GENE*ie* Report: NM_012448.4:c.1680+1del

This report was produced for **Demo Admin** of **Demo Account** on Tuesday, 24 September 2024

This report is for research use only. It is not intended for diagnostic or clinical purposes.

Splice-Altering

90% PROBABILITY

- Annotated donor splice-site variant.
- Variant affects an annotated donor and overlapping cryptic donor.
- Risk of cryptic mis-splicing. Competitive cryptic splice-site within 250 nt or in SpliceVault Top4.

NIF	Similar Impact	Same Sequence	SpliceVault Top4	Cryptic Risk
★★★	☆☆☆	☆☆☆	Mixed Frames	Yes

Variant	NM_012448.4:c.1680+1del		
Gene	*STAT5B*	**Coordinates (GRCh38)**	17:42211982 AC>A
Location	(NM_012448.4) Intron 13 donor / Distance from donor: +1		
Variant Databases	VCV000005698 (ClinVar) - Pathogenic		

Native Intron Frequency (NIF)

Relative frequency of a given splice-site sequence among all human splice-site sequences

Zone	Window	Reference (REF)	Variant (VAR)	Frequency		% Scale		NIF Impact VAR/REF
				REF	VAR	REF	VAR	
U5	E4 - D5	CAGGgtgaggag	CAGGtgaggagc	815	0	0.74	0	-100%
U1	E3 - D6	CAGGgtgaggag	CAGGtgaggagc	407	0	0.5	0	-100%
	E2 - D7	CAGGgtgaggag	CAGGtgaggagc	412	0			
U6	E1 - D8	CAGGgtgaggag	CAGGtgaggagc	1099	0	0.9	0	-100%

NIF-ML Power (Machine Learning)	
ML Score	0.94
Pathogenic	100%
Benign	0%
n	176

Cryptic Splice-site Modification

Cryptic splice-site overlapping the annotated splice-site that is modified by this variant

Splice-site Position	Reference (REF)	Variant (VAR)	REF	VAR	SpliceVault Top-10	In Frame
			U5 | U1 | U6	U5 | U1 | U6		
Annotated	CAGGgtgaggag	CAGGtgaggagc	0.74 | 0.50 | 0.90	0.00 | 0.00 | 0.00	N/A	N/A
+1 > -1	CAGGgtgaggag	ACAGGtgaggag	0.74 | 0.50 | 0.90	0.97 | 0.96 | 0.90	N	N

Same Splice-site Variants

Variants affecting the same splice-site as the test variant

Test Variant	Distance from Donor	NIF Impact	Classification	Variant ID
		U5 | U1 | U6		
NM_012448.4:c.1680+1del	+1	-100% | -100% | -100%	P	VCV000005698

Similar Impact Variants	Distance from Donor	NIF Impact	Classification	Variant ID
		U5 | U1 | U6		
No Similar Impact variants reported at this splice-site				

Different Impact Variants	Distance from Donor	NIF Impact	Classification	Variant ID
		U5 | U1 | U6		
No Different Impact variants reported at this splice-site				

Same Sequence Variants

Variants making the same sequence change at a different splice-site

Zone	Window	Reference (REF)	Variant (VAR)	NIF Impact	Pathogenic		Benign	
				VAR/REF	introns	*n*	introns	*n*
U5	E4 - D5	CAGGgtgaggag	CAGGtgaggagc	-100%	0	0	0	0
U1	E3 - D6	CAGGgtgaggag	CAGGtgaggagc	-100%	0	0	0	0
	E2 - D7	CAGGgtgaggag	CAGGtgaggagc		0	0	0	0
U6	E1 - D8	CAGGgtgaggag	CAGGtgaggagc	-100%	0	0	0	0

E4 - D5	NIF Impact	Classification	Variant ID
	U5 | U1 | U6		
No same sequence variants for this window			

E3 - D6	NIF Impact	Classification	Variant ID
	U5 | U1 | U6		
No same sequence variants for this window			

E2 - D7	NIF Impact	Classification	Variant ID
	U5 | U1 | U6		
No same sequence variants for this window			

E1 - D8	NIF Impact	Classification	Variant ID
	U5 | U1 | U6		
No same sequence variants for this window			

SpliceVault Top-10

Natural splicing mistakes around this splice-site that may be enhanced by this variant

Event	Same Frame	Skipped Exons	Cryptic Position	Cryptic mean NIF	Samples (GTEx)	Samples (SRA)	Max Reads (GTEx)	Total Samples	Splice Junction
Annotated Splicing	✓				19,077	179,228	1,536	198,305	chr17:42210498-42211983
Exon Skipping	✓	13			68	840	5	908	chr17:42210498-42216013
Cryptic donor [2 3 4]	✓		+160	0.04	161	505	9	666	chr17:42210498-42211824
Exon Skipping	✓	12-13			27	466	3	493	chr17:42210498-42217159
Cryptic donor			-28	0.00	14	151	2	165	chr17:42210498-42212011
Cryptic donor			-22	0.00	59	18	2	77	chr17:42210498-42212005
Cryptic donor			-10	0.00	0	16	0	16	chr17:42210498-42211993
Cryptic donor [2 3]	✓		+106	0.00	1	12	1	13	chr17:42210498-42211878
Cryptic donor [2 3]	✓		+115	0.04	2	5	1	7	chr17:42210498-42211869
Cryptic donor	✓		-24	0.00	3	1	1	4	chr17:42210498-42212007

[2] Splice-site frame modified by this variant (see Cryptic Splice Site Modification table above)

[3] Splice-site position modified by this variant (see Cryptic Splice Site Modification table above)

[4] Cryptic is >= 50% strength of annotated splice-site

Understanding your report

Assertion and Probability

Splice - Altering

Clinical and genetic evidence indicate this variant has a given probability of altering pre-mRNA splicing for this gene.

Splice-Neutral

Clinical and genetic evidence indicate this variant has a given probability of maintaining the existing pattern of pre-mRNA splicing for this gene

Uncertain

Clinical and genetic evidence for pre-mRNA splicing disruption by this variant is weak and/or conflicting; and cannot be assigned a probability.

Flags

Summary

Native Intron Frequency (NIF)

NIF-ML Power (Machine Learning)

Cryptic Splice-site Modification

Same Splice-site Variants

Same Sequence Variants

SpliceVault Top-10

Report MetaData

REPORT DATE	GENEIE VERSION	API VERSION
24-Sept-2024	0.0.229.0	0.0.50
ML DONOR VERSION	**ML ACCEPTOR VERSION**	**CLINVAR RELEASE**
v1.0.6	v1.0.5	2023-07
HGMD RELEASE		
2019.1		