

Cers2 Cas9-KO Strategy

Designer: Shilei Zhu

Reviewer: Lingyan Wu

Design Date: 2021-6-23

Project Overview

Project Name

Cers2

Project type

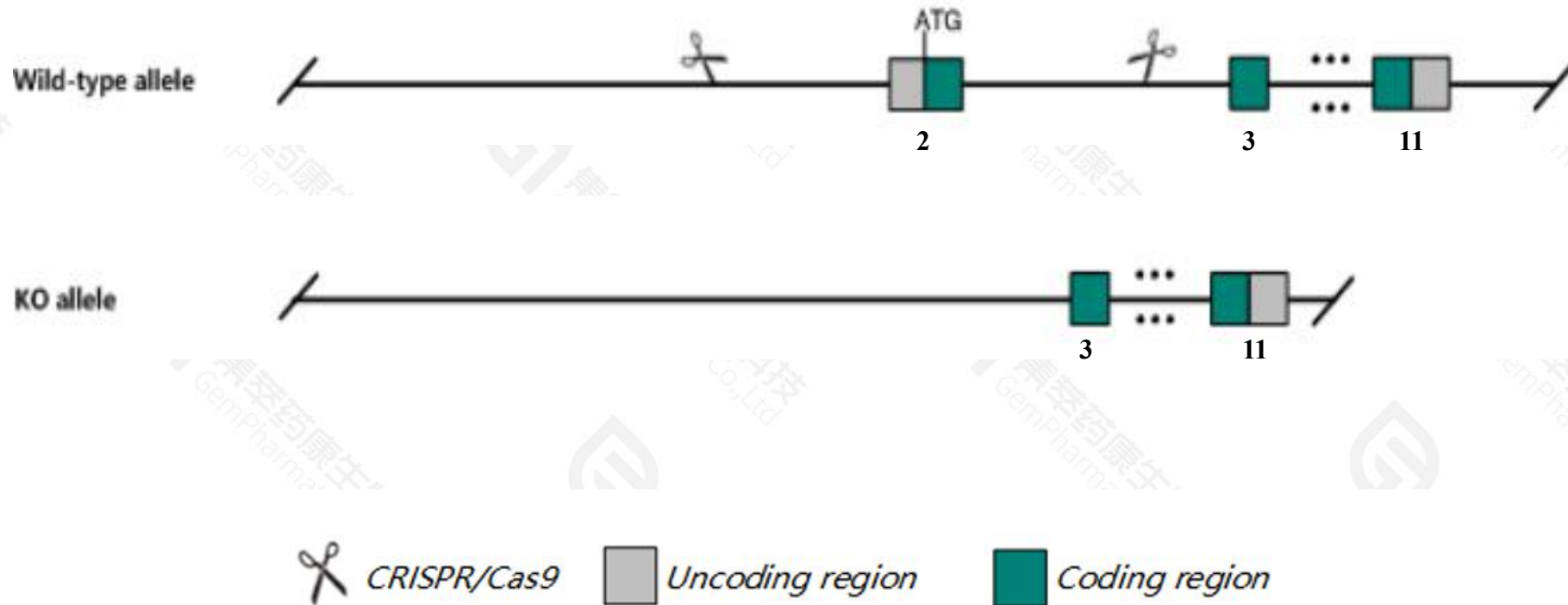
Cas9-KO

Strain background

C57BL/6JGpt

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 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.

- 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.
- 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

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)

