	0.67	0.82	1.00	1.00	0.83
T638A	0.55	0.83	0.68	0.79	0.99	0.99	0.81
G639T	0.59	0.78	0.83	0.83	0.98	0.98	0.85
G639C	0.57	0.79	0.71	0.79	0.99	0.98	0.82
G639A	0.61	0.76	0.87	0.91	0.90	0.90	0.94
C640T	0.74	0.84	0.73	0.88	0.99	0.99	0.88
C640G	0.88	0.72	0.40	0.78	0.98	0.95	0.75
C640A	0.67	0.81	0.57	0.80	1.00	1.00	0.79
A641T	0.54	0.82	0.85	0.83	0.99	1.00	0.85
A641G	0.65	0.77	0.75	0.87	0.94	0.99	0.83
A641C	0.72	0.87	0.72	0.87	1.00	1.00	0.88
C642T	0.61	0.79	0.70	0.81	0.99	0.99	0.82
C642G	0.68	0.83	0.70	0.85	1.00	0.99	0.86
C642A	0.64	0.85	0.69	0.83	1.00	0.99	0.85
T643G	0.62	0.77	0.65	0.79	0.99	0.99	0.80
T643C	0.63	0.78	0.83	0.85	0.98	0.97	0.87
T643A	0.64	0.79	0.69	0.83	0.99	0.99	0.83
G644T	0.56	0.79	0.81	0.81	0.99	0.99	0.84
G644C	0.58	0.75	0.85	0.86	0.94	0.95	0.87
G644A	0.57	0.78	0.76	0.80	0.99	0.99	0.82
G645T	0.51	0.75	0.84	0.79	0.99	0.99	0.81
G645A	0.60	0.75	0.91	0.97	0.85	0.89	0.95
C646T	0.66	0.89	0.56	0.83	1.00	0.99	0.83
C646G	0.62	0.88	0.69	0.84	1.00	1.00	0.85
C646A	0.55	0.86	0.73	0.82	1.00	1.00	0.84
G647T	0.34	0.83	0.72	0.65	0.99	0.98	0.70
G647C	0.62	0.85	0.51	0.78	1.00	0.99	0.78
G647A	0.62	0.83	0.66	0.82	1.00	1.00	0.82
A648T	0.58	0.76	0.71	0.80	0.98	0.99	0.81

A648G	0.59	0.87	0.54	0.78	1.00	1.00	0.79
A648C	0.57	0.80	0.68	0.79	1.00	1.00	0.82
C649T	0.61	0.81	0.67	0.81	1.00	0.99	0.83
C649G	0.72	0.80	0.76	0.88	0.97	0.99	0.87
C649A	0.67	0.78	0.79	0.87	0.96	0.93	0.91
T650G	0.54	0.71	0.80	0.79	0.96	0.93	0.84
T650C	0.61	0.84	0.55	0.79	1.00	1.00	0.78
T650A	0.56	0.80	0.66	0.78	1.00	0.99	0.80
G651T	0.66	0.80	0.76	0.85	0.98	1.00	0.85
G651C	0.59	0.68	0.63	0.76	0.92	0.95	0.74
G651A	0.57	0.79	0.72	0.79	0.99	0.98	0.82
C652T	0.58	0.81	0.65	0.79	1.00	1.00	0.80
C652G	0.62	0.81	0.93	0.93	0.92	0.93	0.95
C652A	0.50	0.81	0.93	0.82	0.99	0.98	0.86
A653T	0.65	0.75	0.66	0.82	0.96	1.00	0.80
A653G	0.66	0.89	0.44	0.79	1.00	1.00	0.76
A653C	0.61	0.80	0.56	0.77	0.99	0.99	0.77
C654T	0.49	0.75	0.90	0.85	0.91	0.96	0.84
C654G	0.61	0.87	0.59	0.82	1.00	1.00	0.82
C654A	0.57	0.81	0.75	0.82	0.98	1.00	0.83
T655G	0.49	0.72	0.92	0.87	0.88	0.90	0.89
T655C	0.60	0.81	0.69	0.81	0.99	1.00	0.82
T655A	0.61	0.80	0.70	0.81	1.00	0.99	0.83
TG656T	0.57	0.64	0.99	1.00	0.74	0.78	1.00
G656T	0.60	0.79	0.72	0.81	0.99	0.98	0.83
G656C	0.63	0.84	0.76	0.84	1.00	0.99	0.87
G656A	0.61	0.80	0.64	0.80	0.99	1.00	0.80
G657C	0.60	0.79	0.82	0.83	0.98	0.96	0.87
G657A	0.59	0.77	0.79	0.82	0.98	0.98	0.84
T658G	0.56	0.91	0.57	0.79	1.00	1.00	0.80
T658C	0.61	0.80	0.70	0.81	1.00	0.99	0.82
T658A	0.49	0.75	0.81	0.77	0.99	0.99	0.79
C659T	0.65	0.83	0.61	0.82	1.00	1.00	0.82
C659A	0.70	0.78	0.57	0.80	1.00	0.99	0.80
T660C	0.62	0.81	0.61	0.79	1.00	0.99	0.80
T660A	0.57	0.78	0.67	0.78	0.99	0.99	0.79
T661G	0.81	0.80	0.60	0.86	0.98	0.99	0.83
T661C	0.65	0.81	0.65	0.82	1.00	1.00	0.82
T661A	0.62	0.79	0.74	0.82	0.99	1.00	0.83
C662T	0.63	0.87	0.45	0.76	0.99	0.99	0.74
C662A	0.63	0.90	0.51	0.82	1.00	1.00	0.80
A663T	0.60	0.83	0.64	0.80	1.00	1.00	0.81
A663G	0.61	0.80	0.76	0.82	0.99	0.99	0.84
A663C	0.59	0.78	0.54	0.73	0.99	1.00	0.73
G664T	0.64	0.82	0.70	0.83	1.00	1.00	0.84
G664C	0.62	0.81	0.58	0.79	0.99	1.00	0.79
G664A	0.54	0.70	0.81	0.82	0.91	0.91	0.85
C665T	0.61	0.82	0.63	0.80	1.00	0.99	0.81
C665G	0.64	0.87	0.69	0.84	1.00	0.99	0.86
C665A	0.61	0.78	0.66	0.80	0.98	0.99	0.80
T666G	0.71	0.83	0.41	0.78	0.98	1.00	0.73
T666C	0.68	0.81	0.57	0.80	1.00	1.00	0.80
T666A	0.57	0.77	0.77	0.80	0.99	0.98	0.83

