

Inpp5f Cas9-KO Strategy

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Project Overview

Project Name

Inpp5f

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Inpp5f* gene. The schematic diagram is as follows:



Technical routes

- The *Inpp5f* gene has 9 transcripts. According to the structure of *Inpp5f* gene, exon3-exon16 of *Inpp5f*-201 (ENSMUST00000043138.12) transcript is recommended as the knockout region. The region contains 1780bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Inpp5f* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Mice homozygous for a gene trap allele exhibit increased isoproterenol-induced cardiac hypertrophy.
- The flox region contains the Gm43580 gene, which may delete it after Cre.
- The *Inpp5f* gene is located on 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)

Inpp5f inositol polyphosphate-5-phosphatase F [*Mus musculus* (house mouse)]

Gene ID: 101490, updated on 13-Mar-2020

Summary

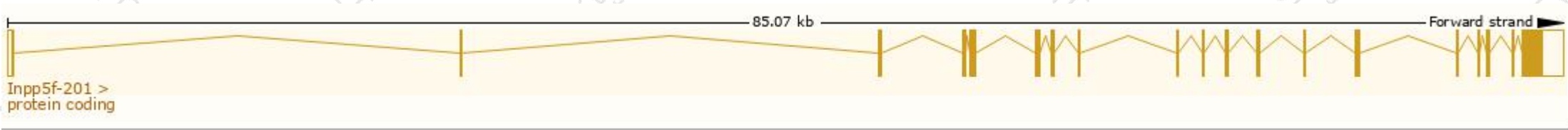
Official Symbol	Inpp5f provided by MGI
Official Full Name	inositol polyphosphate-5-phosphatase F provided by MGI
Primary source	MGI:MGI:2141867
See related	Ensembl:ENSMUSG000000042105
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	SAC2; cl-27; hSAC2; AI115354; AW561896; mKIAA0966; 5830435P03Rik
Expression	Broad expression in CNS E18 (RPKM 34.5), whole brain E14.5 (RPKM 23.5) and 18 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

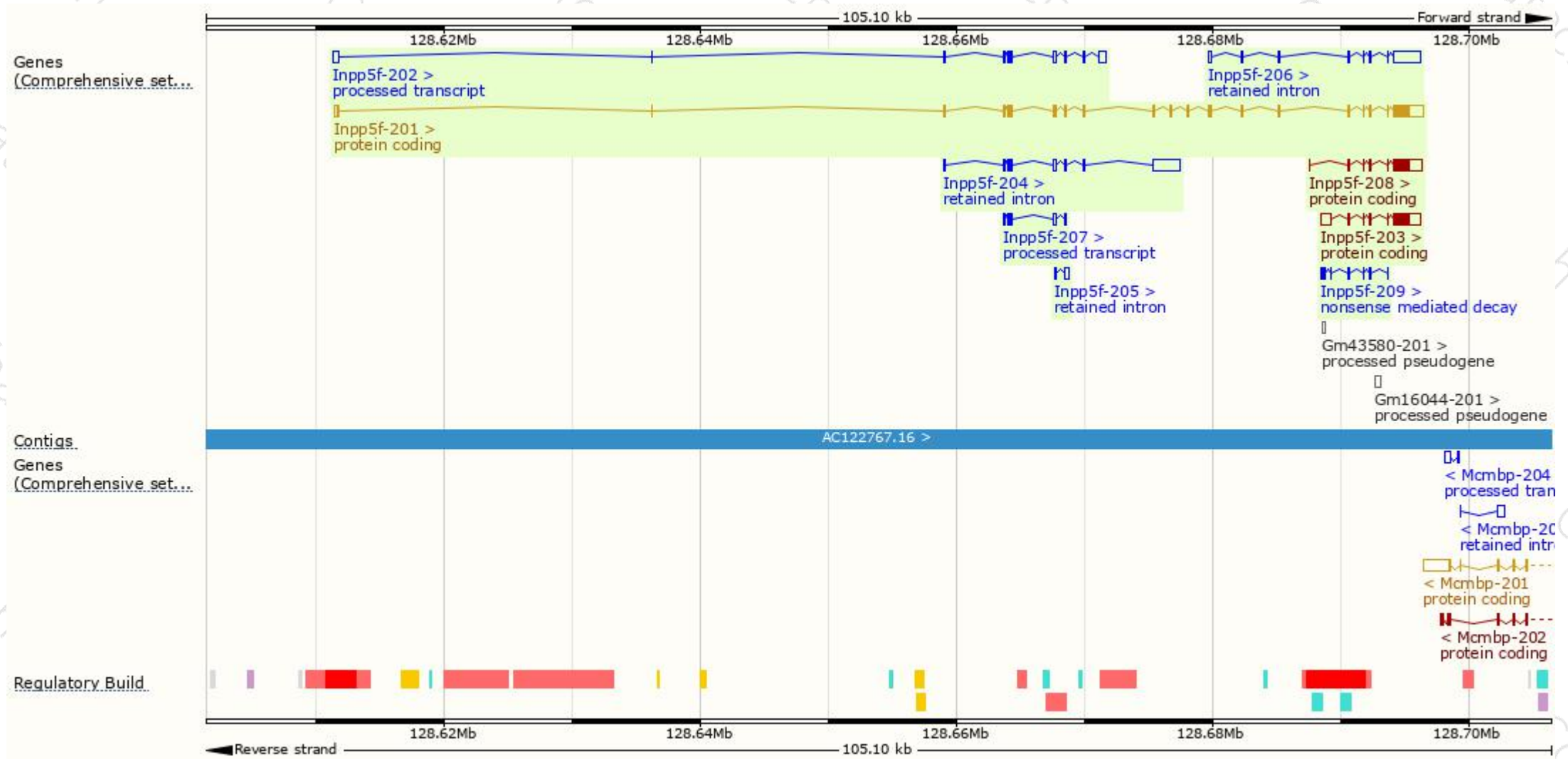
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Inpp5f-201	ENSMUST00000043138.12	4734	1132aa	Protein coding	CCDS21899	B2RQ14 Q8CDA1	TSL:1 GENCODE basic APPRIS P1
Inpp5f-203	ENSMUST00000118605.1	3220	505aa	Protein coding	CCDS85430	Q8CDA1	TSL:1 GENCODE basic
Inpp5f-208	ENSMUST00000151237.4	2609	441aa	Protein coding	-	Q8CDA1	TSL:1 GENCODE basic
Inpp5f-209	ENSMUST00000202419.2	559	121aa	Nonsense mediated decay	-	A0A0J9YU13	TSL:5
Inpp5f-202	ENSMUST00000098007.10	1906	No protein	Processed transcript	-	-	TSL:1
Inpp5f-207	ENSMUST00000148815.1	684	No protein	Processed transcript	-	-	TSL:3
Inpp5f-204	ENSMUST00000129085.7	3126	No protein	Retained intron	-	-	TSL:5
Inpp5f-206	ENSMUST00000142075.7	2939	No protein	Retained intron	-	-	TSL:1
Inpp5f-205	ENSMUST00000130789.1	468	No protein	Retained intron	-	-	TSL:2

