Psd2 Cas9-CKO Strategy

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Project Overview

Project Name	***Psd2***
Project type	**Cas9-CKO**
Strain background	**C57BL/6J**

Conditional Knockout strategy

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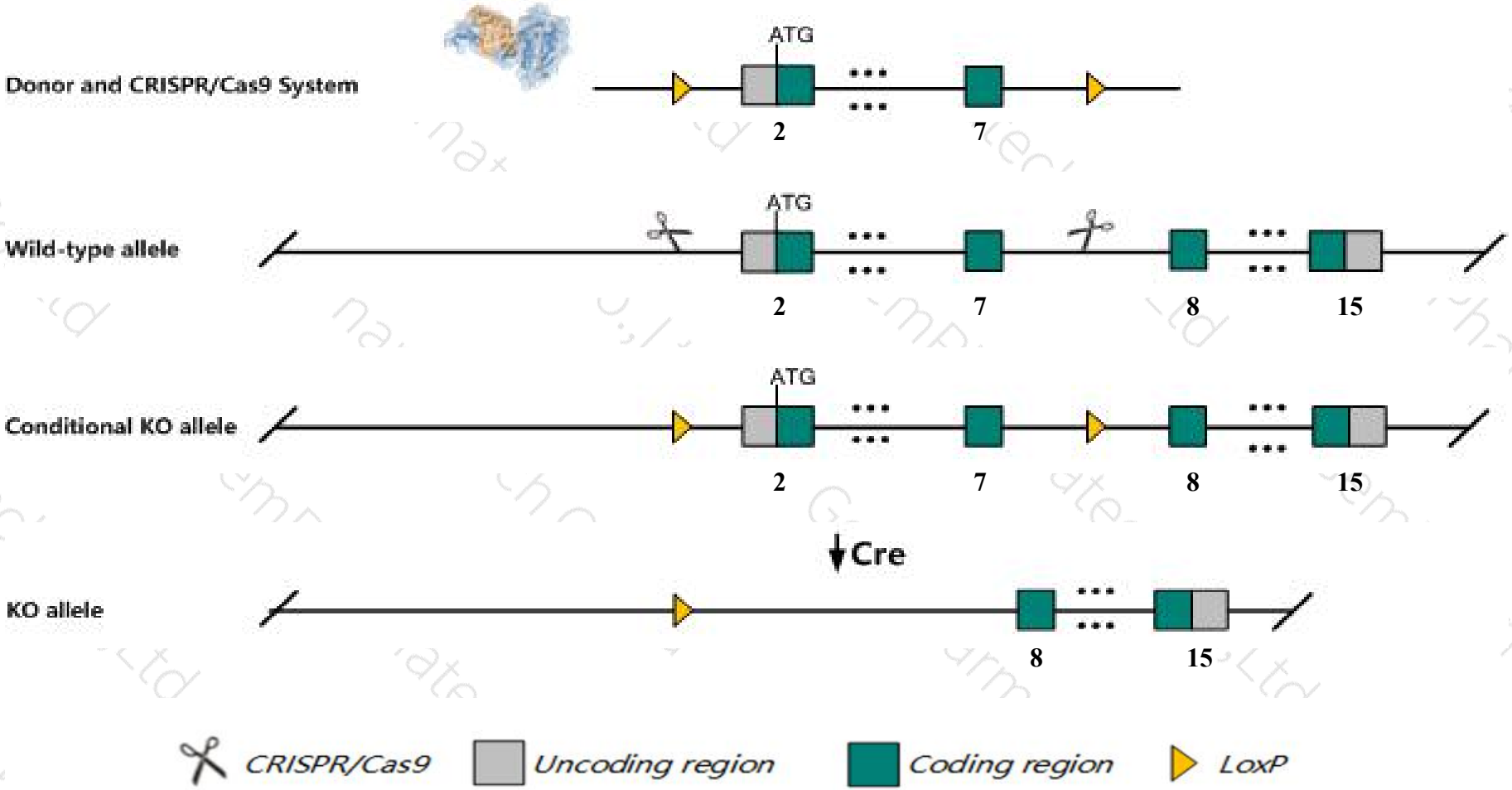
This model will use CRISPR/Cas9 technology to edit the *Psd2* gene. The schematic diagram is as follows:



Technical routes

- The *Psd2* gene has 6 transcripts. According to the structure of *Psd2* gene, exon2-exon7 of *Psd2-201* (ENSMUST00000115716.8) transcript is recommended as the knockout region.The region contains start codon ATG. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Psd2* gene. The brief process is as follows:CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6J mice.Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6J mice.

- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice

- According to the existing MGI data,mice homozygous for a null allele display a decrease in the density of asymmetric synapses in the middle molecular layer but no cerebellum-related behavioral defects.

- The *Psd2* gene is located on the Chr18. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Psd2 pleckstrin and Sec7 domain containing 2 [Mus musculus (house mouse)]

Gene ID: 74002, updated on 13-Mar-2020

Summary

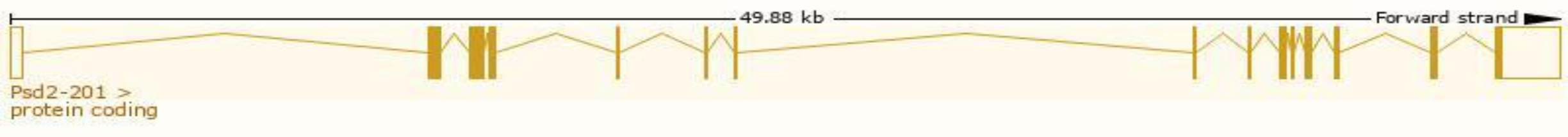
Official Symbol	Psd2 provided by MGI
Official Full Name	pleckstrin and Sec7 domain containing 2 provided by MGI
Primary source	MGI:MGI:1921252
See related	Ensembl:ENSMUSG00000024347
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	6330404E20Rik, AW125584, EFA6C
Expression	Biased expression in cerebellum adult (RPKM 18.6), CNS E18 (RPKM 14.6) and 6 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

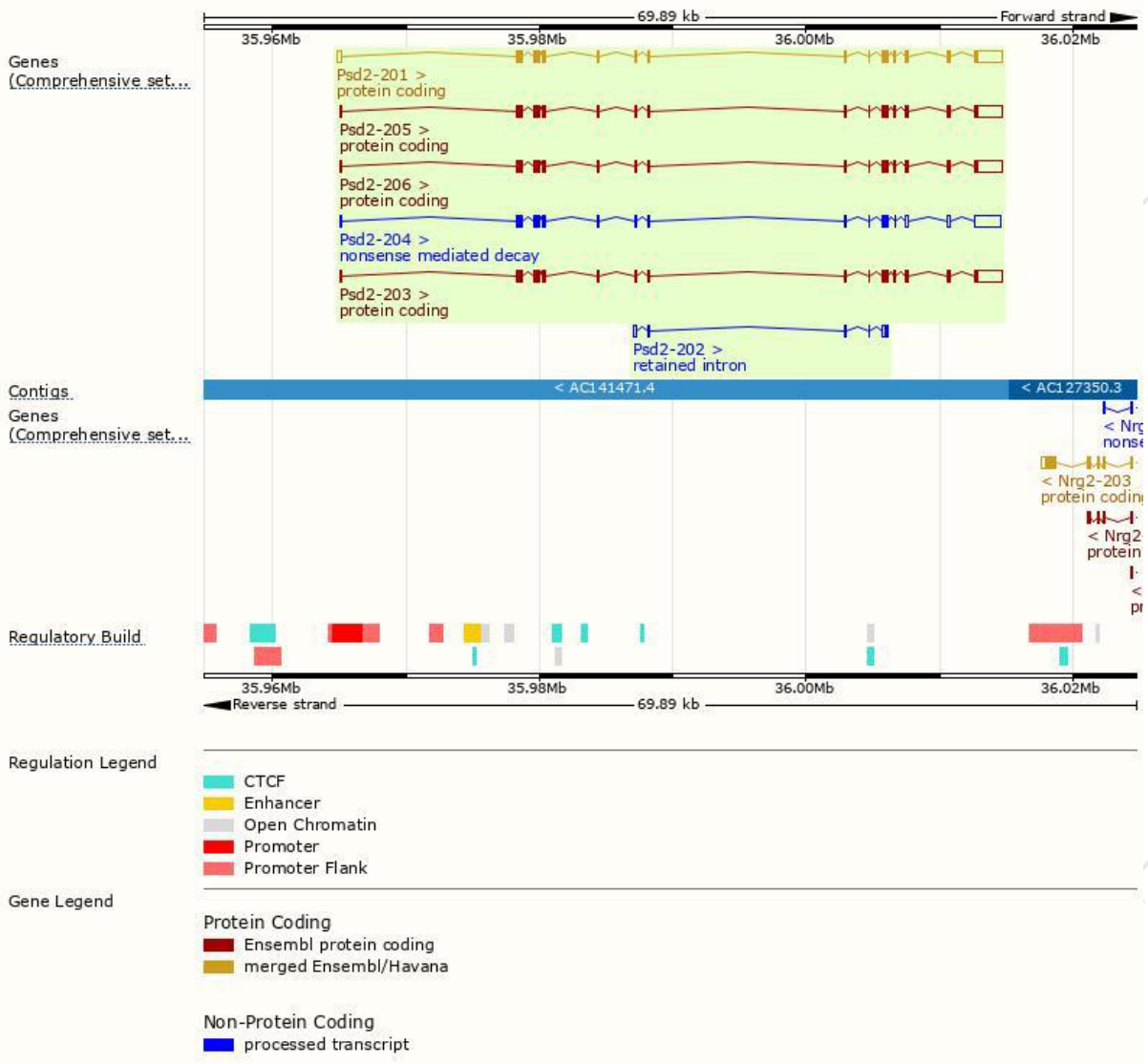
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Psd2-201	ENSMUST00000115716.8	4607	770aa	Protein coding	CCDS37767	Q6P1I6	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P3
Psd2-206	ENSMUST00000177432.7	4367	767aa	Protein coding	CCDS79612	Q6P1I6	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
Psd2-205	ENSMUST00000176873.7	4375	771aa	Protein coding	-	Q6P1I6	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
Psd2-203	ENSMUST00000175734.1	4300	771aa	Protein coding	-	Q6P1I6	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
Psd2-204	ENSMUST00000176472.7	4123	554aa	Nonsense mediated decay	-	H3BK80	TSL:1
Psd2-202	ENSMUST00000175720.1	674	No protein	Retained intron	-	-	TSL:5