A667T	0.59	0.74	0.75	0.81	0.97	0.97	0.83
A667G	0.57	0.81	0.68	0.79	1.00	1.00	0.81
C668T	0.62	0.82	0.68	0.82	1.00	1.00	0.83
C668A	0.59	0.86	0.67	0.82	1.00	1.00	0.83
T669G	0.65	0.63	0.66	0.83	0.86	0.85	0.85
T669C	0.63	0.81	0.63	0.81	0.99	1.00	0.81
T669A	0.60	0.82	0.76	0.83	1.00	0.99	0.86
TG670T	0.74	0.66	0.96	1.00	0.81	0.83	1.00
G670T	0.61	0.83	0.68	0.81	1.00	0.99	0.83
G670C	0.54	0.80	0.79	0.80	0.99	1.00	0.83
G670A	0.67	0.78	0.66	0.82	1.00	1.00	0.82
G671T	0.73	0.74	0.96	1.00	0.84	0.86	1.00
G671A	0.54	0.76	0.76	0.79	0.98	0.99	0.81
GT672G	0.81	0.94	0.98	0.94	0.99	0.98	0.98
T672G	0.71	0.86	0.62	0.87	0.99	1.00	0.85
T672C	0.64	0.75	0.75	0.83	0.97	0.98	0.83
T672A	0.57	0.79	0.73	0.80	0.99	0.98	0.83
TG673T	0.76	0.83	0.73	0.87	1.00	0.99	0.88
G673T	0.63	0.78	0.75	0.82	0.99	0.99	0.84
G673C	0.42	0.77	0.79	0.72	0.98	0.99	0.75
G673A	0.62	0.78	0.63	0.79	0.99	0.98	0.80
G674T	0.59	0.77	0.73	0.79	1.00	0.93	0.87
G674C	0.64	0.84	0.59	0.82	0.99	1.00	0.81
G674A	0.51	0.77	0.86	0.80	0.99	0.98	0.84
C675T	0.62	0.83	0.72	0.83	1.00	0.99	0.85
C675G	0.72	0.84	0.59	0.84	1.00	1.00	0.83
C675A	0.61	0.75	0.70	0.80	0.98	0.98	0.81
G676T	0.63	0.85	0.59	0.82	1.00	1.00	0.81
G676C	0.48	0.76	0.82	0.77	0.99	0.99	0.80
G676A	0.66	0.83	0.62	0.82	1.00	1.00	0.82
G677T	0.74	0.85	0.61	0.86	1.00	1.00	0.85
G677A	0.58	0.62	0.65	0.73	0.86	0.74	0.86
A678T	0.65	0.80	0.66	0.81	0.99	0.99	0.81
A678G	0.62	0.83	0.59	0.80	0.99	1.00	0.79
AG679A	0.79	0.82	0.93	1.00	0.89	0.90	1.00
G679T	0.59	0.76	0.75	0.80	0.99	0.99	0.82
G679A	0.58	0.80	0.81	0.82	0.99	1.00	0.85
G680T	0.55	0.73	0.71	0.78	0.96	1.00	0.76
G680A	0.66	0.80	0.72	0.84	0.99	1.00	0.84
GA681G	0.80	0.87	0.83	0.93	0.97	1.00	0.91
A681T	0.66	0.80	0.57	0.79	1.00	1.00	0.78
A681G	0.64	0.87	0.72	0.85	1.00	1.00	0.86
A682T	0.60	0.81	0.71	0.81	0.99	0.99	0.83
A682G	0.67	0.84	0.63	0.83	1.00	0.99	0.84
G683T	0.64	0.76	0.82	0.87	0.94	0.90	0.94
G683C	0.64	0.69	0.77	0.91	0.86	0.86	0.92
G683A	0.49	0.75	0.80	0.76	0.98	0.99	0.79
C684T	0.65	0.80	0.70	0.82	0.99	0.99	0.83
C684G	0.66	0.91	0.53	0.85	1.00	1.00	0.83
C684A	0.56	0.79	0.75	0.81	0.98	1.00	0.82
A685T	0.61	0.79	0.71	0.81	1.00	0.99	0.82
A685G	0.61	0.79	0.71	0.81	0.99	0.98	0.83
A685C	0.49	0.78	0.60	0.71	0.98	0.99	0.72

