**Ejemplo comparación de resultados predictores in sillico**

Cambio de estudio CPLANE1 c.938+1393T>A (chr5:37237464 T/A,  COSV57073620 o NM_001384732.1: c.938+1393T>A)

Exón 7 e intrones adyacentes:

```
tataataatagatctctgtgtcaccagaattataaataatggttacagtaaaataattt
aatagttttcttgtcttttttttcctttctag
GCAACTCAGGTATTATTTATAAACACACTGAATTTTGTTACTCTCTGTGGTAGCCTTAAA
GGATGTAGTAACAAGAGTCCCGTGGTTCCAGCTACACTTATTAG
gtaagaactcttttgtctgtctttttttttctttttttttcttttaaaagagatgggtctctg
tcaggtgtggtagctcacacctgtaattctagcactttgggaaaccaaggtgagaggatc
acttgagctcaggagtttgagaccagcttgggcaacataatgagacctcatcttactaa
aaaataaaagaaattagccgagcatggtggtggacacctgtagtcccagctacttgaga
ggctgagctaggggtatcacctgaacgtgggtgatagaggctgcagtgagctatgatct
tgccactgcactccagtctgagcaacagagcaagacccatctcaaaaaaaaaaaaaaaa
aaaaaaaagaaaggctgggcgctgtggctcacgcctgtaatcccagcactttgggagg
ctgaggtaggtggatcacctgaggtcaggagtttgagaccagcctggccaaaatggtgaa
accccatctctactaaaaaaaatacaaaaaaaaaaaattagccaagtgtggtggcatgtt
cctgtagtcccagctacttgggaggttgaggcataagaattgcttgaacccaggaggcgg
aggttgccatgagctgagatcgcactactgcactccagcctggatgacagagggagactc
tgtcacacacacaaaaaaagatggggtcttacttattgcccaagctggagtgtagtgg
tgtgatcatagctcactgcagcgttgaactctcggggctcagtcattccttcctcatcctt
ctgagtagctggggactacaggtgtgtgtcactgtatgtagctaatttttttaaagttttt
tgtagagacagggtcttgctatattgaccatgctggtcttgaacttctggccttaagtga
tcctcccatcttggcctcctaaagtgctgggattacaggcctgagccatcatgcccagcc
taaaagtcactttatataaggaaggccttaaatactttttttttttttgagatggagtctc
actctgtcacccaggctggagtgcagtggtgtgatctcggctaactgcaagctctgcctc
ccgggctcacgccattctcctgcctcagcctcccgcgtagctgggattaaaggcgcccgt
caccatgcccggataattttttttgtatttttttttagtagagatgggggtttcaccgtgtta
gccaggatggtctcaatctcctgacctcgtgatccactcgccttggcctcccaaagtgct
cggattacaggcgtaagccaccgtgcctggccataggtgcatatttcttacatgcatatg
ttgtgtagtggtgaagtgtgggcttttagtattaatagtgaacattgtacccaacagata
atttttcaacccacactcccctccgtctttagtagtctccaatgcctattattccact
ctgtatgtcatgtgtaccccattgtttagtccctactataagttagaatatgtagtatt
tgacttctgtttctgagtgatttttacctaggataatgacctcagttccatccatgtta
```

El cambio se encuentra en segunda posición justo antes del exón 7 (la **t** en color rojo subrayada de azul).

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                              Donor splice sites, direct strand
---------------------------------                              ---------------------------------
        pos 5'->3'  phase strand  confidence  5'     exon intron    3'          pos 5'->3'  phase strand  confidence  5'     exon intron    3'
        102         1      +       0.32      GGCAACTCAG^GTATTATTTA           102         1      +       0.32      GGCAACTCAG^GTATTATTTA
        197         2      +       0.47      CACTTATTAG^GTAAGAACTC           197         2      +       0.47      CACTTATTAG^GTAAGAACTC
        306         1      +       0.54      GGAAACCAAG^GTGAGAGGAT           306         1      +       0.54      GGAAACCAAG^GTGAGAGGAT
        622         0      +       0.41      GGAGGCTGAG^GTAGGTGGAT           622         0      +       0.41      GGAGGCTGAG^GTAGGTGGAT
        997         2      +       0.46      GGGACTACAG^GTGTGTGTCA           997         2      +       0.46      GGGACTACAG^GTGTGTGTCA

