

***Ruvbl2* Cas9-KO Strategy**

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Project Overview

Project Name

Ruvbl2

Project type

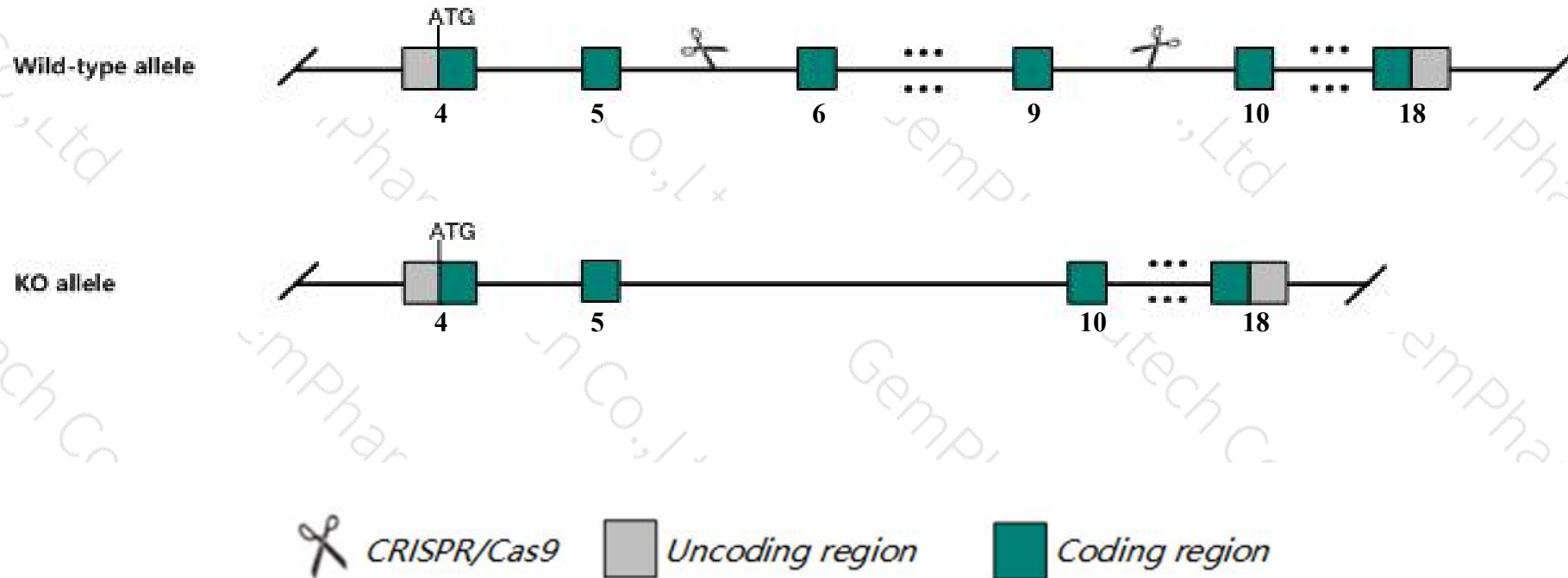
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ruvbl2* gene. The schematic diagram is as follows:



- The *Ruvbl2* gene has 8 transcripts. According to the structure of *Ruvbl2* gene, exon6-exon9 of *Ruvbl2-205* (ENSMUST00000211214.1) transcript is recommended as the knockout region. The region contains 395bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ruvbl2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for an ENU-induced allele exhibit lethality. Mice heterozygous for a knock-out allele exhibit impaired T cell development and maximal T dependent antibody responses.
- The *Ruvbl2* 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)

Ruvbl2 RuvB-like protein 2 [Mus musculus (house mouse)]

