Ejemplo comparación de resultados predictores in sillico
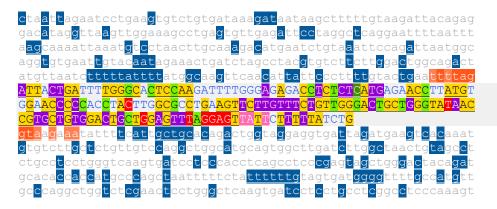
Cambio de estudio CHEK2 c.1116C>T (chr22:28695853 C/T, rs79357544 o NM_007194.4:c.1116C>T)

Exón 11 e intrones adyacentes:

```
ctaattagaatcctgaagtgtctgtgataaagataataagcttttttgtaagattacagag
gacataggttaagttggaaagcctgagtgttgagattcctaggctcaggaattttaattt
aagcaaaattaaatgtcctaacttgcaaagacatgaatctgtaaattccagattaatggc
aggtgtgaattgtacaatagaaactgatctagcctacgtgtcttcttggactggcagact
atgttaatcttttattttatggcaagttcaacattattcccttttgtactgaattttag
ATTACTGATTTGGGCACTCCAAGATTTGGGAGAGACCTCTCTCATGAGAACCTTATGT
GGAACCCCCACCTACTTGGCGCCTGAAGTTCTTGTTTCTGTTGGGACTGCTGGGTATAAC
CGTGCTGTGGACTGCTGGAGTTTAGGAGTTATTCTTTTTATCTG
gtaagaaatattttcattgctgcacagactggtaggaggtgattagatgaagtcacaaat
gtgtcttgctctgttgtccaggctggcatgcagtggcttgatcttggctaactgtagcct
ctgcctcctgggtcaagtgatcctcccacctcagcctccgagtagctgggactacagat
gcacaccaccatgcccagctaattttttctattttttgtagtgatggggttttgccatgtt
gcccaggctggtctcgaactcctgggctcaagtgatcctcctgcctcggcctcccaaagt
```

El cambio se encuentra en la primera fila del exón 7 (la segunda **c** en color verde).

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'
          465        2     +        0.44      TTTTTATCTG^GTAAGAAATA            465        2     +        0.44      TTTTTATCTG^GTAAGAAATA
          496        1     +        0.34      GCACAGACTG^GTAGGAGGTG            496        1     +        0.34      GCACAGACTG^GTAGGAGGTG

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'
    375         557         0     -        0.63      CAGGCGCCAA^GTAGGTGGGG       375         557         0     -        0.60      CAGGCGCCAA^GTAGGTGGGG
    371         561         1     -        0.59      CGCCAAGTAG^GTGGGGGTTC       371         561         1     -        0.55      CGCCAAGTAG^GTGGGGGTTC

Acceptor splice sites, direct strand                           Acceptor splice sites, direct strand
------------------------------------                           ------------------------------------
   No acceptor site predictions above threshold.                  No acceptor site predictions above threshold.

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'
    462         470         0     -        0.27      TTCTTACCAG^ATAAAAGAA       462         470         0     -        0.27      TTCTTACCAG^ATAAAAGAA
```

No cambios.

Splice Site Prediction by Neural Network (NNSplice)

Donor site predictions for 85.53.15.54.28126.0 :

Start	End	Score	Exon	Intron
176	190	0.64	atggcag**gt**gtgaat	
458	472	1.00	ttatctg**gt**aagaaa	
489	503	0.74	cagactg**gt**aggagg	

Donor site predictions for 85.53.15.54.27974.0 :

Start	End	Score	Exon	Intron
176	190	0.64	atggcag**gt**gtgaat	
458	472	1.00	ttatctg**gt**aagaaa	
489	503	0.74	cagactg**gt**aggagg	

Acceptor site predictions for 85.53.15.54.28126.0 :

Start	End	Score	Intron	Exon
280	320	0.81	cccttttgtactgaatttt**ag**attactgattttgggcactc	
525	565	0.53	gtgtcttgctctgttgtcc**ag**gctggcatgcagtggcttga	
598	638	0.46	caagtgatcctcccacctc**ag**cctcccgagtagctgggact	
664	704	0.98	taatttttctattttttgt**ag**tgatggggttttgccatgtt	

Acceptor site predictions for 85.53.15.54.27974.0 :

Start	End	Score	Intron	Exon
280	320	0.81	cccttttgtactgaatttt**ag**attactgattttgggcactc	
525	565	0.53	gtgtcttgctctgttgtcc**ag**gctggcatgcagtggcttga	
598	638	0.46	caagtgatcctcccacctc**ag**cctcccgagtagctgggact	
664	704	0.98	taatttttctattttttgt**ag**tgatggggttttgccatgtt	

No hay cambios.

