

Ejemplo comparación de resultados predictores in silico

Cambio de estudio TP53 c.1024C>T (chr17:7670685 C/T, COSV52665487o NM_000546.6: c.1024C>T)

Exón 10 e intrones adyacentes:

```
cctgtagtccdagctactcgggaggctgaggcacaagaatcacttgaaaccagaggcgg  
agattgcaatcagccaagattgcaccattgcactcccgctgggaacagagtgagacc  
catctcaaaaataaataaataaataatttttaaaagtcagctgtataggtaattgaagtga  
gtttctactaaatgcattgttgettttgtacggtcataaagtcaaacattgttaaattga  
ccatcttttaactcagggtactgtgtataacttacttctccccctcctctgttgctgcag  
ATCCGTGGGCGTGAGCGCTTCGAGATGTTCCGAGAGCTGAATGAGCCCTTGGAACCAAG  
GATGCCCAGGCTGGGAAGGAGCCAGCGGGAGCAGGGCTCACTCCAG  
gtgagtgacctcagcccccttcctggccctactccctgccttcctcagggttgaaagccat  
aggattccattctcatctctgccttcattggtcaaaggcagctgaccccatctcatctgggtc  
ccagccctgcaagacatttttttagtcttcctccggttgaaatctataaccaattctt  
gcctcagtgatccacagaacatcacaacccaggggacgagtggtggatacttctttgcat  
tctcgcgaactcccagcccagagctggagggtctcaaggagggtcctaataattgtgtaa
```

El cambio se encuentra en la primera línea del exón 10 (la **c** en color rojo).

Se va a obtener los resultados que produce analizar esta variable con los diferente predictores y ver cuál de ellos es más preciso.

NetGene2

Donor splice sites, direct strand

| pos 5'→3' | phase | strand | confidence | 5' | exon | intron | 3' |
|-----------|-------|--------|------------|------------|------|------------|----|
| 408 | 2 | + | 0.93 | CTCACTCCAG | ^ | GTGAGTGACC | H |

Donor splice sites, complement strand

| pos 3'→5' | pos 5'→3' | phase | strand | confidence | 5' | exon | intron | 3' |
|-----------|-----------|-------|--------|------------|------------|------|------------|----|
| 275 | 433 | 0 | - | 0.93 | AGGGGGAGAA | ^ | GTAAGTATAT | H |

Acceptor splice sites, direct strand

| pos 5'→3' | phase | strand | confidence | 5' | intron | exon | 3' |
|-----------|-------|--------|------------|------------|--------|------------|----|
| 256 | 1 | + | 0.43 | TTTAACTCAG | ^ | GTACTGTGTA | |
| 300 | 0 | + | 1.00 | GTTGCTGCAG | ^ | ATCCGTGGGC | H |
| 315 | 0 | + | 0.19 | TGGGCGTGAG | ^ | CGCTTCGAGA | |
| 324 | 0 | + | 0.07 | GCGCTTCGAG | ^ | ATGTTCCGAG | |
| 454 | 1 | + | 0.53 | GCCTTCCTAG | ^ | GTTGGAAAGC | |
| 605 | 2 | + | 0.16 | GTATCCACAG | ^ | AACATCCAAA | |

Acceptor splice sites, complement strand

| pos 3'→5' | pos 5'→3' | phase | strand | confidence | 5' | intron | exon | 3' |
|-----------|-----------|-------|--------|------------|------------|--------|------------|----|
| 451 | 257 | 2 | - | 0.17 | TCCAACCTAG | ^ | GAAGGCAGGG | |
| 371 | 337 | 2 | - | 0.67 | TCCTTCCCAG | ^ | CCTGGGCATC | |
| 355 | 353 | 2 | - | 0.18 | CATCCTTGAG | ^ | TTCCAAGGCC | |
| 348 | 360 | 0 | - | 0.18 | GAGTTCCAAG | ^ | GCCTCATTCA | |
| 337 | 371 | 2 | - | 0.17 | CCTCATTGAG | ^ | CTCTCGGAAC | |

