Atg5 Cas9-KO Strategy

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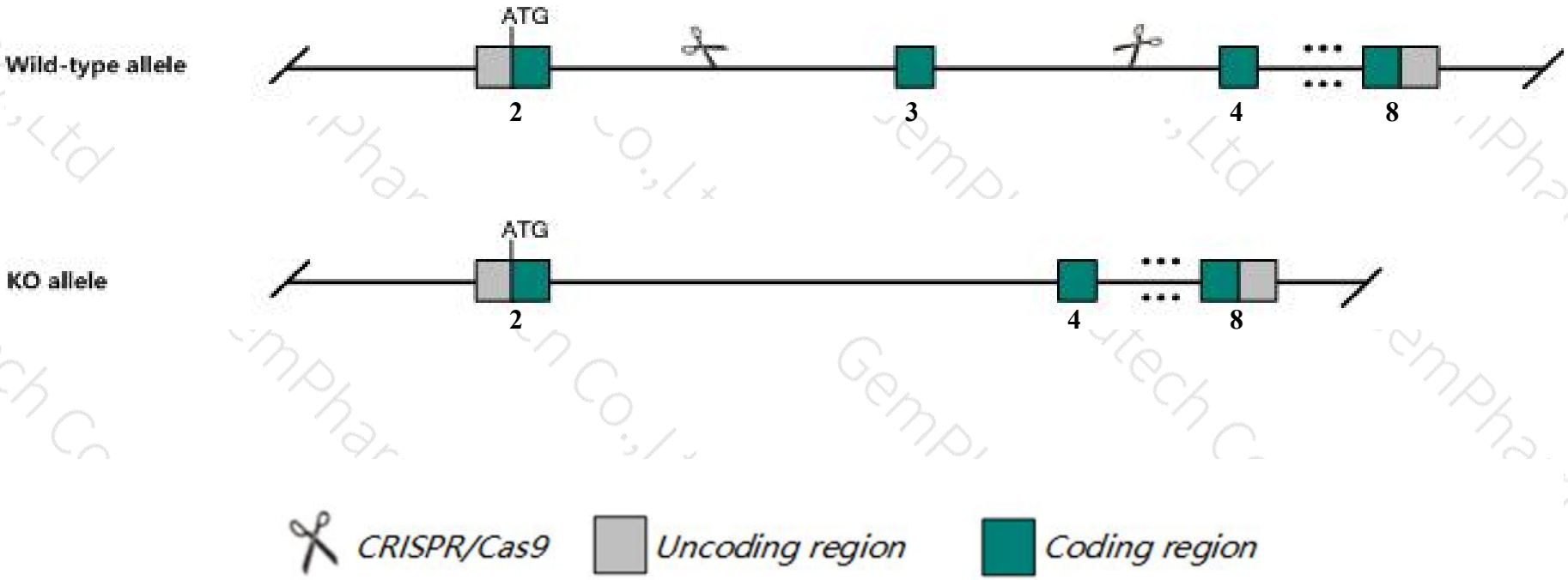
Design Date: 2019-7-22

Project Overview

Project Name	***Atg5***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atg5* gene. The schematic diagram is as follows:



Technical routes

➢ The *Atg5* gene has 2 transcripts. According to the structure of *Atg5* gene, exon3 of *Atg5-201* (ENSMUST00000039286.4) transcript is recommended as the knockout region.The region contains 128bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Atg5* gene. The brief process is as follows: CRISPR/Cas9 system v

Notice

- According to the existing MGI data,Mutation of this gene results in impaired autophagy due to absence of autolysosomes. Homozygotes die within 1 day of birth, have shorter survival times and reduced amino acid levels under fasting conditions. Homozygotes for a gene trap insertion mutationin this gene show no abnormal phenotype.

- The *Atg5* gene is located on the Chr10. 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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Atg5 autophagy related 5 [Mus musculus (house mouse)]

Gene ID: 11793, updated on 2-Apr-2019

Summary

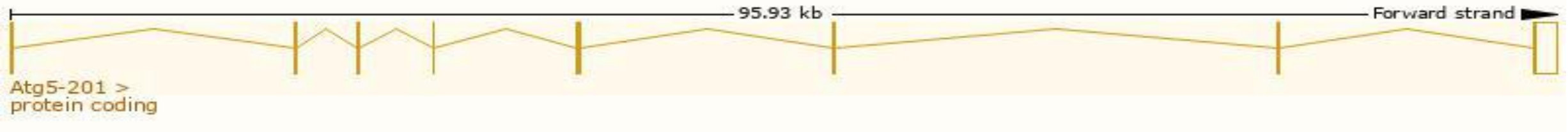
Official Symbol	Atg5 provided by MGI
Official Full Name	autophagy related 5 provided by MGI
Primary source	MGI:MGI:1277186
See related	Ensembl:ENSMUSG00000038160
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2010107M05Rik, 3110067M24Rik, AW319544, Apg5l, Atg5l, C88337, Paddy
Summary	The protein encoded by this gene, in combination with autophagy protein 12, functions as an E1-like activating enzyme in a ubiquitin-like conjugating system. The encoded protein is involved in several cellular processes, including autophagic vesicle formation, mitochondrial quality control after oxidative damage, negative regulation of the innate antiviral immune response, lymphocyte development and proliferation, MHC II antigen presentation, adipocyte differentiation, and apoptosis. Two transcript variants encoding different protein isoforms have been found for this gene. [provided by RefSeq, Sep 2015]
Expression	Ubiquitous expression in placenta adult (RPKM 9.7), bladder adult (RPKM 9.2) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

