

Rsad2 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Rsad2

Project type

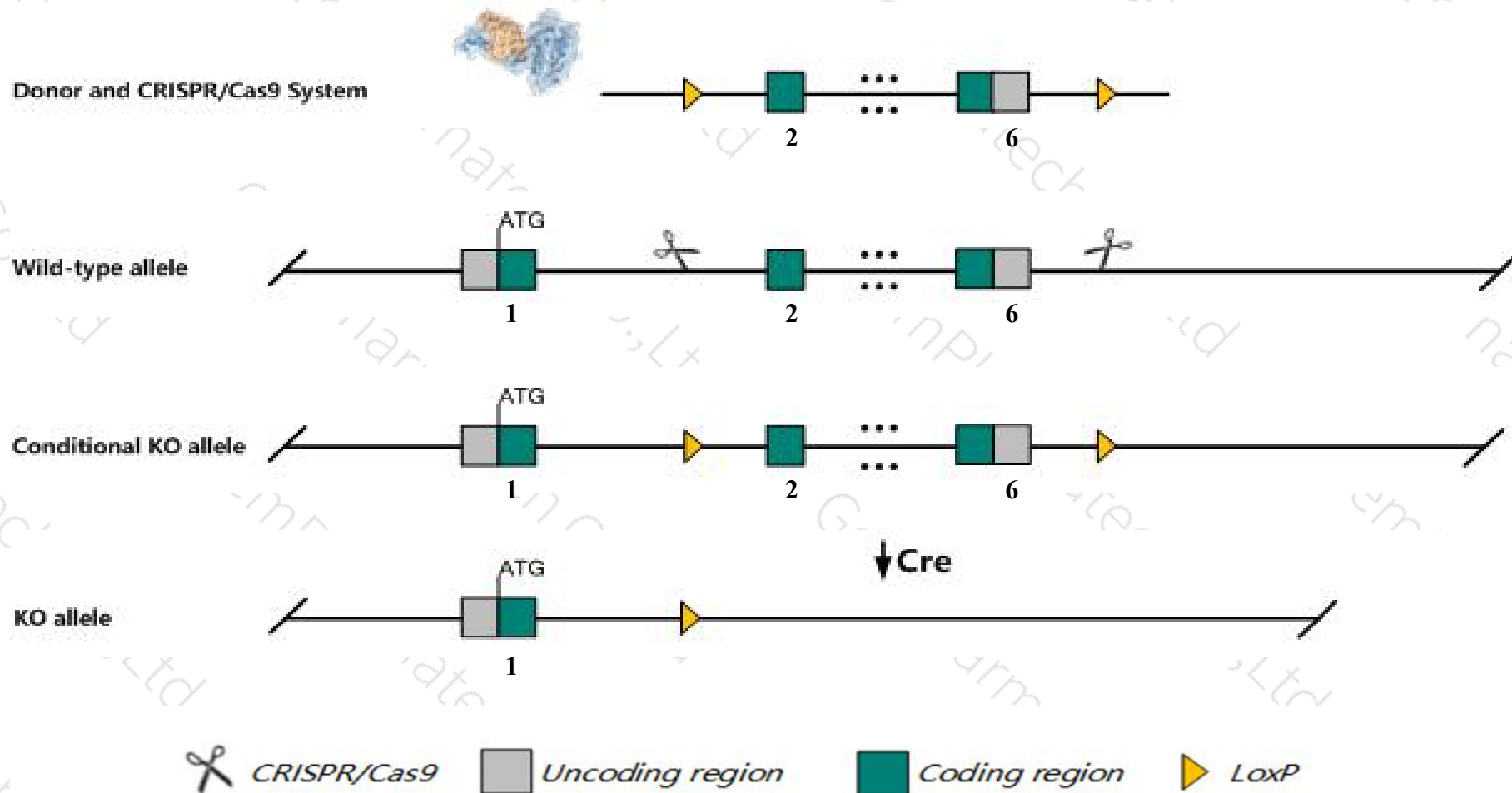
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rsad2* gene. The schematic diagram is as follows:



