

Lztr1 Cas9-CKO Strategy

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Project Overview

Project Name

Lztr1

Project type

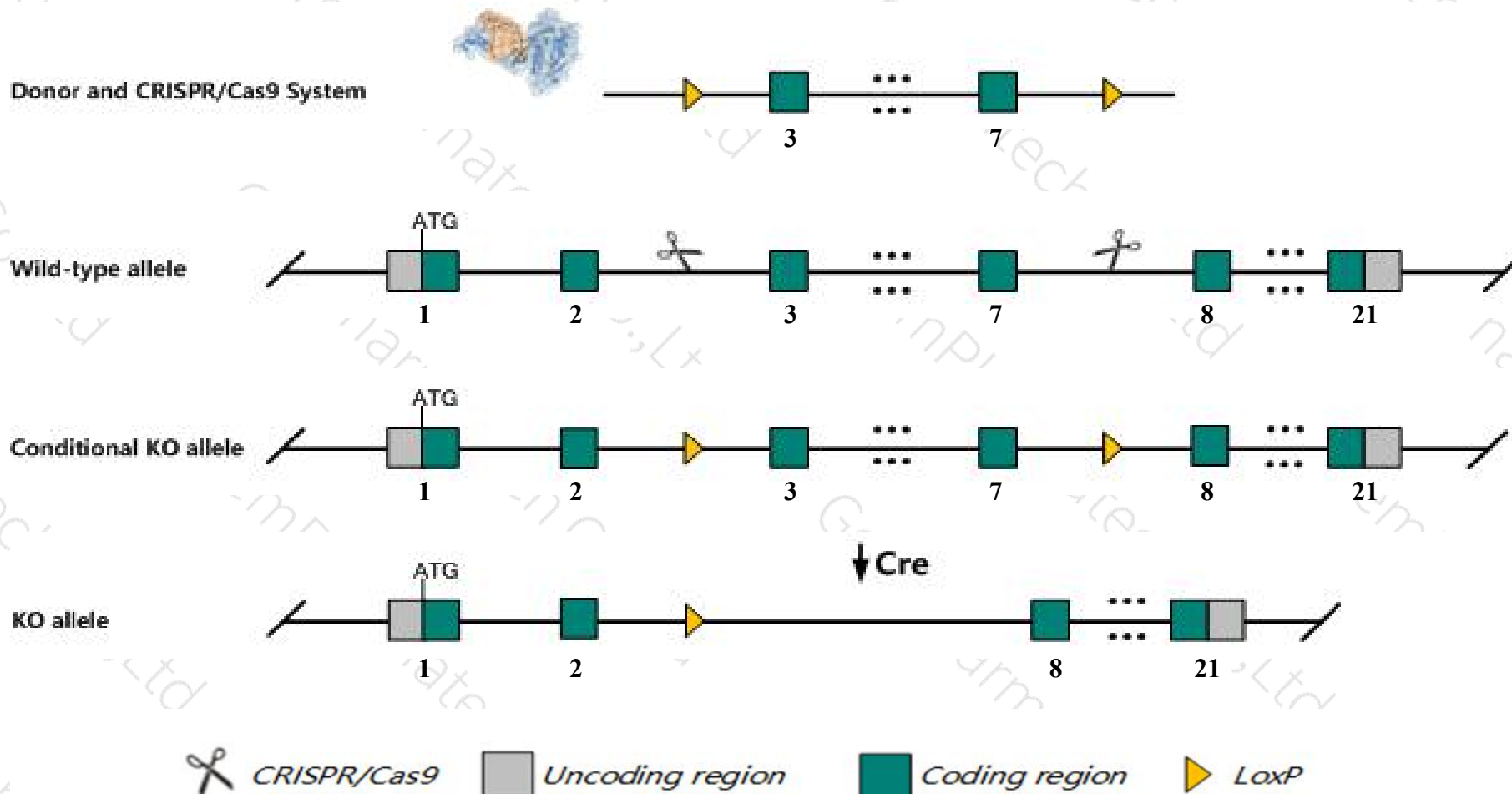
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Lztr1* gene. The schematic diagram is as follows:



Technical routes

- The *Lztr1* gene has 14 transcripts. According to the structure of *Lztr1* gene, exon3-exon7 of *Lztr1*-201 (ENSMUST00000023444.10) transcript is recommended as the knockout region. The region contains 388bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Lztr1* 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.

