

Inpp5d Cas9-KO Strategy

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Project Overview

Project Name

Inpp5d

Project type

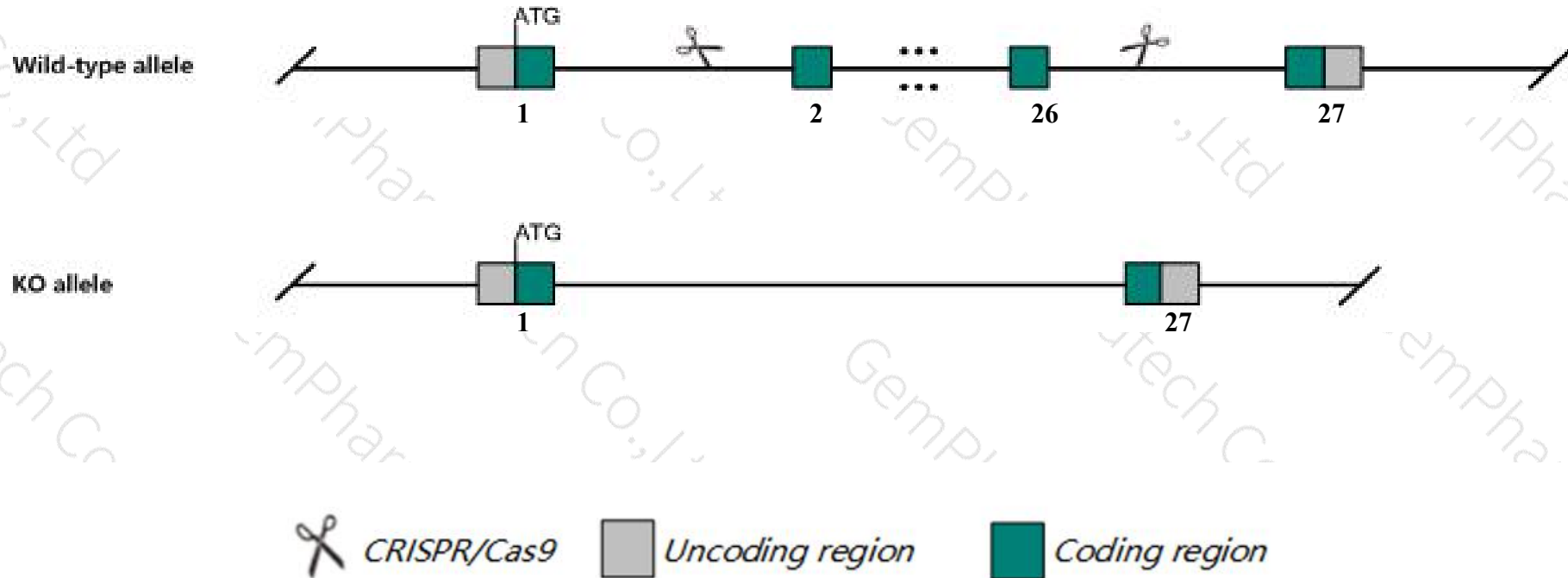
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Inpp5d* gene. The schematic diagram is as follows:



- The *Inpp5d* gene has 11 transcripts. According to the structure of *Inpp5d* gene, exon2-exon26 of *Inpp5d-210* (ENSMUST00000169754.7) transcript is recommended as the knockout region. The region contains 3430bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Inpp5d* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous null mice fail to reject fully mismatched allogeneic marrow grafts, do not develop graft versus host disease, and show enhanced survival after such transplants. Homozygous splice site mutants exhibit wasting, granulocytic lung infiltration and defective cytolysis by NK cells and CTLs.
- The *Inpp5d* gene is located on the Chr1. 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)

Inpp5d inositol polyphosphate-5-phosphatase D [*Mus musculus* (house mouse)]

Gene ID: 16331, updated on 12-Aug-2019

Summary

- Official Symbol** Inpp5d provided by [MGI](#)
- Official Full Name** inositol polyphosphate-5-phosphatase D provided by [MGI](#)
- Primary source** [MGI:MGI:107357](#)
- See related** [Ensembl:ENSMUSG00000026288](#)
- 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** SHIP; SHIP1; SHIP-1; s-SHIP; SIP-145; p150Ship
- Expression** Broad expression in spleen adult (RPKM 30.1), genital fat pad adult (RPKM 21.2) and 20 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 1 D; 1 44.44 cM

See Inpp5d in [Genome Data Viewer](#)

