Atg9b Cas9-KO *Strategy*

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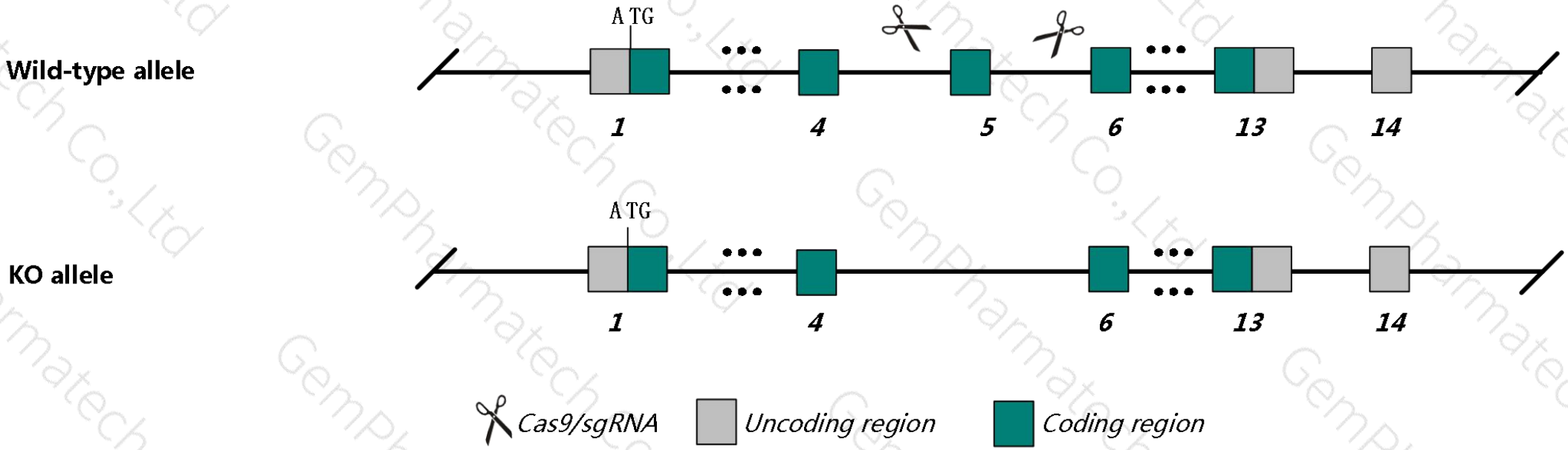
Project Overview

Project Name	***Atg9b***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atg9b* gene. The schematic diagram is as follows:



Technical routes

- The *Atg9b* gene has 3 transcripts.According to the structure of *Atg9b* gene, exon 5 of *Atg9b*-201(ENSMUST00000059401.6)transcript is recommended as the knockout region.The region contains 142 bp coding sequence.Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Atg9b* 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.

Notice

- The *Atg9b* gene is located on the Chr 5 . 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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Atg9b autophagy related 9B [*Mus musculus* (house mouse)]

Gene ID: 213948, updated on 31-Jan-2019

Summary

Official Symbol	Atg9b provided by MGI
Official Full Name	autophagy related 9B provided by MGI
Primary source	MGI:MGI:2685420
See related	Ensembl:ENSMUSG00000038295
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	eONE; sONE; Gm574; Apg912; Apg9l2; Apgdc2; Nos3as
Expression	Broad expression in stomach adult (RPKM 10.7), lung adult (RPKM 3.8) and 19 other tissues See more
Orthologs	human all

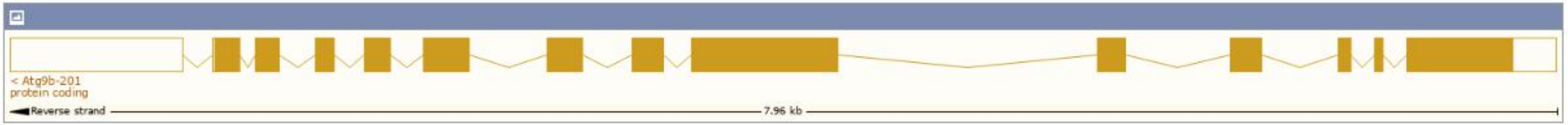
Transcript information（Ensembl）

The gene has 3 transcripts, and all transcripts are shown below:

