#### Ejemplo comparación de resultados predictores in sillico

Cambio de estudio OR10H2 c.612T>C (chr19:15728655 T/C, COSV59947296 o NM\_013939.2:c.612T>C)

#### Exón 1 e intrones adyacentes:

tagtaatgettacettgtaaggcaggtgtaaagatttetgtatatgacaacactcatcac atagtaggtgetcagtaaatgttaaaagcatgtttacttccacaactcttgatctgtatg tetttatetgagttttaatttttgagttatagtagctttattaagatgtaattcacetac catacaatgtacecattagagcgcacatttetgtggtttttgcgtattcagagttatgca accatcatgacaatctggcttagagtattttagtcatccaaaaaagaaacccaaatccta El cambio se encuentra en la línea 11 del exón 7 (la t 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 (no cambios)

Donor splice s	sites, direc	t strand	l							
						Donor splice	sites. direct	strand		
	pos 5'->3' 141	phase 1	strand +	confidence 0.54	5' exon intron 3' AGCACTTAAG^GTGAGTGATC		pos 5'->3'		confidence 0.54	
Donor splice	sites, compl	ement st	rand						0.54	AGCACTTAAG^GTGAGTGATC
pos 3'->5'	pos 5'->3'	phase	strand	confidence	5' exon intron 3'	Donor splice s	sites, comple	ement strand		
1521	121	2	-	0.36	ACATTGTATG^GTAGGTGAAT	noc 2' \5'	pos 5'->3'	phase strand	confidence	5' exon intron 3'
1354	288	2	-	0.46	GCCTTACAAG^GTAAGCATTA	1521	121	2 -	0.36	ACATTGTATG^GTAGGTGAAT
1161	481	0	-	0.70	TGAGGACTGC^GTAGGTGGTG	1354	288	2 -	0.46	GCCTTACAAG^GTAAGCATTA
1059	583	0	-	0.83	CCACAATAAG^GTGAGAGGCA	1161	481	0 -	0.70	TGAGGACTGC^GTAGGTGGTG
671	971	1	-	0.34	GCCCATGACG^GTGAGCAGGA	1059	583	0 -	0.83	CCACAATAAG^GTGAGAGGCA
504	1138	2	-	0.45	ACAGGAAGAG^GTACATGGGC	671	971	1 -	0.34	GCCCATGACG^GTGAGCAGGA
429	1213	2	-	0.58	GCGTGAACAG^GTACATCAGC	504	1138	2 -	0.45	ACAGGAAGAG^GTACATGGGC
344	1298	1	-	0.71	AGACATGGAG^GTGTGGTTTA	429	1213	2 -	0.58	GCGTGAACAG^GTACATCAGC
109	1533	1	-	0.34	CTGACACAAA^GTAAGAATTT	344	1298	1 -	0.71	AGACATGGAG^GTGTGGTTTA
						109	1533	1 -	0.34	CTGACACAAA^GTAAGAATTT
Acceptor splic	ce sites, di	rect str	and							
	51 .21				51 4-4 31	Acceptor spli		rect strand		
	pos 5'->3'	phase 2		confidence						5' intron exon 3'
	119 313		+	0.43 0.97	TTTGTGTCAG^GACCTGCACA		pos 5'->3'	phase strand 2 +	confidence 0.43	
	641	1 2	+		CCCCAACTAG^GGGTGGCCGT TCTCCTTCAG^CTTCGGCTTC		119 313	1 +	0.43	TTTGTGTCAG^GACCTGCACA CCCCAACTAG^GGGTGGCCGT
				0.27			641	2 +	0.27	TCTCCTTCAG^CTTCGGCTTC
	882 907	0 1	+	0.19 0.18	TCTGTTGAAG^TTGGCCTGTG AATGTACCAG^CTGTGGCCCT		882	2 + 0 +	0.19	TCTGTTGAG^CTTGGCCTGTG
	1205	2	7	0.33	TCAGCCTCAG^GAACAAAGAA		907	1 +	0.19	AATGTACCAG^CTGTGGCCCT
	1205	2	+	0.55	TCAGCCTCAG GAACAAAGAA		1205	2 +	0.33	TCAGCCTCAG^GAACAAAGAA
							1203	- '	0.55	TERGEETERG GRACHARGAN
Acceptor spii	ce sites. com	mplement	strand							
Acceptor splic	ce sites, com	mplement 	strand			Acceptor spli	e sites, cor	mplement strand	l	
pos 3'->5'	ce sites, com  pos 5'->3'			confidence	5' intron exon 3'					
					5' intron exon 3' ATTCTATCAG^CACTTCCACA	pos 3'->5'	pos 5'->3'	phase strand	confidence	
pos 3'->5'	pos 5'->3'	phase		confidence		pos 3'->5' 1291	pos 5'->3' 351	phase strand 2 -	confidence 0.21	ATTCTATCAG^CACTTCCACA
pos 3'->5' 1291	pos 5'->3' 351	phase 2		confidence 0.21	ATTCTATCAG^CACTTCCACA	pos 3'->5' 1291 1277	pos 5'->3' 351 365	phase strand 2 - 1 -	confidence 0.21 0.47	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT
pos 3'->5' 1291 1277	pos 5'->3' 351 365	phase 2 1	strand - -	confidence 0.21 0.47	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT	pos 3'->5' 1291 1277 1269	pos 5'->3' 351 365 373	phase strand 2 - 1 - 0 -	confidence 0.21 0.47 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAG^GTGCCTGAGG
pos 3'->5' 1291 1277 1269	pos 5'->3' 351 365 373	phase 2 1 0	strand - - -	confidence 0.21 0.47 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAG^GTGCCTGAGG	pos 3'->5' 1291 1277 1269 1260	pos 5'->3' 351 365 373 382	phase strand 2 - 1 - 0 - 0 -	confidence 0.21 0.47 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAGGAATAGAGTG
pos 3'->5' 1291 1277 1269 1260	pos 5'->3' 351 365 373 382	phase 2 1 0	strand - - -	confidence 0.21 0.47 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAG^GAATAGAGTG	pos 3'->5' 1291 1277 1269 1260 1254	pos 5'->3' 351 365 373 382 388	phase strand 2 - 1 - 0 - 0 -	confidence 0.21 0.47 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAG^GAATAGAGTG TGAGGAATAGAGTG
pos 3'->5' 1291 1277 1269 1260 1254	pos 5'->3' 351 365 373 382 388	phase 2 1 0 0	strand - - -	confidence 0.21 0.47 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAG^GAATAGAGTG TGAGGAATAG^AGTGTGCTGA	pos 3'->5' 1291 1277 1269 1260 1254 1252	pos 5'->3' 351 365 373 382 388 390	phase strand 2 - 1 - 0 - 0 - 0 - 0 -	confidence 0.21 0.47 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAG^GAATAGAGTG TGAGGAATAG^AGTGTGCTGA AGGAATAGAG^TGTGCTGA
