

***Kdm1b* Cas9-CKO Strategy**

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Project Overview

Project Name

Kdm1b

Project type

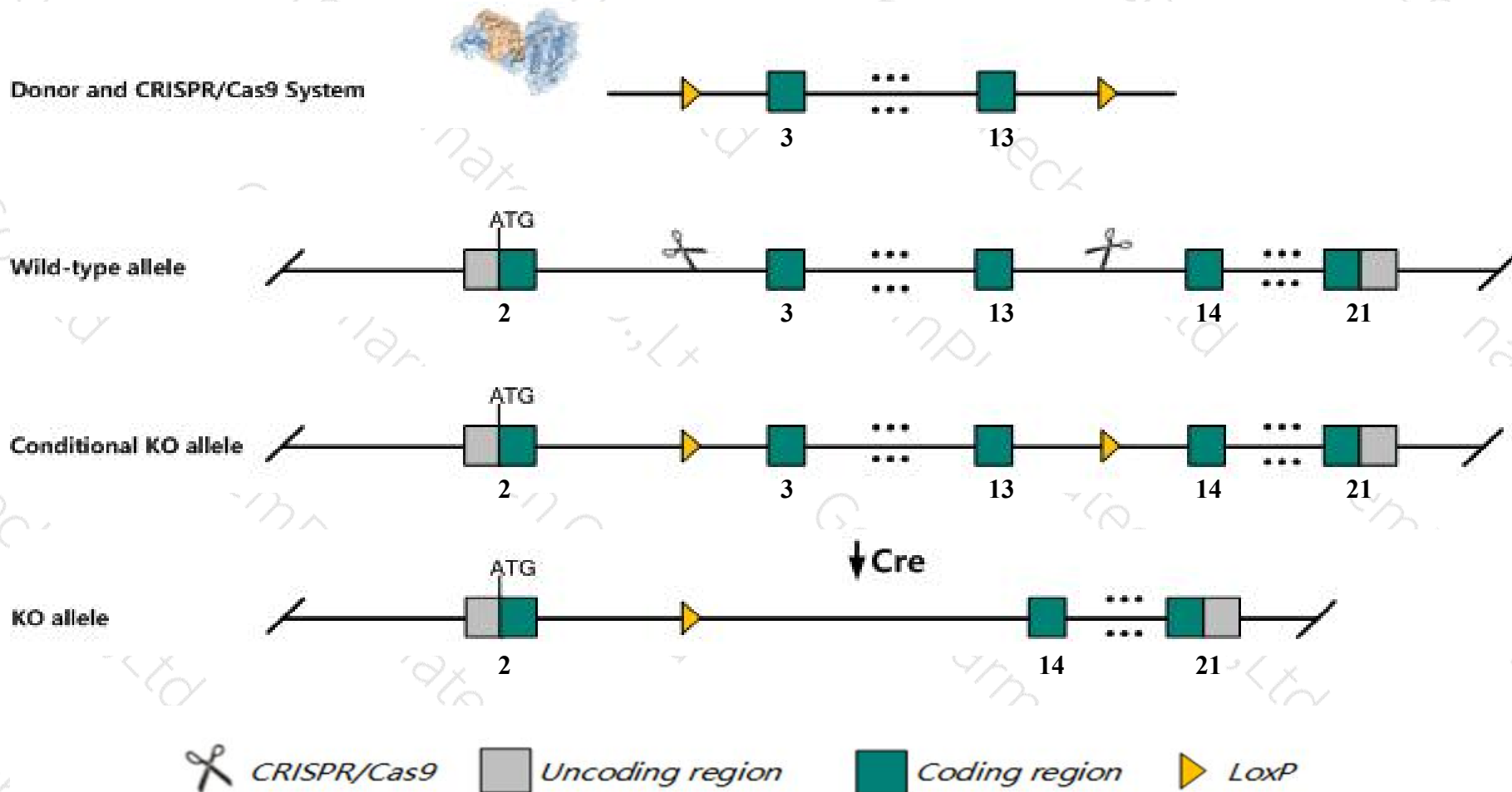
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Kdm1b* gene. The schematic diagram is as follows:



Technical routes

- The *Kdm1b* gene has 5 transcripts. According to the structure of *Kdm1b* gene, exon3-exon13 of *Kdm1b-201* (ENSMUST00000037025.15) transcript is recommended as the knockout region. The region contains 1462bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Kdm1b* 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 null mice of both sexes are viable, grossly normal and male mice are fertile; however, heterozygous progeny of homozygous null mothers display severe placental defects, embryonic growth impairment, neural tube defects and pericardial edema, and do not survive past E10.5.
- The floxed region is near to the N-terminal of *Tpmt* gene, this strategy may influence the regulatory function of the N-terminal of *Tpmt* gene.
- The *Kdm1b* 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)

Kdm1b lysine (K)-specific demethylase 1B [*Mus musculus* (house mouse)]

Gene ID: 218214, updated on 10-Oct-2019

Summary

- Official Symbol** Kdm1b provided by [MGI](#)
- Official Full Name** lysine (K)-specific demethylase 1B provided by [MGI](#)
- Primary source** [MGI:MGI:2145261](#)
- See related** [Ensembl:ENSMUSG00000038080](#)
- 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** Aof1; AI482520; 4632428N09Rik
- Expression** Ubiquitous expression in bladder adult (RPKM 25.1), liver E14 (RPKM 13.2) and 27 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 13; 13 A5 See Kdm1b in [Genome Data Viewer](#)

Exon count: 23

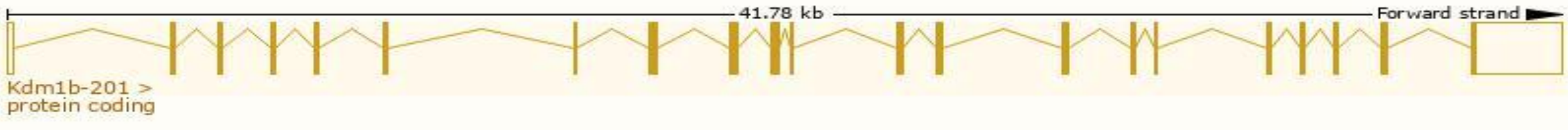
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	13	NC_000079.6 (47043373..47085279)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	13	NC_000079.5 (47138908..47179982)

Transcript information (Ensembl)

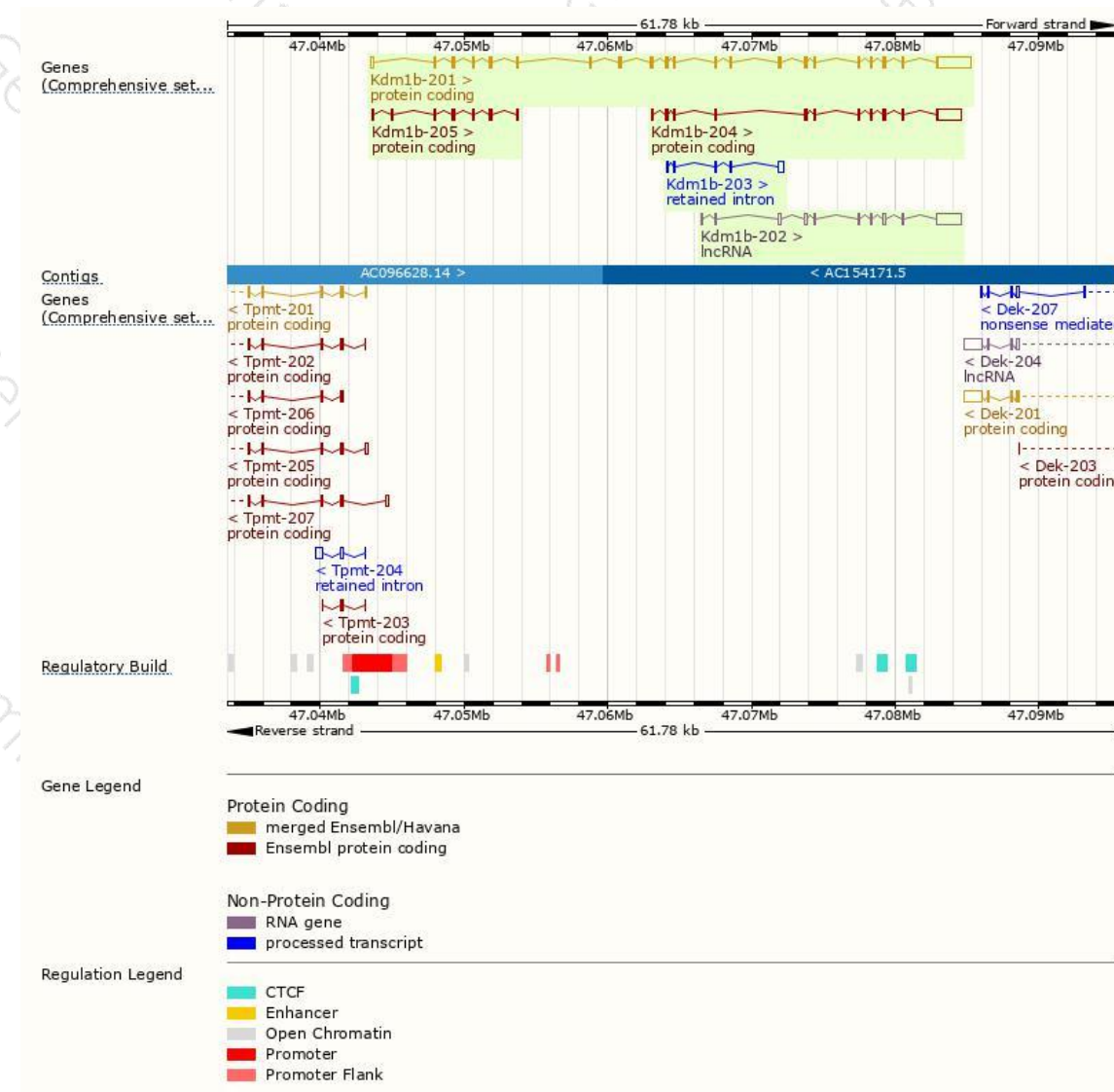
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Kdm1b-201	ENSMUST00000037025.15	4987	826aa	Protein coding	CCDS26489	Q8CIG3	TSL:1 GENCODE basic APPRIS P1
Kdm1b-204	ENSMUST00000143518.2	2969	443aa	Protein coding	-	F6V3V2	CDS 5' incomplete TSL:1
Kdm1b-205	ENSMUST00000143868.1	736	176aa	Protein coding	-	D3Z353	CDS 3' incomplete TSL:3
Kdm1b-203	ENSMUST00000131120.7	870	No protein	Retained intron	-	-	TSL:3
Kdm1b-202	ENSMUST00000128977.2	2876	No protein	lncRNA	-	-	TSL:1

