

Atg16l2 Cas9-KO Strategy

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Project Overview

Project Name

Atg16l2

Project type

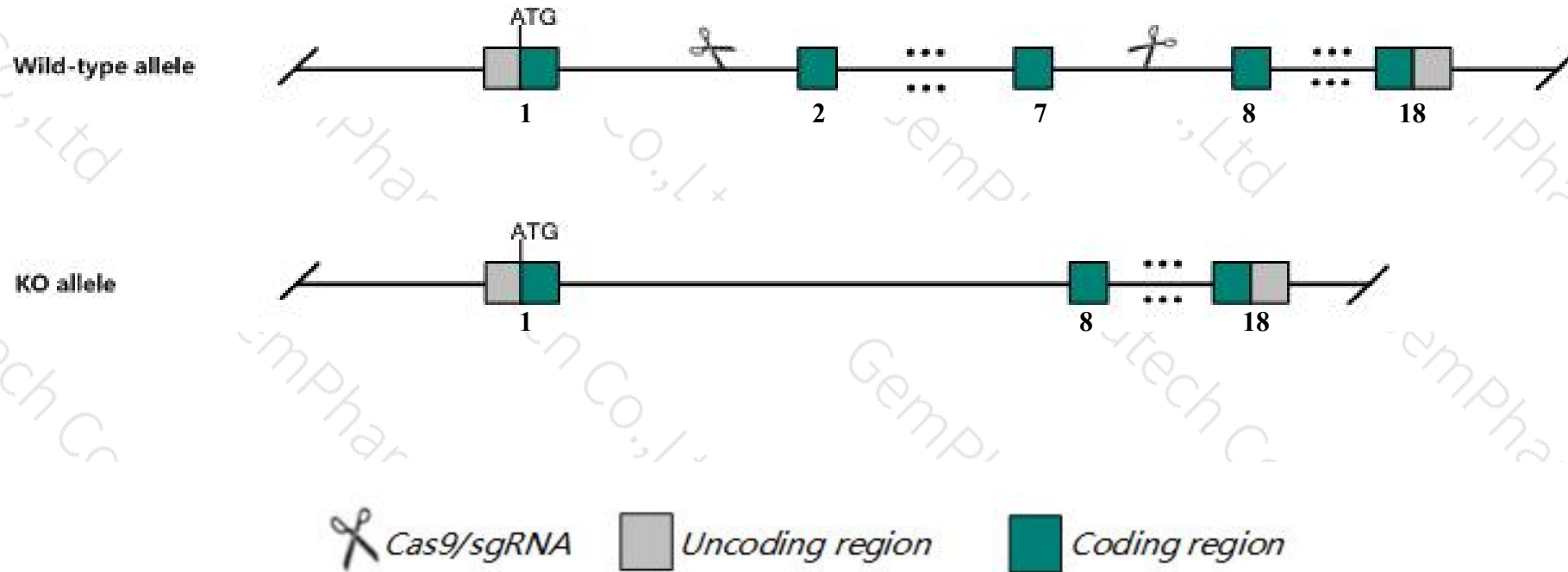
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atg16l2* gene. The schematic diagram is as follows:



- The *Atg16l2* gene has 17 transcripts. According to the structure of *Atg16l2* gene, exon2-exon7 of *Atg16l2-201* (ENSMUST00000120267.8) transcript is recommended as the knockout region. The region contains 709bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Atg16l2* 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, Mice homozygous for an ENU-induced allele exhibit lymphopenia.
- The *Atg16l2* 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)

Atg16l2 autophagy related 16-like 2 (*S. cerevisiae*) [*Mus musculus* (house mouse)]