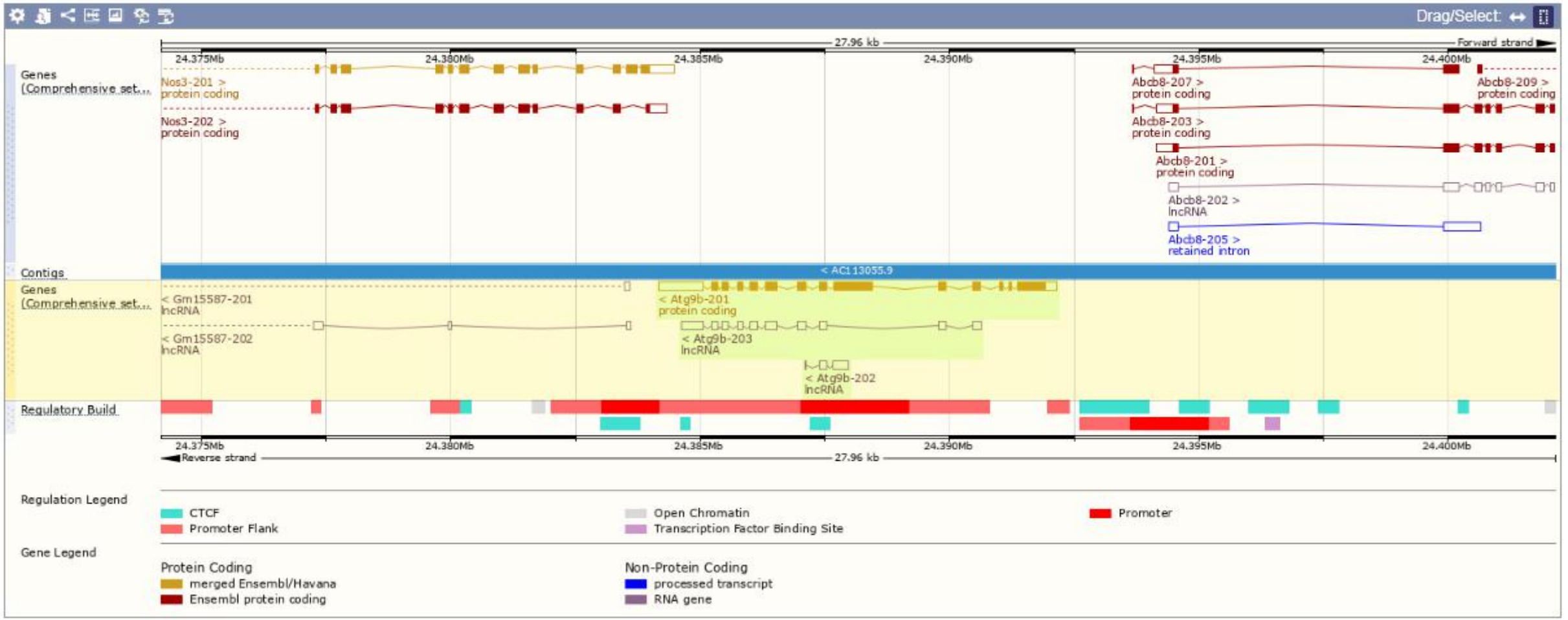
Show/hide columns (1 hidden) Filter

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atg9b-203	ENSMUST00000138716.7	1837	No protein	lncRNA	-	-	TSL:5
Atg9b-202	ENSMUST00000128831.1	490	No protein	lncRNA	-	-	TSL:3
Atg9b-201	ENSMUST00000059401.6	3902	922aa	Protein coding	CCDS39027	Q6EBV9	TSL:1 GENCODE basic APPRIS P1

