

***Rad18* Cas9-KO Strategy**

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Project Overview

Project Name

Rad18

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rad18* gene. The schematic diagram is as follows:



- The *Rad18* gene has 8 transcripts. According to the structure of *Rad18* gene, exon2-exon4 of *Rad18-201* (ENSMUST00000068487.11) transcript is recommended as the knockout region. The region contains 215bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rad18* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Male mice homozygous for a null allele exhibit age-dependent decrease in fertility, germ cell number, and testes weight with progressive degeneration of seminiferous tubules.
- The *Rad18* gene is located on the Chr6. 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)

Rad18 RAD18 E3 ubiquitin protein ligase [*Mus musculus* (house mouse)]

Gene ID: 58186, updated on 10-Oct-2019

Summary

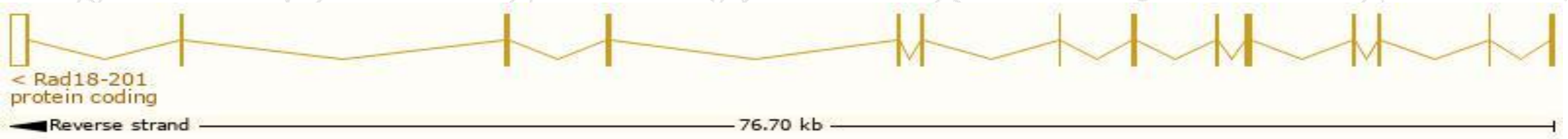
Official Symbol	Rad18 provided by MGI
Official Full Name	RAD18 E3 ubiquitin protein ligase provided by MGI
Primary source	MGI:MGI:1890476
See related	Ensembl:ENSMUSG00000030254
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Rad18sc; 2810024C04Rik
Expression	Broad expression in testis adult (RPKM 6.5), liver E14 (RPKM 4.9) and 19 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

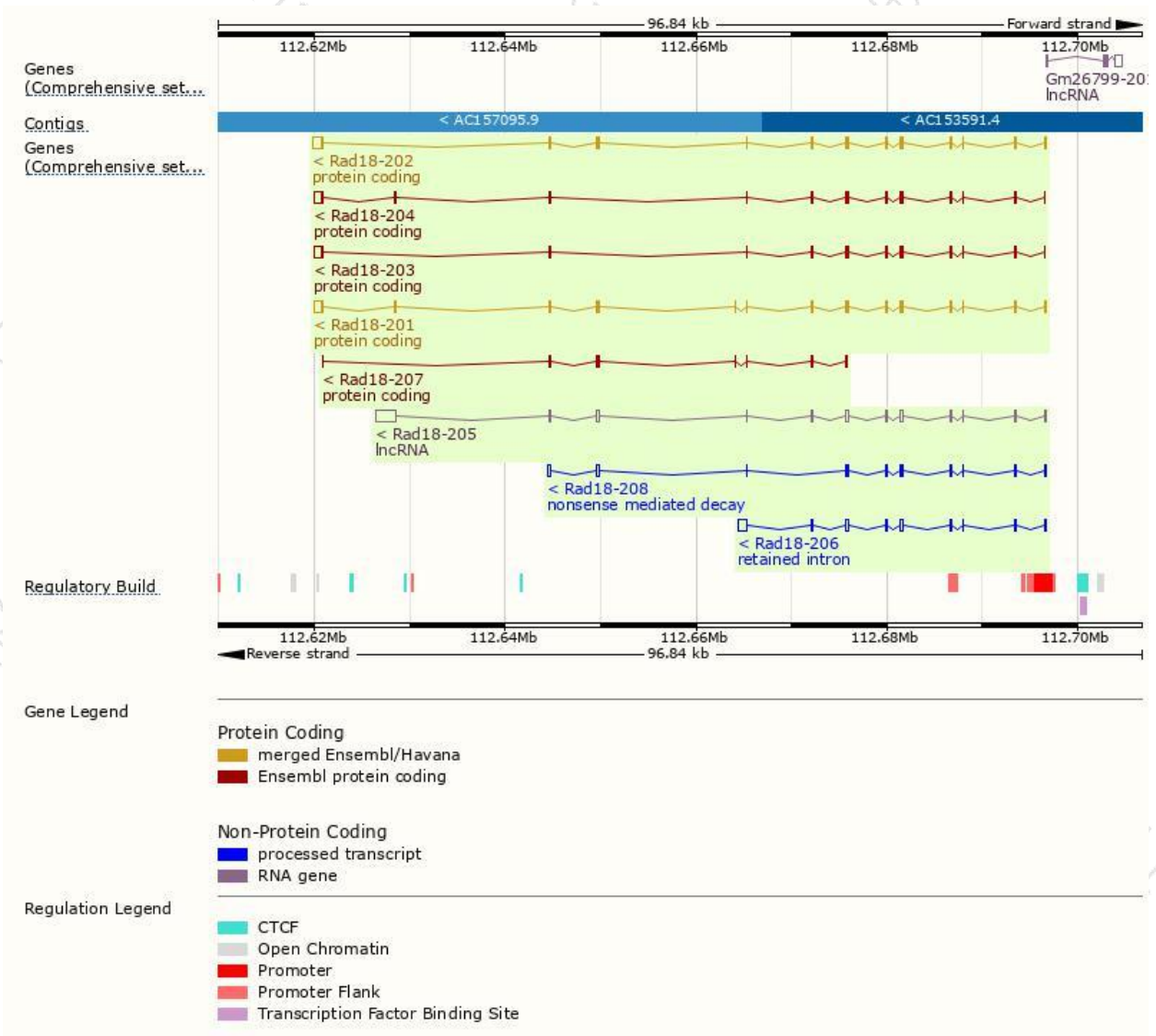
The gene has 8 transcripts,all transcripts are shown below:

Name ▲	Transcript ID ▲	bp ▲	Protein ▲	Biotype ▲	CCDS ▲	UniProt ▲	Flags ▲
Rad18-201	ENSMUST00000068487.11	2577	556aa	Protein coding	CCDS51870	E9Q392	TSL:1 GENCODE basic APPRIS ALT2
Rad18-202	ENSMUST00000077088.10	2577	509aa	Protein coding	CCDS39589	Q9QXK2	TSL:1 GENCODE basic APPRIS P3
Rad18-203	ENSMUST000000113180.7	2136	428aa	Protein coding	-	D3Z734	TSL:5 GENCODE basic APPRIS ALT2
Rad18-204	ENSMUST000000113182.7	2220	449aa	Protein coding	-	D3Z733	TSL:5 GENCODE basic APPRIS ALT2
Rad18-205	ENSMUST000000132590.7	3535	No protein	lncRNA	-	-	TSL:1
Rad18-206	ENSMUST000000135092.1	2004	No protein	Retained intron	-	-	TSL:1
Rad18-207	ENSMUST000000142079.1	724	241aa	Protein coding	-	F6ZKR0	CDS 5' and 3' incomplete TSL:5
Rad18-208	ENSMUST000000156063.1	1496	309aa	Nonsense mediated decay	-	W4VSP9	TSL:5