Donor splice sites, complement strand                          Donor splice sites, complement strand
---------------------------------                              ---------------------------------
   pos 3'->5'  pos 5'->3'  phase strand  confidence  5'    exon intron  3'     pos 3'->5'  pos 5'->3'  phase strand  confidence  5'    exon intron  3'
   890         867         0      -       0.46      TGGGCAATAA^GTAAGACCCC       890         867         0      -       0.46      TGGGCAATAA^GTAAGACCCC

Acceptor splice sites, direct strand                           Acceptor splice sites, direct strand
---------------------------------                              ---------------------------------
        pos 5'->3'  phase strand  confidence  5'   intron exon     3'          pos 5'->3'  phase strand  confidence  5'   intron exon     3'
        92          1      +       0.00      TCCTTTCTAG^GCAACTCAGG           92          1      +       0.00      TCCTTTCTAG^GCAACTCAGG

Acceptor splice sites, complement strand                       Acceptor splice sites, complement strand
---------------------------------                              ---------------------------------
   pos 3'->5'  pos 5'->3'  phase strand  confidence  5'    intron exon  3'     pos 3'->5'  pos 5'->3'  phase strand  confidence  5'    intron exon  3'
   147         1610        0      -       0.26      ATCCTTTAAG^GCTACCACAG       147         1610        0      -       0.26      ATCCTTTAAG^GCTACCACAG
```

# Splice Site Prediction by Neural Network (NNSplice)

## Donor site predictions for 10.42.3.123.574320.0 :

| Start | End | Score | Exon | Intron |
|-------|------|-------|------|--------|
| 95 | 109 | 0.89 | aactcag**gt**attatt | |
| 190 | 204 | 1.00 | ttattag**gt**aagaac | |
| 254 | 268 | 0.63 | ctgtcag**gt**gtggta | |
| 299 | 313 | 0.99 | aaccaag**gt**gagagg | |
| 615 | 629 | 0.94 | ggctgag**gt**aggtgg | |
| 633 | 647 | 0.66 | acctgag**gt**caggag | |
| 990 | 1004 | 0.95 | actacag**gt**gtgtgt | |
| 1002 | 1016 | 0.65 | tgtcact**gt**atgtag | |
| 1462 | 1476 | 0.92 | tacaggc**gt**aagcca | |
| 1486 | 1500 | 0.42 | gccatag**gt**gcatat | |
| 1632 | 1646 | 0.52 | ccactct**gt**atgtcc | |

## Donor site predictions for 10.42.0.139.5 /4332.0 :

## Acceptor site predictions for 10.42.3.123.574320.0 :

| Start | End | Score | Intron | Exon |
|-------|------|-------|--------|------|
| 72 | 112 | 0.99 | tgtctttttttttcctttct**ag**gcaactcaggtattatttat | |
| 223 | 263 | 0.97 | tttctttttttcttttaaa**ag**agatgggtctctgtcaggtg | |
| 964 | 1004 | 0.80 | cttcctcatccttctgagt**ag**ctgggactacaggtgtgtgt | |
| 1011 | 1051 | 0.64 | atgtagctaatttttttaa**ag**tttttgtagagacagggtc | |
| 1021 | 1061 | 0.82 | tttttttaaagtttttgt**ag**agacagggtcttgctatatt | |
| 1186 | 1226 | 0.74 | aaatactttttttttttg**ag**atggagtctcactctgtcac | |
| 1284 | 1324 | 0.88 | cacgccattctcctgcctc**ag**cctcccgcgtagctgggatt | |
| 1352 | 1392 | 0.98 | attttttgtattttttt**ag**tagagatggggtttcaccgt | |
| 1472 | 1512 | 0.81 | agccaccgtgcctggccat**ag**gtgcatatttcttacatgca | |
| 1590 | 1630 | 0.93 | cactccctcccgtctttt**ag**tagtctccaatgcctattat | |

## Acceptor site predictions for 10.42.0.139.574332.0 :

## Spliceman

| Point mutation | Wildtype (wt) | Mutation (mt) | L1 distance | Ranking (L1) |
|---|---|---|---|---|
| aaccc(t/a)cactc | cctcac | ccacac | 26763 | 54% |

## Human Splicing Finder

| 🔴 No significant impact on splicing signals. | No significant impact on splicing signals. |
|---|---|

## SVM-BPfinder

