

# *Pik3c2a* Cas9-KO Strategy

Designer: Huimin Su

# Project Overview

**Project Name**

*Pik3c2a*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pik3c2a* gene. The schematic diagram is as follows:



- The *Pik3c2a* gene has 7 transcripts. According to the structure of *Pik3c2a* gene, exon3 of *Pik3c2a-201* (ENSMUST00000170430.2) transcript is recommended as the knockout region. The region contains 104bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pik3c2a* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a gene trap allele show chronic renal failure and a range of renal lesions that precede immune involvement. Mice heterozygous for a kinase-inactivating allele show defects in platelet formation, platelet membrane morphology and dynamics, and an enrichment of barbell proplatelets.
- The *Pik3c2a* 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)

## Pik3c2a phosphatidylinositol-4-phosphate 3-kinase catalytic subunit type 2 alpha [Mus musculus (house mouse)]

Gene ID: 18704, updated on 19-Feb-2019

### Summary



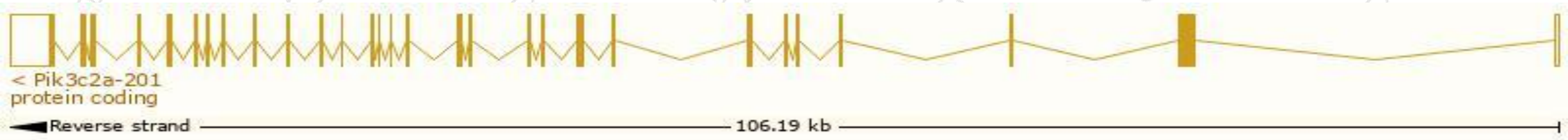
<b>Official Symbol</b>	Pik3c2a provided by <a href="#">MGI</a>
<b>Official Full Name</b>	phosphatidylinositol-4-phosphate 3-kinase catalytic subunit type 2 alpha provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1203729</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000030660</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	Cpk-m, PI3KC2
<b>Expression</b>	Ubiquitous expression in placenta adult (RPKM 5.5), limb E14.5 (RPKM 4.0) and 25 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

