



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	95	5	90	10	94	6
Synonymous	33	67	96	4	44	46	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: 11 : 85974750, G→C

Position:	chr11:85974750	Ref. allele:	G	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.5876	5.7230	0.6814	0.8185	0.0000	0.2400
Exp. accuracy:	0.93	0.92	0.94	0.57	0.93	0.58

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 85974777, T→C

Position:	chr11:85974777	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs200565799	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	0.0090	0.3471	0.1083	0.0000	0.3000
Exp. accuracy:	0.96	0.95	0.97	0.87	0.93	0.57

External links

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

Variant: 11 : 85974780, C→T

Position:	chr11:85974780	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	11.8800	0.5722	0.4095	0.0000	0.2800
Exp. accuracy:	0.96	0.83	0.97	0.72	0.93	0.55

External links

[GenBank] [UCSC] [Ensemble]

Variant:	11 : 85974795, A→G				
Position:	chr11:85974795	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	0.4050	0.7045	0.6867	0.0000	0.2200
Exp. accuracy:	0.96	0.95	0.94	0.69	0.93	0.59

External links

[GenBank] [UCSC] [Ensemble]

Variant:	11 : 85974807, T→C				
Position:	chr11:85974807	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.5853	5.0280	0.7135	0.8323	0.0000	0.2100
Exp. accuracy:	0.93	0.93	0.93	0.57	0.93	0.60

External links

[GenBank] [UCSC] [Ensemble]

Variant:	11 : 85981138, A→C				
Position:	chr11:85981138	Ref. allele:	A	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs76719109	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.4724	6.8470	0.6763	0.9410	0.0000	0.2800
Exp. accuracy:	0.93	0.92	0.94	0.88	0.93	0.55

External links

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

Variant: 11 : 85981138, A→T

Position:	chr11:85981138	Ref. allele:	A	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.4825	6.9340	0.6506	0.9278	0.0000	0.2800
Exp. accuracy:	0.93	0.92	0.96	0.82	0.93	0.55

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 85981150, G→A

Position:	chr11:85981150	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs12295435	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	12.0500	0.5906	0.4934	0.0000	0.2600
Exp. accuracy:	0.96	0.83	0.97	0.70	0.93	0.54

External links

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

Variant: 11 : 85981153, T→C

Position:	chr11:85981153	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.5814	8.3060	0.7544	0.8430	0.0000	0.2400
Exp. accuracy:	0.93	0.92	0.90	0.57	0.93	0.58

External links

[GenBank] [UCSC] [Ensemble]

Variant:	11 : 85981222, <i>T</i> → <i>C</i>				
Position:	chr11:85981222	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.5518	9.6600	0.7521	0.8790	0.0000	0.2400
Exp. accuracy:	0.93	0.91	0.90	0.64	0.93	0.58

External links

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

Variant:	11 : 85981753, <i>G</i> → <i>A</i>				
Position:	chr11:85981753	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.5867	9.6870	0.6784	0.8295	0.0000	0.3900
Exp. accuracy:	0.93	0.91	0.94	0.57	0.93	0.52

External links

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

Variant:	11 : 85981762, <i>T</i> → <i>A</i>				
Position:	chr11:85981762	Ref. allele:	T	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.4534	7.7210	0.6798	0.9539	0.0000	0.4200
Exp. accuracy:	0.93	0.91	0.94	0.92	0.93	0.54

External links

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

Variant: 11 : 85981765, G→A

Position:	chr11:85981765	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	11.1000	0.7879	0.2926	0.0000	0.4600
Exp. accuracy:	0.96	0.88	0.89	0.73	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 85981873, G→A

Position:	chr11:85981873	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs371001564	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.4266	13.5900	0.8618	0.9569	0.0000	0.4300
Exp. accuracy:	0.88	0.73	0.90	0.93	0.93	0.54

