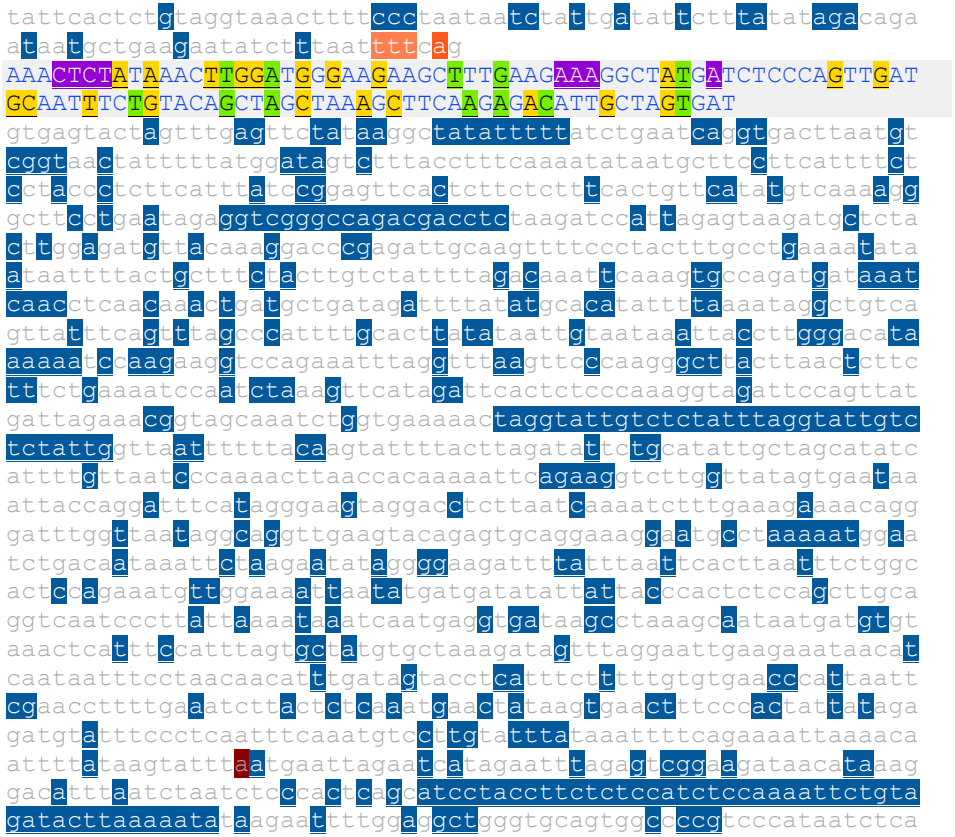
**Ejemplo comparación de resultados predictores in sillico**

Cambio de estudio NEB c.6915+1336A>G (chr 2:151652656 A/G,  NM_001164507.2: c.6915+1336A>G)

Exón 50 e intrones adyacentes:



El cambio se encuentra en la antepenúltima línea del intrón 50 (la **a** en color granate).

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' |
|---|---|---|---|---|
| 199 | 0 | + | 0.91 | TGCTAGTGAT^GTGAGTACTA H |
| 834 | 1 | + | 0.31 | GAAAAACTAG^GTATTGTCTC |

Donor splice sites, complement strand

| pos 3'->5' | pos 5'->3' | phase | strand | confidence | 5' exon intron 3' |
|---|---|---|---|---|---|
| 1612 | 87 | 0 | - | 0.00 | TGGAGAGAAG^GTAGGATGCT |
| 1368 | 331 | 2 | - | 0.35 | AAGAAATGAG^GTACTATCAA |
| 728 | 971 | 1 | - | 0.54 | GAAGAGTTAA^GTAAGCCCTT |
| 667 | 1032 | 0 | - | 0.37 | ATGTCCCAAG^GTAATTTATT |
| 323 | 1376 | 1 | - | 0.39 | AATGAAGAGG^GTAGGAGAAA |
| 287 | 1412 | 1 | - | 0.37 | ATTTTGAAAG^GTAAAGACTA |

Acceptor splice sites, direct strand

| pos 5'->3' | phase | strand | confidence | 5' intron exon 3' |
|---|---|---|---|---|
| 115 | 1 | + | 0.07 | GGATGGGAAG^AAGCTTTGAA |
| 531 | 0 | + | 0.57 | TCTATTTTAG^ACAAATTCAA |
| 850 | 0 | + | 0.33 | CTCTATTTAG^GTATTGTCTC |

