GemPharmatech™

Ppip5k2 Cas9-CKO Strategy

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Reviewer: Xingkai Xiao

Design Date: 2024-1-12

Overview

Target Gene Name

- *Ppip5k2*

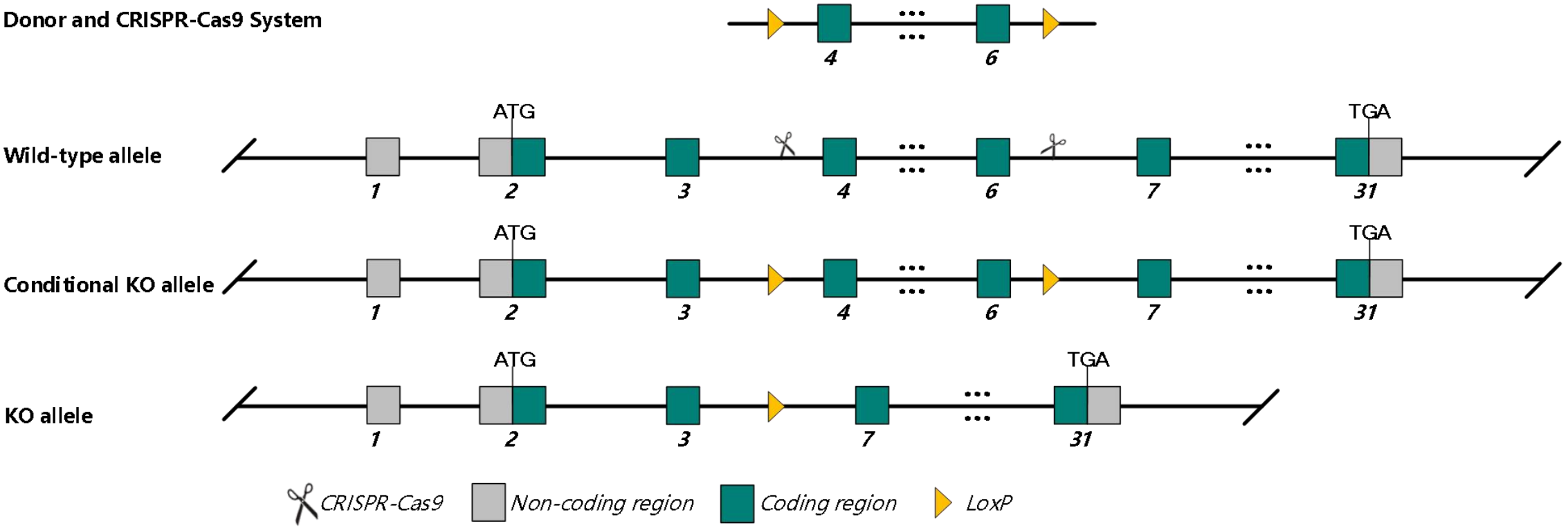
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Ppip5k2* gene.

Technical Information

- The *Ppip5k2* gene has 7 transcripts. According to the structure of *Ppip5k2* gene, exon 4-6 of *Ppip5k2*-202 (ENSMUST00000112845.8) is recommended as the knockout region. The region contains 332 bp of coding sequence. Knocking out the region will result in disruption of gene function.
- In this project we use CRISPR-Cas9 technology to modify *Ppip5k2* gene. The brief process is as follows: CRISPR-Cas9 system and Donor 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- 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.

Gene Information

Ppip5k2 diphosphoinositol pentakisphosphate kinase 2 [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 227399, updated on 23-Nov-2023