Donor splice sites, direct strand

| pos 5'→3' | phase | strand | confidence | 5' | exon | intron | 3' |
|-----------|-------|--------|------------|------------|------|------------|----|
| 408 | 2 | + | 0.86 | CTCACTCCAG | ^ | GTGAGTGACC | |

Donor splice sites, complement strand

| pos 3'→5' | pos 5'→3' | phase | strand | confidence | 5' | exon | intron | 3' |
|-----------|-----------|-------|--------|------------|------------|------|------------|----|
| 275 | 433 | 0 | - | 0.93 | AGGGGGAGAA | ^ | GTAAGTATAT | H |

Acceptor splice sites, direct strand

| pos 5'→3' | phase | strand | confidence | 5' | intron | exon | 3' |
|-----------|-------|--------|------------|------------|--------|------------|----|
| 256 | 1 | + | 0.33 | TTTAACTCAG | ^ | GTACTGTGTA | |
| 300 | 0 | + | 1.00 | GTTGCTGCAG | ^ | ATCCGTGGGC | H |
| 315 | 0 | + | 0.20 | TGGGCGTGAG | ^ | CGCTTCGAGA | |
| 324 | 0 | + | 0.07 | GCGCTTCGAG | ^ | ATGTTCTGAG | |
| 454 | 1 | + | 0.53 | GCCTTCCTAG | ^ | GTTGGAAAGC | |
| 605 | 2 | + | 0.16 | GTATCCACAG | ^ | AACATCCAAA | |

Acceptor splice sites, complement strand

| pos 3'→5' | pos 5'→3' | phase | strand | confidence | 5' | intron | exon | 3' |
|-----------|-----------|-------|--------|------------|------------|--------|------------|----|
| 451 | 257 | 2 | - | 0.17 | TCCAACCTAG | ^ | GAAGGCAGGG | |
| 371 | 337 | 2 | - | 0.51 | TCCTTCCCAG | ^ | CCTGGGCATC | |
| 355 | 353 | 2 | - | 0.17 | CATCCTTGAG | ^ | TTCCAAGGCC | |
| 348 | 360 | 0 | - | 0.18 | GAGTTCCAAG | ^ | GCCTCATTCA | |
| 337 | 371 | 2 | - | 0.17 | CCTCATTGAG | ^ | CTCTCAGAAC | |
| 330 | 378 | 0 | - | 0.19 | CAGCTCTCAG | ^ | AACATCTCGA | |

Aparece un nuevo sitio *acceptor* en la secuencia mutante. Si se empleara este en vez del normal, se perderían 39 nt del exón.

Splice Site Prediction by Neural Network (NNSplice)

Donor site predictions for 85.53.81.31.8031.0 :

| Start | End | Score | Exon | Intron |
|-------|-----|-------|---------|------------------|
| 105 | 119 | 0.53 | caacaga | gt gagacc |
| 160 | 174 | 0.76 | tgtatag | gt acttga |
| 250 | 264 | 0.90 | aactcag | gt actgtg |
| 401 | 415 | 1.00 | actccag | gt gagtga |

Donor site predictions for 85.53.81.31.8053.0 :

| Start | End | Score | Exon | Intron |
|-------|-----|-------|---------|------------------|
| 105 | 119 | 0.53 | caacaga | gt gagacc |
| 160 | 174 | 0.76 | tgtatag | gt acttga |
| 250 | 264 | 0.90 | aactcag | gt actgtg |
| 401 | 415 | 1.00 | actccag | gt gagtga |

Acceptor site predictions for 85.53.81.31.8031.0 :

| Start | End | Score | Intron | Exon |
|-------|-----|-------|----------------------|--------------------------------|
| 236 | 276 | 0.73 | ttgaaccatcttttaactc | ag gtactgtgtatatacttact |
| 280 | 320 | 0.96 | ccccctcctctgttgctgc | ag atccgtgggcgtgagcgctt |
| 434 | 474 | 0.98 | cctactcccctgccttcct | ag gttggaaagccataggattc |
| 585 | 625 | 0.49 | cttgccctcagtgtatccac | ag aacatccaaaccaggagcg |