Exon count: 29

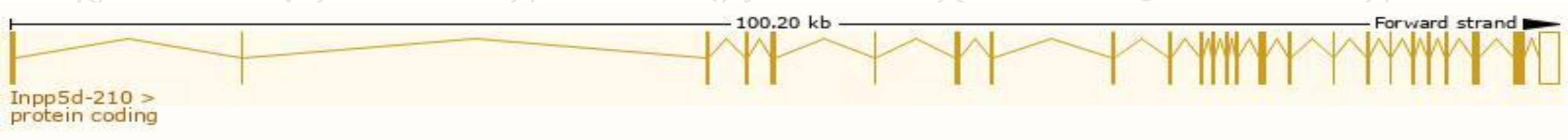
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	1	NC_000067.6 (87620312..87720510)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	1	NC_000067.5 (89516887..89617083)

Transcript information (Ensembl)

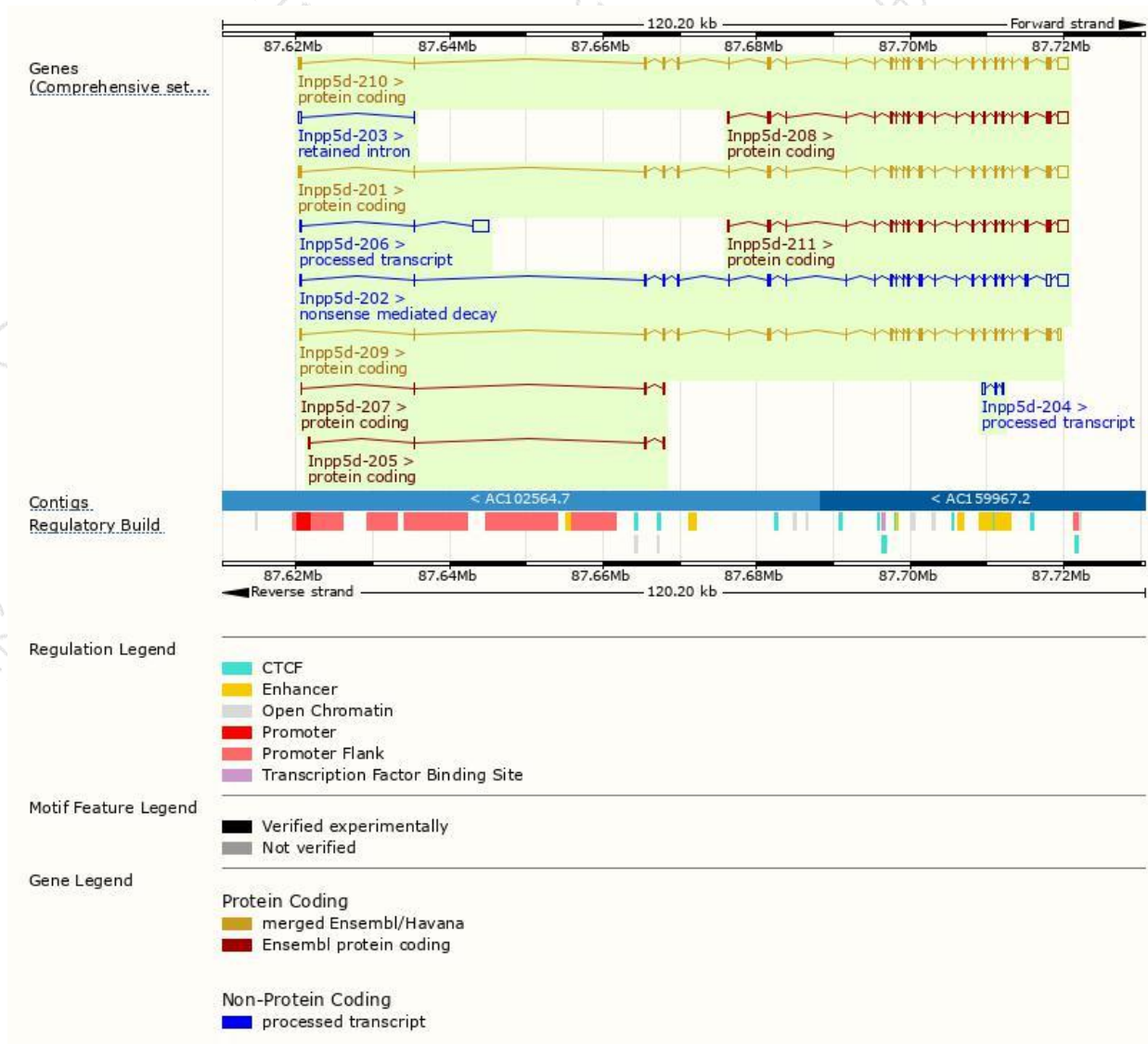
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Inpp5d-210	ENSMUST00000169754.7	4937	1191aa	Protein coding	CCDS35655	Q9ES52	TSL:1 GENCODE basic APPRIS P3
Inpp5d-201	ENSMUST00000442275.14	4880	1190aa	Protein coding	CCDS48311	Q9ES52	TSL:1 GENCODE basic APPRIS ALT2
Inpp5d-209	ENSMUST00000168783.7	3854	1130aa	Protein coding	CCDS48310	Q9ES52	TSL:1 GENCODE basic APPRIS ALT2
Inpp5d-208	ENSMUST00000167032.1	4125	928aa	Protein coding	-	Q9ES52	TSL:2 GENCODE basic
Inpp5d-211	ENSMUST00000170300.7	3942	867aa	Protein coding	-	Q9ES52	TSL:2 GENCODE basic
Inpp5d-207	ENSMUST00000165554.1	370	124aa	Protein coding	-	F7BZA7	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
Inpp5d-205	ENSMUST00000163576.1	344	35aa	Protein coding	-	E9Q752	CDS 3' incomplete TSL:3
Inpp5d-202	ENSMUST00000072999.12	4677	959aa	Nonsense mediated decay	-	Q9ES52	TSL:1
Inpp5d-206	ENSMUST00000164592.7	2480	No protein	Processed transcript	-	-	TSL:1
Inpp5d-204	ENSMUST00000163548.1	577	No protein	Processed transcript	-	-	TSL:2
Inpp5d-203	ENSMUST00000163222.1	364	No protein	Retained intron	-	-	TSL:2