G686T	0.55	0.79	0.76	0.81	0.98	1.00	0.82
G686C	0.72	0.78	0.70	0.85	0.98	0.98	0.85
G686A	0.56	0.75	0.75	0.78	1.00	0.99	0.80
C687T	0.65	0.77	0.62	0.82	0.97	0.99	0.80
C687G	0.61	0.78	0.57	0.76	0.99	0.98	0.77
C687A	0.62	0.85	0.68	0.83	1.00	1.00	0.85
T688G	0.61	0.78	0.69	0.80	1.00	0.99	0.81
T688C	0.55	0.76	0.68	0.78	0.97	1.00	0.77
T688A	0.60	0.79	0.63	0.80	0.97	1.00	0.78
A689T	0.66	0.78	0.70	0.82	1.00	0.99	0.83
A689G	0.63	0.78	0.74	0.83	0.99	0.99	0.84
A689C	0.66	0.80	0.76	0.83	1.00	1.00	0.85
G690T	0.79	0.89	0.57	0.90	0.97	1.00	0.85
G690C	0.78	0.91	0.69	0.90	1.00	1.00	0.90
G690A	0.62	0.91	0.33	0.64	0.96	0.93	0.61
G691T	0.93	0.79	0.07	0.64	0.51	0.50	0.28
G691A	0.60	0.89	0.07	0.37	0.58	0.29	0.27
T692G	0.79	0.86	0.04	0.53	0.55	0.48	0.16
T692C	0.66	0.81	0.11	0.36	0.61	0.22	0.49
T692A	0.69	0.84	0.05	0.27	0.83	0.10	0.67
G693T	0.43	0.84	0.16	0.28	0.53	0.17	0.47
G693C	0.86	0.90	0.25	0.76	1.00	0.99	0.68
G693A	0.50	0.75	0.79	0.78	0.98	0.99	0.80
A694T	0.60	0.90	0.14	0.52	0.46	0.52	0.27
A694G	0.57	0.90	0.28	0.43	0.92	0.94	0.37
A694C	0.59	0.96	0.32	0.69	0.99	0.98	0.65
G695T	0.54	0.90	0.29	0.61	0.54	0.84	0.34
G695A	0.66	0.88	0.12	0.46	0.58	0.44	0.34
T696C	0.72	0.88	0.44	0.81	1.00	1.00	0.78
T696A	0.74	0.87	0.64	0.87	1.00	0.97	0.89
T697G	0.91	0.79	0.78	1.00	0.89	0.87	1.00
T697C	0.66	0.83	0.63	0.83	1.00	0.99	0.83
T697A	0.49	0.72	0.78	0.75	0.97	0.96	0.79
C698T	0.64	0.80	0.71	0.83	0.98	0.99	0.84
C698A	0.53	0.74	0.71	0.75	0.98	0.99	0.76
T699C	0.55	0.77	0.77	0.78	1.00	0.98	0.82
T699A	0.57	0.81	0.69	0.79	1.00	0.99	0.81
C700T	0.53	0.79	0.74	0.78	1.00	1.00	0.80
C700G	0.66	0.79	0.68	0.87	0.94	1.00	0.83
C700A	0.60	0.78	0.59	0.77	0.99	1.00	0.77
T701G	0.37	0.91	0.96	0.80	0.98	1.00	0.87
T701C	0.61	0.78	0.66	0.79	0.99	0.99	0.80
T701A	0.58	0.81	0.73	0.81	1.00	1.00	0.83
TG702T	0.80	0.72	0.82	1.00	0.84	0.84	1.00
G702T	0.64	0.79	0.87	0.90	0.93	0.92	0.94
G702C	0.55	0.83	0.68	0.79	0.99	1.00	0.81
G702A	0.60	0.81	0.73	0.82	1.00	1.00	0.83
C703T	0.53	0.78	0.80	0.80	0.99	0.99	0.83
C703G	0.39	0.65	0.96	0.80	0.83	0.81	0.89
C703A	0.61	0.78	0.61	0.78	0.99	1.00	0.78
CT704C	0.69	0.77	0.77	0.87	0.96	0.93	0.91
T704G	0.72	0.80	0.84	0.96	0.90	0.92	0.96
T704C	0.54	0.77	0.76	0.78	1.00	0.96	0.84

T704A	0.64	0.77	0.70	0.81	1.00	1.00	0.82
T704TC	0.35	0.78	1.00	0.79	0.90	0.89	0.91

The following tables were obtained with the Human Splicing Finder, Version 3.1

http://www.umd.be/HSF/ and FO Desmet, Hamroun D, Lalande M, Collod-Beroud G, Claustres M, Beroud C. Human Splicing Finder: an online bioinformatics tool to predict splicing signals. Nucleic Acid Research, 2009

ESE Finder matrices for SRp40, SC35, SF2/ASF and SRp55 proteins

Cartegni L., Wang J., Zhu Z., Zhang M. Q., Krainer A. R.; 2003. ESEfinder: a web resource to identify exonic splicing enhancers, Nucleic Acid Research, 2003, Vol. 31, No.13 3568-3571

Sequence Position	cDNA Position	Linked SR protein	Enhancer motif
+3	SRp40	TGAGAGG	84.79
+11	SC35	AGCTTCCA	76.46
+12	SC35	GCTTCCAG	76.34
+16	SRp40	CCAGAGC	82.46
+17	SF2/ASF (IgM-BRCA1)	CAGAGCA	80.54
+17	SF2/ASF	CAGAGCA	80.02
+20	SRp55	AGCAGC	74.95
+23	SRp55	AGCAGC	74.95
+25	SF2/ASF (IgM-BRCA1)	CAGCTGT	76.00
+25	SF2/ASF	CAGCTGT	76.06
+31	SRp55	TGCCGC	76.16
+33	SF2/ASF (IgM-BRCA1)	CCGCCTT	72.77
+42	SRp55	TGAATA	76.10
+51	SC35	GGTCCGAG	84.63
+58	SC35	GACCCCCA	91.09
+60	SF2/ASF (IgM-BRCA1)	CCCCCAG	72.38
+61	SRp40	CCCCAGG	83.47
+61	SF2/ASF (IgM-BRCA1)	CCCCAGG	71.38
+62	SF2/ASF (IgM-BRCA1)	CCCAGGG	87.62
+62	SF2/ASF	CCCAGGG	82.18
+74	SRp40	TGGCAGG	79.46
+75	SF2/ASF (IgM-BRCA1)	GGCAGGG	72.77
+75	SF2/ASF	GGCAGGG	80.37
+85	SF2/ASF (IgM-BRCA1)	CTGAGTG	74.69
+86	SRp40	TGAGTGC	78.20
+90	SC35	TGCCCGAG	75.54
+90	SF2/ASF (IgM-BRCA1)	TGCCCGA	73.00
+90	SF2/ASF	TGCCCGA	74.43
+93	SF2/ASF (IgM-BRCA1)	CCGAGGG	84.69
+93	SF2/ASF	CCGAGGG	80.72
+105	SC35	AGCTGCTG	82.36
+107	SRp40	CTGCTGG	78.86
+107	SF2/ASF (IgM-BRCA1)	CTGCTGG	71.15

