



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	61	0	60	1	61	0
Synonymous	55	6	61	0	1	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: X : 19536447, G→A

Position:	chrX:19536447	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	7.1800	0.7355	0.2855	0.0000	0.3700
Exp. accuracy:	0.96	0.91	0.91	0.73	0.93	0.56

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19537720, C→T

Position:	chrX:19537720	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	11.9700	0.8057	0.6143	0.0000	0.6600
Exp. accuracy:	0.96	0.83	0.90	0.69	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19537729, C→T

Position:	chrX:19537729	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	14.3600	0.7041	0.3061	0.0000	0.5800
Exp. accuracy:	0.96	0.73	0.94	0.73	0.93	0.65

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19537752, A→G

Position:	chrX:19537752	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	9.1330	0.6802	0.3487	0.0000	0.6200
Exp. accuracy:	0.96	0.92	0.94	0.73	0.93	0.66

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19541936, C→T

Position:	chrX:19541936	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	13.5700	0.6133	0.5550	0.0000	0.6000
Exp. accuracy:	0.96	0.73	0.96	0.70	0.93	0.64

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19541975, T→G

Position:	chrX:19541975	Ref. allele:	T	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	?
Score:	-1.0000	2.6240	0.5131	0.0507	0.0000	0.4800
Exp. accuracy:	0.96	0.95	0.97	0.94	0.93	0.43

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19541987, C→T

Position:	chrX:19541987	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs61740276	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	13.6100	0.6618	0.5557	0.0000	0.5900
Exp. accuracy:	0.96	0.73	0.95	0.70	0.93	0.62

External links

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

Variant: X : 19541993, G→A

Position:	chrX:19541993	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs11552353	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	13.7100	0.7168	0.2459	0.0000	0.5000
Exp. accuracy:	0.96	0.73	0.93	0.73	0.93	0.51

External links

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

Variant: X : 19541993, G→C

Position:	chrX:19541993	Ref. allele:	G	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	10.7100	0.5989	0.3103	0.0000	0.5000
Exp. accuracy:	0.96	0.88	0.96	0.73	0.93	0.51

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19542005, G→A					
Position:	chrX:19542005	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	10.6400	0.7234	0.5747	0.0000	0.5400
Exp. accuracy:	0.96	0.88	0.93	0.70	0.93	0.62

External links

[\[GenBank\]](#) [\[UCSC\]](#) [\[Ensemble\]](#)

Variant: X : 19542011, C→T					
Position:	chrX:19542011	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs140545590	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	15.6200	0.7293	0.0958	0.0000	0.5700
Exp. accuracy:	0.96	0.73	0.91	0.87	0.93	0.68

External links

[\[dbSNP\]](#) [\[GenBank\]](#) [\[HaploReg\]](#) [\[RegulomeDB\]](#) [\[UCSC\]](#) [\[Ensemble\]](#)

Variant: X : 19542038, C→T					
Position:	chrX:19542038	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs150468291	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	11.8800	0.5898	0.0442	0.0000	0.5200
Exp. accuracy:	0.96	0.83	0.97	0.96	0.93	0.58

External links

[\[dbSNP\]](#) [\[GenBank\]](#) [\[HaploReg\]](#) [\[RegulomeDB\]](#) [\[UCSC\]](#) [\[Ensemble\]](#)

Variant: X : 19542044, G→A

Position:	chrX:19542044	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs199710100	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	5.5370	0.5913	0.3367	0.0000	0.5100
Exp. accuracy:	0.96	0.92	0.96	0.73	0.93	0.55

External links

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

Variant: X : 19542053, C→T

Position:	chrX:19542053	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs200949699	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	?
Score:	-1.0000	10.8700	0.7399	0.0192	0.0000	0.4800
Exp. accuracy:	0.96	0.88	0.91	0.96	0.93	0.43

External links

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

Variant: X : 19542071, T→C

Position:	chrX:19542071	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	4.1700	0.6976	0.6541	0.0000	0.6600
Exp. accuracy:	0.96	0.94	0.94	0.69	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19542097, G→A

Position:	chrX:19542097	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	0.6800	0.6000	0.3557	0.0000	0.5500
Exp. accuracy:	0.96	0.95	0.96	0.73	0.93	0.66

