Axl Cas9-KO Strategy

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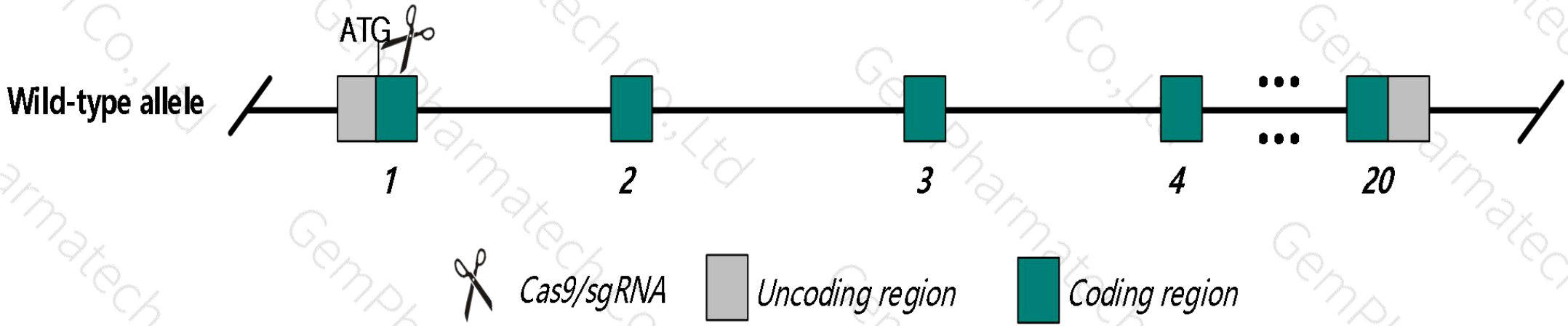
Project Overview

Project Name	***Axl***
Project type	**Cas9-KO**
Strain background	**BALB/cJ**

Knockout strategy

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



Technical routes

- The *Axl* gene has 8 transcripts. According to the structure of *Axl* gene, exon1 of MGP_BALBcJ_T0082410.1 transcript is recommended as the knockout region. Screening mouse model of frameshift mutation.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 BALB/cJ 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 BALB/cJ mice.

Notice

- 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）

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

Gene ID: 26362, updated on 21-May-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	Ark; Ufo; Tyro7; AI323647
Expression	Broad expression in ovary adult (RPKM 53.4), mammary gland adult (RPKM 42.5) and 28 other tissues See more
Orthologs	human all

