

***Rad51* Cas9-CKO Strategy**

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Project Overview

Project Name

Rad51

Project type

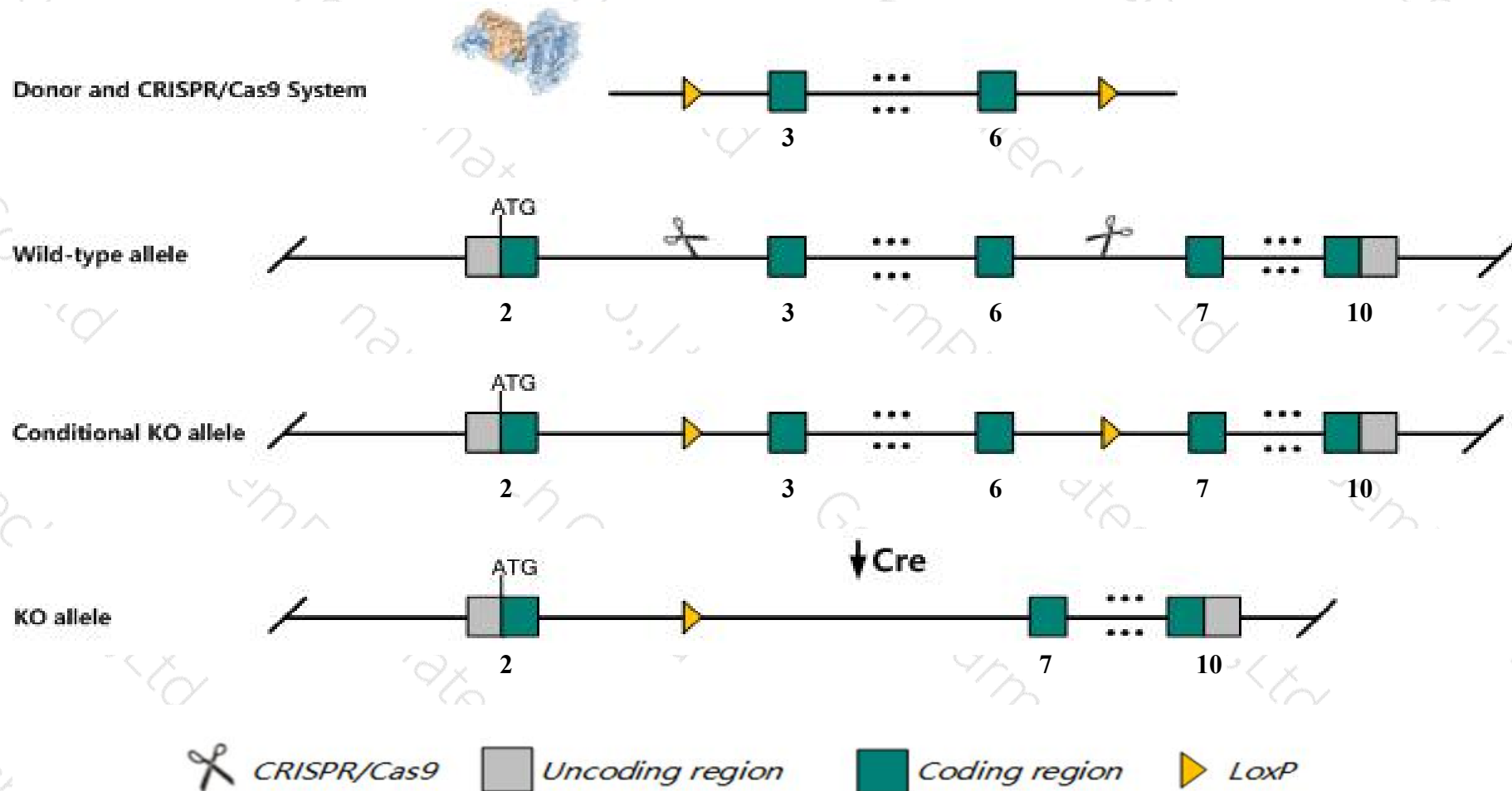
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rad51* gene. The schematic diagram is as follows:



- The *Rad51* gene has 8 transcripts. According to the structure of *Rad51* gene, exon3-exon6 of *Rad51-201* (ENSMUST00000028795.9) transcript is recommended as the knockout region. The region contains 443bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rad51* 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, homozygotes for targeted null mutations die prior to implantation, usually by the eight-cell stage.
- The *Rad51* gene is located on the Chr2. 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)

Rad51 RAD51 recombinase [Mus musculus (house mouse)]

Gene ID: 19361, updated on 13-Mar-2020

Summary



Official Symbol Rad51 provided by [MGI](#)

Official Full Name RAD51 recombinase provided by [MGI](#)

Primary source [MGI:MGI:97890](#)

See related [Ensembl:ENSMUSG00000027323](#)

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 AV304093, Rad51a, Reca

Expression Biased expression in placenta adult (RPKM 14.2), liver E14 (RPKM 13.5) and 13 other tissues [See more](#)

Orthologs [human](#) [all](#)

Transcript information (Ensembl)

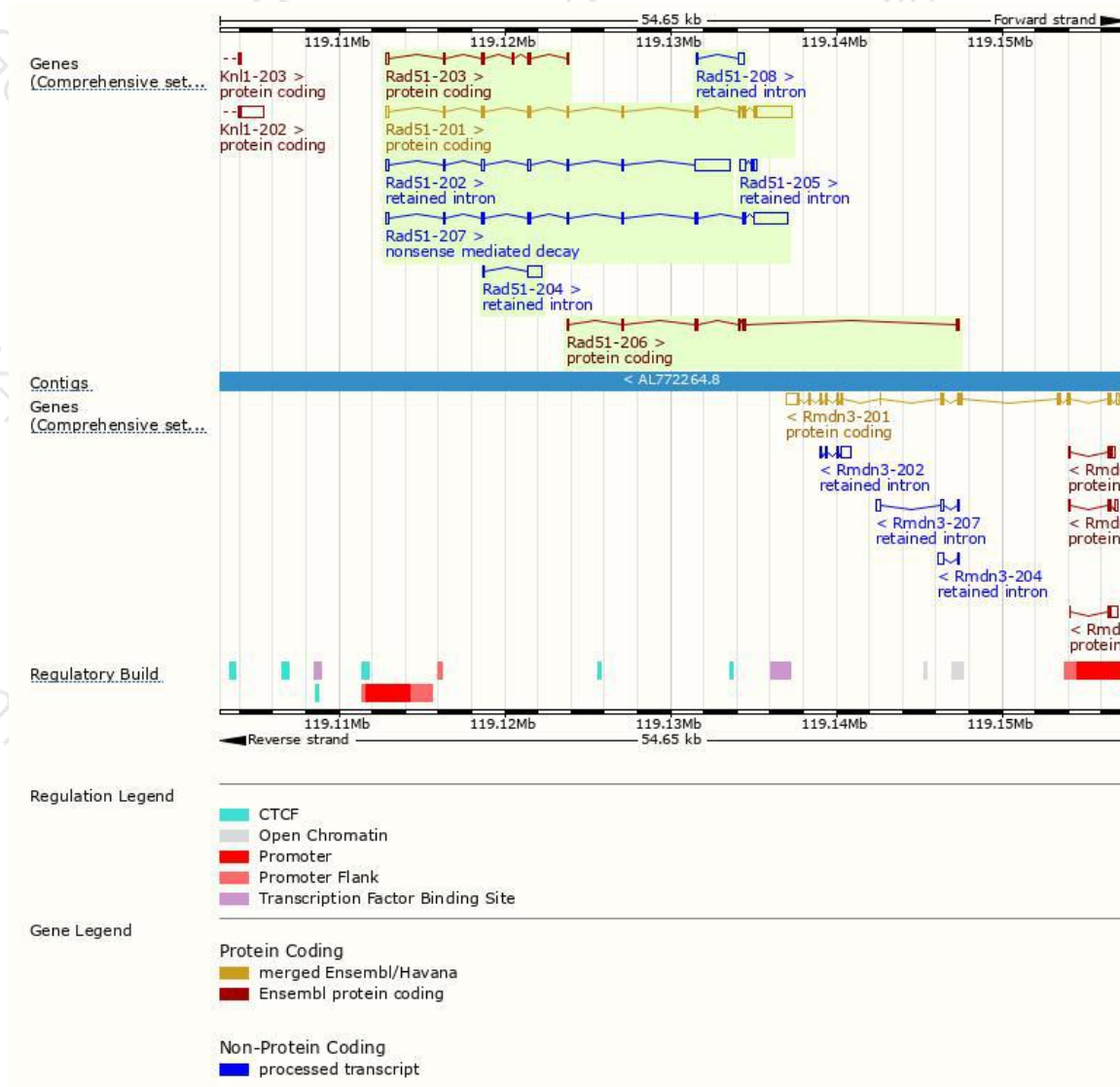
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rad51-201	ENSMUST00000028795.9	3368	339aa	Protein coding	CCDS16590	Q08297	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Rad51-203	ENSMUST00000140939.7	779	178aa	Protein coding	-	A3KGI2	CDS 3' incomplete TSL:5
Rad51-206	ENSMUST00000151406.1	738	237aa	Protein coding	-	F7AT35	CDS 5' incomplete TSL:3
Rad51-207	ENSMUST00000152327.7	2975	220aa	Nonsense mediated decay	-	D6RCK1	TSL:1
Rad51-202	ENSMUST00000110828.1	2849	No protein	Retained intron	-	-	TSL:1
Rad51-204	ENSMUST00000141389.1	887	No protein	Retained intron	-	-	TSL:2
Rad51-205	ENSMUST00000143934.1	557	No protein	Retained intron	-	-	TSL:3
Rad51-208	ENSMUST00000154683.1	482	No protein	Retained intron	-	-	TSL:2

