

# *Cers2* Cas9-CKO Strategy

**Designer: Shilei Zhu**

**Reviewer: Lingyan Wu**

**Design Date: 2021-6-23**

# Project Overview

---

**Project Name**

*Cers2*

---

**Project type**

**Cas9-CKO**

---

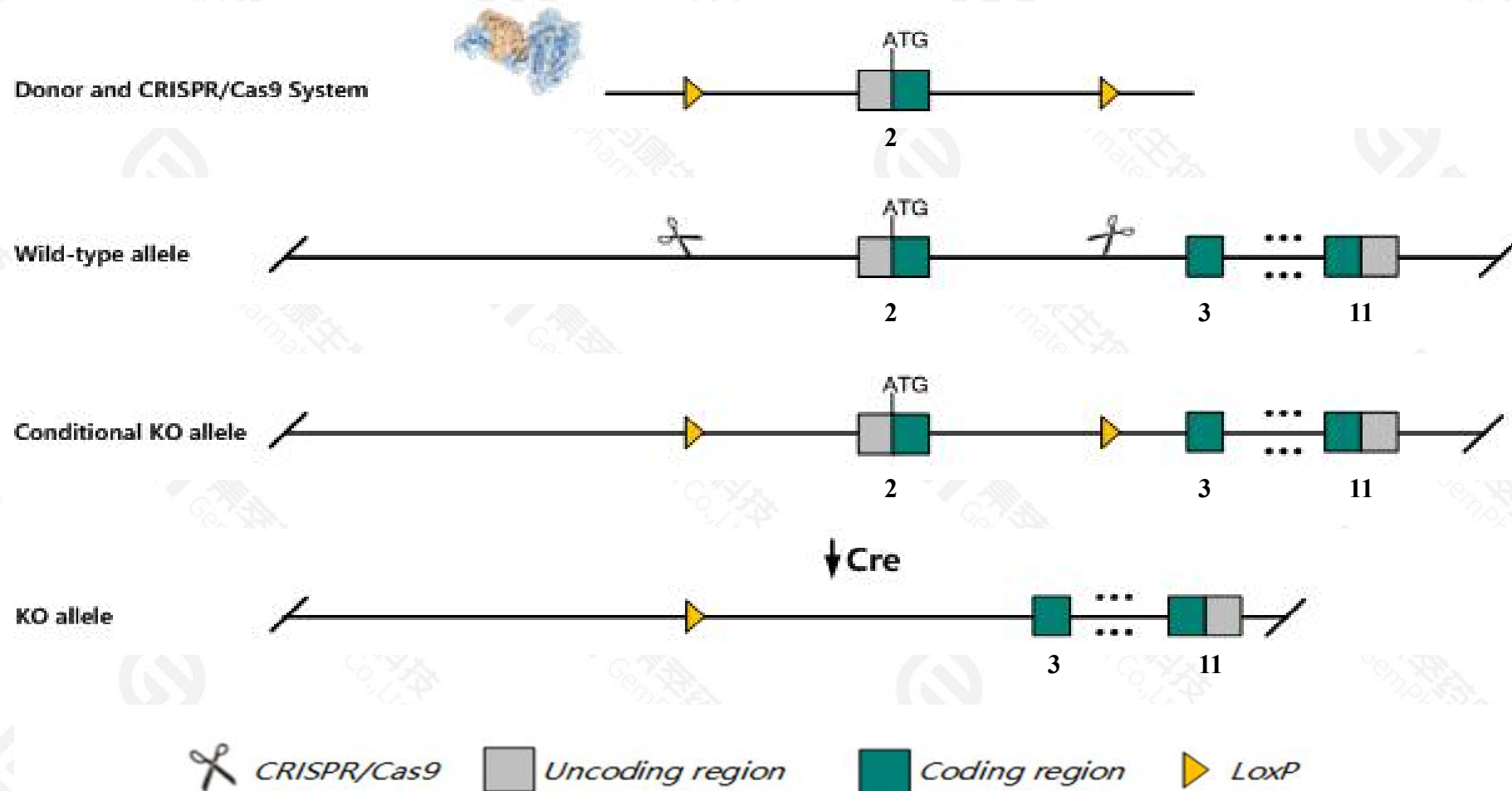
**Strain background**

**C57BL/6JGpt**

---

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cers2* gene. The schematic diagram is as follows:



- The *Cers2* gene has 9 transcripts. According to the structure of *Cers2* gene, exon2 of *Cers2*-201(ENSMUST00000015858.12) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cers2* 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 a gene trapped allele exhibit abnormal ceramide species and myelin sheath defects and develop hepatocellular carcinoma.
- The Intron2 is only 406bp, loxp insertion may affect mRNA splicing.
- The *Cers2* gene is located on the Chr3. 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)

## Cers2 ceramide synthase 2 [Mus musculus (house mouse)]

Gene ID: 76893, updated on 22-Dec-2020

### Summary



**Official Symbol** Cers2 provided by [MGI](#)

**Official Full Name** ceramide synthase 2 provided by [MGI](#)

**Primary source** [MGI:MGI:1924143](#)

**See related** [Ensembl:ENSMUSG00000015714](#)

**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** 0610013I17Rik, AI225939, Cer, L, Lass2, TRH3, Trh

**Expression** Ubiquitous expression in liver adult (RPKM 73.3), placenta adult (RPKM 50.3) and 28 other tissues [See more](#)

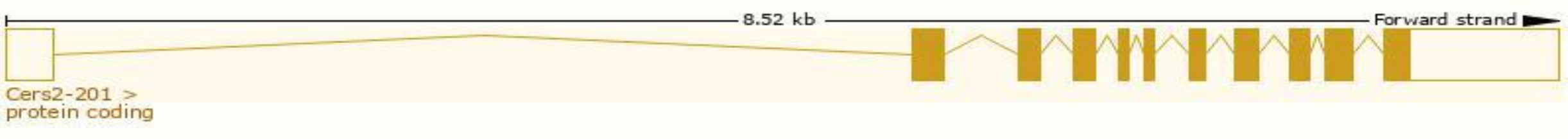
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