Acceptor site predictions for 85.53.81.31.8053.0 :

| Start | End | Score | Intron | Exon |
|-------|-----|-------|----------------------|--------------------------------|
| 236 | 276 | 0.73 | ttgaaccatcttttaactc | ag gtactgtgtatatacttact |
| 280 | 320 | 0.96 | ccccctcctctgttgctgc | ag atccgtgggcgtgagcgctt |
| 434 | 474 | 0.98 | cctactcccctgccttcct | ag gttggaaagccataggattc |
| 585 | 625 | 0.49 | cttgccctcagtgtatccac | ag aacatccaaaccaggagcg |

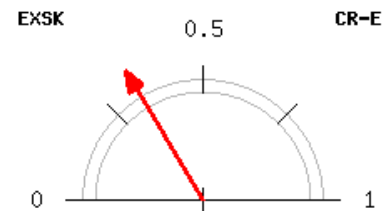
Spliceman

| Point mutation | Wildtype (wt) | Mutation (mt) | L1 distance | Ranking (L1) |
|-----------------|---------------|---------------|-------------|--------------|
| tgttc(c/t)gagag | ttccga | ttctga | 31375 | 83% |

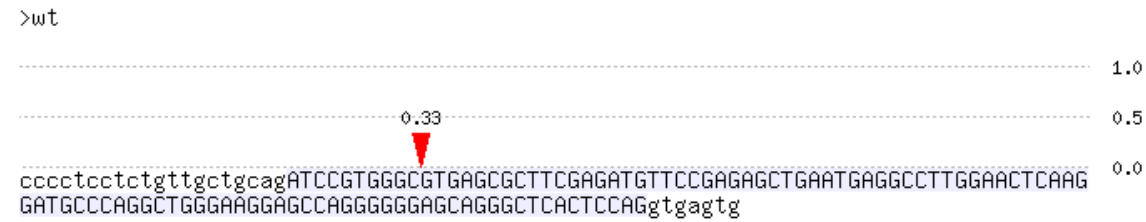
CRYP-SKIP

Results for sequence wt

| | |
|--|--------|
| Exon length (bp) | 107 |
| PESS (≤ -2.62) density | 0.00 |
| NN 5'ss score density | 0.05 |
| SF2/ASF score density | 8.11 |
| FAS-ESS (hex2) density | 5.61 |
| EIE score density | 364.52 |
| Probability of cryptic splice site activation (P_{CR-E}) | 0.33 |



Parece que hay un sitio críptico de *splicing* dentro del propio exón, pero el cambio de interés no lo toma en consideración, por lo que no debe considerar que tenga algún efecto en el *splicing*.



Human Splicing Finder

| Type | ↑↓ | Interpretation | ↑↓ |
|------|--|--|----|
| | No significant impact on splicing signals. | No significant impact on splicing signals. | |

| seq_id | agez | ss_dist | bpeq | bp_scr | y_cont | ppt_off | ppt_len | ppt_scr | svm_scr | | | |
|--------|------|---------|-----------|--------|------------------|---------|----------------|---------|---------|------------|------------|--|
| wt | 39 | 195 | gcgtgagcg | | 0.0665569413265 | | 0.50263157895 | 102 | 37 | 60 | -5.3064548 | |
| wt | 39 | 169 | agctgaagt | | 0.6549809828792 | | 0.512195121951 | 76 | 37 | 60 | -3.4280638 | |
| wt | 39 | 143 | gaatgagcg | | -1.146357913713 | | 0.51875 72 | 37 | 60 | -3.8769748 | | |
| wt | 39 | 151 | aactgaagg | | -0.6515038326258 | | 0.520547945205 | 58 | 37 | 60 | -2.7975469 | |
| wt | 39 | 108 | ggctcactc | | 1.92343889622 | | 0.621359223301 | 15 | 37 | 60 | 0.9650518 | |
| wt | 39 | 98 | agctgagtg | | -0.804796826506 | | 0.634408802151 | 5 | 37 | 60 | 0.53401634 | |
| wt | 39 | 94 | gagtgacct | | 2.14773755094 | | 0.651685393258 | 1 | 37 | 60 | 1.9488463 | |
| wt | 39 | 89 | acctgacct | | 0.174971006769 | | 0.642857142857 | 2 | 31 | 55 | 1.0636861 | |
| wt | 39 | 27 | ctctcatcc | | 0.982359041544 | | 0.596909090909 | 1 | 12 | 21 | 1.1095986 | |
| wt | 39 | 16 | ttctcatgg | | 0.02323227581103 | | 0.369363636364 | 11 | 0 | 0 | -0.1679278 | |