Acceptor splice sites, complement strand

| pos 3'->5' | pos 5'->3' | phase | strand | confidence | 5' intron exon 3' |
|---|---|---|---|---|---|
| 1022 | 677 | 1 | - | 0.53 | TCTTTCAAAG^ATTTTGATTA |
| 819 | 880 | 1 | - | 0.17 | TTTTCACCAG^ATTTGCTACC |
| 488 | 1211 | 2 | - | 0.33 | ATATTTTCAG^GCAAAGTAGG |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**Splice Site Prediction by Neural Network (NNSplice)**

## Donor site predictions for 10.42.0.139.574515.0 :

| Start | End | Score | Exon | Intron |
|---|---|---|---|---|
| 192 | 206 | 0.95 | tagtgat | gtgagtac |
| 240 | 254 | 0.64 | gaatcag | gtgactta |
| 254 | 268 | 0.96 | aatgtcg | gtaactat |
| 419 | 433 | 0.81 | cattaga | gtaagatg |
| 777 | 791 | 0.91 | cccaaag | gtagattc |
| 1243 | 1257 | 0.58 | caatgag | gtgataag |

## Acceptor site predictions for 10.42.0.139.574515.0 :

| Start | End | Score | Intron | Exon |
|---|---|---|---|---|
| 35 | 75 | 0.92 | ctattgatattctttatat | agacagaataatgctgaagaat |
| 226 | 266 | 0.51 | ctatatttttatctgaatc | aggtgacttaatgtcggtaact |
| 511 | 551 | 0.99 | ctttctacttgtctattttt | agacaaattcaaagtgccagat |
| 830 | 870 | 0.89 | ctaggtattgtctctatttt | aggtattgtctctattggttaa |
| 1145 | 1185 | 0.57 | acttaatttctggcactcc | aaaatgttggaaaattaatat |
| 1199 | 1239 | 0.75 | tacccactctccagcttgc | aggtcaatcccttattaaaata |
| 1437 | 1477 | 0.48 | tgaactttcccactattat | agagatgtatttccctcaattt |

## Donor site predictions for 10.42.1.119.574527.0 :

| Start | End | Score | Exon | Intron |
|---|---|---|---|---|
| 192 | 206 | 0.95 | tagtgat | gtgagtac |
| 240 | 254 | 0.64 | gaatcag | gtgactta |
| 254 | 268 | 0.96 | aatgtcg | gtaactat |
| 419 | 433 | 0.81 | cattaga | gtaagatg |
| 777 | 791 | 0.91 | cccaaag | gtagattc |
| 1243 | 1257 | 0.58 | caatgag | gtgataag |

## Acceptor site predictions for 10.42.1.119.574527.0 :

| Start | End | Score | Intron | Exon |
|---|---|---|---|---|
| 35 | 75 | 0.92 | ctattgatattctttatat | agacagaataatgctgaagaat |
| 226 | 266 | 0.51 | ctatatttttatctgaatc | aggtgacttaatgtcggtaact |
| 511 | 551 | 0.99 | ctttctacttgtctattttt | agacaaattcaaagtgccagat |
| 830 | 870 | 0.89 | ctaggtattgtctctatttt | aggtattgtctctattggttaa |
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| 1199 | 1239 | 0.75 | tacccactctccagcttgc | aggtcaatcccttattaaaata |
| 1437 | 1477 | 0.48 | tgaactttcccactattat | agagatgtatttccctcaattt |

## Spliceman

| Point mutation | Wildtype (wt) | Mutation (mt) | L1 distance | Ranking (L1) |
|---|---|---|---|---|
| tattt(a/g)atgaa | tttaat | tttgat | 29966 | 74% |

## Human Splicing Finder

| Alteration of auxiliary sequences | Significant alteration of ESE / ESS motifs ratio (3) |
|---|---|

| Algorithm/Matix | position | sequence |
|---|---|---|
| ESS_hnRNPA1 (ESS Site Broken) | chr2:151652657 | TAATGA |
| RESCUE ESE (New ESE Site) | chr2:151652657 | TGATGA |
| IIE (New ESS Site) | chr2:151652657 | TGATGA |
| Sironi_motif2 (New ESS Site) | chr2:151652657 | TGATGAA |
| PESS (ESS Site Broken) | chr2:151652657 | TAATGAAT |
| PESS (ESS Site Broken) | chr2:151652659 | TTTAATGA |
| EIE (New ESE Site) | chr2:151652660 | ATTTGA |
| IIE (New ESS Site) | chr2:151652660 | ATTTGA |
| PESS (ESS Site Broken) | chr2:151652661 | TATTTAAT |

