



PredictSNP overview

Date: 2017/03/06

Genome version: GRCh38/hg38

PredictSNP version: 2.1

If you use PredictSNP and obtain scientific results that you publish, we would ask you to acknowledge the usage of PredictSNP by referencing the article below.

Bendl, J., Musil, M., Stourac, J., Zendulka, J., Damborsky, J., Brezovsky, J., 2016: PredictSNP2: A unified platform for accurately evaluating SNP effects by exploiting the different characteristics of variants in distinct genomic regions. *PLOS Computational Biology* 12: e1004962

	PredictSNP2		CADD		DANN		FATHMM		FunSeq2		GWAVA	
	Neu	Del	Neu	Del	Neu	Del	Neu	Del	Neu	Del	Neu	Del
Regulatory	0	0	0	0	0	0	0	0	0	0	0	0
Splicing	0	0	0	0	0	0	0	0	0	0	0	0
Missense	0	0	0	0	0	0	96	0	93	3	94	2
Synonymous	74	22	96	0	43	49	0	0	0	0	0	0
Nonsense	0	0	0	0	0	0	0	0	0	0	0	0
Others	0	0	0	0	0	0	0	0	0	0	0	0

Variant: 21 : 32634876, $T \rightarrow C$					
Position:	chr21:32634876	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	deleterious	neutral	deleterious	neutral	deleterious
Score:	-0.0974	19.5900	0.6048	0.8948	0.0000	0.6500
Exp. accuracy:	0.88	0.69	0.96	0.71	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32638911, $C \rightarrow A$					
Position:	chr21:32638911	Ref. allele:	C	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs372695378	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	?
Score:	-1.0000	11.0800	0.3700	0.6560	0.0000	0.4900
Exp. accuracy:	0.96	0.88	0.97	0.69	0.93	0.43

External links

[dbSNP] [GenBank] [RegulomeDB] [UCSC] [Ensemble]
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Variant: 21 : 32638911, $C \rightarrow T$					
Position:	chr21:32638911	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	?
Score:	-1.0000	10.5800	0.3930	0.3106	0.0000	0.4900
Exp. accuracy:	0.96	0.88	0.97	0.73	0.93	0.43

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32638947, $T \rightarrow A$					
Position:	chr21:32638947	Ref. allele:	T	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	9.8270	0.6017	0.0519	0.0000	0.5100
Exp. accuracy:	0.96	0.91	0.96	0.94	0.93	0.55

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32638950, $C \rightarrow T$					
Position:	chr21:32638950	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	deleterious	neutral	neutral	neutral	deleterious
Score:	-0.6000	15.6700	0.7138	0.7348	0.0000	0.6800
Exp. accuracy:	0.95	0.58	0.93	0.69	0.93	0.70

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32638989, $T \rightarrow A$					
Position:	chr21:32638989	Ref. allele:	T	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	1.0220	0.5861	0.0407	0.0000	0.5200
Exp. accuracy:	0.96	0.95	0.97	0.96	0.93	0.58

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32639016, $T \rightarrow G$					
Position:	chr21:32639016	Ref. allele:	T	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	2.4550	0.5013	0.0443	0.0000	0.5300
Exp. accuracy:	0.96	0.95	0.97	0.96	0.93	0.64

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32639034, $A \rightarrow C$					
Position:	chr21:32639034	Ref. allele:	A	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	0.0030	0.5101	0.2148	0.0000	0.5500
Exp. accuracy:	0.96	0.95	0.97	0.77	0.93	0.66

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32639037, $C \rightarrow T$					
Position:	chr21:32639037	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	12.1300	0.5678	0.6645	0.0000	0.7300
Exp. accuracy:	0.96	0.83	0.97	0.69	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32639058, <i>C</i> → <i>T</i>					
Position:	chr21:32639058	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	8.5430	0.4633	0.0083	0.0000	0.5700
Exp. accuracy:	0.96	0.92	0.97	0.96	0.93	0.68

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32639061, <i>G</i> → <i>A</i>					
Position:	chr21:32639061	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs201117151	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	0.2980	0.4000	0.0613	0.0000	0.5700
Exp. accuracy:	0.96	0.95	0.97	0.92	0.93	0.68

External links

[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]

Variant: 21 : 32639070, <i>A</i> → <i>C</i>					
Position:	chr21:32639070	Ref. allele:	A	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs150595970	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	0.0020	0.5074	0.0572	0.0000	0.5600
Exp. accuracy:	0.96	0.95	0.97	0.92	0.93	0.69

External links

[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]

Variant: 21 : 32639076, C→A					
Position:	chr21:32639076	Ref. allele:	C	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs138579227	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	?
Score:	-1.0000	8.8030	0.3735	0.0334	0.0000	0.4900
Exp. accuracy:	0.96	0.92	0.97	0.96	0.93	0.43

External links

[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]

Variant: 21 : 32639076, C→T					
Position:	chr21:32639076	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	?
Score:	-1.0000	7.8260	0.4095	0.0391	0.0000	0.4900
Exp. accuracy:	0.96	0.91	0.97	0.96	0.93	0.43

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32639091, C→T					
Position:	chr21:32639091	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.4698	11.3300	0.6755	0.9441	0.0000	0.7300
Exp. accuracy:	0.93	0.88	0.94	0.90	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32639102, $G \rightarrow A$					
Position:	chr21:32639102	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs2230766	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5849	7.4630	0.6621	0.8221	0.0000	0.6200
Exp. accuracy:	0.93	0.91	0.95	0.57	0.93	0.66

External links

[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]

Variant: 21 : 32639675, $C \rightarrow T$					
Position:	chr21:32639675	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	7.2500	0.5045	0.0228	0.0000	0.5700
Exp. accuracy:	0.96	0.91	0.97	0.96	0.93	0.68

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32639684, $T \rightarrow C$					
Position:	chr21:32639684	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	0.0280	0.3747	0.0275	0.0000	0.5400
Exp. accuracy:	0.96	0.95	0.97	0.96	0.93	0.62

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32639708, A→G					
Position:	chr21:32639708	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	6.2540	0.5898	0.1492	0.0000	0.5100
Exp. accuracy:	0.96	0.93	0.97	0.83	0.93	0.55

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32639729, C→T					
Position:	chr21:32639729	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	12.9300	0.5706	0.6424	0.0000	0.5300
Exp. accuracy:	0.96	0.77	0.97	0.69	0.93	0.64

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32639732, C→T					
Position:	chr21:32639732	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	12.0900	0.7299	0.5451	0.0000	0.5400
Exp. accuracy:	0.96	0.83	0.91	0.70	0.93	0.62