Spliceman

Point mutation	Wildtype (wt)	Mutation (mt)	L1 distance	Ranking (L1)
cactc(c/t)aagat	actcca	actcta	28351	64%

CRYP-SKIP

Results for sequence wt

Exon length (bp)	164
PESS (<=-2.62) density	4.88
NN 5'ss score density	0.02
SF2/ASF score density	6.14
FAS-ESS (hex2) density	9.76
EIE score density	478.54
Probability of cryptic splice site activation (P_{CR-E})	0.10


```
>wt
cctttgtactgaattttagATTACTGATTTTGGGCACTCCAAGATTTTGGGAGAGACCTCTCTCATGAGAACCTTATGT
```



```
GGAACCCCCACCTACTTGGCGCCTGAAGTTCTTGTTTCTGTTGGGACTGCTGGGTATAACCGTGCTGTGGACTGCTGGAG
TTTAGGAGTTATTCTTTTTATCTGgtaagaa
```

No efecto.

Human Splicing Finder

Type	↑↓	Interpretation	↑↓
⊖ 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	33	484	ggctcagga	-1.05317020216	0.526096033403	112	9	20	-6.7437695
wt	33	475	atttttaatt	-4.8626284941	0.527659574468	103	9	20	-7.6651626
wt	33	474	tttttaattt	-0.995102413301	0.528784648188	102	9	20	-6.0871817
wt	33	470	aatttaagc	-3.75943326416	0.52688172043	98	9	20	-6.9169692
wt	33	469	atttaagca	-1.62647998171	0.528017241379	97	9	20	-6.0181521
wt	33	460	aaattaaat	-3.05381608375	0.531868131868	88	9	20	-6.006093
wt	33	459	aattaaatg	-0.734047569933	0.533039647577	87	9	20	-5.0341173
wt	33	450	tcctaactt	2.53660466385	0.532584269663	78	9	20	-3.1839646
wt	33	435	acatgaatc	-1.69367963902	0.537209302326	63	9	20	-3.8893522
wt	33	427	ctgtaaatt	-0.485796759865	0.537914691943	55	9	20	-2.9097946
wt	33	416	agattaatg	-3.29544668823	0.537712895377	44	9	20	-3.313689
wt	33	415	gattaatgg	0.90935737182	0.539024390244	43	9	20	-1.6035876
wt	33	403	gtgtgaatt	-0.955994067854	0.545226130653	31	9	20	-1.572378
wt	33	384	aactgatct	1.39746682692	0.554089709763	12	9	20	0.55464395
wt	33	345	atgttaatc	-3.32740454133	0.55	2	14	31	-0.56122983
wt	33	344	tgttaatct	0.741542252947	0.551622418879	1	14	31	1.0957775
wt	33	336	tttttattt	-4.34020649867	0.543806646526	1	6	13	-1.0641769
wt	33	331	attttatgg	-3.558387177	0.539877300613	15	14	29	-1.4964497
wt	33	320	agttcaaca	-1.5039769505	0.542857142857	4	14	29	0.0051929858
wt	33	314	acattattc	-3.24790672016	0.543689320388	1	11	25	-0.52473759
wt	33	298	tactgaatt	0.591670668885	0.532423208191	45	10	20	-1.8567056
wt	33	292	attttagat	-5.17290259882	0.529616724739	39	10	20	-3.7349249
wt	33	287	agattactg	-1.3389265645	0.531914893617	34	10	20	-1.9165083
wt	33	283	tactgattt	0.990758475835	0.532374100719	30	10	20	-0.75098487
wt	33	245	ctctcatga	0.97307688348	0.529166666667	19	13	21	-0.053346584
wt	33	242	tcatgagaa	-2.54842163591	0.53164556962	16	13	21	-1.2414841
wt	33	234	accttatgt	-1.15931800217	0.532751091703	8	13	21	-0.19084075
wt	33	205	gcctgaagt	0.65582503996	0.525	3	14	30	0.91770435
wt	33	172	gtataaccg	1.71913595622	0.520958083832	30	15	33	-0.3483717
wt	33	147	agtttagga	-5.285122617	0.521126760563	5	15	33	-1.5083574
