

Cadps2 Cas9-KO Strategy

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Reviewer:	
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Project Overview

Project Name

Cadps2

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cadps2* gene. The schematic diagram is as follows:



- The *Cadps2* gene has 13 transcripts. According to the structure of *Cadps2* gene, exon5-exon6 of *Cadps2*-205 (ENSMUST00000115358.8) transcript is recommended as the knockout region. The region contains 359bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cadps2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a null allele exhibit defects in cerebellum, Purkinje cell and interneuron morphology, paired-pulse facilitation, and behaviors including emotional behavior, vestibuloocular reflex, circadian and sleep patterns, social investigation and nurturing behavior.
- Transcripts *Cadps2*-210/211 lncRNA may be unaffected.
- The *Cadps2* gene is located on the Chr6. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risk of the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

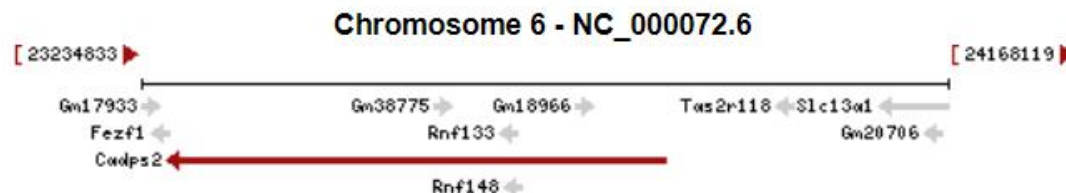
Cadps2 Ca²⁺-dependent activator protein for secretion 2 [*Mus musculus* (house mouse)]

Gene ID: 320405, updated on 10-Dec-2019

Summary



Official Symbol	Cadps2 provided by MGI
Official Full Name	Ca ²⁺ -dependent activator protein for secretion 2 provided by MGI
Primary source	MGI:MGI:2443963
See related	Ensembl:ENSMUSG00000017978
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Cpd2; Caps2; Caps-2; A230044C21Rik
Expression	Biased expression in cerebellum adult (RPKM 18.3), cortex adult (RPKM 6.9) and 9 other tissues See more
Orthologs	human all

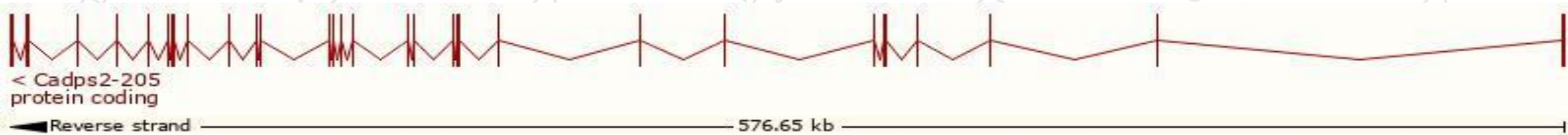


Transcript information (Ensembl)

