

TL1 Cas9-KO Strategy

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Project Overview

Project Name

Tll1

Project type

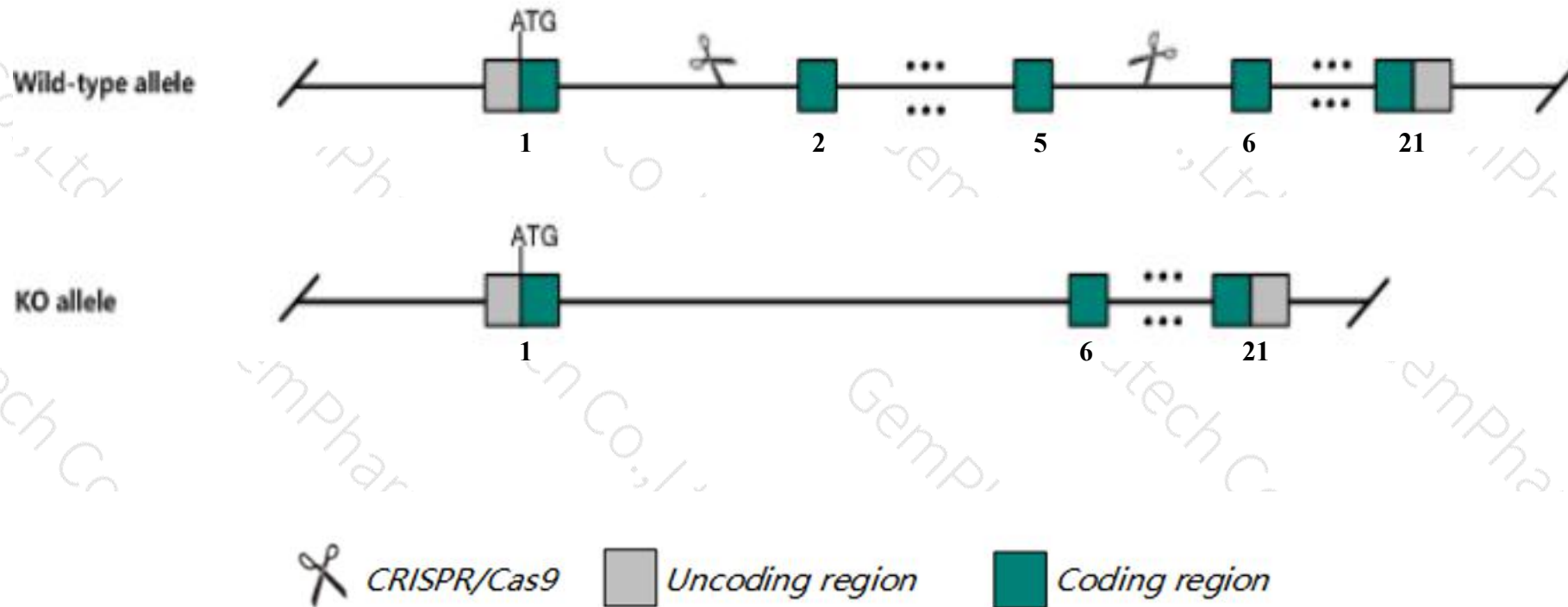
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tll1* gene. The schematic diagram is as follows:



- The *Tll1* gene has 4 transcripts. According to the structure of *Tll1* gene, exon2-exon5 of *Tll1-201* (ENSMUST00000066166.5) transcript is recommended as the knockout region. The region contains 463bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Tll1* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, homozygous null mice are embryonic lethal with death at midgestation from cardiac failure. cardiac defects include incomplete formation of the ventricular septum and abnormal positioning of the heart and aorta.
- Transcript *Tll1-203* may not be affected.
- The *Tll1* 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)

Tll1 tolloid-like [Mus musculus (house mouse)]