External links

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

Variant: 11 : 85981903, G→A

Position:	chr11:85981903	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.4624	12.2500	0.5484	0.9565	0.0000	0.4000
Exp. accuracy:	0.93	0.83	0.97	0.93	0.93	0.56

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 85981942, A→C

Position:	chr11:85981942	Ref. allele:	A	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.5683	0.1730	0.6676	0.8631	0.0000	0.4300
Exp. accuracy:	0.93	0.95	0.95	0.60	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 85981945, A→G

Position:	chr11:85981945	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.4553	9.1930	0.7753	0.9543	0.0000	0.4700
Exp. accuracy:	0.93	0.92	0.90	0.92	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 85981972, T→C

Position:	chr11:85981972	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.5184	7.4540	0.6746	0.9028	0.0000	0.4300
Exp. accuracy:	0.93	0.91	0.94	0.75	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 85983936, T→G

Position:	chr11:85983936	Ref. allele:	T	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.4801	10.2000	0.6877	0.9275	0.0000	0.6000
Exp. accuracy:	0.93	0.88	0.94	0.82	0.93	0.64

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 85983951, T→G

Position:	chr11:85983951	Ref. allele:	T	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5321	7.6520	0.6450	0.8891	0.0000	0.6000
Exp. accuracy:	0.93	0.91	0.96	0.68	0.93	0.64

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 85983957, T→C

Position:	chr11:85983957	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs149179479	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5823	7.8000	0.7254	0.7912	0.0000	0.5500
Exp. accuracy:	0.93	0.91	0.93	0.57	0.93	0.66

External links

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

Variant: 11 : 85990278, A→C

Position:	chr11:85990278	Ref. allele:	A	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.4171	0.6510	0.7134	0.9916	0.0000	0.4400
Exp. accuracy:	0.88	0.95	0.93	0.97	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 85990287, A→G

Position:	chr11:85990287	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.5284	0.1160	0.7023	0.8933	0.0000	0.4300
Exp. accuracy:	0.93	0.95	0.94	0.71	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 85990320, A→G

Position:	chr11:85990320	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.4707	6.7040	0.5990	0.9514	0.0000	0.4700
Exp. accuracy:	0.93	0.92	0.96	0.91	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 85990338, G→A

Position:	chr11:85990338	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5100	9.7780	0.7530	0.9068	0.0000	0.5000
Exp. accuracy:	0.93	0.91	0.90	0.75	0.93	0.51

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 85990344, A→G

Position:	chr11:85990344	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	?
Score:	-0.4148	4.3540	0.7340	0.9908	0.0000	0.4900
Exp. accuracy:	0.88	0.94	0.91	0.97	0.93	0.43

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 85990368, A→G

Position:	chr11:85990368	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	?
Score:	-0.5362	8.6900	0.5310	0.9008	0.0000	0.4900
Exp. accuracy:	0.93	0.92	0.97	0.71	0.93	0.43

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 85990371, A→C

Position:	chr11:85990371	Ref. allele:	A	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	?
Score:	-0.5219	0.6420	0.7202	0.9000	0.0000	0.4900
Exp. accuracy:	0.93	0.95	0.93	0.71	0.93	0.43

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 85990371, A→G

Position:	chr11:85990371	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	?
Score:	-0.5482	6.9260	0.7300	0.8794	0.0000	0.4900
Exp. accuracy:	0.93	0.92	0.91	0.64	0.93	0.43

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 85996869, T→C

Position:	chr11:85996869	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs151035490	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	6.9350	0.7513	0.7689	0.0000	0.5600
Exp. accuracy:	0.96	0.92	0.90	0.69	0.93	0.69

External links

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

Variant: 11 : 85996869, T→G

Position:	chr11:85996869	Ref. allele:	T	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5621	8.6160	0.7347	0.8684	0.0000	0.5600
Exp. accuracy:	0.93	0.92	0.91	0.60	0.93	0.69

