Cers4 Cas9-KO Strategy

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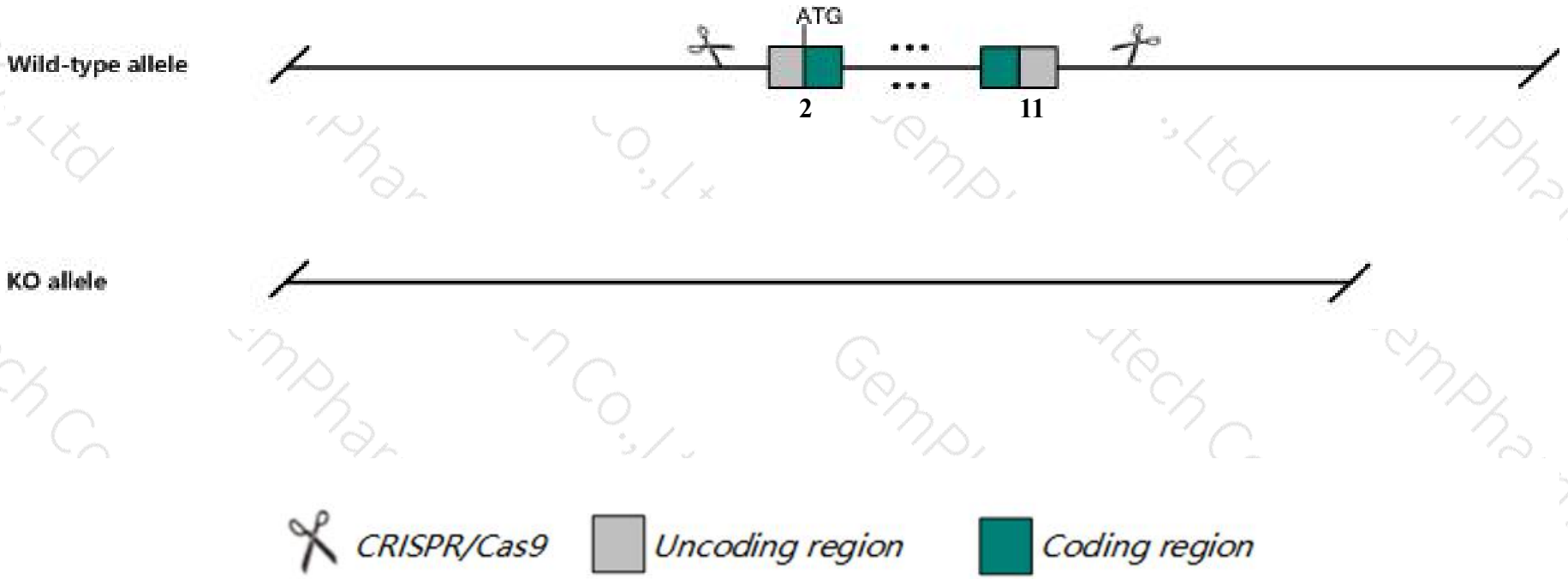
Project Overview

Project Name	***Cers4***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cers4* gene. The schematic diagram is as follows:



Technical routes

➢ The *Cers4* gene has 9 transcripts. According to the structure of *Cers4* gene, exon2-exon11 of *Cers4-201* (ENSMUST00000008350.15) transcript is recommended as the knockout region.The region contains all of the coding sequence.Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Cers4* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ According to the existing MGI data,Mice homozygous for a knock-out allele exhibit altered lipid composition of the sebum and hair follicle dystrophy that results in a progressive form of alopecia.