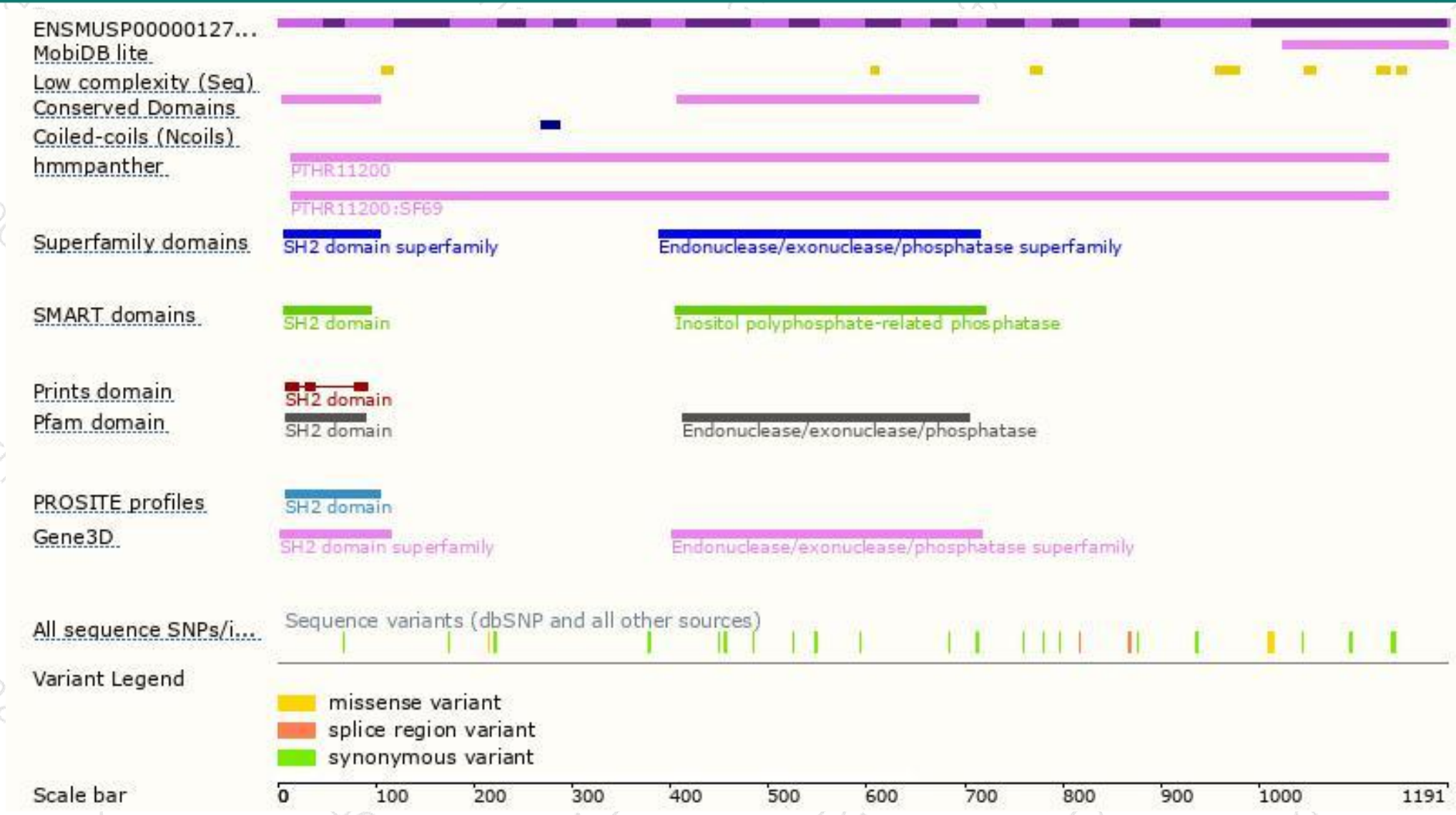
The strategy is based on the design of *Inpp5d-210* transcript,The transcription is shown below