Gene ID: 20174, updated on 7-Apr-2019

Summary



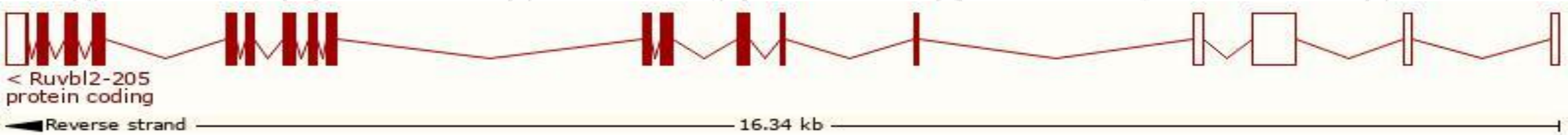
Official Symbol	Ruvbl2 provided by MGI
Official Full Name	RuvB-like protein 2 provided by MGI
Primary source	MGI:MGI:1342299
See related	Ensembl:ENSMUSG000000003868
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	mp47, p47
Expression	Ubiquitous expression in testis adult (RPKM 61.6), CNS E11.5 (RPKM 48.3) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

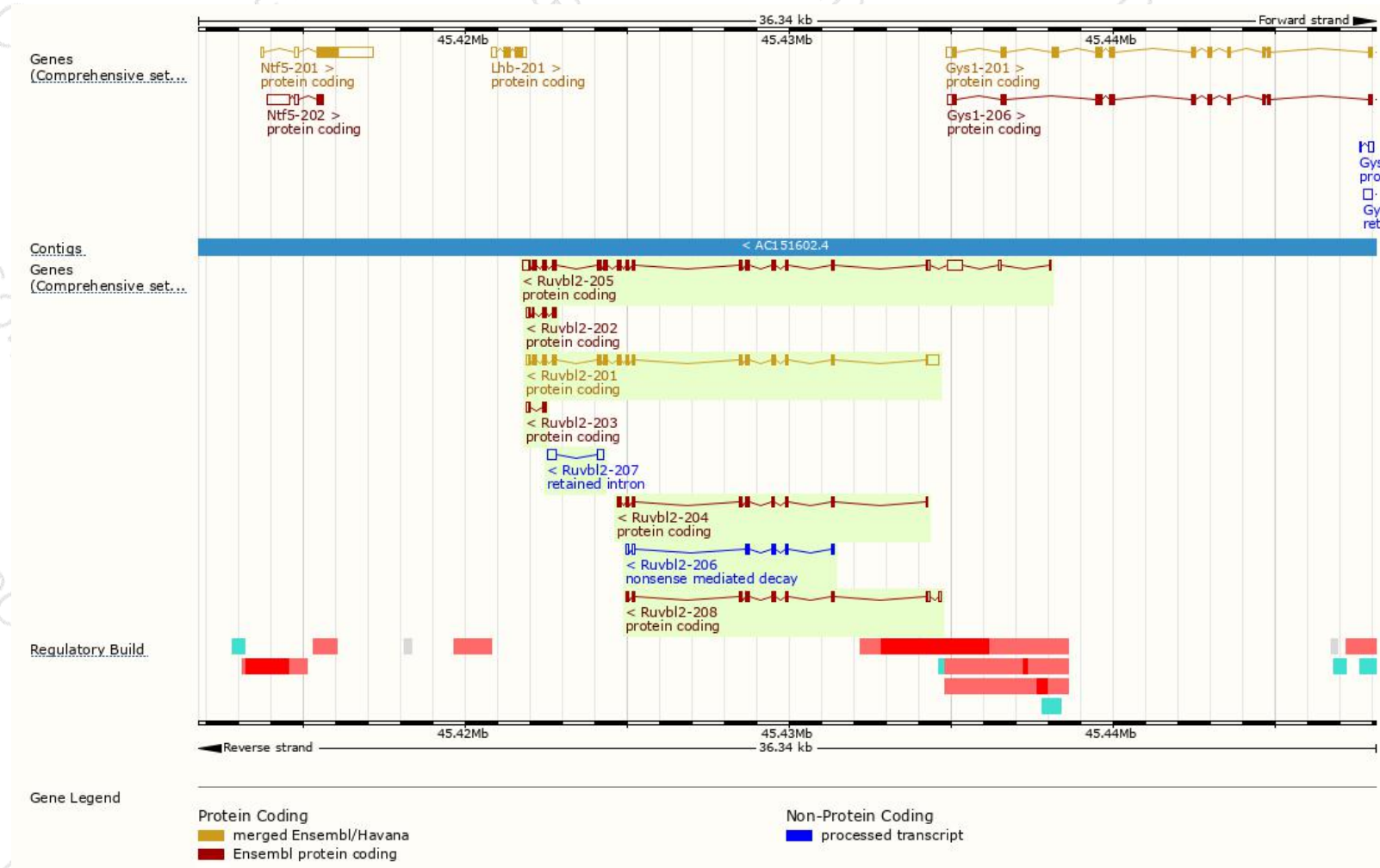
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ruvbl2-205	ENSMUST00000211214.1	2312	463aa	Protein coding	CCDS21243	Q3TXT7 Q9WTM5	TSL:1 GENCODE basic APPRIS P1
Ruvbl2-201	ENSMUST00000107771.11	1834	463aa	Protein coding	CCDS21243	Q3TXT7 Q9WTM5	TSL:1 GENCODE basic APPRIS P1
Ruvbl2-208	ENSMUST00000211666.1	846	221aa	Protein coding	-	A0A1B0GSR4	CDS 3' incomplete TSL:3
Ruvbl2-204	ENSMUST00000210439.1	725	237aa	Protein coding	-	A0A1B0GRW3	CDS 3' incomplete TSL:5
Ruvbl2-202	ENSMUST00000209426.1	396	104aa	Protein coding	-	A0A1B0GR89	CDS 5' incomplete TSL:3
Ruvbl2-203	ENSMUST00000210271.1	219	48aa	Protein coding	-	A0A1B0GRT1	CDS 5' incomplete TSL:3
Ruvbl2-206	ENSMUST00000211440.1	585	134aa	Nonsense mediated decay	-	A0A1B0GT54	CDS 5' incomplete TSL:5
Ruvbl2-207	ENSMUST00000211478.1	474	No protein	Retained intron	-	-	TSL:3