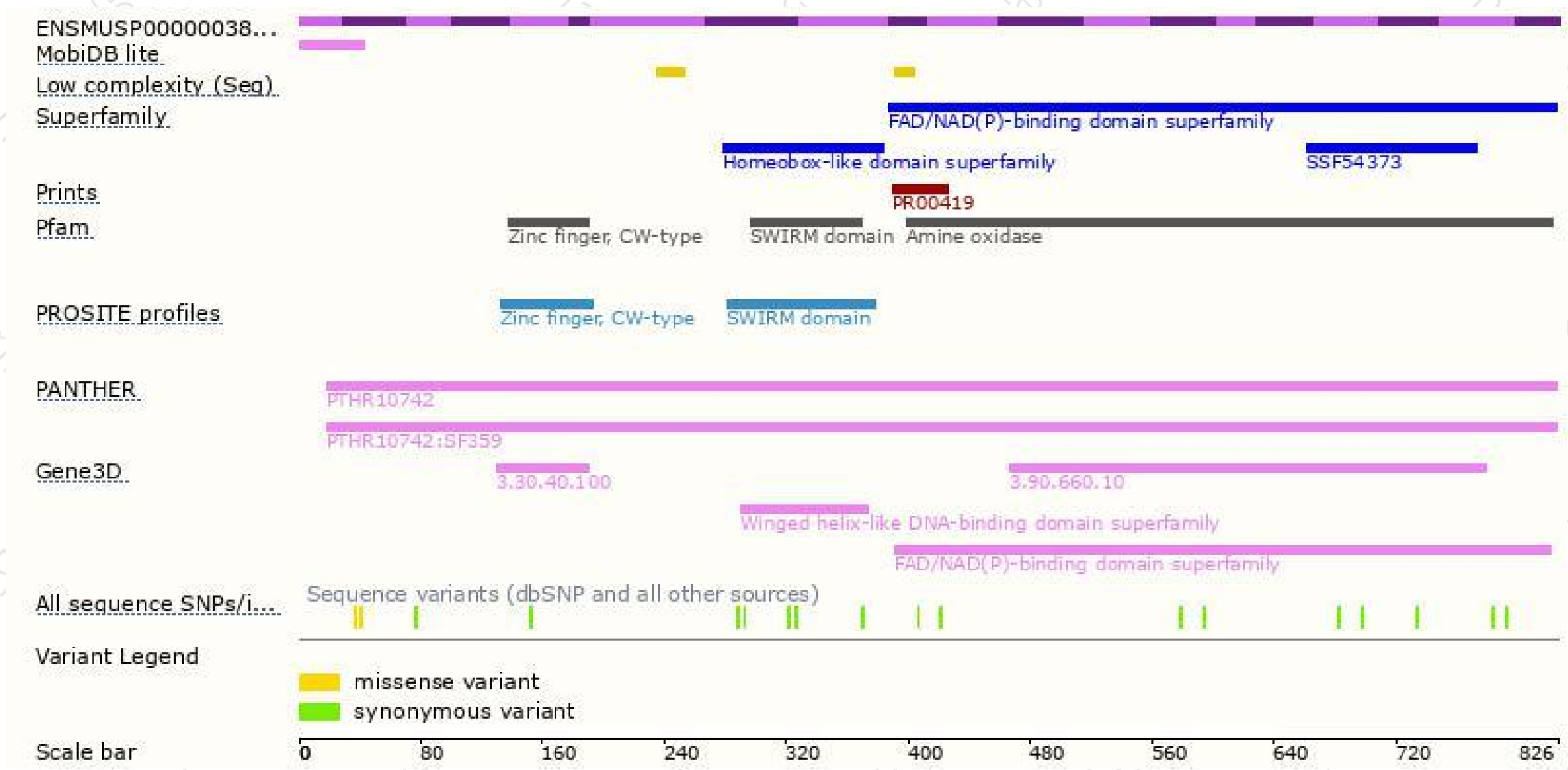
The strategy is based on the design of *Kdm1b-201* transcript,The transcription is shown below