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 85996890, C→T

Position:	chr11:85996890	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs372958249	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.4350	13.7700	0.7898	0.9566	0.0000	0.5300
Exp. accuracy:	0.88	0.73	0.89	0.93	0.93	0.64

External links

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

Variant: 11 : 85996893, C→T

Position:	chr11:85996893	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	12.7100	0.5206	0.0505	0.0000	0.5400
Exp. accuracy:	0.96	0.79	0.97	0.94	0.93	0.62

External links

[GenBank] [UCSC] [Ensemble]

Variante: 11 : 85996908, A→G

Position:	chr11:85996908	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	5.1300	0.5613	0.6872	0.0000	0.5000
Exp. accuracy:	0.96	0.93	0.97	0.69	0.93	0.51

External links

[GenBank] [UCSC] [Ensemble]

Variante: 11 : 85996917, C→A

Position:	chr11:85996917	Ref. allele:	C	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.4656	15.2900	0.7052	0.9333	0.0000	0.5000
Exp. accuracy:	0.93	0.73	0.93	0.86	0.93	0.51

External links

[GenBank] [UCSC] [Ensemble]

Variante: 11 : 85996923, T→C

Position:	chr11:85996923	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5841	7.9990	0.7160	0.8225	0.0000	0.5400
Exp. accuracy:	0.93	0.91	0.93	0.57	0.93	0.62

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86000660, G→A

Position:	chr11:86000660	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5888	11.7200	0.6518	0.8446	0.0000	0.5600
Exp. accuracy:	0.93	0.83	0.96	0.57	0.93	0.69

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86000660, G→T

Position:	chr11:86000660	Ref. allele:	G	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	10.1300	0.6781	0.7739	0.0000	0.5600
Exp. accuracy:	0.96	0.88	0.94	0.69	0.93	0.69

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86000678, G→A

Position:	chr11:86000678	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs145725396	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.4137	13.9400	0.6360	0.9874	0.0000	0.5700
Exp. accuracy:	0.88	0.73	0.97	0.97	0.93	0.68

External links

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

Variant: 11 : 86000684, T→G

Position:	chr11:86000684	Ref. allele:	T	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs200575473	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.4812	11.6500	0.6654	0.9279	0.0000	0.6300
Exp. accuracy:	0.93	0.83	0.95	0.82	0.93	0.66

External links

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

Variant: 11 : 86000687, A→G

Position:	chr11:86000687	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5654	9.2110	0.7452	0.8623	0.0000	0.6100
Exp. accuracy:	0.93	0.91	0.91	0.57	0.93	0.64

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86000696, C→A

Position:	chr11:86000696	Ref. allele:	C	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	deleterious	neutral	neutral	neutral	deleterious
Score:	-0.6078	16.4500	0.6252	0.4003	0.0000	0.6500
Exp. accuracy:	0.95	0.58	0.96	0.72	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86000696, C→T

Position:	chr11:86000696	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	13.3300	0.6099	0.5595	0.0000	0.6500
Exp. accuracy:	0.96	0.74	0.96	0.70	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86000702, T→G

Position:	chr11:86000702	Ref. allele:	T	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5370	10.2900	0.5631	0.8959	0.0000	0.5800
Exp. accuracy:	0.93	0.88	0.97	0.71	0.93	0.65

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86000714, T→C

Position:	chr11:86000714	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs141849542	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	9.2410	0.7283	0.6247	0.0000	0.6000
Exp. accuracy:	0.96	0.91	0.93	0.69	0.93	0.64

External links

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

Variant: 11 : 86000729, A→G

Position:	chr11:86000729	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs201745810	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	9.8280	0.7121	0.2832	0.0000	0.6000
Exp. accuracy:	0.96	0.91	0.93	0.73	0.93	0.64

External links

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

Variant: 11 : 86000762, T→C

Position:	chr11:86000762	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs150582057	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5452	8.5530	0.5867	0.8825	0.0000	0.6700
Exp. accuracy:	0.93	0.92	0.97	0.64	0.93	0.70