+116	SRp40	TTACACT	82.04
+118	SRp40	ACACTGC	87.13
+121	SF2/ASF (IgM-BRCA1)	CTGCCTG	73.15
+122	SRp40	TGCCTGG	79.22
+127	SC35	GGCTTTCG	79.41
+133	SRp55	CGCTTC	76.04
+134	SC35	GCTTCCTA	79.84
+139	SRp40	CTACCCC	78.62
+140	SC35	TACCCCCA	78.49
+145	SRp40	CCACCCC	80.48
+146	SF2/ASF (IgM-BRCA1)	CACCCCA	81.92
+146	SF2/ASF	CACCCCA	79.27
+155	SF2/ASF (IgM-BRCA1)	CACCCAG	77.62
+155	SF2/ASF	CACCCAG	75.01
+157	SF2/ASF (IgM-BRCA1)	CCCAGTG	75.69
+158	SRp40	CCAGTGC	80.96
+173	SC35	TTCCACTG	80.52
+175	SRp40	CCACTGA	82.10
+184	SRp40	CCTGAGG	81.26
+185	SF2/ASF (IgM-BRCA1)	CTGAGGA	89.92
+185	SF2/ASF	CTGAGGA	88.47
+186	SRp55	TGAGGA	74.82
+205	SRp40	TTTGAGG	81.56
+216	SRp40	TGTAAGG	79.40
+229	SF2/ASF (IgM-BRCA1)	GGCAGGG	72.77
+229	SF2/ASF	GGCAGGG	80.37
+262	SF2/ASF (IgM-BRCA1)	CAGCCTA	79.77
+262	SF2/ASF	CAGCCTA	80.43
+264	SC35	GCCTACTG	83.22
+266	SRp40	CTACTGG	94.49
+275	SC35	GGTCCTCA	79.23
+278	SRp40	CCTCATG	79.46
+279	SF2/ASF (IgM-BRCA1)	CTCATGA	80.54
+279	SF2/ASF	CTCATGA	78.80
+289	SRp40	TCTCTGC	87.13
+292	SRp40	CTGCAGG	80.36
+293	SRp55	TGCAGG	75.65
+293	SF2/ASF (IgM-BRCA1)	TGCAGGA	74.54
+293	SF2/ASF	TGCAGGA	76.65
+297	SC35	GGATATTG	78.92
+309	SC35	GGGCGCTG	80.33
+315	SRp55	TGTGGC	80.97
+320	SF2/ASF (IgM-BRCA1)	CTGACTG	76.31

+320	SF2/ASF	CTGACTG	75.42
+321	SRp40	TGACTGT	79.34
+325	SRp55	TGTGTG	74.82
+329	SRp55	TGGGTA	74.12
+341	SC35	TGACCGTG	75.60
+344	SF2/ASF (IgM-BRCA1)	CCGTGGG	71.92
+354	SRp40	TGAGAGC	79.70
+358	SC35	AGCTGCCA	75.66
+360	SF2/ASF (IgM-BRCA1)	CTGCCAG	71.38
+365	SF2/ASF (IgM-BRCA1)	AGCACGA	75.92
+365	SF2/ASF	AGCACGA	82.76
+375	SF2/ASF (IgM-BRCA1)	CCGGGGG	71.46
+376	SF2/ASF (IgM-BRCA1)	CGGGGGG	78.92
+390	SRp40	TGTCTGC	82.22
+395	SC35	GCCCCCTG	87.52
+396	SF2/ASF (IgM-BRCA1)	CCCCCTG	74.15
+401	SC35	TGCCCCCA	80.70
+403	SF2/ASF (IgM-BRCA1)	CCCCCAT	73.92
+407	SC35	CATCCCTG	81.81
+409	SRp40	TCCCTGC	79.04
+413	SRp55	TGCAGC	86.98
+422	SF2/ASF	GCCAGGA	77.23
+426	SC35	GGATGGTG	81.32
+431	SC35	GTGCCCCA	75.11
+439	SRp40	TTGCAGG	82.51
+440	SRp55	TGCAGG	75.65
+440	SF2/ASF (IgM-BRCA1)	TGCAGGT	72.77
+440	SF2/ASF	TGCAGGT	74.61
+450	SF2/ASF (IgM-BRCA1)	CAGCCCA	79.00
+450	SF2/ASF	CAGCCCA	77.81
+453	SF2/ASF (IgM-BRCA1)	CCCAGCT	76.46
+455	SF2/ASF (IgM-BRCA1)	CAGCTGG	74.46
+455	SF2/ASF	CAGCTGG	73.85
+461	SC35	GACCTCCC	75.29
+464	SF2/ASF (IgM-BRCA1)	CTCCCTG	76.08
+465	SRp40	TCCCTGG	84.13
+466	SF2/ASF (IgM-BRCA1)	CCCTGGG	74.85
+473	SRp40	AAACACG	78.32
+474	SF2/ASF	AACACGG	81.13
+475	SRp40	ACACGGG	78.44
+476	SF2/ASF (IgM-BRCA1)	CACGGGC	72.00
+482	SF2/ASF (IgM-BRCA1)	CAGAGGG	89.92
+482	SF2/ASF	CAGAGGG	90.74