pos 3'->5' 1291 1277 1269 1260 1254 1252	pos 5'->3' 351 365 373 382 388 390	phase 2 1 0 0 0	strand - - -	confidence 0.21 0.47 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAG^GAATAGAGTG TGAGGAATAG^AGTGTGCTGA AGGAATAGAGTGTGCTGA	pos 3'->5' 1291 1277 1269 1260 1254 1252 1243	pos 5'->3' 351 365 373 382 388 390 399	phase strand 2 - 1 - 0 - 0 - 0 - 0 - 0 -	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTCACTCAGGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAGGAGAATAGAGTG TGAGGAATAGAGTGAGAGAGTAGTGCTGA AGGAATAGAGTAGTGCTGAGGGTGTGTGTGAGGAGTGCTGAGGGTGTGTGT
pos 3'->5' 1291 1277 1269 1260 1254 1252 1243	pos 5'->3' 351 365 373 382 388 390 399	phase 2 1 0 0 0 0 0 0 0	strand - - -	confidence 0.21 0.47 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAG^GAATAGAGTG TGAGGAATAGAGTGTGCTGA AGGAATAGAGTGTGTGAGGAATAGAGGG GTGTGCTGAGAGAAGAGGCTGAGGG	pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239	pos 5'->3' 351 365 373 382 388 390 399 403	phase strand 2 - 1 - 0 - 0 - 0 - 0 - 1 - 1 -	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAG^GAATAGAGTG TGAGGAATAGAAGTGTGCTGA AGGAATAGAG^TGTGCTGAGG GTGTGCTGAG^GAAGGTCCTC GCTGAGGAAAGGTCCTCTCA
pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239	pos 5'->3' 351 365 373 382 388 390 399 403	phase 2 1 0 0 0 0 0 0 1	strand - - -	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAG^GGTGCCTGAGG GGTGCCTGAG^GAATAGAGTG TGAGGAATAGAGTGTGCTGA AGGAATAGAGTGTGCTGA GGTGTGCTGAGAGGTCCTC GCTGAGAGAAGGTCCTC GCTGAGGAAGGTCCTC	pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216	pos 5'->3' 351 365 373 382 388 390 399 403 426	phase strand 2	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTITCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAG^GAATAGAGTG TGAGGAATAGAGTGTGTGAGAGAGAATAGAGATTAGTGTGAGGATAGAGATAGAGATCTC GCTGAGGAAAGAGTCCTC GCTGAGGAAGAGTCCTCACACACCTTCAGAGAGTCCTTCACACACCTTCAG
pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216	pos 5'->3' 351 365 373 382 388 390 399 403 426	phase 2 1 0 0 0 0 0 1 0 0	strand - - - - - - -	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAG^GAATAGAGTG TGAGGAATAGAGTGTGCTGA AGGAATAGAGTGTGCTGA AGGAATAGAGTGTGCTGAGG GTTGCTGAGGAGAGTCCTC GCTGAGGAAGAGTCCTCTTCA CAACCTTCAG^TTCTTTTGTTC	pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019	pos 5'->3' 351 365 373 382 388 390 399 403 426 623	phase strand 2 - 1 - 0 - 0 - 0 - 1 - 0 - 2 - 2 -	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTCCTAGCT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAGGAGAATAGAGTG TGAGGAATAGAGTGTGCTGA AGGAATAGAGATTGCTGA GTGTGCTGAGGAGAGGTCCTC GCTGAGGAAGAGTCCTCTCA CAACCTTCAG^TCTTTGTTC CGACCTTCAG^CAGAGGGAT CGACCTTCAG^CAGAAGGGAT
pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019	pos 5'->3' 351 365 373 382 388 390 399 403 426 623	phase 2 1 0 0 0 0 0 1 0 2	strand - - - - - - -	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAG^GAATAGAGTG TGAGGAATAG^AGTGTGCTGA AGGAATAGAGATGTGCTGAG GTGTGCTGAG^GAAGGTCCTC GCTGAGGAAGAGTCCTCTTCA CAACCTTCAG^TTCTTTGTTC CGACCTTCAG^CAGAAGGGAT	pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019	pos 5'->3' 351 365 373 382 388 390 399 403 426 623 626	phase strand 2 - 1 - 0 - 0 - 0 - 1 - 0 - 2 - 1 - 2 -	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT ASCTACTCAG^GTGCCTGAGG GGTGCCTGAGG^GAATAGAGTG TGAGGAATAG^AGTGTGCTGA AGGAATAGAGAGTGTGCTGAGG GTGTGCTGAG^GAAGGTCCTC GCTGAGGAAGGTCCTCTCA CAACCTTCAG^TTCTTTGTTC GACCTTCAG^CAGAAGGAT CCTTCAGCAGAAGGGAT CCTTCAGCAGAAGGGAT
pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019	pos 5'->3' 351 365 373 382 388 390 399 403 426 623 626	phase 2 1 0 0 0 0 0 1 0 2 2 2	strand - - - - - - -	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAG^GTGCCTGAGG GTTGCCTGAG^GAATAGAGTG TGAGGAATAGAGTGTGCTGA AGGAATAGAGTGTGCTGA GTGTGCTGAG^GAAGGTCCTC GCTGAGGAAGAGTCCTC CAACCTTCAG^CAGAAGGATCTTTCA CAACCTTCAG^CAGAAGGGATCCTC CGACCTTCAG^CAGAAGGGAT CCTTCAGCAAGAAGGGAT	pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019 1016	pos 5'->3' 351 365 373 382 388 390 399 403 426 623 626 629	phase strand 2	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTITCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAG^GAATAGAGTG TGAGGAATAGAGATGGTGTGA AGGAATAGAG^TGTGCTGAG GTGTGCTGAG^GAAGGTCCTC GCTGAGGAAG^GTCCTCTCA CAACCTTCAG^TCCTTTTATC CGACCTTCAG^AGAGGGAT CCTTCAGCAGAAGGGAT CCTTCAGCAGAAGGGAT CCTTCAGCAGAAGGGAT TCAGCAGAAGGGAT
pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019 1016 1013	pos 5'->3' 351 365 373 382 388 390 399 403 426 623 626 629	phase 2 1 0 0 0 0 0 1 0 2 2 2 2	strand - - - - - - -	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAG^GAATAGAGTG TGAGGAATAGAGTG TGAGGAATAGAGTG GTGGTGCTGAG AGGAATAGAGTGTCTGA AGGAATAGAGTGTCTCA GTGAGGAAGAGTCCTC GCTGAGGAAGAGTCCTCTTCA CAACCTTCAG^TCAGTCTTTCA CAACCTTCAG^TCAGGAAGGGAT CCTTCAGCAGAAGGGATCTT TCAGCAGAAG	pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019 1016 1013 1002	pos 5'->3' 351 365 373 382 388 399 403 426 623 626 629 640	phase strand 2	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTCACTCAGGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAGGAGAATAGAGTG TGAGGAATAGAGTGTGCTGA AGGAATAGAGATTGCTGA AGGAATAGAGATTGCTGAGG GTGTGCTGAGGAGAGGTCCTC GCTGAGGAAGAGTCCTCTTCA CAACCTTCAGATTCTTTTTTC CGACCTTCAG^ACAGAGGGAT CCTTCAGCAGAAAGGGATCTT TCAGCAGAAAGGGATCTT TCAGCAGAAAGGGATCTT TCAGCAGAAAGGGATCTT TCAGCAGAAAGGGATCTTCAA GATCTTCAAG^ATGTCGCCCA
pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019 1016 1013 1002	pos 5'->3' 351 365 373 382 388 390 399 403 426 623 626 629 640	phase 2 1 0 0 0 0 0 1 0 2 2 2 1 1	strand	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CACTACCAGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAG^GAATAGAGTG TGAGGAATAG^AGTGTGCTGA AGGAATAGAGATGTGCTGAG GTGTGCTGAG^GAAGGTCCTC GCTGAGGAAGAGTCCTCTTCA CAACCTTCAG^TTCTTTGTTC CGACCTTCAG^AGGAGGGAT CCTTCAGAGAGGGATCTT TCAGCAGAAGGGATCTT TCAGCAGAAGGGATCTT TCAGCAGAAGGGATCTTCAA GATCTTCAAG^ATGTCGGCCA	pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019 1016 1013 1002 888	pos 5'->3' 351 365 373 382 388 390 399 403 426 623 626 629 640 754	phase strand 2	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAG^GAATAGAGTG TGAGGAATAG^AGTGTGCTGA AGGAATAGAGATGTGCTGA AGGAATAGAGAGTCCTCTCA CAACCTTCAG^TTCTTTGTTC CGACCTTCAG^AGAAGGGAT CCTTCAGCAGAAGGGATCTT TCAGCAGAAGGGATCTT TCAGCAGAAGGGATCTT AGCAGGAGGAGGATCTTCAA GATCTTCAGCAGAAGGGATCTT AGCAGGAGAGAGGATCTTCAA GATCTTCAGGACAGAGGATCTTCAA ATTTCCACACAGAGCCAACTTCA
pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019 1016 1013 1002 888	pos 5'->3' 351 365 373 382 388 390 399 403 426 623 626 629 640 754	phase 2 1 0 0 0 0 1 1 0 2 2 2 1 1 2 2	strand	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAG^GAATTAGAGTG TGAGGAATAGAGTGTGCTGA AGGAATAGAG^AGTGTGCTGA GGTGGCTGAGAGAAGGTCCTC GCTGAGGAAGAGTCCTCTTCA CAACCTTCAG^CAGAAGGGATCTTC TCAGCCAGAAGGGATCTTTCAC GACCTTCAG^CAGAAGGGATCTT TCAGCAGAAGGGATCTTCAA GATCTTCAAGAATCTGCACA ATTTCCACAGAGGCCAACTTCA	pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019 1016 1013 1002 888 828	pos 5'->3' 351 365 373 382 388 390 399 403 426 623 626 629 640 754 814	phase strand 2	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.19 0.19 0.10	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAG^GAGATAGAGTG TGAGGAATAGAG^TGTGCTGAG AGGAATAGAG^TGTGCTGAG GGTGCTGAG^GAAGGGTCCTC GCTGAGGAAG^GTCCTCTAC CAACCTTCAG^TCTTTTGTTC CGACCTTCAG^AGAGGGAT CCTTCAGCAGAAGGGAT CCTTCAGCAGAAGGGAT TCAGCAGAAGGGAT CTTCAGCAGAAGGGAT CTTCAGCAGAAGGGAT TCAGCAGAAGAGGAACTTCA GATCTCAAG^AAGTCATCA GATCTCAAG^AAAGTCAGTT GGGCCA
pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019 1016 1013 1002 888 828	pos 5'->3' 351 365 373 382 388 390 493 426 623 623 626 629 640 754 814	phase 2 1 0 0 0 0 1 0 2 2 2 1 1 2 0 0 0 0	strand	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAGGTGGCTGAGG GGTGCCTGAGGAGTAGAGTG TGAGGAATAGAGTG TGAGGAATAGAGTG GGTGCTGAGAGAGTGCTGA AGGAATAGAGTGTGCTGA GGTGTGCTGAGAGAAGGTCCTC GCTGAGGAAGGTCTCTTCA CAACCTTCAG^TTCTTTGTTC CGACCTTCAGCAGAGGGAT CCTTCAGCAGAAGGGAT TCTCAGCAGAAGGGATCTT TCAGCAGAAGGGATCTTCAA GATCTTCAAGATTCGGCCA ATTTCCACAGAGTAGTCGGCCA GGATCCACAGAGAAGTCATT	pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019 1016 1013 1002 888 828 828	pos 5'->3' 351 365 373 382 388 399 403 426 623 626 629 640 754 814 818	phase strand 2	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTCACTCAGGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAGGAGAATAGAGTG TGAGGAATAGAATGTGCTGA AGGAATAGAGATTGCTGA AGGAATAGAGATTGCTGAGG GTGTGCTGAGGAGAGGTCCTC GCTGAGGAAGAGTCCTCTTCA CAACCTTCAGATTCTTTTGTTC CGACCTTCAG^CAGAAGGGAT CCTTCAGCAG^AAGGGATCTT TCAGCAGAAAGAGGATCTTCAA GATCTTCAGAGAAGGGATCTTCA GATCTTCAGAGGAGACTCTCA GGATCACAGAAGGAACTTCA GGATCCACAGAAGGACACTTCA GGATCCACAGAAGGAACTTCA
pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019 1016 1013 1002 888 828 828	pos 5'->3' 351 365 373 382 388 390 403 426 623 626 629 640 754 814 818	phase 2 1 0 0 0 0 1 0 2 2 1 1 2 2 1 2 0 1 1	strand	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CACTTCCACA TCCACACCAG^CACTACTCAGGT AGCTACTCAG^GAGATAGAGTG GGTGCCTGAG^GAATAGAGTG TGAGGAATAGAATGTGCTGAG AGGAATAGAGATGTGCTGAG GTGTGCTGAG^GAAGGTCCTC GCTGAGGAAG^GTCCTCTTCA CAACCTTCAG^TTCTTTGTTC CGACCTTCAG^CAGAAGGGAT CCTTCAGCAG^AAGGGATCTTCA GATCTTCAAGAAGAGGATCTTCA GATCTCCACAG^AAGGGATCTTCA GATCTCCACAG^AAGAGTCTTCA GGATCCACAGAAAAGTCAGTT CCACAGAAAAGATCAGTT CCACAGAAAAGATCAGTT	pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019 1016 1013 1002 888 828 824 820	pos 5'->3' 351 365 373 382 388 390 399 403 426 623 626 629 640 754 814 818 822	phase strand 2	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTCACTCAGGT AGCTACTTCAG^GTGCCTGAGG GGTGCCTGAGGAGATAGAGTG TGAGGAATAGAGTGTGCTGA AGGAATAGAGAGTGTGCTGA AGGAATAGAGAGTCCTCTCCA CAACCTTCAG^CTCTCTCA CAACCTTCAG^CAGAAGGGAT CCTTCAGCAGAAGGGAT TCAGCAGAAGAGGATCTT TCAGCAGAAGAGGATCTT TCAGCAGAAGAGGATCTT AGCAGAAGAGAGTCCTCAA GATCTTCAAGATTCCAGCCA ATTTCCACGAGAAGAGTCCTCA GGATCCACAGAAAGTCAGTT CCACAGAAAGTCAGTTT CCACAGAAAGTCAGTTT CCACAGAAAGTCAGTTT
pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019 1016 1013 1002 888 828 824 820	pos 5'->3' 351 365 373 382 388 390 399 403 426 623 626 629 640 754 814 818 822	phase 2 1 0 0 0 0 0 1 1 0 2 2 2 1 1 2 0 0 1 2 2 0 1 2 0	strand	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAGAGTGCCTGAGG GGTGCCTGAGAGAATAGAGTG TGAGGAATAGAGTGTGCTGAG AGGAATAGAGTGTGCTGAG GTGTGCTGAGAGAGGGTCCTC GCTGAGGAGAGGTCCTCTTCA CAACCTTCAGACAGAAGGGATCCTT CCAGCAGAAGGGATCTTTCAAGCAGAAGGGATCTTTCAGCAGAAGGGATCTTTCAGCAGAAGGGATCTTCAGAGAAGGAATCCTTCAAGATTGTCGCCA ATTTCCACAGAAGAGCACTTCA GGATCCACAGAAGAGTCAGTT CCACAGAAAGATCAGTTGCAAAAGACAGATTCCATGGAAAAGACTCAGTTGGAAAAGACAGATTGAGTTGGAAAAAGTCAGTTGGAAAAGTCAGTTGGAAAAAGTCAGTTGGAAAAAGTCAGTTGGAAAAAGTCAGTTGGAAAAAGTCAGTTGGAAAAAGTCAGTTGGAAAAAGTCAGTTGGAAAAAGTCAGTTGGAAAAAGTCAGTTGGAAAAAGTCAGTTGGAAAAGTCAGTTGGAAAAAGTCAGTTGGAAAAGTCAGTTGGAAAAAGTCAGTTGGAAAAGTCAGTTGGAAAAGTCAGTTGGAAAAAGTCAGTTGAGAAAAGTCAGTTGAGAAAAGTCAGTTGAGAAAAGTCAGTTGGAAAAGTCAGTTGGAAAAGTCAGTTGGAAAAGTCAGTTGGAAAAGTCAGTTGGAAAAGTCAGTTGGAAAAGTCAGTTGGAAAAGTCAGTGAGAAAGTCAGTTGGAAAAGTCAGTTGGAAAAGTCAGTGGAAAAGTCAGTGAGAAAAGTCAGTGAGAAAAGTCAGTTGGAAAAGTCAGTTGAGAAAAGTCAGTTGAGAAAAGTCAGTTGAGAAAAGTCAGTTGAGAAAAGTCAGTTGAGAAAAGTCAGTTGAGAAAAGTCAGTTGAGAAAAGTCAGTTGAGAAAAGTCAGTTGAGAAAAGTCAGTTGAGAAAAAGTCAGTGAGAAAAAGTCAGTGAGAAAAGTCAGTGAGAAAAGTAAGT	pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019 1016 1013 1002 888 828 824 820 804	pos 5'->3' 351 365 373 382 388 390 399 403 426 623 626 629 640 754 814 818 822 838	phase strand 2	confidence	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAG^GAGATAGAGTG TGAGGAATAGAG^TGTGCTGAG GGTGTGCTGAGAGAGAGGTCCTC GCTGAGGAAGAGAGTCCTC GCTGAGGAAGAGTCCTCACACACCTCAGCAGAGAGAGTCCTCACACACCTTCAGCAGAAGGGAT CCTTCAGCAGAAGAGGATCTT TCAGCAGAAGAGGATCTT TCAGCAGAAGAGGATCTT TCAGCAGAAGAGGATCTTCAA GATCTTCAGCAGAAGGGATCTTCAACAGAGAGAGAGTCTTCAGCAGAAAGTCATTCAACAGAGCCAACTTCAAGATCTCAAGATCTCAAGATCAGTTCCACAGAAAGTCAGTTCCACAGAAAGTCAGTTGCAAAAGTCAGTTGGAAAAGAGAAAGCCAGTTAGAAAAGTCAGTTGGAAAAGAGAAGAGAAGTCAGTTGGAAAAGAGAAGAGAGAG
pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019 1016 1013 1002 888 828 824 820 804	pos 5'->3' 351' 365' 373' 382' 388' 390' 493' 426' 623' 626' 629' 640' 754' 814' 818' 822' 838'	phase 2 1 0 0 0 0 1 1 0 2 2 2 1 2 0 1 2 0 0	strand	confidence 0,21 0,47 0,18 0,18 0,18 0,18 0,18 0,18 0,18 0,18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAGGTGGCCTGAGG GGTGCCTGAGGGAGTAGCTGACTGA AGGAATAGAGTGGCTGA AGGAATAGAGTGTGCTGA AGGAATAGAGTGTGCTGA GGTGTGCTGAGGAAGGTCCTC GCTGAGGAAGGATCCTCTTCA CAACCTTCAGCAGAAGGGATCTT TCAGCAGAAGGGATCTTTCAGCAGAAGGGATCTTTCAGAGAAAGGATCTTCAGAGAAGGATCTTCAGCAGAAGGATCTTCAGAGAAAGTCAGTTCCACAGAAGTCAGAAGGAATCTCCACAGAAGAGAATTCCACCACAGAAAGTCAGTTCCACAGAAAGTCAGTTGGAA AGAAAGTCAGCTTGGAAAATG AAGGCCGAGAGAGTCACCCCA	pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019 1016 1013 1002 888 828 824 820	pos 5'->3' 351 365 373 382 388 390 399 403 426 623 626 629 640 754 814 818 822	phase strand 2	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CACTTCCACAC TCCACACCAG^CACTCCTCAGG GGTGCCTGAGGAGAATAGAGTG TGAGGAATAGAATTGCTGA AGGAATAGAGATTGCTGA AGGAATAGAGATTGCTGAGA GTGTGCTGAGGAGAGGTCCTC GCTGAGGAAGAGTCCTCTTCA CAACCATTCAGATTCTTTGTTC CGACCTTCAG^CAGAAGGGAT CCTTCAGCAGCAAGAGGAT CCTTCAGCAGCAAGAGGAT TCAGCAGAAGAGGATCTTCAA GATCTTCAGAGAGAGGATCTTCAA GATCTTCAGAGAGAGGATCTTCAA GATCTTCAGAGAGAGGATCTTCA GATCTCAAGAGAGGATCTTCA GATCTCACAGAAAGTGCACTTCA AGATCACAGAAAGTTGGAAATTG AATGGCCGAGAGTGTTGGAA AGAAAGTCAGATTGGAAAATG AATGGCCGAGAGTGTCACCCC CATGACCGAGAGCCCCCC
pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019 1016 1013 1002 888 828 824 820 804 780	pos 5'->3' 351 365 373 382 388 390 399 403 426 623 626 629 640 754 811 818 822 838 862	phase 2 1 0 0 0 0 1 1 0 2 2 1 2 0 1 2 0 0 0 0	strand	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CACTTCCACA TCCACACCAG^CACTACTCAGGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAG^GAATAGAGTG TGAGGAATAGAATGTGCTGA AGGAATAGAATGTGCTGAG GTGTGCTGAG^GAAGGTCCTC GCTGAGGAAGAGTCCTCTTCA CAACCTTCAGA^TCTTTGTTC CGACCTTCAG^CAGAAGGGAT CCTTCAGAGAGGGATCTT TCAGCAGAAGAGGGATCTT TCAGCAGAAGAGGGATCTTCAA GATCTTCAAGATGTCGGCCA ATTTCCACAGAAGAGTCAGTTCA GGATCCACAGAAAGATCAGTT CCACAGAAAAGATCAGTTGCAAAAGGAACCACCACGAAATGAAAAGAAGATCAGTTGGAAAATG AAAAGTCAGAGAAGGTCACCACCA CATGACCGAGAGCCACCACCCCC CATGACCCAGGAACCTCACCACCAC CATGACCCAGAACTCACCACCACCACCACCACCACCACCACCACCACCAC	pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019 1016 1013 1002 888 828 824 820 804 780 773	pos 5'->3' 351 365 373 382 388 390 399 403 426 623 626 629 640 754 814 818 822 838 862 869	phase strand 2	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.19 0.19 0.19 0.34 0.18 0.17 0.33 0.17 0.07 0.07 0.07 0.07 0.07	ATTCTATCAG^CACTITCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAG^GAATAGAGTG TGAGGAATAGAGATG TGAGGAATAGAGATGCTGA AGGAATAGAGATGCTGAG GTTGCTGAG^GAAGGGTCCTC GCTGAGGAAGAGATCCTTCA CACCTITCAG^TTCTITGTTC CGACCTITCAG^CAGAAGGGAT CCTTCAGCAGAAGGGATCTT TCAGCAGAAGGGATCTT TCAGCAGAAGGGATCTTCAA GATCTTCAAG^ATGTCGGCCA ATTTCCACAG^GCCAACTTCA GGATCCACAGAAGAGTCAGTT CCACAGAGACAGTGGAA AGAAGTCAGTTGGAA AGAAGTCAGATTGGAAAATG AGAAGTCAGATTGAAAATG AGAAGTCAGATTCAGTGGAA AGAAGTCAGATTGAAAATG CCAGGAGCCACACCACCACCACCACCACCACCACCACCAGCCC GAGCCACCAG^CCCCAGGAGCC
pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019 1016 1013 1002 888 828 824 820 804 780 773	pos 5'->3' 351 365 373 382 388 390 399 403 426 623 626 629 640 754 814 818 822 838 862 869	phase 2 1 0 0 0 0 0 1 0 2 2 2 0 0 1 2 0 0 0 1 1 2 0 0 1 1 2 0 0 1 1 1 1	strand	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAGAGTGCCTGAGG GGTGCCTGAGGGAATAGAATG TGAGGAATAGAGTGTGCTGAG AGGAATAGAGTGTGCTGAGG GTTGCTGAGAGAAGGTCCTC GCTGAGGAAGAGTCCTCTTCA CAACCTTCAGAGAGAGGGAT CCTTCAGAGAAGGGATCTT TCAGCAGAAGGGATCTTTCAA GATCTTCAAGAAGGGATCTTCAA GATCTTCAAGAAGGGATCTTCA GGATCCACAGAAGGGATCTTCA GGATCCACAGAAGGGATCTCAA GATCTTCAAGAAGTCAGTT CCACAGAAAGATCAGTT CCACAGAAAGATCAGTTGGAAA AGAAGTCAGAGAGAGTACCACCA CATGACCGAGACCCACCACCA CATGACCGAGACCACCACCA CATGACCGAGACCCACCACCA	pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019 1016 1013 1002 888 828 824 820 804 780 773 768	pos 5'->3' 351 365 373 382 388 390 399 403 426 623 626 629 640 754 814 818 822 838 862 869 874	phase strand 2	confidence	ATTCTATCAG^CACTITCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAG^GAGTAGAGTG TGAGGAATAGAG^TGTGCTGA AGGAATAGAG^TGTGCTGAGG GTGTGCTGAG^GAGAGGTCCTC GCTGAGGAAG^GTCCTCTTCA CAACCTTCAG^TCTCTTTGTTC CGACCTTCAG^CAGAAGGGAT CCTTCAGCAG^AAGGGATCTT TCAGCAGAAG^GGATCTT TCAGCAGAAG^GGATCTT TCAGCAGAAG^GGATCTTCAA GATCTTCAGG^ATGTCGGCCA ATTTCCACAG^AGCCAACTTCA GGATCCACAG^AGAGTCATTCA GGATCCACAG^AGAGTCAGTT CCACAGAAAG^TCAGTTGGAA AGAAGTCAG^TTGGAAAATG AATGGCCGAG^CACCACCACCC CATGACCGAG^CCCCCGGAGCCA ACCAGCCCAG^CCCCCGGAGCCA ACCAGCCCCAG^CCCC
pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019 1016 1013 1002 888 828 824 820 804 780 773 768	pos 5'->3' 351 365 373 382 388 390 399 403 426 623 626 629 640 754 814 818 822 838 862 869 874	phase 2 1 0 0 0 0 1 1 0 2 2 2 1 2 0 0 1 1 2 0 0 0 1 1 1 1	strand	confidence 0,21 0,47 0,18 0,18 0,18 0,18 0,18 0,18 0,18 0,18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CACTTCCACA TCCACACCAG^CACTACTCAGGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAG^GAATAGAGTG TGAGGAATAG^AGTGTGCTGA AGGAATAGAGATGTGTGCTGA AGGAATAGAGATGTGCTCAG GTGTGCTGAG^GAAGGTCCTC GCTGAGGAAG^GTCCTCTTCA CAACCTTCAG^TTCTTTTTTC CGACCTTCAG^AAAGGGATCTT TCAGCAGAAG^AAGGGATCTT TCAGCAGAAG^ATGTCTTCAA GATCTTCAAG^ATGTGGGCA ATTTCCACAG^AAGTCACTTCA GGATCCACAGAAGGTCACTTCA GGATCCACAGAAGATCAGTT CCACAGAAAGTCAGTTGGAA AGGAAAGTCAGTTGGAA AGAAAGTCAGATGAAAAGT AATGGCCGAG^CACCACCACC CATGACCGAG^CCACCAGCCC GAGCCACCAG^CCCAGGAGCA ACCAGCCCAG^CCCCAGGAGCA	pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019 1016 1013 1002 888 828 824 820 804 780 773	pos 5'->3' 351 365 373 382 388 390 399 403 426 623 626 629 640 