

# Slc17a7 Cas9-KO Strategy

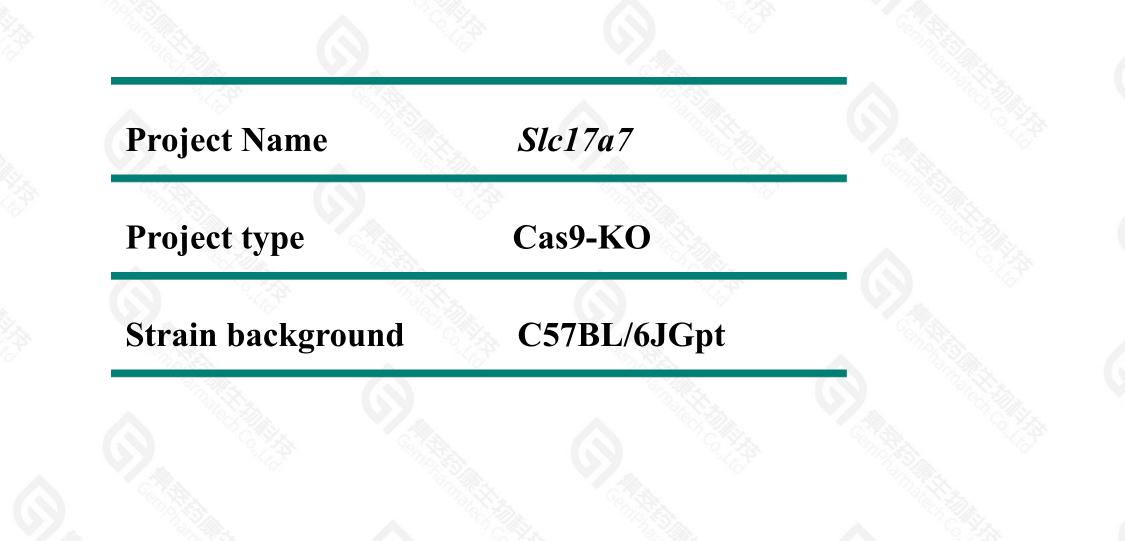
Designer: Lingyan Wu

**Reviewer: Miaomiao Cui** 

**Design Date: 2021-9-22** 

## **Project Overview**





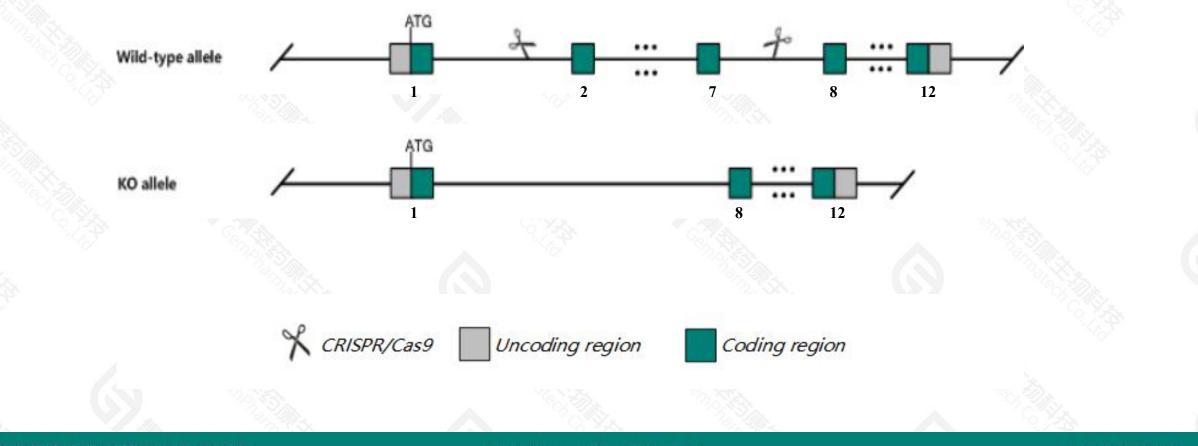
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## **Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the *Slc17a7* gene. The schematic diagram is as follows:



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> The *Slc17a7* gene has 5 transcripts. According to the structure of *Slc17a7* gene, exon2-exon7 of *Slc17a7*-201(ENSMUST00000085374.7) transcript is recommended as the knockout region. The region contains 805bp coding sequence. Knock out the region will result in disruption of protein function.

> In this project we use CRISPR/Cas9 technology to modify *Slc17a7* gene. The brief process is as follows: CRISPR/Cas9 system were microinjected into the fertilized eggs of C57BL/6JGpt 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/6JGpt mice.