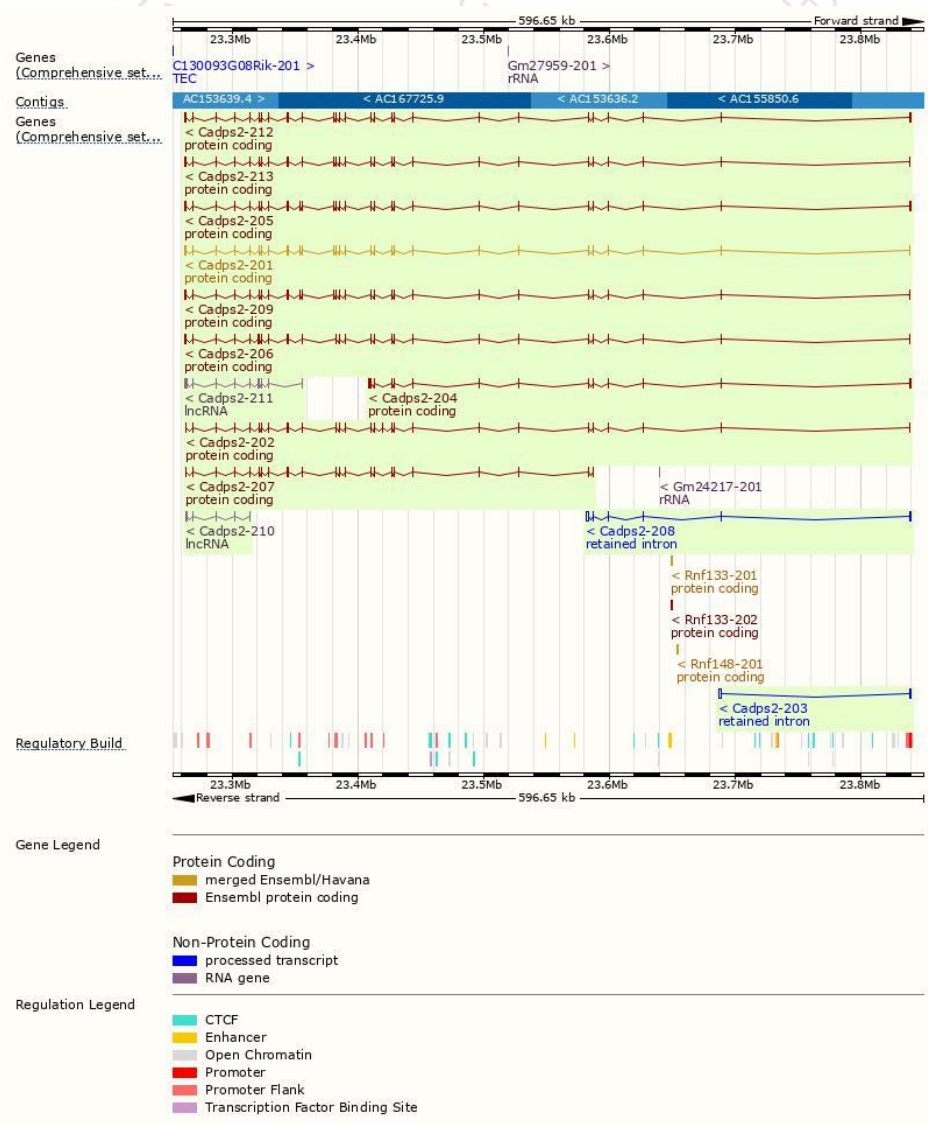
The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Translation ID	Biotype	CCDS	UniProt	Flags
Cadps2-205	ENSMUST00000115358.8	4848	1264aa	ENSMUSP00000111015.2	Protein coding	CCDS57412	Q8BYR5	TSL:5 GENCODE basic APPRIS ALT2
Cadps2-201	ENSMUST0000018122.13	4723	1304aa	ENSMUSP0000018122.7	Protein coding	CCDS39439	A4PI81 Q8BYR5	TSL:5 GENCODE basic APPRIS P3
Cadps2-206	ENSMUST00000115361.8	4571	1259aa	ENSMUSP00000111018.2	Protein coding	CCDS57411	Q8BYR5	TSL:1 GENCODE basic
Cadps2-204	ENSMUST00000115356.2	3533	768aa	ENSMUSP00000111013.2	Protein coding	CCDS57413	Q8BYR5	TSL:1 GENCODE basic
Cadps2-212	ENSMUST00000163871.8	4969	1304aa	ENSMUSP00000128905.2	Protein coding	-	E9Q835	TSL:5 GENCODE basic APPRIS ALT1
Cadps2-213	ENSMUST00000166458.8	4598	1275aa	ENSMUSP00000125972.2	Protein coding	-	E9Q5C0	TSL:5 GENCODE basic
Cadps2-209	ENSMUST00000142913.8	4533	1275aa	ENSMUSP00000138167.1	Protein coding	-	S4R1C6	TSL:5 GENCODE basic
Cadps2-202	ENSMUST00000069074.13	3935	1297aa	ENSMUSP00000064876.8	Protein coding	-	A0A0M3HEP6	TSL:5 GENCODE basic
Cadps2-207	ENSMUST00000125350.7	2735	899aa	ENSMUSP00000115866.1	Protein coding	-	F6SH36	CDS 5' incomplete TSL:5
Cadps2-208	ENSMUST00000136279.1	3031	No protein	-	Retained intron	-	-	TSL:1
Cadps2-203	ENSMUST00000115355.1	2118	No protein	-	Retained intron	-	-	TSL:1
Cadps2-211	ENSMUST00000156986.7	1931	No protein	-	lncRNA	-	-	TSL:1
Cadps2-210	ENSMUST00000152131.1	744	No protein	-	lncRNA	-	-	TSL:3