- The *Rsad2* gene has 3 transcripts. According to the structure of *Rsad2* gene, exon2-exon6 of *Rsad2*-201 (ENSMUST00000020970.9) transcript is recommended as the knockout region. The region contains 740bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rsad2* gene. The brief process is as follows: CRISPR/Cas9 system and Donor 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.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, Mice homozygous for a null allele exhibit impaired T-helper 2 differentiation.
- The *Rsad2* gene is located on the Chr12. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Rsad2 radical S-adenosyl methionine domain containing 2 [Mus musculus (house mouse)]

Gene ID: 58185, updated on 31-Jan-2019

Summary



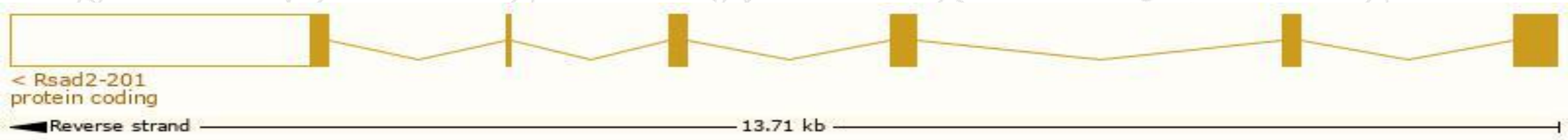
Official Symbol	Rsad2 provided by MGI
Official Full Name	radical S-adenosyl methionine domain containing 2 provided by MGI
Primary source	MGI:MGI:1929628
See related	Ensembl:ENSMUSG00000020641
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2510004L01Rik, Vig1, cig5
Expression	Biased expression in liver E18 (RPKM 29.0), spleen adult (RPKM 9.1) and 7 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

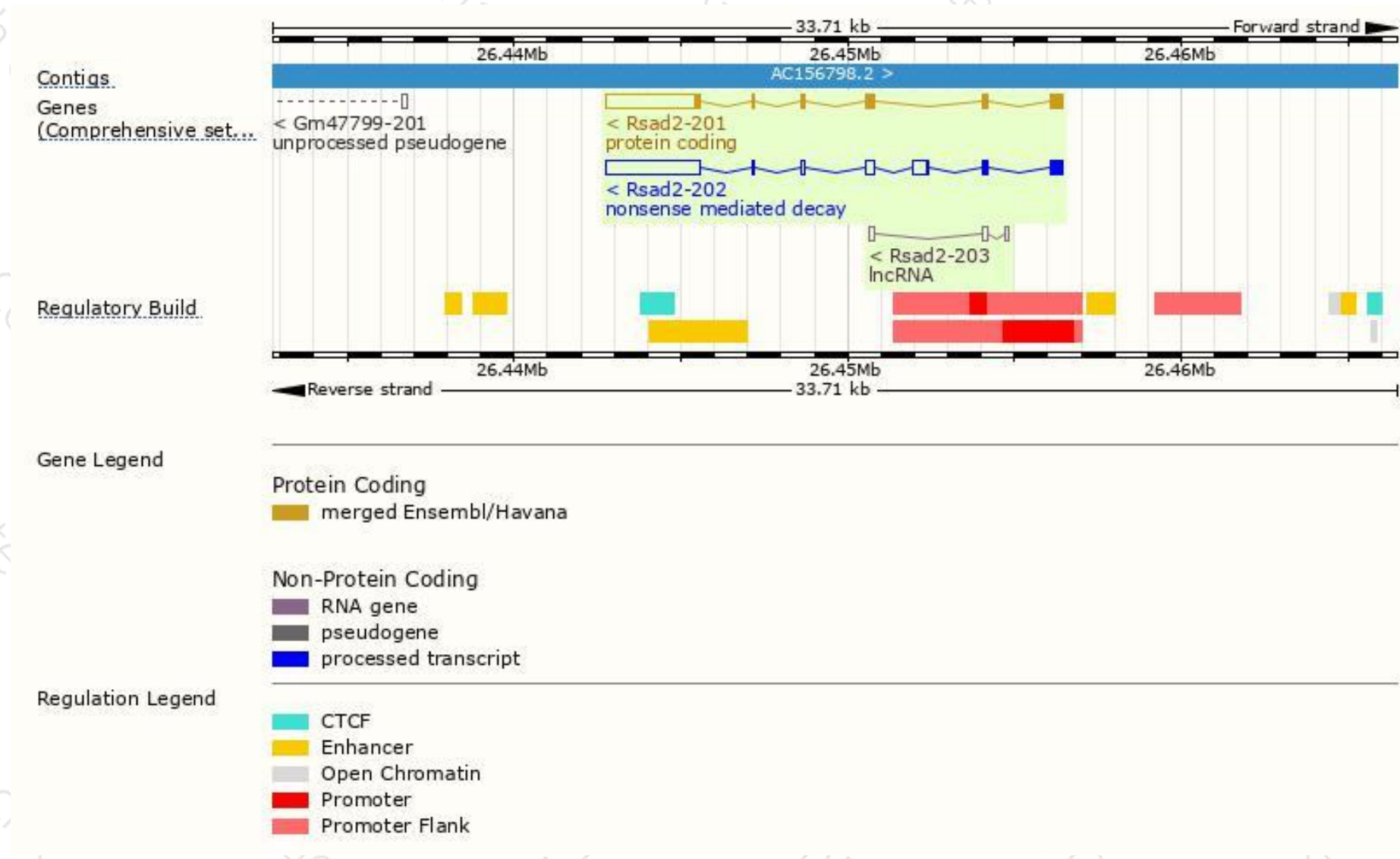
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rsad2-201	ENSMUST00000020970.9	3782	362aa	Protein coding	CCDS25848	Q8CBB9	TSL:1 GENCODE basic APPRIS P1
Rsad2-202	ENSMUST00000137792.6	4189	187aa	Nonsense mediated decay	-	D6RJ49	TSL:1
Rsad2-203	ENSMUST00000142732.1	430	No protein	lncRNA	-	-	TSL:2

