

Erc2 Cas9-KO Strategy

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Project Overview

Project Name

Ercc2

Project type

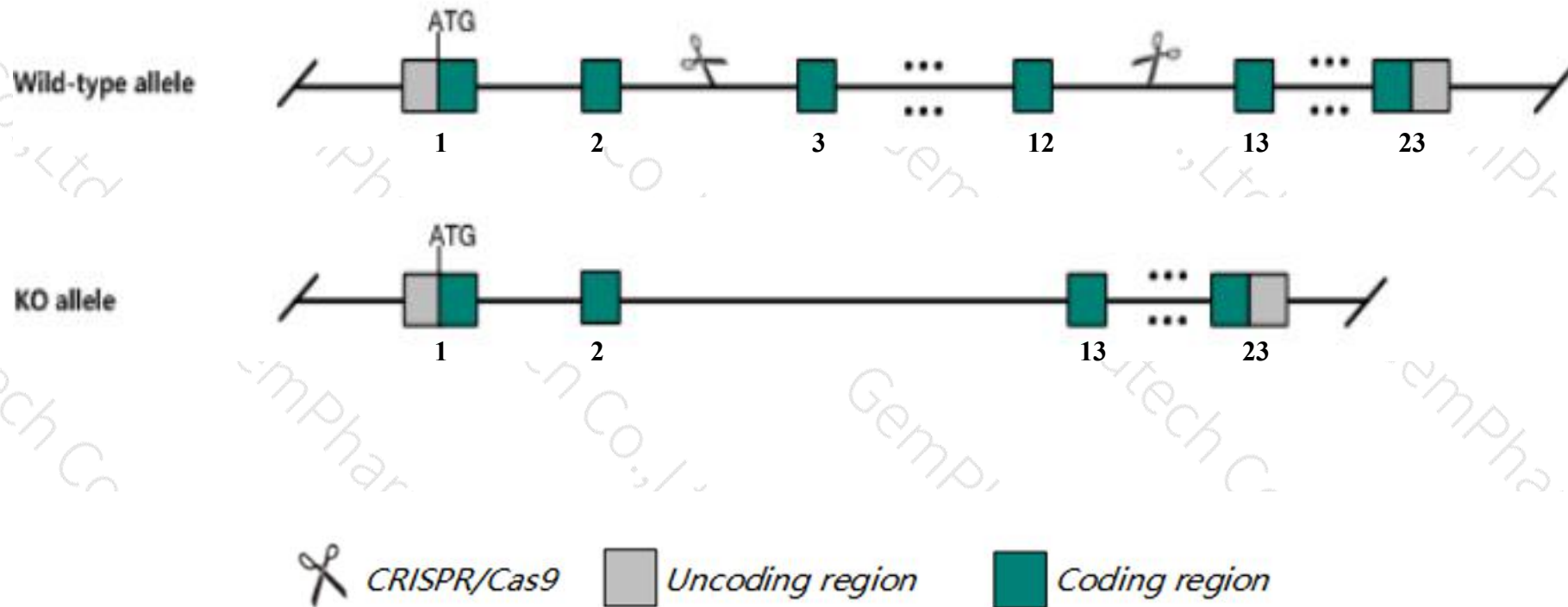
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ercc2* gene. The schematic diagram is as follows:



- The *Ercc2* gene has 10 transcripts. According to the structure of *Ercc2* gene, exon3-exon12 of *Ercc2-201* (ENSMUST00000062831.15) transcript is recommended as the knockout region. The region contains 1132bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ercc2* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, homozygotes for a targeted null mutation die prior to implantation. homozygotes for a targeted missense mutation exhibit brittle and greying hair, cachexia, infertility, osteosclerosis, osteoporosis, reduced lifespan, uv sensitivity, and skin defects.
- The KO region contains functional region of the *Ercc2* gene. Knockout the region may affect the function of *Mir343* gene
- The *Ercc2* 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)

Ercc2 excision repair cross-complementing rodent repair deficiency, complementation group 2 [Mus musculus (house mouse)]

