

Cers3 Cas9-KO Strategy

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Project Overview

Project Name

Cers3

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cers3* gene. The schematic diagram is as follows:



- The *Cers3* gene has 2 transcripts. According to the structure of *Cers3* gene, exon3 of *Cers3*-201(ENSMUST00000066475.10) transcript is recommended as the knockout region. The region contains 115bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cers3* 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 knock-out allele exhibit a lethal skin barrier disruption defect due to a lack of ultra-long-chain acyl ceramides, impaired stratum corneum desquamation, accelerated lamellar body biogenesis and extrusion, and delayed keratinocyte cornification.
- The *Cers3* gene is located on the Chr7. 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.

Gene information (NCBI)

Cers3 ceramide synthase 3 [Mus musculus (house mouse)]

Gene ID: 545975, updated on 13-Mar-2020

Summary



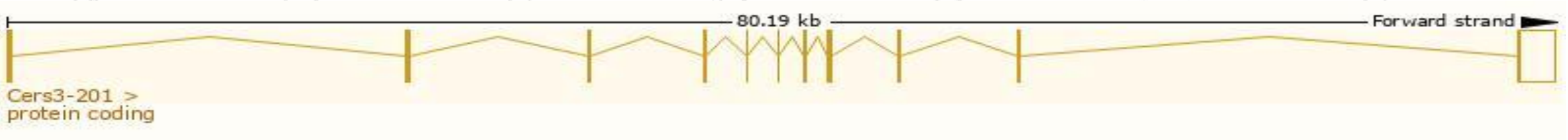
Official Symbol	Cers3 provided by MGI
Official Full Name	ceramide synthase 3 provided by MGI
Primary source	MGI:MGI:2681008
See related	Ensembl:ENSMUSG00000030510
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4930550L11Rik, Gm488, Lass3, T3L, mCerS3
Expression	Biased expression in bladder adult (RPKM 14.7), testis adult (RPKM 13.6) and 3 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

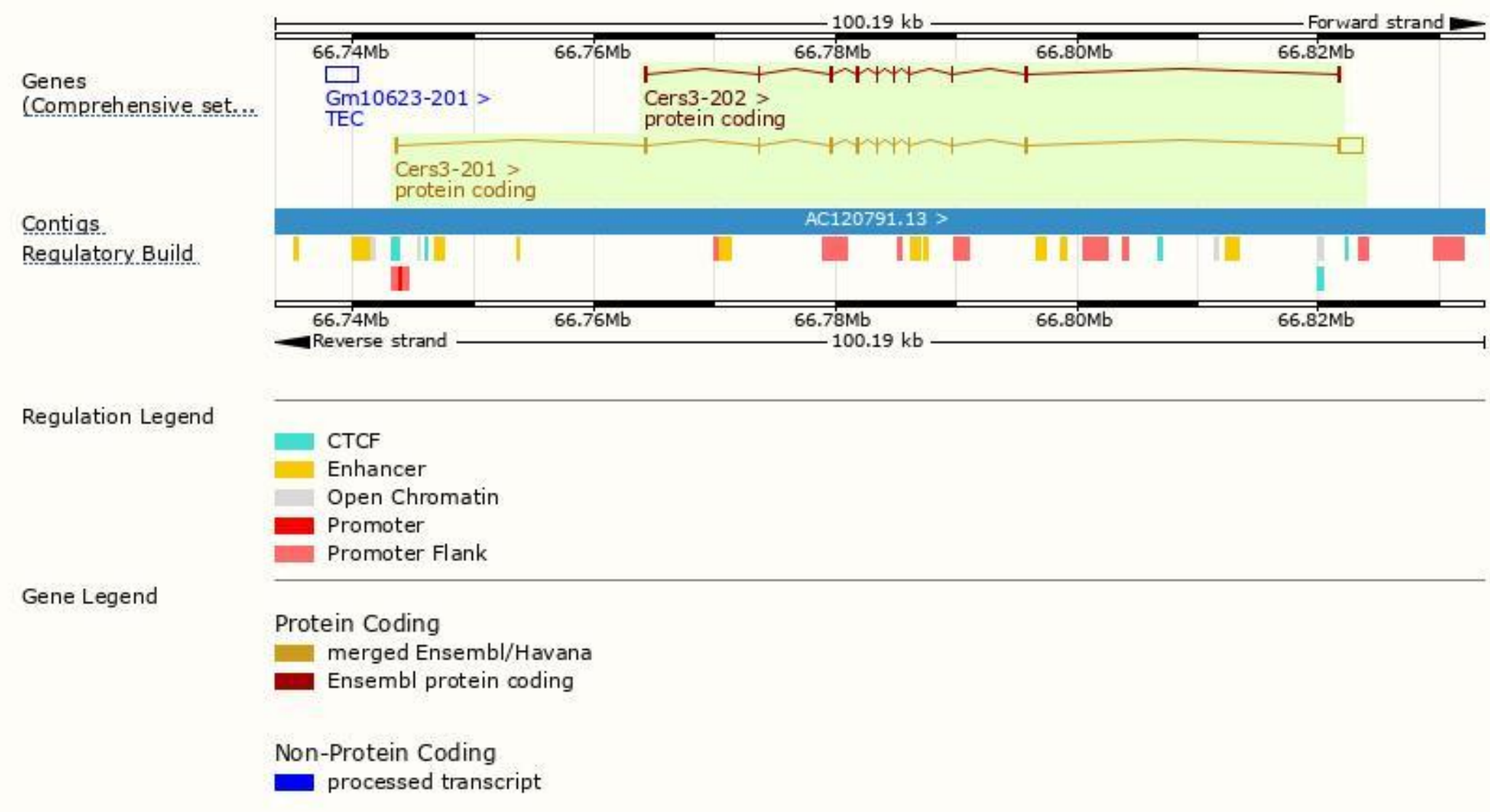
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cers3-201	ENSMUST00000066475.10	3250	419aa	Protein coding	CCDS52268	Q1A3B0	TSL:1 GENCODE basic
Cers3-202	ENSMUST00000208521.1	1159	383aa	Protein coding	-	Q1A3B0	TSL:1 GENCODE basic APPRIS P1