- The *Lztr1* gene is located on the Chr16. 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.
- Transcript *Lztr1*-202&207&2018&213 may not be affected . And the effect on transcript *Lztr1*-204 is unknown.
- 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)

Lztr1 leucine-zipper-like transcriptional regulator, 1 [Mus musculus (house mouse)]

Gene ID: 66863, updated on 19-Mar-2019

Summary



Official Symbol Lztr1 provided by [MGI](#)

Official Full Name leucine-zipper-like transcriptional regulator, 1 provided by [MGI](#)

Primary source [MGI:MGI:1914113](#)

See related [Ensembl:ENSMUSG00000022761](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as 1200003E21Rik, AI591627, AW550890

Summary This gene encodes a member of the BR-C, ttk and bab-kelch superfamily that, in humans, localizes to the Golgi network and is associated with the ras / mitogen-activated protein kinase pathway. Loss-of-function mutations in the human ortholog are associated with glioblastoma multiforme, schwannomatosis, Noonan syndrome, and DiGeorge syndrome. [provided by RefSeq, Sep 2016]

Expression Ubiquitous expression in ovary adult (RPKM 35.0), CNS E18 (RPKM 32.2) and 28 other tissues [See more](#)

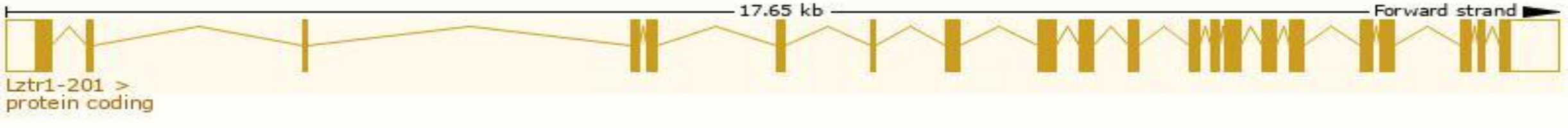
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