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32639735, $G \rightarrow A$					
Position:	chr21:32639735	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	1.3590	0.4995	0.0180	0.0000	0.5400
Exp. accuracy:	0.96	0.95	0.97	0.96	0.93	0.62

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32639777, $C \rightarrow T$					
Position:	chr21:32639777	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	0.0180	0.5145	0.0413	0.0000	0.5500
Exp. accuracy:	0.96	0.95	0.97	0.96	0.93	0.66

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32641902, $G \rightarrow A$					
Position:	chr21:32641902	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	10.3700	0.7078	0.7077	0.0000	0.3300
Exp. accuracy:	0.96	0.88	0.93	0.69	0.93	0.56

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32641905, $T \rightarrow C$					
Position:	chr21:32641905	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	1.9360	0.5330	0.0543	0.0000	0.2600
Exp. accuracy:	0.96	0.95	0.97	0.94	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32641926, $T \rightarrow C$					
Position:	chr21:32641926	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	6.6930	0.6679	0.7505	0.0000	0.2400
Exp. accuracy:	0.96	0.92	0.95	0.69	0.93	0.58

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32641938, $T \rightarrow A$					
Position:	chr21:32641938	Ref. allele:	T	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.4236	13.2000	0.7736	0.9583	0.0000	0.3700
Exp. accuracy:	0.88	0.74	0.90	0.93	0.93	0.56

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32643453, A→G					
Position:	chr21:32643453	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	0.5670	0.6900	0.3045	0.0000	0.5000
Exp. accuracy:	0.96	0.95	0.94	0.73	0.93	0.51

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32645653, C→T					
Position:	chr21:32645653	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	deleterious	neutral	neutral	neutral
Score:	-0.5383	13.9600	0.9226	0.0365	0.0000	0.2300
Exp. accuracy:	0.93	0.73	0.87	0.96	0.93	0.59

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32645659, A→T					
Position:	chr21:32645659	Ref. allele:	A	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs376132504	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	14.1000	0.7860	0.1405	0.0000	0.2200
Exp. accuracy:	0.96	0.73	0.90	0.85	0.93	0.59

External links

[dbSNP] [GenBank] [RegulomeDB] [UCSC] [Ensemble]
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Variant: 21 : 32645668, $T \rightarrow C$					
Position:	chr21:32645668	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs368850131	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	14.9100	0.5617	0.6249	0.0000	0.2000
Exp. accuracy:	0.96	0.73	0.97	0.69	0.93	0.60

External links

[dbSNP]	[GenBank]	[RegulomeDB]	[UCSC]	[Ensemble]
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Variant: 21 : 32645704, $G \rightarrow C$					
Position:	chr21:32645704	Ref. allele:	G	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs372510070	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	10.1300	0.6013	0.7575	0.0000	0.1900
Exp. accuracy:	0.96	0.88	0.96	0.69	0.93	0.60

External links

[dbSNP]	[GenBank]	[RegulomeDB]	[UCSC]	[Ensemble]
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Variant: 21 : 32645713, $C \rightarrow T$					
Position:	chr21:32645713	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	deleterious	neutral	neutral	neutral
Score:	-0.5474	6.2110	0.9147	0.0309	0.0000	0.2400
Exp. accuracy:	0.93	0.93	0.87	0.96	0.93	0.58

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32645752, <i>C</i> → <i>A</i>					
Position:	chr21:32645752	Ref. allele:	C	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs376395608	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	9.5660	0.7063	0.4347	0.0000	0.2800
Exp. accuracy:	0.96	0.91	0.93	0.72	0.93	0.55

External links

[dbSNP] [GenBank] [RegulomeDB] [UCSC] [Ensemble]
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Variant: 21 : 32645752, <i>C</i> → <i>T</i>					
Position:	chr21:32645752	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	9.4420	0.8825	0.3224	0.0000	0.2800
Exp. accuracy:	0.96	0.91	0.90	0.73	0.93	0.55

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32646403, <i>G</i> → <i>A</i>					
Position:	chr21:32646403	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	2.9250	0.5066	0.0144	0.0000	0.2400
Exp. accuracy:	0.96	0.95	0.97	0.96	0.93	0.58

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32646412, A→G					
Position:	chr21:32646412	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	1.2660	0.4711	0.0991	0.0000	0.3100
Exp. accuracy:	0.96	0.95	0.97	0.87	0.93	0.53

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32646430, T→C					
Position:	chr21:32646430	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	4.1360	0.7459	0.3716	0.0000	0.2800
Exp. accuracy:	0.96	0.94	0.91	0.72	0.93	0.55

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32646445, G→A					
Position:	chr21:32646445	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	8.1540	0.4897	0.0569	0.0000	0.2400
Exp. accuracy:	0.96	0.91	0.97	0.92	0.93	0.58

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32646460, A→G					
Position:	chr21:32646460	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	0.3150	0.5101	0.0398	0.0000	0.2700
Exp. accuracy:	0.96	0.95	0.97	0.96	0.93	0.55

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32646487, G→A					
Position:	chr21:32646487	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.5837	11.9300	0.6914	0.8450	0.0000	0.3300
Exp. accuracy:	0.93	0.83	0.94	0.57	0.93	0.56

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32646490, G→C					
Position:	chr21:32646490	Ref. allele:	G	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.4537	10.0500	0.7592	0.9539	0.0000	0.4100
Exp. accuracy:	0.93	0.91	0.90	0.92	0.93	0.56

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32646496, A→C					
Position:	chr21:32646496	Ref. allele:	A	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.5982	0.2960	0.5772	0.7913	0.0000	0.3100
Exp. accuracy:	0.93	0.95	0.97	0.57	0.93	0.53

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32646496, A→G					
Position:	chr21:32646496	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	5.3940	0.5963	0.1808	0.0000	0.3100
Exp. accuracy:	0.96	0.92	0.96	0.80	0.93	0.53

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32646517, G→A					
Position:	chr21:32646517	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	8.9180	0.6091	0.0929	0.0000	0.3100
Exp. accuracy:	0.96	0.92	0.96	0.87	0.93	0.53

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32646580, A→T					
Position:	chr21:32646580	Ref. allele:	A	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs141637663	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	0.0050	0.5353	0.0390	0.0000	0.3500
Exp. accuracy:	0.96	0.95	0.97	0.96	0.93	0.54

External links

[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]

Variant: 21 : 32646583, A→G					
Position:	chr21:32646583	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.5406	5.7140	0.6696	0.8865	0.0000	0.3500
Exp. accuracy:	0.93	0.92	0.94	0.68	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32646595, A→G					
Position:	chr21:32646595	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	5.0290	0.6510	0.0212	0.0000	0.3600
Exp. accuracy:	0.96	0.93	0.96	0.96	0.93	0.55