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19542098, G→A

Position:	chrX:19542098	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	0.1980	0.5993	0.0417	0.0000	0.5000
Exp. accuracy:	0.96	0.95	0.96	0.96	0.93	0.51

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19542098, G→C

Position:	chrX:19542098	Ref. allele:	G	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	0.0110	0.3655	0.0732	0.0000	0.5000
Exp. accuracy:	0.96	0.95	0.97	0.90	0.93	0.51

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19542098, G→T

Position:	chrX:19542098	Ref. allele:	G	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs376960635	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	0.0090	0.4426	0.0587	0.0000	0.5000
Exp. accuracy:	0.96	0.95	0.97	0.92	0.93	0.51

External links

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

Variant: X : 19542104, G→C

Position:	chrX:19542104	Ref. allele:	G	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	0.0100	0.3369	0.3712	0.0000	0.5000
Exp. accuracy:	0.96	0.95	0.97	0.72	0.93	0.51

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19542107, C→T

Position:	chrX:19542107	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs143070322	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	9.9830	0.3822	0.0139	0.0000	0.5200
Exp. accuracy:	0.96	0.91	0.97	0.96	0.93	0.58

External links

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

Variant: X : 19542110, C→G					
Position:	chrX:19542110	Ref. allele:	C	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	5.6680	0.3192	0.0487	0.0000	0.5100
Exp. accuracy:	0.96	0.92	0.97	0.94	0.93	0.55

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19542110, C→T					
Position:	chrX:19542110	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	9.0050	0.4109	0.0212	0.0000	0.5100
Exp. accuracy:	0.96	0.92	0.97	0.96	0.93	0.55

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19542131, C→G					
Position:	chrX:19542131	Ref. allele:	C	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	5.0970	0.4500	0.0955	0.0000	0.5400
Exp. accuracy:	0.96	0.93	0.97	0.87	0.93	0.62

External links

[GenBank] [UCSC] [Ensemble]

Variant:	X : 19542137, G→A					
Position:	chrX:19542137	Ref. allele:	G	Alt. allele:	A	
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1	
RS number:	-	Clin. sign.:	-	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	?
Score:	-1.0000	1.0280	0.4294	0.0381	0.0000	0.4800
Exp. accuracy:	0.96	0.95	0.97	0.96	0.93	0.43

External links

[\[GenBank\]](#) [\[UCSC\]](#) [\[Ensemble\]](#)

Variant:	X : 19542146, T→C					
Position:	chrX:19542146	Ref. allele:	T	Alt. allele:	C	
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1	
RS number:	-	Clin. sign.:	-	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	1.1540	0.4126	0.0915	0.0000	0.5200
Exp. accuracy:	0.96	0.95	0.97	0.87	0.93	0.58

External links

[\[GenBank\]](#) [\[UCSC\]](#) [\[Ensemble\]](#)

Variant:	X : 19542158, C→T					
Position:	chrX:19542158	Ref. allele:	C	Alt. allele:	T	
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1	
RS number:	rs373830746	Clin. sign.:	-	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	10.8500	0.6118	0.0358	0.0000	0.5000
Exp. accuracy:	0.96	0.88	0.96	0.96	0.93	0.51

External links

[\[dbSNP\]](#) [\[GenBank\]](#) [\[RegulomeDB\]](#) [\[UCSC\]](#) [\[Ensemble\]](#)

Variant: X : 19542167, C→T

Position:	chrX:19542167	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs199899970	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	9.5680	0.5552	0.0288	0.0000	0.5100
Exp. accuracy:	0.96	0.91	0.97	0.96	0.93	0.55

External links

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

Variant: X : 19542176, T→G

Position:	chrX:19542176	Ref. allele:	T	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	?
Score:	-1.0000	6.9050	0.4208	0.0510	0.0000	0.4800
Exp. accuracy:	0.96	0.92	0.97	0.94	0.93	0.43

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19545946, A→G

Position:	chrX:19545946	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	4.9020	0.5696	0.3319	0.0000	0.5900
Exp. accuracy:	0.96	0.93	0.97	0.73	0.93	0.62