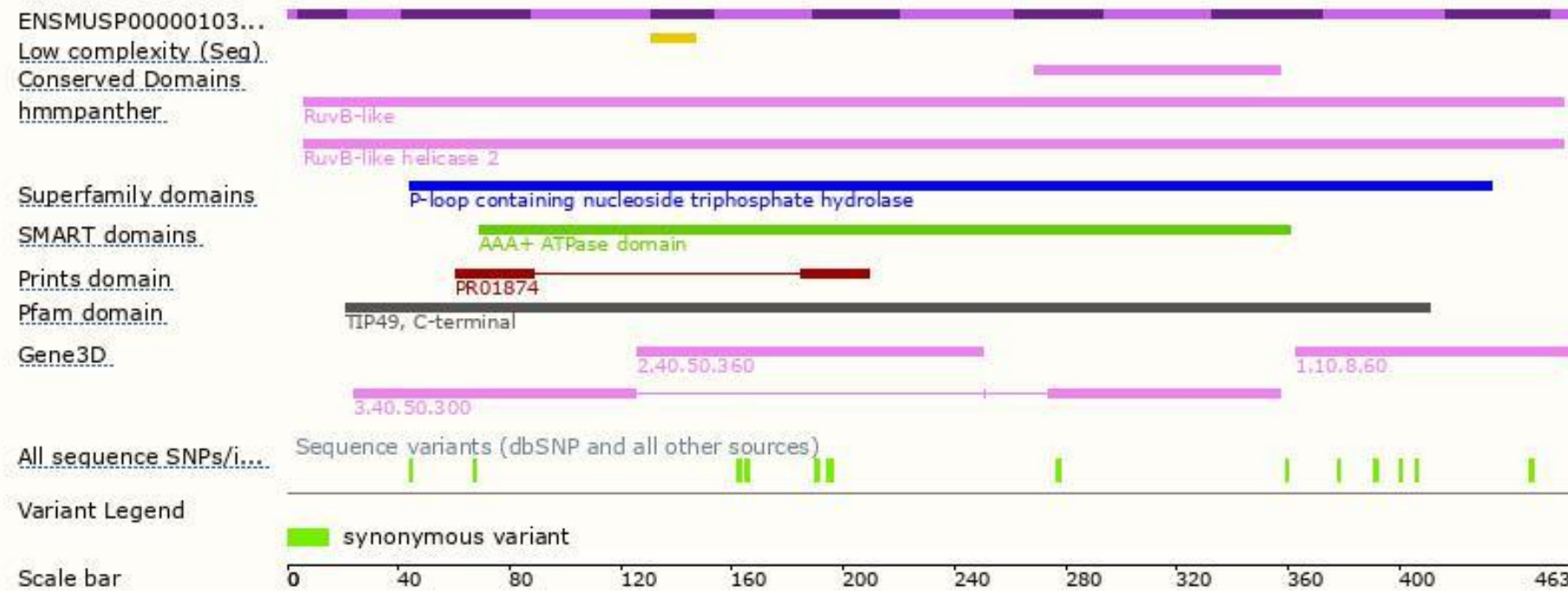
The strategy is based on the design of *Ruvbl2-205* transcript,The transcription is shown below



