

Cabp1 Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Cabp1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cabp1* gene. The schematic diagram is as follows:



- The *Cabp1* gene has 7 transcripts. According to the structure of *Cabp1* gene, exon2-exon5 of *Cabp1*-204 (ENSMUST00000112113.7) transcript is recommended as the knockout region. The region contains 433bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cabp1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knockout allele are viable and fertile and show no apparent motor deficits, but they are affected in the transmission of responses to light through the retinal circuits.
- Some amino acids will remain at the N-terminus and some functions may be retained.
- The *Cabp1* gene is located on the Chr5. 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)

Cabp1 calcium binding protein 1 [Mus musculus (house mouse)]

Gene ID: 29867, updated on 9-Apr-2019

Summary



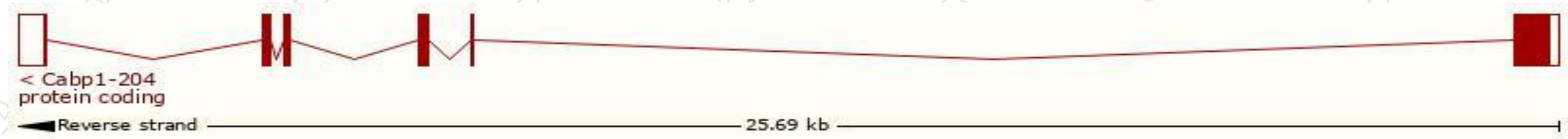
Official Symbol	Cabp1 provided by MGI
Official Full Name	calcium binding protein 1 provided by MGI
Primary source	MGI:MGI:1352750
See related	Ensembl:ENSMUSG00000029544
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	caldendrin
Expression	Biased expression in cortex adult (RPKM 57.2), frontal lobe adult (RPKM 41.4) and 5 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