Gene ID: 73683, updated on 31-Jan-2019

Summary

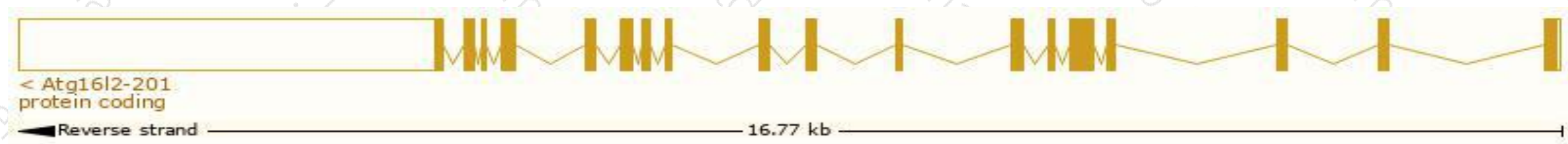
Official Symbol	Atg16l2 provided by MGI
Official Full Name	autophagy related 16-like 2 (<i>S. cerevisiae</i>) provided by MGI
Primary source	MGI:MGI:1920933
See related	Ensembl:ENSMUSG00000047767
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2410118P20Rik
Expression	Ubiquitous expression in spleen adult (RPKM 5.6), thymus adult (RPKM 4.5) and 27 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

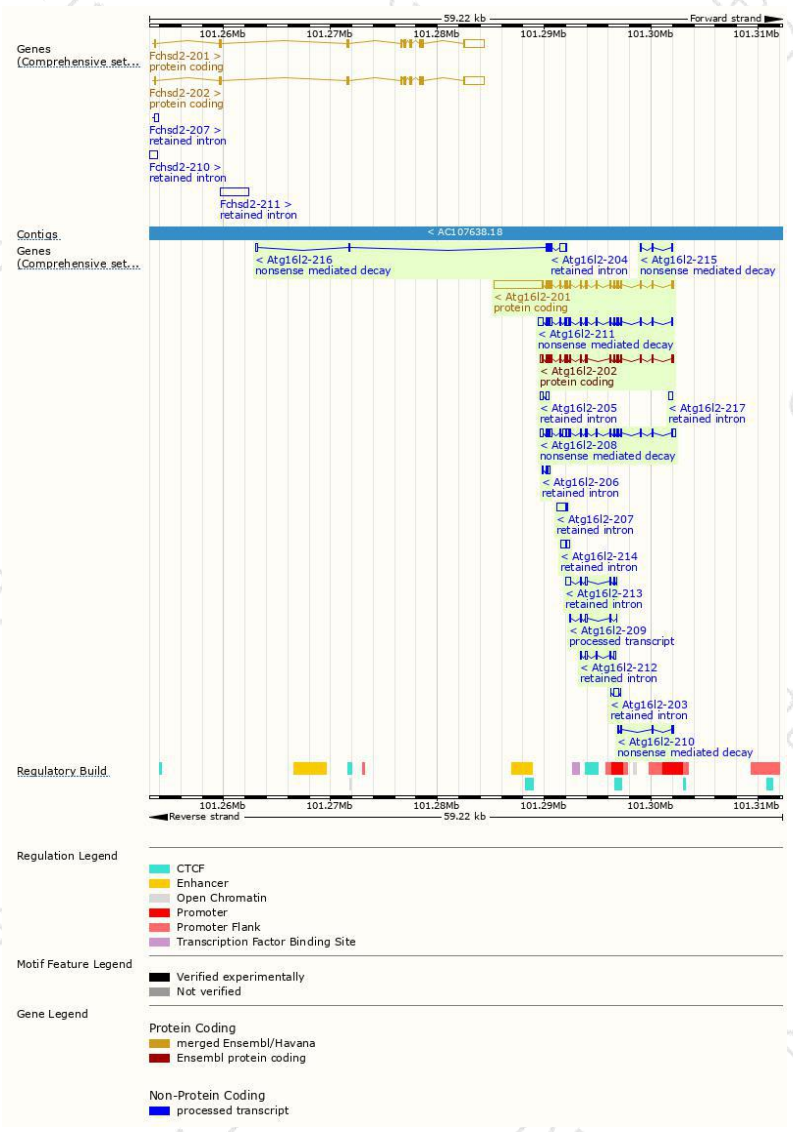
The gene has 17 transcripts,all transcripts are shown below:

Show/hide columns (1 hidden)						Filter			
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags		
Atg16l2-217	ENSMUST00000209093.1	374	No protein	Retained intron	-	-	TSL:NA		
Atg16l2-216	ENSMUST00000207740.1	473	46aa	Nonsense mediated decay	-	A0A140LIS0	CDS 5' incomplete	TSL:3	
Atg16l2-215	ENSMUST00000207121.1	358	44aa	Nonsense mediated decay	-	A0A140LHW3	TSL:3		
Atg16l2-214	ENSMUST00000153327.1	706	No protein	Retained intron	-	-	TSL:2		
Atg16l2-213	ENSMUST00000151297.7	829	No protein	Retained intron	-	-	TSL:3		
Atg16l2-212	ENSMUST00000146445.1	584	No protein	Retained intron	-	-	TSL:3		
Atg16l2-211	ENSMUST00000143630.7	2501	403aa	Nonsense mediated decay	-	Q6KAU8	TSL:5		
Atg16l2-210	ENSMUST00000140553.1	459	81aa	Nonsense mediated decay	-	D6RHC1	TSL:3		
Atg16l2-209	ENSMUST00000140059.1	377	No protein	lncRNA	-	-	TSL:5		
Atg16l2-208	ENSMUST00000139609.7	2655	403aa	Nonsense mediated decay	-	Q6KAU8	TSL:5		
Atg16l2-207	ENSMUST00000134531.1	878	No protein	Retained intron	-	-	TSL:2		
Atg16l2-206	ENSMUST00000131988.1	423	No protein	Retained intron	-	-	TSL:2		
Atg16l2-205	ENSMUST00000124617.1	608	No protein	Retained intron	-	-	TSL:2		
Atg16l2-204	ENSMUST00000123970.1	637	No protein	Retained intron	-	-	TSL:3		
Atg16l2-203	ENSMUST00000123835.1	518	No protein	Retained intron	-	-	TSL:5		
Atg16l2-202	ENSMUST00000122116.7	2083	602aa	Protein coding	-	D3Z653	TSL:1	GENCODE basic	APPRIS ALT2
Atg16l2-201	ENSMUST00000120267.8	6459	623aa	Protein coding	CCDS52329	G9M4M8 Q6KAU8	TSL:1	GENCODE basic	APPRIS P2