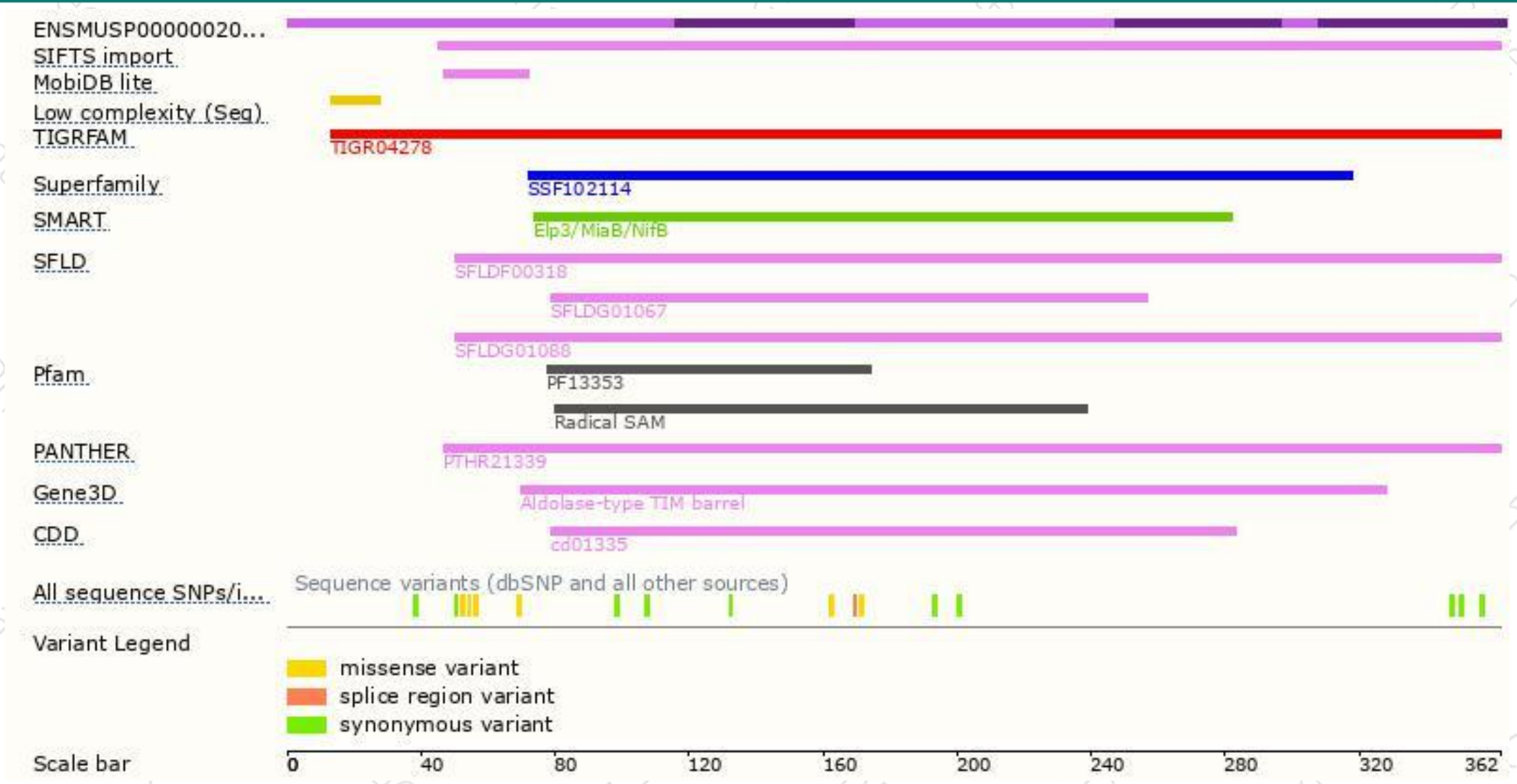
The strategy is based on the design of *Rsad2-201* transcript,The transcription is shown below



