Atp13a5 Cas9-KO Strategy

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Overview

Target Gene Name
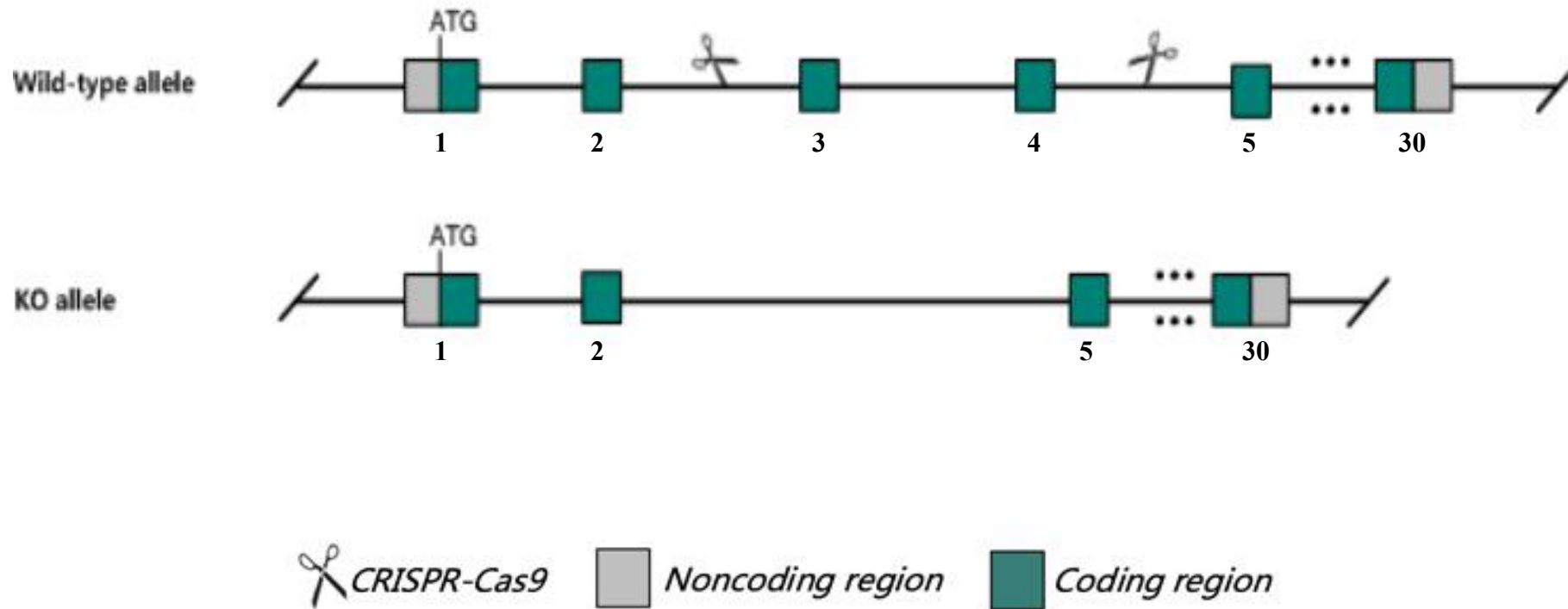
- Atp13a5

Project Type

- Cas9-KO

Genetic Background

- C57BL/6NGpt

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Strain Strategy

Technical Information

- The *Atp13a5* gene has 4 transcripts. According to the structure of *Atp13a5* gene, exon3-exon4 of *Atp13a5*-MGP_C57BL6NJ_T0044389.1 transcript is recommended as the knockout region. The region contains 218bp coding sequence. Knocking out the region will result in disruption of protein function.

- In this project we use CRISPR-Cas9 technology to modify *Atp13a5* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs were microinjected into the fertilized eggs of C57BL/6NGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6NGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.

Gene Information

Atp13a5 ATPase type 13A5 [*Mus musculus* (house mouse)]

⬇ Download Datasets

Gene ID: 268878, updated on 27-Feb-2024

▲ Summary   ⤒ ?

Official Symbol	Atp13a5 provided by MGI
Official Full Name	ATPase type 13A5 provided by MGI
Primary source	MGI:MGI:2444068
See related	Ensembl:ENSMUSG00000048939 AllianceGenome:MGI:2444068
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	C630015F21Rik
Summary	Predicted to enable ATP binding activity; ATP hydrolysis activity; and metal ion binding activity. Predicted to be involved in cellular calcium ion homeostasis. Predicted to be located in membrane. Predicted to be integral component of membrane. Is expressed in lung; musculature; nervous system; sensory organ; and urinary system. Orthologous to human ATP13A5 (ATPase 13A5). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Biased expression in cortex adult (RPKM 2.3), frontal lobe adult (RPKM 2.2) and 6 other tissues See more
Orthologs	human all
NEW	**Try the new Gene table** **Try the new Transcript table**

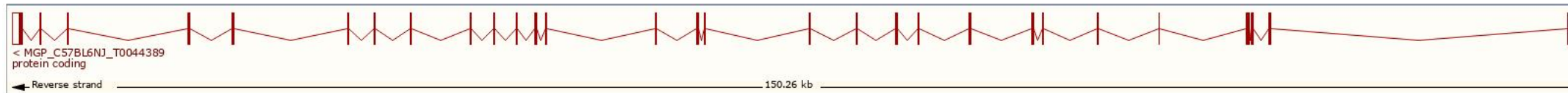Source: https://www.ncbi.nlm.nih.gov/

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Transcript Information

The gene has 4 transcripts,all transcripts are shown below:

Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
MGP_C57BL6NJ_T0044391.1	-	3789	1171aa	Protein coding		-	-
MGP_C57BL6NJ_T0044392.1	-	728	227aa	Protein coding		-	-
MGP_C57BL6NJ_T0044390.1	-	4572	949aa	Nonsense mediated decay		-	-
MGP_C57BL6NJ_T0044389.1	-	4598	1216aa	Protein coding	CCDS28095, CCDS70705	D3YU82 D3YV41 D6RHM2 Q3TYU2	Ensembl Canonical

The strategy is based on the design of *Atp13a5*-MGP_C57BL6NJ_T0044389.1 transcript, the transcription is shown below:
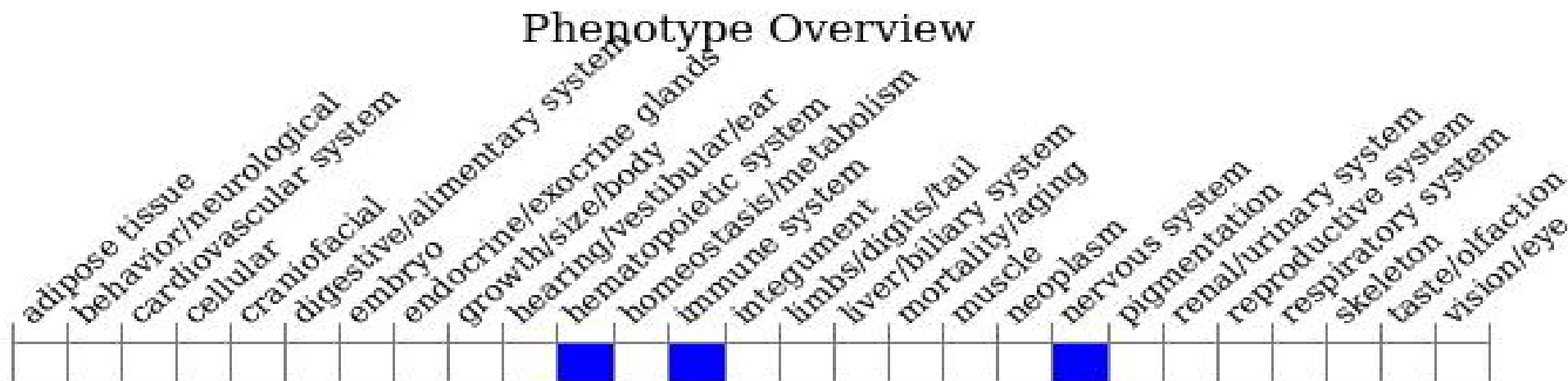
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Genomic Information

Source: : https://www.ensembl.org

Protein Information

Source: : https://www.ensembl.org
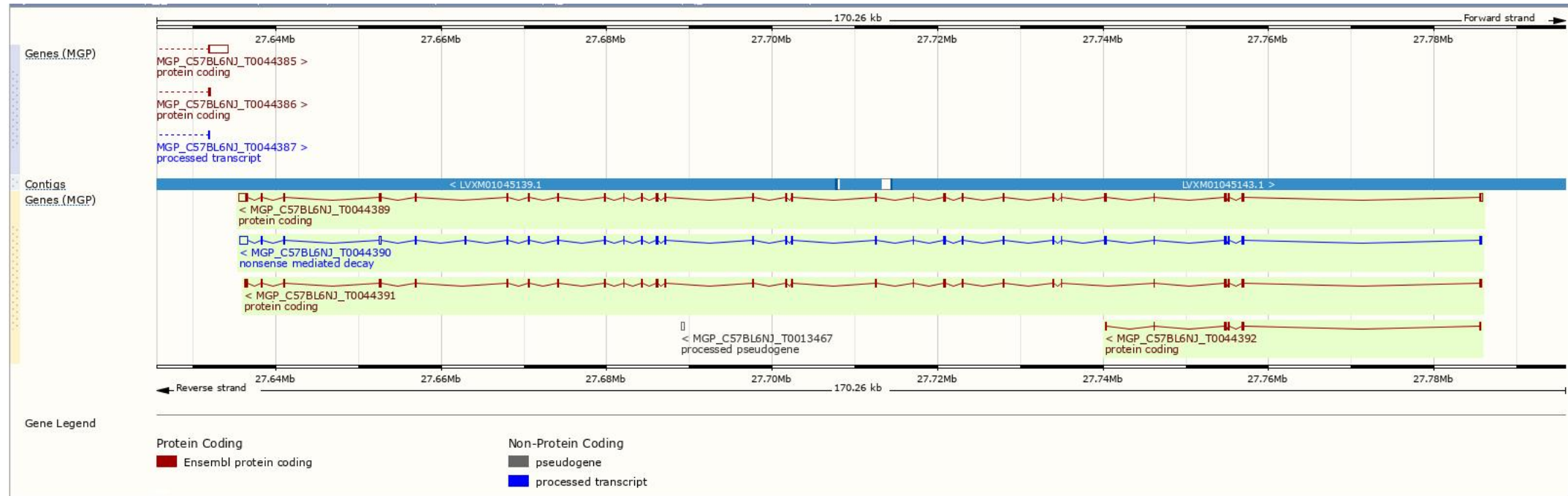
Mouse Phenotype Information (MGI)

Phenotype Overview

- Homozygous mutant mice show a decreased mean percentage of natural killer cells when compared with controls. Male homozygous mutant mice exhibit impaired sensorimotor gating/attention during prepulse inhibition testing.

Source: https://www.informatics.jax.org

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Important Information

- *Atp13a5* is located on Chr16. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is on the same chromosome.

- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risks of the mutation on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

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