Gene ID: 13871, updated on 13-Mar-2020

Summary

Official Symbol Ercc2 provided by [MGI](#)

Official Full Name excision repair cross-complementing rodent repair deficiency, complementation group 2 provided by [MGI](#)

Primary source [MGI:MGI:95413](#)

See related [Ensembl:ENSMUSG00000030400](#)

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 AA407812, AU020867, AW240756, CXPDP, Ercc-2, Mhdarco15, RCO015, XPD

Expression Ubiquitous expression in thymus adult (RPKM 38.9), ovary adult (RPKM 35.9) and 28 other tissues [See more](#)

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

Transcript information（Ensembl）

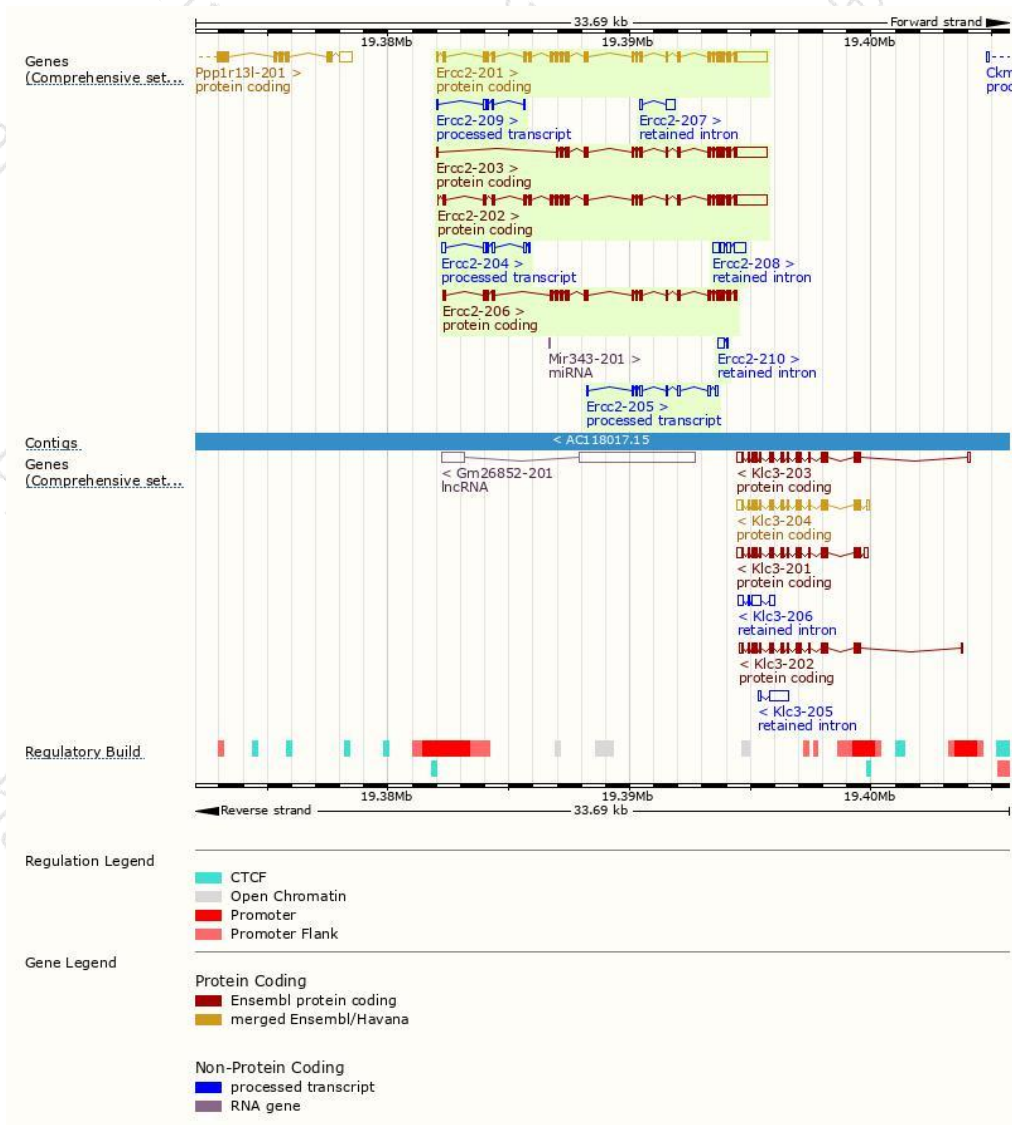
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ercc2-201	ENSMUST0000062831.15	3578	760aa	Protein coding	CCDS20900	Q08811	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
Ercc2-202	ENSMUST00000108460.7	3485	739aa	Protein coding	-	E9Q6K1	TSL:1 GENCODE basic
Ercc2-203	ENSMUST00000108461.7	2799	508aa	Protein coding	-	D3Z700	TSL:1 GENCODE basic
Ercc2-206	ENSMUST00000129249.1	2071	684aa	Protein coding	-	F6YA33	CDS 5' incomplete TSL:5
Ercc2-205	ENSMUST00000128167.1	684	No protein	Processed transcript	-	-	TSL:3
Ercc2-204	ENSMUST00000127363.1	607	No protein	Processed transcript	-	-	TSL:5
Ercc2-209	ENSMUST00000136055.7	311	No protein	Processed transcript	-	-	TSL:5
Ercc2-208	ENSMUST00000135693.1	994	No protein	Retained intron	-	-	TSL:2
Ercc2-207	ENSMUST00000129291.1	485	No protein	Retained intron	-	-	TSL:3
Ercc2-210	ENSMUST00000145039.1	286	No protein	Retained intron	-	-	TSL:2