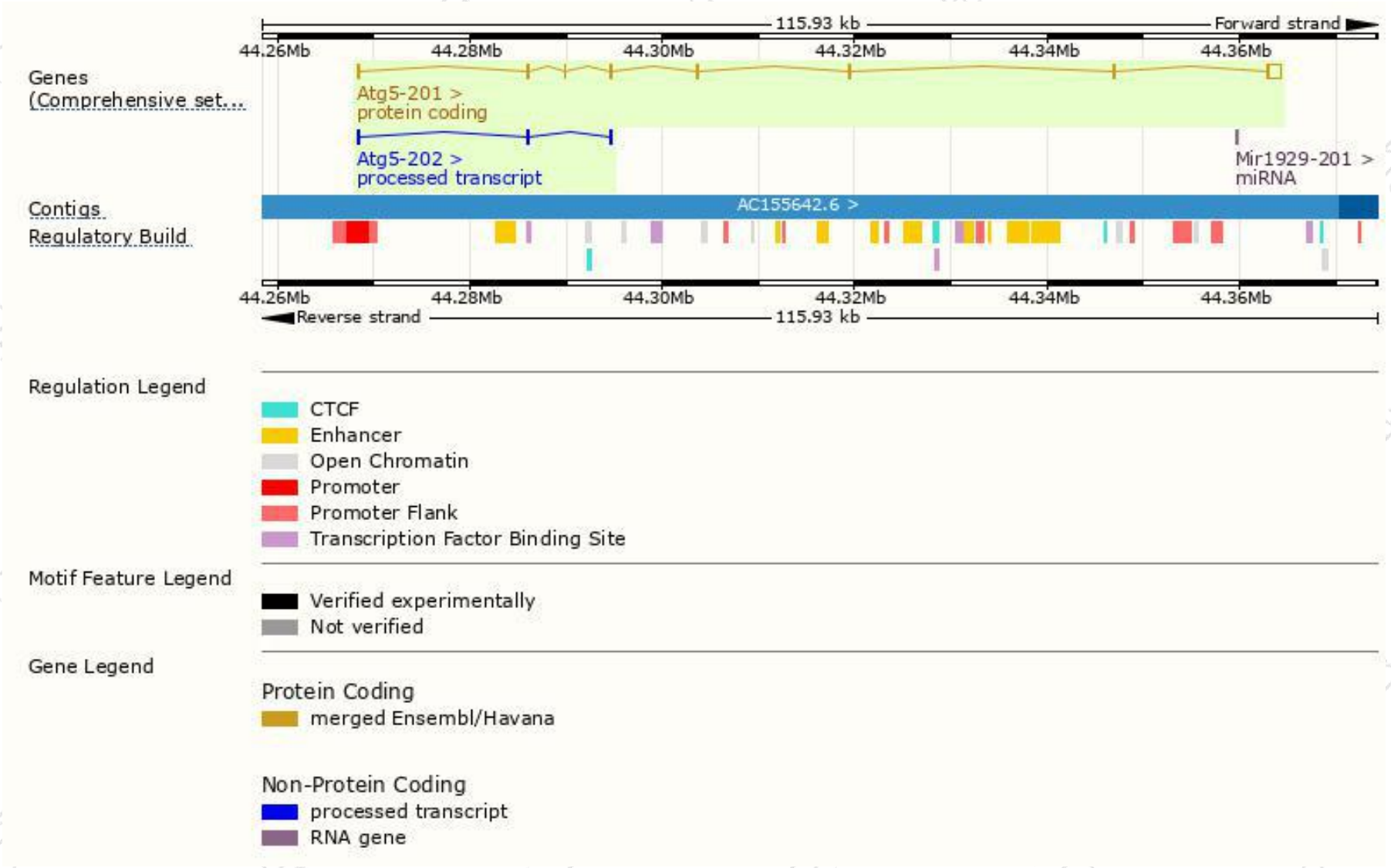
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atg5-201	ENSMUST00000039286.4	2352	275aa	Protein coding	CCDS23824	Q99J83	TSL:1 GENCODE basic APPRIS P1
Atg5-202	ENSMUST00000217412.1	415	No protein	Processed transcript	-	-	TSL:3

