

***Sec14l2* Cas9-KO Strategy**

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Reviewer:

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Project Overview

Project Name

Sec14l2

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sec14l2* gene. The schematic diagram is as follows:



- The *Sec14l2* gene has 6 transcripts. According to the structure of *Sec14l2* gene, exon2-exon8 of *Sec14l2-201* (ENSMUST00000003681.7) transcript is recommended as the knockout region. The region contains 610bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sec14l2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a null allele exhibit decreased cholesterol synthesis and plasma levels under fasting conditions compared to wild-type mice.
- The KO region contains functional region of the *Gm11955* gene. Knockout the region may affect the function of *Gm11955* gene.
- The *Sec14l2* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Sec14l2 SEC14-like lipid binding 2 [Mus musculus (house mouse)]

Gene ID: 67815, updated on 31-Jan-2019

Summary



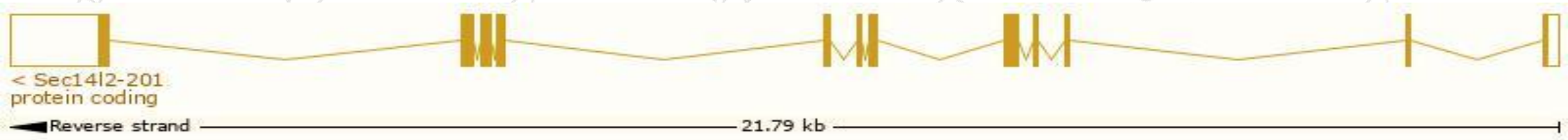
Official Symbol	Sec14l2 provided by MGI
Official Full Name	SEC14-like lipid binding 2 provided by MGI
Primary source	MGI:MGI:1915065
See related	Ensembl:ENSMUSG000000003585
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1300013M05Rik, Spf, TAP
Expression	Biased expression in liver adult (RPKM 140.8), liver E18 (RPKM 27.5) and 6 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

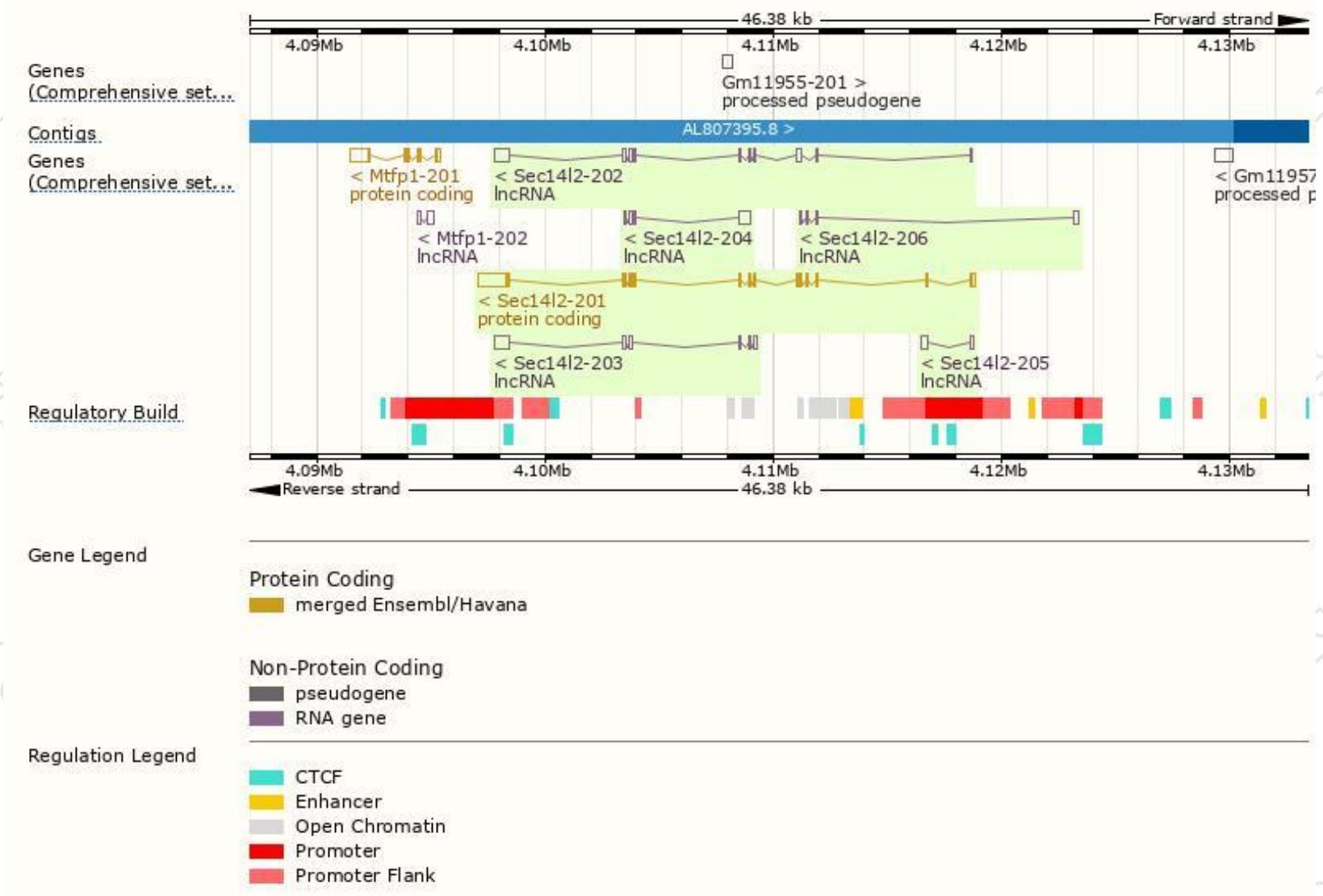
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sec14l2-201	ENSMUST00000003681.7	2631	403aa	Protein coding	CCDS24377	Q99J08	TSL:1 GENCODE basic APPRIS P1
Sec14l2-202	ENSMUST00000123901.7	1624	No protein	lncRNA	-	-	TSL:5
Sec14l2-203	ENSMUST00000132421.7	1229	No protein	lncRNA	-	-	TSL:5
Sec14l2-204	ENSMUST00000133631.1	880	No protein	lncRNA	-	-	TSL:3
Sec14l2-205	ENSMUST00000136420.1	429	No protein	lncRNA	-	-	TSL:2
Sec14l2-206	ENSMUST00000145173.1	423	No protein	lncRNA	-	-	TSL:5