```
seq_id  agez    ss_dist bp_seq  bp_scr   y_cont   ppt_off ppt_len ppt_scr svm_scr
wt      30      74      tggtgaagt       -0.345123087746 0.579710144928  48      22      40      -2.2118104
wt      30      60      cttttagta       -4.47378177514 0.6      34      22      40      -2.9356458
wt      30      54      gtattaata       -3.66992421558  0.612244897959  28      22      40      -2.237153
wt      30      53      tattaatag       0.0984647972875 0.625   27      22      40      -0.69423271
wt      30      47      tagtgaaca       -0.389189961415 0.666666666667  21      22      40      -0.49192555
wt      30      27      agataattt       -1.66524815352  0.863636363636  1       22      40      0.33801921
wt      30      20      ttttcaacc       -1.09324308372  0.866666666667  2       14      27      0.37856061
mut     30      74      tggtgaagt       -0.345123087746 0.565217391304  48      22      35      -2.2630703
mut     30      60      cttttagta       -4.47378177514 0.581818181818  34      22      35      -2.9880972
mut     30      54      gtattaata       -3.66992421558  0.591836734694  28      22      35      -2.2903234
mut     30      53      tattaatag       0.0984647972875 0.604166666667  27      22      35      -0.74754048
mut     30      47      tagtgaaca       -0.389189961415 0.642857142857  21      22      35      -0.54619456
mut     30      27      agataattt       -1.66524815352  0.818181818182  1       22      35      0.27675949
mut     30      20      ttttcaacc       -1.09324308372  0.8      2       14      22      0.31045001
```

**Variant Effect Predictor tool**

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ENST00000508244.5:c.938+1393T>A | 5:37237464-37237464 | T | intron_variant, NMD_transcript_variant | CPLANE1 | ENSG00000197603 | Transcript | ENST00000425232.7 | nonsense_mediated_decay | - | - | COSV57073620 |
| ENST00000508244.5:c.938+1393T>A | 5:37237464-37237464 | T | intron_variant | CPLANE1 | ENSG00000197603 | Transcript | ENST00000508244.5 | protein_coding | - | - | COSV57073620 |
| ENST00000508244.5:c.938+1393T>A | 5:37237464-37237464 | T | intron_variant | CPLANE1 | ENSG00000197603 | Transcript | ENST00000651892.1 | protein_coding | - | - | COSV57073620 |
| ENST00000508244.5:c.938+1393T>A | 5:37237464-37237464 | T | intron_variant, non_coding_transcript_variant | CPLANE1 | ENSG00000197603 | Transcript | ENST00000675547.1 | processed_transcript | - | - | COSV57073620 |
| ENST00000508244.5:c.938+1393T>A | 5:37237464-37237464 | T | intron_variant, non_coding_transcript_variant | CPLANE1 | ENSG00000197603 | Transcript | ENST00000676290.1 | retained_intron | - | - | COSV57073620 |

**ESEfinder**

Solo se obtiene un resultado positivo para las matrices 5'SS. Pero las puntuaciones no se alteran en la secuencia mutante, por lo que no se tendrá en cuenta.

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| 1559 (-198) | cattgtacccaacagataatttttcaaccc | -1.87550 | 1559 (-198) | cattgtacccaacagataatttttcaaccc | 4.27160 | 1559 (-198) | cattgtacccaacagataatttttcaaccc | -2.44240 | 1559 (-198) | cattgtacccaacagataatttttcaaccc | 4.16710 |
| 1559 (-198) | cattgtacccaacagataatttttcaaccc | -1.87550 | 1559 (-198) | cattgtacccaacagataatttttcaaccc | 4.27160 | 1559 (-198) | cattgtacccaacagataatttttcaaccc | -2.44240 | 1559 (-198) | cattgtacccaacagataatttttcaaccc | 4.16710 |