Gene ID: 21892, updated on 13-Mar-2020

Summary



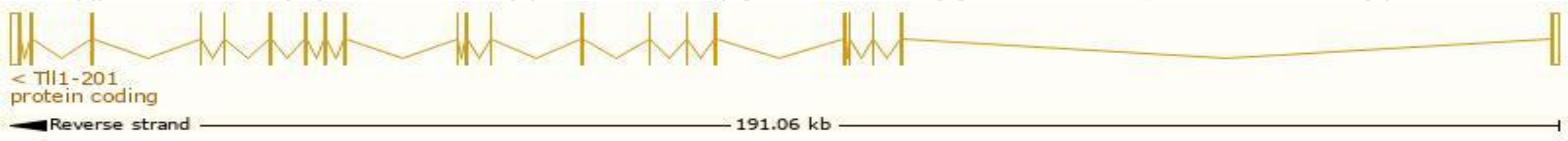
Official Symbol	Tll1 provided by MGI
Official Full Name	tolloid-like provided by MGI
Primary source	MGI:MGI:106923
See related	Ensembl:ENSMUSG00000053626
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Tll, Tll-1, b2b2476Clo
Expression	Biased expression in cerebellum adult (RPKM 2.0), limb E14.5 (RPKM 0.7) and 13 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

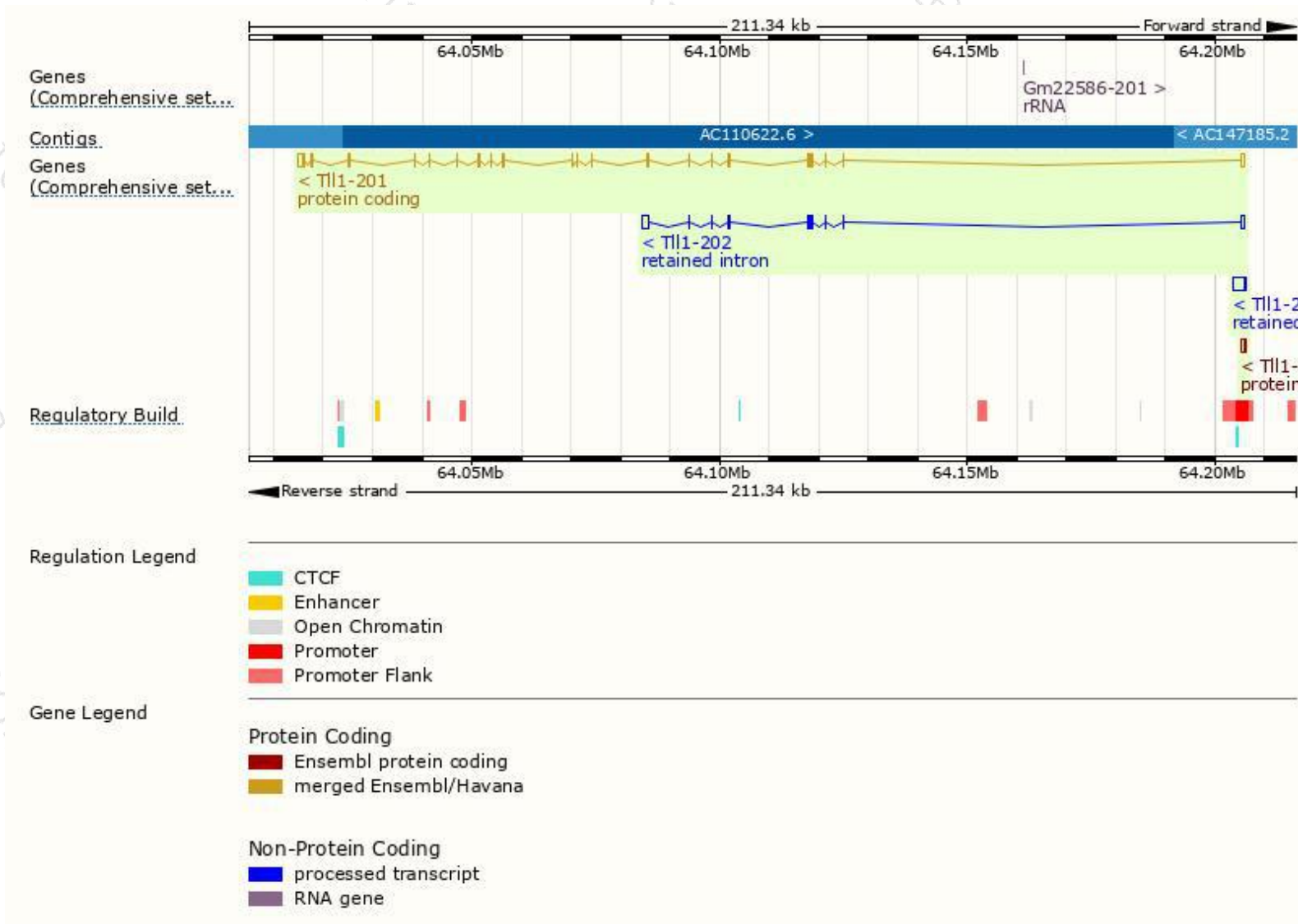
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
TI11-201	ENSMUST00000066166.5	4767	1013aa	Protein coding	CCDS40352	G3X9F5	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
TI11-203	ENSMUST00000210256.1	687	8aa	Protein coding	-	A0A1B0GRW8	CDS 3' incomplete TSL:1
TI11-202	ENSMUST00000209451.1	2908	No protein	Retained intron	-	-	TSL:1
TI11-204	ENSMUST00000211755.1	2516	No protein	Retained intron	-	-	TSL:1