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32650212, $T \rightarrow G$					
Position:	chr21:32650212	Ref. allele:	T	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	0.7940	0.4203	0.0117	0.0000	0.5000
Exp. accuracy:	0.96	0.95	0.97	0.96	0.93	0.51

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32650224, $A \rightarrow G$					
Position:	chr21:32650224	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs111774827	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	1.7200	0.7276	0.0524	0.0000	0.5300
Exp. accuracy:	0.96	0.95	0.93	0.94	0.93	0.64

External links

[dbSNP]	[GenBank]	[HaploReg]	[RegulomeDB]	[UCSC]	[Ensemble]
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Variant: 21 : 32650229, $G \rightarrow A$					
Position:	chr21:32650229	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5231	9.2030	0.7341	0.8977	0.0000	0.6100
Exp. accuracy:	0.93	0.92	0.91	0.71	0.93	0.64

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32650230, $G \rightarrow A$					
Position:	chr21:32650230	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	9.8810	0.6832	0.7438	0.0000	0.5900
Exp. accuracy:	0.96	0.91	0.94	0.69	0.93	0.62

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32650230, $G \rightarrow T$					
Position:	chr21:32650230	Ref. allele:	G	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs191969474	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5834	3.7680	0.6814	0.8286	0.0000	0.5900
Exp. accuracy:	0.93	0.94	0.94	0.57	0.93	0.62

External links

[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]

Variant: 21 : 32650245, $T \rightarrow C$					
Position:	chr21:32650245	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs115204185	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	0.5940	0.4993	0.0509	0.0000	0.5300
Exp. accuracy:	0.96	0.95	0.97	0.94	0.93	0.64

External links

[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]

Variant: 21 : 32650266, $T \rightarrow C$					
Position:	chr21:32650266	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	7.5390	0.6618	0.7087	0.0000	0.6800
Exp. accuracy:	0.96	0.91	0.95	0.69	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32650284, $T \rightarrow C$					
Position:	chr21:32650284	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	0.2240	0.6264	0.6602	0.0000	0.7100
Exp. accuracy:	0.96	0.95	0.97	0.69	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32653302, $G \rightarrow A$					
Position:	chr21:32653302	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs374794895	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	deleterious	neutral	deleterious	neutral	neutral
Score:	-0.1244	16.8700	0.7756	0.7957	0.0000	0.3900
Exp. accuracy:	0.88	0.58	0.90	0.57	0.93	0.52

External links

[dbSNP] [GenBank] [RegulomeDB] [UCSC] [Ensemble]
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Variant: 21 : 32656743, $G \rightarrow A$					
Position:	chr21:32656743	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	10.0300	0.6158	0.5623	0.0000	0.6400
Exp. accuracy:	0.96	0.91	0.96	0.70	0.93	0.68

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32656767, $T \rightarrow C$					
Position:	chr21:32656767	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5847	5.8230	0.7158	0.8046	0.0000	0.6500
Exp. accuracy:	0.93	0.92	0.93	0.57	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32656791, $C \rightarrow T$					
Position:	chr21:32656791	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs115263361	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.4960	11.5700	0.7265	0.9126	0.0000	0.6500
Exp. accuracy:	0.93	0.88	0.93	0.77	0.93	0.70

External links

[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]

Variant: 21 : 32656793, A→G					
Position:	chr21:32656793	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	4.0080	0.7407	0.1025	0.0000	0.6100
Exp. accuracy:	0.96	0.94	0.91	0.87	0.93	0.64

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32656821, T→G					
Position:	chr21:32656821	Ref. allele:	T	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	6.4490	0.5096	0.0558	0.0000	0.5700
Exp. accuracy:	0.96	0.93	0.97	0.94	0.93	0.68

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32656851, C→T					
Position:	chr21:32656851	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs375526059	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	12.1000	0.4774	0.7066	0.0000	0.6600
Exp. accuracy:	0.96	0.83	0.97	0.69	0.93	0.70

External links

[dbSNP] [GenBank] [RegulomeDB] [UCSC] [Ensemble]
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Variant: 21 : 32656860, $T \rightarrow C$					
Position:	chr21:32656860	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5929	1.5310	0.6071	0.8319	0.0000	0.6600
Exp. accuracy:	0.93	0.95	0.96	0.57	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32656890, $G \rightarrow A$					
Position:	chr21:32656890	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs373366653	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	10.5700	0.6107	0.5430	0.0000	0.7000
Exp. accuracy:	0.96	0.88	0.96	0.70	0.93	0.70

External links

[dbSNP] [GenBank] [RegulomeDB] [UCSC] [Ensemble]
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Variant: 21 : 32656896, $G \rightarrow A$					
Position:	chr21:32656896	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	10.2000	0.5438	0.0399	0.0000	0.6000
Exp. accuracy:	0.96	0.88	0.97	0.96	0.93	0.64

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32657035, A→G					
Position:	chr21:32657035	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs61756207	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	4.7310	0.4105	0.0695	0.0000	0.3600
Exp. accuracy:	0.96	0.93	0.97	0.90	0.93	0.55

External links

[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]

Variant: 21 : 32657038, G→A					
Position:	chr21:32657038	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.5975	3.6800	0.3607	0.8619	0.0000	0.3300
Exp. accuracy:	0.93	0.94	0.97	0.57	0.93	0.56

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32657041, C→A					
Position:	chr21:32657041	Ref. allele:	C	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.4412	13.2000	0.7650	0.9481	0.0000	0.4200
Exp. accuracy:	0.88	0.74	0.90	0.91	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32657062, C→A					
Position:	chr21:32657062	Ref. allele:	C	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	15.5600	0.4748	0.0470	0.0000	0.4400
Exp. accuracy:	0.96	0.73	0.97	0.94	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32657062, C→T					
Position:	chr21:32657062	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	14.1700	0.4416	0.0328	0.0000	0.4400
Exp. accuracy:	0.96	0.73	0.97	0.96	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32657095, A→G					
Position:	chr21:32657095	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	6.3040	0.4945	0.1296	0.0000	0.4200
Exp. accuracy:	0.96	0.93	0.97	0.85	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32657738, <i>C</i> → <i>T</i>					
Position:	chr21:32657738	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs143244716	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	13.4900	0.5785	0.5982	0.0000	0.3700
Exp. accuracy:	0.96	0.73	0.97	0.69	0.93	0.56

External links

[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]