Aparece un nuevo BP, pero tiene una puntuación muy negativo, por lo que no lo tendremos en cuenta.

| | | | | | | | | | | | | | | | | |
|-----------------------------|------------------------------------|---|---|------|---------------------------------|------------|-----------------------------------|-------------------------|-------|------|-----|-----|-----|---------|---|---|
| ENST00000445888.6.c.1024C>T | 17-7670685-7670685 | A | 3_prime_UTR_variant | TP53 | ENSG00000141510 | Transcript | ENST00000610623.4 | protein_coding | 7/8 | 966 | - | - | - | - | - | rs730882029 CM004908 COSV52665487 |
| ENST00000445888.6.c.1024C>T | 17-7670685-7670685 | A | 3_prime_UTR_variant | TP53 | ENSG00000141510 | Transcript | ENST00000618944.4 | protein_coding | 7/8 | 1039 | - | - | - | - | - | rs730882029 CM004908 COSV52665487 |
| ENST00000445888.6.c.1024C>T | 17-7670685-7670685 | A | stop_gained | TP53 | ENSG00000141510 | Transcript | ENST00000619186.4 | protein_coding | 6/7 | 906 | 547 | 183 | R/* | CGA/TGA | - | rs730882029 CM004908 COSV52665487 |
| ENST00000445888.6.c.1024C>T | 17-7670685-7670685 | A | stop_gained | TP53 | ENSG00000141510 | Transcript | ENST00000619485.4 | protein_coding | 10/11 | 1160 | 907 | 303 | R/* | CGA/TGA | - | rs730882029 CM004908 COSV52665487 |
| ENST00000445888.6.c.1024C>T | 17-7670685-7670685 | A | stop_gained | TP53 | ENSG00000141510 | Transcript | ENST00000620739.4 | protein_coding | 10/11 | 1214 | 907 | 303 | R/* | CGA/TGA | - | rs730882029 CM004908 COSV52665487 |
| ENST00000445888.6.c.1024C>T | 17-7670685-7670685 | A | 3_prime_UTR_variant | TP53 | ENSG00000141510 | Transcript | ENST00000622645.4 | protein_coding | 11/12 | 1290 | - | - | - | - | - | rs730882029 CM004908 COSV52665487 |
| ENST00000445888.6.c.1024C>T | 17-7670685-7670685 | A | stop_gained NMD_transcript_variant | TP53 | ENSG00000141510 | Transcript | ENST00000635293.1 | nonsense_mediated_decay | 10/12 | 1167 | 907 | 303 | R/* | CGA/TGA | - | rs730882029 CM004908 COSV52665487 |