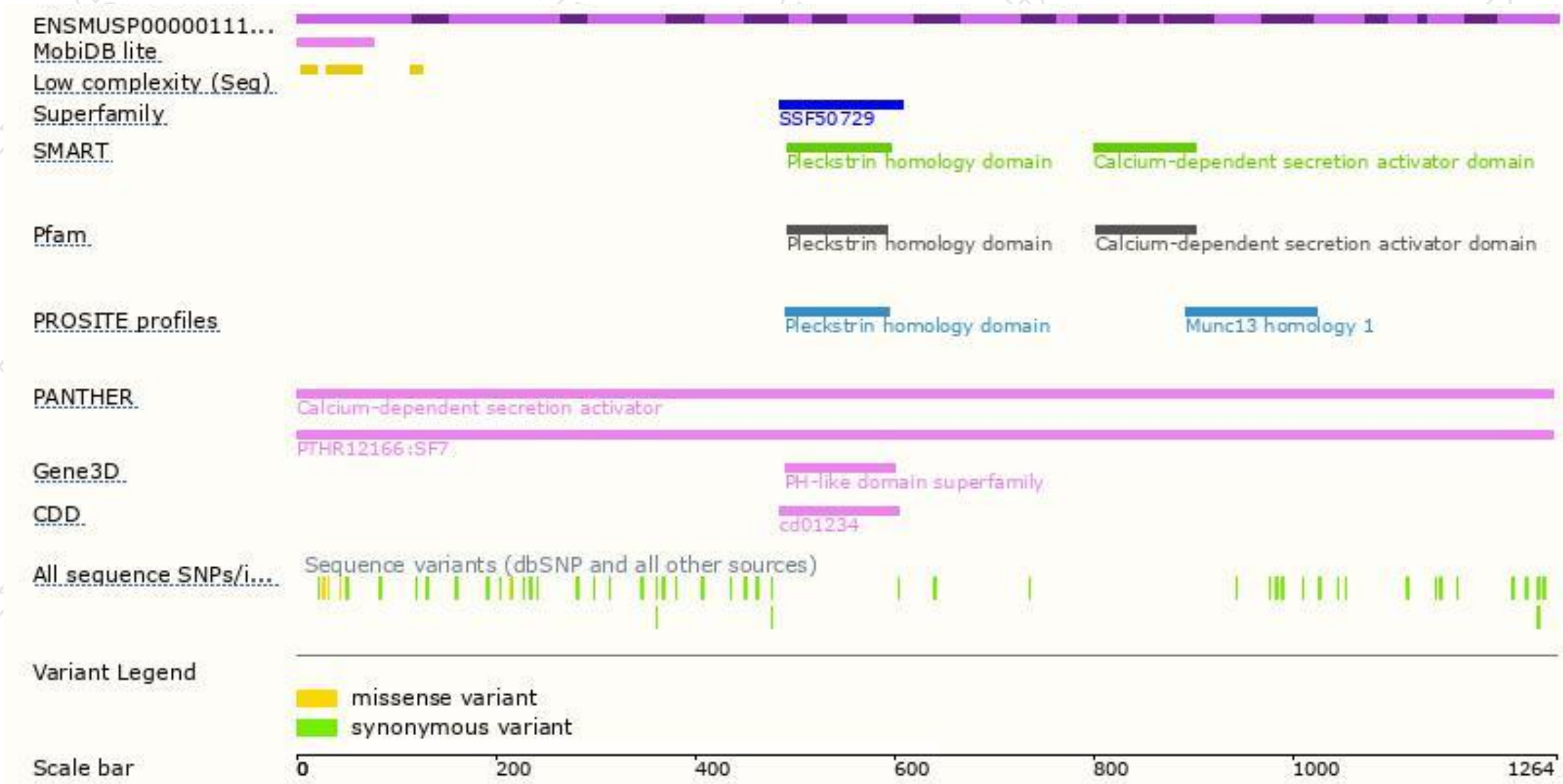
The strategy is based on the design of *Cadps2-205* transcript,The transcription is shown below