The strategy is based on the design of *Psd2-201* transcript,the transcription is shown below:

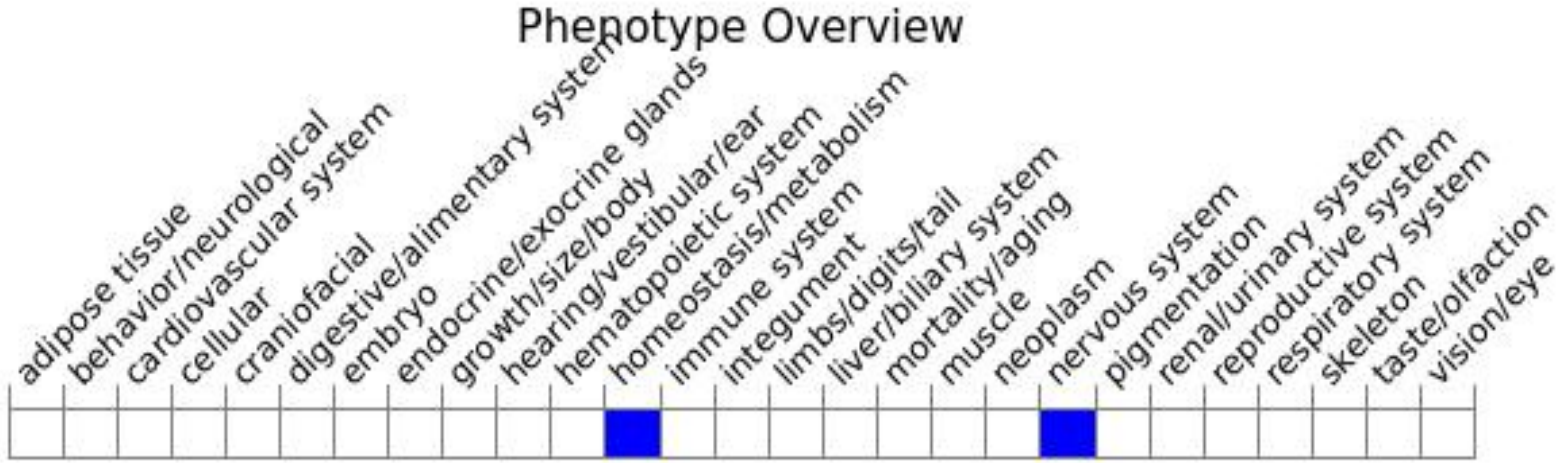


Genomic location distribution



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 display a decrease in the density of asymmetric synapses in the middle molecular layer but no cerebellum-related behavioral defects.

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

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