External links

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

Variant: 11 : 86000768, T→A

Position:	chr11:86000768	Ref. allele:	T	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5501	11.6200	0.7071	0.8778	0.0000	0.6600
Exp. accuracy:	0.93	0.88	0.93	0.64	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86000774, C→T

Position:	chr11:86000774	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs372267972	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5807	13.6800	0.6379	0.8103	0.0000	0.7400
Exp. accuracy:	0.93	0.73	0.97	0.57	0.93	0.70

External links

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

Variant: 11 : 86001062, T→C

Position:	chr11:86001062	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5280	4.1600	0.6360	0.8956	0.0000	0.5100
Exp. accuracy:	0.93	0.94	0.97	0.71	0.93	0.55

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86001071, T→A

Position:	chr11:86001071	Ref. allele:	T	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	15.3200	0.6531	0.5199	0.0000	0.5800
Exp. accuracy:	0.96	0.73	0.96	0.70	0.93	0.65

External links

[GenBank] [UCSC] [Ensemble]

Variant:	11 : 86001071, T→G				
Position:	chr11:86001071	Ref. allele:	T	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	13.1200	0.6518	0.5751	0.0000	0.5800
Exp. accuracy:	0.96	0.74	0.96	0.70	0.93	0.65

External links

[GenBank] [UCSC] [Ensemble]

Variant:	11 : 86001080, C→T				
Position:	chr11:86001080	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5855	14.6800	0.5928	0.8509	0.0000	0.5600
Exp. accuracy:	0.93	0.73	0.96	0.57	0.93	0.69

External links

[GenBank] [UCSC] [Ensemble]

Variant:	11 : 86001095, C→T				
Position:	chr11:86001095	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5079	13.8400	0.7642	0.9016	0.0000	0.5000
Exp. accuracy:	0.93	0.73	0.90	0.71	0.93	0.51

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86001101, *G*→*C*

Position:	chr11:86001101	Ref. allele:	G	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.4781	9.1710	0.6993	0.9416	0.0000	0.5100
Exp. accuracy:	0.93	0.92	0.94	0.88	0.93	0.55

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86001106, *G*→*A*

Position:	chr11:86001106	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.4577	12.2500	0.7478	0.9427	0.0000	0.5400
Exp. accuracy:	0.93	0.83	0.91	0.90	0.93	0.62

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86001110, *T*→*A*

Position:	chr11:86001110	Ref. allele:	T	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	12.7800	0.7079	0.6762	0.0000	0.5600
Exp. accuracy:	0.96	0.77	0.93	0.69	0.93	0.69

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86001110, T→C

Position:	chr11:86001110	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs139625756	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	9.0250	0.7043	0.2603	0.0000	0.5600
Exp. accuracy:	0.96	0.92	0.94	0.73	0.93	0.69

External links

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

Variant: 11 : 86001116, A→G

Position:	chr11:86001116	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.4813	9.6180	0.7092	0.9293	0.0000	0.5200
Exp. accuracy:	0.93	0.91	0.93	0.82	0.93	0.58

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86001122, T→A

Position:	chr11:86001122	Ref. allele:	T	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs111469150	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.4103	12.9700	0.7187	0.9720	0.0000	0.5100
Exp. accuracy:	0.88	0.77	0.93	0.97	0.93	0.55

External links

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

Variant: 11 : 86001149, T→C

Position:	chr11:86001149	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.4747	7.8220	0.7392	0.9288	0.0000	0.5400
Exp. accuracy:	0.93	0.91	0.91	0.82	0.93	0.62

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86003413, T→C

Position:	chr11:86003413	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs200195910	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	?
Score:	-0.5038	9.6710	0.7788	0.9053	0.0000	0.4900
Exp. accuracy:	0.93	0.91	0.90	0.75	0.93	0.43

