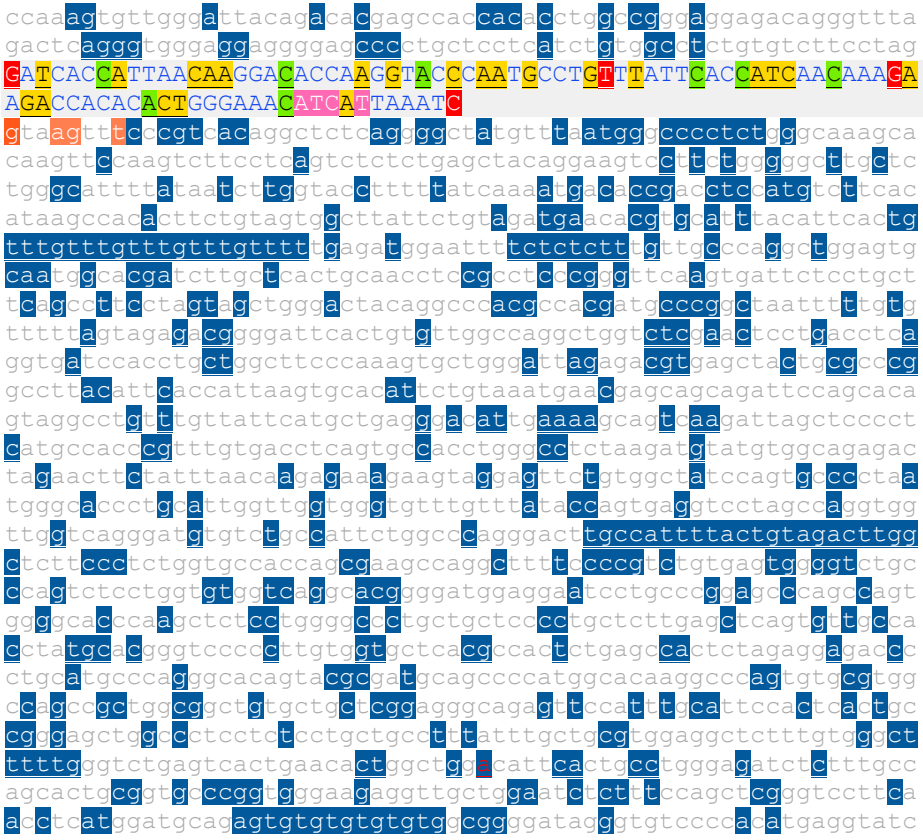
Ejemplo comparación de resultados predictores in sillico

Cambio de estudio AC093668.1 c.425+1352A>G (chr7:102568483 A/G, rs78060501)

Exón 4 e intrones adyacentes:



El cambio se encuentra en la antepenúltima fila del intrón 4 (la **a** 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

pos 5'->3'	phase	strand	confidence	5' exon intron 3'
211	2	+	0.80	TCATTAAATC^GTAAGTTTCC
1156	1	+	0.34	TTCCCCGTCT^GTGAGTGGGG

Donor splice sites, complement strand

pos 3'->5'	pos 5'->3'	phase	strand	confidence	5' exon intron 3'
1467	244	0	-	0.41	GCTCCCGGCA^GTGAGTGGAA
757	954	1	-	0.49	AATGGTGAAT^GTAAGGCCGG
376	1335	0	-	0.42	AGACATGGAG^GTCGGTGTCA
353	1358	2	-	0.80	TGATAAAAAG^GTACCAAGAT

Acceptor splice sites, direct strand

pos 5'->3'	phase	strand	confidence	5' intron exon 3'
120	2	+	0.92	GTCTTCCTAG^GATCACCATT
136	0	+	0.19	CATTAACAAG^GACACCAAGG
145	0	+	0.18	GGACACCAAG^GTACCCAATG
501	2	+	0.27	TGTTGCCCAG^GCTGGAGTGC

Acceptor splice sites, complement strand

pos 3'->5'	pos 5'->3'	phase	strand	confidence	5' intron exon 3'
1179	532	0	-	0.14	ACCACACCAG^GAGACTGGGC
1176	535	0	-	0.07	ACACCAGGAG^ACTGGGCAGA
1167	544	0	-	0.07	GACTGGGCAG^ACCCCACTCA
1154	557	1	-	0.14	CCACTCACAG^ACGGGGAAAA
939	772	1	-	0.28	TGTTAAATAG^AAGTTCTAGT
833	878	2	-	0.25	TGTCCCTCAG^CATGAATAAC
779	932	0	-	0.33	TCATTTACAG^AATGTGCACT
419	1292	0	-	0.17	TCATCTACAG^AATAAGCCAC
191	1520	0	-	0.17	TGTTTCCCAG^TGTGTGGTCT
37	1674	1	-	0.00	TCCCGGCCAG^GTGTGGTGGC

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Aparece un sitio *acceptor* en la secuencia mutante (en azul). Si este fuera lo suficientemente fuerte como para que el *spliceosome* lo detectara y hubiera más adelante en el intrón un *donor* críptico, se podría producir la inclusión de un exón críptico.