Variant: 21 : 32657774, <i>G</i> → <i>A</i>					
Position:	chr21:32657774	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	8.5780	0.5745	0.2086	0.0000	0.3500
Exp. accuracy:	0.96	0.92	0.97	0.77	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32657780, <i>G</i> → <i>A</i>					
Position:	chr21:32657780	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.5462	9.4670	0.6116	0.8871	0.0000	0.3500
Exp. accuracy:	0.93	0.91	0.96	0.68	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32657792, $G \rightarrow C$					
Position:	chr21:32657792	Ref. allele:	G	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.4865	6.3800	0.6285	0.9269	0.0000	0.4500
Exp. accuracy:	0.93	0.93	0.97	0.82	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32657804, $G \rightarrow A$					
Position:	chr21:32657804	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs374390032	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	6.9650	0.5392	0.1236	0.0000	0.3900
Exp. accuracy:	0.96	0.92	0.97	0.85	0.93	0.52

External links

[dbSNP] [GenBank] [RegulomeDB] [UCSC] [Ensemble]
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Variant: 21 : 32657825, $A \rightarrow G$					
Position:	chr21:32657825	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	6.7350	0.3924	0.5107	0.0000	0.3800
Exp. accuracy:	0.96	0.92	0.97	0.70	0.93	0.55

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32657831, <i>C</i> → <i>T</i>					
Position:	chr21:32657831	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs61753644	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	14.3300	0.7188	0.0717	0.0000	0.4200
Exp. accuracy:	0.96	0.73	0.93	0.90	0.93	0.54

External links

[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]

Variant: 21 : 32657840, <i>G</i> → <i>A</i>					
Position:	chr21:32657840	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs367656251	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	10.7000	0.6158	0.6999	0.0000	0.4400
Exp. accuracy:	0.96	0.88	0.96	0.69	0.93	0.54

External links

[dbSNP] [GenBank] [RegulomeDB] [UCSC] [Ensemble]
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Variant: 21 : 32657846, <i>C</i> → <i>T</i>					
Position:	chr21:32657846	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	13.5000	0.5218	0.3516	0.0000	0.4500
Exp. accuracy:	0.96	0.73	0.97	0.73	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32657852, $T \rightarrow C$					
Position:	chr21:32657852	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	1.1260	0.5781	0.5349	0.0000	0.3600
Exp. accuracy:	0.96	0.95	0.97	0.70	0.93	0.55

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32657870, $A \rightarrow G$					
Position:	chr21:32657870	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs145411448	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	8.3340	0.7317	0.6058	0.0000	0.3700
Exp. accuracy:	0.96	0.92	0.91	0.69	0.93	0.56

External links

[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]

Variant: 21 : 32664916, $T \rightarrow C$					
Position:	chr21:32664916	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs138073731	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	1.8820	0.7093	0.2747	0.0000	0.5800
Exp. accuracy:	0.96	0.95	0.93	0.73	0.93	0.65

External links

[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]

Variant: 21 : 32664922, A→G					
Position:	chr21:32664922	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs142455194	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.4994	7.0540	0.6901	0.9165	0.0000	0.6800
Exp. accuracy:	0.93	0.92	0.94	0.77	0.93	0.70

External links

[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]

Variant: 21 : 32664961, A→G					
Position:	chr21:32664961	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5394	8.3270	0.6005	0.8918	0.0000	0.7000
Exp. accuracy:	0.93	0.92	0.96	0.68	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32664976, T→C					
Position:	chr21:32664976	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	6.0080	0.6599	0.3859	0.0000	0.6000
Exp. accuracy:	0.96	0.93	0.95	0.72	0.93	0.64

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32664991, A→T					
Position:	chr21:32664991	Ref. allele:	A	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	0.8760	0.7049	0.5747	0.0000	0.6100
Exp. accuracy:	0.96	0.95	0.94	0.70	0.93	0.64

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32665000, G→A					
Position:	chr21:32665000	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	9.1170	0.6179	0.3291	0.0000	0.6400
Exp. accuracy:	0.96	0.92	0.96	0.73	0.93	0.68

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32665003, A→G					
Position:	chr21:32665003	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	7.6620	0.7626	0.5857	0.0000	0.6600
Exp. accuracy:	0.96	0.91	0.90	0.70	0.93	0.70

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32665012, $G \rightarrow A$					
Position:	chr21:32665012	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs149236383	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	9.4040	0.7231	0.0698	0.0000	0.6600
Exp. accuracy:	0.96	0.91	0.93	0.90	0.93	0.70

External links

[dbSNP]	[GenBank]	[HaploReg]	[RegulomeDB]	[UCSC]	[Ensemble]
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Variant: 21 : 32665045, $A \rightarrow G$					
Position:	chr21:32665045	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs144454116	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	0.9100	0.4083	0.7634	0.0000	0.6500
Exp. accuracy:	0.96	0.95	0.97	0.69	0.93	0.70

External links

[dbSNP]	[GenBank]	[HaploReg]	[RegulomeDB]	[UCSC]	[Ensemble]
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Variant: 21 : 32665048, $G \rightarrow A$					
Position:	chr21:32665048	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5965	8.0820	0.5314	0.8422	0.0000	0.7200
Exp. accuracy:	0.93	0.91	0.97	0.57	0.93	0.70

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32665051, A→G					
Position:	chr21:32665051	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs148784824	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5675	6.4820	0.5665	0.8723	0.0000	0.6100
Exp. accuracy:	0.93	0.93	0.97	0.60	0.93	0.64

External links

[dbSNP]	[GenBank]	[HaploReg]	[RegulomeDB]	[UCSC]	[Ensemble]
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Variant: 21 : 32665060, T→C					
Position:	chr21:32665060	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs112875942	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	4.5000	0.5580	0.0283	0.0000	0.5900
Exp. accuracy:	0.96	0.93	0.97	0.96	0.93	0.62

External links

[dbSNP]	[GenBank]	[HaploReg]	[RegulomeDB]	[UCSC]	[Ensemble]
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Variant: 21 : 32665946, A→C					
Position:	chr21:32665946	Ref. allele:	A	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	0.0800	0.7140	0.2582	0.0000	0.3700
Exp. accuracy:	0.96	0.95	0.93	0.73	0.93	0.56

External links

[GenBank]	[UCSC]	[Ensemble]
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PredictSNP overview

Date: 2017/03/06

Genome version: GRCh38/hg38

PredictSNP version: 2.1

If you use PredictSNP and obtain scientific results that you publish, we would ask you to acknowledge the usage of PredictSNP by referencing the article below.