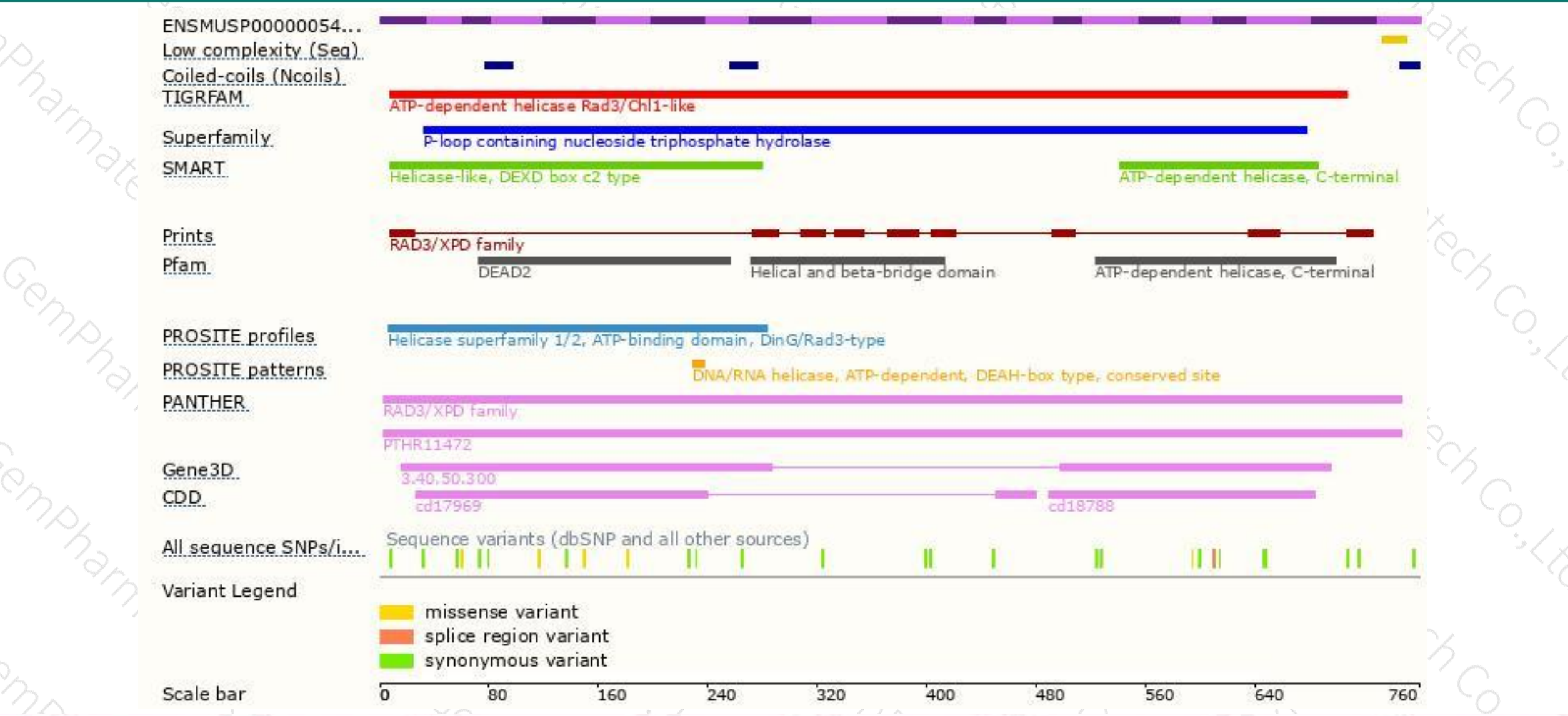
The strategy is based on the design of *Ercc2-201* transcript,the transcription is shown below:



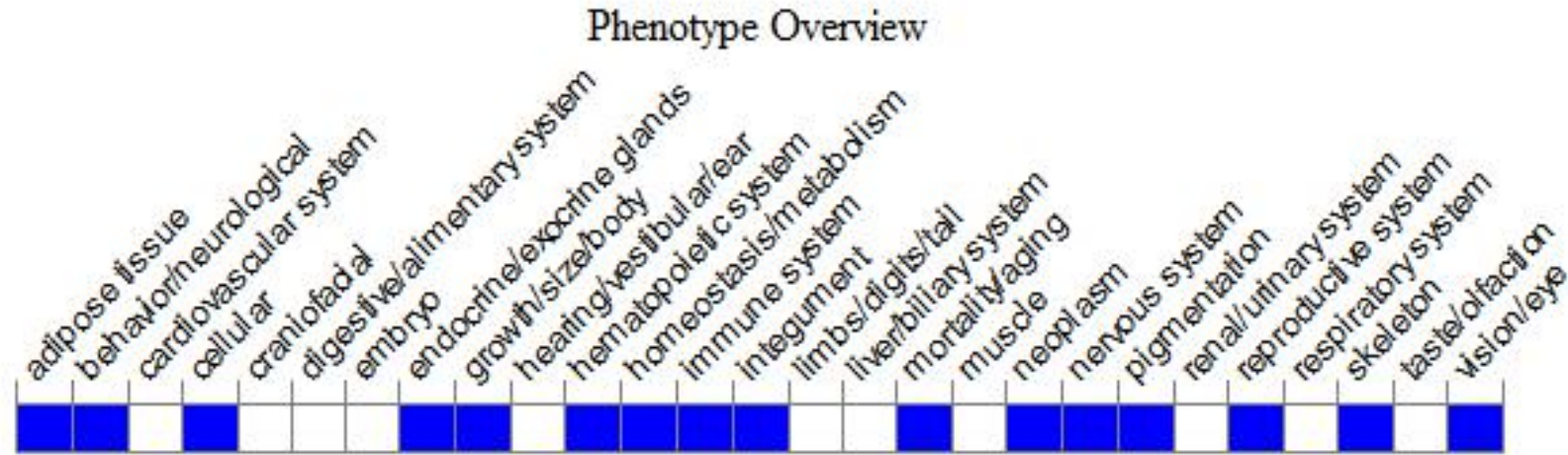
Genomic location distribution



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/>).

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

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