

***Rere* Cas9-CKO Strategy**

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Project Overview

Project Name

Rere

Project type

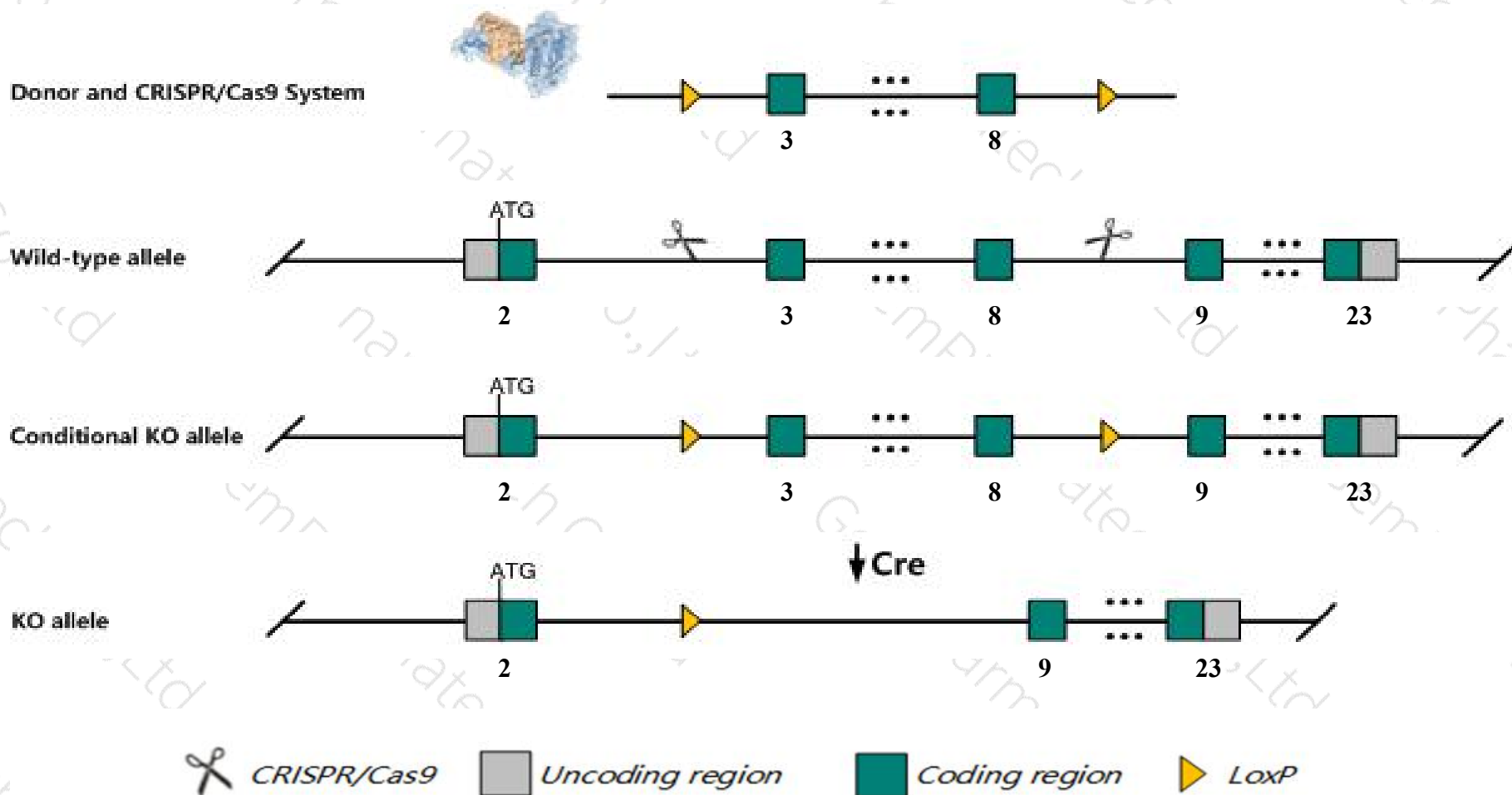
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