wt	33	140	gagttattc	-2.8039058943	0.533333333333	1	12	29	-0.31697161
wt	33	131	tttttatct	-3.50785622612	0.507936507937	13	13	22	-1.4255946
wt	33	123	tggtaagaa	-1.09689641737	0.508474576271	5	13	22	0.024970455
wt	33	111	ttttcattg	-1.29807077245	0.509433962264	44	20	30	-2.4475967
wt	33	85	aggtgatta	-1.17766320873	0.55	18	20	30	-0.74159349
wt	33	82	tgattagat	-3.29528255368	0.545454545455	15	20	30	-1.3823147
wt	33	77	agatgaagt	-2.14921626834	0.569444444444	10	20	30	-0.60933585
wt	33	72	aagtcacaa	-1.69262394357	0.582089552239	5	20	30	-0.10998281
wt	33	26	gcttgatct	-0.023915899769	0.666666666667	21	0	0	-0.72153728
wt	33	16	ggctaactg	3.0387153898	0.727272727273	11	0	0	1.1301848

seq_id	agez	ss_dist	bp_seq	bp_scr	y_cont	ppt_off	ppt_len	ppt_scr	svm_scr
mut	33	484	ggctcagga	-1.05317020216	0.526096033403	112	9	20	-6.7437695
mut	33	475	atttttaatt	-4.8626284941	0.527659574468	103	9	20	-7.6651626
mut	33	474	tttttaattt	-0.995102413301	0.528784648188	102	9	20	-6.0871817
mut	33	470	aatttaagc	-3.75943326416	0.52688172043	98	9	20	-6.9169692
mut	33	469	atttaagca	-1.62647998171	0.528017241379	97	9	20	-6.0181521
mut	33	460	aaattaaat	-3.05381608375	0.531868131868	88	9	20	-6.006093
mut	33	459	aattaaatg	-0.734047569933	0.533039647577	87	9	20	-5.0341173
mut	33	450	tcctaactt	2.53660466385	0.532584269663	78	9	20	-3.1839646
mut	33	435	acatgaatc	-1.69367963902	0.537209302326	63	9	20	-3.8893522
mut	33	427	ctgtaaatt	-0.485796759865	0.537914691943	55	9	20	-2.9097946
mut	33	416	agattaatg	-3.29544668823	0.537712895377	44	9	20	-3.313689
mut	33	415	gattaatgg	0.90935737182	0.539024390244	43	9	20	-1.6035876
mut	33	403	gtgtgaatt	-0.955994067854	0.545226130653	31	9	20	-1.572378
mut	33	384	aactgatct	1.39746682692	0.554089709763	12	9	20	0.55464395
mut	33	345	atgttaatc	-3.32740454133	0.55	2	14	31	-0.56122983
mut	33	344	tgttaatct	0.741542252947	0.551622418879	1	14	31	1.0957775
mut	33	336	tttttattt	-4.34020649867	0.543806646526	1	6	13	-1.0641769
mut	33	331	attttatgg	-3.558387177	0.539877300613	15	14	29	-1.4964497
mut	33	320	agttcaaca	-1.5039769505	0.542857142857	4	14	29	0.0051929858
mut	33	314	acattattc	-3.24790672016	0.543689320388	1	11	25	-0.52473759
mut	33	298	tactgaatt	0.591670668885	0.532423208191	45	10	20	-1.8567056
mut	33	292	attttagat	-5.17290259882	0.529616724739	39	10	20	-3.7349249
mut	33	287	agattactg	-1.3389265645	0.531914893617	34	10	20	-1.9165083
mut	33	283	tactgattt	0.990758475835	0.532374100719	30	10	20	**-0.75098487**
mut	33	268	**ctctaagat**	0.293088363061	0.528517110266	15	10	20	-0.075926555
mut	33	245	ctctcatga	0.97307688348	0.529166666667	19	13	21	-0.053346584
mut	33	242	tcatgagaa	-2.54842163591	0.53164556962	16	13	21	-1.2414841
mut	33	234	accttatgt	-1.15931800217	0.532751091703	8	13	21	-0.19084075
mut	33	205	gcctgaagt	0.65582503996	0.525	3	14	30	0.91770435
