

Inpp1 Cas9-KO Strategy

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Project Overview

Project Name

Inpp1l

Project type

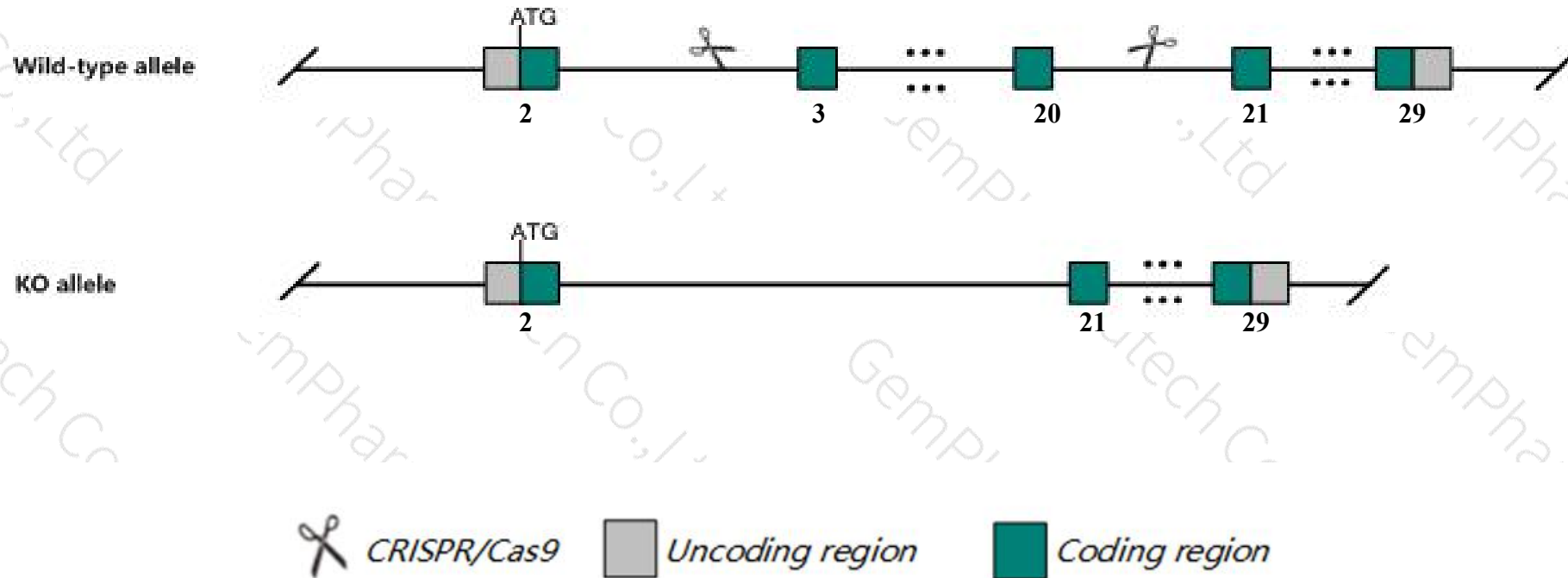
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Inpp1l* gene. The schematic diagram is as follows:



- The *Inpp11* gene has 9 transcripts. According to the structure of *Inpp11* gene, exon3-exon20 of *Inpp11-201* (ENSMUST00000035836.13) transcript is recommended as the knockout region. The region contains 2033bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Inpp11* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous mice display decreased postnatal growth, decreased circulating levels of leptin, free fatty acids, triglycerides, and total cholesterol, and resistance to diet-induced obesity.
- The knockout region is near to the N-terminal of *Gm10602* gene, this strategy may influence the regulatory function of the N-terminal of *Gm10602* gene.
- Transcript *Inpp1l*-205&208 may not be affected. And the effect on transcript *Inpp1l*-204&207 is unknown.
- The *Inpp1l* 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)

Inpp1 inositol polyphosphate phosphatase-like 1 [*Mus musculus* (house mouse)]

Gene ID: 16332, updated on 10-Oct-2019

Summary

- Official Symbol** Inpp1 provided by [MGI](#)
- Official Full Name** inositol polyphosphate phosphatase-like 1 provided by [MGI](#)
- Primary source** [MGI:MGI:1333787](#)
- See related** [Ensembl:ENSMUSG00000032737](#)
- 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** 51C; SHIP2
- Expression** Ubiquitous expression in ovary adult (RPKM 43.9), heart adult (RPKM 33.8) and 26 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 7; 7 E2 [See Inpp1 in Genome Data Viewer](#)