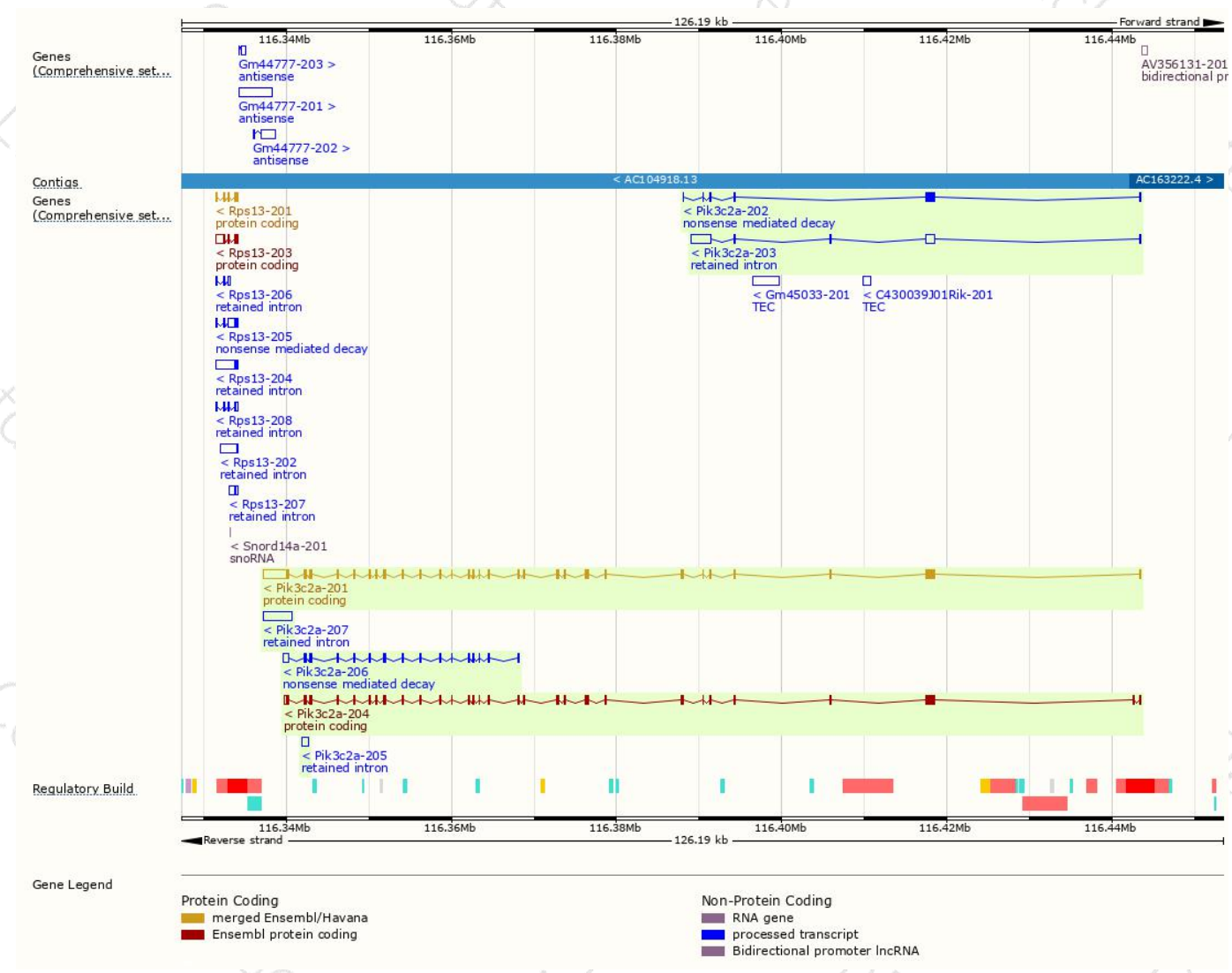
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pik3c2a-201	<a href="#">ENSMUST00000170430.2</a>	8044	<a href="#">1686aa</a>	Protein coding	<a href="#">CCDS52371</a>	<a href="#">F8VPL2</a>	TSL:5 GENCODE basic APPRIS P1
Pik3c2a-204	<a href="#">ENSMUST00000206219.1</a>	5670	<a href="#">1686aa</a>	Protein coding	<a href="#">CCDS52371</a>	<a href="#">F8VPL2</a>	TSL:5 GENCODE basic APPRIS P1
Pik3c2a-206	<a href="#">ENSMUST00000206385.1</a>	2830	<a href="#">448aa</a>	Nonsense mediated decay	-	<a href="#">A0A0U1RNT0</a>	CDS 5' incomplete TSL:1
Pik3c2a-202	<a href="#">ENSMUST00000205378.1</a>	1710	<a href="#">364aa</a>	Nonsense mediated decay	-	<a href="#">A0A0U1RNH9</a>	TSL:1
Pik3c2a-203	<a href="#">ENSMUST00000205767.1</a>	3849	No protein	Retained intron	-	-	TSL:2
Pik3c2a-207	<a href="#">ENSMUST00000206805.1</a>	3354	No protein	Retained intron	-	-	TSL:NA
Pik3c2a-205	<a href="#">ENSMUST00000206248.1</a>	741	No protein	Retained intron	-	-	TSL:NA

The strategy is based on the design of *Pik3c2a-201* transcript,The transcription is shown below

