

Ap3b1 Cas9-CKO Strategy

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Project Overview

Project Name

Ap3b1

Project type

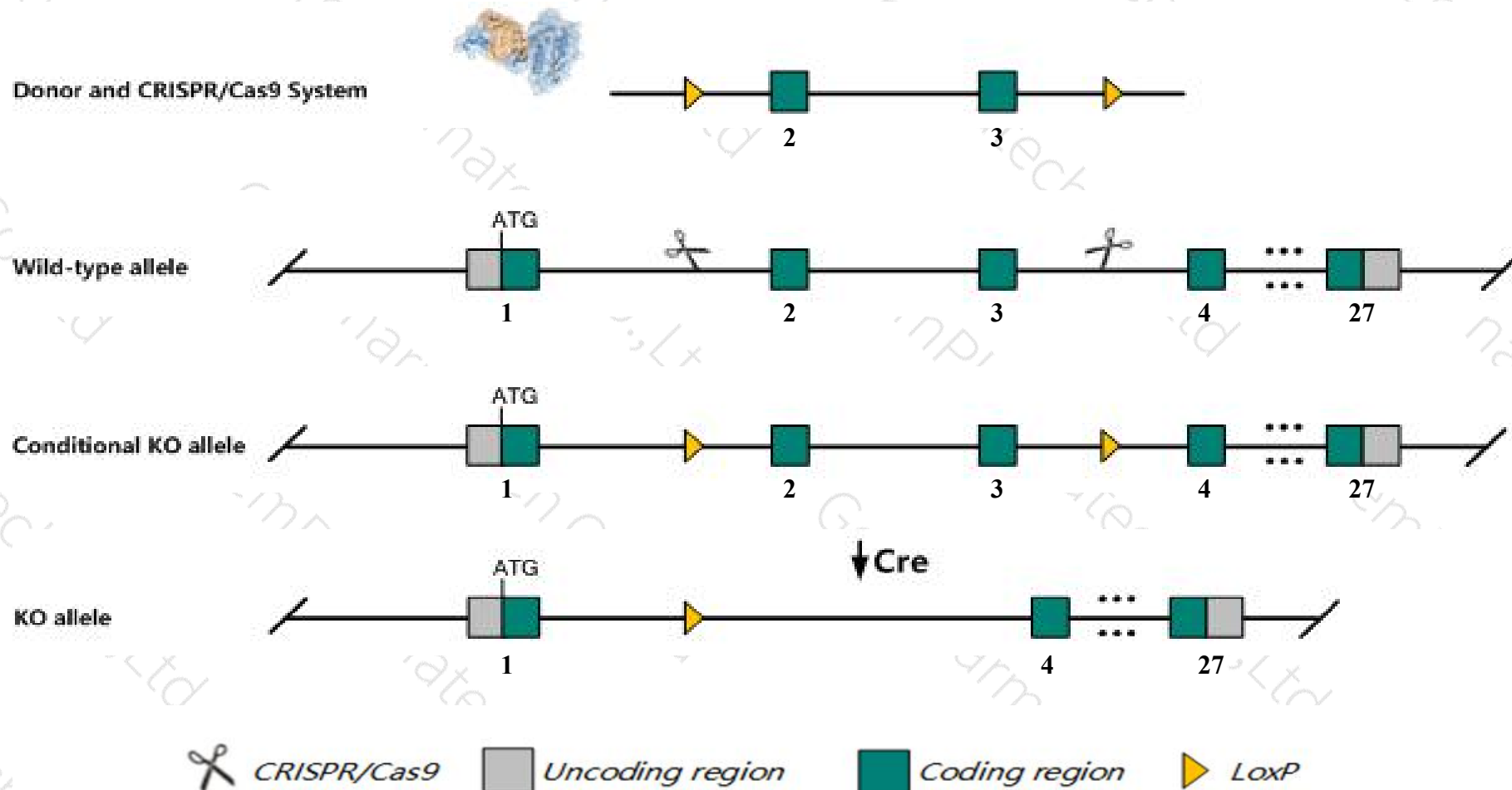
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ap3b1* gene. The schematic diagram is as follows:



Technical routes

- The *Ap3b1* gene has 5 transcripts. According to the structure of *Ap3b1* gene, exon2-exon3 of *Ap3b1-201* (ENSMUST00000022196.4) transcript is recommended as the knockout region. The region contains 151bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ap3b1* gene. The brief process is as follows: CRISPR/Cas9 system 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 will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, Homozygous mutants exhibit hypopigmentation, elevated kidney levels of lysosomal enzymes, platelet storage pool deficiency, reduced ipsilateral projections from the retina to brain, reduced sensitivity of dark-adapted retina and shortened life span.
- Transcript *Ap3b1*-202&203&204 may not be affected.
- The effect on transcript *Ap3b1*-205 is unknown.
- The *Ap3b1* gene is located on the Chr13. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Ap3b1 adaptor-related protein complex 3, beta 1 subunit [*Mus musculus* (house mouse)]

Gene ID: 11774, updated on 12-Aug-2019

Summary

Official Symbol	Ap3b1 provided by MGI
Official Full Name	adaptor-related protein complex 3, beta 1 subunit provided by MGI
Primary source	MGI:MGI:1333879
See related	Ensembl:ENSMUSG00000021686
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	pe; AP-3; Hps2; rim2; pearl; C78395; beta3A; AU015684
Expression	Ubiquitous expression in testis adult (RPKM 20.5), placenta adult (RPKM 16.4) and 28 other tissues See more
Orthologs	human all

Genomic context

Location: 13 C3; 13 49.22 cM

See Ap3b1 in [Genome Data Viewer](#)

Exon count: 28

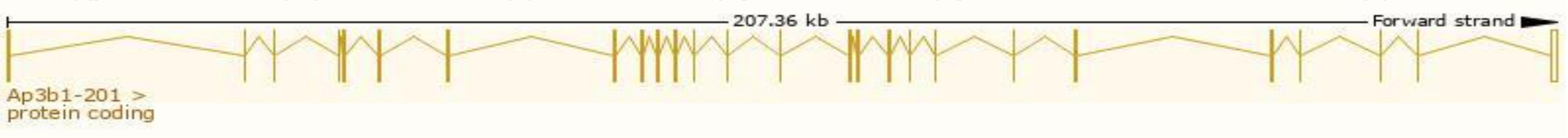
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	13	NC_000079.6 (94358960..94566316)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	13	NC_000079.5 (95128915..95336271)

Transcript information (Ensembl)

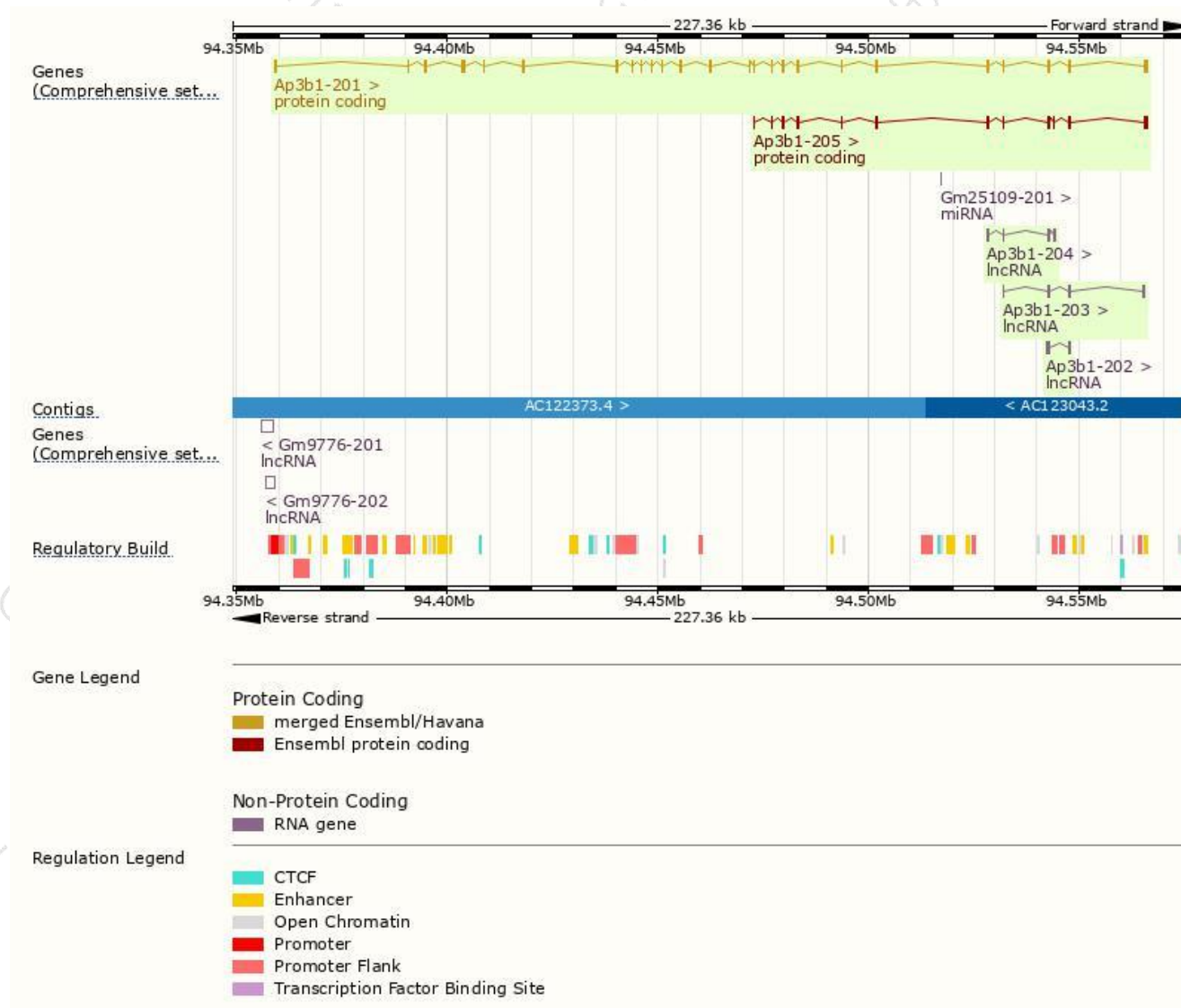
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ap3b1-201	ENSMUST00000022196.4	4021	1105aa	Protein coding	CCDS26693	Q9Z1T1	TSL:1 GENCODE basic APPRIS P1
Ap3b1-205	ENSMUST000000231916.1	2008	484aa	Protein coding	-	A0A338P6V5	CDS 5' incomplete
Ap3b1-204	ENSMUST000000222383.1	579	No protein	lncRNA	-	-	TSL:3
Ap3b1-203	ENSMUST000000221206.1	413	No protein	lncRNA	-	-	TSL:3
Ap3b1-202	ENSMUST000000220505.1	364	No protein	lncRNA	-	-	TSL:5

