

Map2k7 Cas9-CKO Strategy

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Project Overview

Project Name

Map2k7

Project type

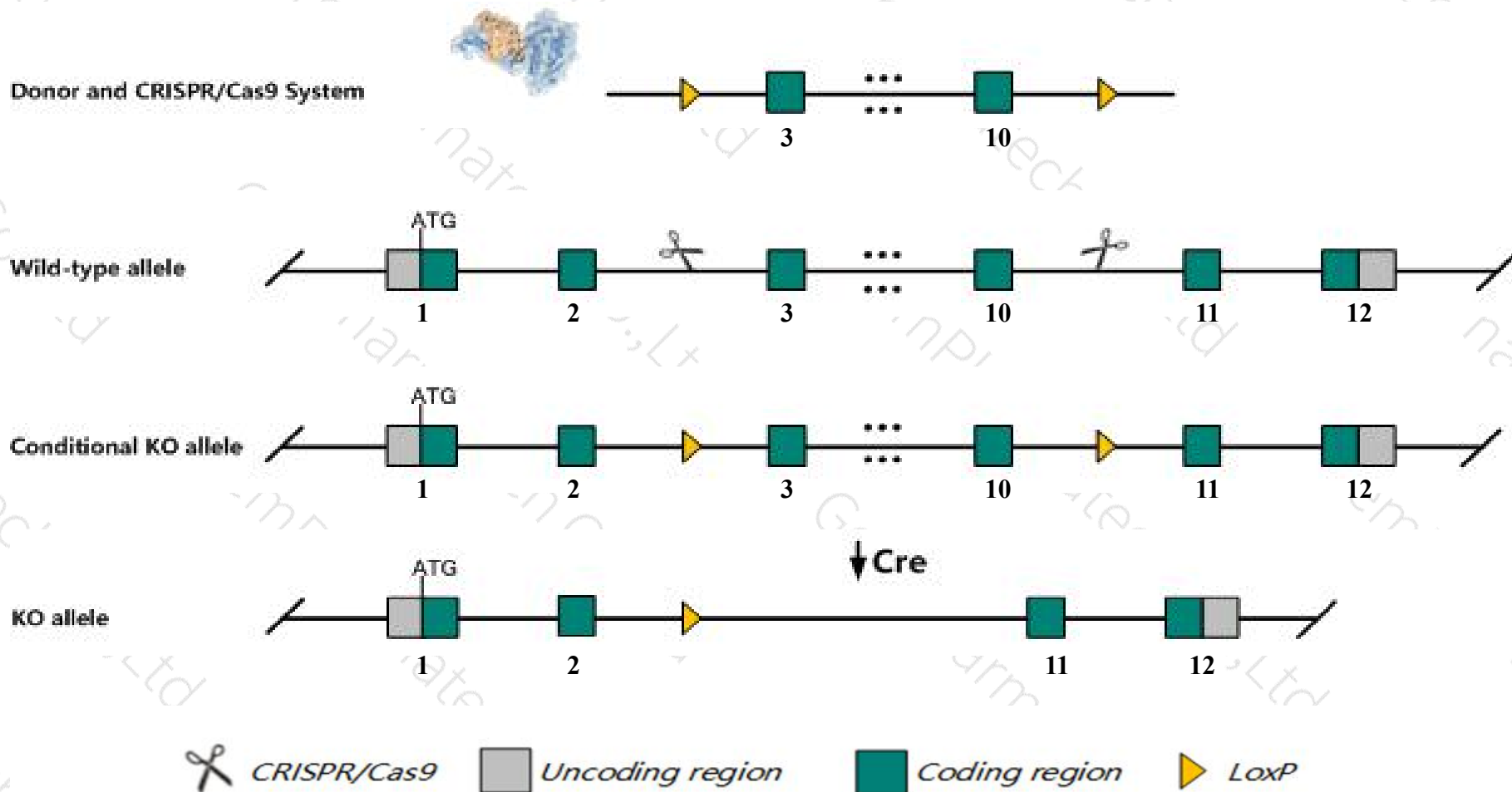
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Map2k7* gene. The schematic diagram is as follows:



- The *Map2k7* gene has 10 transcripts. According to the structure of *Map2k7* gene, exon3-exon10 of *Map2k7-201* (ENSMUST00000003027.13) transcript is recommended as the knockout region. The region contains 955bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Map2k7* 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, Mice homozygous for disruptions in this gene die during embryogenesis.
- The knockout region near to the 5'UTR of Tgfbr31 gene. Knockout the region may affect the regulatory function of the 5'UTR of Tgfbr31 gene.
- The Gm49320 gene will be deleted together in this strategy.
- The *Map2k7* gene is located on the Chr8. 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)