+487	SC35	GGCCTACA	80.82
+488	SC35	GCCTACAG	76.95
+490	SRp40	CTACAGG	95.99
+500	SC35	GGCCTGAG	83.47
+503	SF2/ASF (IgM-BRCA1)	CTGAGTT	76.23
+503	SF2/ASF	CTGAGTT	74.08
+516	SC35	TGCCCCCA	80.70
+517	SC35	GCCCCCAG	81.25
+518	SF2/ASF (IgM-BRCA1)	CCCCCAG	72.38
+519	SRp40	CCCCAGG	83.47
+519	SF2/ASF (IgM-BRCA1)	CCCCAGG	71.38
+520	SF2/ASF (IgM-BRCA1)	CCCAGGT	89.15
+520	SF2/ASF	CCCAGGT	84.39
+524	SC35	GGTCTGCG	82.30
+527	SF2/ASF (IgM-BRCA1)	CTGCGTA	74.85
+528	SRp55	TGCGTA	93.71
+547	SC35	ATATCCTG	77.63
+553	SRp55	TGGGTA	74.12
+565	SRp55	TGCGGC	90.89
+567	SF2/ASF (IgM-BRCA1)	CGGCCAG	76.92
+568	SC35	GGCCAGGG	77.26
+577	SF2/ASF (IgM-BRCA1)	CAGATGG	77.62
+577	SF2/ASF	CAGATGG	79.62
+583	SC35	GGGTCCCA	77.69
+584	SC35	GGTCCCAC	76.34
+585	SC35	GTCCCACA	81.50
+587	SF2/ASF (IgM-BRCA1)	CCCACAG	75.54
+588	SRp40	CCACAGA	83.59
+589	SRp55	CACAGA	75.40
+589	SF2/ASF (IgM-BRCA1)	CACAGAG	79.15
+589	SF2/ASF	CACAGAG	77.23
+590	SRp40	ACAGAGC	78.32
+591	SF2/ASF (IgM-BRCA1)	CAGAGCA	80.54
+591	SF2/ASF	CAGAGCA	80.02
+598	SF2/ASF (IgM-BRCA1)	CGCTCCT	72.77
+607	SC35	GTATCCTG	88.38
+613	SRp55	TGCTGC	76.16
+615	SF2/ASF (IgM-BRCA1)	CTGCCTT	74.69
+622	SRp55	TGCTGC	76.16
+622	SC35	TGCTGCTG	80.52
+625	SRp55	TGCTGC	76.16
+628	SC35	TGCTTGTG	75.72
+632	SRp55	TGTGGC	80.97

+639	SRp40	GCACTGG	83.53
+640	SF2/ASF (IgM-BRCA1)	CACTGGC	72.46
+642	SF2/ASF (IgM-BRCA1)	CTGGCGA	78.31
+642	SF2/ASF	CTGGCGA	75.13
+644	SC35	GGCGACTG	80.58
+646	SRp40	CGACTGC	86.35
+651	SRp40	GCACTGG	83.53
+652	SF2/ASF (IgM-BRCA1)	CACTGGT	81.62
+652	SF2/ASF	CACTGGT	80.14
+657	SC35	GTCTTCAG	83.65
+659	SRp40	CTTCAGC	84.61
+663	SC35	AGCTACTG	84.94
+665	SRp40	CTACTGG	94.49
+675	SF2/ASF (IgM-BRCA1)	CGGAGGA	95.46
+675	SF2/ASF	CGGAGGA	92.37
+682	SRp55	AGCAGC	74.95
+695	SC35	GTTCTCTG	87.83
+697	SRp40	TCTCTGC	87.13

RESCUE ESE hexamers

Fairbrother WG, Yeh RF, Sharp PA, Burge CB. Predictive identification of exonic splicing enhancers in human genes. Science. 2002 Aug 9;297(5583):1007-13

Sequence Position	cDNA Position	Enhancer motif
40	+40	CCTGAA
100	+100	GATGGA
177	+177	ACTGAA
178	+178	CTGAAG
179	+179	TGAAGC
187	+187	GAGGAG
248	+248	CTGAAA
249	+249	TGAAAG
321	+321	TGACTG
335	+335	TCAACG
471	+471	GGAAAC
472	+472	GAAACA
482	+482	CAGAGG
658	+658	TCTTCA
659	+659	CTTCAG
676	+676	GGAGGA
677	+677	GAGGAA
678	+678	AGGAAG

680	+680	GAAGCA
681	+681	AAGCAG

Predicted PESE Octamers from Zhang & Chasin.