mut	33	172	gtataaccg	1.71913595622	0.520958083832	30	15	33	-0.3483717
mut	33	147	agtttagga	-5.285122617	0.521126760563	5	15	33	-1.5083574
mut	33	140	gagttattc	-2.8039058943	0.533333333333	1	12	29	-0.31697161
mut	33	131	tttttatct	-3.50785622612	0.507936507937	13	13	22	-1.4255946
mut	33	123	tggtaagaa	-1.09689641737	0.508474576271	5	13	22	0.024970455
mut	33	111	ttttcattg	-1.29807077245	0.509433962264	44	20	30	-2.4475967
mut	33	85	aggtgatta	-1.17766320873	0.55	18	20	30	-0.74159349
mut	33	82	tgattagat	-3.29528255368	0.545454545455	15	20	30	-1.3823147
mut	33	77	agatgaagt	-2.14921626834	0.569444444444	10	20	30	-0.60933585
mut	33	72	aagtcacaa	-1.69262394357	0.582089552239	5	20	30	-0.10998281
mut	33	26	gcttgatct	-0.023915899769	0.666666666667	21	0	0	-0.72153728
mut	33	16	ggctaactg	3.0387153898	0.727272727273	11	0	0	1.1301848

Variant Effect Predictor tool

Uploaded variation	Location	Allele	Consequence	Symbol	Gene	Feature type	Feature	Biotype	Exon	cDNA position	CDS position	Protein position	Amino acids	Codons	Existing variation
ENST00000404276.6:c.1116C>T	22:28695853-28695853	A	synonymous_variant	CHEK2	ENSG00000183765	Transcript	ENST00000348295.7	protein_coding	10/14	1101	1029	343	S	TCC/TCT	rs79357544
ENST00000404276.6:c.1116C>T	22:28695853-28695853	A	synonymous_variant	CHEK2	ENSG00000183765	Transcript	ENST00000382580.6	protein_coding	12/16	1321	1245	415	S	TCC/TCT	rs79357544
ENST00000404276.6:c.1116C>T	22:28695853-28695853	A	synonymous_variant	CHEK2	ENSG00000183765	Transcript	ENST00000402731.5	protein_coding	9/13	1029	1029	343	S	TCC/TCT	rs79357544
ENST00000404276.6:c.1116C>T	22:28695853-28695853	A	synonymous_variant	CHEK2	ENSG00000183765	Transcript	ENST00000403642.5	protein_coding	8/12	843	843	281	S	TCC/TCT	rs79357544
ENST00000404276.6:c.1116C>T	22:28695853-28695853	A	synonymous_variant	CHEK2	ENSG00000183765	Transcript	ENST00000404276.6	protein_coding	11/15	1174	1116	372	S	TCC/TCT	rs79357544
ENST00000404276.6:c.1116C>T	22:28695853-28695853	A	synonymous_variant	CHEK2	ENSG00000183765	Transcript	ENST00000405598.5	protein_coding	12/16	1308	1116	372	S	TCC/TCT	rs79357544
ENST00000404276.6:c.1116C>T	22:28695853-28695853	A	3_prime_UTR_variant, NMD_transcript_variant	CHEK2	ENSG00000183765	Transcript	ENST00000416671.5	nonsense_mediated_decay	12/16	1890	-	-	-	-	rs79357544
ENST00000404276.6:c.1116C>T	22:28695853-28695853	A	3_prime_UTR_variant, NMD_transcript_variant	CHEK2	ENSG00000183765	Transcript	ENST00000417588.5	nonsense_mediated_decay	9/13	1025	-	-	-	-	rs79357544
ENST00000404276.6:c.1116C>T	22:28695853-28695853	A	downstream_gene_variant	CHEK2	ENSG00000183765	Transcript	ENST00000425190.6	protein_coding	-	-	-	-	-	-	rs79357544
ENST00000404276.6:c.1116C>T	22:28695853-28695853	A	downstream_gene_variant	CHEK2	ENSG00000183765	Transcript	ENST00000433028.6	nonsense_mediated_decay	-	-	-	-	-	-	rs79357544