Map2k7 mitogen-activated protein kinase kinase 7 [Mus musculus (house mouse)]

Gene ID: 26400, updated on 23-Feb-2019

Summary



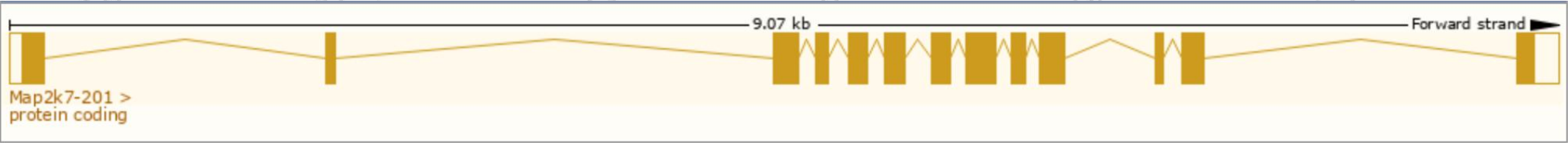
Official Symbol	Map2k7 provided by MGI
Official Full Name	mitogen-activated protein kinase kinase 7 provided by MGI
Primary source	MGI:MGI:1346871
See related	Ensembl:ENSMUSG00000002948
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	5930412N11Rik, JNKK 2, Jnkk2, MAPKK 7, MEK 7, Mapkk7, Mek7, Mkk7, Prkmk7, sek2
Expression	Ubiquitous expression in testis adult (RPKM 34.8), adrenal adult (RPKM 26.2) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

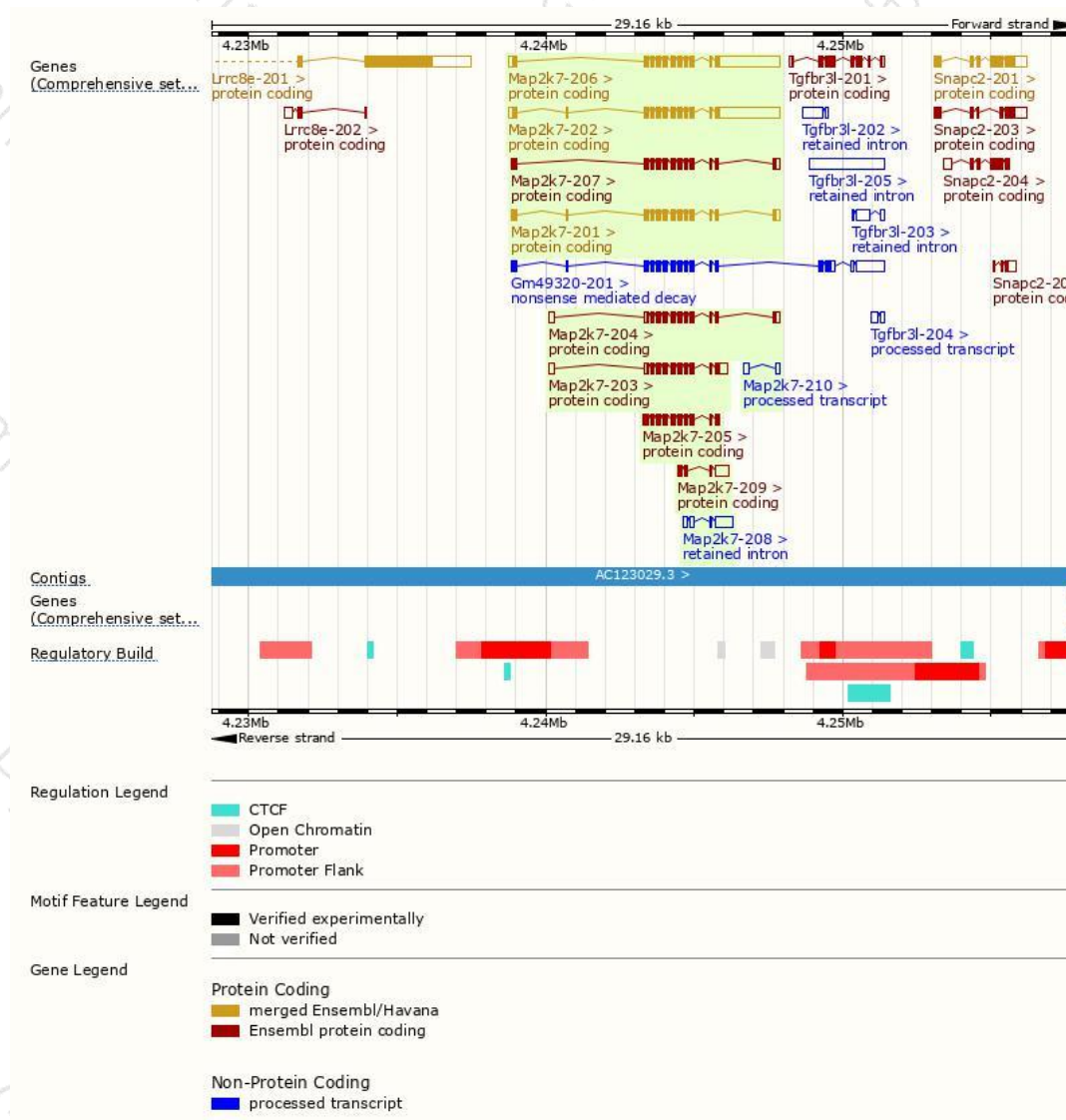
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Map2k7-202	ENSMUST00000062686.10	3525	435aa	Protein coding	CCDS52474	Q8CE90	TSL:1 GENCODE basic APPRIS ALT1
Map2k7-206	ENSMUST00000110998.8	3497	419aa	Protein coding	CCDS40209	Q8CE90	TSL:1 GENCODE basic APPRIS P3
Map2k7-201	ENSMUST00000003027.13	1626	468aa	Protein coding	CCDS40208	Q8CE90	TSL:1 GENCODE basic
Map2k7-203	ENSMUST00000110994.8	1600	346aa	Protein coding	CCDS80854	Q8CE90	TSL:1 GENCODE basic
Map2k7-207	ENSMUST00000110999.7	1578	452aa	Protein coding	CCDS80852	Q8CE90	TSL:1 GENCODE basic
Map2k7-204	ENSMUST00000110995.7	1558	379aa	Protein coding	CCDS80853	Q8CE90	TSL:1 GENCODE basic
Map2k7-205	ENSMUST00000110996.1	1188	391aa	Protein coding	-	Q8CE90	TSL:1 GENCODE basic
Map2k7-209	ENSMUST00000129866.7	760	79aa	Protein coding	-	A0A140LHN8	CDS 5' incomplete TSL:3
Map2k7-210	ENSMUST00000207247.1	324	No protein	Processed transcript	-	-	TSL:2
Map2k7-208	ENSMUST00000129537.1	934	No protein	Retained intron	-	-	TSL:2