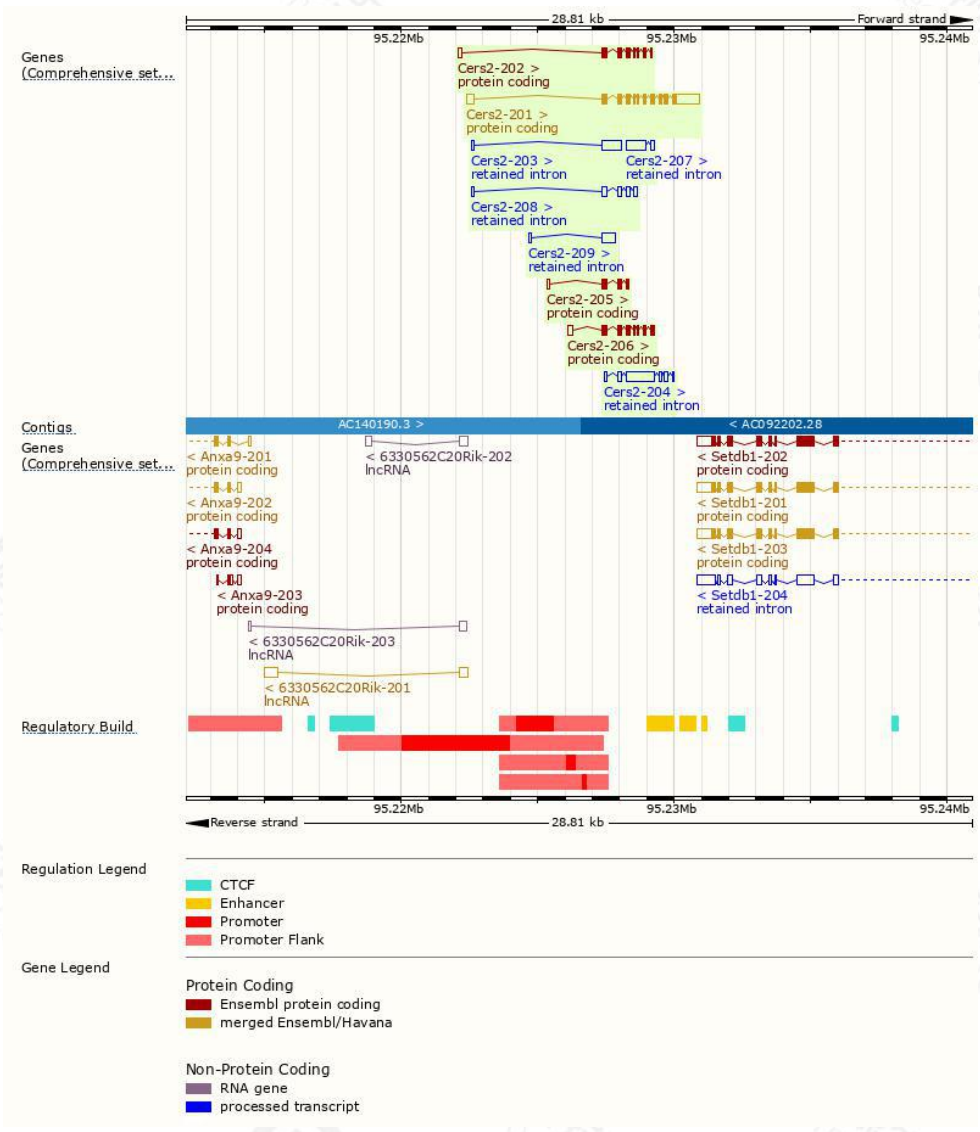
The gene has 9 transcripts,all transcripts are shown below:

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

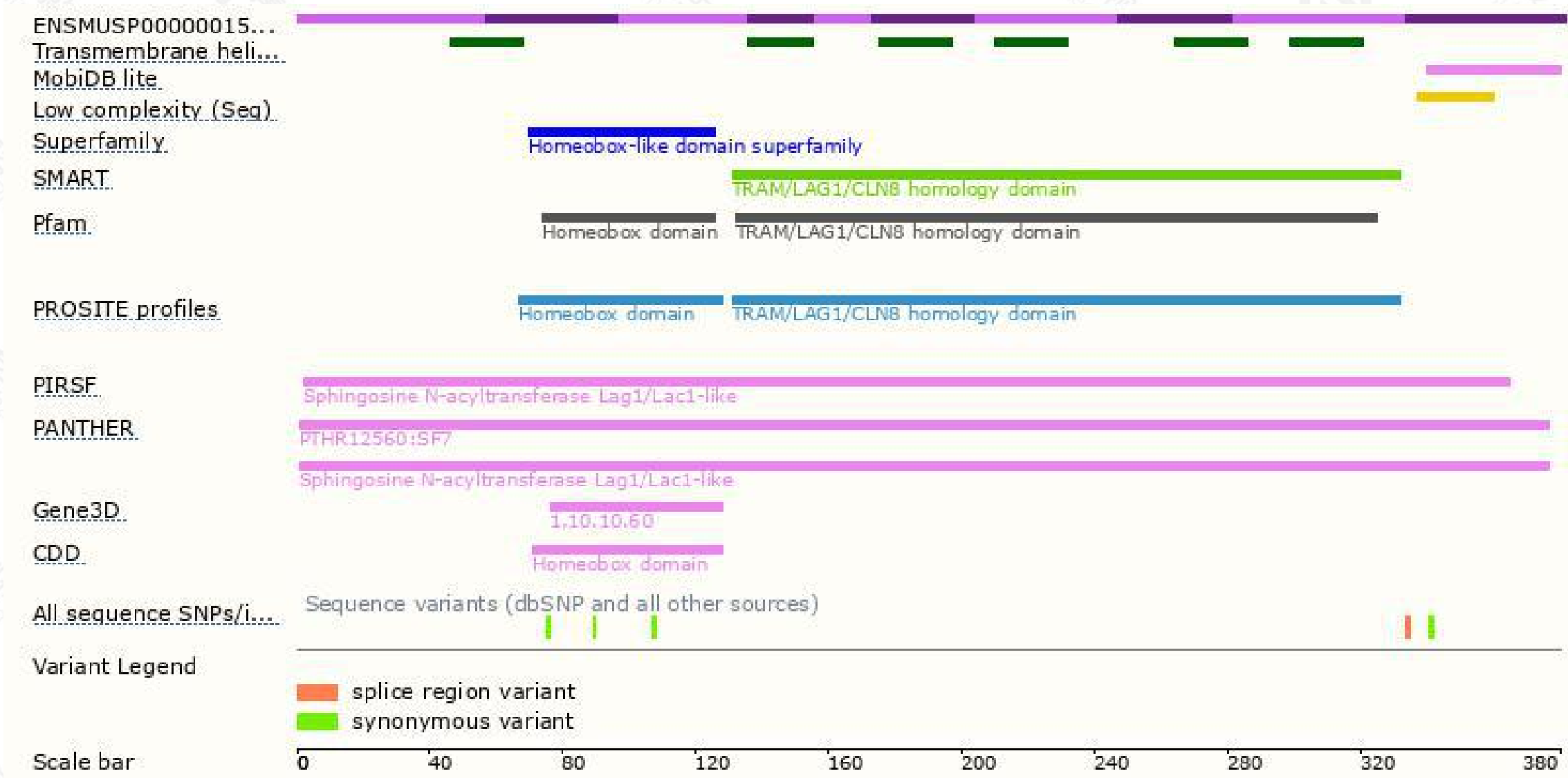
The strategy is based on the design of *Cers2-201* transcript,the transcription is shown below:



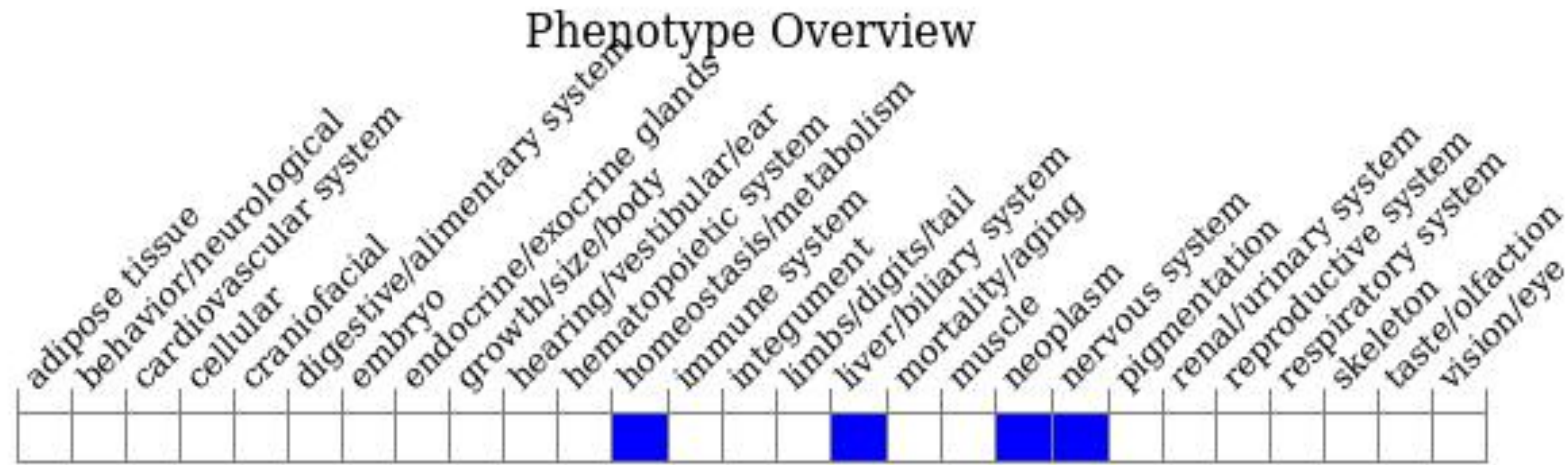
Genomic location distribution



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