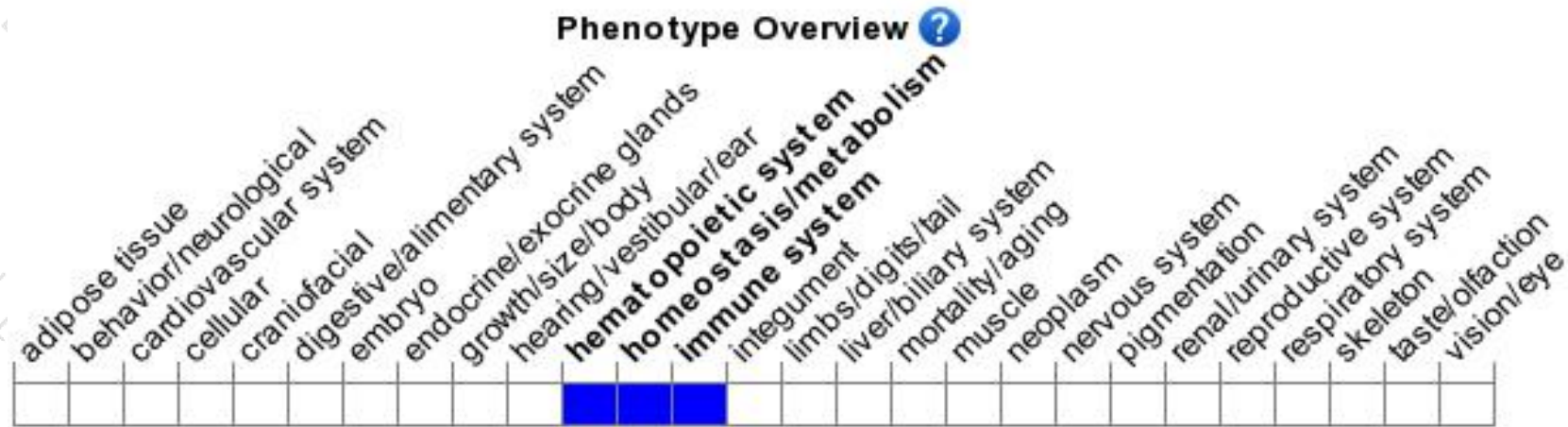
Genomic location distribution



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/>).

According to the existing MGI data, Mice homozygous for a null allele exhibit impaired T-helper 2 differentiation.

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

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