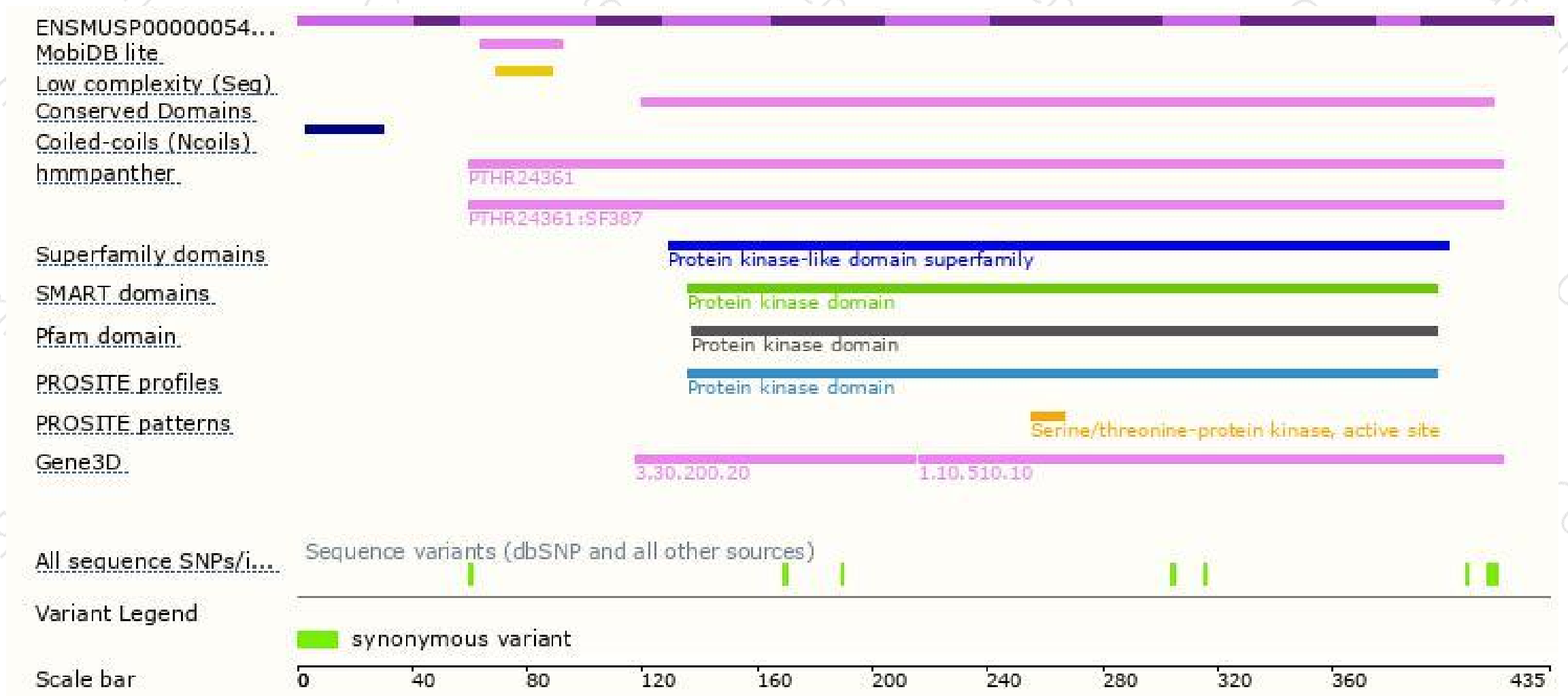
The strategy is based on the design of *Map2k7-201* transcript,The transcription is shown below