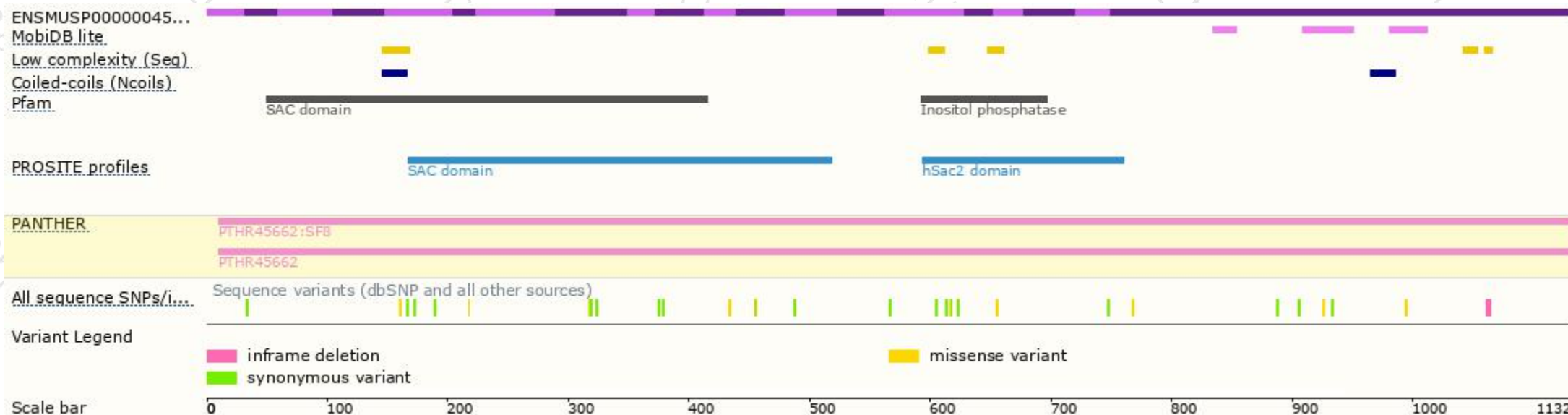
The strategy is based on the design of *Inpp5f-201* transcript,The transcription is shown below



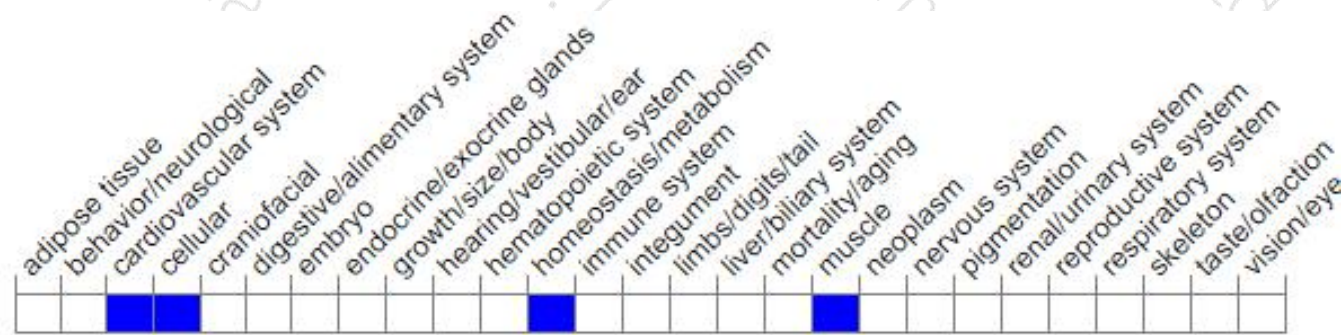
Genomic location distribution



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 exhibit increased isoproterenol-induced cardiac hypertrophy.

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

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