## SVM-BPfinder

| seq_id | agez | ss_dist | bp_seq | bp_scr | y_cont | ppt_off | ppt_len | ppt_scr | svm_scr |
|---|---|---|---|---|---|---|---|---|---|
| wt | 15 | 78 | ttttcagaa | -2.70211898349 | 0.356164383562 | 15 | 6 | 13 | -1.3695675 |
| wt | 15 | 70 | aaattaaaa | -3.55055560732 | 0.369230769231 | 7 | 6 | 13 | -1.191164 |
| wt | 15 | 69 | aattaaaac | -0.709023521857 | 0.375 | 6 | 6 | 13 | -0.01340828 |
| wt | 15 | 59 | attttataa | -4.94195942364 | 0.351851851852 | 54 | 0 | 0 | -4.8377043 |
| wt | 15 | 56 | ttataagta | -2.02610137058 | 0.352941176471 | 51 | 0 | 0 | -3.5057613 |
| wt | 15 | 49 | tatttaatg | -3.20745702824 | 0.318181818182 | 44 | 0 | 0 | -3.5364559 |
| wt | 15 | 48 | atttaatga | -0.706554062214 | 0.325581395349 | 43 | 0 | 0 | -2.491546 |
| wt | 15 | 45 | taatgaatt | -1.02793661227 | 0.325 | 40 | 0 | 0 | -2.4276752 |
| wt | 15 | 41 | gaattagaa | -3.43859928475 | 0.305555555556 | 36 | 0 | 0 | -3.1246504 |
| wt | 15 | 35 | gaatcatag | -1.77467332989 | 0.3 | 30 | 0 | 0 | -2.095149 |
| wt | 15 | 26 | aatttagag | -4.39996390828 | 0.238095238095 | 21 | 0 | 0 | -2.5733829 |
| mut | 15 | 78 | ttttcagaa | -2.70211898349 | 0.356164383562 | 15 | 6 | 13 | -1.3695675 |
| mut | 15 | 70 | aaattaaaa | -3.55055560732 | 0.369230769231 | 7 | 6 | 13 | -1.191164 |
| mut | 15 | 69 | aattaaaac | -0.709023521857 | 0.375 | 6 | 6 | 13 | -0.01340828 |
| mut | 15 | 59 | attttataa | -4.94195942364 | 0.351851851852 | 54 | 0 | 0 | -4.8377043 |
| mut | 15 | 56 | ttataagta | -2.02610137058 | 0.352941176471 | 51 | 0 | 0 | -3.5057613 |
| mut | 15 | 48 | atttgatga | -0.70062753547 | 0.325581395349 | 43 | 0 | 0 | -2.4892255 |
| mut | 15 | 45 | tgatgaatt | -1.37180623181 | 0.325 | 40 | 0 | 0 | -2.5623165 |
| mut | 15 | 41 | gaattagaa | -3.43859928475 | 0.305555555556 | 36 | 0 | 0 | -3.1246504 |
| mut | 15 | 35 | gaatcatag | -1.77467332989 | 0.3 | 30 | 0 | 0 | -2.095149 |
| mut | 15 | 26 | aatttagag | -4.39996390828 | 0.238095238095 | 21 | 0 | 0 | -2.5733829 |

Desaparece uno de los BP (49) mientras que los otros cambian a raíz de la presencia de la mutación (48 y 45). Como todos tienen puntuaciones positivas, no se van a tener en cuenta.

## Variant Effect Predictor tool

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| ENST00000604864.5:c.6915+1336A>G | 2:151652656-151652656 | C | intron_variant | NEB | ENSG00000183091 | Transcript | ENST00000172853.14 | protein_coding | - |
| ENST00000604864.5:c.6915+1336A>G | 2:151652656-151652656 | C | intron_variant | NEB | ENSG00000183091 | Transcript | ENST00000397345.7 | protein_coding | - |
| ENST00000604864.5:c.6915+1336A>G | 2:151652656-151652656 | C | intron_variant | NEB | ENSG00000183091 | Transcript | ENST00000409198.5 | protein_coding | - |
| ENST00000604864.5:c.6915+1336A>G | 2:151652656-151652656 | C | intron_variant | NEB | ENSG00000183091 | Transcript | ENST00000427231.6 | protein_coding | - |
| ENST00000604864.5:c.6915+1336A>G | 2:151652656-151652656 | C | intron_variant | NEB | ENSG00000183091 | Transcript | ENST00000603639.5 | protein_coding | - |
| ENST00000604864.5:c.6915+1336A>G | 2:151652656-151652656 | C | intron_variant | NEB | ENSG00000183091 | Transcript | ENST00000604864.5 | protein_coding | - |
| ENST00000604864.5:c.6915+1336A>G | 2:151652656-151652656 | C | intron_variant | NEB | ENSG00000183091 | Transcript | ENST00000618972.4 | protein_coding | - |

**ESEfinder**

No se obtienen puntuaciones positivas para ninguna predicción en ninguna de las secuencias.