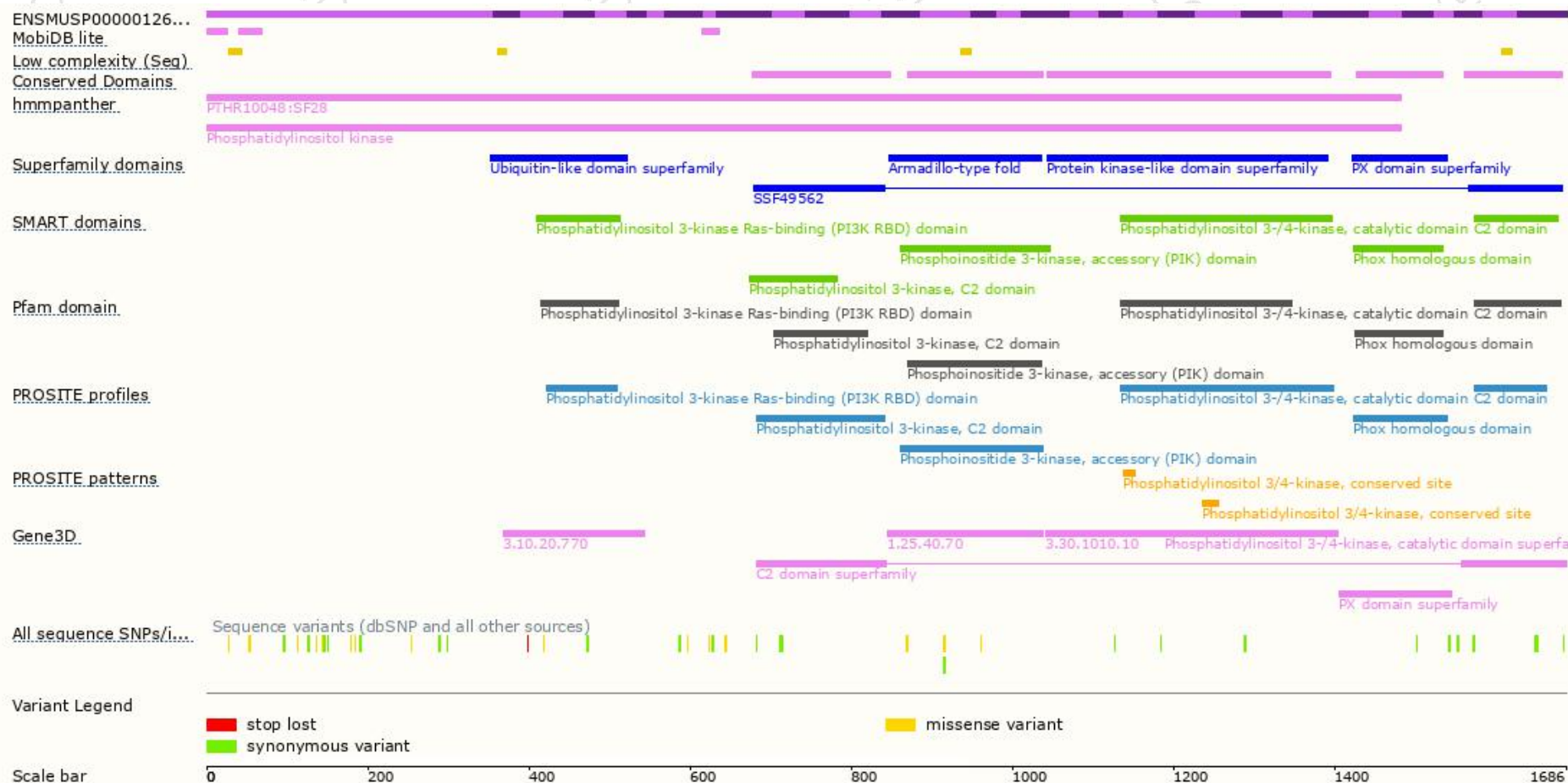


# Genomic location distribution

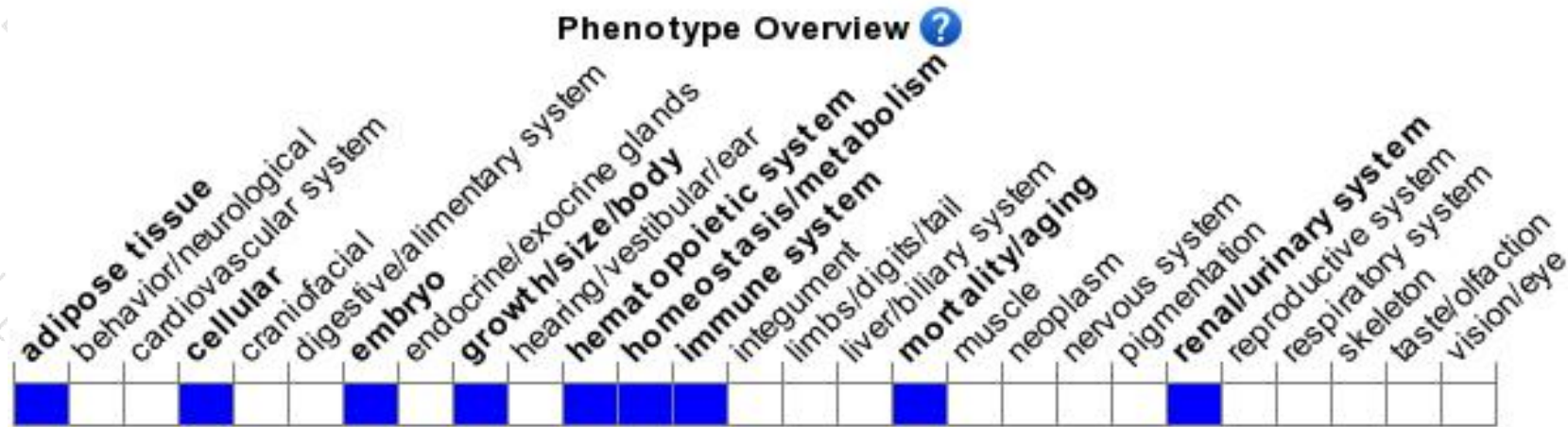




# Protein domain



# 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, Mice homozygous for a gene trap allele show chronic renal failure and a range of renal lesions that precede immune involvement. Mice heterozygous for a kinase-inactivating allele show defects in platelet formation, platelet membrane morphology and dynamics, and an enrichment of barbell proplatelets.

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

Tel: 400-9660890