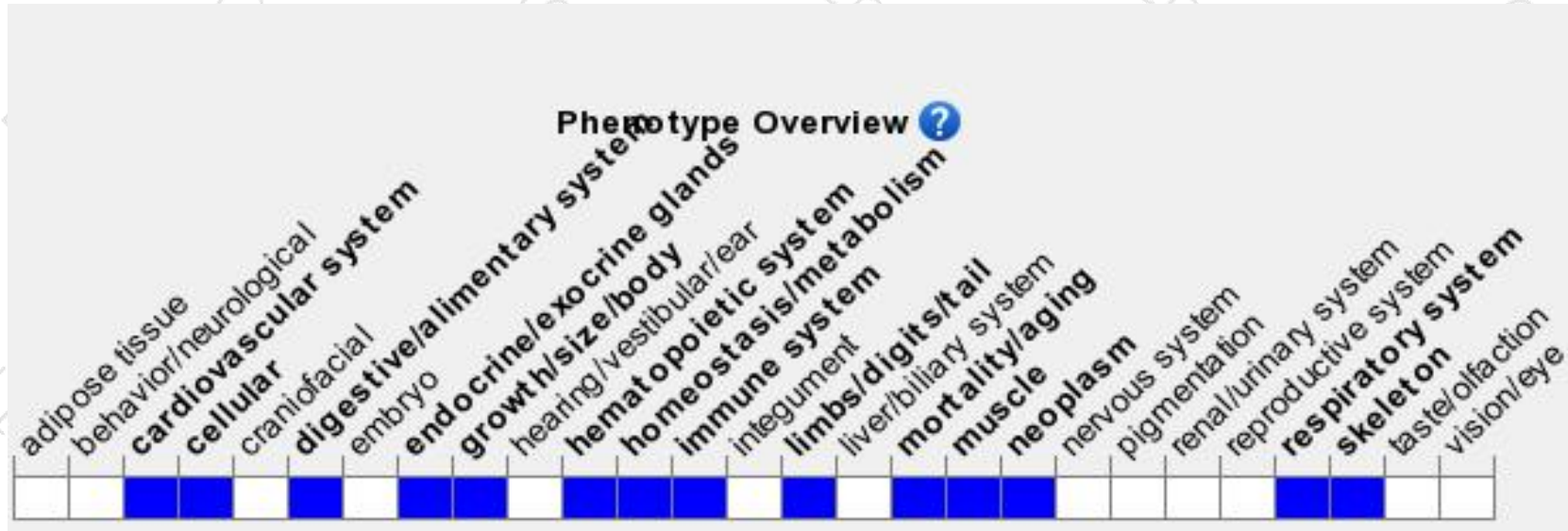
Genomic location distribution



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, Homozygous null mice fail to reject fully mismatched allogeneic marrow grafts, do not develop graft versus host disease, and show enhanced survival after such transplants. Homozygous splice site mutants exhibit wasting, granulocytic lung infiltration and defective cytotoxicity by NK cells and CTLs.

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

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