Cacna1g Cas9-KO Strategy

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Project Overview

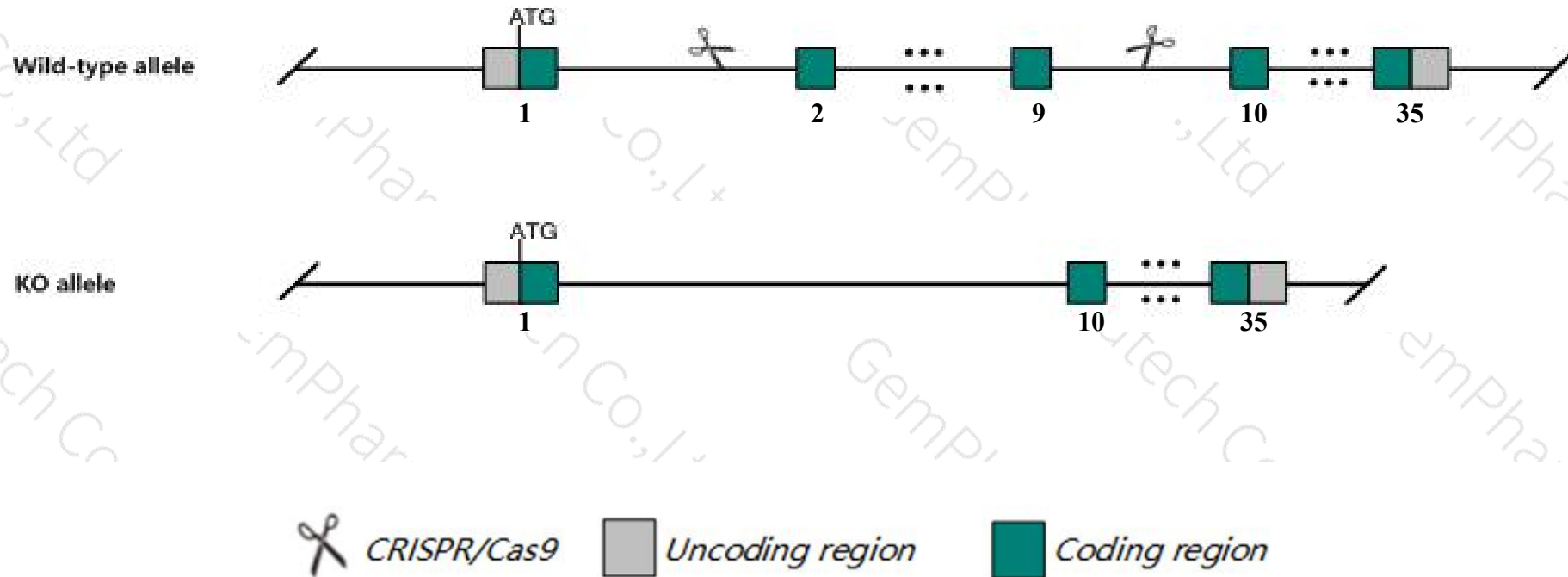|	
Project Name	*Cacna1g*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cacna1g* gene. The schematic diagram is as follows:

➢ The *Cacna1g* gene has 16 transcripts. According to the structure of *Cacna1g* gene, exon2-exon9 of *Cacna1g-201* (ENSMUST00000021234.14) transcript is recommended as the knockout region.The region contains 2059bp coding sequence Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Cacna1g* gene. The brief process is as follows: CRISPR/Cas9 syst

➢ According to the existing MGI data,Homozygote null mice display disrupted sleeping patterns, altered amounts of activity, abnormal action potentials in the brain, prolonged electrical conductance in the heart, and resistance to diet-induced obesity.

➢ Transcript *Cacna1g*-212&213&214&215 may not be affected.

➢ The *Cacna1g* gene is located on the Chr11. 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）

Cacna1g   **calcium channel, voltage-dependent, T type, alpha 1G subunit** [*Mus musculus* (house mouse)]

Gene ID: 12291, updated on 29-Oct-2019

⌃ Summary

Official Symbol	Cacna1g provided by MGI
Official Full Name	calcium channel, voltage-dependent, T type, alpha 1G subunit provided by MGI
Primary source	MGI:MGI:1201678
See related	Ensembl:ENSMUSG00000020866
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	a1G; [a]1G; Cav3.1d; alpha-1G; mKIAA1123
Expression	Biased expression in limb E14.5 (RPKM 50.1), cerebellum adult (RPKM 19.2) and 10 other tissues See more
Orthologs	human all