Exon count: 30

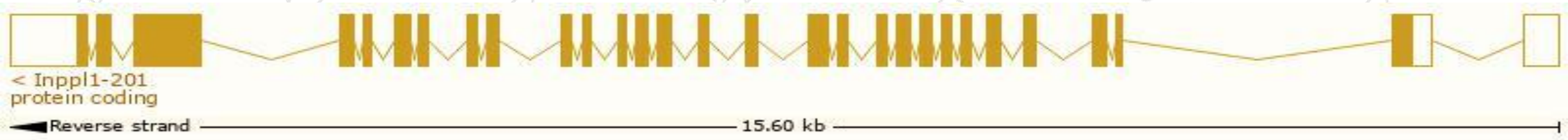
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	7	NC_000073.6 (101822632..101838226, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	7	NC_000073.5 (108971146..108986740, complement)

Transcript information (Ensembl)

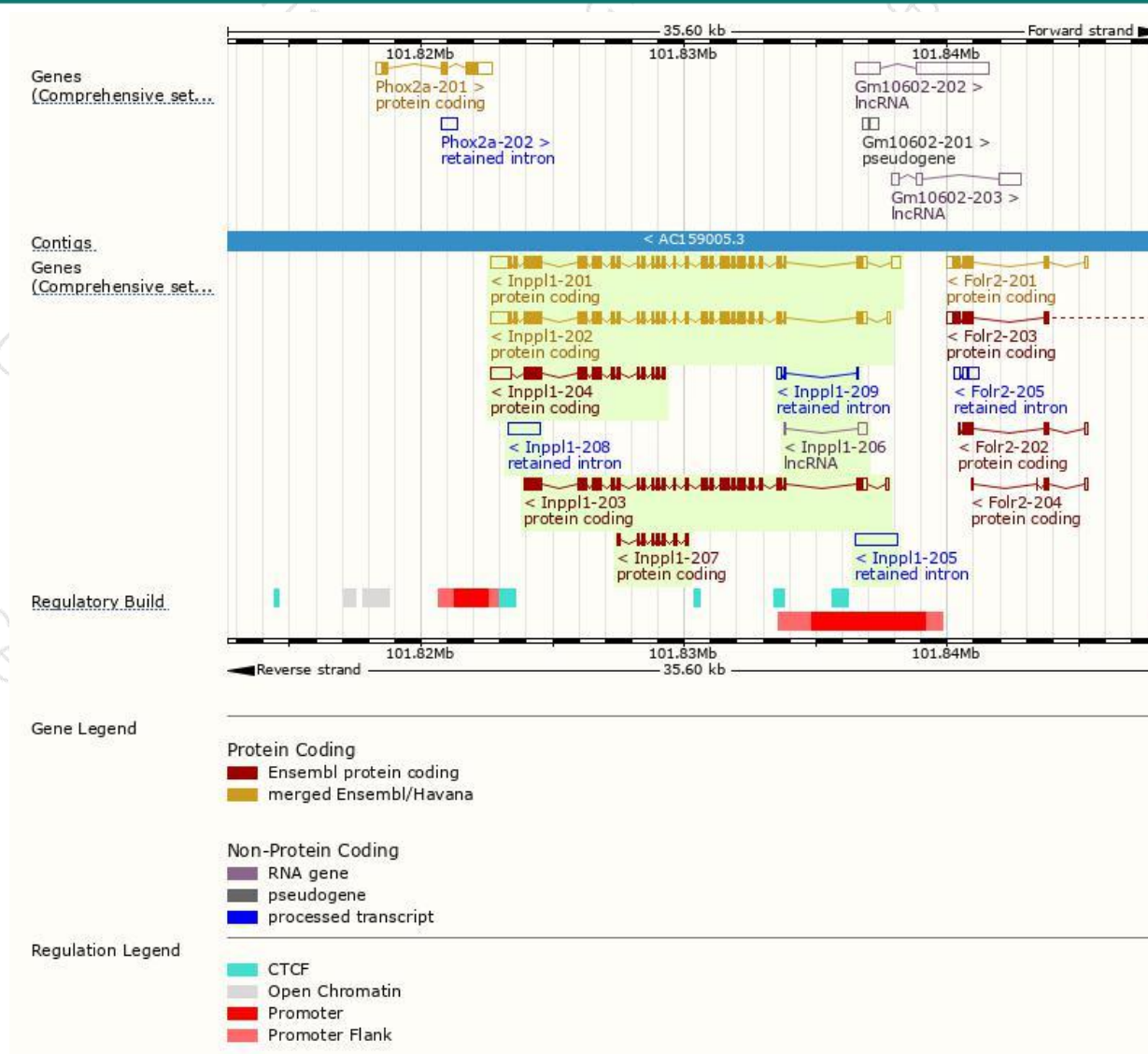
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Inpp1l-201	ENSMUST00000035836.13	4995	1257aa	Protein coding	CCDS21515	Q6P549	TSL:1 GENCODE basic APPRIS P1
Inpp1l-202	ENSMUST00000165052.7	4730	1257aa	Protein coding	CCDS21515	Q6P549	TSL:1 GENCODE basic APPRIS P1
Inpp1l-203	ENSMUST00000185929.1	3817	1166aa	Protein coding	-	A0A087WPT7	CDS 3' incomplete TSL:1
Inpp1l-204	ENSMUST00000186316.1	2559	603aa	Protein coding	-	A0A1B0GR64	CDS 5' incomplete TSL:1
Inpp1l-207	ENSMUST00000210116.1	828	276aa	Protein coding	-	A0A1B0GST7	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Inpp1l-205	ENSMUST00000209481.1	1624	No protein	Retained intron	-	-	TSL:NA
Inpp1l-208	ENSMUST00000211436.1	1186	No protein	Retained intron	-	-	TSL:NA
Inpp1l-209	ENSMUST00000211514.1	269	No protein	Retained intron	-	-	TSL:2
Inpp1l-206	ENSMUST00000209861.1	398	No protein	lncRNA	-	-	TSL:5