Bendl, J., Musil, M., Stourac, J., Zendulka, J., Damborsky, J., Brezovsky, J., 2016: PredictSNP2: A unified platform for accurately evaluating SNP effects by exploiting the different characteristics of variants in distinct genomic regions. *PLOS Computational Biology* 12: e1004962

	PredictSNP2		CADD		DANN		FATHMM		FunSeq2		GWAVA	
	Neu	Del	Neu	Del	Neu	Del	Neu	Del	Neu	Del	Neu	Del
Regulatory	0	0	0	0	0	0	0	0	0	0	0	0
Splicing	0	0	0	0	0	0	0	0	0	0	0	0
Missense	0	0	0	0	0	0	92	3	80	15	92	3
Synonymous	71	24	95	0	38	56	0	0	0	0	0	0
Nonsense	0	0	0	0	0	0	0	0	0	0	0	0
Others	0	0	0	0	0	0	0	0	0	0	0	0

Variant: 21 : 32666033, $G \rightarrow A$					
Position:	chr21:32666033	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	10.3600	0.6301	0.2944	0.0000	0.3600
Exp. accuracy:	0.96	0.88	0.97	0.73	0.93	0.55

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32666045, $G \rightarrow C$					
Position:	chr21:32666045	Ref. allele:	G	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.5271	6.6890	0.7187	0.8901	0.0000	0.3900
Exp. accuracy:	0.93	0.92	0.93	0.68	0.93	0.52

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32666054, $G \rightarrow A$					
Position:	chr21:32666054	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs116024329	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5206	10.3900	0.7098	0.8970	0.0000	0.5400
Exp. accuracy:	0.93	0.88	0.93	0.71	0.93	0.62

External links

[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]

Variant: 21 : 32666117, A→G					
Position:	chr21:32666117	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	0.0990	0.6204	0.2256	0.0000	0.3900
Exp. accuracy:	0.96	0.95	0.96	0.73	0.93	0.52

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32666120, A→G					
Position:	chr21:32666120	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs140112176	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	9.1980	0.5913	0.7713	0.0000	0.4000
Exp. accuracy:	0.96	0.92	0.96	0.69	0.93	0.56

External links

[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]

Variant: 21 : 32666129, A→C					
Position:	chr21:32666129	Ref. allele:	A	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.5846	1.9540	0.6813	0.8254	0.0000	0.3500
Exp. accuracy:	0.93	0.95	0.94	0.57	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32666135, C→T					
Position:	chr21:32666135	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	deleterious	deleterious	deleterious	deleterious	neutral	deleterious
Score:	0.4739	17.8800	0.9175	0.9194	0.0000	0.5800
Exp. accuracy:	0.93	0.56	0.87	0.78	0.93	0.65

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32666447, A→G					
Position:	chr21:32666447	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs116801038	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	6.4180	0.6744	0.5351	0.0000	0.6000
Exp. accuracy:	0.96	0.93	0.94	0.70	0.93	0.64

External links

[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]

Variant: 21 : 32666465, A→G					
Position:	chr21:32666465	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	0.4020	0.6873	0.6449	0.0000	0.6000
Exp. accuracy:	0.96	0.95	0.94	0.69	0.93	0.64

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32666471, <i>C</i> → <i>T</i>					
Position:	chr21:32666471	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5705	12.7700	0.7538	0.8007	0.0000	0.6500
Exp. accuracy:	0.93	0.77	0.90	0.57	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32666480, <i>G</i> → <i>A</i>					
Position:	chr21:32666480	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	15.0200	0.6909	0.4826	0.0000	0.6800
Exp. accuracy:	0.96	0.73	0.94	0.72	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32666498, <i>A</i> → <i>G</i>					
Position:	chr21:32666498	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	8.6180	0.6635	0.2106	0.0000	0.5900
Exp. accuracy:	0.96	0.92	0.95	0.77	0.93	0.62

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32666555, $G \rightarrow C$					
Position:	chr21:32666555	Ref. allele:	G	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs115658799	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	7.9110	0.7381	0.6668	0.0000	0.6800
Exp. accuracy:	0.96	0.91	0.91	0.69	0.93	0.70

External links

[dbSNP]	[GenBank]	[HaploReg]	[RegulomeDB]	[UCSC]	[Ensemble]
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Variant: 21 : 32666561, $C \rightarrow T$					
Position:	chr21:32666561	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs371628726	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5572	12.5900	0.6576	0.8680	0.0000	0.7500
Exp. accuracy:	0.93	0.79	0.95	0.60	0.93	0.70

External links

[dbSNP]	[GenBank]	[RegulomeDB]	[UCSC]	[Ensemble]
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Variant: 21 : 32670371, $A \rightarrow G$					
Position:	chr21:32670371	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5011	12.8100	0.8291	0.8824	0.0000	0.6000
Exp. accuracy:	0.93	0.77	0.90	0.64	0.93	0.64

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32673398, <i>C</i> → <i>T</i>					
Position:	chr21:32673398	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5778	12.4200	0.6952	0.8289	0.0000	0.7400
Exp. accuracy:	0.93	0.79	0.94	0.57	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32673425, <i>T</i> → <i>C</i>					
Position:	chr21:32673425	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	1.2620	0.3748	0.3714	0.0000	0.6500
Exp. accuracy:	0.96	0.95	0.97	0.72	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32673437, <i>A</i> → <i>G</i>					
Position:	chr21:32673437	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	7.0930	0.5946	0.1078	0.0000	0.6200
Exp. accuracy:	0.96	0.92	0.96	0.87	0.93	0.66

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32673455, G→A						
Position:	chr21:32673455	Ref. allele:	G	Alt. allele:	A	
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1	
RS number:	-	Clin. sign.:	-	-		
Results						
Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	10.7800	0.6253	0.0638	0.0000	0.6000
Exp. accuracy:	0.96	0.88	0.96	0.92	0.93	0.64
External links						
[GenBank] [UCSC] [Ensemble]						

Variant: 21 : 32673455, G→C						
Position:	chr21:32673455	Ref. allele:	G	Alt. allele:	C	
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1	
RS number:	rs150180190	Clin. sign.:	-	-		
Results						
Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	9.3760	0.6443	0.1476	0.0000	0.6000
Exp. accuracy:	0.96	0.91	0.96	0.83	0.93	0.64
External links						
[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]						

Variant: 21 : 32673470, T→C						
Position:	chr21:32673470	Ref. allele:	T	Alt. allele:	C	
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1	
RS number:	rs111686118	Clin. sign.:	-	-		
Results						
Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	7.8290	0.6601	0.2352	0.0000	0.5800
Exp. accuracy:	0.96	0.91	0.95	0.73	0.93	0.65
External links						
[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]						

Variant: 21 : 32673485, A→G					
Position:	chr21:32673485	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	4.0460	0.4159	0.5720	0.0000	0.6600
Exp. accuracy:	0.96	0.94	0.97	0.70	0.93	0.70

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32673503, A→G					
Position:	chr21:32673503	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.4825	7.9160	0.6606	0.9304	0.0000	0.7500
Exp. accuracy:	0.93	0.91	0.95	0.82	0.93	0.70