The gene has 9 transcripts,all transcripts are shown below:

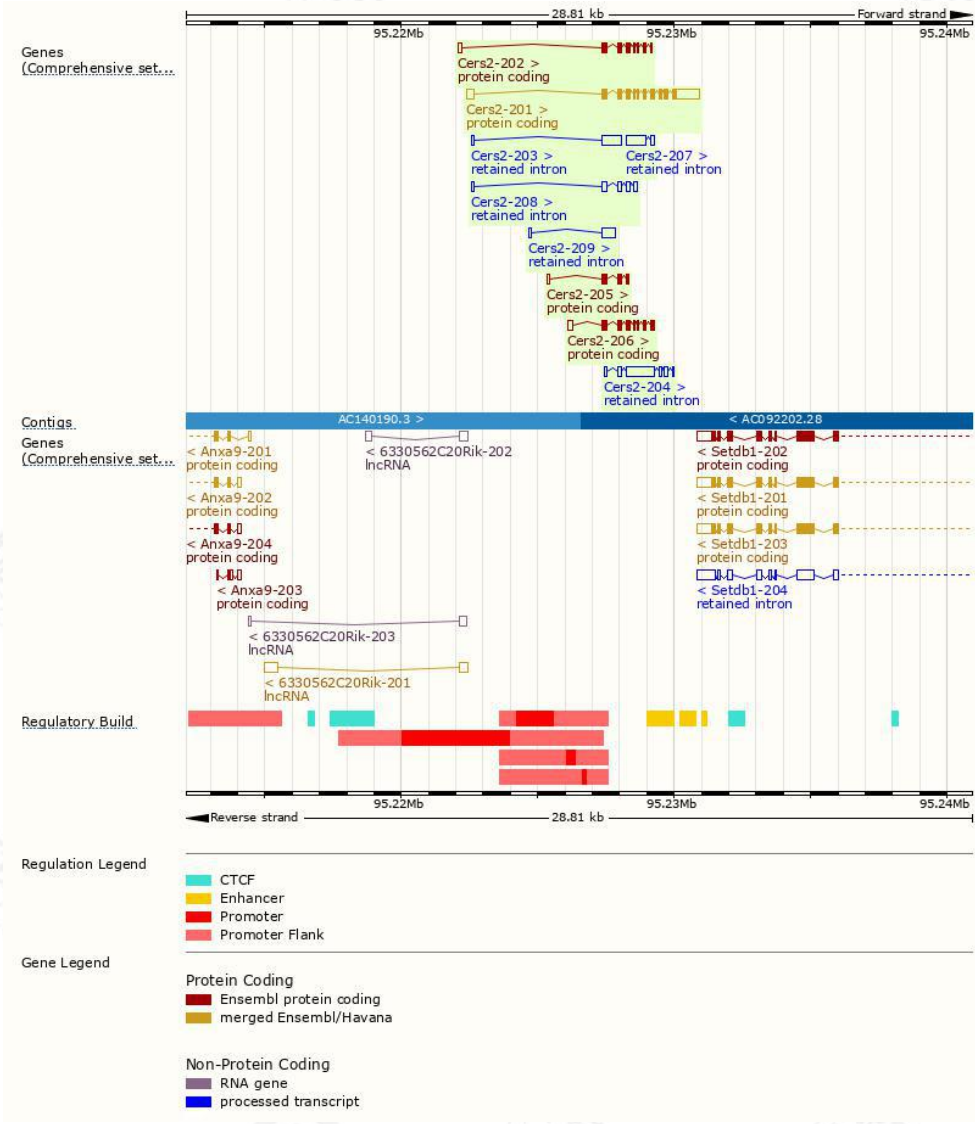
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cers2-201	<a href="#">ENSMUST00000015858.12</a>	2216	<a href="#">380aa</a>	Protein coding	<a href="#">CCDS17612</a>		TSL:1 , GENCODE basic , APPRIS P1 ,
Cers2-206	<a href="#">ENSMUST00000139866.2</a>	900	<a href="#">245aa</a>	Protein coding	-		CDS 3' incomplete , TSL:5 ,
Cers2-202	<a href="#">ENSMUST00000129267.8</a>	775	<a href="#">220aa</a>	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Cers2-205	<a href="#">ENSMUST00000139498.8</a>	495	<a href="#">130aa</a>	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Cers2-204	<a href="#">ENSMUST00000134702.3</a>	1524	No protein	Retained intron	-		TSL:5 ,
Cers2-207	<a href="#">ENSMUST00000142398.2</a>	855	No protein	Retained intron	-		TSL:3 ,
Cers2-203	<a href="#">ENSMUST00000133748.2</a>	811	No protein	Retained intron	-		TSL:2 ,
Cers2-208	<a href="#">ENSMUST00000154055.8</a>	624	No protein	Retained intron	-		TSL:2 ,
Cers2-209	<a href="#">ENSMUST00000156850.3</a>	583	No protein	Retained intron	-		TSL:2 ,