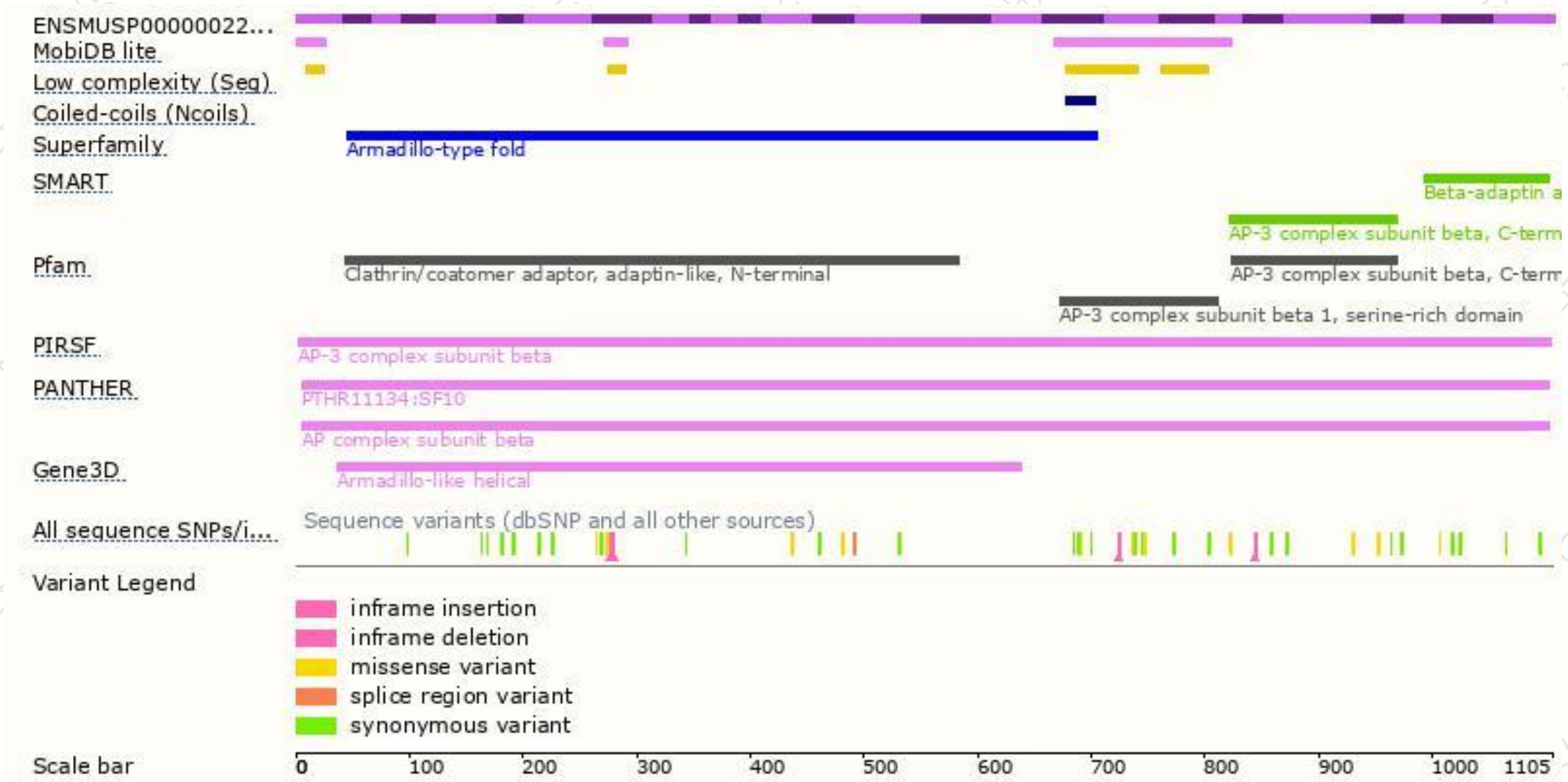
The strategy is based on the design of *Ap3b1-201* transcript,The transcription is shown below