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32678652, A→G					
Position:	chr21:32678652	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5021	5.4020	0.7042	0.9121	0.0000	0.6000
Exp. accuracy:	0.93	0.92	0.94	0.77	0.93	0.64

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32678697, A→G					
Position:	chr21:32678697	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	7.6050	0.6239	0.7269	0.0000	0.6300
Exp. accuracy:	0.96	0.91	0.96	0.69	0.93	0.66

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32678714, G→A					
Position:	chr21:32678714	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5351	9.6110	0.7255	0.8823	0.0000	0.7300
Exp. accuracy:	0.93	0.91	0.93	0.64	0.93	0.70

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32678763, C→T					
Position:	chr21:32678763	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5805	12.7200	0.6315	0.8547	0.0000	0.7800
Exp. accuracy:	0.93	0.79	0.97	0.57	0.93	0.70

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32681571, C→T					
Position:	chr21:32681571	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	deleterious	neutral	neutral	neutral	neutral
Score:	-0.6228	16.0700	0.5418	0.2211	0.0000	0.4400
Exp. accuracy:	0.95	0.58	0.97	0.77	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32681592, A→C					
Position:	chr21:32681592	Ref. allele:	A	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs76972835	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5586	2.8150	0.6379	0.8776	0.0000	0.5300
Exp. accuracy:	0.93	0.95	0.97	0.64	0.93	0.64

External links

[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]

Variant: 21 : 32681595, C→G					
Position:	chr21:32681595	Ref. allele:	C	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5766	10.9400	0.7581	0.8501	0.0000	0.6500
Exp. accuracy:	0.93	0.88	0.90	0.57	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32681600, A→G					
Position:	chr21:32681600	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	?
Score:	-1.0000	9.8710	0.7252	0.0956	0.0000	0.4800
Exp. accuracy:	0.96	0.91	0.93	0.87	0.93	0.43

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32681604, A→G					
Position:	chr21:32681604	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs111655347	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	9.6770	0.7661	0.7521	0.0000	0.4700
Exp. accuracy:	0.96	0.91	0.90	0.69	0.93	0.54

External links

[dbSNP]	[GenBank]	[HaploReg]	[RegulomeDB]	[UCSC]	[Ensemble]
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Variant: 21 : 32681607, C→T					
Position:	chr21:32681607	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	14.2500	0.6322	0.6506	0.0000	0.5200
Exp. accuracy:	0.96	0.73	0.97	0.69	0.93	0.58

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32684044, <i>G</i> → <i>A</i>					
Position:	chr21:32684044	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5729	13.2800	0.6937	0.8234	0.0000	0.5900
Exp. accuracy:	0.93	0.74	0.94	0.57	0.93	0.62

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32684056, <i>C</i> → <i>T</i>					
Position:	chr21:32684056	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	13.7100	0.6221	0.7637	0.0000	0.7300
Exp. accuracy:	0.96	0.73	0.96	0.69	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32684062, <i>A</i> → <i>G</i>					
Position:	chr21:32684062	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	2.9090	0.7608	0.6969	0.0000	0.5600
Exp. accuracy:	0.96	0.95	0.90	0.69	0.93	0.69

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32684071, T→C					
Position:	chr21:32684071	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	5.5050	0.6601	0.7866	0.0000	0.6100
Exp. accuracy:	0.96	0.92	0.95	0.69	0.93	0.64

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32685759, A→G					
Position:	chr21:32685759	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	4.9380	0.7161	0.6459	0.0000	0.7900
Exp. accuracy:	0.96	0.93	0.93	0.69	0.93	0.70

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32685765, A→G					
Position:	chr21:32685765	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5822	6.6240	0.7146	0.8215	0.0000	0.7700
Exp. accuracy:	0.93	0.92	0.93	0.57	0.93	0.70

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32685789, <i>T</i> → <i>G</i>					
Position:	chr21:32685789	Ref. allele:	T	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	10.1700	0.7884	0.7722	0.0000	0.6400
Exp. accuracy:	0.96	0.88	0.89	0.69	0.93	0.68

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32685864, <i>G</i> → <i>A</i>					
Position:	chr21:32685864	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.4762	8.3670	0.5476	0.9518	0.0000	0.7800
Exp. accuracy:	0.93	0.92	0.97	0.92	0.93	0.70

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32685885, <i>A</i> → <i>G</i>					
Position:	chr21:32685885	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	4.8840	0.5681	0.7710	0.0000	0.6500
Exp. accuracy:	0.96	0.93	0.97	0.69	0.93	0.70

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32687017, $T \rightarrow C$					
Position:	chr21:32687017	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs145522240	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	7.4870	0.6963	0.3840	0.0000	0.3300
Exp. accuracy:	0.96	0.91	0.94	0.72	0.93	0.56

External links

[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]

Variant: 21 : 32687044, $A \rightarrow G$					
Position:	chr21:32687044	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	8.9340	0.6402	0.4990	0.0000	0.3700
Exp. accuracy:	0.96	0.92	0.97	0.70	0.93	0.56

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32687062, $T \rightarrow C$					
Position:	chr21:32687062	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	5.6370	0.7936	0.6741	0.0000	0.3300
Exp. accuracy:	0.96	0.92	0.89	0.69	0.93	0.56

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32688314, A→G					
Position:	chr21:32688314	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs372016074	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	deleterious	neutral	neutral	neutral	deleterious
Score:	-0.5972	15.7400	0.7650	0.6625	0.0000	0.6700
Exp. accuracy:	0.93	0.58	0.90	0.69	0.93	0.70

External links

[dbSNP] [GenBank] [RegulomeDB] [UCSC] [Ensemble]
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Variant: 21 : 32688320, T→G					
Position:	chr21:32688320	Ref. allele:	T	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	deleterious	neutral	neutral	neutral	deleterious
Score:	-0.5913	17.1000	0.7985	0.6816	0.0000	0.7100
Exp. accuracy:	0.93	0.58	0.89	0.69	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32688323, A→G					
Position:	chr21:32688323	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	deleterious	neutral	neutral	neutral	deleterious
Score:	-0.5953	17.3400	0.7087	0.7305	0.0000	0.7000
Exp. accuracy:	0.93	0.58	0.93	0.69	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32688326, <i>G</i> → <i>A</i>					
Position:	chr21:32688326	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs148732160	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	15.2800	0.8163	0.2542	0.0000	0.6100
Exp. accuracy:	0.96	0.73	0.90	0.73	0.93	0.64

External links

[dbSNP]	[GenBank]	[HaploReg]	[RegulomeDB]	[UCSC]	[Ensemble]
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Variant: 21 : 32694234, <i>C</i> → <i>T</i>					
Position:	chr21:32694234	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs188892266	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	13.6300	0.5668	0.0296	0.0000	0.5700
Exp. accuracy:	0.96	0.73	0.97	0.96	0.93	0.68