External links

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

Variant: 11 : 86003427, A→G

Position:	chr11:86003427	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.4941	8.5750	0.7693	0.9135	0.0000	0.4600
Exp. accuracy:	0.93	0.92	0.90	0.77	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86011033, T→C

Position:	chr11:86011033	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.4795	9.1330	0.7432	0.9265	0.0000	0.7500
Exp. accuracy:	0.93	0.92	0.91	0.82	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86011036, A→C

Position:	chr11:86011036	Ref. allele:	A	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5490	6.1350	0.8235	0.8672	0.0000	0.7200
Exp. accuracy:	0.93	0.93	0.90	0.60	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86011129, A→G

Position:	chr11:86011129	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.5982	2.8440	0.5645	0.8185	0.0000	0.6900
Exp. accuracy:	0.93	0.95	0.97	0.57	0.93	0.70

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86012300, T→C

Position:	chr11:86012300	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs375495535	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.4585	4.5400	0.6037	0.9616	0.0000	0.3900
Exp. accuracy:	0.93	0.93	0.96	0.94	0.93	0.52

External links

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

Variant: 11 : 86012339, C→A

Position:	chr11:86012339	Ref. allele:	C	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	deleterious	neutral	deleterious	neutral	neutral
Score:	-0.1308	17.2300	0.7450	0.8174	0.0000	0.4400
Exp. accuracy:	0.88	0.58	0.91	0.57	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86012351, G→A

Position:	chr11:86012351	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.4679	13.8500	0.6356	0.9464	0.0000	0.5100
Exp. accuracy:	0.93	0.73	0.97	0.90	0.93	0.55

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86012351, G→C

Position:	chr11:86012351	Ref. allele:	G	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.4561	10.9400	0.6702	0.9575	0.0000	0.5100
Exp. accuracy:	0.93	0.88	0.94	0.93	0.93	0.55

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86012354, A→G

Position:	chr11:86012354	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs149334225	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	?
Score:	-0.5438	12.2000	0.6703	0.8787	0.0000	0.4800
Exp. accuracy:	0.93	0.83	0.94	0.64	0.93	0.43

External links

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

Variant: 11 : 86012357, A→G

Position:	chr11:86012357	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs79317992	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.5084	10.0600	0.7306	0.9093	0.0000	0.4700
Exp. accuracy:	0.93	0.91	0.91	0.75	0.93	0.54

External links

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

Variant: 11 : 86012363, T→C

Position:	chr11:86012363	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs199846387	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.4828	9.7910	0.6885	0.9264	0.0000	0.4100
Exp. accuracy:	0.93	0.91	0.94	0.82	0.93	0.56

External links

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

Variant: 11 : 86014894, C→T

Position:	chr11:86014894	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs592297	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	12.9000	0.6510	0.4728	0.0000	0.3600
Exp. accuracy:	0.96	0.77	0.96	0.72	0.93	0.55

External links

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

Variant: 11 : 86014923, G→A

Position:	chr11:86014923	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs186932606	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.5206	11.6400	0.6788	0.8999	0.0000	0.3500
Exp. accuracy:	0.93	0.83	0.94	0.71	0.93	0.54

External links

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

Variant: 11 : 86014963, C→G

Position:	chr11:86014963	Ref. allele:	C	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	deleterious	neutral	deleterious	deleterious	deleterious	neutral
Score:	0.5498	15.5400	0.9477	0.9140	4.0000	0.3700
Exp. accuracy:	0.93	0.73	0.87	0.77	1.00	0.56

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86022369, T→C

Position:	chr11:86022369	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	deleterious	neutral	deleterious	neutral	deleterious
Score:	-0.0534	15.7700	0.8477	0.9024	0.0000	0.5100
Exp. accuracy:	0.88	0.58	0.90	0.75	0.93	0.55