Zhang XH, Chasin LA. Computational definition of sequence motifs governing constitutive exon splicing. Genes Dev. 2004 Jun 1;18(11):1241-50

Sequence Position	cDNA Position	Enhancer motif	Motif value (0-100)
9	+9	GCAGCTTC	30.44
21	+21	GCAGCAGC	10.87
24	+24	GCAGCTGT	39.34
25	+25	CAGCTGTG	38.37
57	+57	AGACCCCC	38.13
81	+81	GAATCTGA	30.83
101	+101	ATGGAGCT	30.38
156	+156	ACCCAGTG	26.53
176	+176	CACTGAAG	38.12
177	+177	ACTGAAGC	37.74
184	+184	CCTGAGGA	44.48
185	+185	CTGAGGAG	48.52
186	+186	TGAGGAGC	40.81
187	+187	GAGGAGCA	57.89
188	+188	AGGAGCAT	33.2
245	+245	GATCTGAA	36.71
268	+268	ACTGGCTG	31.31
338	+338	ACGTGACC	31.54
360	+360	CTGCCAGC	47.59
454	+454	CCAGCTGG	42.69
455	+455	CAGCTGGA	49.24
457	+457	GCTGGACC	40.48
505	+505	GAGTTGCC	30.64
508	+508	TTGCCACC	24.19
511	+511	CCACCTGC	26.78
513	+513	ACCTGCCC	55
609	+609	ATCCTGCT	23.21
610	+610	TCCTGCTG	44.28
618	+618	CCTTTGCT	32.21
622	+622	TGCTGCTG	34.72
657	+657	GTCTTCAG	34.58
673	+673	GGCGGAGG	1.21
676	+676	GGAGGAAG	47.57
677	+677	GAGGAAGC	42.39

Ratio PESE/PESS: 6.8

Silencer motifs from Sironi et al.

Sironi M, Menozzi G, Riva L, Cagliani R, Comi GP, Bresolin N, Giorda R, Pozzoli U. Silencer elements as possible inhibitors of pseudoexon splicing. Nucleic Acids Res. 2004 Mar 19;32(5):1783-91

Sequence Position	cDNA Position	Sironi's motif	Silencer motif
+1	Motif 2 - [T/G]G[T/A]GGGG	TGTGAGAG	72.42
+3	Motif 1 - CTAGAGGT	TGAGAGGC	80.93
+3	Motif 2 - [T/G]G[T/A]GGGG	TGAGAGGC	80.20
+5	Motif 2 - [T/G]G[T/A]GGGG	AGAGGCAG	62.54
+12	Motif 3 - TCTCCCAA	GCTTCCAG	76.97
+16	Motif 1 - CTAGAGGT	CCAGAGCA	79.23
+29	Motif 2 - [T/G]G[T/A]GGGG	TGTGCCGC	66.35
+36	Motif 3 - TCTCCCAA	CCTTCCTG	69.14
+46	Motif 2 - [T/G]G[T/A]GGGG	TATGTGGT	66.35
+48	Motif 2 - [T/G]G[T/A]GGGG	TGTGGTCC	73.23
+51	Motif 3 - TCTCCCAA	GGTCCGAG	62.64
+55	Motif 1 - CTAGAGGT	CGAGACCC	64.72
+59	Motif 3 - TCTCCCAA	ACCCCCAG	77.56
+63	Motif 1 - CTAGAGGT	CCAGGGAT	68.31
+67	Motif 2 - [T/G]G[T/A]GGGG	GGATGGGT	86.07
+68	Motif 2 - [T/G]G[T/A]GGGG	GATGGGTG	68.12
+70	Motif 2 - [T/G]G[T/A]GGGG	TGGGTGGC	70.71
+71	Motif 2 - [T/G]G[T/A]GGGG	GGGTGGCA	66.56
+72	Motif 2 - [T/G]G[T/A]GGGG	GGTGGCAG	69.35
+75	Motif 2 - [T/G]G[T/A]GGGG	GGCAGGGA	69.39
+76	Motif 2 - [T/G]G[T/A]GGGG	GCAGGGAA	66.30
+86	Motif 2 -	TGAGTGCC	70.18

	[T/G]G[T/A]GGGG		
+92	Motif 1 - CTAGAGGT	CCCGAGGG	72.64
+94	Motif 1 - CTAGAGGT	CGAGGGGA	73.01
+94	Motif 2 - [T/G]G[T/A]GGGG	CGAGGGGA	87.24
+99	Motif 2 - [T/G]G[T/A]GGGG	GGATGGAG	75.24
+100	Motif 2 - [T/G]G[T/A]GGGG	GATGGAGC	63.28
+101	Motif 1 - CTAGAGGT	ATGGAGCT	68.62
+103	Motif 2 - [T/G]G[T/A]GGGG	GGAGCTGC	60.23
+108	Motif 2 - [T/G]G[T/A]GGGG	TGCTGGCT	69.63
+120	Motif 3 - TCTCCCAA	ACTGCCTG	66.29
+134	Motif 3 - TCTCCCAA	GCTTCCTA	71.27
+135	Motif 3 - TCTCCCAA	CTTCCTAC	66.41
+138	Motif 3 - TCTCCCAA	CCTACCCC	67.86
+140	Motif 3 - TCTCCCAA	TACCCCCA	65.38
+141	Motif 3 - TCTCCCAA	ACCCCCAC	77.98
+145	Motif 3 - TCTCCCAA	CCACCCCA	73.01
+146	Motif 3 - TCTCCCAA	CACCCCAT	63.78
+150	Motif 3 - TCTCCCAA	CCATCCAC	63.64
+153	Motif 3 - TCTCCCAA	TCCACCCA	61.63
+154	Motif 3 - TCTCCCAA	CCACCCAG	80.41
+158	Motif 1 - CTAGAGGT	CCAGTGCC	65.60
+160	Motif 3 - TCTCCCAA	AGTGCCAA	65.08
+171	Motif 3 - TCTCCCAA	AGTTCCAC	61.79
+184	Motif 1 - CTAGAGGT	CCTGAGGA	72.58
+186	Motif 2 - [T/G]G[T/A]GGGG	TGAGGAGC	80.20
+193	Motif 3 - TCTCCCAA	CATGCCAT	61.93
+205	Motif 1 - CTAGAGGT	TTTGAGGT	74.76
+205	Motif 2 - [T/G]G[T/A]GGGG	TTTGAGGT	66.35
+207	Motif 2 - [T/G]G[T/A]GGGG	TGAGGTAA	69.37
+216	Motif 2 - [T/G]G[T/A]GGGG	TGTAAGGG	68.11
+217	Motif 2 - [T/G]G[T/A]GGGG	GTAAGGGA	61.98
+218	Motif 1 - CTAGAGGT	TAAGGGAT	60.88
+218	Motif 2 - [T/G]G[T/A]GGGG	TAAGGGAT	69.37
+222	Motif 1 - CTAGAGGT	GGATAGGG	62.30

