

Axl Cas9-KO Strategy

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Date: 2020/2/13

Project Overview

Project Name

Axl

Project type

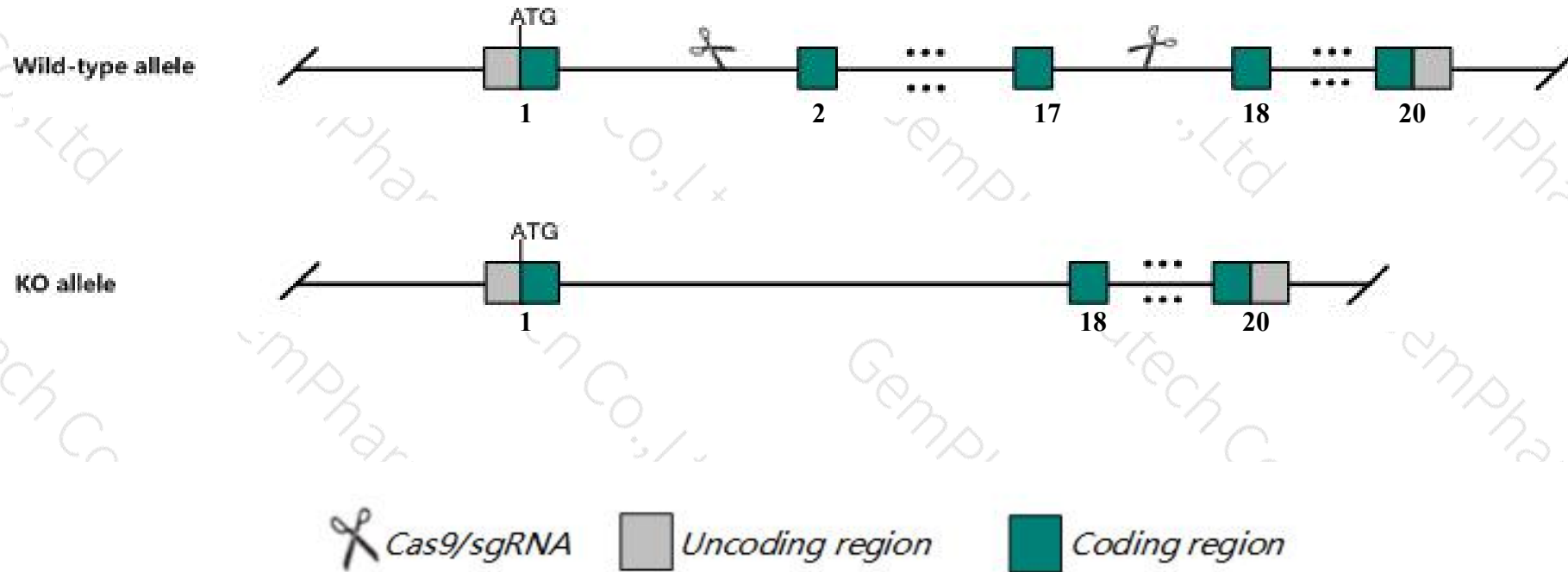
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Axl* gene has 8 transcripts. According to the structure of *Axl* gene, exon2-exon17 of *Axl-201* (ENSMUST00000002677.10) transcript is recommended as the knockout region. The region contains 1954bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Axl* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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, Homozygous mutant mice are phenotypically normal, however in conjunction with mutations in other related receptor tyrosine kinases, mutations of this gene results in fertility defects, autoimmunity abnormalities, and aberrant apoptosis.
- The *Axl* 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)

Axl AXL receptor tyrosine kinase [Mus musculus (house mouse)]

