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Menu

Functional Impact Assessment

Variant Data Overview

Gene Expression Overview

SuRE Profiles

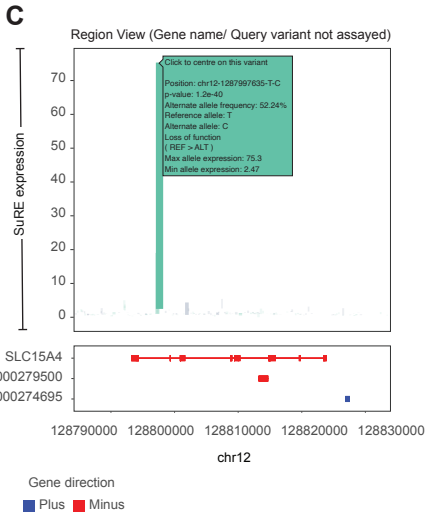
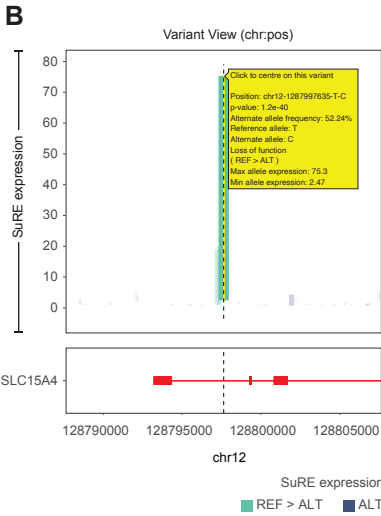
Highlighted Variant

Transcription Factor Binding Site Impact (TFBSi)

Genome Aggregation Database (gnomAD) Viewer

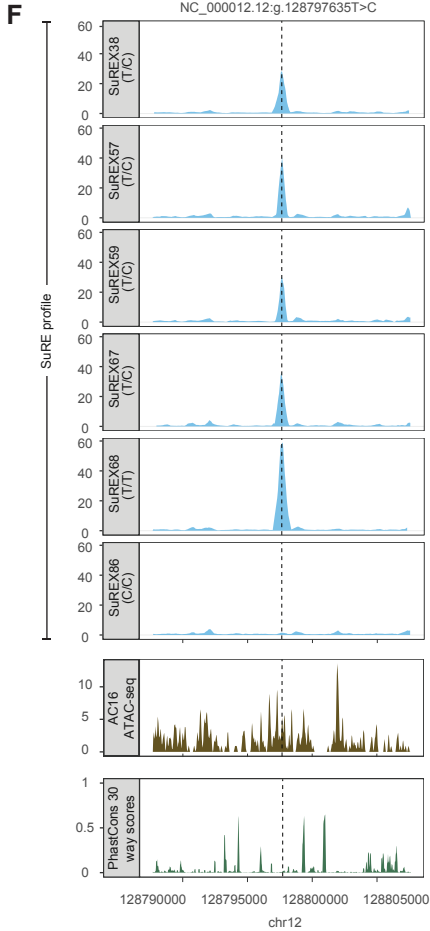
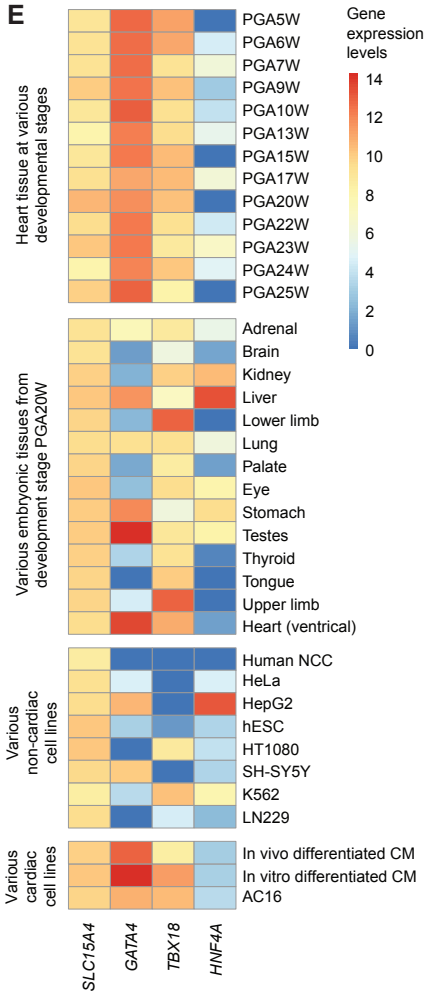
ClinVar Viewer

Uploaded Tracks Viewer



D

Chromosome	Position	REF allele	ALT allele	rsID	Population allele frequency gnomAD 3.1.2	SuREX38	SuREX57	SuREX59	SuREX67	SuREX68	SuREX86	REF allele coverage	ALT allele coverage	REF allele mean expression	ALT allele mean expression	p-value	Description
chr12	128797243	C	T	rs9738216	0.5175	0/1	0/1	0/1	0/1	0/0	1/1	169	165	19.022476	0.9542911	0.0000001	raQTL
chr12	128797293	A	G	rs9738836	0.2975	1/1	0/0	0/0	0/1	0/0	0/1	232	69	19.980296	1.3218745	0.0218883	not_raQTL
chr12	128797393	A	AG	rs11461172	0.5332	0/1	0/1	0/1	0/0	0/0	1/1	173	63	20.017592	1.0016241	0.0000022	raQTL
chr12	128797635	T	C	rs35907548	0.5224	0/1	0/1	0/1	0/1	0/0	1/1	187	182	75.317003	2.4701912	0.0000000	raQTL
chr12	128798604	T	C	rs7960920	0.4738	0/1	0/1	0/1	0/0	0/0	1/1	135	101	1.236906	1.9050211	0.4845033	not_raQTL



G

gnomAD browser

gnomAD v4.1.0

Help us continue to improve gnomAD by taking 5 minutes to fill out our [user survey](#).

SNV

12-128797635

T-C

(GRCh38)

Copy variant ID

Gene page

Dataset: gnomAD v4.1.0

Exons: No data

Genomes: 79799

Total: 79799

Allele Count: 152072

Allele Number: 0.5247

Allele Frequency: 0.6107

Gprmax Filtering AF (95% confidence): 21877

Number of homozygotes: 21877



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National Library of Medicine

ClinVar

NM_003060.4(SLC22A5):c...

Classification

Benign

criteria provided, multiple submitters, no conflicts

No data submitted for somatic clinical impact

No data submitted for oncogen