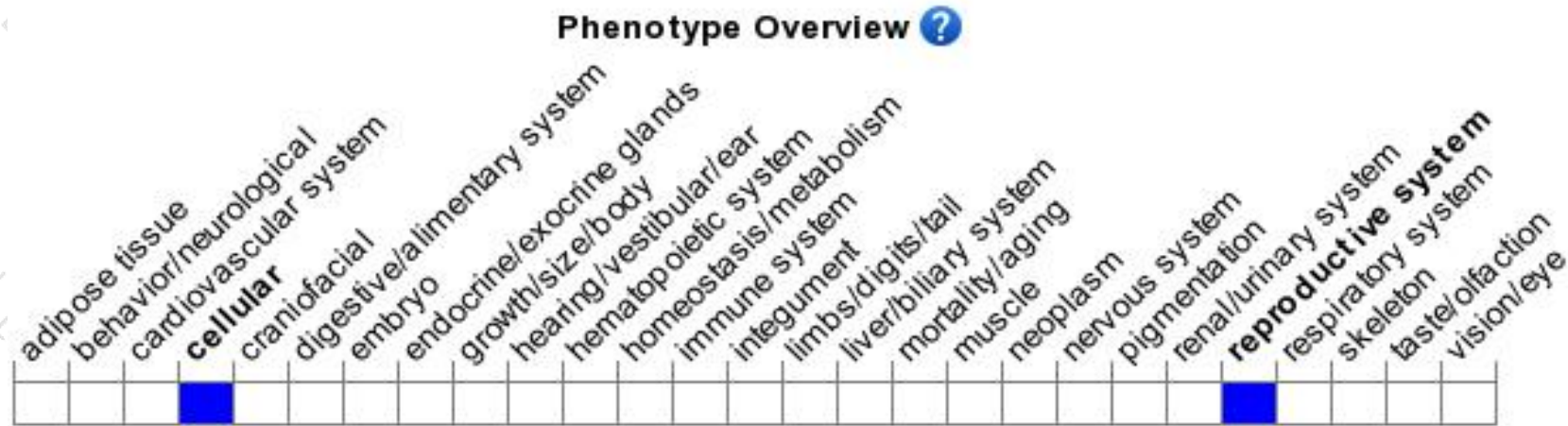
Genomic location distribution



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 null mice of both sexes are viable, grossly normal and male mice are fertile; however, heterozygous progeny of homozygous null mothers display severe placental defects, embryonic growth impairment, neural tube defects and pericardial edema, and do not survive past E10.5.

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

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