Gene ID: 26362, updated on 30-Mar-2019

Summary



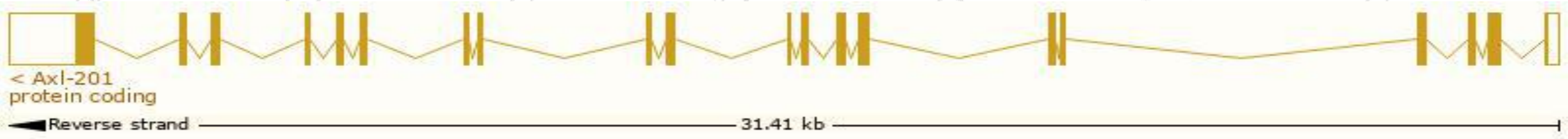
Official Symbol	Axl provided by MGI
Official Full Name	AXL receptor tyrosine kinase provided by MGI
Primary source	MGI:MGI:1347244
See related	Ensembl:ENSMUSG00000002602
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI323647, Ark, Tyro7, Ufo
Expression	Broad expression in ovary adult (RPKM 53.4), mammary gland adult (RPKM 42.5) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

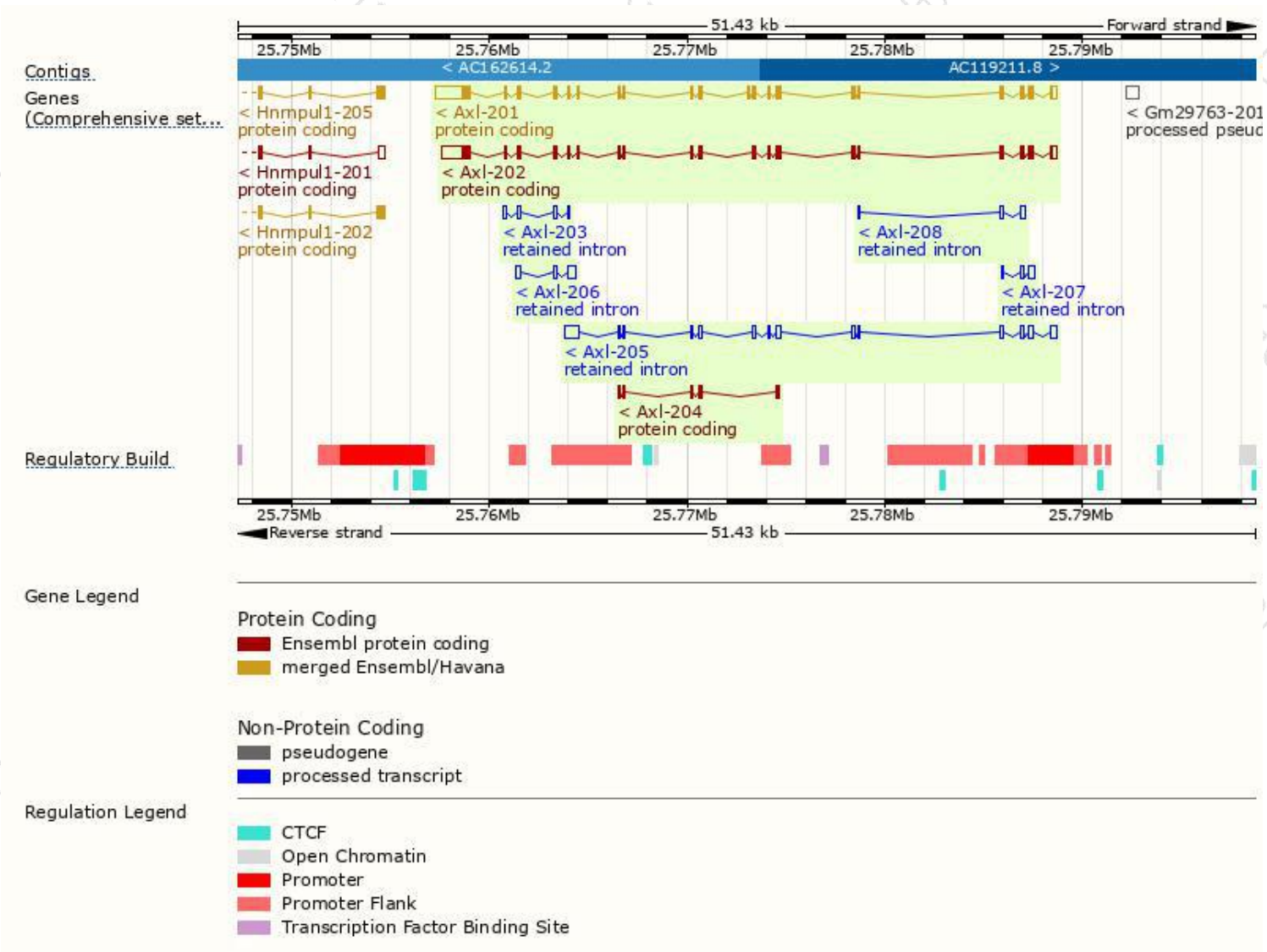
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Axl-201	ENSMUST00000002677.10	4265	888aa	Protein coding	CCDS20996	Q00993	TSL:1 GENCODE basic APPRIS P3
Axl-202	ENSMUST00000085948.10	3899	879aa	Protein coding	CCDS57528	Q6PE80	TSL:1 GENCODE basic APPRIS ALT2
Axl-204	ENSMUST00000132038.2	563	188aa	Protein coding	-	F6YPR4	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Axl-205	ENSMUST00000132989.7	2609	No protein	Retained intron	-	-	TSL:2
Axl-206	ENSMUST00000137211.1	777	No protein	Retained intron	-	-	TSL:3
Axl-203	ENSMUST00000124442.7	602	No protein	Retained intron	-	-	TSL:2
Axl-207	ENSMUST00000137383.1	455	No protein	Retained intron	-	-	TSL:3
Axl-208	ENSMUST00000147680.1	382	No protein	Retained intron	-	-	TSL:3