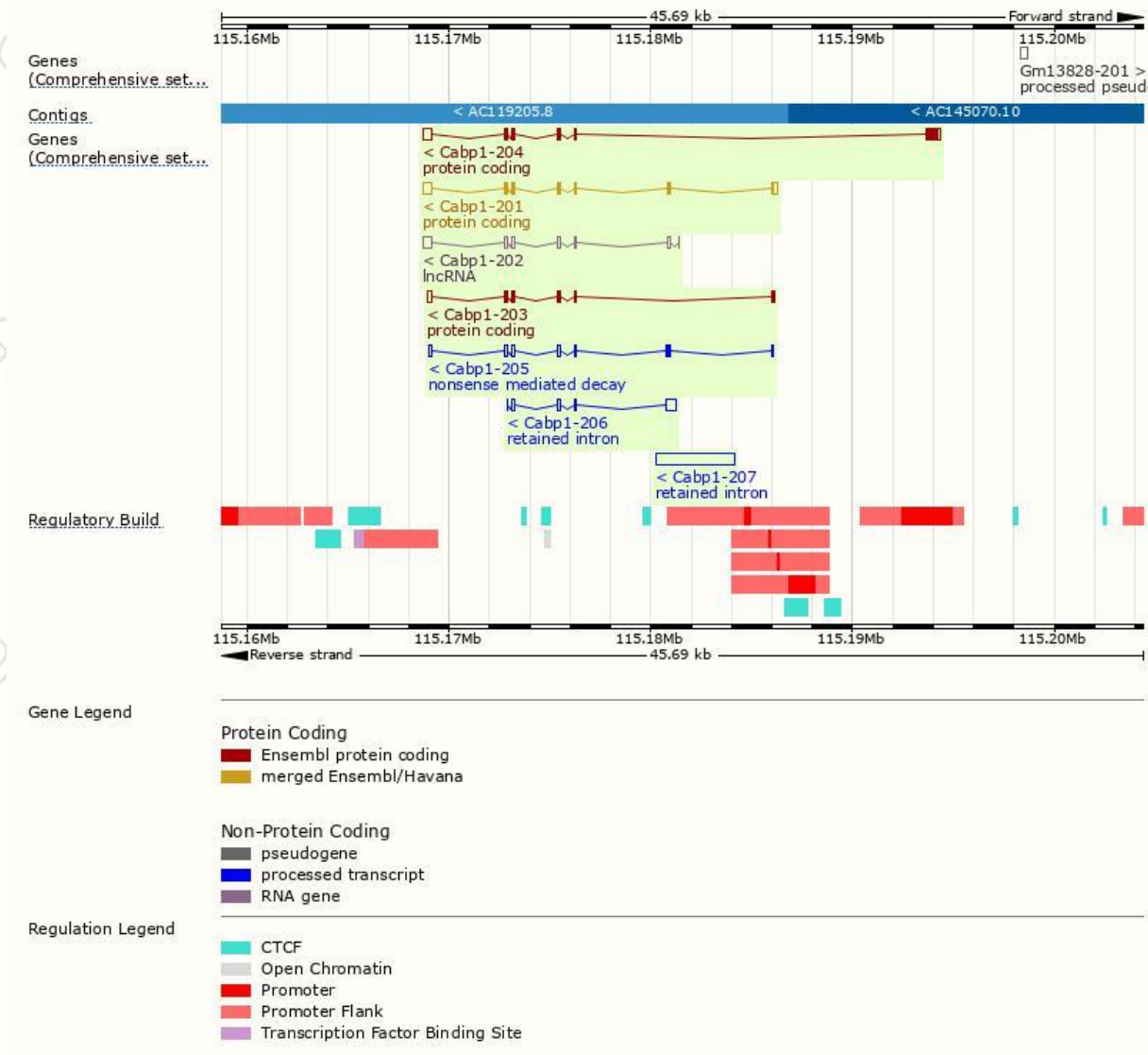
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cabp1-204	ENSMUST00000112113.7	1621	350aa	Protein coding	CCDS80379	D3Z1M4	TSL:1 GENCODE basic
Cabp1-201	ENSMUST00000031519.13	1370	227aa	Protein coding	CCDS19582	Q9JLK7	TSL:1 GENCODE basic APPRIS P3
Cabp1-203	ENSMUST00000112112.1	746	167aa	Protein coding	CCDS80378	Q9JLK7	TSL:1 GENCODE basic APPRIS ALT 1
Cabp1-205	ENSMUST00000145197.8	840	85aa	Nonsense mediated decay	-	Q812F6	TSL:2
Cabp1-207	ENSMUST00000201900.1	3914	No protein	Retained intron	-	-	TSL:NA
Cabp1-206	ENSMUST00000151775.1	783	No protein	Retained intron	-	-	TSL:5
Cabp1-202	ENSMUST00000112109.7	1071	No protein	lncRNA	-	-	TSL:1