➢ The *Cers4* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information（NCBI）

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Cers4 ceramide synthase 4 [Mus musculus (house mouse)]

Gene ID: 67260, updated on 31-Jan-2019

Summary

Official Symbol	Cers4 provided by MGI
Official Full Name	ceramide synthase 4 provided byMGI
Primary source	MGI:MGI:1914510
See related	Ensembl:ENSMUSG00000008206
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	2900019C14Rik, Lass4, Trh1
Expression	Ubiquitous expression in genital fat pad adult (RPKM 11.0), lung adult (RPKM 8.8) and 23 other tissuesSee more
Orthologs	human all

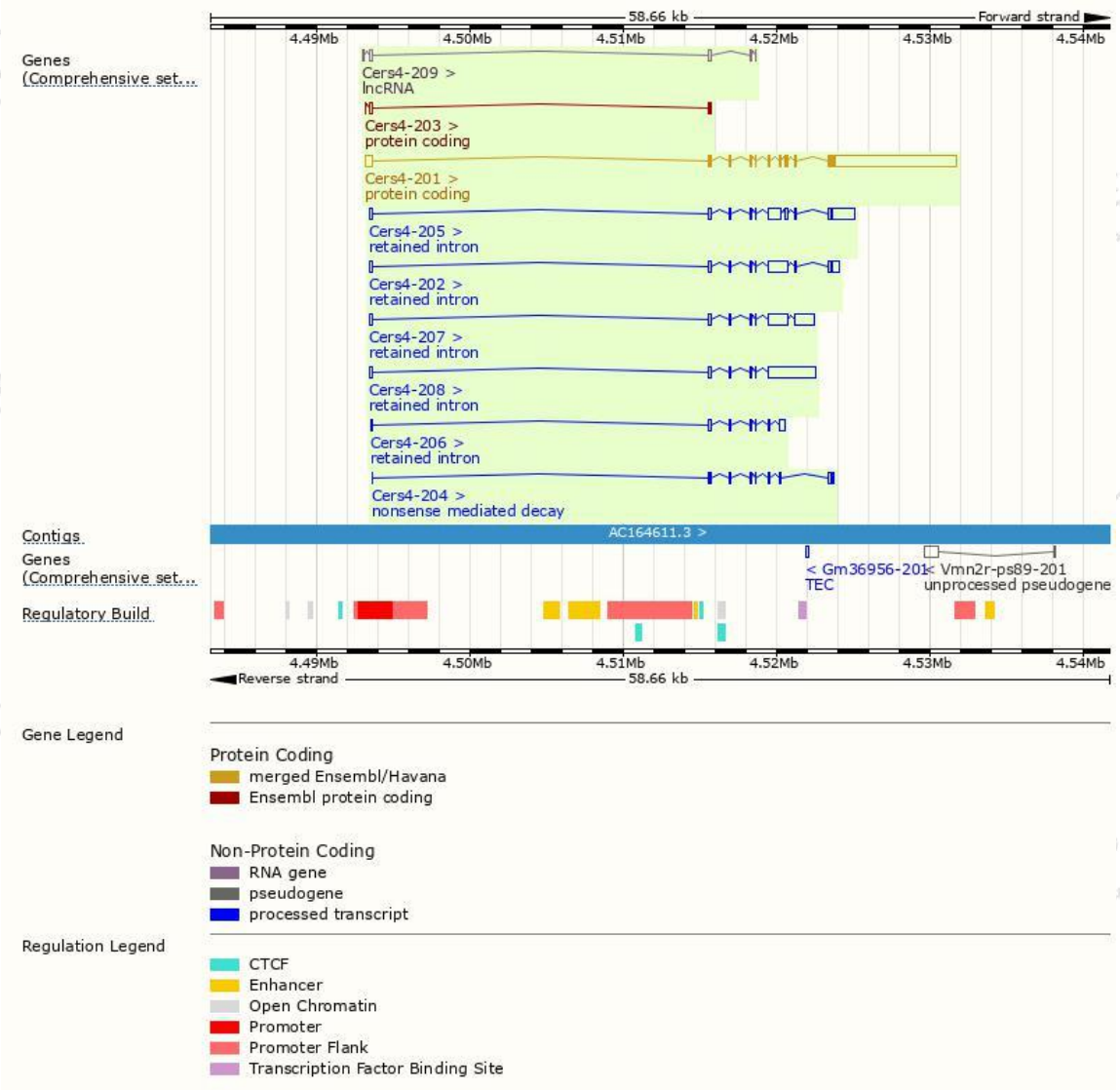
Transcript information（Ensembl）

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