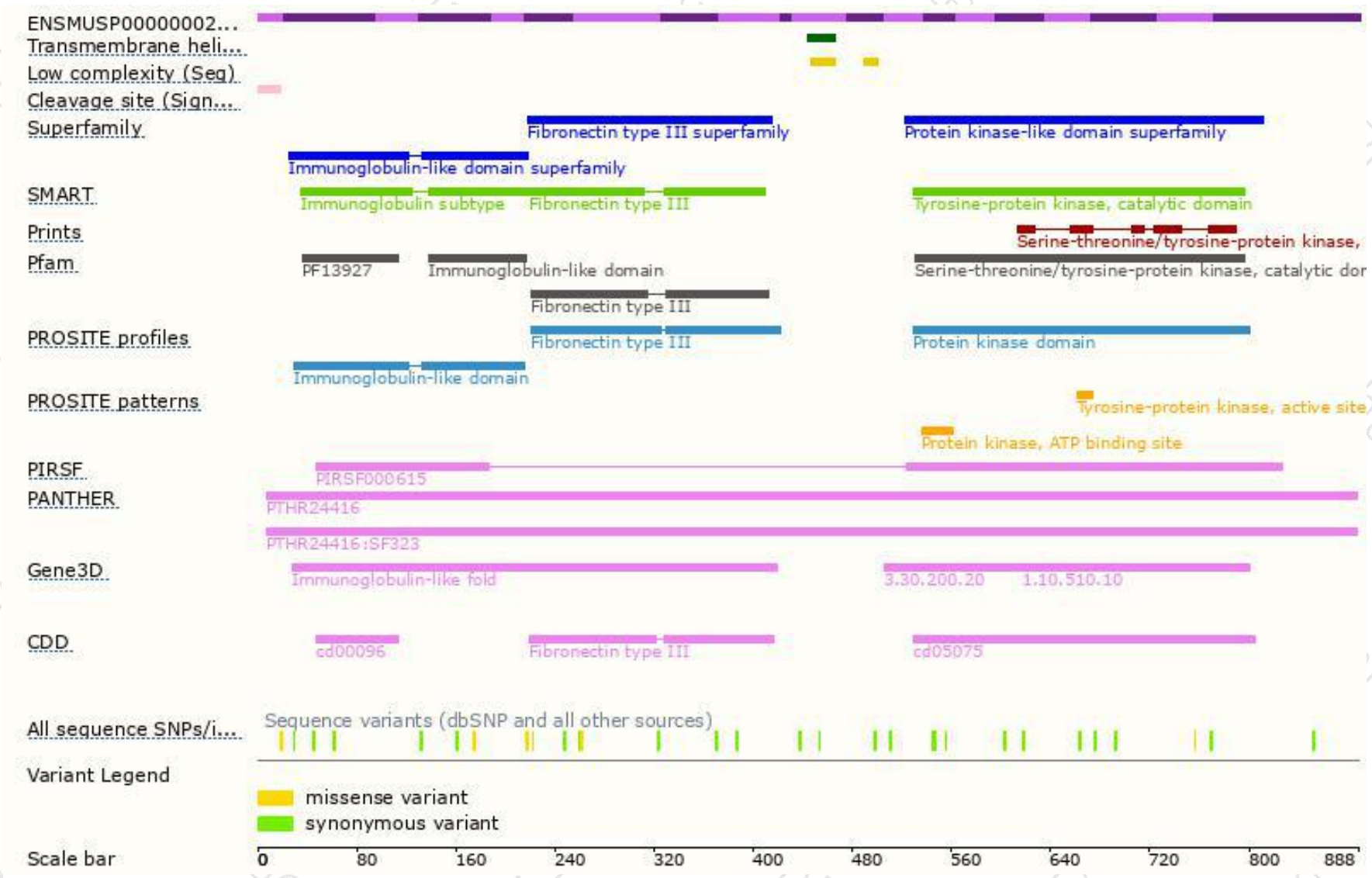
The strategy is based on the design of *Axl-201* transcript,The transcription is shown below