+222	Motif 2 - [T/G]G[T/A]GGGG	GGATAGGG	69.17
+223	Motif 2 - [T/G]G[T/A]GGGG	GATAGGGG	65.03
+224	Motif 1 - CTAGAGGT	ATAGGGGC	71.07
+224	Motif 2 - [T/G]G[T/A]GGGG	ATAGGGGC	73.38
+225	Motif 2 - [T/G]G[T/A]GGGG	TAGGGGCA	60.69
+229	Motif 2 - [T/G]G[T/A]GGGG	GGCAGGGA	69.39
+230	Motif 2 - [T/G]G[T/A]GGGG	GCAGGGAC	66.30
+238	Motif 2 - [T/G]G[T/A]GGGG	AGTTGGGG	85.37
+239	Motif 2 - [T/G]G[T/A]GGGG	GTTGGGGA	80.18
+253	Motif 2 - [T/G]G[T/A]GGGG	AGTAGGGG	78.18
+254	Motif 1 - CTAGAGGT	GTAGGGGC	68.44
+254	Motif 2 - [T/G]G[T/A]GGGG	GTAGGGGC	77.13
+255	Motif 2 - [T/G]G[T/A]GGGG	TAGGGGCC	60.69
+266	Motif 1 - CTAGAGGT	CTACTGGC	60.99
+271	Motif 2 - [T/G]G[T/A]GGGG	GGCTGGTC	64.52
+283	Motif 3 - TCTCCCAA	TGACCCTC	62.90
+287	Motif 3 - TCTCCCAA	CCTCTCTG	69.14
+293	Motif 2 - [T/G]G[T/A]GGGG	TGCAGGAT	61.64
+300	Motif 2 - [T/G]G[T/A]GGGG	TATTGGGC	75.30
+301	Motif 2 - [T/G]G[T/A]GGGG	ATTGGGCT	66.40
+305	Motif 2 - [T/G]G[T/A]GGGG	GGCTGGGC	76.58
+306	Motif 2 - [T/G]G[T/A]GGGG	GCTGGGCG	70.15
+308	Motif 2 - [T/G]G[T/A]GGGG	TGGGCGCT	60.69
+313	Motif 2 - [T/G]G[T/A]GGGG	GCTGTGGC	63.28
+315	Motif 2 - [T/G]G[T/A]GGGG	TGTGGCTG	71.20
+325	Motif 2 - [T/G]G[T/A]GGGG	TGTGTGGG	83.25

+327	Motif 2 - [T/G]G[T/A]GGGG	TGTGGGTA	88.10
+345	Motif 2 - [T/G]G[T/A]GGGG	CGTGGGTG	78.23
+347	Motif 2 - [T/G]G[T/A]GGGG	TGGGTGGT	70.71
+348	Motif 2 - [T/G]G[T/A]GGGG	GGGTGGTG	64.52
+349	Motif 2 - [T/G]G[T/A]GGGG	GGTGGTGA	80.18
+351	Motif 2 - [T/G]G[T/A]GGGG	TGGTGAGA	62.75
+352	Motif 2 - [T/G]G[T/A]GGGG	GGTGAGAG	69.35
+354	Motif 1 - CTAGAGGT	TGAGAGCT	78.48
+354	Motif 2 - [T/G]G[T/A]GGGG	TGAGAGCT	70.18
+359	Motif 3 - TCTCCCAA	GCTGCCAG	76.97
+367	Motif 1 - CTAGAGGT	CACGAGTT	69.74
+374	Motif 2 - [T/G]G[T/A]GGGG	TCCGGGGG	70.71
+375	Motif 2 - [T/G]G[T/A]GGGG	CCGGGGGG	60.84
+376	Motif 2 - [T/G]G[T/A]GGGG	CGGGGGGA	77.74
+377	Motif 2 - [T/G]G[T/A]GGGG	GGGGGGAC	73.71
+387	Motif 2 - [T/G]G[T/A]GGGG	GGTTGTCT	62.20
+392	Motif 3 - TCTCCCAA	TCTGCCCC	73.67
+395	Motif 3 - TCTCCCAA	GCCCCCTG	69.41
+399	Motif 3 - TCTCCCAA	CCTGCCCC	67.86
+401	Motif 3 - TCTCCCAA	TGCCCCCA	64.49
+402	Motif 3 - TCTCCCAA	GCCCCCAT	75.65
+407	Motif 3 - TCTCCCAA	CATCCCTG	72.88
+417	Motif 2 - [T/G]G[T/A]GGGG	GCTTGGCC	62.20
+426	Motif 2 - [T/G]G[T/A]GGGG	GGATGGTG	74.01
+427	Motif 2 - [T/G]G[T/A]GGGG	GATGGTGC	63.28
+432	Motif 3 - TCTCCCAA	TGCCCCAT	68.71
+440	Motif 2 - [T/G]G[T/A]GGGG	TGCAGGTA	60.41
+444	Motif 2 - [T/G]G[T/A]GGGG	GGTAGGCA	71.91