⌃ Genomic context

**Location:**   11; 11 D

See Cacna1g in Genome Data Viewer

Exon count: 40

| Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	11	NC_000077.6 (94408391..94474400, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	11	NC_000077.5 (94269705..94335512, complement)

Transcript information（Ensembl）

The gene has 16 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cacna1g-201	ENSMUST00000021234.14	8139	2272aa	Protein coding	CCDS48885	E9PWL1	TSL:5 GENCODE basic APPRIS ALT2
Cacna1g-202	ENSMUST00000100561.9	8125	2295aa	Protein coding	CCDS25255	Q5SUG4	TSL:1 GENCODE basic APPRIS P3
Cacna1g-208	ENSMUST00000107790.7	8035	2265aa	Protein coding	CCDS48886	Q5SUF9	TSL:1 GENCODE basic APPRIS ALT2
Cacna1g-205	ENSMUST00000107786.7	7984	2248aa	Protein coding	CCDS48884	Q5SUG1	TSL:1 GENCODE basic APPRIS ALT2
Cacna1g-207	ENSMUST00000107789.7	8383	2381aa	Protein coding	-	Q5SUF7	TSL:5 GENCODE basic APPRIS ALT2
Cacna1g-203	ENSMUST00000103166.8	8104	2288aa	Protein coding	-	Q5SUF6	TSL:5 GENCODE basic APPRIS ALT2
Cacna1g-211	ENSMUST00000107793.7	8071	2277aa	Protein coding	-	Q5SUG0	TSL:5 GENCODE basic APPRIS ALT2
Cacna1g-206	ENSMUST00000107788.7	8050	2270aa	Protein coding	-	Q5SUG3	TSL:5 GENCODE basic APPRIS ALT2
Cacna1g-209	ENSMUST00000107791.7	8002	2254aa	Protein coding	-	Q5SUF8	TSL:5 GENCODE basic APPRIS ALT2
Cacna1g-210	ENSMUST00000107792.7	7981	2247aa	Protein coding	-	Q5SUF5	TSL:5 GENCODE basic APPRIS ALT2
Cacna1g-204	ENSMUST00000107785.1	7523	2176aa	Protein coding	-	Q5SUG2	TSL:5 GENCODE basic APPRIS ALT2
Cacna1g-216	ENSMUST00000152811.1	4878	No protein	lncRNA	-	-	TSL:5
Cacna1g-214	ENSMUST00000142190.1	797	No protein	lncRNA	-	-	TSL:2
Cacna1g-212	ENSMUST00000133000.1	784	No protein	lncRNA	-	-	TSL:3
Cacna1g-215	ENSMUST00000146160.1	749	No protein	lncRNA	-	-	TSL:3
Cacna1g-213	ENSMUST00000133331.1	434	No protein	lncRNA	-	-	TSL:2

The strategy is based on the design of *Cacna1g-201* transcript,The transcription is shown below

