Ift80 Cas9-CKO *Strategy*

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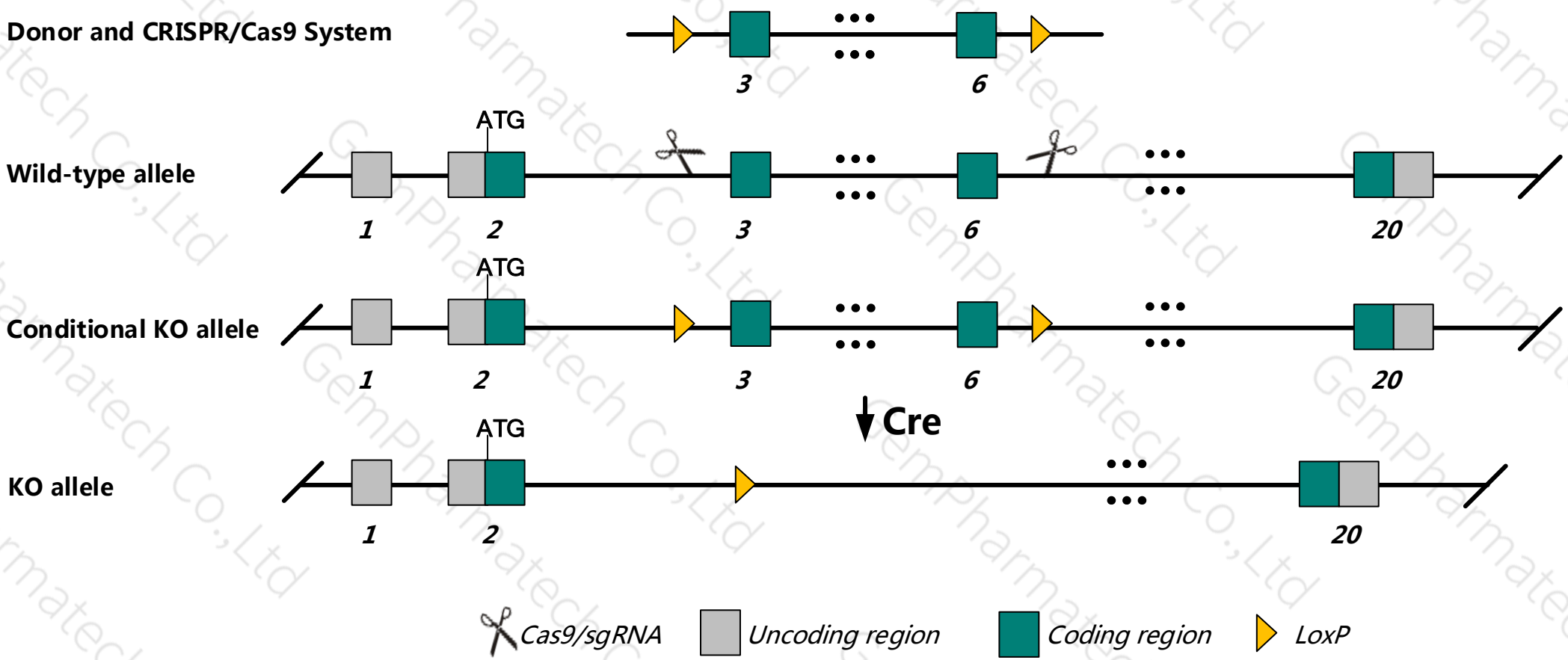
Project Overview

Project Name	***Ift80***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ift80* gene. The schematic diagram is as follows:



Technical routes

- The *Ift80* gene has12 transcripts.According to the structure of *Ift80* gene, exon3-exon6 of *Ift80*-202 (ENSMUST00000107812.7) transcript is recommended as the knockout region.The region contains 512bp coding sequence.Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Ift80* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed.Cas9, sgRNA and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice.Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- The flox mice was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues or cell types.

