

# *Map2k4* Cas9-CKO Strategy

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# Project Overview

**Project Name**

*Map2k4*

**Project type**

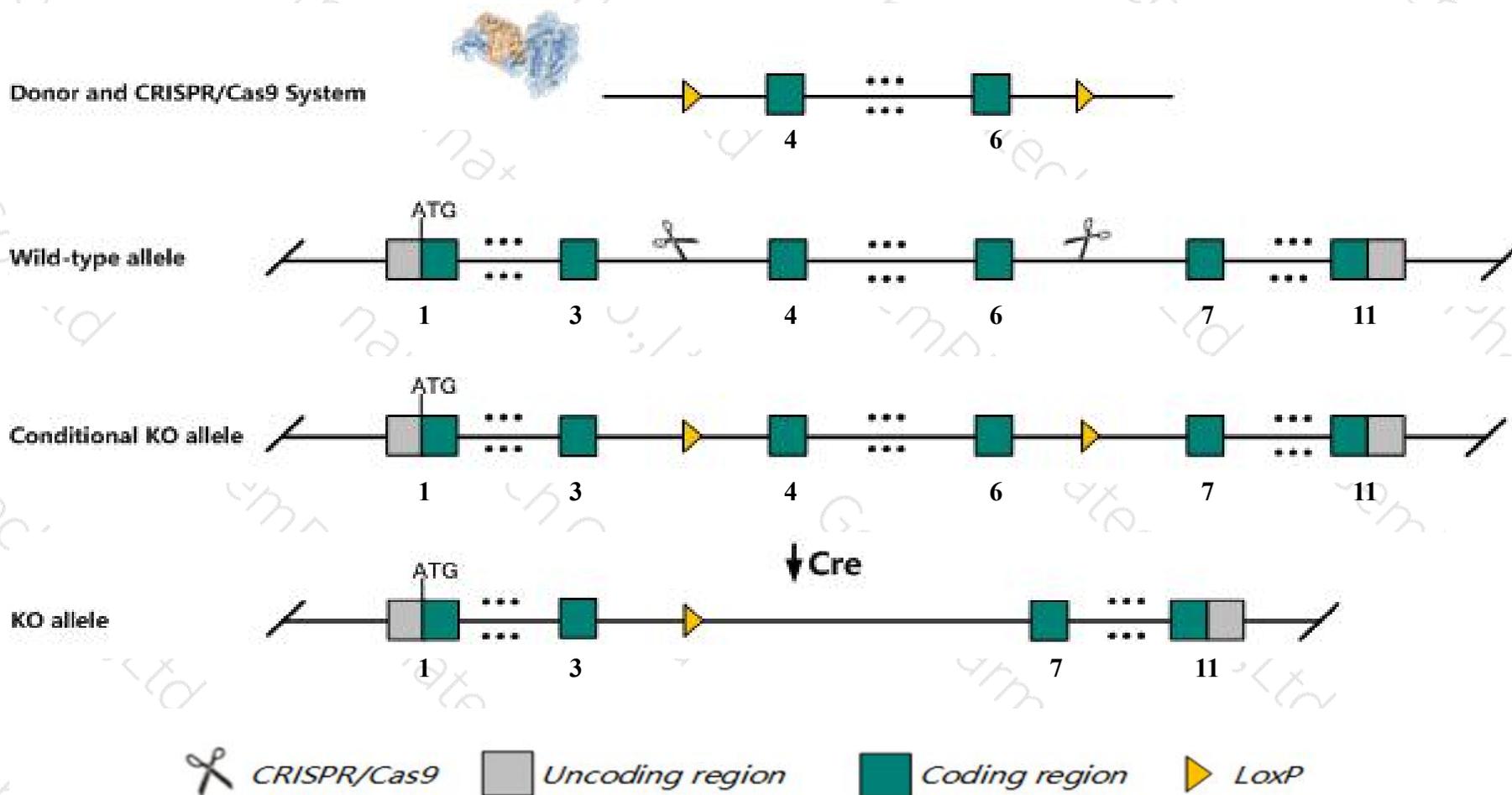
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Map2k4* gene. The schematic diagram is as follows:



- The *Map2k4* gene has 7 transcripts. According to the structure of *Map2k4* gene, exon4-exon6 of *Map2k4-201*(ENSMUST00000046963.9) transcript is recommended as the knockout region. The region contains 292bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Map2k4* 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, homozygotes for targeted null mutations exhibit abnormal liver development with a deficiency of parenchymal hepatocytes, severe anemia, and lethality before embryonic day 14.0.
- The effect of transcripts 202,204 is unknown.
- The *Map2k4* gene is located on the Chr11. 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)