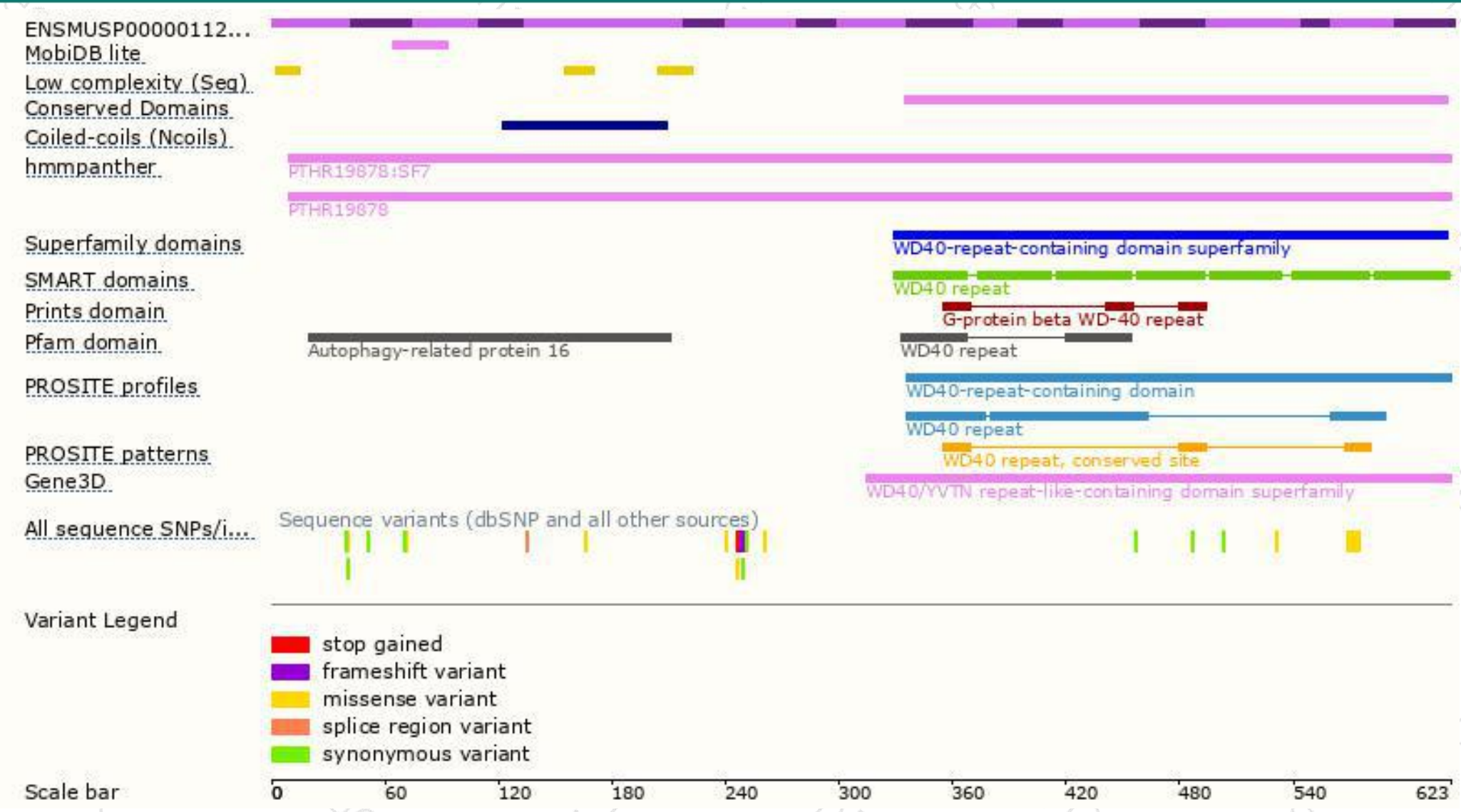
The strategy is based on the design of *Atg16l2-201* transcript,The transcription is shown below



Genomic location distribution

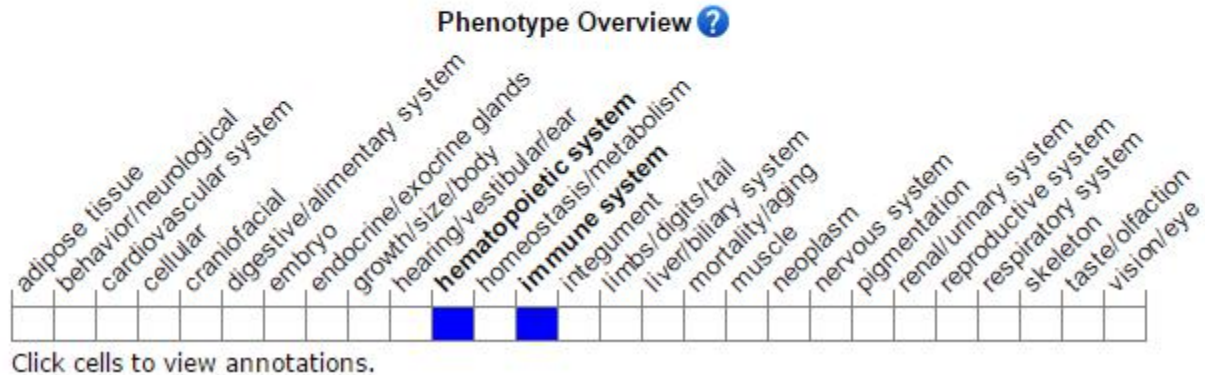


Protein domain



Mouse phenotype description(MGI)

less ▼ **Phenotype Summary** 1 phenotype from 1 allele in 1 genetic background
17 phenotype references



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,Mice homozygous for an ENU-induced allele exhibit lymphopenia.

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

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