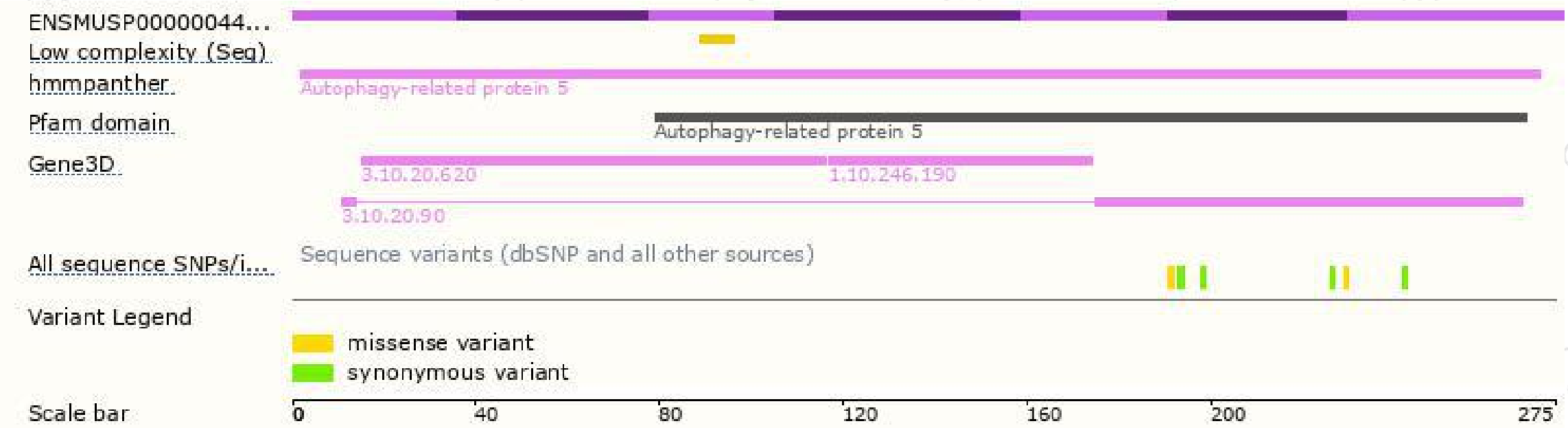
The strategy is based on the design of *Atg5-201* transcript,The transcription is shown below



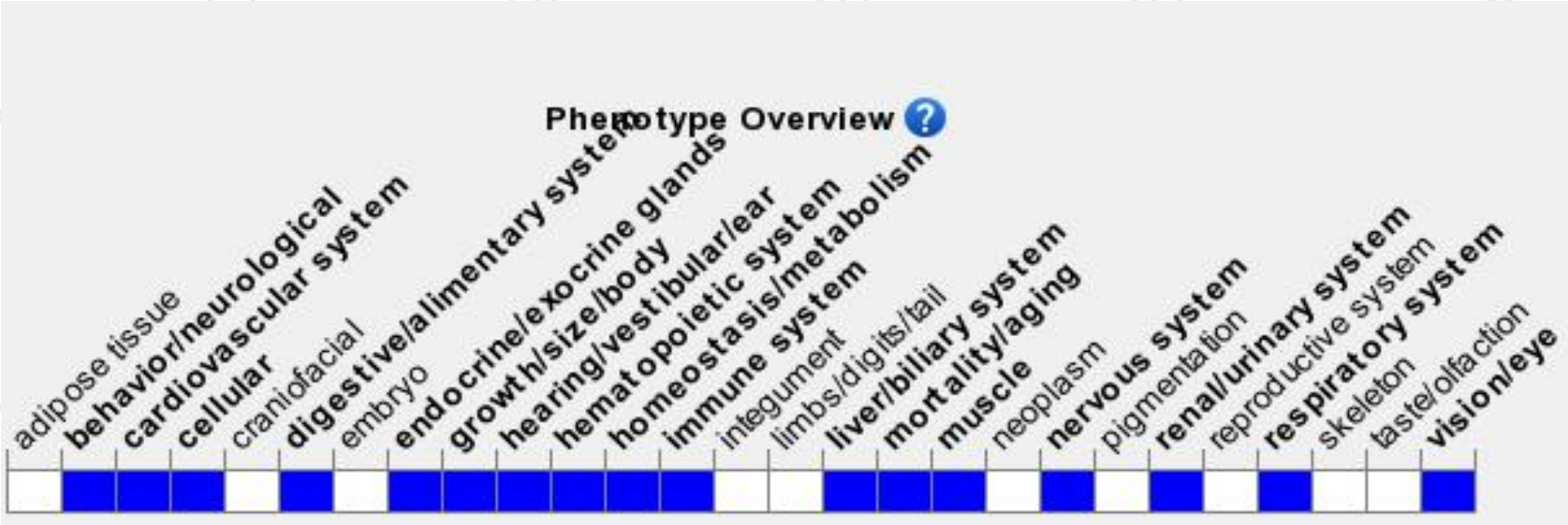
Genomic location distribution



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/).

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

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