## Map2k4 mitogen-activated protein kinase kinase 4 [Mus musculus (house mouse)]

Gene ID: 26398, updated on 13-Mar-2020

### Summary



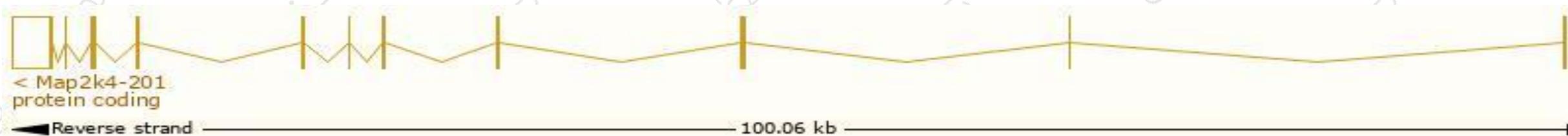
<b>Official Symbol</b>	Map2k4 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	mitogen-activated protein kinase kinase 4 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1346869</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000033352</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	JNKK1, MAPKK 4, MEK4, MKK4, PRKMK4, Sek1, Serk1
<b>Expression</b>	Ubiquitous expression in cerebellum adult (RPKM 19.2), cortex adult (RPKM 18.8) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

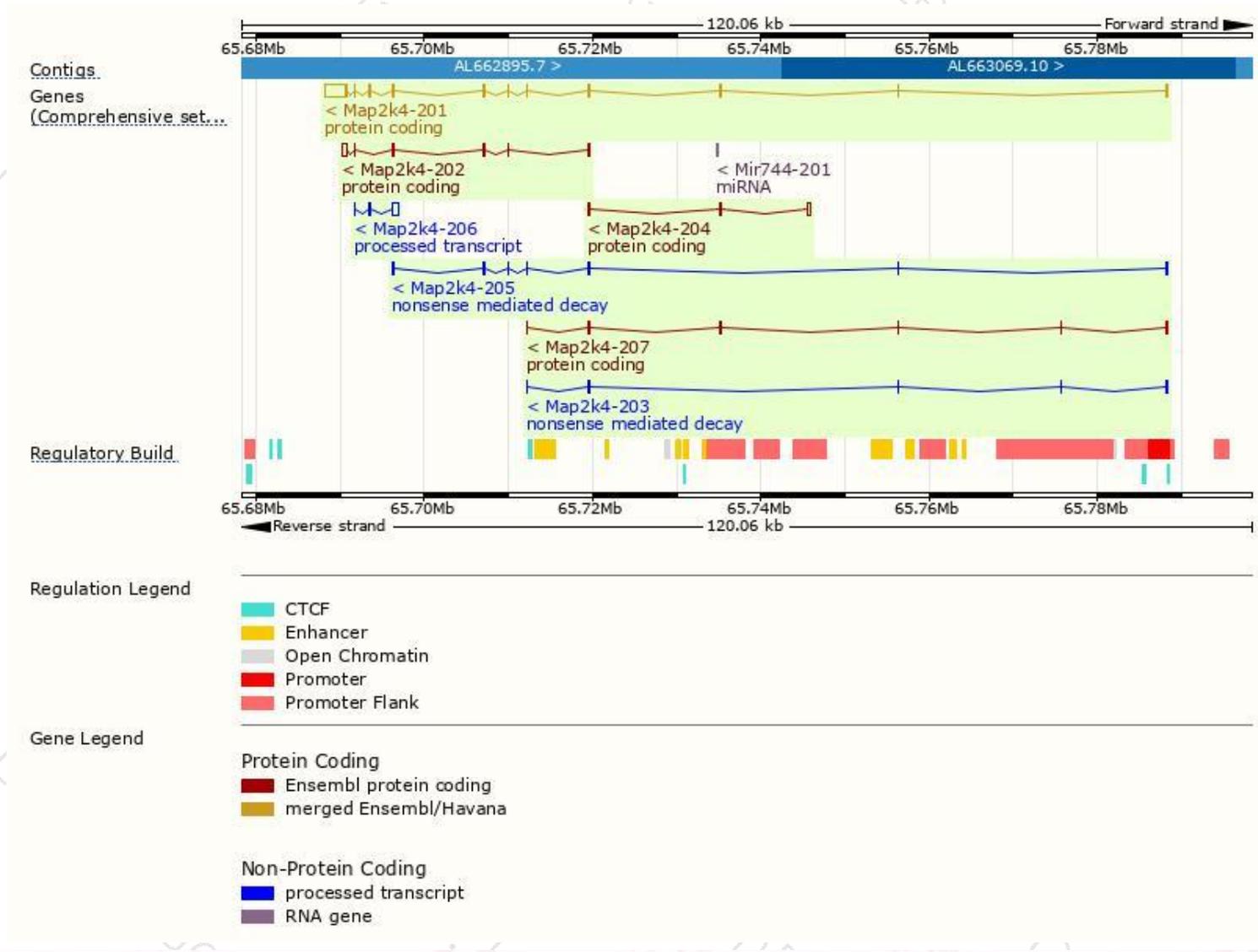
The gene has 7 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Map2k4-201	<a href="#">ENSMUST00000046963.9</a>	3695	<a href="#">397aa</a>	Protein coding	<a href="#">CCDS24844</a>	<a href="#">P47809 Q543X6</a>	TSL:1 GENCODE basic APPRIS P1
Map2k4-202	<a href="#">ENSMUST00000125598.7</a>	896	<a href="#">130aa</a>	Protein coding	-	<a href="#">M0QW52</a>	CDS 5' incomplete TSL:5
Map2k4-207	<a href="#">ENSMUST00000152096.7</a>	661	<a href="#">206aa</a>	Protein coding	-	<a href="#">B1ATL6</a>	CDS 3' incomplete TSL:2
Map2k4-204	<a href="#">ENSMUST00000138093.1</a>	527	<a href="#">34aa</a>	Protein coding	-	<a href="#">A0A2I3BQK8</a>	CDS 3' incomplete TSL:3
Map2k4-205	<a href="#">ENSMUST00000140301.7</a>	751	<a href="#">90aa</a>	Nonsense mediated decay	-	<a href="#">M0QWR0</a>	TSL:3
Map2k4-203	<a href="#">ENSMUST00000130009.1</a>	484	<a href="#">101aa</a>	Nonsense mediated decay	-	<a href="#">M0QWG5</a>	TSL:3
Map2k4-206	<a href="#">ENSMUST00000140740.1</a>	922	No protein	Processed transcript	-	-	TSL:5