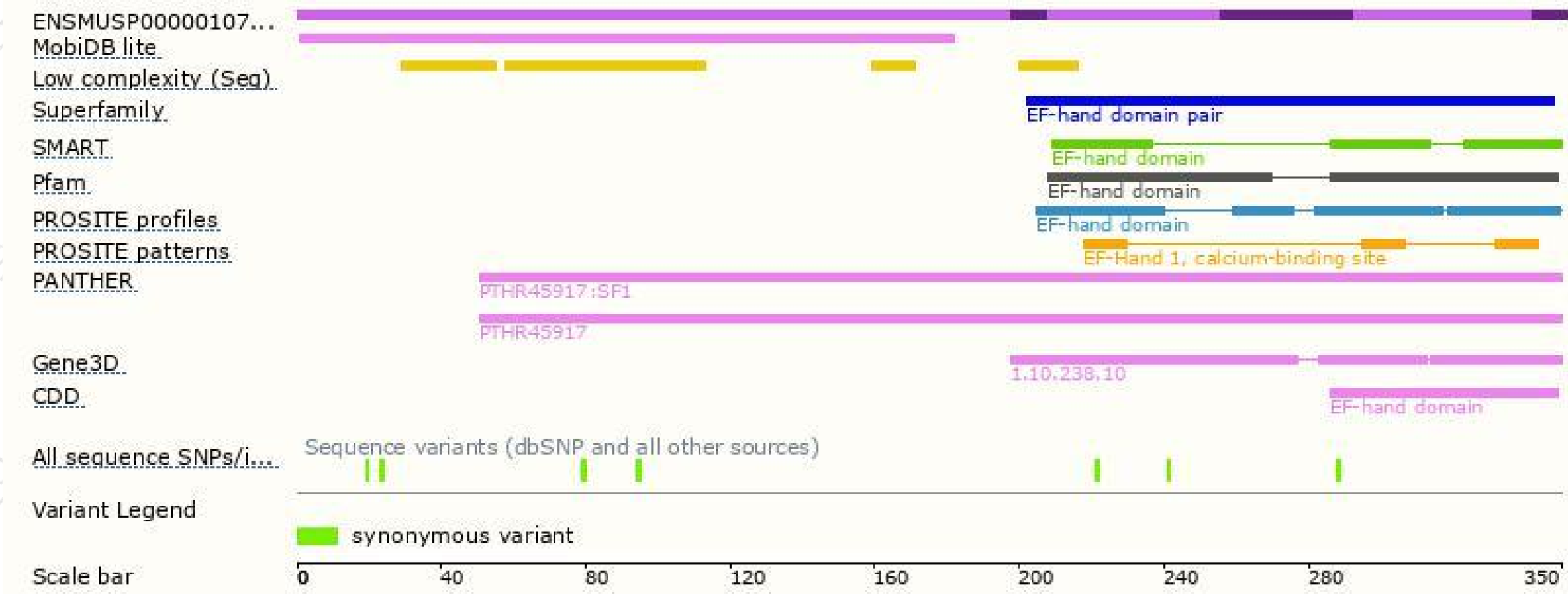
The strategy is based on the design of *Cabp1-204* transcript,The transcription is shown below



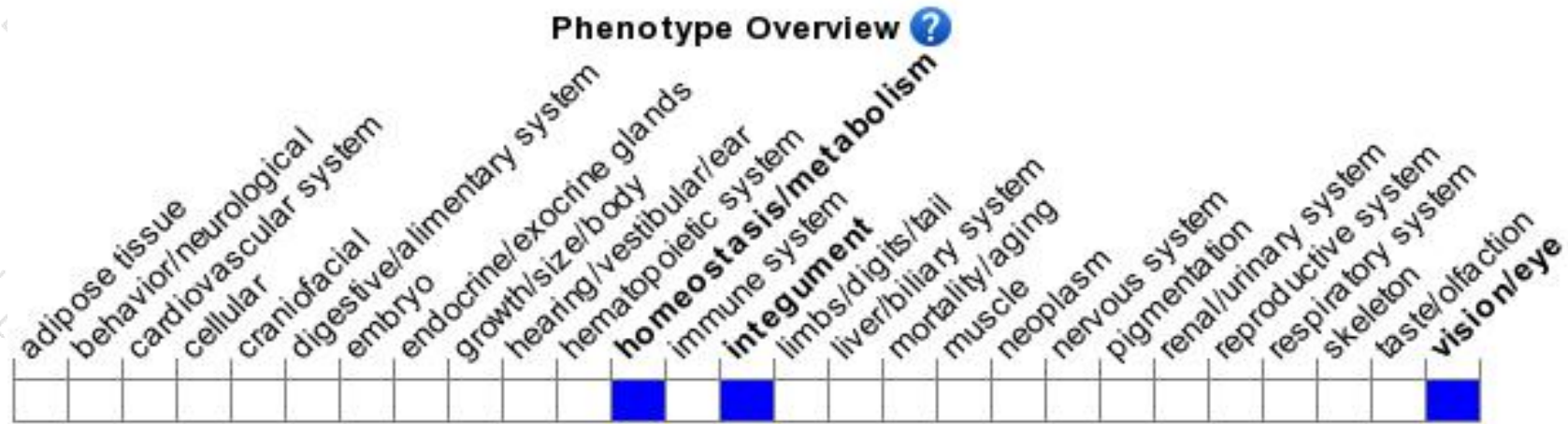
Genomic location distribution



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 knockout allele are viable and fertile and show no apparent motor deficits, but they are affected in the transmission of responses to light through the retinal circuits.

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

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