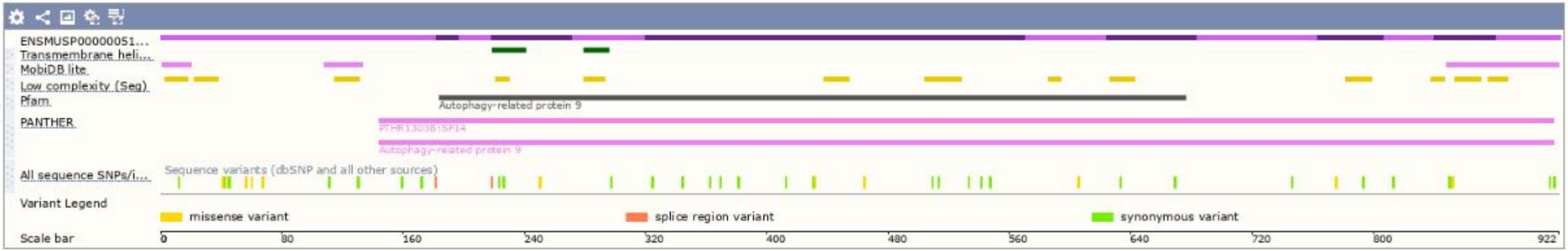
The strategy is based on the design of *Atg9b-201* transcript,The transcription is shown below



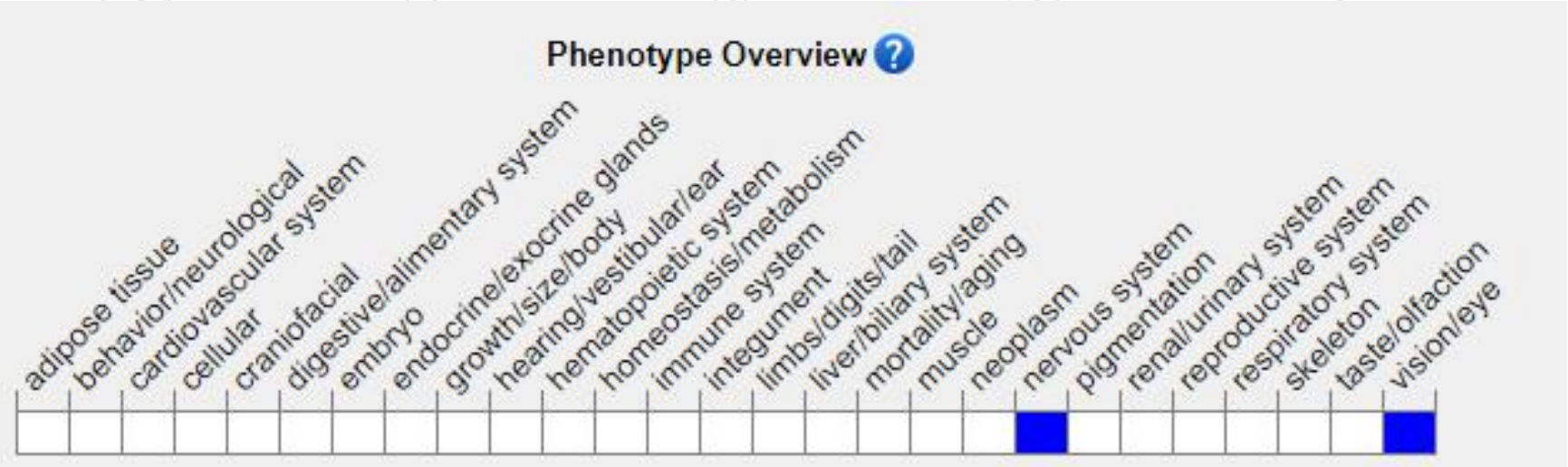
Genomic location (Ensembl)



Protein domain (Ensembl)



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,Mutations in this locus affect cell-cycle regulation and apoptos is. Null homozygotes show high, early-onset tumor incidence; some have persistent hyaloid vasculature and cataracts. Truncated or temperature-sensitive alleles cause early aging phenotypes.

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

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