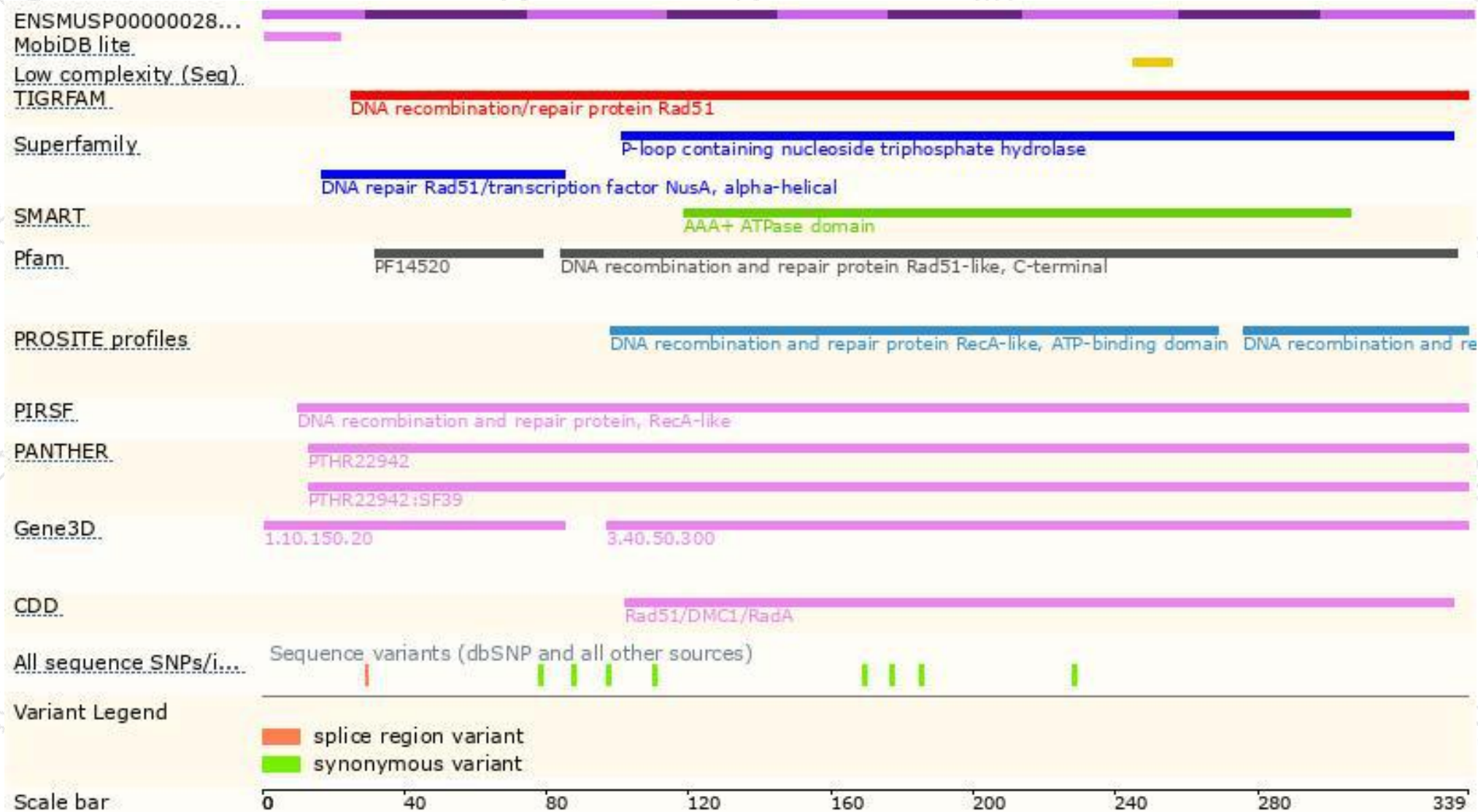
The strategy is based on the design of *Rad51-201* transcript,the transcription is shown below:



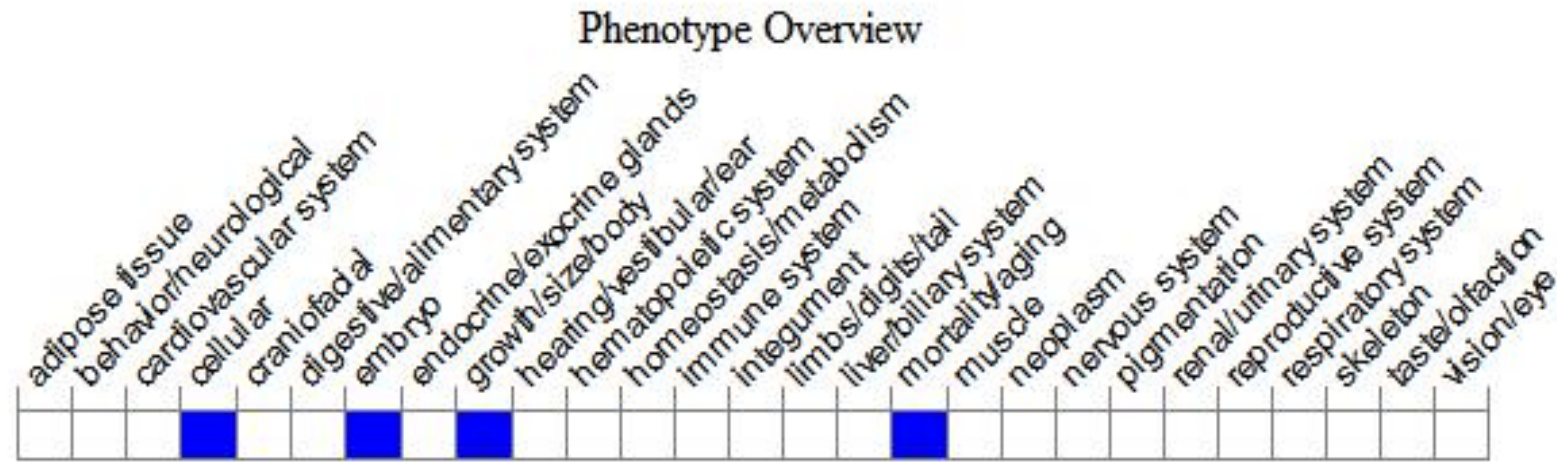
Genomic location distribution



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, homozygotes for targeted null mutations die prior to implantation, usually by the eight-cell stage.

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

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