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86022375, C→T

Position:	chr11:86022375	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	13.4200	0.7679	0.6904	0.0000	0.5000
Exp. accuracy:	0.96	0.74	0.90	0.69	0.93	0.51

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86022396, A→C

Position:	chr11:86022396	Ref. allele:	A	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	5.5420	0.7228	0.7505	0.0000	0.4200
Exp. accuracy:	0.96	0.92	0.93	0.69	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86022453, T→C

Position:	chr11:86022453	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	deleterious	neutral
Score:	-0.3751	9.9620	0.8690	0.7566	3.0000	0.4200
Exp. accuracy:	0.88	0.91	0.90	0.69	1.00	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86022465, A→G

Position:	chr11:86022465	Ref. allele:	A	Alt. allele:	G
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	deleterious	neutral	neutral	deleterious	deleterious	neutral
Score:	0.0917	8.8790	0.8691	0.9342	4.0000	0.4200
Exp. accuracy:	0.93	0.92	0.90	0.86	1.00	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86022468, T→C

Position:	chr11:86022468	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	deleterious	neutral	deleterious	neutral	deleterious	neutral
Score:	0.1113	13.3200	0.9639	0.2183	3.0000	0.3200
Exp. accuracy:	0.93	0.74	0.87	0.77	1.00	0.53

External links

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

Variant: 11 : 86026296, C→T

Position:	chr11:86026296	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs202207283	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	14.1700	0.7042	0.7677	0.0000	0.3000
Exp. accuracy:	0.96	0.73	0.94	0.69	0.93	0.57

External links

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

Variant: 11 : 86026323, T→C

Position:	chr11:86026323	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs148486517	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	neutral
Score:	-0.5799	9.1020	0.7808	0.8600	0.0000	0.4600
Exp. accuracy:	0.93	0.92	0.90	0.57	0.93	0.54

External links

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

Variant:	11 : 86026335, C→T					
Position:	chr11:86026335	Ref. allele:	C	Alt. allele:	T	
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM	
RS number:	-	Clin. sign.:	-	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	deleterious	neutral	neutral	neutral	neutral
Score:	-0.6391	16.8800	0.5891	0.0861	0.0000	0.3600
Exp. accuracy:	0.95	0.58	0.97	0.88	0.93	0.55

External links

[GenBank] [UCSC] [Ensemble]

Variant:	11 : 86031481, C→T					
Position:	chr11:86031481	Ref. allele:	C	Alt. allele:	T	
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM	
RS number:	-	Clin. sign.:	-	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	?
Score:	-1.0000	14.5300	0.7411	0.7343	0.0000	0.4800
Exp. accuracy:	0.96	0.73	0.91	0.69	0.93	0.43

External links

[GenBank] [UCSC] [Ensemble]

Variant:	11 : 86031523, C→G					
Position:	chr11:86031523	Ref. allele:	C	Alt. allele:	G	
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM	
RS number:	-	Clin. sign.:	-	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	?
Score:	-0.5575	12.3300	0.6918	0.8695	0.0000	0.4900
Exp. accuracy:	0.93	0.83	0.94	0.60	0.93	0.43

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86031523, C→T

Position:	chr11:86031523	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs140266798	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	?
Score:	-1.0000	13.6500	0.6654	0.7859	0.0000	0.4900
Exp. accuracy:	0.96	0.73	0.95	0.69	0.93	0.43

External links

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

Variant: 11 : 86031559, G→A

Position:	chr11:86031559	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs142062212	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.4756	10.9000	0.6150	0.9470	0.0000	0.5500
Exp. accuracy:	0.93	0.88	0.96	0.91	0.93	0.66

External links

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

Variant: 11 : 86031571, T→C

Position:	chr11:86031571	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs151105998	Clin. sign.:	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	deleterious
Score:	-1.0000	9.3380	0.6938	0.2327	0.0000	0.5200
Exp. accuracy:	0.96	0.91	0.94	0.73	0.93	0.58