Notice

- According to the existing MGI data，Mice homozygous for a hypomorphic gene trap allele exhibit partial perinatal lethality, decreased body size, postnatal growth retardation, shortened long bones, constricted thoracic cage, periaxial polydactyly, and small cranium.
- The *Ift80* gene is located on the Chr3. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information （NCBI）

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Ift80 intraflagellar transport 80 [*Mus musculus* (house mouse)]

Gene ID: 68259, updated on 12-May-2019

Summary

Official Symbol	Ift80 provided by MGI
Official Full Name	intraflagellar transport 80 provided by MGI
Primary source	MGI:MGI:1915509
See related	Ensembl:ENSMUSG00000027778
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	Wdr56; mKIAA1374; 4921524P20Rik
Expression	Broad expression in testis adult (RPKM 8.7), CNS E11.5 (RPKM 6.3) and 21 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

The gene has 12 transcripts, and all transcripts are shown below:

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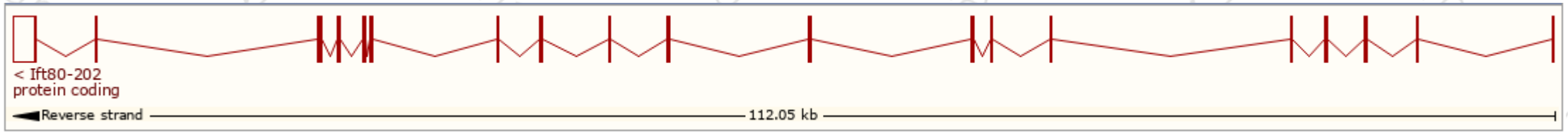
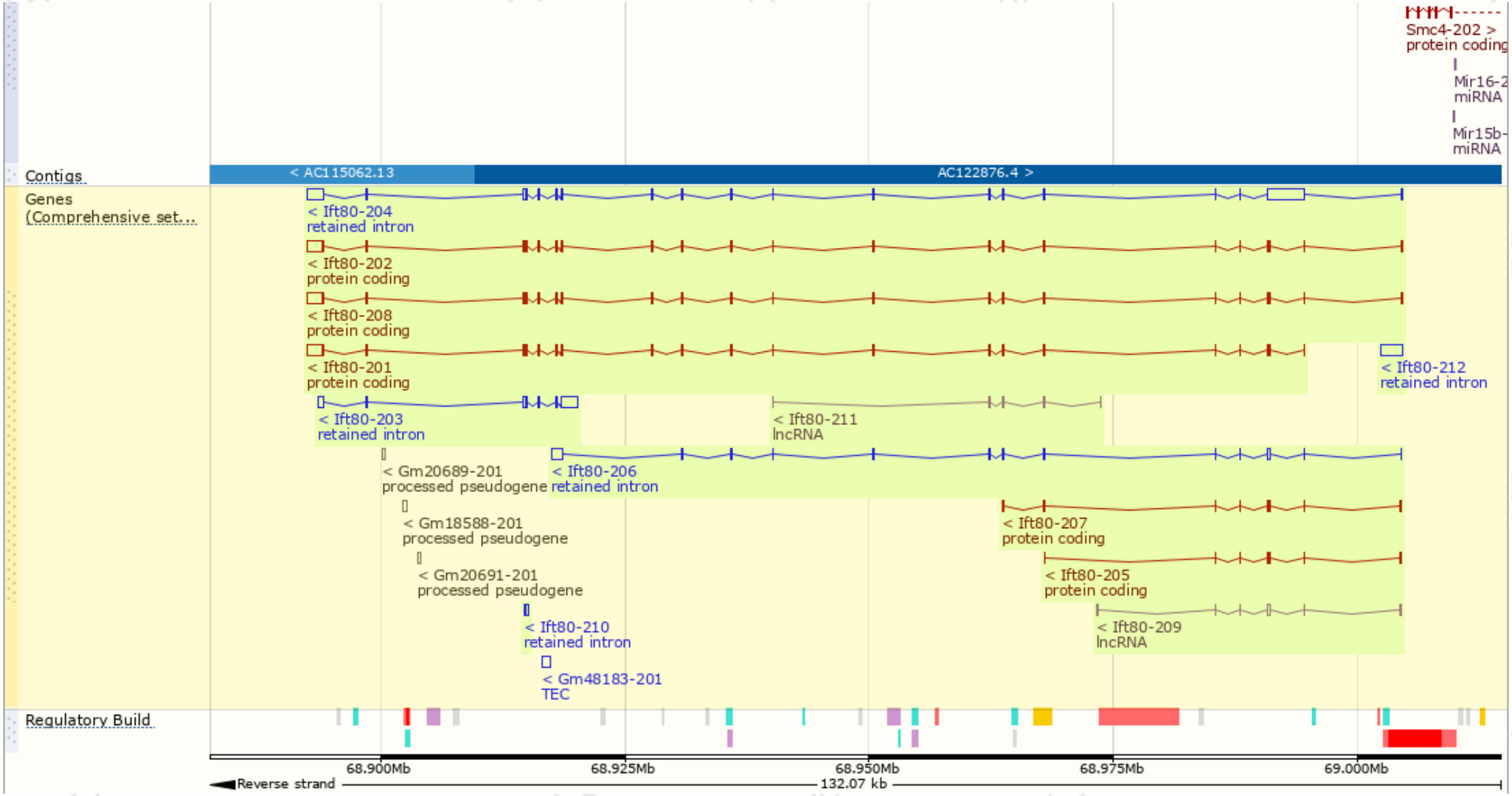
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ift80-202	ENSMUST00000107812.7	4063	777aa	Protein coding	CCDS38451	Q8K057	TSL:5 GENCODE basic APPRIS P1
Ift80-201	ENSMUST00000029347.13	3880	777aa	Protein coding	CCDS38451	Q8K057	TSL:5 GENCODE basic APPRIS P1
Ift80-208	ENSMUST00000169064.7	4064	777aa	Protein coding	-	Q8K057	TSL:1 GENCODE basic APPRIS P1
Ift80-207	ENSMUST00000154741.7	755	209aa	Protein coding	-	D3YWI8	CDS 3' incomplete TSL:5
Ift80-205	ENSMUST00000148031.1	741	158aa	Protein coding	-	D3Z157	CDS 3' incomplete TSL:5
Ift80-204	ENSMUST00000136448.7	7616	No protein	Retained intron	-	-	TSL:2
Ift80-203	ENSMUST00000136176.1	2860	No protein	Retained intron	-	-	TSL:1
Ift80-206	ENSMUST00000152502.7	2608	No protein	Retained intron	-	-	TSL:5
Ift80-212	ENSMUST00000192467.1	2231	No protein	Retained intron	-	-	TSL:NA
Ift80-210	ENSMUST00000176189.1	241	No protein	Retained intron	-	-	TSL:3
Ift80-209	ENSMUST00000176135.1	653	No protein	lncRNA	-	-	TSL:3
Ift80-211	ENSMUST00000176754.1	525	No protein	lncRNA	-	-	TSL:2

