

Mpp5 Cas9-KO Strategy

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Project Overview



Project Name

Mpp5

Project type

Cas9-KO

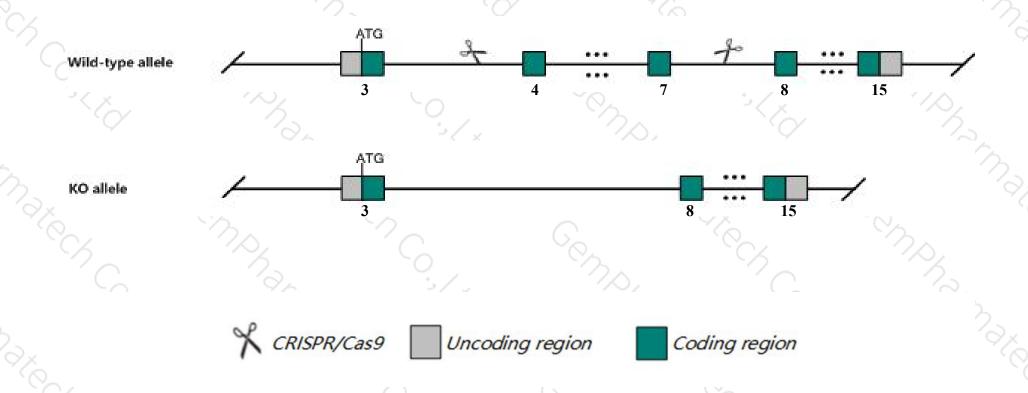
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Mpp5 gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Mpp5* gene has 5 transcripts. According to the structure of *Mpp5* gene, exon4-exon7 of *Mpp5-201*(ENSMUST00000082024.6) transcript is recommended as the knockout region. The region contains 596bp coding sequence.

 Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify Mpp5 gene. The brief process is as follows: CRISPR/Cas9 system

Notice



- > According to the existing MGI data, Mice homozygous for a floxed allele activated in cortical neuron exhibit loss of cortex neurons due to premature differentiation and increased apoptosis. These mice also exhibit behavioral defects but are otherwise viable and fertile. Heterozygous mice exhibit an intermediate phenotype.
- ➤ Transcript *Mpp5*-202&203 may not be affected.
- The *Mpp5* gene is located on the Chr12. 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)



Mpp5 membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5) [Mus musculus (house mouse)]

Gene ID: 56217, updated on 10-Oct-2019

Summary

☆ ?

Official Symbol Mpp5 provided by MGI

Official Full Name membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5) provided by MGI

Primary source MGI:MGI:1927339

See related Ensembl: ENSMUSG00000021112

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 Pals1; Al255216; Al644496; 3830420B02Rik

Expression Ubiquitous expression in placenta adult (RPKM 4.8), CNS E11.5 (RPKM 4.1) and 24 other tissues See more

Orthologs <u>human</u> all

Genomic context



Location: 12; 12 C3

See Mpp5 in Genome Data Viewer

Exon count: 16

Annotation release	Status	Assembly	Chr	Location	
<u>108</u>	current	GRCm38.p6 (GCF_000001635.26)	12	NC_000078.6 (7874888278840714)	
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	12	NC_000078.5 (7984993479941701)	

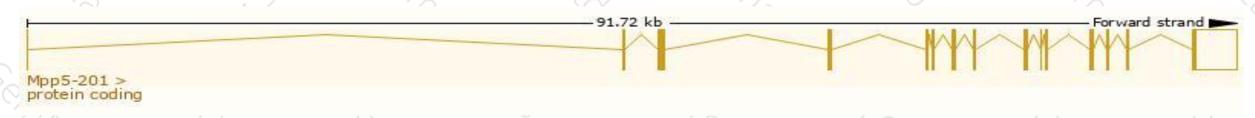
Transcript information (Ensembl)



The gene has 5 transcripts, all transcripts are shown below:

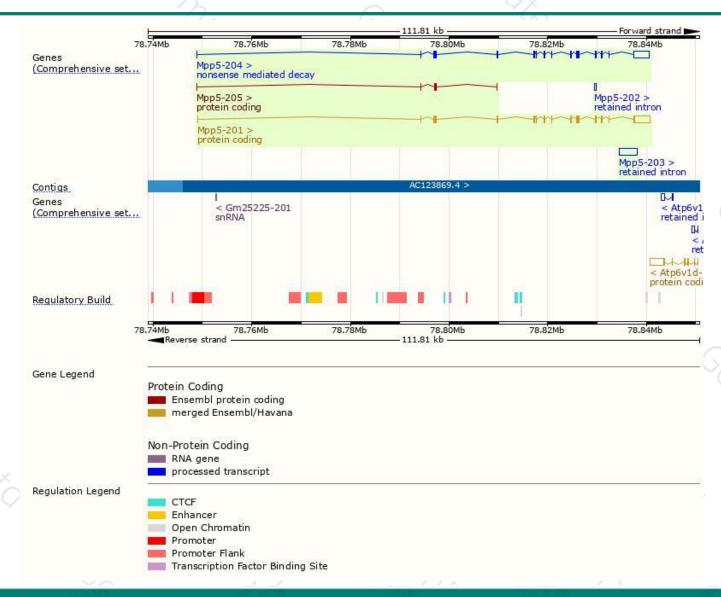
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mpp5-201	ENSMUST00000082024.6	5470	675aa	Protein coding	CCDS26001	B2RRY4 Q9JLB2	TSL:1 GENCODE basic APPRIS P1
Mpp5-205	ENSMUST00000219667.1	413	<u>93aa</u>	Protein coding	-8	A0A1W2P7Z6	CDS 3' incomplete TSL:5
Mpp5-204	ENSMUST00000219197.1	5283	285aa	Nonsense mediated decay	2	A0A1W2P6P0	TSL:1
Mpp5-203	ENSMUST00000219180.1	3619	No protein	Retained intron	Eq.	15 <u>2</u> 8	TSL:NA
Mpp5-202	ENSMUST00000218726.1	424	No protein	Retained intron	-	1271	TSL:NA

The strategy is based on the design of Mpp5-201 transcript, The transcription is shown below



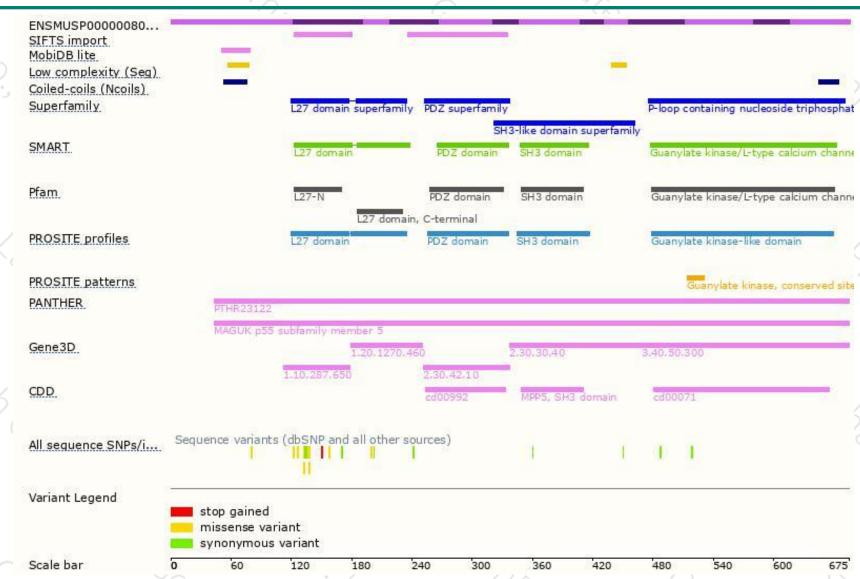
Genomic location distribution





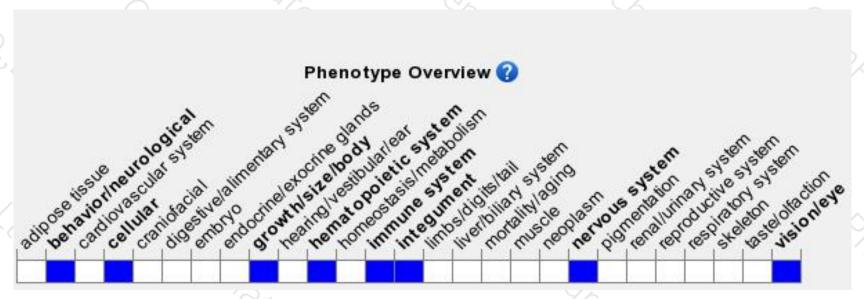
Protein domain





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 floxed allele activated in cortical neuron exhibit loss of cortex neurons due to premature differentiation and increased apoptosis. These mice also exhibit behavioral defects but are otherwise viable and fertile. Heterozygous mice exhibit an intermediate phenotype.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