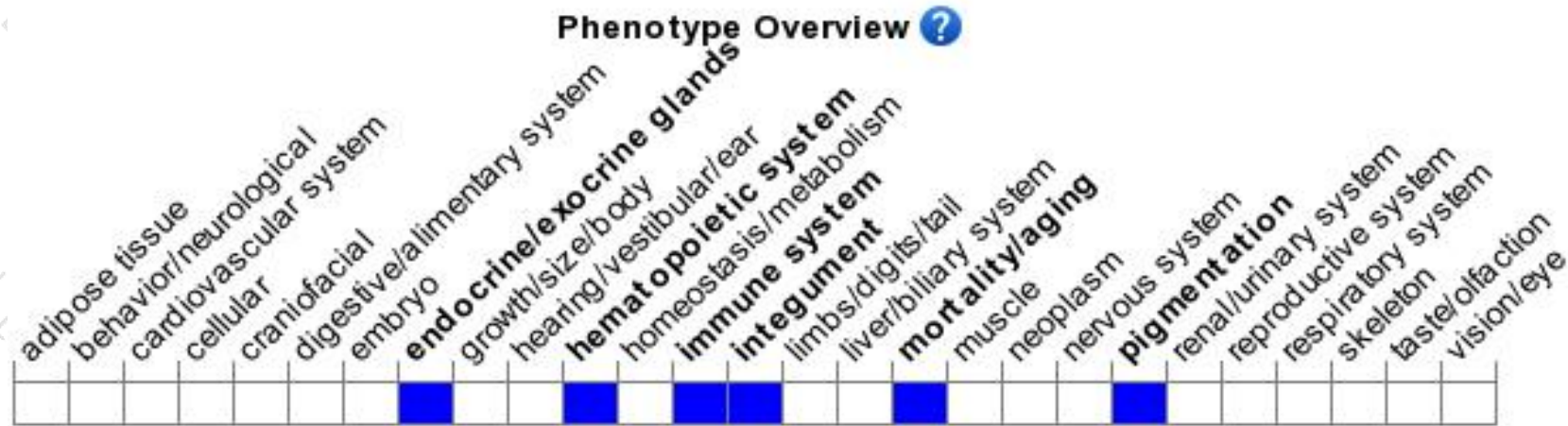
Genomic location distribution



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, Mice homozygous for an ENU-induced allele exhibit lethality. Mice heterozygous for a knock-out allele exhibit impaired T cell development and maximal T dependent antibody responses.

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

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