External links

[dbSNP]	[GenBank]	[HaploReg]	[RegulomeDB]	[UCSC]	[Ensemble]
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Variant: 21 : 32694258, <i>A</i> → <i>C</i>					
Position:	chr21:32694258	Ref. allele:	A	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs111290161	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	1.3760	0.6920	0.5849	0.0000	0.5700
Exp. accuracy:	0.96	0.95	0.94	0.70	0.93	0.68

External links

[dbSNP]	[GenBank]	[HaploReg]	[RegulomeDB]	[UCSC]	[Ensemble]
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Variant: 21 : 32694270, <i>G</i> → <i>A</i>					
Position:	chr21:32694270	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	9.0600	0.6930	0.5216	0.0000	0.6000
Exp. accuracy:	0.96	0.92	0.94	0.70	0.93	0.64

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32694282, <i>G</i> → <i>T</i>					
Position:	chr21:32694282	Ref. allele:	G	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	7.3420	0.7499	0.6291	0.0000	0.5800
Exp. accuracy:	0.96	0.91	0.91	0.69	0.93	0.65

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32694306, <i>C</i> → <i>T</i>					
Position:	chr21:32694306	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	10.0700	0.5729	0.0737	0.0000	0.5300
Exp. accuracy:	0.96	0.91	0.97	0.90	0.93	0.64

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32695060, $T \rightarrow C$					
Position:	chr21:32695060	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs372354458	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	1.3350	0.6394	0.5486	0.0000	0.4600
Exp. accuracy:	0.96	0.95	0.97	0.70	0.93	0.54

External links

[dbSNP]	[GenBank]	[RegulomeDB]	[UCSC]	[Ensemble]
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Variant: 21 : 32695078, $G \rightarrow A$					
Position:	chr21:32695078	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs376985894	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	10.7200	0.6535	0.7199	0.0000	0.5900
Exp. accuracy:	0.96	0.88	0.96	0.69	0.93	0.62

External links

[dbSNP]	[GenBank]	[RegulomeDB]	[UCSC]	[Ensemble]
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Variant: 21 : 32695153, $G \rightarrow A$					
Position:	chr21:32695153	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5542	10.4200	0.6845	0.8774	0.0000	0.6300
Exp. accuracy:	0.93	0.88	0.94	0.64	0.93	0.66

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32695165, $C \rightarrow T$					
Position:	chr21:32695165	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	15.2200	0.6383	0.3533	0.0000	0.5500
Exp. accuracy:	0.96	0.73	0.97	0.73	0.93	0.66

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32695189, $T \rightarrow C$					
Position:	chr21:32695189	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs61756694	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	0.3310	0.3817	0.7043	0.0000	0.6100
Exp. accuracy:	0.96	0.95	0.97	0.69	0.93	0.64

External links

[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]

Variant: 21 : 32695207, $T \rightarrow A$					
Position:	chr21:32695207	Ref. allele:	T	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	6.8870	0.6255	0.1308	0.0000	0.6000
Exp. accuracy:	0.96	0.92	0.96	0.85	0.93	0.64

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32695273, A→C					
Position:	chr21:32695273	Ref. allele:	A	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	0.2470	0.7887	0.6499	0.0000	0.6000
Exp. accuracy:	0.96	0.95	0.89	0.69	0.93	0.64

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32699849, A→G					
Position:	chr21:32699849	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	7.3580	0.6219	0.5457	0.0000	0.2900
Exp. accuracy:	0.96	0.91	0.96	0.70	0.93	0.56

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32699855, A→T					
Position:	chr21:32699855	Ref. allele:	A	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs369978981	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	0.0030	0.5222	0.0331	0.0000	0.3100
Exp. accuracy:	0.96	0.95	0.97	0.96	0.93	0.53

External links

[dbSNP] [GenBank] [RegulomeDB] [UCSC] [Ensemble]
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Variant: 21 : 32699864, $T \rightarrow C$					
Position:	chr21:32699864	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs376163066	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	0.7560	0.6044	0.2289	0.0000	0.3300
Exp. accuracy:	0.96	0.95	0.96	0.73	0.93	0.56

External links

[dbSNP] [GenBank] [RegulomeDB] [UCSC] [Ensemble]
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Variant: 21 : 32699867, $T \rightarrow C$					
Position:	chr21:32699867	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	0.5510	0.4695	0.1922	0.0000	0.3300
Exp. accuracy:	0.96	0.95	0.97	0.80	0.93	0.56

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32699882, $C \rightarrow A$					
Position:	chr21:32699882	Ref. allele:	C	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	deleterious	neutral	neutral	neutral	neutral
Score:	-0.6367	15.9500	0.6268	0.0692	0.0000	0.2900
Exp. accuracy:	0.95	0.58	0.97	0.90	0.93	0.56

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32699882, C→T					
Position:	chr21:32699882	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs151248057	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	14.9300	0.6617	0.0459	0.0000	0.2900
Exp. accuracy:	0.96	0.73	0.95	0.96	0.93	0.56

External links

[dbSNP]	[GenBank]	[HaploReg]	[RegulomeDB]	[UCSC]	[Ensemble]
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Variant: 21 : 32699896, A→G					
Position:	chr21:32699896	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs140461566	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	2.8860	0.7027	0.3456	0.0000	0.3500
Exp. accuracy:	0.96	0.95	0.94	0.73	0.93	0.54

External links

[dbSNP]	[GenBank]	[HaploReg]	[RegulomeDB]	[UCSC]	[Ensemble]
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Variant: 21 : 32699912, A→G					
Position:	chr21:32699912	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs113672883	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	8.7950	0.7482	0.7776	0.0000	0.3300
Exp. accuracy:	0.96	0.92	0.91	0.69	0.93	0.56

External links

[dbSNP]	[GenBank]	[HaploReg]	[RegulomeDB]	[UCSC]	[Ensemble]
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Variant: 21 : 32699924, T→C					
Position:	chr21:32699924	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs377218872	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	8.8810	0.6325	0.5020	0.0000	0.3200
Exp. accuracy:	0.96	0.92	0.97	0.70	0.93	0.53

External links

[dbSNP] [GenBank] [RegulomeDB] [UCSC] [Ensemble]
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Variant: 21 : 32699933, A→G					
Position:	chr21:32699933	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	8.1060	0.6190	0.5789	0.0000	0.3100
Exp. accuracy:	0.96	0.91	0.96	0.70	0.93	0.53

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32699966, T→C					
Position:	chr21:32699966	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs144142216	Clin. sign.:	-	-	

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	7.5850	0.7021	0.1915	0.0000	0.3400
Exp. accuracy:	0.96	0.91	0.94	0.80	0.93	0.56