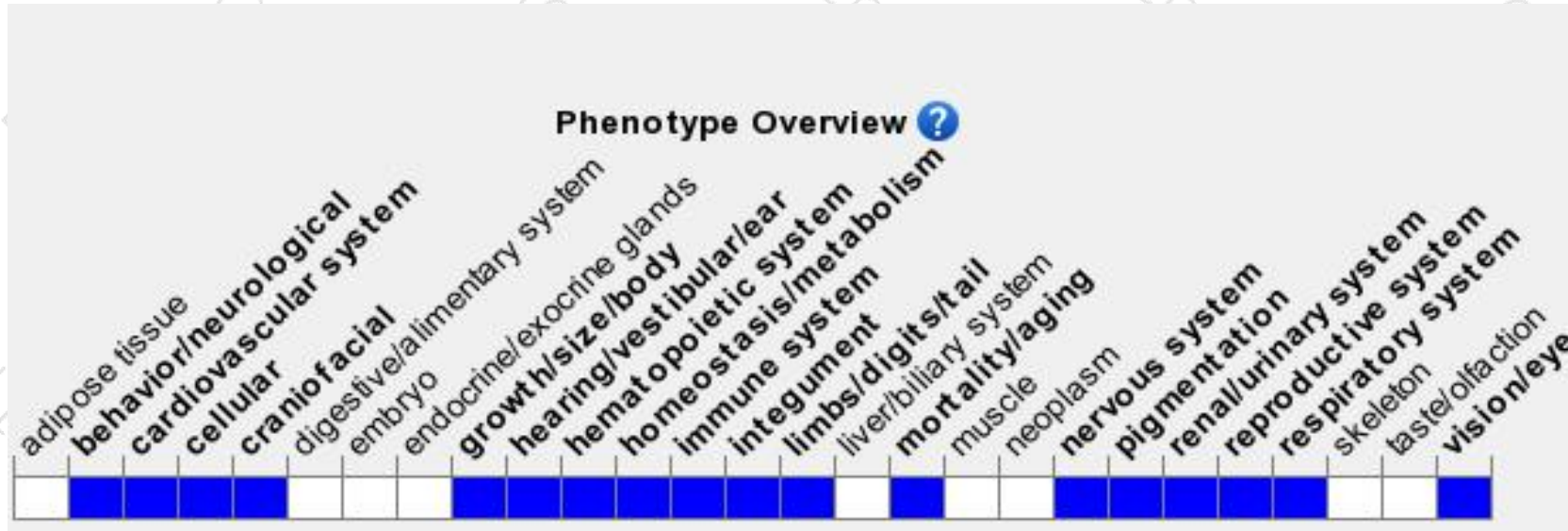
Genomic location distribution



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, Homozygous mutants exhibit hypopigmentation, elevated kidney levels of lysosomal enzymes, platelet storage pool deficiency, reduced ipsilateral projections from the retina to brain, reduced sensitivity of dark-adapted retina and shortened life span.

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

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