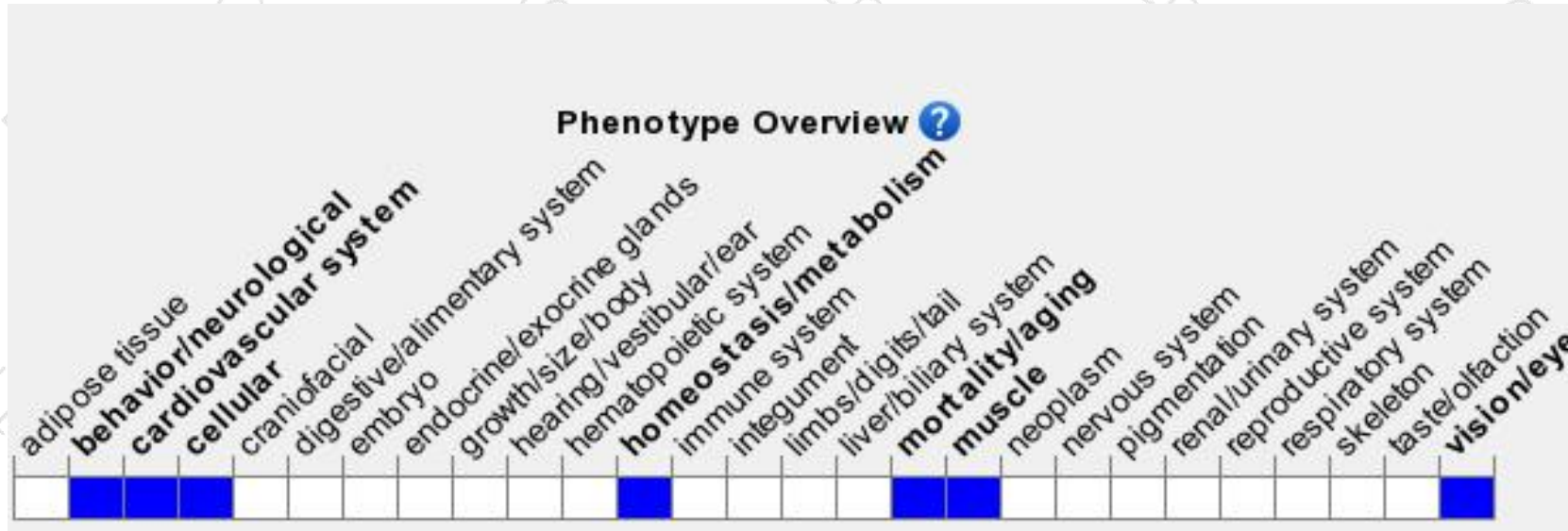
Genomic location distribution



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, Mice homozygous for disruptions in this gene die during embryogenesis.

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

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