

Wrn Cas9-CKO Strategy

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Project Overview



Project Name

Wrn

Project type

Cas9-CKO

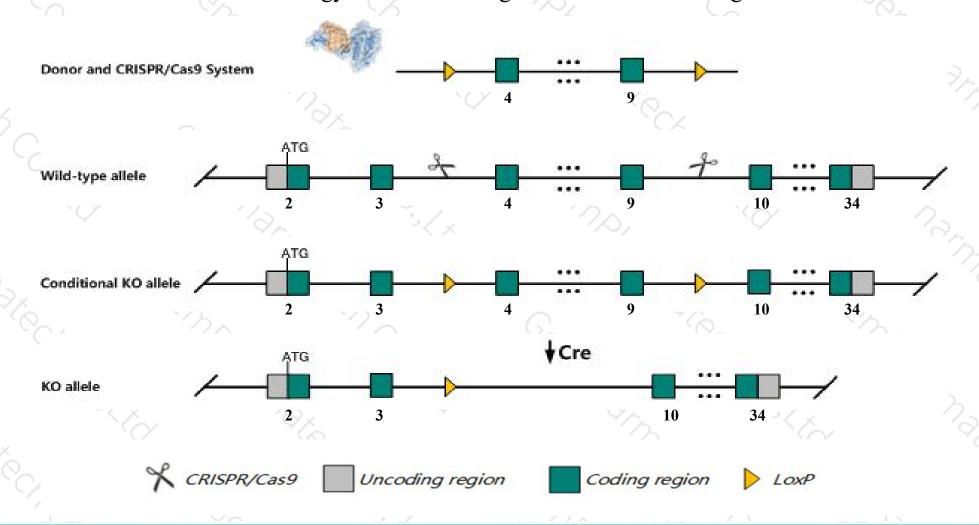
Strain background

C57BL/6JGpt

Conditional Knockout strategy



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



Technical routes



- The *Wrn* gene has 4 transcripts. According to the structure of *Wrn* gene, exon4-exon9 of *Wrn-202* (ENSMUST00000033991.12) transcript is recommended as the knockout region. The region contains 1057bp coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Wrn* 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.

Notice



- ➤ According to the existing MGI data, Homozygous mutants show enhanced frequency and variety of tumors in conjunction with Trp53 knockout alleles. Homozygotes also have an elevated frequency of somatic reversion of the pink-eyed dilution unstable mutation.
- > The Wrn gene is located on the Chr8. 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)



Wrn Werner syndrome RecQ like helicase [Mus musculus (house mouse)]

Gene ID: 22427, updated on 31-Jan-2019

Summary

☆ ?

Official Symbol Wrn provided by MGI

Official Full Name Werner syndrome RecQ like helicase provided by MGI

Primary source MGI:MGI:109635

See related Ensembl: ENSMUSG00000031583

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 Al846146

Expression Ubiquitous expression in liver E14 (RPKM 4.4), liver E14.5 (RPKM 3.9) and 25 other tissuesSee more

Orthologs human all

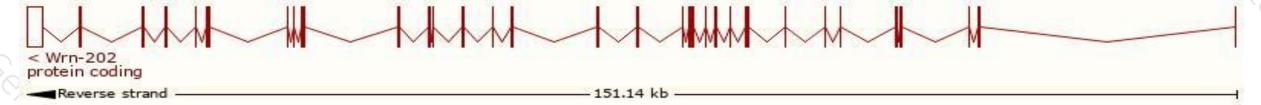
Transcript information (Ensembl)



The gene has 4 transcripts, all transcripts are shown below:

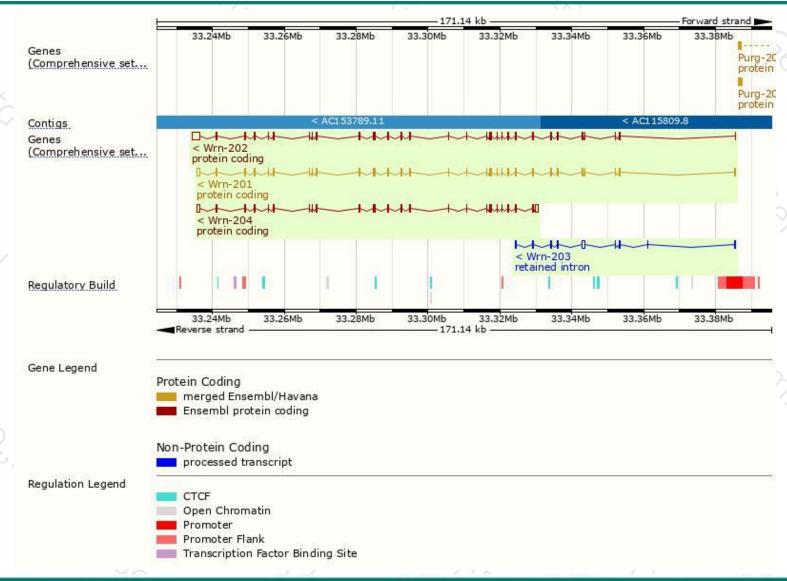
Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST00000033991.12	6262	1401aa	Protein coding	CCDS22229	009053	TSL:5 GENCODE basic APPRIS P1
ENSMUST00000033990.6	5019	<u>1401aa</u>	Protein coding	CCDS22229	009053	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000211498.1	4856	1158aa	Protein coding	-	A0A1B0GR54	TSL:1 GENCODE basic
ENSMUST00000209293.1	1921	No protein	Retained intron		120	TSL:1
	ENSMUST00000033991.12 ENSMUST00000033990.6 ENSMUST00000211498.1	ENSMUST00000033991.12 6262 ENSMUST00000033990.6 5019 ENSMUST00000211498.1 4856	ENSMUST00000033991.12 6262 1401aa ENSMUST00000033990.6 5019 1401aa ENSMUST00000211498.1 4856 1158aa	ENSMUST00000033991.12 6262 1401aa Protein coding ENSMUST00000033990.6 5019 1401aa Protein coding ENSMUST000000211498.1 4856 1158aa Protein coding	ENSMUST00000033991.12 6262 1401aa Protein coding CCDS22229 ENSMUST00000033990.6 5019 1401aa Protein coding CCDS22229 ENSMUST00000211498.1 4856 1158aa Protein coding -	ENSMUST00000033991.12 6262 1401aa Protein coding CCDS22229 009053 ENSMUST00000033990.6 5019 1401aa Protein coding CCDS22229 009053 ENSMUST00000211498.1 4856 1158aa Protein coding - A0A1B0GR54

The strategy is based on the design of Wrn-202 transcript, The transcription is shown below



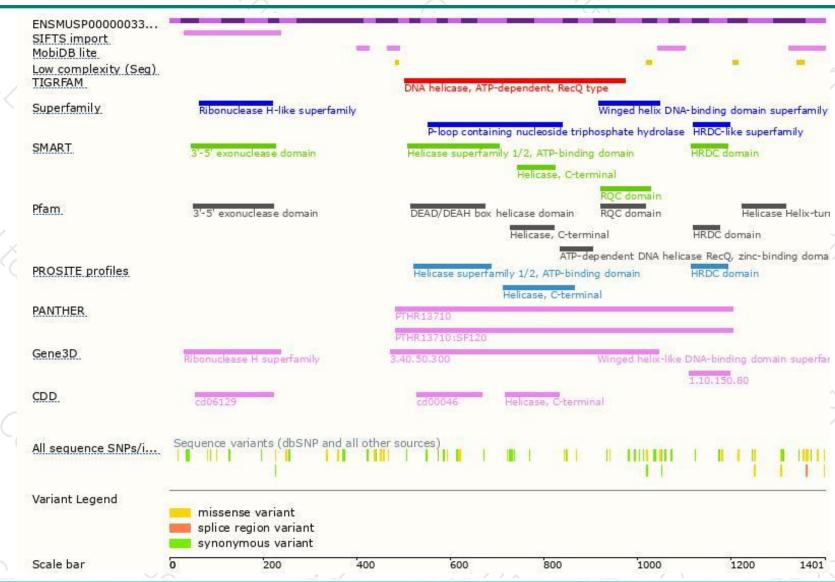
Genomic location distribution





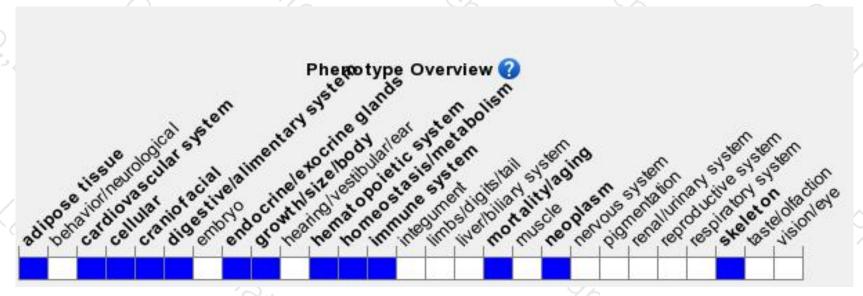
Protein domain





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, Homozygous mutants show enhanced frequency and variety of tumors in conjunction wit Trp53 knockout alleles. Homozygotes also have an elevated frequency of somatic reversion of the pink-eyed dilution unstable mutation.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