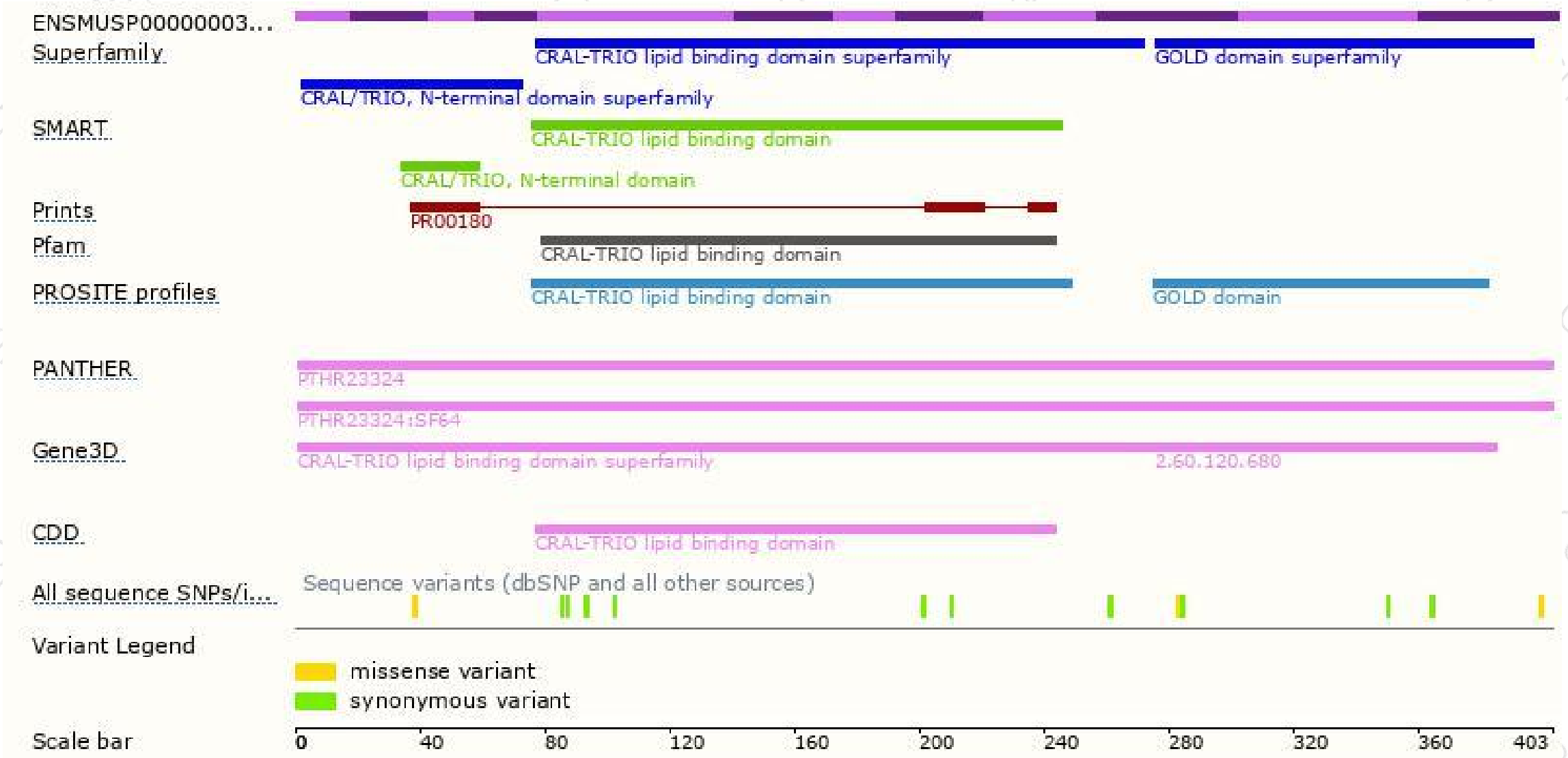
The strategy is based on the design of *Sec14l2-201* transcript,The transcription is shown below