ENST00000404276.6:c.1116C>T	22:28695853-28695853	A	3_prime_UTR_variant, NMD_transcript_variant	CHEK2	ENSG00000183765	Transcript	ENST00000433728.5	nonsense_mediated_decay	9/13	1054	-	-	-	-	rs79357544
ENST00000404276.6:c.1116C>T	22:28695853-28695853	A	synonymous_variant	CHEK2	ENSG00000183765	Transcript	ENST00000434810.5	protein_coding	6/10	347	348	116	S	TCC/TCT	rs79357544
ENST00000404276.6:c.1116C>T	22:28695853-28695853	A	downstream_gene_variant	CHEK2	ENSG00000183765	Transcript	ENST00000439346.5	nonsense_mediated_decay	-	-	-	-	-	-	rs79357544
ENST00000404276.6:c.1116C>T	22:28695853-28695853	A	downstream_gene_variant	CHEK2	ENSG00000183765	Transcript	ENST00000447421.5	protein_coding	-	-	-	-	-	-	rs79357544
ENST00000404276.6:c.1116C>T	22:28695853-28695853	A	3_prime_UTR_variant, NMD_transcript_variant	CHEK2	ENSG00000183765	Transcript	ENST00000448511.5	nonsense_mediated_decay	10/14	1006	-	-	-	-	rs79357544
ENST00000404276.6:c.1116C>T	22:28695853-28695853	A	intron_variant	CHEK2	ENSG00000183765	Transcript	ENST00000456369.5	protein_coding	-	-	-	-	-	-	rs79357544
ENST00000404276.6:c.1116C>T	22:28695853-28695853	A	downstream_gene_variant	CHEK2	ENSG00000183765	Transcript	ENST00000464581.5	protein_coding	-	-	-	-	-	-	rs79357544
ENST00000404276.6:c.1116C>T	22:28695853-28695853	A	downstream_gene_variant	CHEK2	ENSG00000183765	Transcript	ENST00000491919.5	retained_intron	-	-	-	-	-	-	rs79357544
ENST00000404276.6:c.1116C>T	22:28695853-28695853	A	non_coding_transcript_exon_variant	CHEK2	ENSG00000183765	Transcript	ENST00000648295.1	processed_transcript	7/11	668	-	-	-	-	rs79357544
ENST00000404276.6:c.1116C>T	22:28695853-28695853	A	synonymous_variant	CHEK2	ENSG00000183765	Transcript	ENST00000649563.1	protein_coding	8/12	562	453	151	S	TCC/TCT	rs79357544
ENST00000404276.6:c.1116C>T	22:28695853-28695853	A	synonymous_variant	CHEK2	ENSG00000183765	Transcript	ENST00000650281.1	protein_coding	12/16	1276	1116	372	S	TCC/TCT	rs79357544

ESEfinder

Comparando la única predicción con valores positivos para 3'SS con su correspondiente en la secuencia mutante, los valores se reducen minimamente, por lo que no tendrá efecto en el *splicing.*

| 310 (-622) | TTTGGGCACTCCAAGATTTTGGGAGAGACC | -10.46370 | | 310 (-622) | TTTGGGCACTCCAAGATTTTGGGAGAGACC | 3.75060 | | 310 (-622) | TTTGGGCACTCCAAGATTTTGGGAGAGACC | -10.85920 | | 310 (-622) | TTTGGGCACTCCAAGATTTTGGGAGAGACC | 3.58190 |

| 310 (-622) | TTTGGGCACTCTAAGATTTTGGGAGAGACC | -11.28110 | | 310 (-622) | TTTGGGCACTCTAAGATTTTGGGAGAGACC | 3.28600 | | 310 (-622) | TTTGGGCACTCTAAGATTTTGGGAGAGACC | -11.66820 | | 310 (-622) | TTTGGGCACTCTAAGATTTTGGGAGAGACC | 3.10620 |

Si hacemos lo mismo para la búsqueda de ESE, pasa lo mismo, por lo que no habrá cambios en los ESE.