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19545958, C→T

Position:	chrX:19545958	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	14.1600	0.5692	0.0482	0.0000	0.5700
Exp. accuracy:	0.96	0.73	0.97	0.94	0.93	0.68

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19545961, G→A

Position:	chrX:19545961	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	6.2010	0.6533	0.0883	0.0000	0.5800
Exp. accuracy:	0.96	0.93	0.96	0.88	0.93	0.65

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19545976, C→T

Position:	chrX:19545976	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	15.5400	0.7234	0.2793	0.0000	0.5900
Exp. accuracy:	0.96	0.73	0.93	0.73	0.93	0.62

External links

[GenBank] [UCSC] [Ensemble]

Variant:	X : 19545979, A→G				
Position:	chrX:19545979	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	8.4100	0.6846	0.6995	0.0000	0.7400
Exp. accuracy:	0.96	0.92	0.94	0.69	0.93	0.70

External links

[\[GenBank\]](#) [\[UCSC\]](#) [\[Ensemble\]](#)

Variant:	X : 19546009, G→C				
Position:	chrX:19546009	Ref. allele:	G	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs370412822	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	11.8300	0.6293	0.6028	0.0000	0.5900
Exp. accuracy:	0.96	0.83	0.97	0.69	0.93	0.62

External links

[\[dbSNP\]](#) [\[GenBank\]](#) [\[RegulomeDB\]](#) [\[UCSC\]](#) [\[Ensemble\]](#)

Variant:	X : 19546018, G→A				
Position:	chrX:19546018	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	10.9400	0.6479	0.6411	0.0000	0.7300
Exp. accuracy:	0.96	0.88	0.96	0.69	0.93	0.70

External links

[\[GenBank\]](#) [\[UCSC\]](#) [\[Ensemble\]](#)

Variant: X : 19546021, G→A

Position:	chrX:19546021	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs148651015	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5771	9.7600	0.5955	0.8623	0.0000	0.7800
Exp. accuracy:	0.93	0.91	0.96	0.57	0.93	0.70

External links

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

Variant: X : 19546024, G→A

Position:	chrX:19546024	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs201790502	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	13.8800	0.7217	0.1968	0.0000	0.6900
Exp. accuracy:	0.96	0.73	0.93	0.77	0.93	0.70

External links

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

Variant: X : 19546045, G→T

Position:	chrX:19546045	Ref. allele:	G	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5886	6.3620	0.6651	0.8389	0.0000	0.7200
Exp. accuracy:	0.93	0.93	0.95	0.57	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19549980, G→A

Position:	chrX:19549980	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs141233913	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.4714	10.3500	0.7728	0.9261	0.0000	0.6900
Exp. accuracy:	0.93	0.88	0.90	0.82	0.93	0.70

External links

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

Variant: X : 19549992, C→T

Position:	chrX:19549992	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	14.7300	0.6358	0.0095	0.0000	0.5000
Exp. accuracy:	0.96	0.73	0.97	0.96	0.93	0.51

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19550007, T→C

Position:	chrX:19550007	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	0.5080	0.6383	0.0454	0.0000	0.5500
Exp. accuracy:	0.96	0.95	0.97	0.96	0.93	0.66

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19550031, C→T

Position:	chrX:19550031	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs372371711	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	14.8200	0.6260	0.1259	0.0000	0.5700
Exp. accuracy:	0.96	0.73	0.96	0.85	0.93	0.68

External links

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

Variant: X : 19550034, A→G

Position:	chrX:19550034	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	4.3410	0.5299	0.1750	0.0000	0.6700
Exp. accuracy:	0.96	0.94	0.97	0.80	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19550058, T→C

Position:	chrX:19550058	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs35665839	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	3.6880	0.6719	0.0902	0.0000	0.5600
Exp. accuracy:	0.96	0.94	0.94	0.88	0.93	0.69

External links

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

Variant: X : 19550064, G→A

Position:	chrX:19550064	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs139733939	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	14.6800	0.7157	0.4265	0.0000	0.5200
Exp. accuracy:	0.96	0.73	0.93	0.72	0.93	0.58

External links

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

Variant: X : 19550079, T→C

Position:	chrX:19550079	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	5.3900	0.7964	0.7601	0.0000	0.7000
Exp. accuracy:	0.96	0.92	0.89	0.69	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19550081, A→G

