

Mpp6 Cas9-KO Strategy

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Reviewer:

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Design Date:

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Project Overview



Project Name

Mpp6

Project type

Cas9-KO

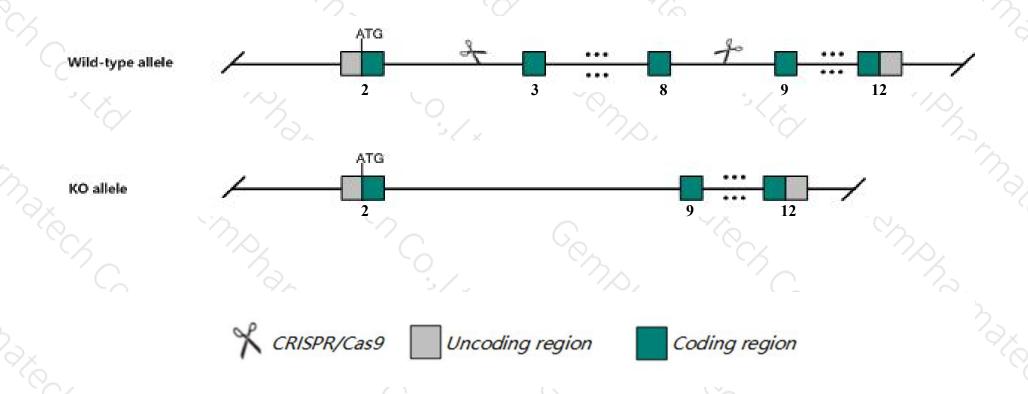
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Mpp6 gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Mpp6* gene has 9 transcripts. According to the structure of *Mpp6* gene, exon3-exon8 of *Mpp6-209*(ENSMUST00000204545.2) transcript is recommended as the knockout region. The region contains 832bp coding sequence.

 Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Mpp6* gene. The brief process is as follows: CRISPR/Cas9 system

Notice



- > The *Mpp6* 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)



Mpp6 membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6) [Mus musculus (house mouse)]

Gene ID: 56524, updated on 3-Feb-2019

Summary



Official Symbol Mpp6 provided by MGI

Official Full Name membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6) provided by MGI

Primary source MGI:MGI:1927340

See related Ensembl: ENSMUSG00000038388

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 P55t, Pals2

Expression Broad expression in testis adult (RPKM 14.9), CNS E11.5 (RPKM 12.6) and 23 other tissuesSee more

Orthologs human all

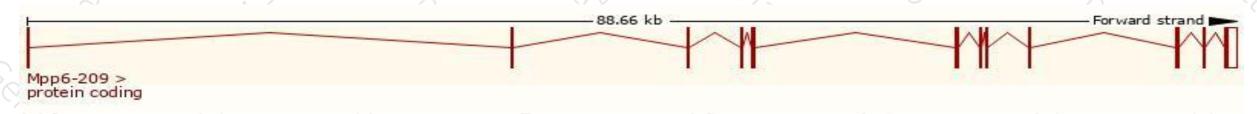
Transcript information (Ensembl)



The gene has 9 transcripts, all transcripts are shown below:

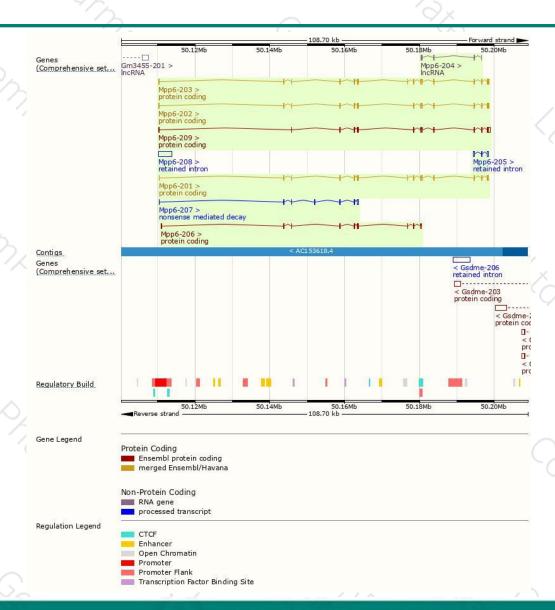
Transcript ID	bp 🍦	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST00000204545.2	2418	<u>539aa</u>	Protein coding	CCDS20128 ₽	B9EHZ5@ Q9JLB0@	TSL:5 GENCODE basic APPRIS P3
ENSMUST00000166318.7	2222	<u>553aa</u>	Protein coding	CCDS51770 ₽	Q3UN60@Q9JLB0@	TSL:1 GENCODE basic APPRIS ALT1
ENSMUST00000036236.14	2161	539aa	Protein coding	CCDS20128 ₽	B9EHZ5 ₽ Q9JLB0 ₽	TSL:1 GENCODE basic APPRIS P3
ENSMUST00000036225.14	1896	553aa	Protein coding	CCDS51770 ₽	Q3UN60@ Q9JLB0@	TSL:1 GENCODE basic APPRISALT1
ENSMUST00000167628.1	1281	315aa	Protein coding	121	E9PWC5₽	CDS 3' incomplete TSL:1
ENSMUST00000171601.7	845	48aa	Nonsense mediated decay	120	E9Q2R8₺	TSL:3
ENSMUST00000167063.1	637	No protein	Processed transcript	130	180	TSL:5
ENSMUST00000203415.1	3523	No protein	Retained intron	17.0	(5)	TSL:NA
ENSMUST00000167319.1	616	No protein	Retained intron	-	-	TSL:2
	ENSMUST00000204545.2 ENSMUST00000166318.7 ENSMUST00000036236.14 ENSMUST00000036225.14 ENSMUST00000167628.1 ENSMUST00000171601.7 ENSMUST00000167063.1 ENSMUST00000203415.1	ENSMUST00000204545.2 2418 ENSMUST00000166318.7 2222 ENSMUST00000036236.14 2161 ENSMUST00000036225.14 1896 ENSMUST00000167628.1 1281 ENSMUST00000171601.7 845 ENSMUST00000167063.1 637 ENSMUST00000203415.1 3523	ENSMUST00000204545.2 2418 539aa ENSMUST00000166318.7 2222 553aa ENSMUST00000036236.14 2161 539aa ENSMUST00000036225.14 1896 553aa ENSMUST00000167628.1 1281 315aa ENSMUST00000171601.7 845 48aa ENSMUST00000167063.1 637 No protein ENSMUST00000203415.1 3523 No protein	ENSMUST00000204545.2 2418 539aa Protein coding ENSMUST00000166318.7 2222 553aa Protein coding ENSMUST00000036236.14 2161 539aa Protein coding ENSMUST00000036225.14 1896 553aa Protein coding ENSMUST00000167628.1 1281 315aa Protein coding ENSMUST00000171601.7 845 48aa Nonsense mediated decay ENSMUST00000167063.1 637 No protein Processed transcript ENSMUST00000203415.1 3523 No protein Retained intron	ENSMUST00000204545.2 2418 539aa I Protein coding CCDS20128 № ENSMUST00000166318.7 2222 553aa I Protein coding CCDS51770 № ENSMUST00000036236.14 2161 539aa I Protein coding CCDS20128 № ENSMUST00000036225.14 1896 553aa I Protein coding CCDS51770 № ENSMUST00000167628.1 1281 315aa I Protein coding - ENSMUST00000171601.7 845 48aa I Nonsense mediated decay - ENSMUST00000167063.1 637 No protein I Processed transcript - ENSMUST00000203415.1 3523 No protein I Retained intron -	ENSMUST00000204545.2 2418 539aa Protein coding CCDS20128 @ B9EHZ5 @ Q9JLB0 @ ENSMUST00000166318.7 2222 553aa Protein coding CCDS51770 @ Q3UN60 @ Q9JLB0 @ ENSMUST00000036236.14 2161 539aa Protein coding CCDS20128 @ B9EHZ5 @ Q9JLB0 @ ENSMUST00000036225.14 1896 553aa Protein coding CCDS51770 @ Q3UN60 @ Q9JLB0 @ ENSMUST00000167628.1 1281 315aa Protein coding - E9PWC5 @ ENSMUST00000171601.7 845 48aa Nonsense mediated decay - E9Q2R8 @ ENSMUST00000167063.1 637 No protein Processed transcript - - - ENSMUST00000203415.1 3523 No protein Retained intron - - -

The strategy is based on the design of *Mpp6-209* transcript, The transcription is shown below



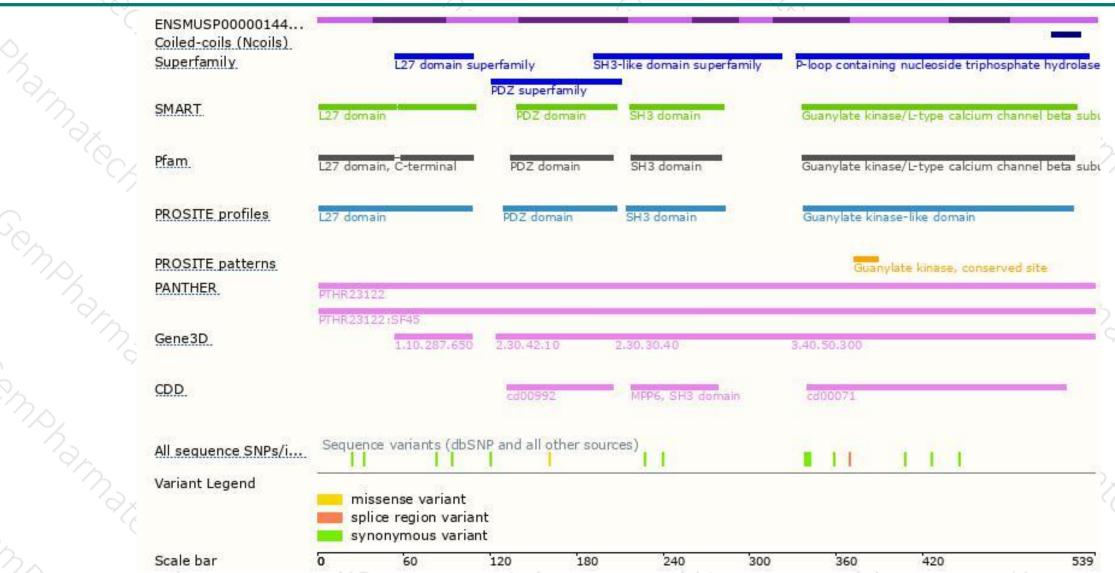
Genomic location distribution





Protein domain







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