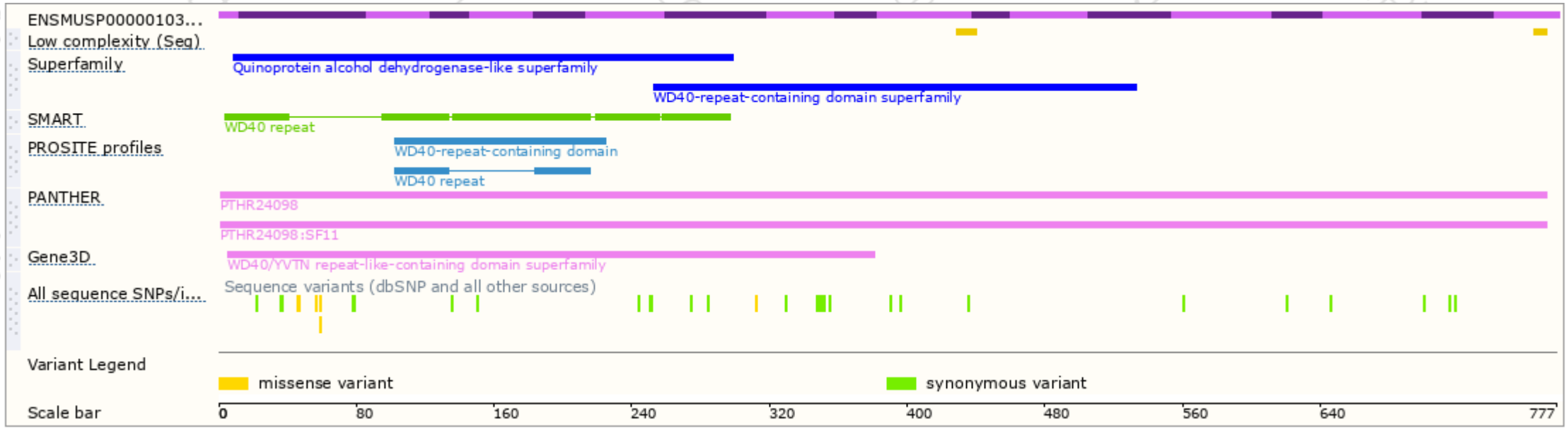
The strategy is based on the design of *Ift80*-202 transcript,The transcription is shown below