Splice Site Prediction by Neural Network (NNSplice)

Donor site predictions for 10.42.1.119.574158.0 :

Start	End	Score	Exon	Intron
139	153	0.86	caccaag	**gt**acccaa
204	218	0.97	ttaaatc	**gt**aagttt
685	699	0.73	acctcag	**gt**gatcca
909	923	0.44	ctaagat	**gt**atgtgg
1149	1163	0.71	cccgtct	**gt**gagtgg

Donor site predictions for 10.42.2.148.574170.0 :

Start	End	Score	Exon	Intron
139	153	0.86	caccaag	**gt**acccaa
204	218	0.97	ttaaatc	**gt**aagttt
685	699	0.73	acctcag	**gt**gatcca
909	923	0.44	ctaagat	**gt**atgtgg
1149	1163	0.71	cccgtct	**gt**gagtgg

Acceptor site predictions for 10.42.1.119.574158.0 :

Start	End	Score	Intron	Exon
100	140	0.94	gtggcctctgtgtcttcct	**ag**gatcaccattaacaaggaca
208	248	0.81	atcgtaagtttcccgtcac	**ag**gctctcaggggctatgttta
287	327	0.55	ctcagtctctctgagctac	**ag**gaagtccttctgggggcttg
404	444	0.82	ctgtagtggcttattctgt	**ag**atgaacacgtgcatttacat
481	521	0.82	ttttctctctttgttgccc	**ag**gctggagtgcaatggcacga
554	594	0.67	caagtgattctcctgcttc	**ag**ccttcctagtagctgggact
566	606	0.84	ctgcttcagccttcctagt	**ag**ctgggactacaggcccacgc
617	657	0.90	ggctaatttttgtgttttt	**ag**tagagacggggattcactgt
1084	1124	0.78	ggacttgccattttactgt	**ag**acttggctcttccctctggt
1617	1657	0.76	gttgctggaatctctttcc	**ag**ctcgggtccttcaacctcat

Acceptor site predictions for 10.42.2.148.574170.0 :

Start	End	Score	Intron	Exon
100	140	0.94	gtggcctctgtgtcttcct	**ag**gatcaccattaacaaggaca
208	248	0.81	atcgtaagtttcccgtcac	**ag**gctctcaggggctatgttta
287	327	0.55	ctcagtctctctgagctac	**ag**gaagtccttctgggggcttg
404	444	0.82	ctgtagtggcttattctgt	**ag**atgaacacgtgcatttacat
481	521	0.82	ttttctctctttgttgccc	**ag**gctggagtgcaatggcacga
554	594	0.67	caagtgattctcctgcttc	**ag**ccttcctagtagctgggact
566	606	0.84	ctgcttcagccttcctagt	**ag**ctgggactacaggcccacgc
617	657	0.90	ggctaatttttgtgttttt	**ag**tagagacggggattcactgt
1084	1124	0.78	ggacttgccattttactgt	**ag**acttggctcttccctctggt
1617	1657	0.76	gttgctggaatctctttcc	**ag**ctcgggtccttcaacctcat

Spliceman

Point mutation	Wildtype (wt)	Mutation (mt)	L1 distance	Ranking (L1)
gctgg(a/g)cattc	gctgga	gctggg	31336	82%

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	16	67	gtctgagtc		1.05629923504	0.548387096774	21	12	16	-0.18772933
wt	16	63	gagtcactg		-0.100031383343	0.551724137931	17	12	16	-0.38621636
wt	16	59	cactgaaca		1.51702510309	0.555555555556	13	12	16	0.50136842
wt	16	41	cattcactg		1.13940374359	0.583333333333	13	10	21	0.4090624
mut	16	67	gtctgagtc		1.05629923504	0.548387096774	21	12	16	-0.18772933
mut	16	63	gagtcactg		-0.100031383343	0.551724137931	17	12	16	-0.38621636
mut	16	59	cactgaaca		1.51702510309	0.555555555556	13	12	16	0.50136842
mut	16	41	cattcactg		1.13940374359	0.583333333333	13	10	21	0.4090624

Variant Effect Predictor tool

rs78060501 SNP

Most severe consequence	intron variant | See all predicted consequences
Alleles	T/C | Highest population MAF: 0.21
Change tolerance	CADD: C:6.578 | GERP: -0.49
Location	Chromosome 7:102568483 (forward strand) | VCF: `7 102568483 rs78060501 T C`

ESEfinder

No hay predicciones positivas ni para la secuencia WT ni la mutante.