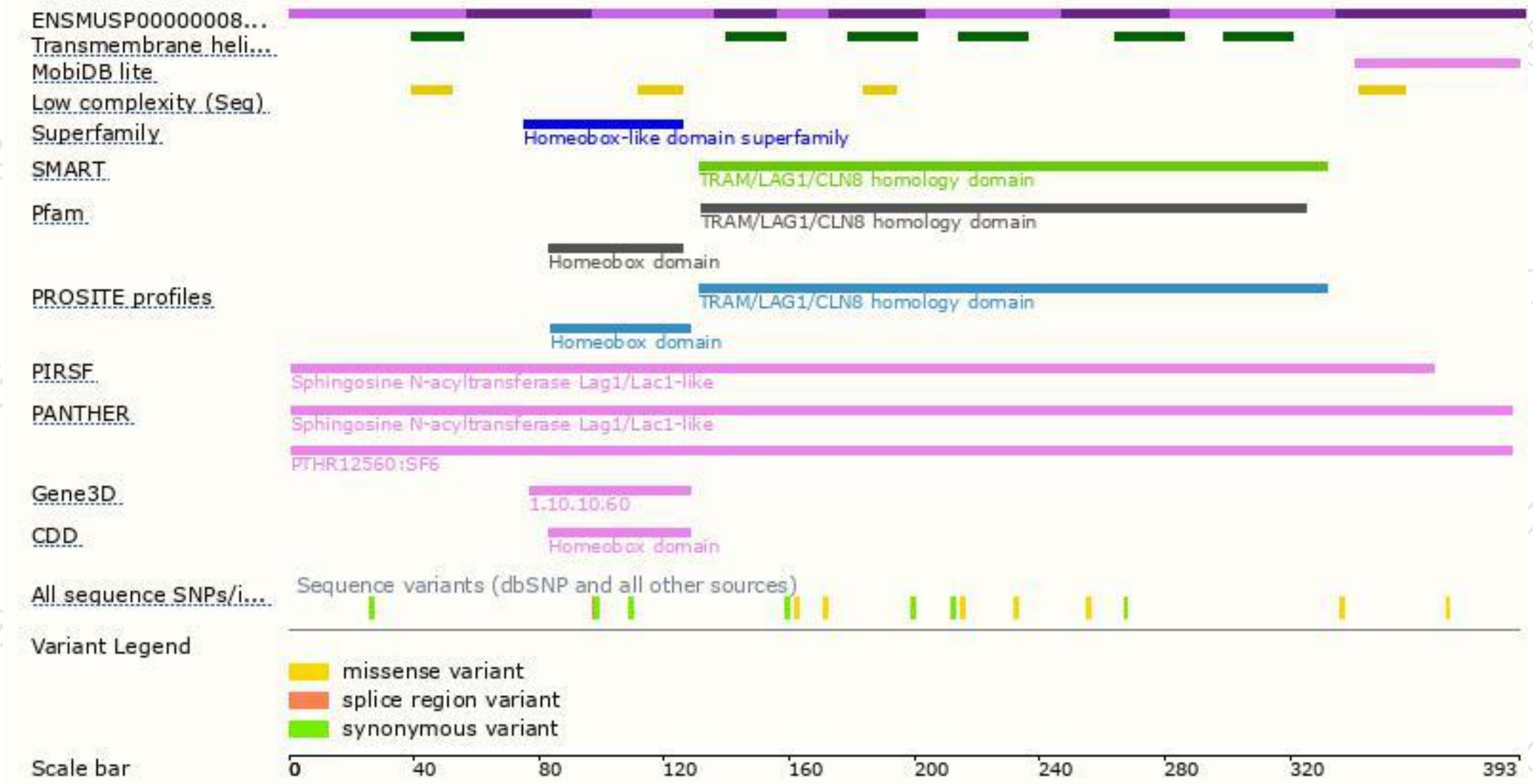
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cers4-201	ENSMUST00000008350.15	9475	393aa	Protein coding	CCDS22086	Q9D6J1	TSL:1 GENCODE basic APPRIS P1
Cers4-203	ENSMUST00000176042.1	387	56aa	Protein coding	-	H3BKZ9	CDS 3' incomplete TSL:3
Cers4-204	ENSMUST00000176130.9	874	211aa	Nonsense mediated decay	-	H3BL50	TSL:5
Cers4-208	ENSMUST00000176932.7	3674	No protein	Retained intron	-	-	TSL:2
Cers4-205	ENSMUST00000176267.8	3369	No protein	Retained intron	-	-	TSL:2
Cers4-207	ENSMUST00000176837.7	3116	No protein	Retained intron	-	-	TSL:1
Cers4-202	ENSMUST00000175781.4	2539	No protein	Retained intron	-	-	TSL:1
Cers4-206	ENSMUST00000176705.1	908	No protein	Retained intron	-	-	TSL:2
Cers4-209	ENSMUST00000177010.9	561	No protein	lncRNA	-	-	TSL:5