+450	Motif 3 - TCTCCCAA	CAGCCCAG	66.96
+456	Motif 2 - [T/G]G[T/A]GGGG	AGCTGGAC	62.00
+463	Motif 3 - TCTCCCAA	CCTCCCTG	86.32
+467	Motif 2 - [T/G]G[T/A]GGGG	CCTGGGAA	62.55
+481	Motif 1 - CTAGAGGT	GCAGAGGG	78.78
+481	Motif 2 - [T/G]G[T/A]GGGG	GCAGAGGG	60.23
+483	Motif 2 - [T/G]G[T/A]GGGG	AGAGGGCC	80.25
+490	Motif 1 - CTAGAGGT	CTACAGGC	76.59
+495	Motif 2 - [T/G]G[T/A]GGGG	GGCTGGGC	76.58
+496	Motif 2 - [T/G]G[T/A]GGGG	GCTGGGCC	70.15
+502	Motif 1 - CTAGAGGT	CCTGAGTT	67.52
+504	Motif 2 - [T/G]G[T/A]GGGG	TGAGTTGC	63.30
+507	Motif 3 - TCTCCCAA	GTTGCCAC	64.83
+514	Motif 3 - TCTCCCAA	CCTGCCCC	67.86
+516	Motif 3 - TCTCCCAA	TGCCCCCA	64.49
+517	Motif 3 - TCTCCCAA	GCCCCCAG	78.83
+519	Motif 1 - CTAGAGGT	CCCCAGGT	64.15
+526	Motif 3 - TCTCCCAA	TCTGCGTA	61.48
+531	Motif 1 - CTAGAGGT	GTAGATGG	65.22
+533	Motif 2 - [T/G]G[T/A]GGGG	AGATGGTG	70.26
+534	Motif 2 - [T/G]G[T/A]GGGG	GATGGTGA	63.28
+550	Motif 2 - [T/G]G[T/A]GGGG	TCCTGGGT	62.75
+551	Motif 2 - [T/G]G[T/A]GGGG	CCTGGGTA	61.33
+555	Motif 2 - [T/G]G[T/A]GGGG	GGTAGAGT	65.03
+556	Motif 1 - CTAGAGGT	GTAGAGTG	68.59
+558	Motif 1 - CTAGAGGT	AGAGTGGT	74.65
+558	Motif 2 - [T/G]G[T/A]GGGG	AGAGTGGT	73.38
+560	Motif 2 - [T/G]G[T/A]GGGG	AGTGGTGC	76.43
+562	Motif 2 - [T/G]G[T/A]GGGG	TGGTGCGG	62.75
+563	Motif 2 - [T/G]G[T/A]GGGG	GGTGCGGC	80.18

+565	Motif 2 - [T/G]G[T/A]GGGG	TGCGGCCA	60.69
+566	Motif 3 - TCTCCCAA	GCGGCCAG	61.64
+570	Motif 1 - CTAGAGGT	CCAGGGCC	65.60
+570	Motif 2 - [T/G]G[T/A]GGGG	CCAGGGCC	60.31
+576	Motif 1 - CTAGAGGT	CCAGATGG	71.33
+578	Motif 2 - [T/G]G[T/A]GGGG	AGATGGGG	82.32
+579	Motif 2 - [T/G]G[T/A]GGGG	GATGGGGT	80.18
+581	Motif 2 - [T/G]G[T/A]GGGG	TGGGGTCC	60.69
+584	Motif 3 - TCTCCCAA	GGTCCCAC	80.25
+586	Motif 3 - TCTCCCAA	TCCCACAG	69.03
+590	Motif 1 - CTAGAGGT	ACAGAGCA	72.40
+599	Motif 3 - TCTCCCAA	GCTCCTTG	67.56
+614	Motif 3 - TCTCCCAA	GCTGCCTT	64.38
+630	Motif 1 - CTAGAGGT	CTTGTGGC	62.30
+632	Motif 2 - [T/G]G[T/A]GGGG	TGTGGCTG	71.20
+665	Motif 1 - CTAGAGGT	CTACTGGT	67.50
+668	Motif 1 - CTAGAGGT	CTGGTGGC	62.30
+669	Motif 2 - [T/G]G[T/A]GGGG	TGGTGGCG	69.63
+670	Motif 2 - [T/G]G[T/A]GGGG	GGTGGCGG	80.18
+672	Motif 2 - [T/G]G[T/A]GGGG	TGGCGGAG	61.64
+673	Motif 2 - [T/G]G[T/A]GGGG	GGCGGAGG	67.64
+674	Motif 1 - CTAGAGGT	GCGGAGGA	63.13
+676	Motif 2 - [T/G]G[T/A]GGGG	GGAGGAAG	66.30
+690	Motif 2 - [T/G]G[T/A]GGGG	GGTGAGTT	68.12

ESS decamers from Wang et al.

Wang Z, Rolish ME, Yeo G, Tung V, Mawson M, Burge CB. Systematic identification and analysis of exonic splicing silencers. Cell. 2004 Dec 17;119(6):831-45

Sequence Position	cDNA Position	Silencer motif
210	+210	GGTAAGTGTA

Predicted PESS Octamers from Zhang & Chasin.

Zhang XH, Chasin LA. Computational definition of sequence motifs governing constitutive exon splicing. Genes Dev. 2004 Jun 1;18(11):1241-50

Sequence Position	cDNA Position	Silencer motif	Motif value (0-100)
68	+68	GATGGGTG	26.14
97	+97	GGGGATGG	33.2
375	+375	CCGGGGGG	2.24
493	+493	CAGGCTGG	3.81
533	+533	AGATGGTG	32.13