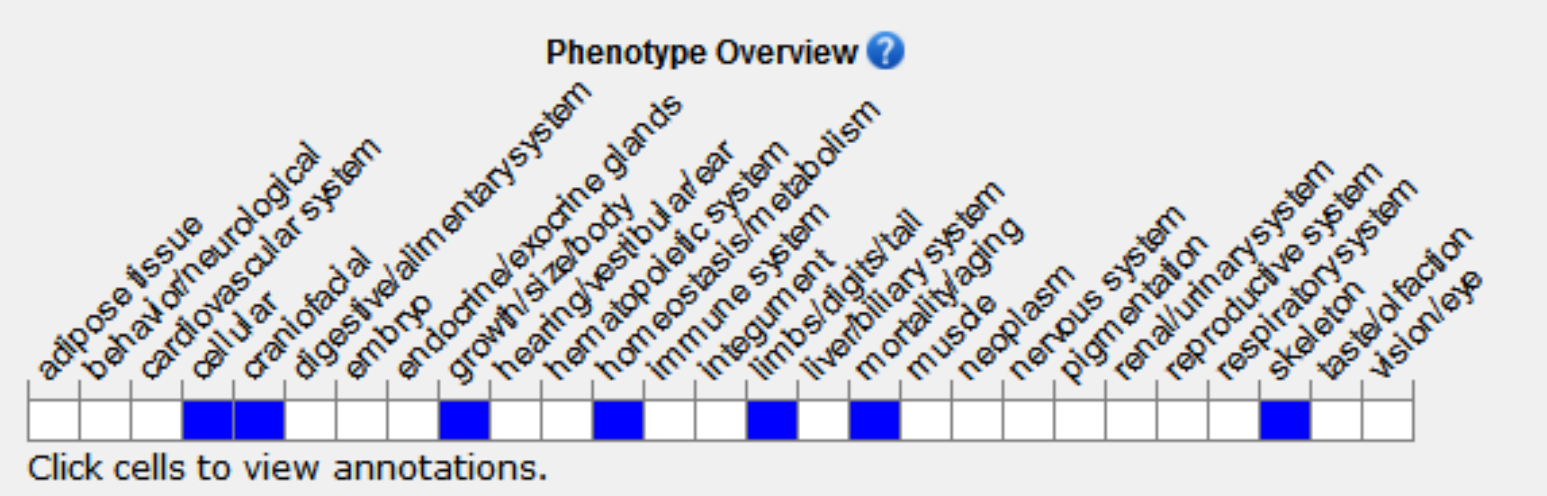
Genomic location distribution



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 hypomorphic gene trap allele exhibit partial perinatal lethality, decreased body size, postnatal growth retardation, shortened long bones, constricted thoracic cage, periaxial polydactyly, and small cranium.

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

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