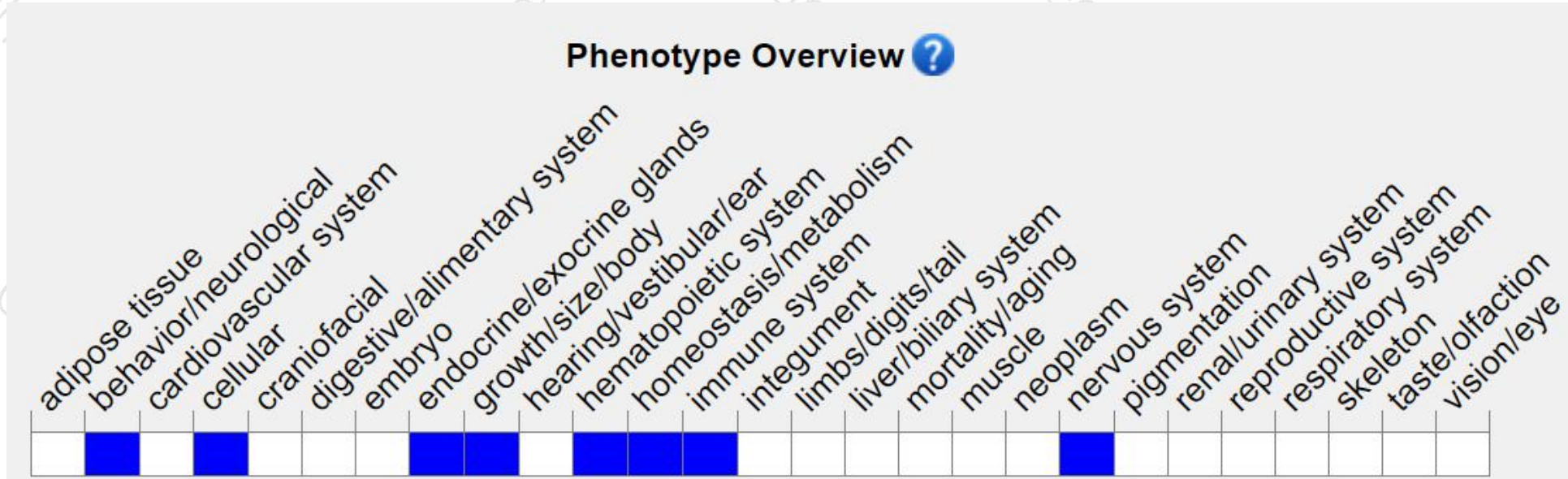
Genomic location distribution



Protein domain



Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).

According to the existing MGI data, Mice homozygous for a null allele exhibit defects in cerebellum, Purkinje cell and interneuron morphology, paired-pulse facilitation, and behaviors including emotional behavior, vestibuloocular reflex, circadian and sleep patterns, social investigation and nurturing behavior.

If you have any questions, you are welcome to inquire.

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