Summary

Official Symbol	Ppip5k2 provided by MGI
Official Full Name	diphosphoinositol pentakisphosphate kinase 2 provided by MGI
Primary source	MGI:MGI:2142810
See related	Ensembl:ENSMUSG00000040648 AllianceGenome:MGI:2142810
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	Vip2; Cfap160; Hisppd1; mKIAA0433; D330021B20
Summary	Enables diphosphoinositol-pentakisphosphate kinase activity and inositol hexakisphosphate kinase activity. Predicted to be involved in inositol metabolic process and inositol phosphate biosynthetic process. Predicted to act upstream of or within sensory perception of sound. Predicted to be located in cytoplasm. Predicted to be active in cytosol. Is expressed in several structures, including alimentary system; genitourinary system; nervous system; sensory organ; and skin. Used to study nonsyndromic deafness. Human ortholog(s) of this gene implicated in autosomal recessive nonsyndromic deafness 100. Orthologous to human PPIP5K2 (diphosphoinositol pentakisphosphate kinase 2). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in CNS E18 (RPKM 10.9), CNS E14 (RPKM 10.8) and 26 other tissues See more
Orthologs	human all
NEW	**Try the new Gene table** **Try the new Transcript table**

Genomic context

Location: 1 D; 1 47.76 cM

See Ppip5k2 in Genome Data Viewer

Exon count: 32

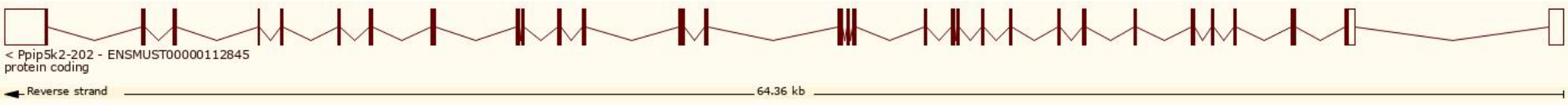
https://www.ncbi.nlm.nih.gov/gene/227399

Transcript Information

The gene has 7 transcripts, all transcripts are shown below:

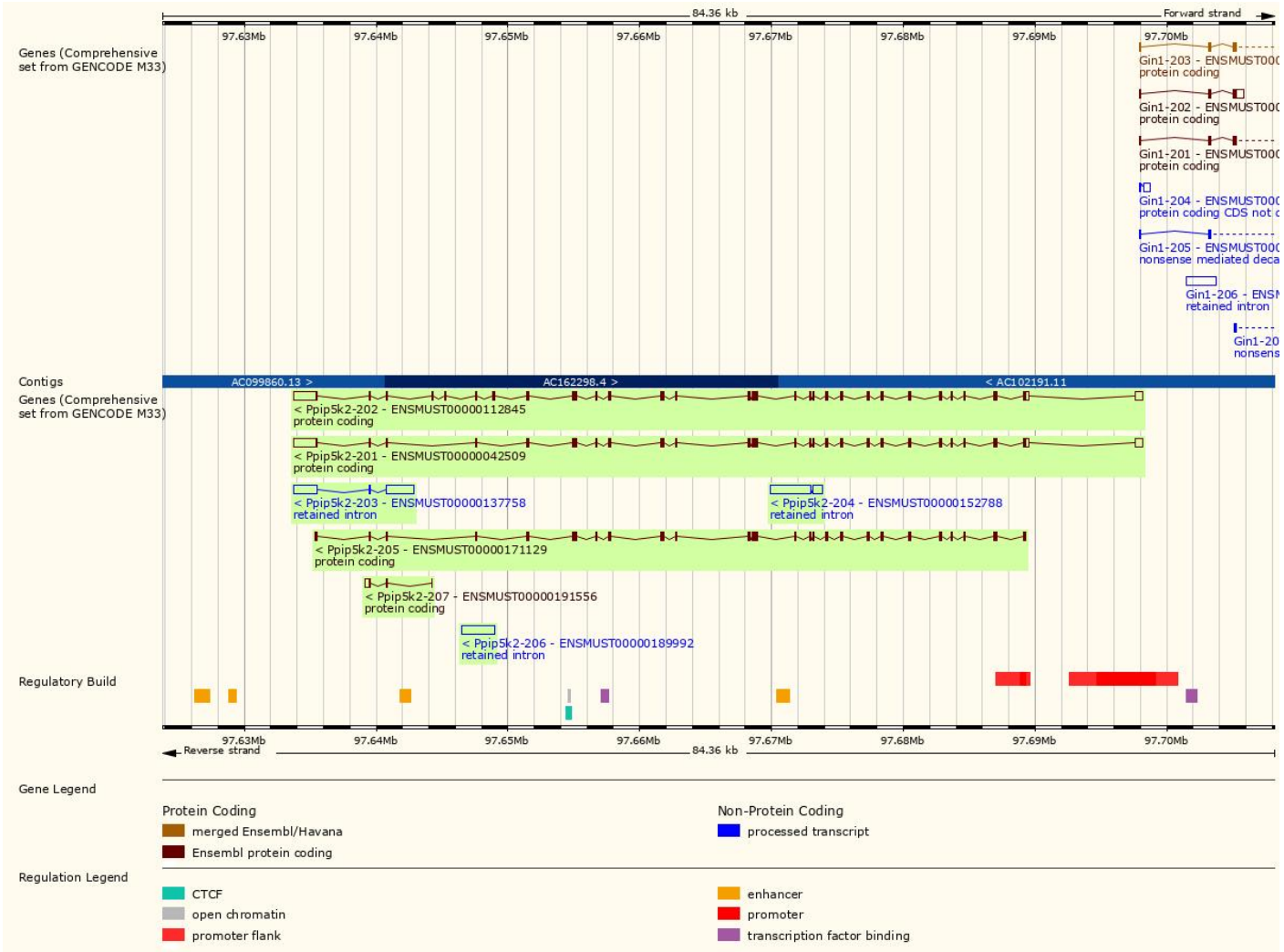
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000042509.13	Ppip5k2-201	5882	1129aa	Protein coding	CCDS35678	Q6ZQB6	GENCODE basic TSL:1
ENSMUST00000112845.8	Ppip5k2-202	6239	1242aa	Protein coding		E9Q9J4	Ensembl Canonical GENCODE basic APPRIS P3 TSL:5
ENSMUST00000137758.2	Ppip5k2-203	4055	No protein	Retained intron		-	TSL:1
ENSMUST00000152788.3	Ppip5k2-204	3844	No protein	Retained intron		-	TSL:1
ENSMUST00000171129.8	Ppip5k2-205	3425	1123aa	Protein coding		Q6ZQB6-3	GENCODE basic APPRIS ALT1 TSL:1
ENSMUST00000189992.2	Ppip5k2-206	2523	No protein	Retained intron		-	TSL:NA
ENSMUST00000191556.2	Ppip5k2-207	561	92aa	Protein coding		A0A087WPZ7	TSL:5 CDS 5' incomplete