External links

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

Variant: 11 : 86031577, G→A

Position:	chr11:86031577	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	deleterious
Score:	-0.4845	11.5400	0.6322	0.9321	0.0000	0.5300
Exp. accuracy:	0.93	0.88	0.97	0.86	0.93	0.64

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86068657, G→A

Position:	chr11:86068657	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	deleterious	deleterious	deleterious	deleterious	neutral	neutral
Score:	0.4592	17.4700	0.9650	0.7963	0.0000	0.3400
Exp. accuracy:	0.93	0.58	0.87	0.57	0.93	0.56

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86068661, C→T

Position:	chr11:86068661	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs150283404	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	deleterious	deleterious	neutral	neutral	neutral
Score:	0.0072	16.6800	0.9680	0.6263	0.0000	0.3100
Exp. accuracy:	0.88	0.58	0.87	0.69	0.93	0.53

External links

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

Variant: 11 : 86068673, C→T

Position:	chr11:86068673	Ref. allele:	C	Alt. allele:	T
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	deleterious	deleterious	neutral	neutral	neutral
Score:	-0.0254	17.3200	0.9581	0.6314	0.0000	0.2700
Exp. accuracy:	0.88	0.58	0.87	0.69	0.93	0.55

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86068703, T→C

Position:	chr11:86068703	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	-	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	deleterious	neutral	neutral	neutral	neutral
Score:	-0.5941	17.4900	0.7616	0.5796	0.0000	0.4700
Exp. accuracy:	0.93	0.58	0.90	0.70	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86068715, T→C

Position:	chr11:86068715	Ref. allele:	T	Alt. allele:	C
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs200624220	Clin. sign.:	-	-	-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	5.2440	0.4790	0.0365	0.0000	0.3800
Exp. accuracy:	0.96	0.92	0.97	0.96	0.93	0.55

External links

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

Variant:	11 : 86068724, G→C					
Position:	chr11:86068724	Ref. allele:	G	Alt. allele:	C	
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM	
RS number:	-	Clin. sign.:	-	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	deleterious	neutral	?
Score:	-0.5947	11.1400	0.5060	0.8078	0.0000	0.4900
Exp. accuracy:	0.93	0.88	0.97	0.57	0.93	0.43

External links

[GenBank] [UCSC] [Ensemble]

Variant:	11 : 86068727, G→T					
Position:	chr11:86068727	Ref. allele:	G	Alt. allele:	T	
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM	
RS number:	-	Clin. sign.:	-	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	neutral	neutral	neutral	neutral	neutral
Score:	-1.0000	9.3130	0.4774	0.7482	0.0000	0.4000
Exp. accuracy:	0.96	0.91	0.97	0.69	0.93	0.56

External links

[GenBank] [UCSC] [Ensemble]

Variant:	11 : 86068754, T→C					
Position:	chr11:86068754	Ref. allele:	T	Alt. allele:	C	
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM	
RS number:	-	Clin. sign.:	-	-		

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	neutral	deleterious	neutral	neutral	neutral	neutral
Score:	-0.5989	16.3400	0.7207	0.4389	0.0000	0.2600
Exp. accuracy:	0.93	0.58	0.93	0.72	0.93	0.54

External links

[GenBank] [UCSC] [Ensemble]

Variant: 11 : 86068757, G→A

Position:	chr11:86068757	Ref. allele:	G	Alt. allele:	A
Region:	exonic	Exonic. func.:	synonymous	Gene ID:	PICALM
RS number:	rs367839126	Clin. sign.:	-		-

Results

Tool:	PredictSNP2	CADD	DANN	FATHMM	FunSeq2	GWAVA
Prediction:	deleterious	deleterious	deleterious	deleterious	neutral	neutral
Score:	0.4858	19.8100	0.9597	0.8890	0.0000	0.4100
Exp. accuracy:	0.93	0.69	0.87	0.68	0.93	0.56

External links

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