Position:	chrX:19550081	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	10.7000	0.7750	0.1567	0.0000	0.6000
Exp. accuracy:	0.96	0.88	0.90	0.83	0.93	0.64

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19569161, G→T

Position:	chrX:19569161	Ref. allele:	G	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	10.8600	0.6618	0.3728	0.0000	0.5100
Exp. accuracy:	0.96	0.88	0.95	0.72	0.93	0.55

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19569185, A→G

Position:	chrX:19569185	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5809	7.3860	0.7111	0.8345	0.0000	0.6100
Exp. accuracy:	0.93	0.91	0.93	0.57	0.93	0.64

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19588648, G→A

Position:	chrX:19588648	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	0.2680	0.4824	0.0728	0.0000	0.5000
Exp. accuracy:	0.96	0.95	0.97	0.90	0.93	0.51

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19588657, C→T

Position:	chrX:19588657	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs145308311	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	12.0400	0.7135	0.4606	0.0000	0.5400
Exp. accuracy:	0.96	0.83	0.93	0.72	0.93	0.62

External links

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

Variant: X : 19588666, C→A

Position:	chrX:19588666	Ref. allele:	C	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	deleterious	neutral	neutral	neutral	deleterious
Score:	-0.6107	15.9900	0.5847	0.6794	0.0000	0.5700
Exp. accuracy:	0.95	0.58	0.97	0.69	0.93	0.68

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19588666, C→T

Position:	chrX:19588666	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs147648876	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	13.0000	0.6798	0.1920	0.0000	0.5700
Exp. accuracy:	0.96	0.77	0.94	0.80	0.93	0.68

External links

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

Variant: X : 19588672, C→T

Position:	chrX:19588672	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	9.9380	0.3696	0.3341	0.0000	0.5700
Exp. accuracy:	0.96	0.91	0.97	0.73	0.93	0.68

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19588675, C→T

Position:	chrX:19588675	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs2290805	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	8.3870	0.7240	0.0057	0.0000	0.5400
Exp. accuracy:	0.96	0.92	0.93	0.96	0.93	0.62

External links

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

Variant: X : 19588684, C→T

Position:	chrX:19588684	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs199796248	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	11.5200	0.7542	0.0234	0.0000	0.5500
Exp. accuracy:	0.96	0.88	0.90	0.96	0.93	0.66

External links

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

Variant: X : 19588717, G→C

Position:	chrX:19588717	Ref. allele:	G	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5932	5.9920	0.6062	0.7935	0.0000	0.6400
Exp. accuracy:	0.93	0.93	0.96	0.57	0.93	0.68

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19588731, G→T

Position:	chrX:19588731	Ref. allele:	G	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.4926	12.8800	0.6286	0.9216	0.0000	0.6700
Exp. accuracy:	0.93	0.77	0.97	0.78	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19588741, T→C

Position:	chrX:19588741	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	3.3960	0.6280	0.4354	0.0000	0.5600
Exp. accuracy:	0.96	0.94	0.97	0.72	0.93	0.69

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19588741, T→G

Position:	chrX:19588741	Ref. allele:	T	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	5.7100	0.6358	0.5045	0.0000	0.5600
Exp. accuracy:	0.96	0.92	0.97	0.70	0.93	0.69

External links

[\[GenBank\]](#) [\[UCSC\]](#) [\[Ensemble\]](#)



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	54	0	54	0	54	0
Synonymous	41	13	54	0	29	24	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: X : 19588744, C→A

Position:	chrX:19588744	Ref. allele:	C	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	13.5600	0.6786	0.0281	0.0000	0.5500
Exp. accuracy:	0.96	0.73	0.94	0.96	0.93	0.66

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19588744, C→T

Position:	chrX:19588744	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	12.8100	0.7393	0.0237	0.0000	0.5500
Exp. accuracy:	0.96	0.77	0.91	0.96	0.93	0.66

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19588756, A→G

Position:	chrX:19588756	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	6.8640	0.6973	0.7487	0.0000	0.6700
Exp. accuracy:	0.96	0.92	0.94	0.69	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19588759, G→A

Position:	chrX:19588759	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs145759622	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	12.8800	0.6534	0.0246	0.0000	0.6000
Exp. accuracy:	0.96	0.77	0.96	0.96	0.93	0.64