754 814 818 822 838 862 869	phase strand 2	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.19 0.19 0.19 0.34 0.18 0.17 0.33 0.17 0.07 0.07 0.07 0.07 0.07	ATTCTATCAG^CACTITCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAG^CTGCCTGAGG GGTGCCTGAG^GAATAGAGTG TGAGGAATAGAGATGAGGATAGAGTG GTGAGGAAAGAGATGCTGA AGGAATAGAGATGCTGCAGAGGAGAGAGTCCTC GCTGAGGAAGAGATCCTTCA CAACCTTCAG^TCAGAAGGGAT CCTTCAGCAGAAGGGATCTT TCAGCAGAGAGGGATCTT TCAGCAGAGAGGGATCTTCAA GATCTTCAGAGAAGGGATCTTCAA GATCTCAAGAGAAGTCAGTT CCACAGAGACAGTCAGTGCACAGAAGGGAT ATTTCCACGAGACAGATCAGTT CCACAGAAGATCAGTT CCACAGAGACAGTCACACCA GAATCCCAGAGAGGAATTCA GAATCCCAGGAGAGTCACCACCA CATGACCGAGACCCACCACCACCACCACCACCACCACCAGCCC GAGCCACCAGCACCCACC
pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019 1016 1013 1002 888 828 824 820 804 780 773 768 727	pos 5'->3' 351 365 373 382 388 390 399 403 426 623 626 629 640 754 814 818 822 838 862 869 874 915	phase 2 1 0 0 0 0 1 2 2 2 1 2 0 0 1 1 2 0 0 1 1 0 0 1 1 0 0 1 1 0 0 0 1 1 0 0 0 1 1 0 0 0 1 1 0 0 0 0 1 1 0 0 0 0 1 1 0 0 0 0 1 1 0 0 0 0 1 1 0	strand	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CACTTCCACA TCCACACCAG^CACTACTCAGGT AGCTACTCAGAGTGCCTGAGG GGTGCCTGAG^GAATAGAGTG TGAGGAATAGAATGTGCTGAG GTGTGCTGAG^GAAGGTCCTC GCTGAGGAAGAGTCCTCTTCA CAACCTTCAG^TTCTTTGTTC CGACCTTCAG^TCTTTTGTTC CGACCTTCAGAAGGGATCTTCA GATCTTCAGAAGGGATCTTCA GATCTTCAGAAGAGGGATCTTCA GATCTTCAAGAAGAGGATCTTCA GATCTCACAGAAAGTCAGTTCA GATCTCACAGAAAGTCAGTTCA GGATCCACAGAAAAGTCAGTT CCACAGAAAGTCAGTTCAGAAATG AATAGCCGAGAGTCACACCA CATGACCGAGAACTCAGCA CATGACCGAGAACTCAGCCC GAGCCACCAGACCCCAGGAGCCA ACCAGCCCAGAGACCACCAGCCC GAGCCCCAGGAGCCACCAGGCCA GGCTCATGAGACACCTGTGTAG	pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019 1016 1013 1002 888 828 824 820 804 780 773 768 727	pos 5'->3' 351 365 373 382 388 399 403 426 623 626 629 640 754 814 818 822 838 862 869 874 915	phase strand 2	confidence	ATTCTATCAG^CACTITCCACA TCCACACCAG^CACTACTCAGGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAGGAGAATAGAGTG TGAGGAATAGAATTGCTGA AGGAATAGAGATTGCTGA AGGAATAGAGATTGCTGAGA GTGTGCTGAGGAGAGGTCCTC GCTGAGGAAGAGTCCTCTTCA CAACCTTCAGATTCTTTGTTC CGACCTTCAG^CAGAAGGGAT CCTTCAGCAGCAAGAGGAT CCTTCAGCAGCAGAAGGGAT CCTTCAGCAGCAGAAGGGAT CCTTCAGCAGCAGAAGGGAT CCTCAGAGAGAGGATCTTCAA GATCTTCAAGAGAGGAGTCTTCAA GATCTTCAAGAGAGGAGACTTCA AGATCTCACAGAAAGTGTTGGAA AGAAAGTGCAGCAGCACACACACACAGAAAGTCAGTTGGAA AGAAAGTCAGATTGGAAAATG AATGGCCGAGAGTCACCACCA CATGACCGAGAGCCACCACACACCACCACACACCACCACCACAGACCCCAGGAGCCA GCCCCCAGGAGCCA
pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019 1016 1013 1002 888 828 824 820 804 780 773 768 727 717	pos 5'->3' 351 365 373 382 388 390 399 403 426 623 626 629 640 754 814 818 822 838 862 874 915 925	phase 2 1 0 0 0 0 0 1 0 2 2 2 0 0 1 1 2 0 0 1 1 1 0 0 1 1 0 0 1	strand	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.18	ATTCTATCAG^CACTTCCACA TCCACACCAG^CACTACCACA TCCACACCAG^CACTACTCAGGT AGCTACTCAGAGTAGCTGAGG GGTGCCTGAG^GAATAGAGTG TGAGGAATAGAGTGTGCTGA AGGAATAGAGTGTGTGAGG GTGTGCTGAG^GAAAGGTCCTC GCTGAGGAAGAGTCCTCTTCA CAACCTTCAG^CAGAAGGGAT CCTTCAG^CAGAAGGGATCTT TCAGCAGAAGGGATCTTCAA GATCTTCAAG^AAGGGATCTTCA GATCTTCAAGAAGGGATCTTCA GGATCACAGAAGAGGATCAGT CCACAGAAAG^TCAGTTCA GGATCCACAGAAGAAGTCAGTT CACAGAAAGTCAGTTGAA AGAAGTCAGTTGGAAAATG AATGGCCGAG^CCCACCCCC GAGCCACCAGCCCAGCCC GAGCCACCAGCCCAGCCC GAGCCACCAGCCCAGCCCA ACCAGCACAGTTGAGACACCAC ACCAGCACCAGCCCAGC	pos 3'->5' 1291 1277 1269 1260 1254 1252 1243 1239 1216 1019 1016 1013 1002 888 828 824 820 804 780 773 768 727 717	pos 5'->3' 351 365 373 382 388 390 399 403 426 623 626 629 640 754 814 818 822 838 862 869 874 915	phase strand 2	confidence 0.21 0.47 0.18 0.18 0.18 0.18 0.18 0.18 0.18 0.17 0.33 0.17 0.07 0.07 0.07 0.07 0.07 0.07 0.07	ATTCTATCAG^CACTTCCACA TCCACACCAG^CTACTCAGGT AGCTACTCAG^GTGCCTGAGG GGTGCCTGAG^GAATAGAGTG TGAGGAATAGAGATGAGGTG TGAGGAATAGAGATGCTGA AGGAATAGAGATGCTGAG GGTGCTGAG^GAAGGGTCCTC GCTGAGGAAGAGTCCTC GCTGAGGAAGAGTCCTC GCACCTTCAG^CAGAAGGGAT CCTTCAGCAGAAGGGATCTT TCAGCAGAGAAGGGATCTTCAGCAGAAGAGGATCTTCAGCAGAAGAGATCTCAG GATCTTCAGG^AAAGGTCATCA GATCTCAAG^AGCAACTCA GGATCCACGAGAAAGTCAGTT CCACAGAAGAGTCAGTTGGAA AGAAGTCAGATTGAAAAATG AGAAGTCAGATTGAAAAATG AGAAGTCAGATTGAAAATG CCAGGAGCCAGCCCA CATGACCGAGAGCAGCCC GAGCCACCAGCACCACCACCACCACGCC GAGCCACCAGGACCACCAGGCCC GAGCCACCAGGACCACCAGGCCC GAGCCACCAGGACCCCA GGCTCATGAGACACGTTGTAG CACGTTGTAGACAGGCCC GGCTCATGAGACACGTTGTAG CACGTTGTAGACAGGCCC GGCTCATGAGACACGCTCAGGGGGGT CACCTGTGTAGACAGGGCGCCCAGGCCCAGGGCCAGGCCCAGGGCGGCCCAGGGCGGC