Technical routes

- The *Rere* gene has 8 transcripts. According to the structure of *Rere* gene, exon3-exon8 of *Rere*-202(ENSMUST00000105682.8) transcript is recommended as the knockout region. The region contains 554bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rere* 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 disruptions in this gene display embryonic lethality with abnormalities in neural tube development, somite development, and in the embryonic heart. Mice homozygous for an ENU-induced allele exhibit narrow snouts, decreased body weight, renal agenesis and small eyes.
- Transcript 204,208 CDS 5' and 3' incomplete the influences is unknown.
- Transcript 205 CDS 5' incomplete the influences is unknown.
- The *Rere* gene is located on the Chr4. 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)

Rere arginine glutamic acid dipeptide (RE) repeats [Mus musculus (house mouse)]

Gene ID: 68703, updated on 13-Mar-2020

Summary



Official Symbol	Rere provided by MGI
Official Full Name	arginine glutamic acid dipeptide (RE) repeats provided by MGI
Primary source	MGI:MGI:2683486
See related	Ensembl:ENSMUSG00000039852
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	1110033A15Rik, AI414665, ARG, ARP, ATN1L, AW742570, Atr2, DNB1, eye, eyes3, mKIAA0458
Expression	Ubiquitous expression in adrenal adult (RPKM 15.0), spleen adult (RPKM 12.9) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

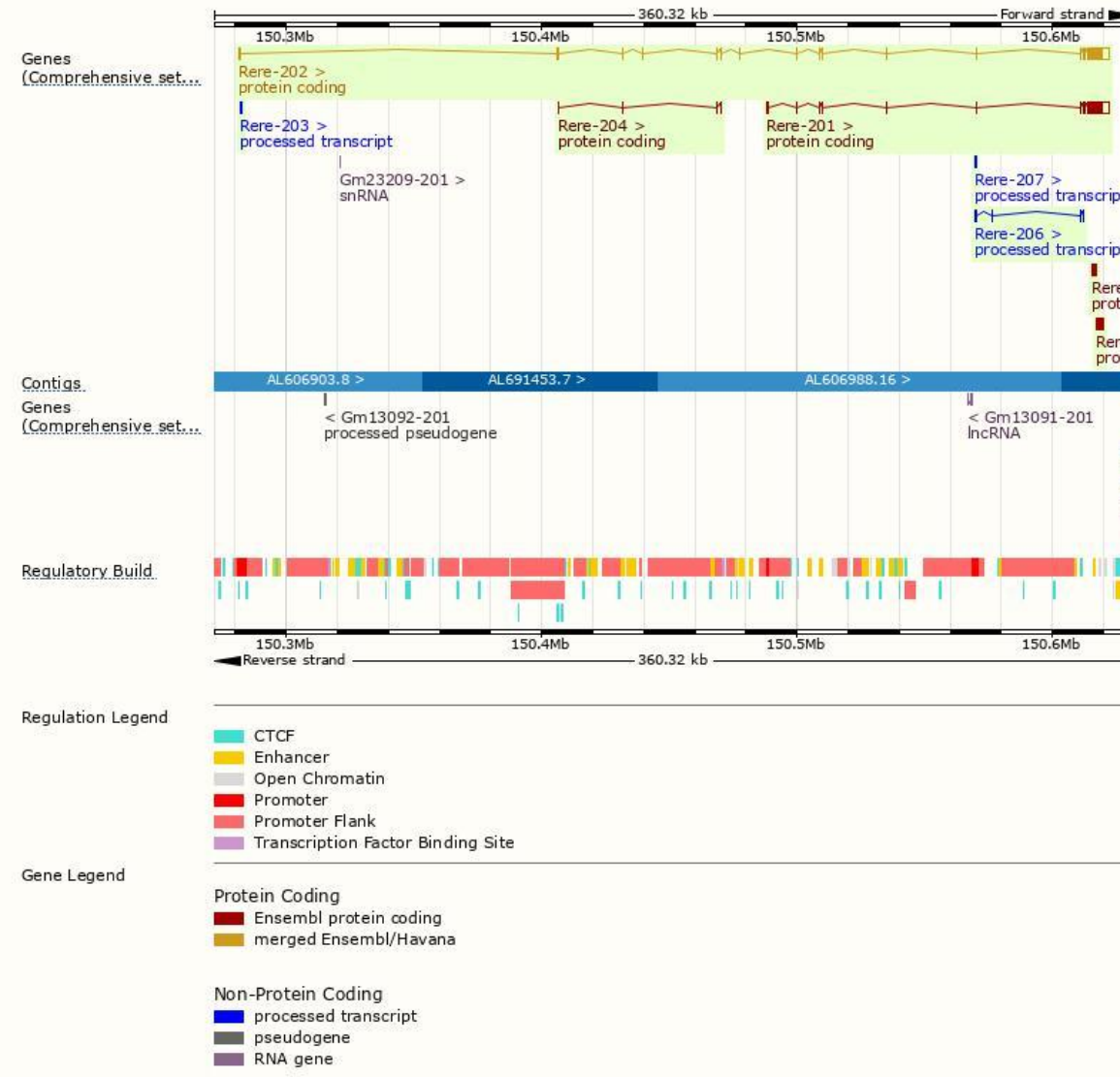
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rere-202	ENSMUST00000105682.8	7728	1558aa	Protein coding	CCDS38979	Q80TZ9	TSL:5 GENCODE basic APPRIS P2
Rere-201	ENSMUST00000105680.8	6503	1290aa	Protein coding	-	A2A7T3	TSL:5 GENCODE basic APPRIS ALT2
Rere-208	ENSMUST00000219467.1	1305	435aa	Protein coding	-	A0A1W2P787	CDS 5' and 3' incomplete TSL:2
Rere-205	ENSMUST00000136646.1	939	199aa	Protein coding	-	A2A7T1	CDS 5' incomplete TSL:1
Rere-204	ENSMUST00000131600.1	535	178aa	Protein coding	-	B1AS11	CDS 5' and 3' incomplete TSL:2
Rere-206	ENSMUST00000137112.1	496	No protein	Processed transcript	-	-	TSL:5
Rere-203	ENSMUST00000129188.1	417	No protein	Processed transcript	-	-	TSL:2
Rere-207	ENSMUST00000142379.1	379	No protein	Processed transcript	-	-	TSL:3