External links

[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]

Variant: 21 : 32699981, A→G					
Position:	chr21:32699981	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	9.8800	0.6187	0.6953	0.0000	0.3800
Exp. accuracy:	0.96	0.91	0.96	0.69	0.93	0.55

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32699993, G→A					
Position:	chr21:32699993	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	9.9700	0.7216	0.0238	0.0000	0.2900
Exp. accuracy:	0.96	0.91	0.93	0.96	0.93	0.56

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32700011, C→T					
Position:	chr21:32700011	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	13.2600	0.5508	0.5797	0.0000	0.3400
Exp. accuracy:	0.96	0.74	0.97	0.70	0.93	0.56

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32700017, $G \rightarrow C$					
Position:	chr21:32700017	Ref. allele:	G	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs192548936	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.5537	8.9800	0.7463	0.8768	0.0000	0.4300
Exp. accuracy:	0.93	0.92	0.91	0.64	0.93	0.54

External links

[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]

Variant: 21 : 32700029, $G \rightarrow A$					
Position:	chr21:32700029	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.5757	10.0800	0.8005	0.8170	0.0000	0.3800
Exp. accuracy:	0.93	0.91	0.90	0.57	0.93	0.55

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32700074, $G \rightarrow A$					
Position:	chr21:32700074	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.5867	9.9660	0.6728	0.8105	0.0000	0.4400
Exp. accuracy:	0.93	0.91	0.94	0.57	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32700079, $G \rightarrow A$					
Position:	chr21:32700079	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.5196	10.2000	0.7328	0.8968	0.0000	0.4500
Exp. accuracy:	0.93	0.88	0.91	0.71	0.93	0.54

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32700098, $A \rightarrow G$					
Position:	chr21:32700098	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	0.0720	0.6492	0.0301	0.0000	0.4700
Exp. accuracy:	0.96	0.95	0.96	0.96	0.93	0.54

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32701986, $G \rightarrow C$					
Position:	chr21:32701986	Ref. allele:	G	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	9.1410	0.7876	0.2648	0.0000	0.4600
Exp. accuracy:	0.96	0.92	0.89	0.73	0.93	0.54

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32701995, $T \rightarrow C$					
Position:	chr21:32701995	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	7.5070	0.7195	0.3393	0.0000	0.4200
Exp. accuracy:	0.96	0.91	0.93	0.73	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32701995, $T \rightarrow G$					
Position:	chr21:32701995	Ref. allele:	T	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	9.8140	0.7124	0.2516	0.0000	0.4200
Exp. accuracy:	0.96	0.91	0.93	0.73	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32702007, $T \rightarrow C$					
Position:	chr21:32702007	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs141138675	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.5722	8.7970	0.6698	0.8692	0.0000	0.4500
Exp. accuracy:	0.93	0.92	0.94	0.60	0.93	0.54

External links

[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]

Variant: 21 : 32702010, $G \rightarrow C$					
Position:	chr21:32702010	Ref. allele:	G	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.4941	8.7750	0.7693	0.9146	0.0000	0.4700
Exp. accuracy:	0.93	0.92	0.90	0.77	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32702016, $T \rightarrow C$					
Position:	chr21:32702016	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs144728528	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	5.3320	0.6940	0.1508	0.0000	0.4400
Exp. accuracy:	0.96	0.92	0.94	0.83	0.93	0.54

External links

[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]

Variant: 21 : 32726776, $C \rightarrow A$					
Position:	chr21:32726776	Ref. allele:	C	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	deleterious	neutral	neutral	neutral	neutral
Score:	-0.4885	21.6000	0.8257	0.4212	0.0000	0.4700
Exp. accuracy:	0.93	0.82	0.90	0.72	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32726797, $G \rightarrow A$					
Position:	chr21:32726797	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	deleterious	neutral	neutral	neutral	deleterious
Score:	-0.4604	22.2000	0.8817	0.4664	0.0000	0.5300
Exp. accuracy:	0.93	0.87	0.90	0.72	0.93	0.64

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32726803, $G \rightarrow C$					
Position:	chr21:32726803	Ref. allele:	G	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs201322530	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	deleterious	neutral	neutral	neutral	deleterious
Score:	-0.4899	21.5000	0.8541	0.6480	0.0000	0.5400
Exp. accuracy:	0.93	0.79	0.90	0.69	0.93	0.62

External links

[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]

Variant: 21 : 32726833, $T \rightarrow G$					
Position:	chr21:32726833	Ref. allele:	T	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	deleterious	neutral	neutral	neutral	deleterious
Score:	-0.5276	21.5000	0.7677	0.1266	0.0000	0.5000
Exp. accuracy:	0.93	0.79	0.90	0.85	0.93	0.51

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32726890, <i>C</i> → <i>T</i>					
Position:	chr21:32726890	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	rs61750221	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	deleterious	neutral	neutral	neutral	deleterious
Score:	-0.4596	22.3000	0.8804	0.3575	0.0000	0.5600
Exp. accuracy:	0.93	0.87	0.90	0.73	0.93	0.69

External links

[dbSNP] [GenBank] [HaploReg] [RegulomeDB] [UCSC] [Ensemble]

Variant: 21 : 32727954, <i>C</i> → <i>G</i>					
Position:	chr21:32727954	Ref. allele:	C	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	deleterious	neutral	neutral	neutral	deleterious
Score:	-0.4597	22.2000	0.8636	0.6965	0.0000	0.6000
Exp. accuracy:	0.93	0.87	0.90	0.69	0.93	0.64

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32727972, <i>T</i> → <i>C</i>					
Position:	chr21:32727972	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	deleterious	neutral	neutral	neutral	deleterious
Score:	-0.6080	19.5900	0.6997	0.0173	0.0000	0.6000
Exp. accuracy:	0.95	0.69	0.94	0.96	0.93	0.64

External links

[GenBank] [UCSC] [Ensemble]

Variant: 21 : 32727987, $G \rightarrow A$					
Position:	chr21:32727987	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	deleterious	deleterious	deleterious	neutral	neutral	deleterious
Score:	0.0282	22.4000	0.9348	0.7578	0.0000	0.5100
Exp. accuracy:	0.93	0.87	0.87	0.69	0.93	0.55

External links

[GenBank]	[UCSC]	[Ensemble]
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Variant: 21 : 32727996, $G \rightarrow A$					
Position:	chr21:32727996	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SYNJ1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	deleterious	deleterious	deleterious	neutral	neutral	neutral
Score:	0.0199	21.4000	0.9425	0.3648	0.0000	0.4100
Exp. accuracy:	0.93	0.79	0.87	0.72	0.93	0.56

External links

[GenBank]	[UCSC]	[Ensemble]
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