The strategy is based on the design of *Cers4-201* transcript,The transcription is shown below

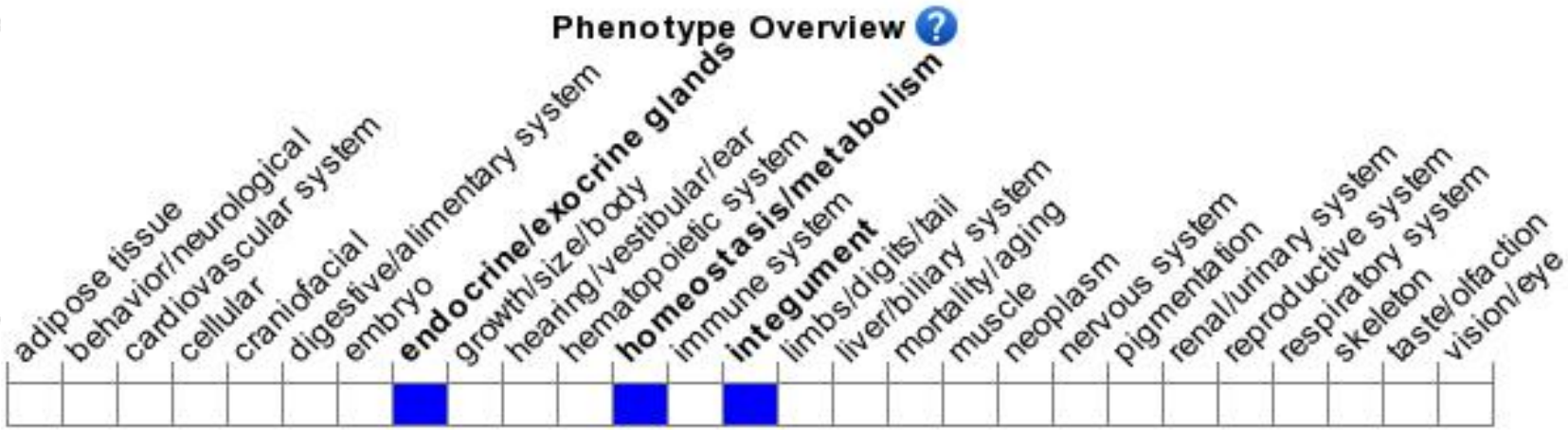
Genomic location distribution



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/).

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

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