The strategy is based on the design of *Inpp1l-201* transcript,The transcription is shown below



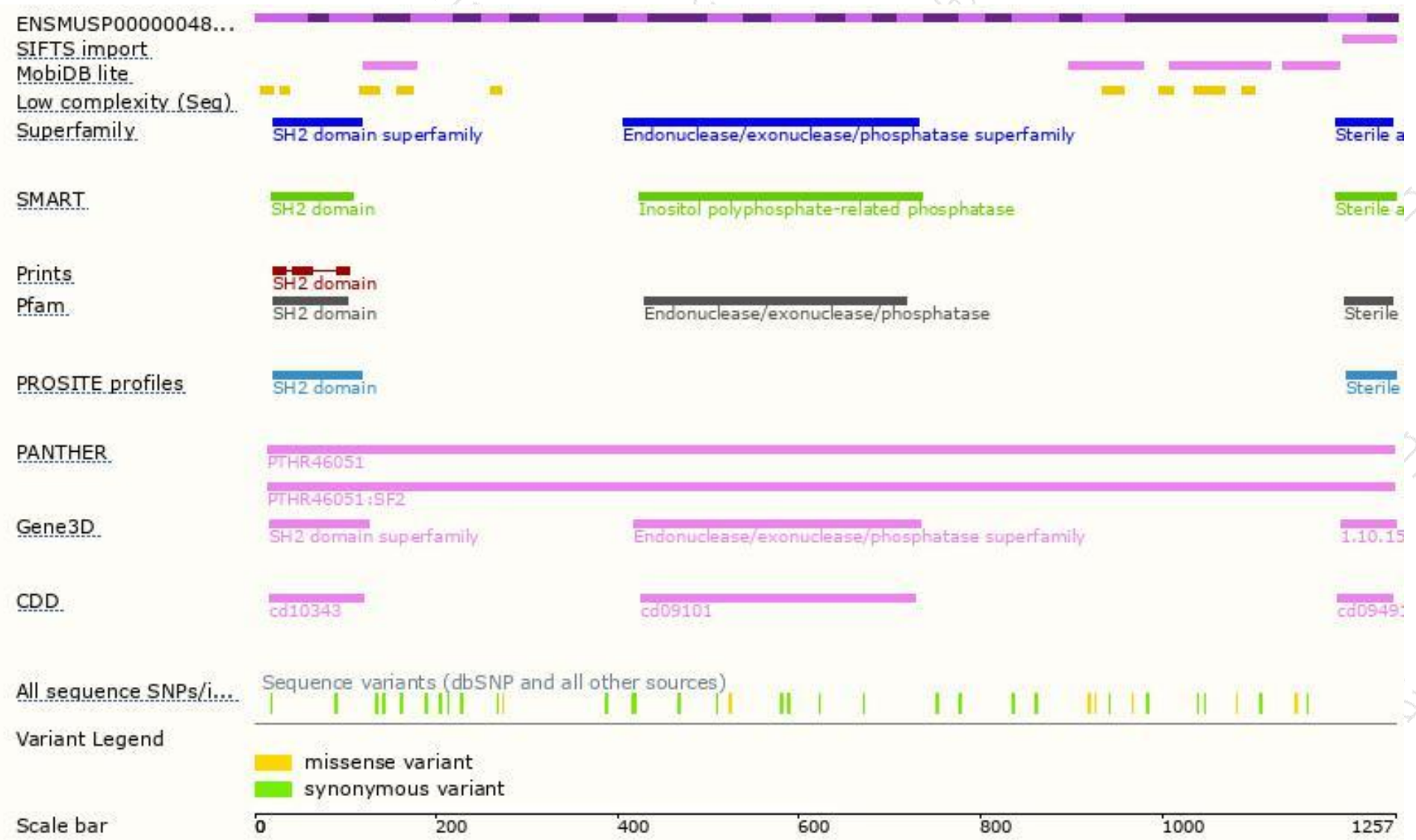
Genomic location distribution



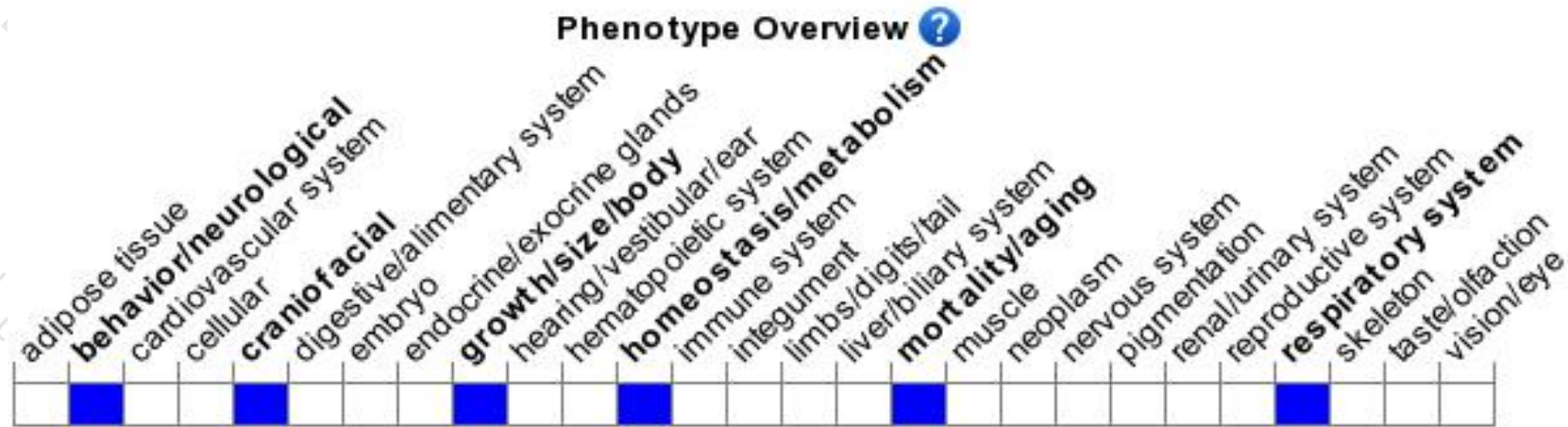
Protein domain



集萃药康
GemPharmatech



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, Homozygous mice display decreased postnatal growth, decreased circulating levels of leptin, free fatty acids, triglycerides, and total cholesterol, and resistance to diet-induced obesity.

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

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