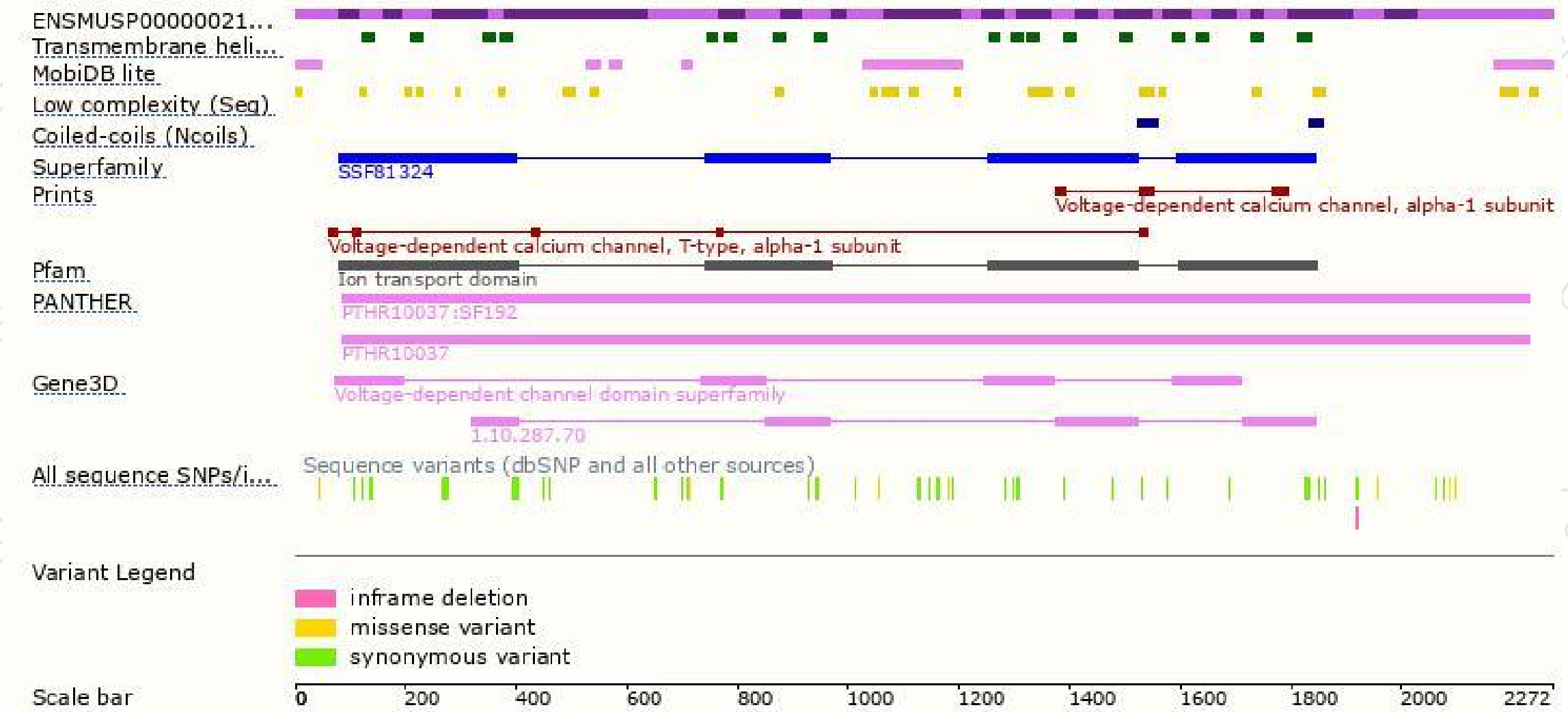< Cacna1g-201
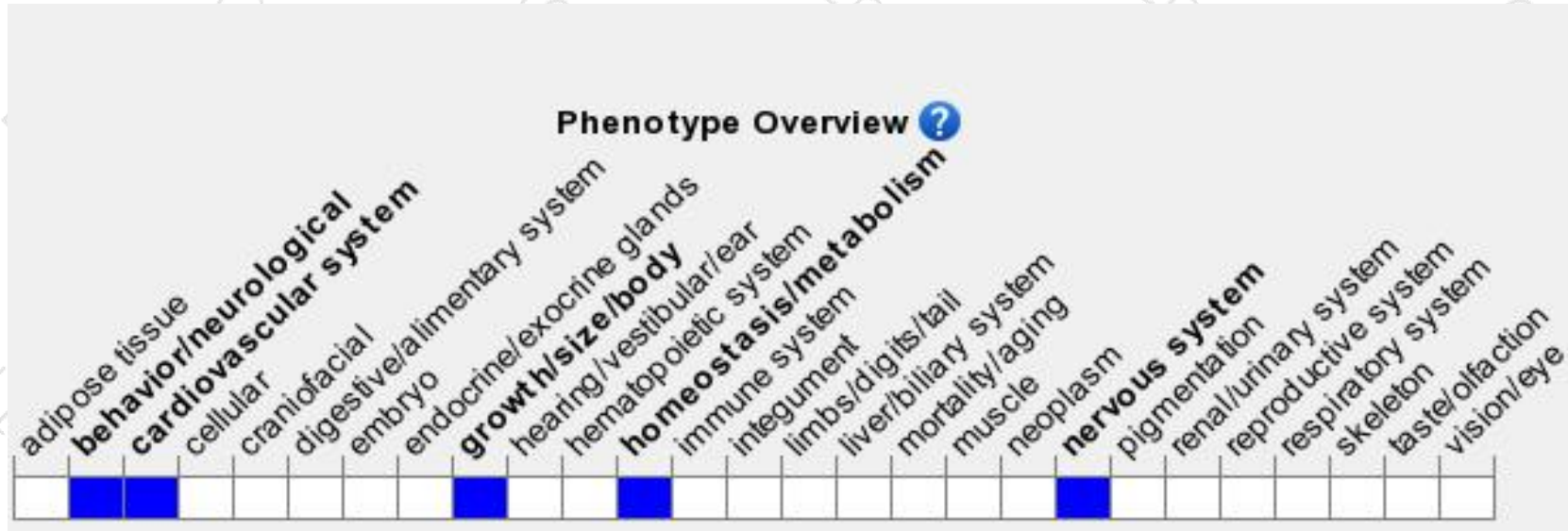protein coding

