Psph Cas9-KO Strategy

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Project Overview

Project Name	*Psph*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

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

Technical routes

➢ The *Psph* gene has 8 transcripts. According to the structure of *Psph* gene, exon4-exon6 of *Psph-201* (ENSMUST00000031399.12) transcript is recommended as the knockout region.The region contains start codon ATG. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Psph* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ The *Psph* gene is located on the Chr5. 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）

Psph phosphoserine phosphatase [*Mus musculus* (house mouse)]
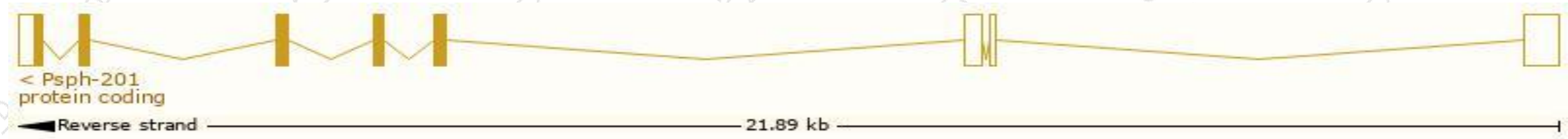
Gene ID: 100678, updated on 12-Aug-2019

Summary

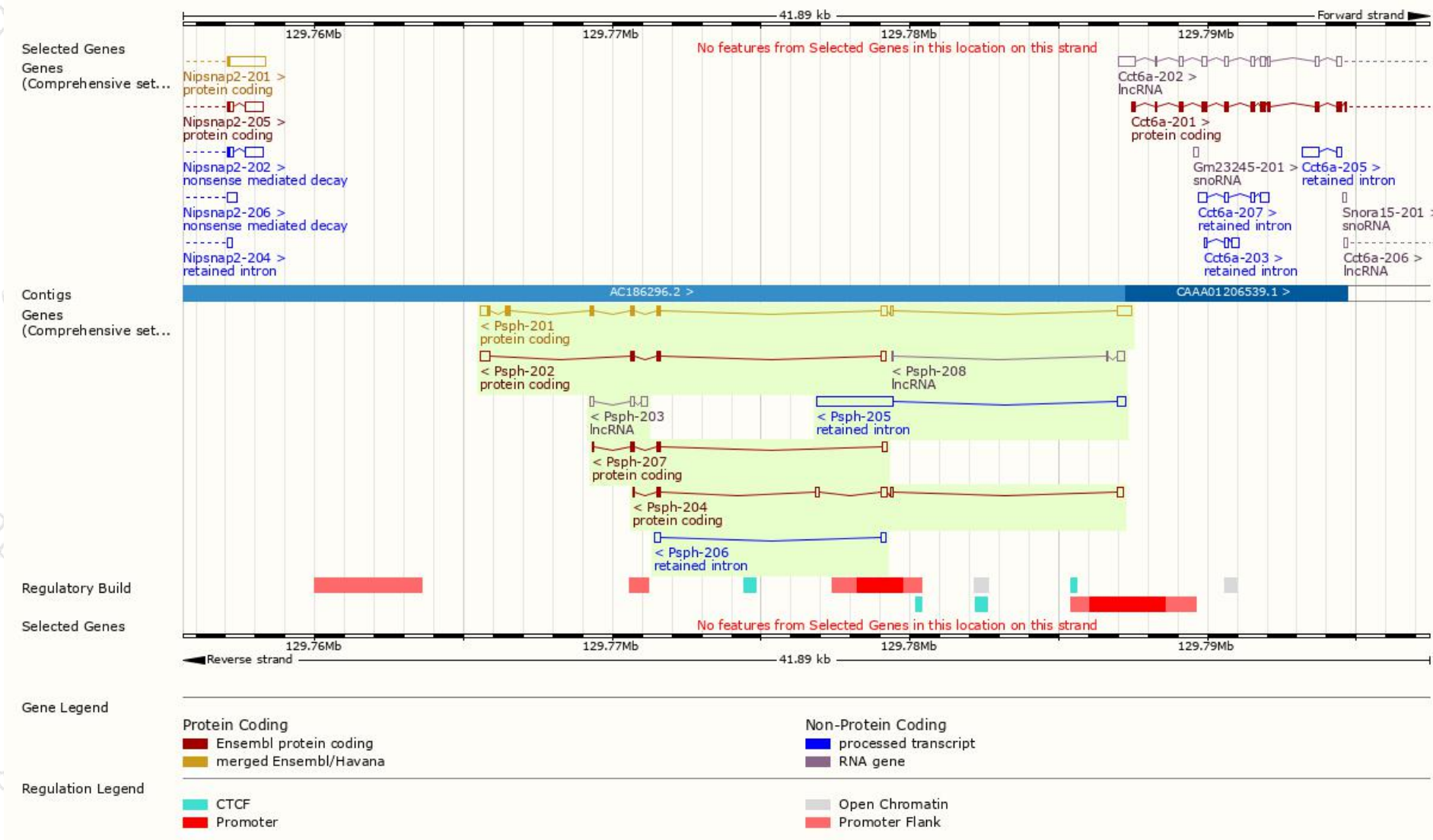|	
Official Symbol	Psph provided by MGI
Official Full Name	phosphoserine phosphatase provided by MGI
Primary source	MGI:MGI:97788
See related	Ensembl:ENSMUSG00000029446
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	PSP; PSPase; AI480570
Expression	Ubiquitous expression in placenta adult (RPKM 14.8), liver E14 (RPKM 8.2) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Psph-201	ENSMUST00000031399.12	1733	225aa	Protein coding	CCDS19699	Q99LS3	TSL:1 GENCODE basic APPRIS P1
Psph-204	ENSMUST00000136507.3	820	60aa	Protein coding	-	D3Z666	CDS 3' incomplete TSL:5
Psph-202	ENSMUST00000118268.8	785	101aa	Protein coding	-	D3Z4T3	TSL:5 GENCODE basic
Psph-207	ENSMUST0000201394.3	510	113aa	Protein coding	-	A0A0J9YVH9	CDS 3' incomplete TSL:3
Psph-205	ENSMUST00000178244.1	2877	No protein	Retained intron	-	-	TSL:1
Psph-206	ENSMUST00000201022.1	398	No protein	Retained intron	-	-	TSL:2
Psph-203	ENSMUST00000136280.1	446	No protein	lncRNA	-	-	TSL:2
Psph-208	ENSMUST0000202374.1	383	No protein	lncRNA	-	-	TSL:3