The strategy is based on the design of *Ppip5k2*-202 transcript, the transcription is shown below:



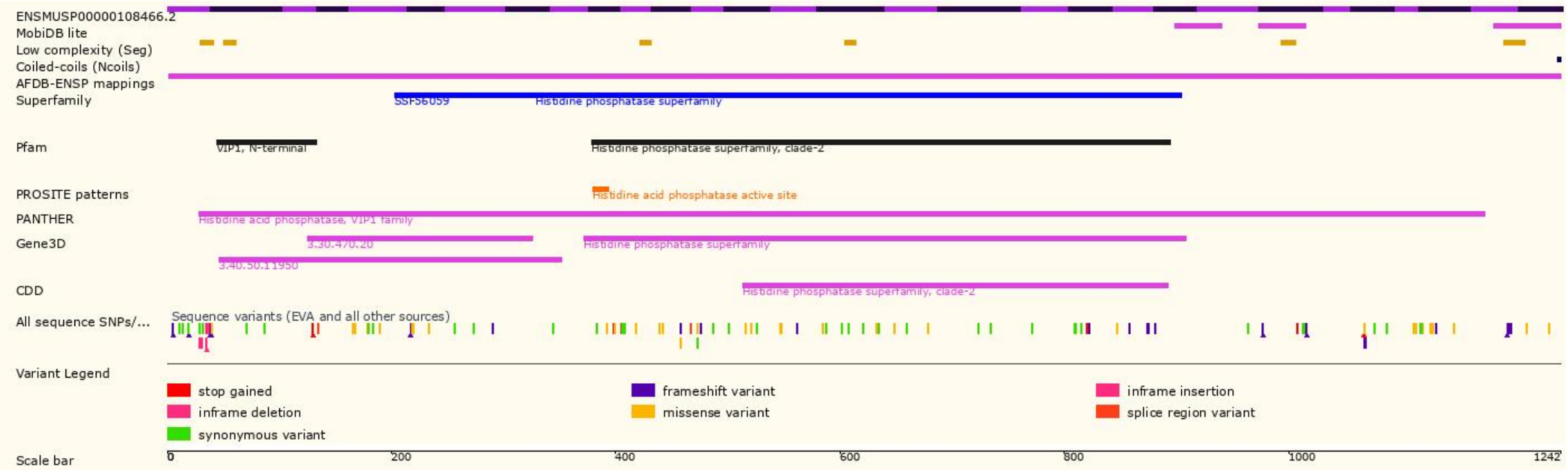
Source: http://asia.ensembl.org/

Genomic Information



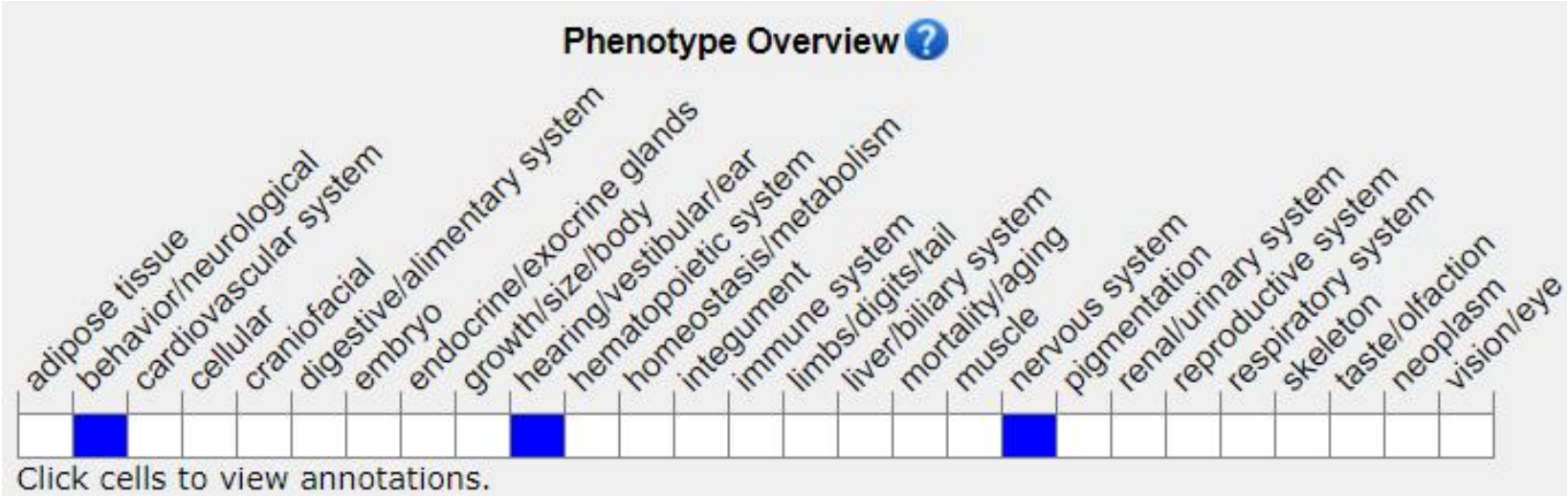
Source: http://asia.ensembl.org/

Protein Information



Source: https://www.ensembl.org

Mouse Phenotype Information (MGI)



Mice homozygous or heterozygous for a targeted deletion of the phosphatase domain exhibit progressive hearing loss with increased auditory-evoked brainstem response (ABR) thresholds and cochlear outer hair cell degeneration.

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

Important Information

- This stratergy may not affect *Ppip5k2*-203, *Ppip5k2*-204, *Ppip5k2*-206 and *Ppip5k2*-207 transcript.
- *Ppip5k2* is located on Chr 1. 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 risk of loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.