| | | | | | | | | | | | | | | | |
|-----------------------------|------------------------------------|---|-------------------------|------|---------------------------------|------------|------------------------------------|----------------------|-------|------|------|-----|-----|---------|---|
| ENST00000445888.6:c.1024C>T | 17-7670685-7670685 | A | stop_gained | TP53 | ENSG00000141510 | Transcript | ENST00000269305.9 | protein_coding | 10/11 | 1166 | 1024 | 342 | R/* | CGA/TGA | rs730882029 , CM004908 , COSV52665487 |
| ENST00000445888.6:c.1024C>T | 17-7670685-7670685 | A | intron_variant | TP53 | ENSG00000141510 | Transcript | ENST00000359597.8 | protein_coding | - | - | - | - | - | - | rs730882029 , CM004908 , COSV52665487 |
| ENST00000445888.6:c.1024C>T | 17-7670685-7670685 | A | intron_variant | TP53 | ENSG00000141510 | Transcript | ENST00000413465.6 | protein_coding | - | - | - | - | - | - | rs730882029 , CM004908 , COSV52665487 |
| ENST00000445888.6:c.1024C>T | 17-7670685-7670685 | A | 3_prime_UTR_variant | TP53 | ENSG00000141510 | Transcript | ENST00000420246.6 | protein_coding | 11/12 | 1290 | - | - | - | - | rs730882029 , CM004908 , COSV52665487 |
| ENST00000445888.6:c.1024C>T | 17-7670685-7670685 | A | stop_gained | TP53 | ENSG00000141510 | Transcript | ENST00000445888.6 | protein_coding | 10/11 | 1160 | 1024 | 342 | R/* | CGA/TGA | rs730882029 , CM004908 , COSV52665487 |
| ENST00000445888.6:c.1024C>T | 17-7670685-7670685 | A | 3_prime_UTR_variant | TP53 | ENSG00000141510 | Transcript | ENST00000455263.6 | protein_coding | 11/12 | 1217 | - | - | - | - | rs730882029 , CM004908 , COSV52665487 |
| ENST00000445888.6:c.1024C>T | 17-7670685-7670685 | A | downstream_gene_variant | TP53 | ENSG00000141510 | Transcript | ENST00000503591.1 | protein_coding | - | - | - | - | - | - | rs730882029 , CM004908 , COSV52665487 |
| ENST00000445888.6:c.1024C>T | 17-7670685-7670685 | A | 3_prime_UTR_variant | TP53 | ENSG00000141510 | Transcript | ENST00000504290.5 | protein_coding | 7/8 | 966 | - | - | - | - | rs730882029 , CM004908 , COSV52665487 |
| ENST00000445888.6:c.1024C>T | 17-7670685-7670685 | A | stop_gained | TP53 | ENSG00000141510 | Transcript | ENST00000504937.5 | protein_coding | 6/7 | 906 | 628 | 210 | R/* | CGA/TGA | rs730882029 , CM004908 , COSV52665487 |
| ENST00000445888.6:c.1024C>T | 17-7670685-7670685 | A | downstream_gene_variant | TP53 | ENSG00000141510 | Transcript | ENST00000505014.5 | retained_intron | - | - | - | - | - | - | rs730882029 , CM004908 , COSV52665487 |
| ENST00000445888.6:c.1024C>T | 17-7670685-7670685 | A | downstream_gene_variant | TP53 | ENSG00000141510 | Transcript | ENST00000508793.5 | protein_coding | - | - | - | - | - | - | rs730882029 , CM004908 , COSV52665487 |
| ENST00000445888.6:c.1024C>T | 17-7670685-7670685 | A | downstream_gene_variant | TP53 | ENSG00000141510 | Transcript | ENST00000509690.5 | protein_coding | - | - | - | - | - | - | rs730882029 , CM004908 , COSV52665487 |
| ENST00000445888.6:c.1024C>T | 17-7670685-7670685 | A | 3_prime_UTR_variant | TP53 | ENSG00000141510 | Transcript | ENST00000510385.5 | protein_coding | 7/8 | 1039 | - | - | - | - | rs730882029 , CM004908 , COSV52665487 |
| ENST00000445888.6:c.1024C>T | 17-7670685-7670685 | A | downstream_gene_variant | TP53 | ENSG00000141510 | Transcript | ENST00000514944.5 | protein_coding | - | - | - | - | - | - | rs730882029 , CM004908 , COSV52665487 |
| ENST00000445888.6:c.1024C>T | 17-7670685-7670685 | A | downstream_gene_variant | TP53 | ENSG00000141510 | Transcript | ENST00000514684.1 | processed_transcript | - | - | - | - | - | - | rs730882029 , CM004908 , COSV52665487 |
| ENST00000445888.6:c.1024C>T | 17-7670685-7670685 | A | intron_variant | TP53 | ENSG00000141510 | Transcript | ENST000005176024.1 | protein_coding | - | - | - | - | - | - | rs730882029 , CM004908 , COSV52665487 |
| ENST00000445888.6:c.1024C>T | 17-7670685-7670685 | A | downstream_gene_variant | TP53 | ENSG00000141510 | Transcript | ENST00000604348.5 | protein_coding | - | - | - | - | - | - | rs730882029 , CM004908 , COSV52665487 |
| ENST00000445888.6:c.1024C>T | 17-7670685-7670685 | A | stop_gained | TP53 | ENSG00000141510 | Transcript | ENST00000610292.4 | protein_coding | 9/10 | 1274 | 907 | 303 | R/* | CGA/TGA | rs730882029 , CM004908 , COSV52665487 |
| ENST00000445888.6:c.1024C>T | 17-7670685-7670685 | A | 3_prime_UTR_variant | TP53 | ENSG00000141510 | Transcript | ENST00000610538.4 | protein_coding | 11/12 | 1217 | - | - | - | - | rs730882029 , CM004908 , COSV52665487 |