### **Splice Site Prediction by Neural Network (NNSplice)**

## **Donor site predictions for 85.53.81.31.7591.0:**

Start	End	Score	Exon Intron
134	148	1.00	acttaag <b>gt</b> gagtga
494	508	0.42	cgcccat <b>gt</b> acctct
924	938	0.89	gggcttg <b>gt</b> atgtat
1351	1365	0.74	ttacctt <b>gt</b> aaggca

## **Donor site predictions for 85.53.81.31.7645.0:**

Start	End	Score	Exon Intron
134	148		acttaag <b>gt</b> gagtga
134	148	1.00	
494	508	0.42	cgcccat <b>gt</b> acctct
1351	1365	0.74	ttacctt <b>gt</b> aaggca

# Acceptor site predictions for 85.53.81.31.7591.0:

Start	End	Score	Intron	Exon
99	139	0.53	taaattctt	actttgtgtc <b>ag</b> gacctgcacaaagcacttaa
172	212	0.74	attattaat	gcctttctgc <b>ag</b> atggagtaaccatggcttgg
227	267	0.85	cgctctcag	atgtcctccc <b>ag</b> gcaggaatcactagacaccc
293	333	0.77	tttcctctc	ttccccaact <b>ag</b> gggtggccgtcatgctgggg
506	546	0.80	tcttcctgt	gcgtcctctc <b>ag</b> tctccgagatcctctacacc
621	661	0.94	tcagatgtt	cttctccttcagcttcggcttcacccactcct
1004	1044	0.61	tgaagatco	cttctgctga <b>ag</b> gtcggaacaaggccttctcc
1111	1151	0.67	cccaaaggt	ccccactctc <b>ag</b> gagggtgacaccctgatggc
1185	1225	0.85	ccccatcat	cttcagcctc <b>ag</b> gaacaaagaactgaaggttg
1244	1284	0.79	tcagcacac	tctattcctc <b>ag</b> gcacctgagtagctggtgtg
1552	1592	0.57	ctgtggttt	ttgcgtattc <b>ag</b> agttatgcaaccatcatgac

## Acceptor site predictions for 85.53.81.31.7645.0:

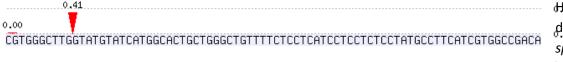
Start	End	Score	Intron	Exon
99	139	0.53	taaattctta	tttgtgtc <b>ag</b> gacctgcacaaagcacttaa
172	212	0.74	attattaatg	cctttctgc <b>ag</b> atggagtaaccatggcttgg
227	267	0.85	cgctctcaga	tgtcctccc <b>ag</b> gcaggaatcactagacaccc
293	333	0.77	tttcctctct	tccccaact $oldsymbol{ag}_{gggtggccgtcatgctgggg}$
506	546	0.80	tcttcctgtg	gtcctctc <b>ag</b> tctccgagatcctctacacc
621	661	0.94	tcagatgttc	$ttctccttc \mathbf{ag}_cttcggcttcacccactcct$
1004	1044	0.61	tgaagatccc	ttctgctga <b>ag</b> gtcggaacaaggccttctcc
1111	1151	0.67	cccaaaggtc	ccactctc <b>ag</b> gagggtgacaccctgatggc
1185	1225	0.85	ccccatcatc	ttcagcctc <b>ag</b> gaacaaagaactgaaggttg
1244	1284	0.79	tcagcacact	tattcctc $oldsymbol{ag}$ gcacctgagtagctggtgtg
1552	1592	0.57	ctgtggtttt	tgcgtattc <b>ag</b> agttatgcaaccatcatgac

Desaparece un sitio *donor* de la secuencia WT a la mutante. Este sitio se encuentra coincidiendo con la región donde está la mutación, pero, como está dentro del exón y no participa de normal en el *splicing* del mRNA, por lo que la mutación no estará afectando al *splicing*.

## **Spliceman**

Point mutation	Wildtype (wt)	Mutation (mt)	L1 distance	Ranking (L1)
gtatg(t/c)atcat	gtatgt	gtatgc	27979	61%

#### **CRYP-SKIP**



Hay otro sitio críptico a solo 5 nt de nuestra posición de interés, pero la T no la marca como posible sitio de splicing, por lo que no estará afectando a este.

## **Human Splicing Finder**



#### **SVM-BPfinder**

 seq\_id
 agez
 ss\_dist
 bp\_seq
 bp\_ser
 y\_cont
 ppt\_off
 ppt\_len
 ppt\_scr
 svm\_scr

 wt
 70
 38
 gtatcatgg
 -1.70767935223
 0.727272727273
 14
 20
 41
 -0.53619841

 seq\_id
 agez
 ss\_dist
 bp\_seq
 bp\_scr
 y\_cont
 ppt\_off
 ppt\_len
 ppt\_scr
 svm\_scr

 mut
 70
 38
 gcatcatgg
 -1.50412238601
 0.7272727272727
 14
 20
 41
 -0.45649622

Son diferentes porque incluyen el cambio (en la segunda posición) pero tienen puntuación negativa, por lo que no se tienen en cuenta.

### **Variant Effect Predictor tool**

ENST00000305899.4:c.612T>C 19:15728655- C	synonymous_variant	OR10H2	ENSG00000171942 Transcript	ENST00000305899.4 protein_coding	1/1	636	612	204	С	TGT/TGC <u>COSV59947296</u>

#### **ESEfinder**

Si realizamos la búsqueda para las regiones de *splicing* que contengan la posición de interés, solo se obtienen dos resultados con puntuaciones positivas para las matrices de 5'SS:

907 (-735) GCTGTGGCCCTGGGCGTGGGCTTGGTATGT 0.89	907 (-735) GCTGTGGCCCTGGGCGTGGGCTTGGTATGT	T -27.22330 907 GCTGTGGCCCTGGGCGTGGGCTTGGT	TGT 0.60710	907 (-735) GCTGTGGCCCTGGGCGTGGGCTTGGTATGT -25.50600
916 CTGGGCGTGGGCTTGGTATGTATCATGGCA 7.4	916 CTGGGCGTGGGCTTGGTATGTATCATGGC	CA -12.79590 916 CTGGGCGTGGGCTTGGTATGTATCA	GGCA 7.18970	916 CTGGGCGTGGGCTTGGTATGTATCATGGCA -13.77820

Si buscamos las predicciones equivalentes para la secuencia mutante, se observa que las puntuaciones para el resultado aumentan ligeramente, mientras que para el segundo se reducen un poco:

907 (-735) GCTGTGGCCCTGGGCGTGGGCTTGGTATGC	1.02170	907 (-735) GCTGTGGCCCTGGGCGTGGGCTTGGTATGC -26.62240	907 (-735) GCTGTGGCCCTGGGCGTGGGCTTGGTATGC	0.87780	907 (-735) GCTGTGGCCCTGGGCGTGGGCTTGGTATGC -24.91840
916 (-726) CTGGGCGTGGGCTTGGTATGCATCATGGCA	6.27240	916 (-726) CTGGGCGTGGGCTTGGTATGCATCATGGCA -12.28830	916 CTGGGCGTGGGCTTGGTATGCATCATGGCA	6.03390	916 (-726) CTGGGCGTGGGCTTGGTATGCATCATGGCA -13.26950

Por lo tanto, para el segundo de los resultados, podríamos decir que un sitio donor está debilitado, lo que podría estar afectando al splicing.

Por otro lado, haciendo la búsqueda de las ESE, las puntuaciones no se ven alteradas de la secuencia WT (arriba) a la mutante, por lo que no habrá cambios en las ESE.