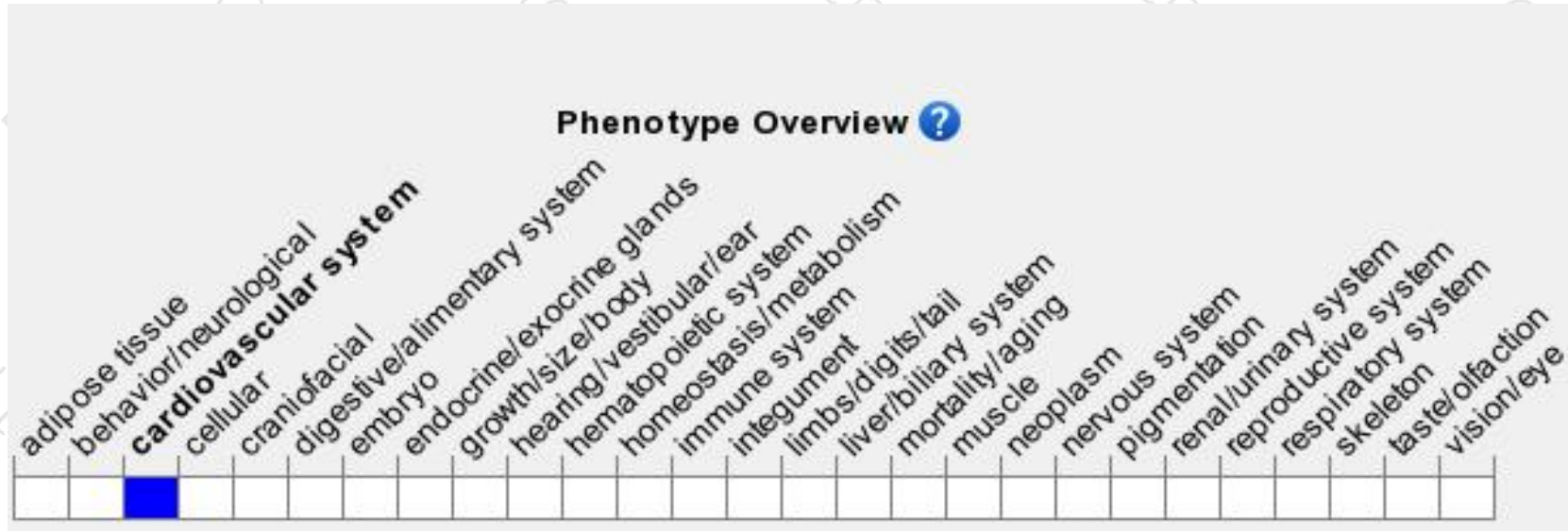
Genomic location distribution



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 mutant mice are phenotypically normal, however in conjunction with mutations in other related receptor tyrosine kinases, mutations of this gene results in fertility defects, autoimmunity abnormalities, and aberrant apoptosis.

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

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