315 (-617)	GCACTCC	-7.32534		315 (-617)	GCACTCC	-5.23164		315 (-617)	GCACTCCA	1.55132		315 (-617)	GCACTCC	2.42608
316 (-616)	CACTCCA	1.56048		316 (-616)	CACTCCA	2.09305		316 (-616)	CACTCCAA	2.35844		316 (-616)	CACTCCA	-5.50352
317 (-615)	ACTCCAA	-3.52285		317 (-615)	ACTCCAA	-2.66920		317 (-615)	ACTCCAAG	-0.20533		317 (-615)	ACTCCAA	-0.45903
318 (-614)	CTCCAAG	-1.35523		318 (-614)	CTCCAAG	0.43451		318 (-614)	CTCCAAGA	-0.74364		318 (-614)	CTCCAAG	2.69227
319 (-613)	TCCAAGA	-0.61058		319 (-613)	TCCAAGA	-0.29850		319 (-613)	TCCAAGAT	-5.00321		319 (-613)	TCCAAGA	-0.02191
320 (-612)	CCAAGAT	-0.98147		320 (-612)	CCAAGAT	0.74058		320 (-612)	CCAAGATT	-5.75640		320 (-612)	CCAAGAT	-1.10544
321 (-611)	CAAGATT	-3.62650		321 (-611)	CAAGATT	-1.76918		321 (-611)	CAAGATTT	-4.10813		321 (-611)	CAAGATT	-2.42761

315 (-617)	GCACTCT	-5.47194		315 (-617)	GCACTCT	-4.03494		315 (-617)	GCACTCTA	2.19576		315 (-617)	GCACTCT	0.88698
316 (-616)	CACTCTA	2.01819		316 (-616)	CACTCTA	2.19705		316 (-616)	CACTCTAA	0.62943		316 (-616)	CACTCTA	-7.22045
317 (-615)	ACTCTAA	-6.04658		317 (-615)	ACTCTAA	-4.48099		317 (-615)	ACTCTAAG	-0.96457		317 (-615)	ACTCTAA	1.03222
318 (-614)	CTCTAAG	-2.81255		318 (-614)	CTCTAAG	-0.82024		318 (-614)	CTCTAAGA	-0.97449		318 (-614)	CTCTAAG	0.30764
319 (-613)	TCTAAGA	-2.92060		319 (-613)	TCTAAGA	-2.36736		319 (-613)	TCTAAGAT	-5.57214		319 (-613)	TCTAAGA	1.32637
320 (-612)	CTAAGAT	-0.37854		320 (-612)	CTAAGAT	0.98936		320 (-612)	CTAAGATT	-4.36800		320 (-612)	CTAAGAT	-1.41750
321 (-611)	TAAGATT	-6.57699		321 (-611)	TAAGATT	-4.87423		321 (-611)	TAAGATTT	-4.12926		321 (-611)	TAAGATT	-2.07092

EX-SKIP

EX-SKIP - Results for submitted sequences

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	8	15	9	65	1236.5415	41	-51.3624	9	11	58	759.7814	50	62.0857	138	128	1.08
mut	8	15	9	65	1236.5415	41	-51.3624	9	10	57	735.3937	46	58.4881	138	122	1.13

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

HOT-SKIP

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>wt
ctaattagaatcctgaagtgtctgtgataaagataataagctttttgtaagattacagaggacataggttaagttggaaa
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No efecto.