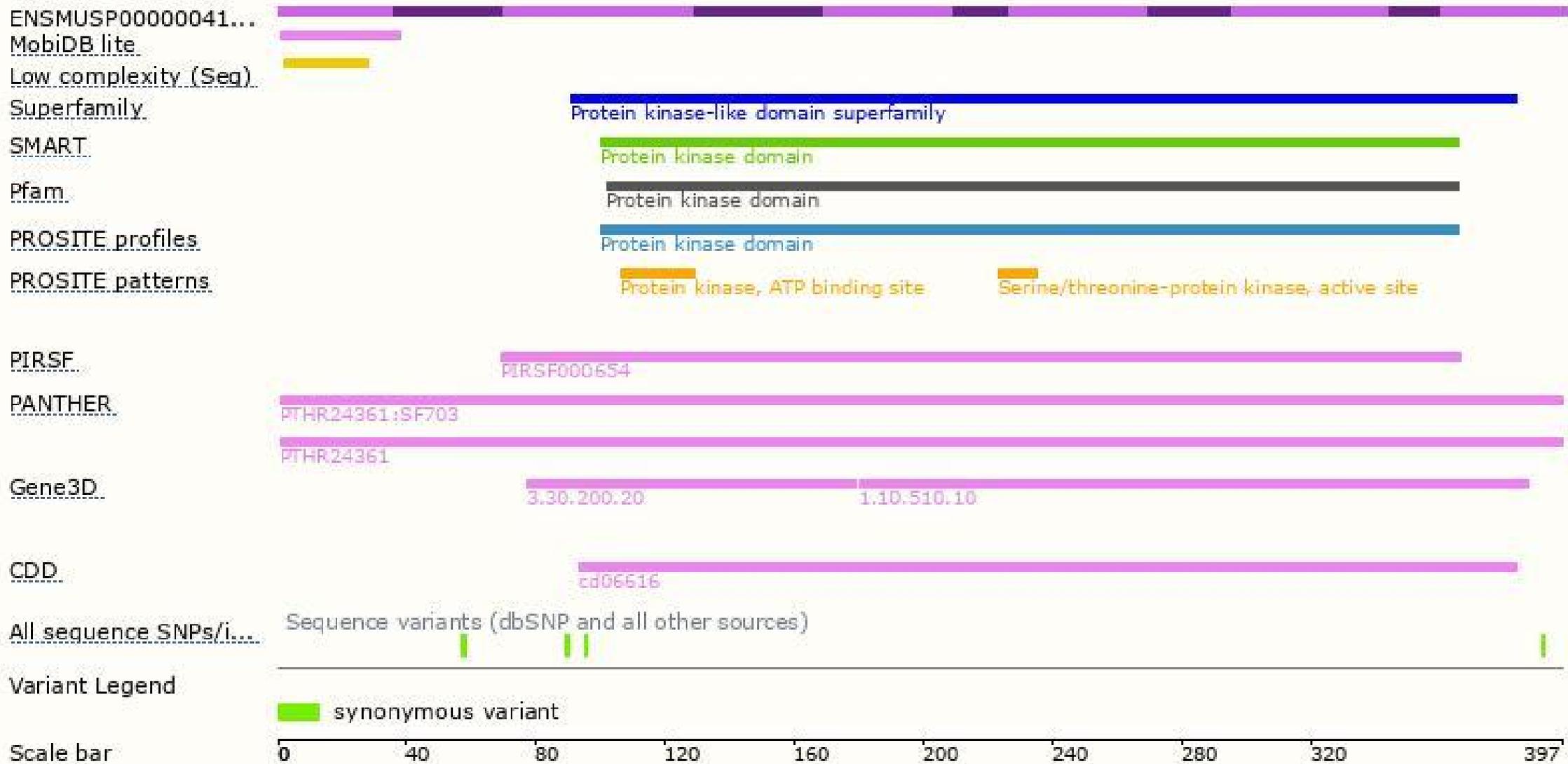
The strategy is based on the design of *Map2k4-201* transcript, the transcription is shown below:



# Genomic location distribution

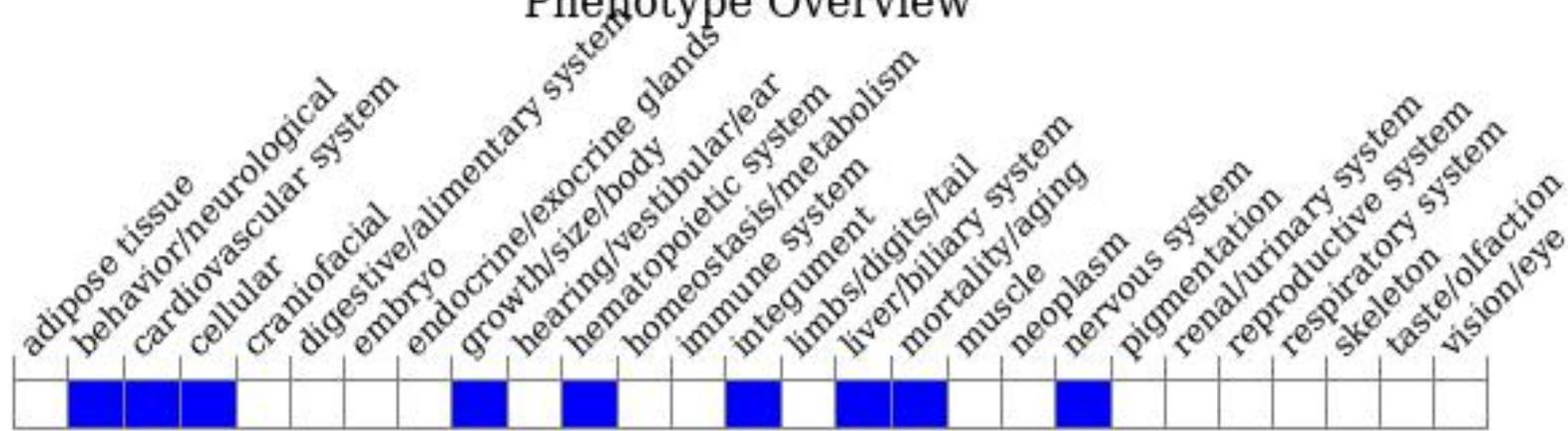


# Protein domain



# Mouse phenotype description(MGI)

## Phenotype Overview



*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, homozygotes for targeted null mutations exhibit abnormal liver development with a deficiency of parenchymal hepatocytes, severe anemia, and lethality before embryonic day 14.0.

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

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