ESEfinder

Para los sitios de *splicing*, no aparece ningún resultado con la posición de interés que tenga puntuaciones positivas, ni tampoco los equivalentes en la secuencia mutante, por lo que no afecta a los sitios de *splicing*.

| | | | | | | | | | | | |
|---------------|---------|----------|---------------|---------|----------|---------------|----------|----------|---------------|---------|----------|
| 325 (-383) | ATGTTCC | -7.04382 | 325 (-383) | ATGTTCC | -5.09141 | 325 (-383) | ATGTTCCG | 0.10981 | 325 (-383) | ATGTTCC | -1.42468 |
| 326 (-382) | TGTTCCG | -4.87402 | 326 (-382) | TGTTCCG | -3.21801 | 326 (-382) | TGTTCCGA | 0.83234 | 326 (-382) | TGTTCCG | 0.02835 |
| 327 (-381) | GTTCCGA | 0.58569 | 327 (-381) | GTTCCGA | -0.40321 | 327 (-381) | GTTCCGAG | 3.29663 | 327 (-381) | GTTCCGA | -1.65798 |
| 328 (-380) | TTCGAG | -2.38611 | 328 (-380) | TTCGAG | -0.96415 | 328 (-380) | TTCGAGA | -1.19004 | 328 (-380) | TTCGAG | 0.49441 |
| 329 (-379) | TCCGAGA | -3.51916 | 329 (-379) | TCCGAGA | -2.01825 | 329 (-379) | TCCGAGAG | -2.74304 | 329 (-379) | TCCGAGA | -0.17721 |
| 330 (-378) | CCGAGAG | 0.70877 | 330 (-378) | CCGAGAG | 1.91666 | 330 (-378) | CCGAGAGC | -9.37330 | 330 (-378) | CCGAGAG | -1.33250 |
| 331 (-377) | CGAGAGC | -3.80709 | 331 (-377) | CGAGAGC | -1.12435 | 331 (-377) | CGAGAGCT | -3.57801 | 331 (-377) | CGAGAGC | 2.57920 |