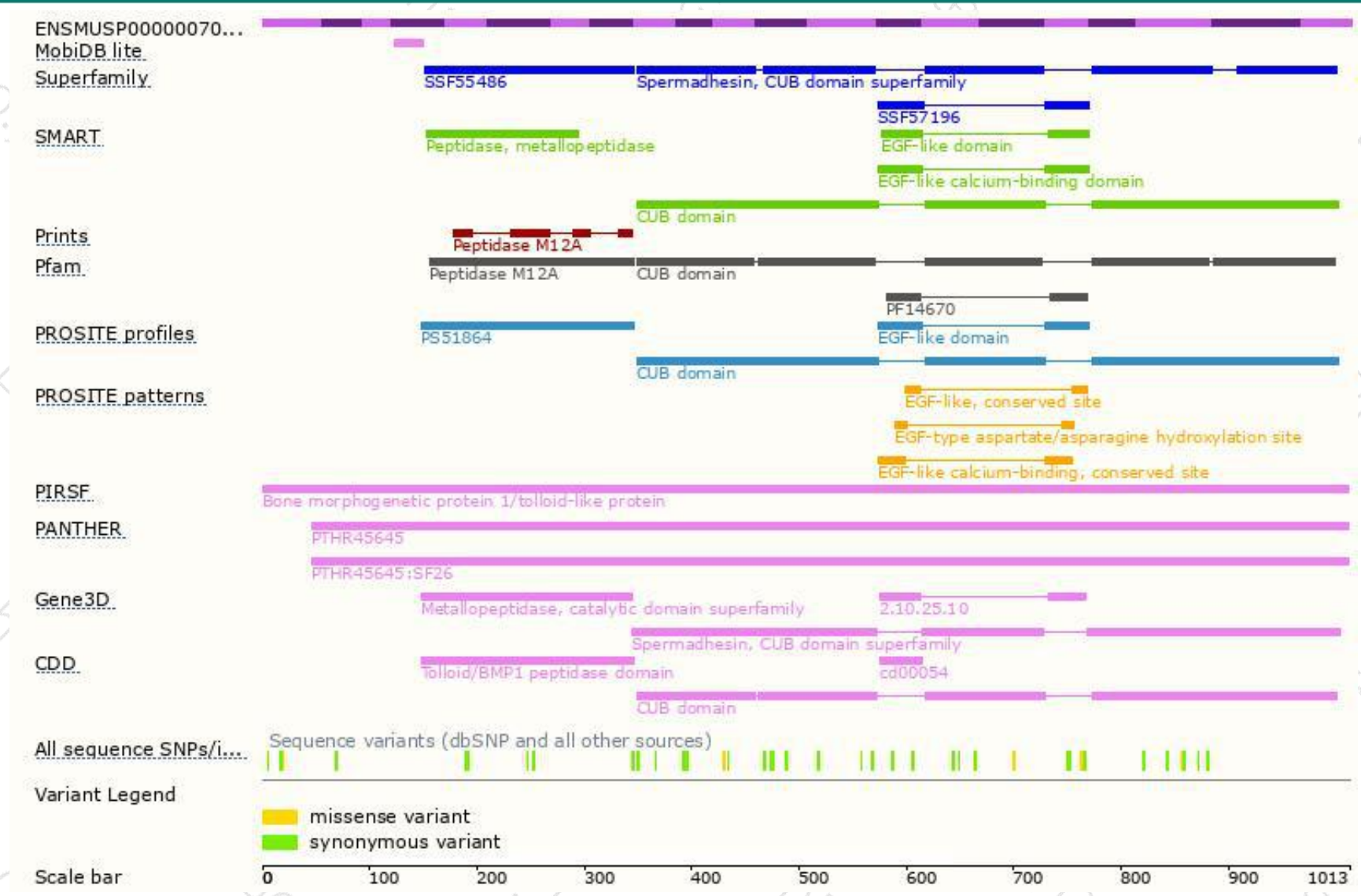
The strategy is based on the design of *TI11-201* transcript,the transcription is shown below