Genomic context

Location: 7 A3; 7 14.02 cM

See Axl in Genome Data Viewer

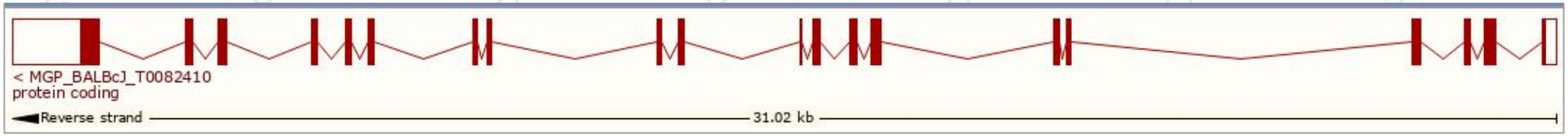
Exon count: 20

Transcript information（Ensembl）

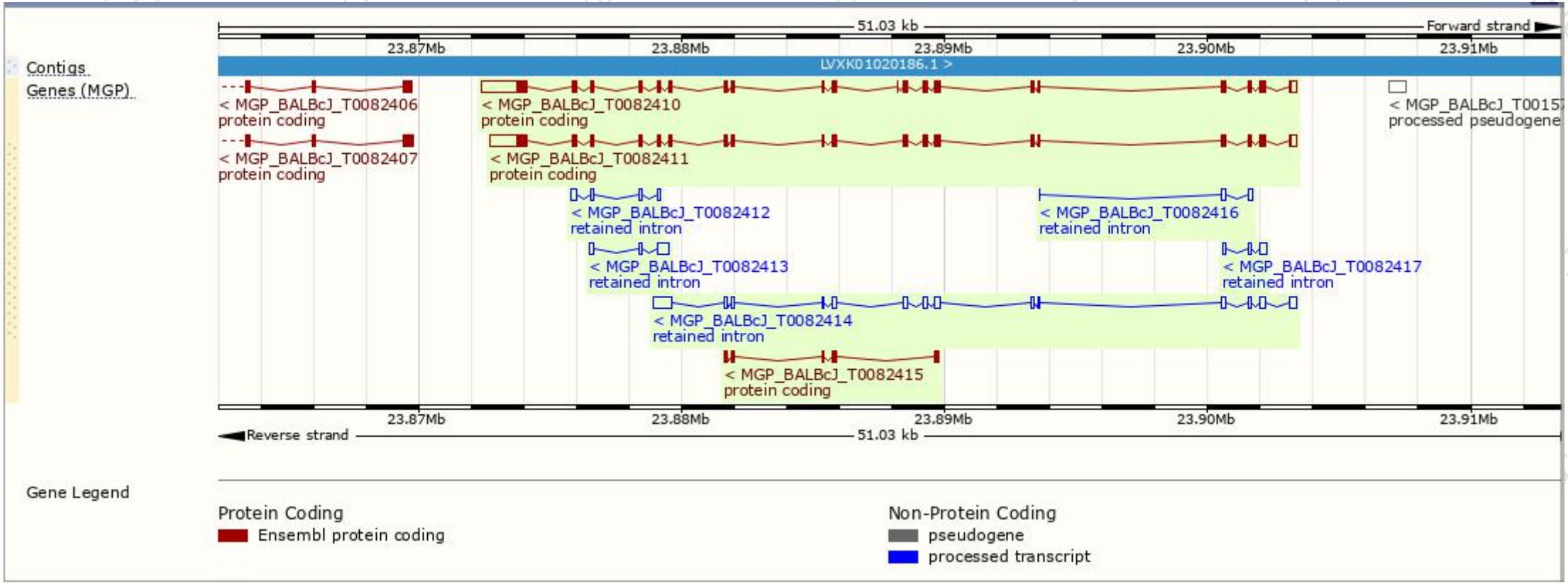
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
-	MGP_BALBcJ_T0082410.1	4265	888aa	Protein coding	CCDS20996, CCDS57528	F6YPR4 Q00993 Q6PE80	-
-	MGP_BALBcJ_T0082411.1	3899	879aa	Protein coding	-	-	-
-	MGP_BALBcJ_T0082415.1	563	187aa	Protein coding	-	-	-
-	MGP_BALBcJ_T0082414.1	2609	No protein	Retained intron	-	-	-
-	MGP_BALBcJ_T0082413.1	777	No protein	Retained intron	-	-	-
-	MGP_BALBcJ_T0082412.1	602	No protein	Retained intron	-	-	-
-	MGP_BALBcJ_T0082417.1	455	No protein	Retained intron	-	-	-
-	MGP_BALBcJ_T0082416.1	382	No protein	Retained intron	-	-	-

The strategy is based on the design of *MGP_BALBcJ_T0082410.1* transcript,The transcription is shown below

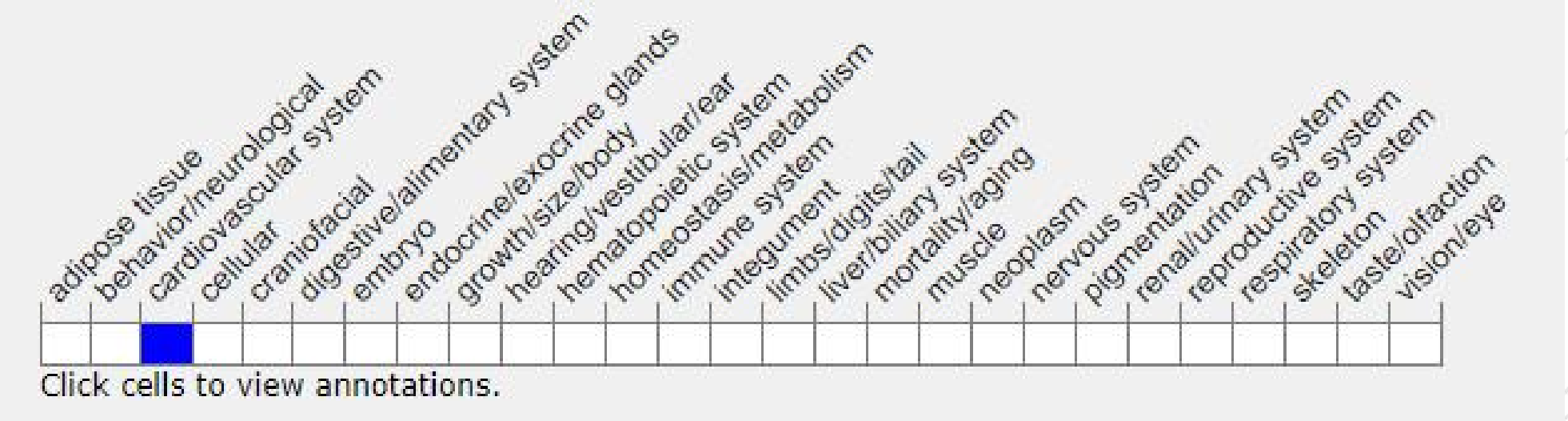


Genomic location distribution



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/marker/MGI:1347244).

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.

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

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