| | | | | | | | | | | | |
|---------------|---------|----------|---------------|---------|----------|---------------|----------|----------|---------------|---------|----------|
| 325 (-383) | ATGTTCT | -5.19043 | 325 (-383) | ATGTTCT | -3.89471 | 325 (-383) | ATGTTCTG | 0.75425 | 325 (-383) | ATGTTCT | -2.96378 |
| 326 (-382) | TGTTCTG | -4.41632 | 326 (-382) | TGTTCTG | -3.11401 | 326 (-382) | TGTTCTGA | -0.89667 | 326 (-382) | TGTTCTG | -1.68857 |
| 327 (-381) | GTTCTGA | -1.93803 | 327 (-381) | GTTCTGA | -2.21500 | 327 (-381) | GTTCTGAG | 2.53739 | 327 (-381) | GTTCTGA | -0.16673 |
| 328 (-380) | TTCTGAG | -3.84343 | 328 (-380) | TTCTGAG | -2.21891 | 328 (-380) | TTCTGAGA | -1.42088 | 328 (-380) | TTCTGAG | -1.89023 |
| 329 (-379) | TCTGAGA | -5.82917 | 329 (-379) | TCTGAGA | -4.08711 | 329 (-379) | TCTGAGAG | -3.31197 | 329 (-379) | TCTGAGA | 1.17107 |
| 330 (-378) | CTGAGAG | 1.31170 | 330 (-378) | CTGAGAG | 2.16544 | 330 (-378) | CTGAGAGC | -7.98489 | 330 (-378) | CTGAGAG | -1.64456 |
| 331 (-377) | TGAGAGC | -6.75758 | 331 (-377) | TGAGAGC | -4.22940 | 331 (-377) | TGAGAGCT | -3.59914 | 331 (-377) | TGAGAGC | 2.93590 |

En cuanto a las ESE, los resultados no cambian mucho entre secuencias.

EX-SKIP

| Seq | PESS (count) | FAS-ESS hex2 (count) | FAS-ESS hex3 (count) | IIE (count) | IIE (sum) | NI-ESS trusted (count) | NI-ESS all (sum) | PESE (count) | RESCUE -ESE (count) | EIE (count) | EIE (sum) | NI-ESE trusted (count) | NI-ESE all (sum) | ESS (total) | ESE (total) | ESS/ESE (ratio) |
|-----|-----------------|----------------------------|----------------------------|----------------|--------------|------------------------------|------------------------|-----------------|---------------------------|----------------|--------------|------------------------------|------------------------|----------------|----------------|--------------------|
| wt | 0 | 6 | 5 | 21 | 245.4405 | 6 | -8.2198 | 4 | 7 | 35 | 376.7962 | 38 | 53.3183 | 38 | 84 | 0.45 |
| mut | 0 | 5 | 5 | 23 | 280.0633 | 5 | -8.0016 | 4 | 7 | 33 | 354.2475 | 39 | 54.5823 | 38 | 83 | 0.46 |

Allele mut has a higher chance of exon skipping than allele wt.

HOT-SKIP

| | | | | | | | | | | | | | | | | | | | | |
|-----|----|---|------------------|--------------|---|---|---|---|---------|---|---------|---|---|---|---------|---|--------|---|---|------|
| 117 | 31 | C | GATGTTCCGAGAGCT | TGTTCCGAGAG | 0 | 2 | 1 | 1 | 7.4238 | 2 | -1.9999 | 0 | 0 | 2 | 22.5487 | 1 | 1.8161 | 6 | 3 | 2.00 |
| 118 | 31 | A | GATGTTCCAGAGAGCT | TGTTCCAGAGAG | 0 | 0 | 0 | 1 | 8.6203 | 1 | -0.9999 | 1 | 1 | 2 | 23.1995 | 3 | 4.1370 | 2 | 7 | 0.29 |
| 119 | 31 | T | GATGTTCTGAGAGCT | TGTTCTGAGAG | 0 | 1 | 1 | 3 | 42.0465 | 1 | -1.7817 | 0 | 0 | 0 | 0.0000 | 2 | 3.0801 | 6 | 2 | 3.00 |
| 120 | 31 | G | GATGTTCCGAGAGCT | TGTTCCGAGAG | 0 | 0 | 0 | 0 | 0.0000 | 0 | -1.5335 | 0 | 0 | 3 | 23.8134 | 2 | 2.7246 | 0 | 5 | 0.00 |