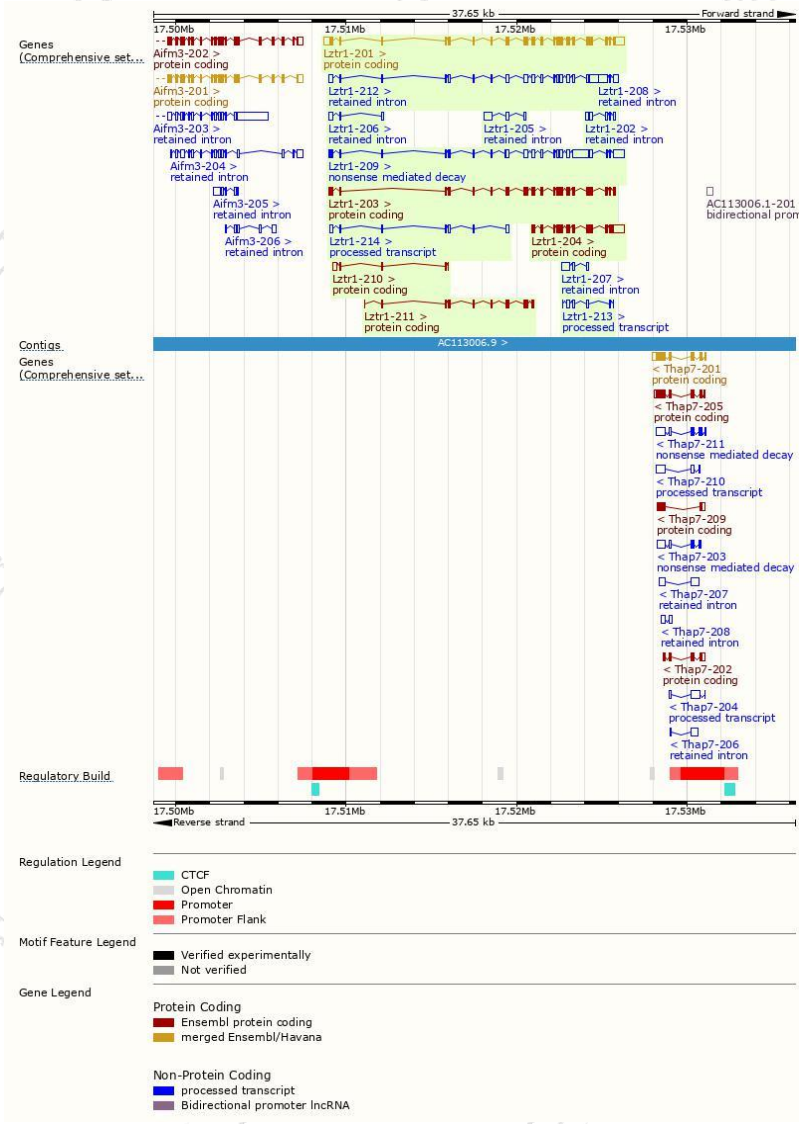
The gene has 14 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lztr1-201	ENSMUST00000023444.10	3394	837aa	Protein coding	CCDS37272	Q9CQ33	TSL:1 GENCODE basic APPRIS P2
Lztr1-203	ENSMUST00000231292.1	2491	818aa	Protein coding	-	A0A338P6P0	GENCODE basic APPRIS ALT 2
Lztr1-204	ENSMUST00000231307.1	2214	529aa	Protein coding	-	A0A338P6Y5	CDS 5' incomplete
Lztr1-211	ENSMUST00000232372.1	902	280aa	Protein coding	-	A0A338P686	CDS 3' incomplete
Lztr1-210	ENSMUST00000232242.1	463	58aa	Protein coding	-	A0A338P6T8	CDS 3' incomplete
Lztr1-209	ENSMUST00000231994.1	3809	225aa	Nonsense mediated decay	-	A0A338P687	
Lztr1-214	ENSMUST00000232644.1	722	No protein	Processed transcript	-	-	
Lztr1-213	ENSMUST00000232438.1	595	No protein	Processed transcript	-	-	
Lztr1-212	ENSMUST00000232379.1	2621	No protein	Retained intron	-	-	
Lztr1-208	ENSMUST00000231746.1	906	No protein	Retained intron	-	-	
Lztr1-207	ENSMUST00000231684.1	774	No protein	Retained intron	-	-	
Lztr1-205	ENSMUST00000231326.1	742	No protein	Retained intron	-	-	
Lztr1-202	ENSMUST00000231230.1	595	No protein	Retained intron	-	-	
Lztr1-206	ENSMUST00000231538.1	469	No protein	Retained intron	-	-	

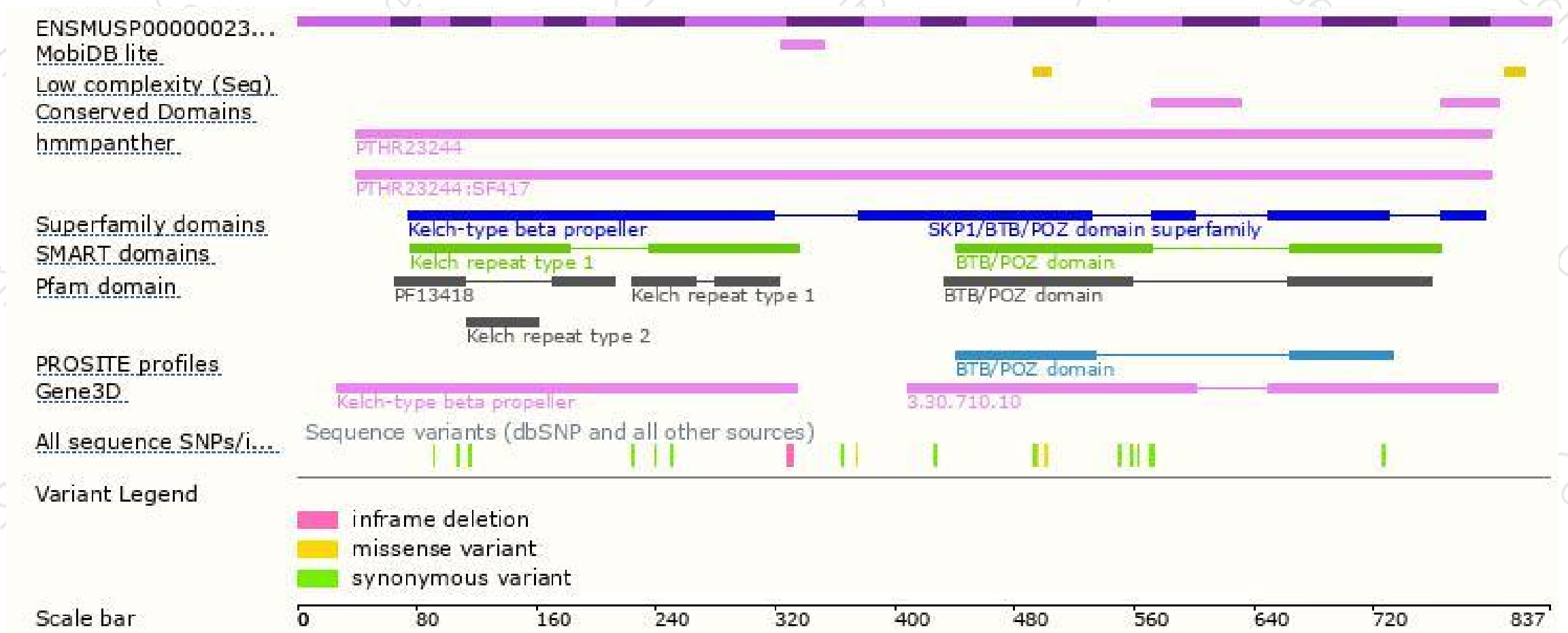
The strategy is based on the design of *Lztr1-201* transcript,The transcription is shown below