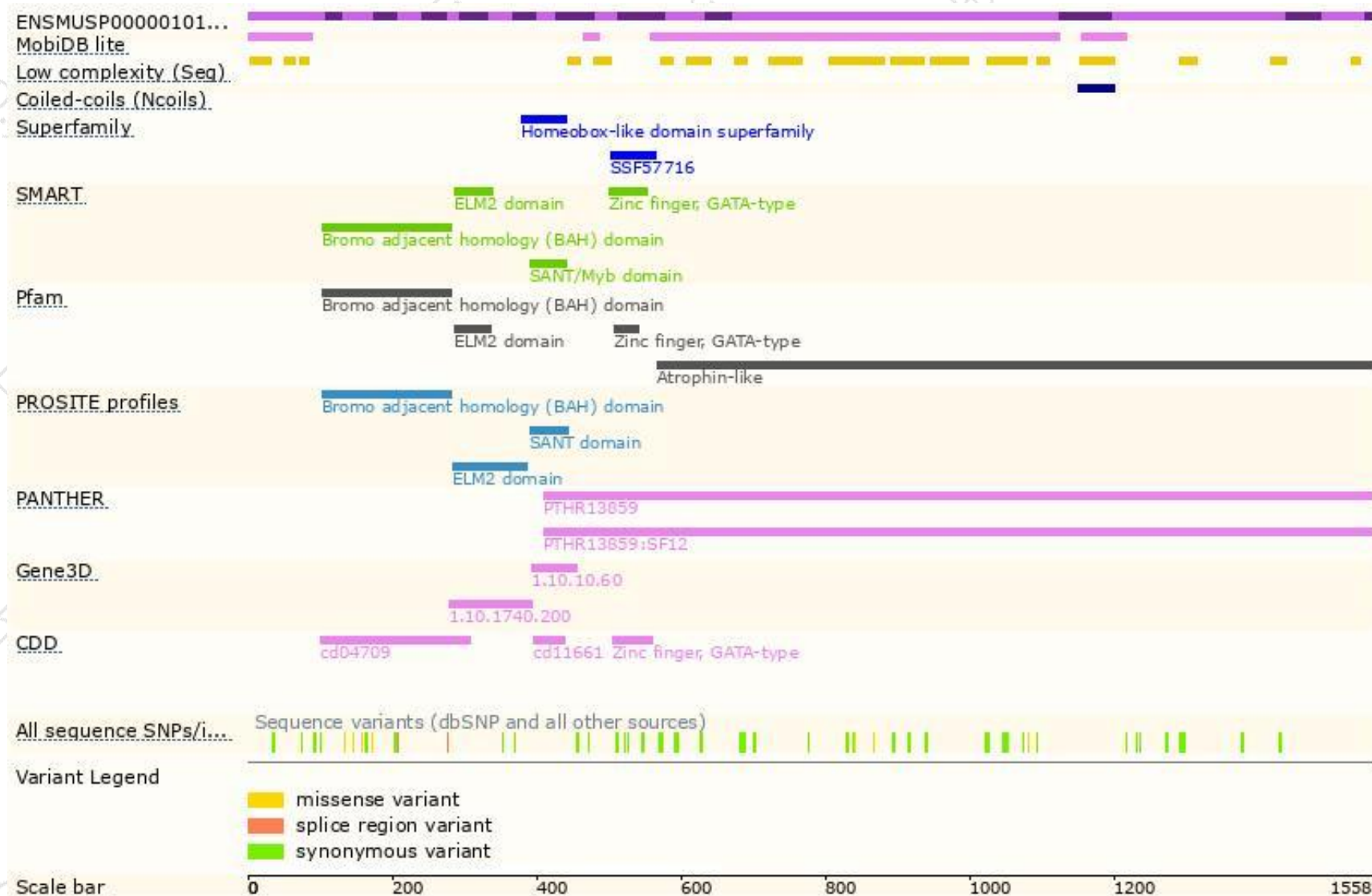
The strategy is based on the design of *Rere-202* transcript,the transcription is shown below:



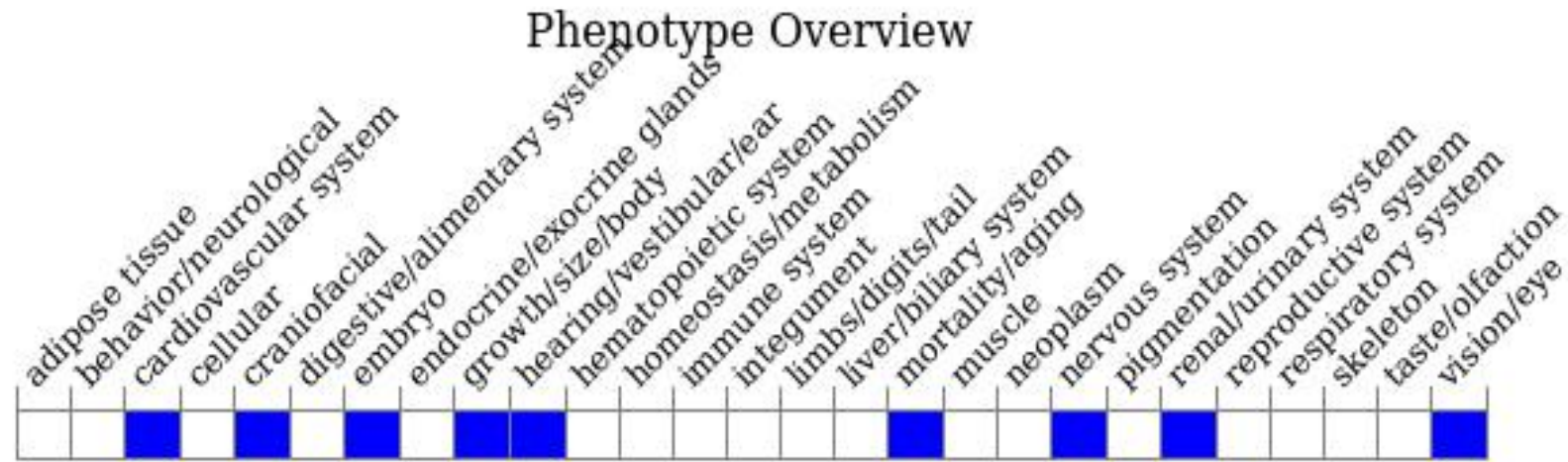
Genomic location distribution



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 disruptions in this gene display embryonic lethality with abnormalities in neural tube development, somite development, and in the embryonic heart. Mice homozygous for an ENU-induced allele exhibit narrow snouts, decreased body weight, renal agenesis and small eyes.

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

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