External links

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

Variant: X : 19588789, T→C

Position:	chrX:19588789	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5883	3.2800	0.6627	0.8493	0.0000	0.6600
Exp. accuracy:	0.93	0.94	0.95	0.57	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19592077, T→C

Position:	chrX:19592077	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs369021832	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.4901	1.6180	0.7888	0.9178	0.0000	0.5800
Exp. accuracy:	0.93	0.95	0.89	0.78	0.93	0.65

External links

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

Variant: X : 19592128, A→G

Position:	chrX:19592128	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.4832	6.3070	0.6568	0.9261	0.0000	0.6400
Exp. accuracy:	0.93	0.93	0.95	0.82	0.93	0.68

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19592131, T→C

Position:	chrX:19592131	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs372562490	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	1.2270	0.6183	0.6865	0.0000	0.6000
Exp. accuracy:	0.96	0.95	0.96	0.69	0.93	0.64

External links

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

Variant: X : 19594965, G→A

Position:	chrX:19594965	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.5583	10.4200	0.7693	0.8699	0.0000	0.3200
Exp. accuracy:	0.93	0.88	0.90	0.60	0.93	0.53

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19594974, G→A

Position:	chrX:19594974	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	11.6200	0.6145	0.3520	0.0000	0.2900
Exp. accuracy:	0.96	0.88	0.96	0.73	0.93	0.56

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19594977, T→G

Position:	chrX:19594977	Ref. allele:	T	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs143742226	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	11.1400	0.7307	0.7865	0.0000	0.3300
Exp. accuracy:	0.96	0.88	0.91	0.69	0.93	0.56

External links

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

Variant: X : 19594995, G→A

Position:	chrX:19594995	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	7.9610	0.6322	0.7596	0.0000	0.3200
Exp. accuracy:	0.96	0.91	0.97	0.69	0.93	0.53

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19607959, C→T

Position:	chrX:19607959	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs3747357	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	10.3700	0.6051	0.0086	0.0000	0.3200
Exp. accuracy:	0.96	0.88	0.96	0.96	0.93	0.53

External links

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

Variant: X : 19607962, T→C

Position:	chrX:19607962	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	0.2600	0.3323	0.1528	0.0000	0.3400
Exp. accuracy:	0.96	0.95	0.97	0.83	0.93	0.56

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19607977, G→A

Position:	chrX:19607977	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	11.6600	0.6895	0.4237	0.0000	0.3100
Exp. accuracy:	0.96	0.83	0.94	0.72	0.93	0.53

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19607986, G→A

Position:	chrX:19607986	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs199869591	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	4.0450	0.7125	0.0635	0.0000	0.3100
Exp. accuracy:	0.96	0.94	0.93	0.92	0.93	0.53

External links

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

Variant: X : 19608013, C→T

Position:	chrX:19608013	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	12.3300	0.6140	0.5219	0.0000	0.3400
Exp. accuracy:	0.96	0.83	0.96	0.70	0.93	0.56

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19608034, G→A

Position:	chrX:19608034	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs372715805	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	9.2320	0.6240	0.0122	0.0000	0.3200
Exp. accuracy:	0.96	0.91	0.96	0.96	0.93	0.53

External links

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

Variant: X : 19608037, G→A

Position:	chrX:19608037	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	11.8700	0.8148	0.2766	0.0000	0.2900
Exp. accuracy:	0.96	0.83	0.90	0.73	0.93	0.56

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19608037, G→T

Position:	chrX:19608037	Ref. allele:	G	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	9.5720	0.7712	0.5145	0.0000	0.2900
Exp. accuracy:	0.96	0.91	0.90	0.70	0.93	0.56

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19631879, G→A

Position:	chrX:19631879	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	9.7570	0.7735	0.6253	0.0000	0.3300
Exp. accuracy:	0.96	0.91	0.90	0.69	0.93	0.56

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19631957, G→A

Position:	chrX:19631957	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	?
Score:	-0.5688	15.0600	0.7694	0.7976	0.0000	0.4800
Exp. accuracy:	0.93	0.73	0.90	0.57	0.93	0.43