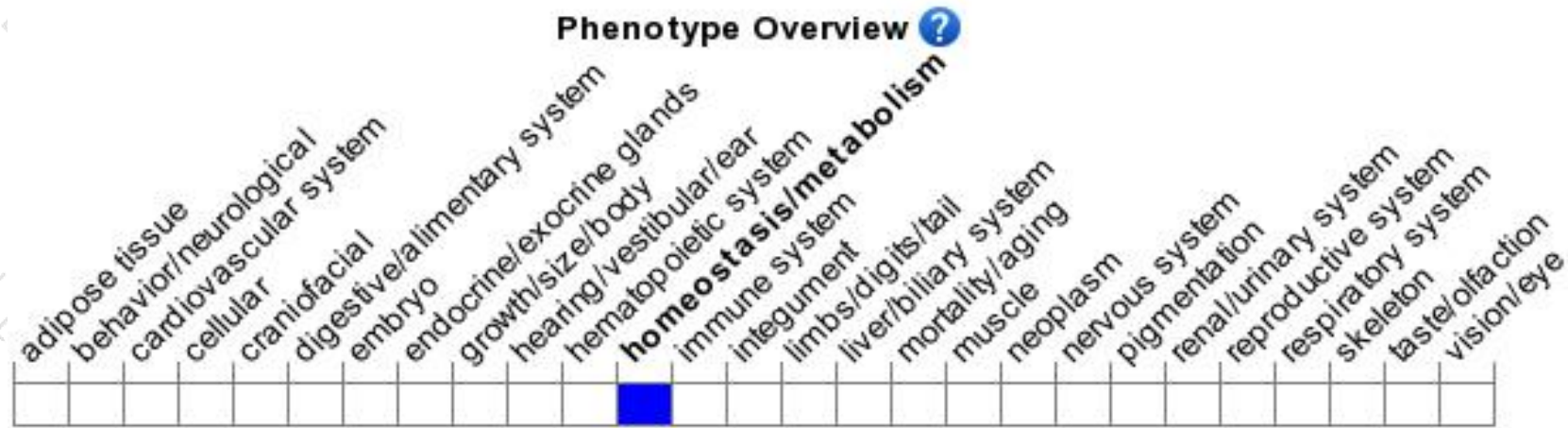
Genomic location distribution



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 null allele exhibit decreased cholesterol synthesis and plasma levels under fasting conditions compared to wild-type mice.

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

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