- According to the existing MGI data, homozygous mutant mice are small and fail to thrive by 3-4 weeks of age.
  Abnormal excitatory post synaptic potential and currents.
- The *Slc17a7* gene is located on the Chr7. 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)

## Slc17a7 solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7 [Mus musculus (house mouse)]

Gene ID: 72961, updated on 7-Mar-2021

#### Summary

Official SymbolSlc17a7 provided by MGIOfficial Full Namesolute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7 provided byMGIPrimary sourceMGI:MGI:1920211See relatedEnsembl:ENSMUSG0000070570Gene typeprotein codingRefSeq statusVALIDATEDOrganismMus musculusLineageEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;<br/>Myomorpha; Muroidea; Murinae; Mus; MusAlso known as2900052E22Rik, Al851913, Vglu, Vglut1ExpressionBiased expression in cortex adult (RPKM 249.8), frontal lobe adult (RPKM 216.5) and 3 other tissues<br/>See more<br/>human all

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## **Transcript information (Ensembl)**

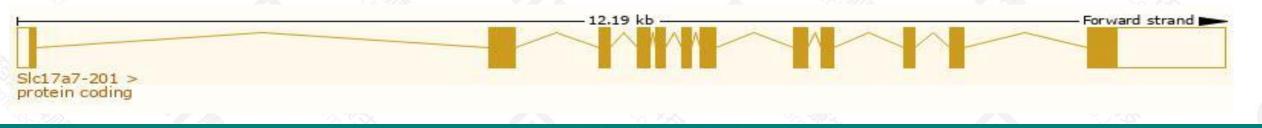


### The gene has 5 transcripts, all transcripts are shown below:

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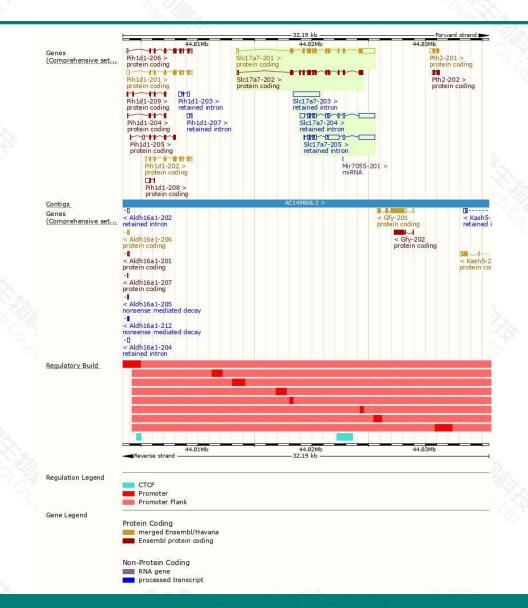
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc17a7-201	ENSMUST0000085374.7	2915	<u>560aa</u>	Protein coding	CCDS52244		TSL:1, GENCODE basic, APPRIS P1,
Slc17a7-202	ENSMUST00000209634.2	1860	<u>585aa</u>	Protein coding	-		TSL:5 , GENCODE basic ,
Slc17a7-205	ENSMUST00000211652.2	3080	No protein	Retained intron	2		TSL:2,
Slc17a7-204	ENSMUST00000210540.2	2722	No protein	Retained intron			TSL:1,
Slc17a7-203	ENSMUST00000210498.2	2346	No protein	Retained intron	Ξ.		TSL:NA ,

The strategy is based on the design of *Slc17a7-201* transcript, the transcription is shown below:



### **Genomic location distribution**





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## **Protein domain**

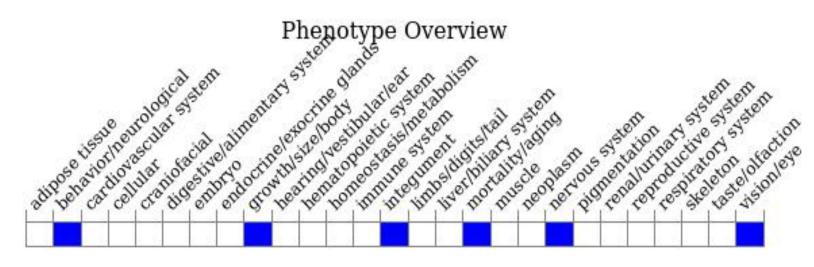


Transmembrane heli       MobiDB lite         Low complexity (Seg)       MFS transporter superfamily         Superfamily       MFS transporter superfamily         Pfam       Major facilitator superfamily         PROSITE profiles       Major facilitator superfamily domain         PANTHER       PTHR116621SF29         Gene3D       1.20.1250.20         CDD       cd17382         All sequence SNPs/i       Sequence variants (dbSNP and all other sources)	
Major facilitator superfamily       Mode       Major facilitator superfamily domain       Major facilitator superfamily domain    <	-
ROSITE profiles       Major facilitator superfamily domain         ANTHER       PTHR11662         PTHR11662:SF29       PTHR11662:SF29         Sene3D       1.20.1250.20         CDD       cd17382	
PTHR11662:SF29 I.20.1250.20 Cd17382	
Sene3D         1.20.1250.20           DD         cd17382	
DD cd17382	
Il sequence SNPs/i Sequence variants (dbSNP and all other sources)	
	0.00
/ariant Legend synonymous variant	
Scale bar <b>0</b> 60 120 180 240 300 360 420 480	

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## 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, homozygous mutant mice are small and fail to thrive by 3-4 weeks of age. Abnormal excitatory post synaptic potential and currents.



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