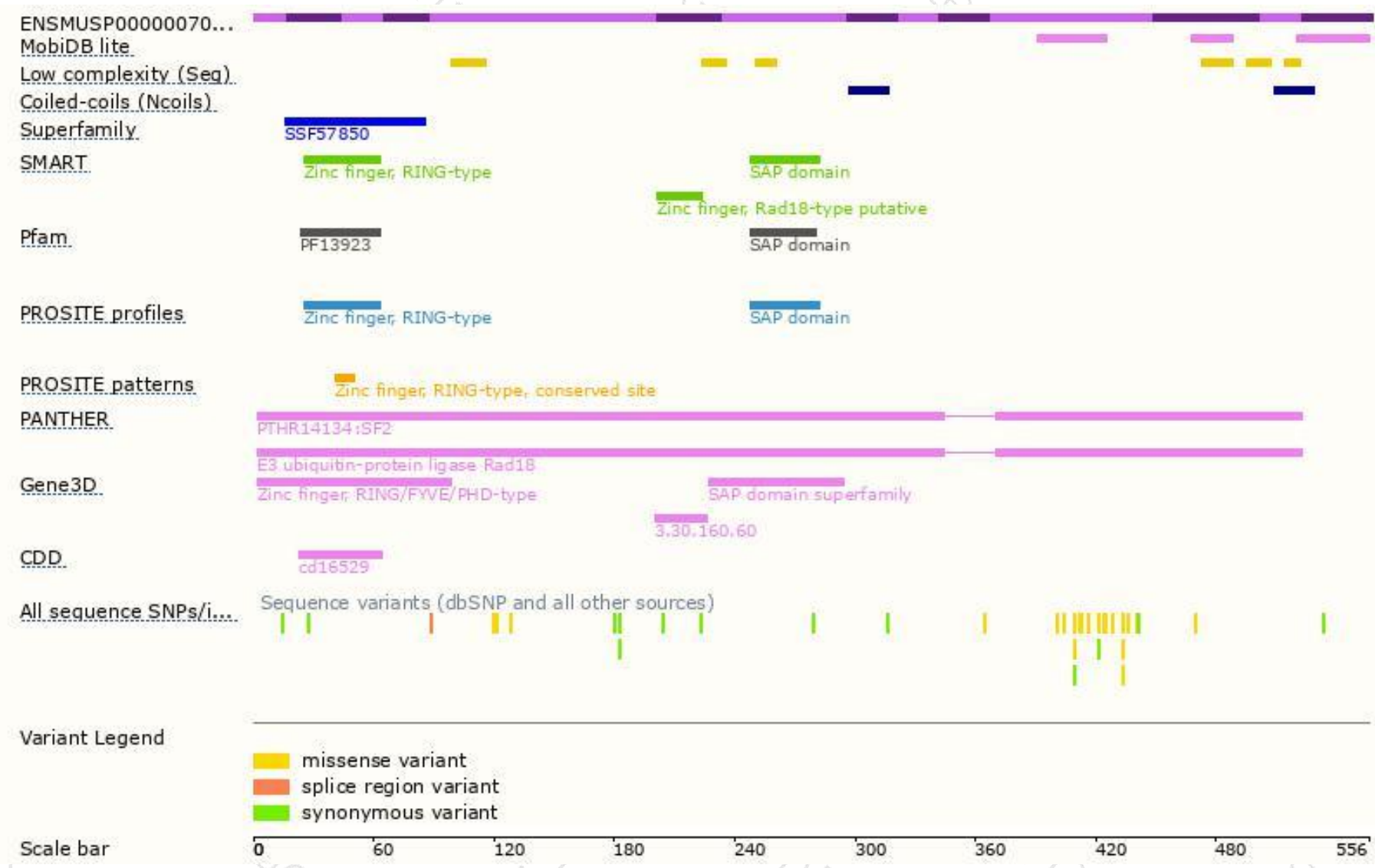
The strategy is based on the design of *Rad18-201* transcript,The transcription is shown below



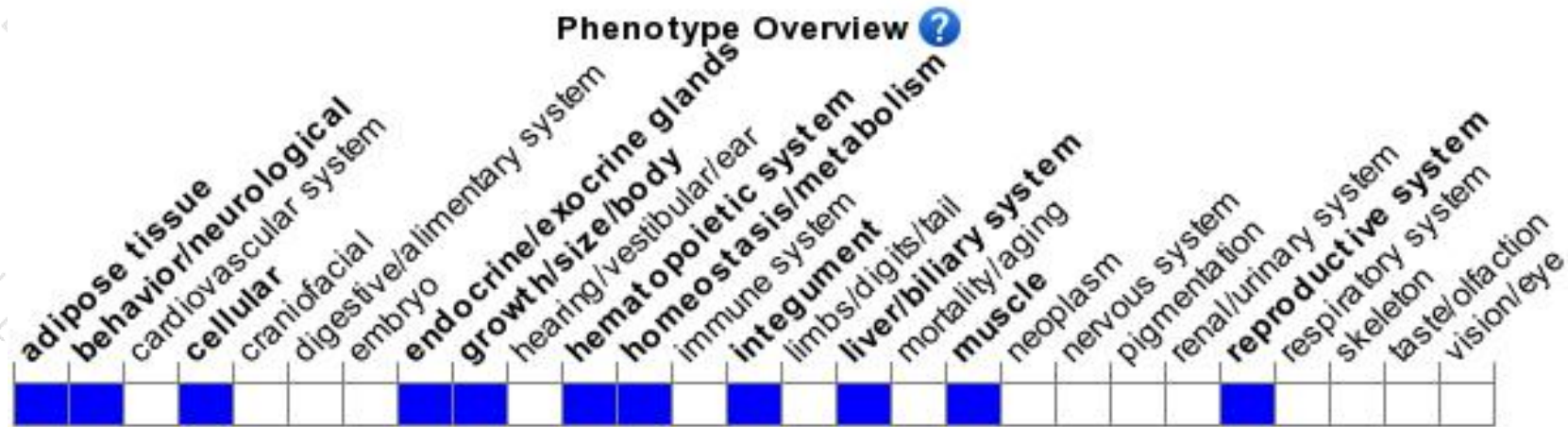
Genomic location distribution



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, Male mice homozygous for a null allele exhibit age-dependent decrease in fertility, germ cell number, and testes weight with progressive degeneration of seminiferous tubules.

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

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