The strategy is based on the design of *Cers3-201* transcript,the transcription is shown below:



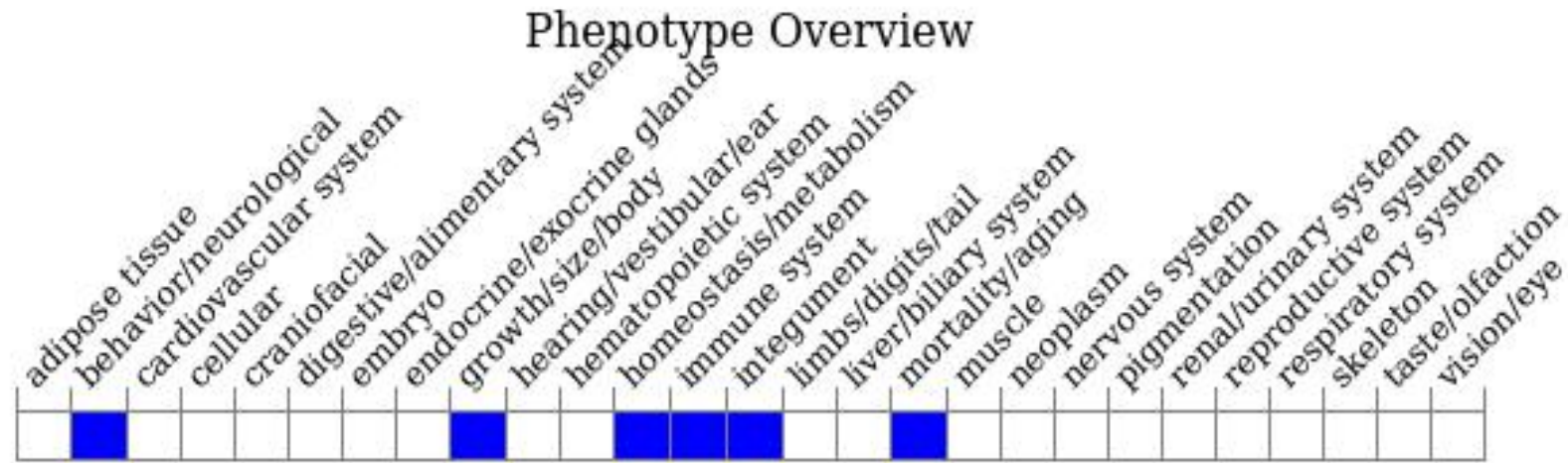
Genomic location distribution



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 knock-out allele exhibit a lethal skin barrier disruption defect due to a lack of ultra-long-chain acyl ceramides, impaired stratum corneum desquamation, accelerated lamellar body biogenesis and extrusion, and delayed keratinocyte cornification.

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

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