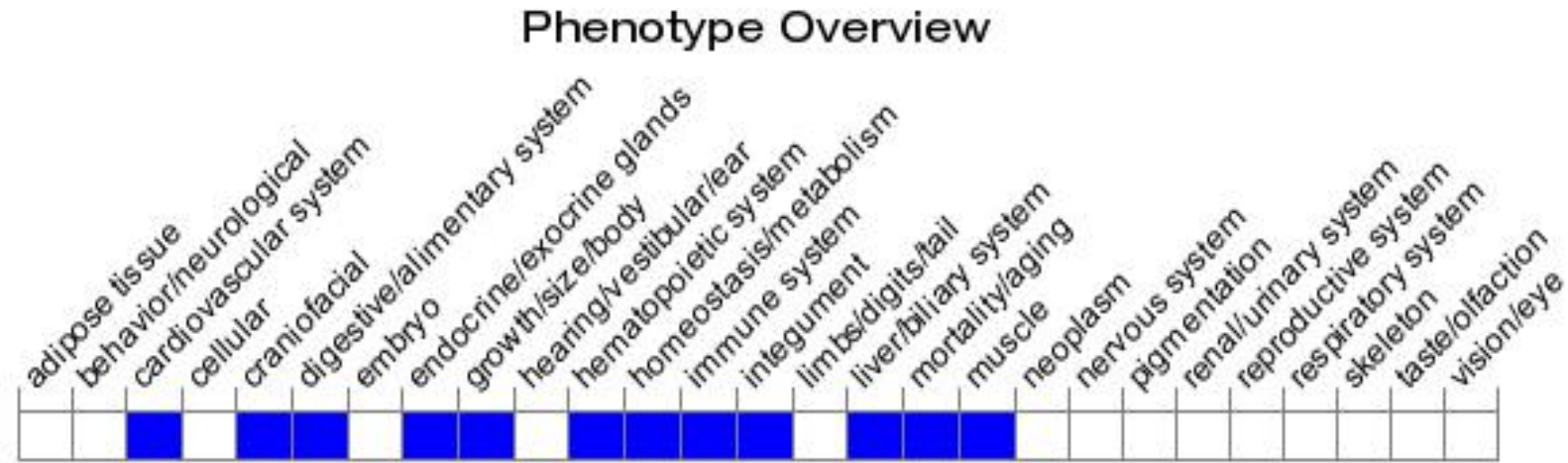
Genomic location distribution



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, homozygous null mice are embryonic lethal with death at midgestation from cardiac failure. Cardiac defects include incomplete formation of the ventricular septum and abnormal positioning of the heart and aorta.

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

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