◀ Reverse strand

65.79 kb
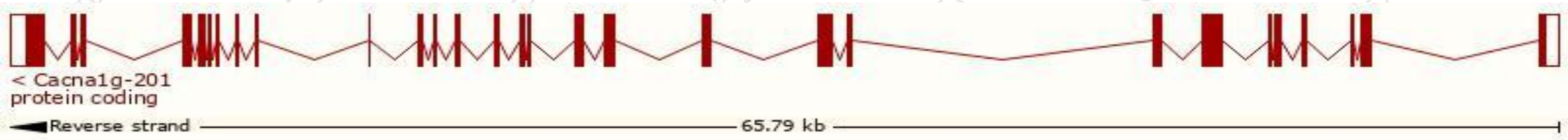
Genomic location distribution
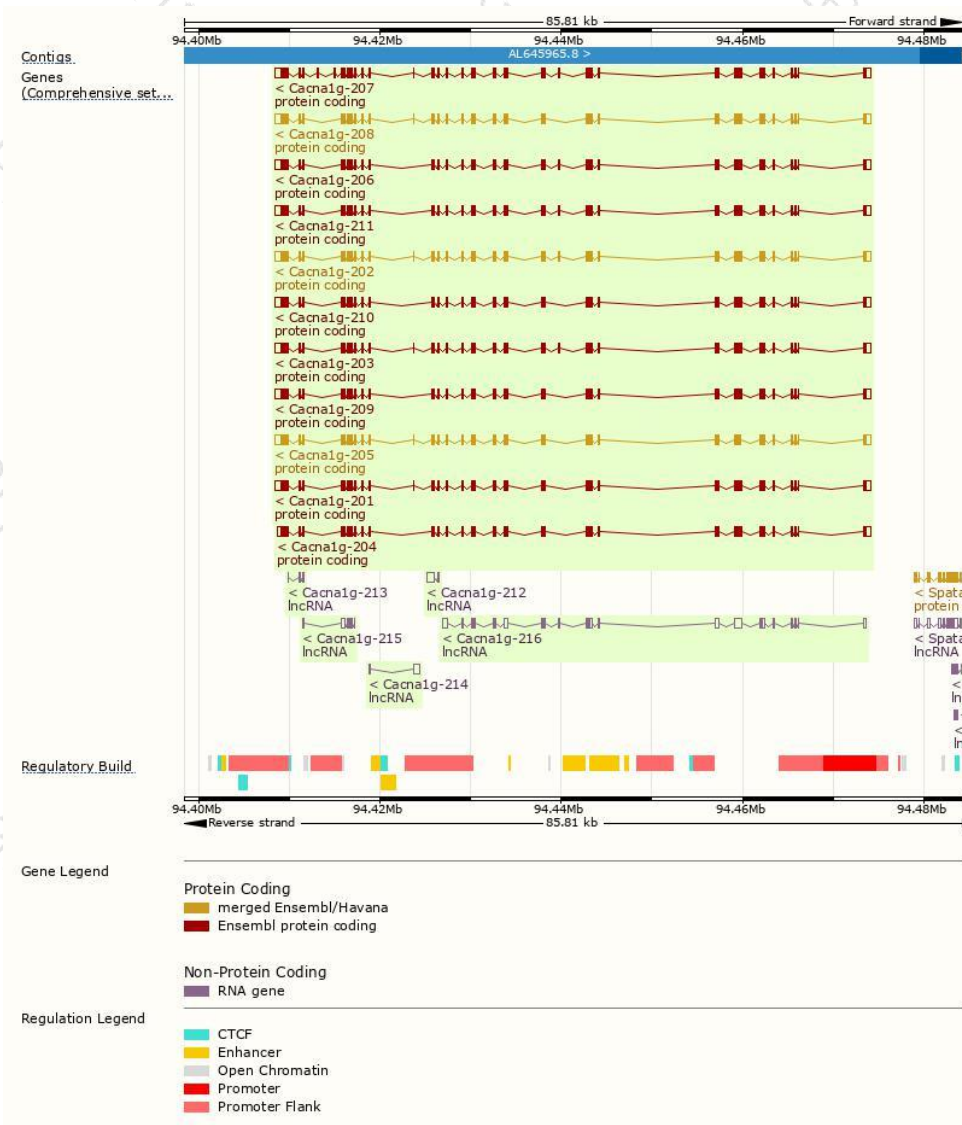
Protein domain

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,Homozygote null mice display disrupted sleeping patterns, altered amounts of activity, abnormal action potentials in the brain, prolonged electrical conductance in the heart, and resistance to diet-induced obesity.

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