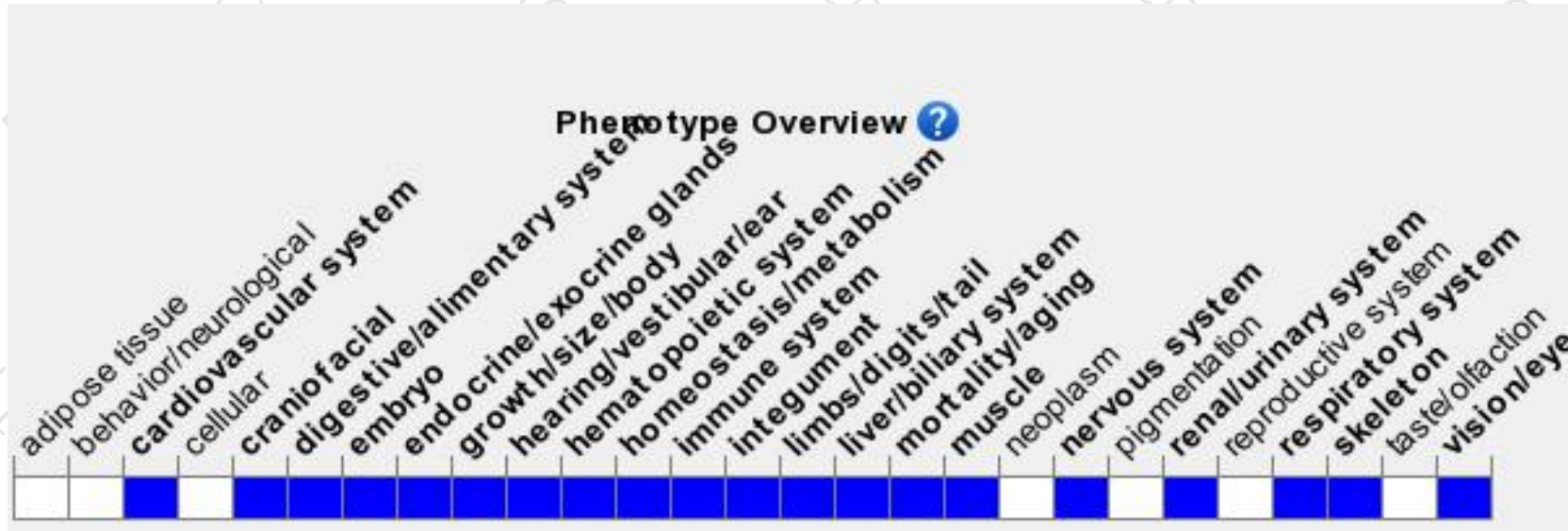The strategy is based on the design of *Psph-201* transcript,The transcription is shown below

< Psph-201
protein coding

◄ Reverse strand

21.89 kb

Genomic location distribution

Protein domain

ENSMUSP00000031...
Conserved Domains
hmmpanther
PTHR43344
PTHR43344:SF2

TIGRFAM domain
TIGR00338
TIGR01488

Superfamily domains
HAD-like superfamily

Structure-Function L...
SFLDG01137

Pfam domain
PF00702

Gene3D
Phosphoserine phosphatase, domain 2
HAD superfamily

All sequence SNPs/i...
Sequence variants (dbSNP and all other sources)

Variant Legend

■ frameshift variant
■ missense variant
■ splice region variant
■ synonymous variant

Scale bar
0   20   40   60   80   100   120   140   160   180   200   225

Mouse phenotype description(MGI)

Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

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If you have any questions, you are welcome to inquire.
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