The strategy is based on the design of *Cers2-201* transcript,the transcription is shown below:



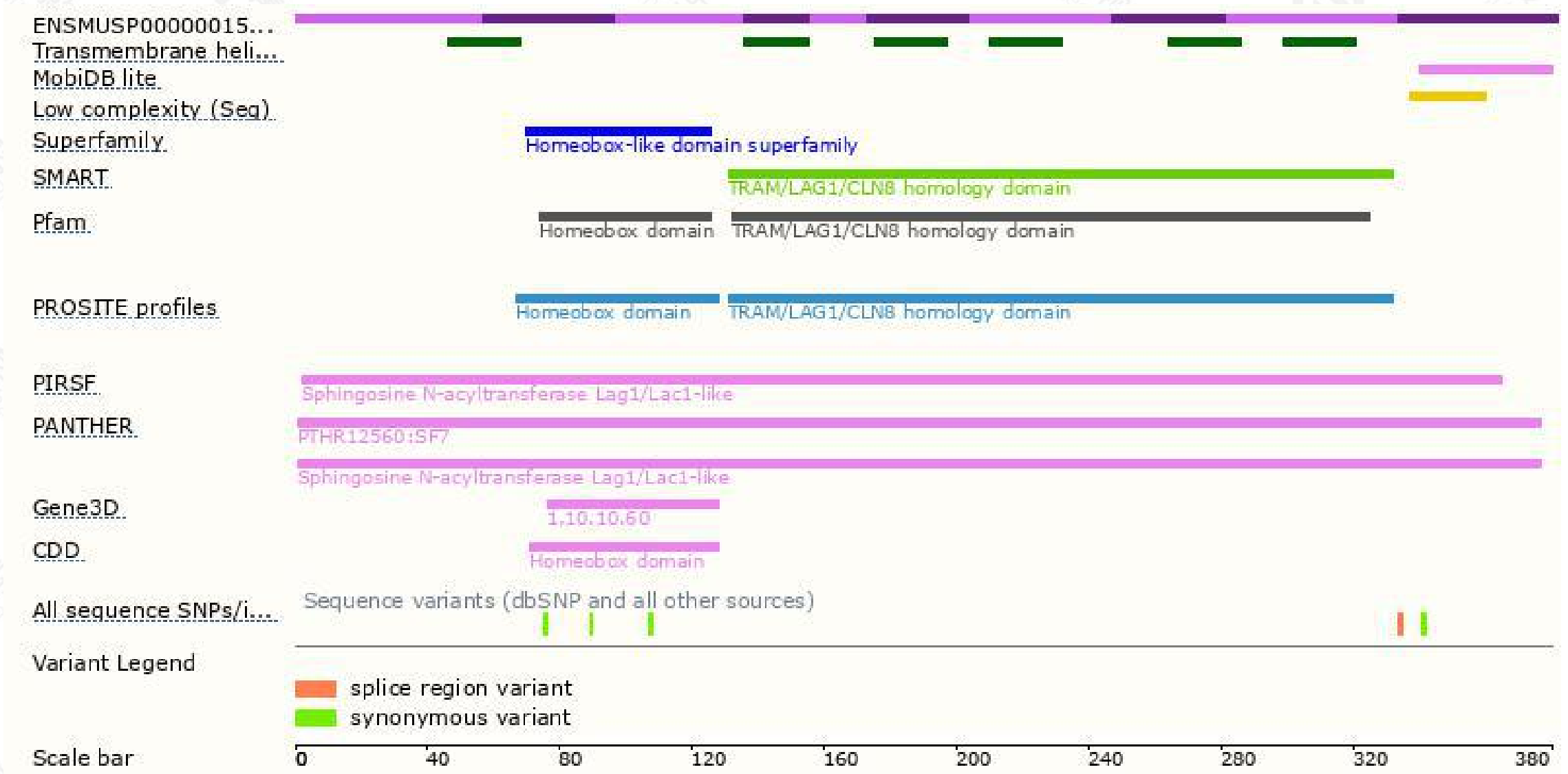


# Genomic location distribution

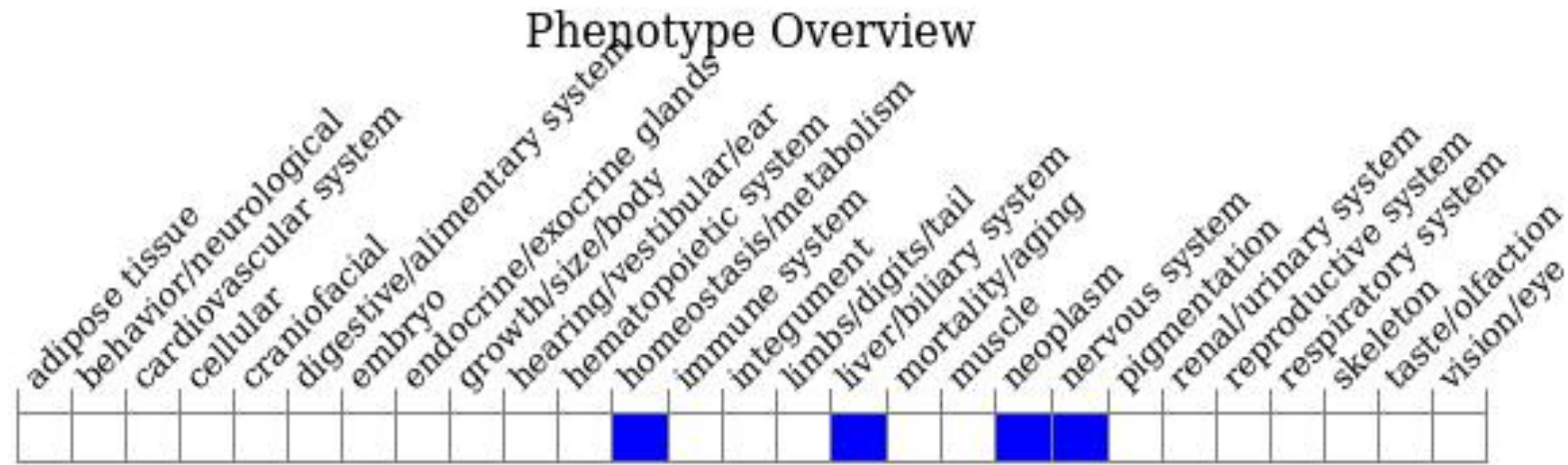




# Protein domain



# 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 a gene trapped allele exhibit abnormal ceramide species and myelin sheath defects and develop hepatocellular carcinoma.

If you have any questions, you are welcome to inquire.  
Tel: 400-9660890