929 (-713)	TGGTATG	-4.87626	929 (-713) TG(	GTATG-3.34	4073	929 (-713)	TGGTATGT	-4.91800	929 (-713)	TGGTATG	-1.51312
930 (-712)	GGTATGT	-0.62242	930 (-712)	TATGT -1.30	0741	930 (-712)	GGTATGTA	1.06014	930 (-712)	GGTATGT	-2.24524
931 (-711)	GTATGTA	-3.59577	931 (-711)	ATGTA -3.10	0536	931 (-711)	GTATGTAT	-1.34752	931 (-711)	GTATGTA	-5.83547
932 (-710)	TATGTAT	-7.03470	932 (-710)	TGTAT -5.31	1189	932 (-710)	TATGTATC	-3.52211	932 (-710)	TATGTAT	-1.90920
933 (-709)	ATGTATC	-6.58612	933 (-709)	GTATC -5.08	8993	933 (-709)	ATGTATCA	-1.78227	933 (-709)	ATGTATC	-2.89588
934 (-708)	TGTATCA	-4.22010	934 (-708)	TATCA -2.93	3387	934 (-708)	TGTATCAT	-2.90758	934 (-708)	TGTATCA	-0.04653
935 (-707)	GTATCAT	-3.80261	935 (-707)	ATCAT -3.3	6147	935 (-707)	GTATCATG	3.28566	935 (-707)	GTATCAT	-3.56316
936 (-706)	TATCATG	-5.03550	936 (-706) TAT	TCATG -4.0	7180	936 (-706)	TATCATGG	-1.04920	936 (-706)	TATCATG	0.98787

929 (-713)	TGGTATG	-4.87626	929 (-713) TGGTATG -3.34073	929 (-713) TGGTATGC -4.91800	929 TGGTATG -1.51312
930 (-712)	GGTATGC	-2.47582	930 (-712) GGTATGC -2.50411	930 (-712) GGTATGCA 0.41570	930 (-712) GGTATGC -0.70614
931 (-711)	GTATGCA	-4.05348	931 (-711) GTATGCA -3.20935	931 (-711) GTATGCAT 0.38150	931 (-711) GTATGCA -4.11854
932 (-710)	TATGCAT	-4.51097	932 (-710) TATGCAT -3.50010	932 (-710) TATGCATC -2.76287	932 (-710) TATGCAT -3.40045
933 (-709)	ATGCATC	-5.12879	933 ATGCATC -3.83518	933 ATGCATCA -1.55143	933 ATGCATC -0.51125
934 (-708)	TGCATCA	-1.91009	934 (-708) TGCATCA -0.86501	934 (-708) TGCATCAT -2.33865	934 (-708) TGCATCA -1.39480
935 (-707)	GCATCAT	-4.40554	935 (-707) GCATCAT -3.61025	935 GCATCATG 1.89726	935 (-707) GCATCAT -3.25111
936 (-706)	CATCATG	-2.08501	936 (-706) CATCATG -0.96675	936 (-706) CATCATGG -1.02807	936 (-706) CATCATG 0.63117

### **EX-SKIP**

Seq	PESS	FAS-ESS hex2	FAS-ESS hex3	IIE	IIE	NI-ESS trusted	NI-ESS all	PESE	RESCUE -ESE	EIE	EIE	NI-ESE trusted	NI-ESE all	ESS	ESE	ESS/ESE
	(count)	(count)	(count)	(count)	(sum)	(count)	(sum)	(count)	(count)	(count)	(sum)	(count)	(sum)	(total)	(total)	(ratio)
wt	16	33	26	262	3696.4485	80	-116.0393	70	51	309	3609.2156	302	453.4088	417	732	0.57
mut	14	33	26	259	3654.6598	79	-114.6174	70	51	310	3617.7994	302	454.6694	411	733	0.56

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

#### **HOT-SKIP**

>wt

 $\verb|ctcaatacattattattaatgcctttctgcagatggagtaaccatggcttggacagatgaaggaggcgctctcagatgtc| \\$ ctcccaggcaggaatcactagacaccccatgctcctaaccactgggtcttctttcctctCTTCCCCAACTAGGGGTGGC CGTCATGCTGGGGCTAAACCACACCTCCATGTCTGAATTCATCCTCGGCTTCTCTGCCTTCCCCCACCTCCAACTGA TGCTCTTCCTGCTGTTCCTGCTGATGTACCTGTTCACGCTGCTGGGCAACCTGCTCATCATGGCCACCGTCTGGAGCGAG CGCAGCCTCCACACGCCCATGTACCTCTTCCTGTGCGTCCTCTCAGTCTCCGAGATCCTCTACACCGTGGCCATCATCCC GCGCATGCTGGCCGACCTGTCCACCCAGCGCTCCATCGCCTTCCTGGCCTGTGCCAGTCAGATGTTCTTCTCCTTCA GCTTCGGCTTCACCCACTCCTTCCTGCTCACCGTCATGGGCTACGACCGCTACGTGGCCATCTGCCACCCCCTGCGCTAC AACGTGCTCATGAGCCCACGGGGCTGCGCCTGCCTGGTGGGCTGCTCCTGGGCTGGTCGGTCATGGGGATGGTGGT GACCTCGGCCATTTTCCAACTGACTTTCTGTGGATCCCATGAGATCCAGCATTTTTTATGTCATGTGCCACCTCTGTTGA CTCCTCATCCTCTCTCTATGCCTTCATCGTGGCCGACATCTTGAAGATCCCTTCTGCTGAAGGTCGGAACAAGGCCTT CTCCACCTGTGCCTCTCACCTTATTGTGGTCATTGTGCACTATGGCTTTTGCCTCTGTCATCTACCTCAAGCCCAAAGGTC CCCACTCTCAGGAGGTGACACCCTGATGGCCACCACCTACGCAGTCCTCACGCCCTTCCTCAGCCCCATCATCTTCAGC CTCAGGAACAAGAACTGAAGGTTGCCATGAAGAGGGCCTTCCTCAGCACACTCTATTCCTCAGGCACCCTGAGTAGCTGG TGTGGAAGTGCTGATAGAATATGATAGGAGGATGACCATCACCTTGTCTGCACAGTGTGGCtagtaatgcttaccttgta agg caggtg taaagatttctg tatatgacaacactcatcacatag taggtgctcagtaaatgttaaaagcatgtttactt $\verb|ccacaactcttgatctgtatgtctttatctgagttttaattttgagttatagtagctttattaagatgtaattcaccta|\\$ ccatacaatgtacccattagagcgcacatttctgtggtttttgcgtattcagagttatgcaaccatcatgacaatctggc ttagagtattttagtcatccaaaaaagaaacccaaatccta

2534	635	Α	TTGGTATATATCATG	GGTATATATCA	3	1	1	1	12.0557	5	-5.4218	0	0	0	0.0000	0	0.0000	11	0	11.00
2535	635	С	TTGGTATCTATCATG	GGTATCTATCA	0	0	0	0	0.0000	1	-2.2605	0	0	1	5.2320	0	0.1489	1	1	1.00
2538	635	Т	TTGGTATTTATCATG	GGTATTTATCA	1	0	0	4	54.3215	5	-5.2486	0	0	1	6.4797	0	0.0000	10	1	10.00