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19683832, C→T

Position:	chrX:19683832	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs111744926	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	9.4010	0.2521	0.0049	0.0000	0.3100
Exp. accuracy:	0.96	0.91	0.97	0.96	0.93	0.53

External links

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

Variant: X : 19683880, T→C

Position:	chrX:19683880	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	5.3740	0.7302	0.6944	0.0000	0.3000
Exp. accuracy:	0.96	0.92	0.91	0.69	0.93	0.57

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19683892, G→A

Position:	chrX:19683892	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs375218887	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.4858	10.5400	0.6290	0.9262	0.0000	0.4600
Exp. accuracy:	0.93	0.88	0.97	0.82	0.93	0.54

External links

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

Variant: X : 19683916, C→T

Position:	chrX:19683916	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	12.4300	0.5659	0.5673	0.0000	0.3000
Exp. accuracy:	0.96	0.79	0.97	0.70	0.93	0.57

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19683952, T→C

Position:	chrX:19683952	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	0.4100	0.5620	0.0367	0.0000	0.2600
Exp. accuracy:	0.96	0.95	0.97	0.96	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19683958, G→A

Position:	chrX:19683958	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	8.2490	0.6158	0.3322	0.0000	0.3400
Exp. accuracy:	0.96	0.92	0.96	0.73	0.93	0.56

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19684006, G→A

Position:	chrX:19684006	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs373105646	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	11.1000	0.7645	0.0585	0.0000	0.4100
Exp. accuracy:	0.96	0.88	0.90	0.92	0.93	0.56

External links

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

Variant: X : 19695622, T→C

Position:	chrX:19695622	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	1.0740	0.5636	0.1528	0.0000	0.5100
Exp. accuracy:	0.96	0.95	0.97	0.83	0.93	0.55

External links

[GenBank] [UCSC] [Ensemble]

Variant:	X : 19695622, T→G					
Position:	chrX:19695622	Ref. allele:	T	Alt. allele:	G	
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1	
RS number:	-	Clin. sign.:	-	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	5.6730	0.5976	0.0587	0.0000	0.5100
Exp. accuracy:	0.96	0.92	0.96	0.92	0.93	0.55

External links

[GenBank] [UCSC] [Ensemble]

Variant:	X : 19695655, C→T					
Position:	chrX:19695655	Ref. allele:	C	Alt. allele:	T	
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1	
RS number:	rs145372202	Clin. sign.:	-	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	12.3200	0.6134	0.0236	0.0000	0.5800
Exp. accuracy:	0.96	0.83	0.96	0.96	0.93	0.65

External links

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

Variant:	X : 19695682, G→A					
Position:	chrX:19695682	Ref. allele:	G	Alt. allele:	A	
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1	
RS number:	-	Clin. sign.:	-	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5883	9.9210	0.6962	0.8588	0.0000	0.6700
Exp. accuracy:	0.93	0.91	0.94	0.57	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant:	X : 19695706, C→T					
Position:	chrX:19695706	Ref. allele:	C	Alt. allele:	T	
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1	
RS number:	-	Clin. sign.:	-	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	14.6900	0.6257	0.4316	0.0000	0.5800
Exp. accuracy:	0.96	0.73	0.96	0.72	0.93	0.65

External links

[GenBank] [UCSC] [Ensemble]

Variant:	X : 19695709, G→A					
Position:	chrX:19695709	Ref. allele:	G	Alt. allele:	A	
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1	
RS number:	rs184591130	Clin. sign.:	-	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	10.0500	0.6394	0.2472	0.0000	0.5800
Exp. accuracy:	0.96	0.91	0.97	0.73	0.93	0.65

External links

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

Variant:	X : 19695721, T→C					
Position:	chrX:19695721	Ref. allele:	T	Alt. allele:	C	
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1	
RS number:	-	Clin. sign.:	-	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.4678	3.1140	0.7356	0.9472	0.0000	0.7700
Exp. accuracy:	0.93	0.94	0.91	0.91	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19706890, C→T

Position:	chrX:19706890	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	11.7100	0.8190	0.5002	0.0000	0.3200
Exp. accuracy:	0.96	0.83	0.90	0.70	0.93	0.53