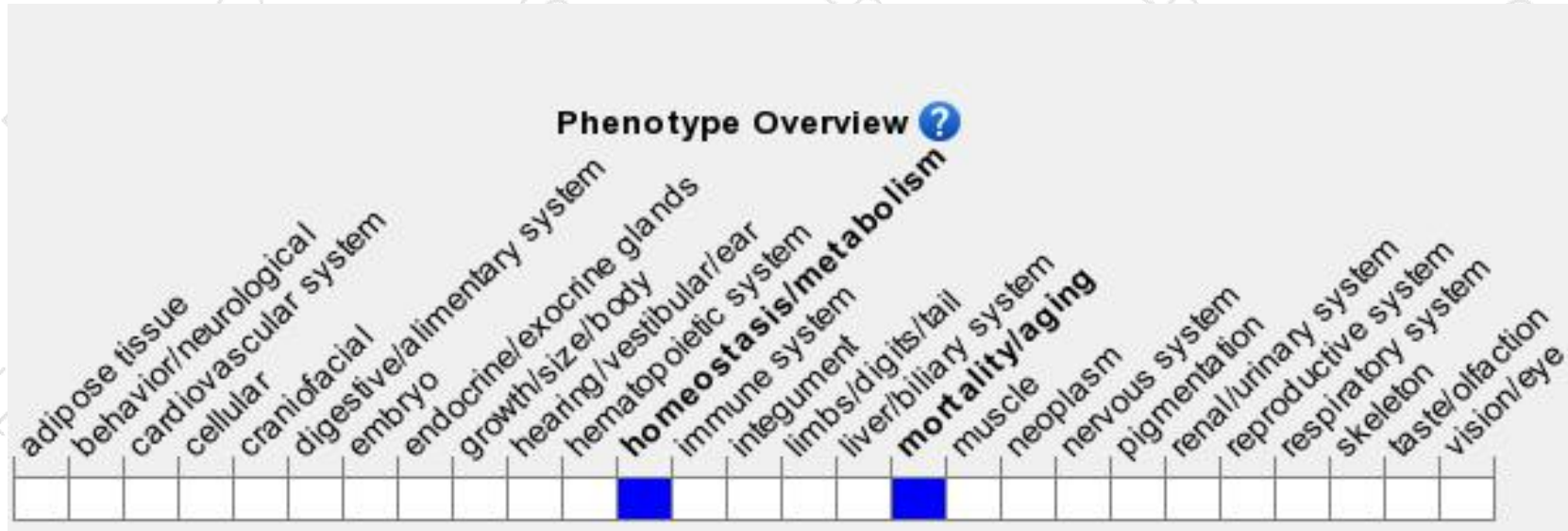
Genomic location distribution



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/>).

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

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