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19706905, G→A

Position:	chrX:19706905	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	10.9800	0.8352	0.0096	0.0000	0.4300
Exp. accuracy:	0.96	0.88	0.90	0.96	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19706929, G→A

Position:	chrX:19706929	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs368141192	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	6.1360	0.7478	0.0135	0.0000	0.4200
Exp. accuracy:	0.96	0.93	0.91	0.96	0.93	0.54

External links

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

Variant: X : 19706944, G→A

Position:	chrX:19706944	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs371576734	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	9.5030	0.5860	0.7846	0.0000	0.5100
Exp. accuracy:	0.96	0.91	0.97	0.69	0.93	0.55

External links

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

Variant: X : 19706983, G→A

Position:	chrX:19706983	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	7.3650	0.8381	0.0111	0.0000	0.3700
Exp. accuracy:	0.96	0.91	0.90	0.96	0.93	0.56

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19746328, G→A

Position:	chrX:19746328	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	9.4230	0.6730	0.7326	0.0000	0.3600
Exp. accuracy:	0.96	0.91	0.94	0.69	0.93	0.55

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19746340, C→T

Position:	chrX:19746340	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs375522869	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	14.1800	0.7016	0.0201	0.0000	0.3600
Exp. accuracy:	0.96	0.73	0.94	0.96	0.93	0.55

External links

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

Variant: X : 19746376, T→C

Position:	chrX:19746376	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	1.5860	0.5733	0.4735	0.0000	0.3300
Exp. accuracy:	0.96	0.95	0.97	0.72	0.93	0.56

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19746379, G→A

Position:	chrX:19746379	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	1.9240	0.7287	0.0212	0.0000	0.3600
Exp. accuracy:	0.96	0.95	0.91	0.96	0.93	0.55

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19746397, A→G

Position:	chrX:19746397	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	11.1800	0.7860	0.7385	0.0000	0.4600
Exp. accuracy:	0.96	0.88	0.90	0.69	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19836149, A→C

Position:	chrX:19836149	Ref. allele:	A	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5585	0.2660	0.7690	0.8673	0.0000	0.6700
Exp. accuracy:	0.93	0.95	0.90	0.60	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19836152, T→C

Position:	chrX:19836152	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5662	3.2830	0.6961	0.8654	0.0000	0.6700
Exp. accuracy:	0.93	0.94	0.94	0.60	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19836161, G→A					
Position:	chrX:19836161	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	9.3650	0.6393	0.6683	0.0000	0.5400
Exp. accuracy:	0.96	0.91	0.97	0.69	0.93	0.62

External links

[\[GenBank\]](#) [\[UCSC\]](#) [\[Ensemble\]](#)

Variant: X : 19836200, G→A					
Position:	chrX:19836200	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs35356139	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.4850	9.8720	0.8514	0.9205	0.0000	0.6300
Exp. accuracy:	0.93	0.91	0.90	0.78	0.93	0.66

External links

[\[dbSNP\]](#) [\[GenBank\]](#) [\[HaploReg\]](#) [\[RegulomeDB\]](#) [\[UCSC\]](#) [\[Ensemble\]](#)

Variant: X : 19836224, G→A					
Position:	chrX:19836224	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5746	13.6100	0.7128	0.7964	0.0000	0.6400
Exp. accuracy:	0.93	0.73	0.93	0.57	0.93	0.68

External links

[\[GenBank\]](#) [\[UCSC\]](#) [\[Ensemble\]](#)

Variant: X : 19836230, C→G

Position:	chrX:19836230	Ref. allele:	C	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	8.6900	0.7045	0.0284	0.0000	0.6200
Exp. accuracy:	0.96	0.92	0.94	0.96	0.93	0.66

External links

[GenBank] [UCSC] [Ensemble]

Variant: X : 19836245, G→A

Position:	chrX:19836245	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	rs7882276	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	9.6710	0.6257	0.7752	0.0000	0.6800
Exp. accuracy:	0.96	0.91	0.96	0.69	0.93	0.70

External links

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

Variant: X : 19836272, T→A

Position:	chrX:19836272	Ref. allele:	T	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	SH3KBP1
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5316	12.4600	0.7807	0.8754	0.0000	0.7200
Exp. accuracy:	0.93	0.79	0.90	0.64	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]
