

# Uril Cas9-CKO Strategy

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Reviewer: Xiaojing Li

**Design Date:** 2020-2-26

# **Project Overview**



**Project Name** 

Uri1

**Project type** 

Cas9-CKO

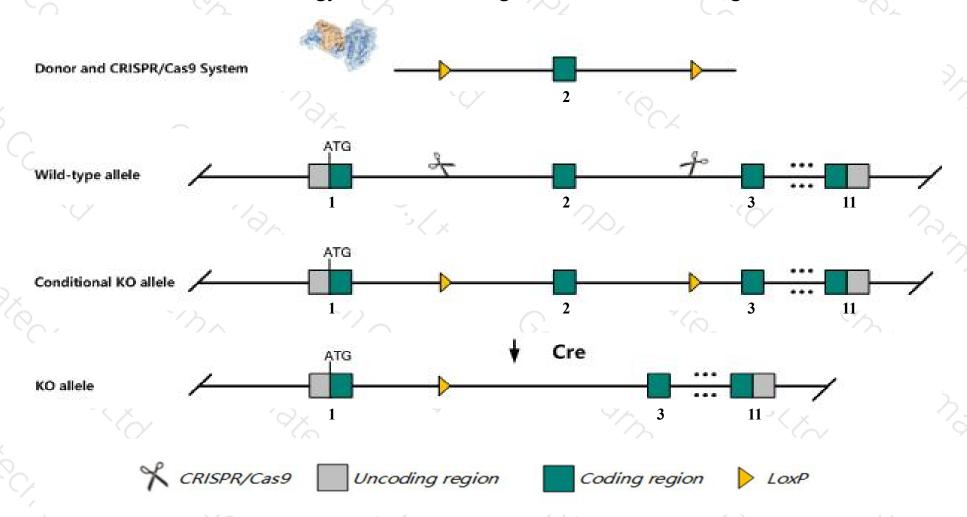
Strain background

C57BL/6JGpt

# Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Uri1* gene. The schematic diagram is as follows:



### Technical routes



- ➤ The *Uri1* gene has 7 transcripts. According to the structure of *Uri1* gene, exon2 of *Uri1-201*(ENSMUST00000085513.5) transcript is recommended as the knockout region. The region contains 35bp coding sequence.

  Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Uri1* 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**



- ➤ The *Uril* 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.
- Transcript 203 CDS 5' incomplete the influences is unknown.
- ➤ 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)



#### Uri1 URI1, prefoldin-like chaperone [Mus musculus (house mouse)]

Gene ID: 19777, updated on 31-Jan-2019

#### Summary

☆ ?

Official Symbol Uri1 provided by MGI

Official Full Name URI1, prefoldin-like chaperone provided by MGI

Primary source MGI:MGI:1342294

See related Ensembl:ENSMUSG00000030421

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 C80913, NNX3, Rmp

Expression Ubiquitous expression in testis adult (RPKM 10.9), bladder adult (RPKM 10.0) and 28 other tissuesSee more

Orthologs <u>human</u> all

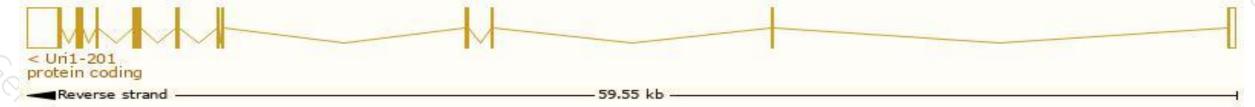
# Transcript information (Ensembl)



The gene has 7 transcripts, all transcripts are shown below:

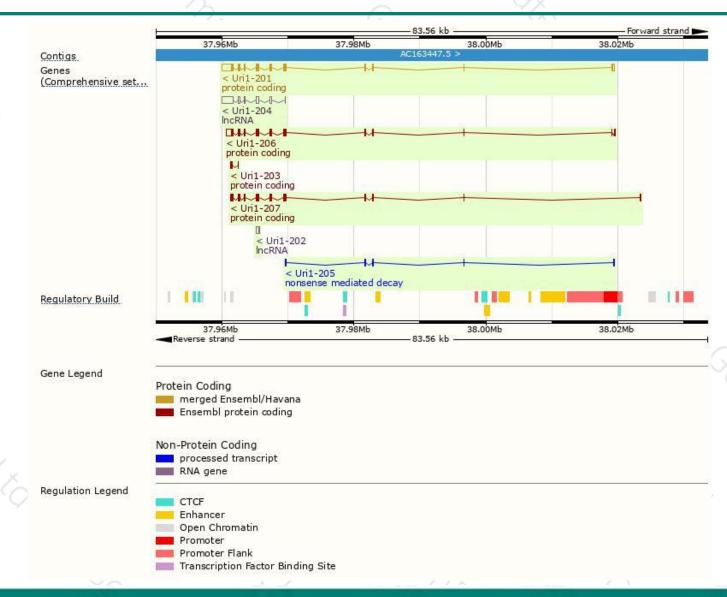
Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST00000085513.5	3441	<u>531aa</u>	Protein coding	CCDS21157	Q3TLD5	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000206327.1	2453	<u>526aa</u>	Protein coding	3953	A0A0U1RPG9	CDS 5' incomplete TSL:5
ENSMUST00000206581.1	1753	<u>533aa</u>	Protein coding	825	A0A0U1RNX4	CDS 5' incomplete TSL:1
ENSMUST00000205918.1	366	94aa	Protein coding	350	A0A0U1RP89	CDS 5' incomplete TSL:5
ENSMUST00000206169.1	440	<u>47aa</u>	Nonsense mediated decay	-	A0A0U1RQB2	CDS 5' incomplete TSL:3
ENSMUST00000205927.1	2630	No protein	IncRNA	350	15 <del>-</del>	TSL:1
ENSMUST00000205809.1	422	No protein	IncRNA	(2)	<u> </u>	TSL:3
	ENSMUST00000085513.5 ENSMUST00000206327.1 ENSMUST00000206581.1 ENSMUST00000205918.1 ENSMUST00000206169.1 ENSMUST00000205927.1	ENSMUST00000085513.5 3441 ENSMUST00000206327.1 2453 ENSMUST00000206581.1 1753 ENSMUST00000205918.1 366 ENSMUST00000206169.1 440 ENSMUST00000205927.1 2630	ENSMUST00000085513.5       3441       531aa         ENSMUST00000206327.1       2453       526aa         ENSMUST00000206581.1       1753       533aa         ENSMUST00000205918.1       366       94aa         ENSMUST00000206169.1       440       47aa         ENSMUST00000205927.1       2630       No protein	ENSMUST00000085513.5         3441         531aa         Protein coding           ENSMUST00000206327.1         2453         526aa         Protein coding           ENSMUST00000206581.1         1753         533aa         Protein coding           ENSMUST00000205918.1         366         94aa         Protein coding           ENSMUST00000206169.1         440         47aa         Nonsense mediated decay           ENSMUST00000205927.1         2630         No protein         IncRNA	ENSMUST00000085513.5         3441         531aa         Protein coding         CCDS21157           ENSMUST00000206327.1         2453         526aa         Protein coding         -           ENSMUST00000206581.1         1753         533aa         Protein coding         -           ENSMUST00000205918.1         366         94aa         Protein coding         -           ENSMUST00000206169.1         440         47aa         Nonsense mediated decay         -           ENSMUST00000205927.1         2630         No protein         IncRNA         -	ENSMUST00000085513.5         3441         531aa         Protein coding         CCDS21157         Q3TLD5           ENSMUST00000206327.1         2453         526aa         Protein coding         -         A0A0U1RPG9           ENSMUST00000206581.1         1753         533aa         Protein coding         -         A0A0U1RNX4           ENSMUST00000205918.1         366         94aa         Protein coding         -         A0A0U1RP89           ENSMUST00000206169.1         440         47aa         Nonsense mediated decay         -         A0A0U1RQB2           ENSMUST00000205927.1         2630         No protein         IncRNA         -         -

The strategy is based on the design of *Uri1-201* transcript, The transcription is shown below



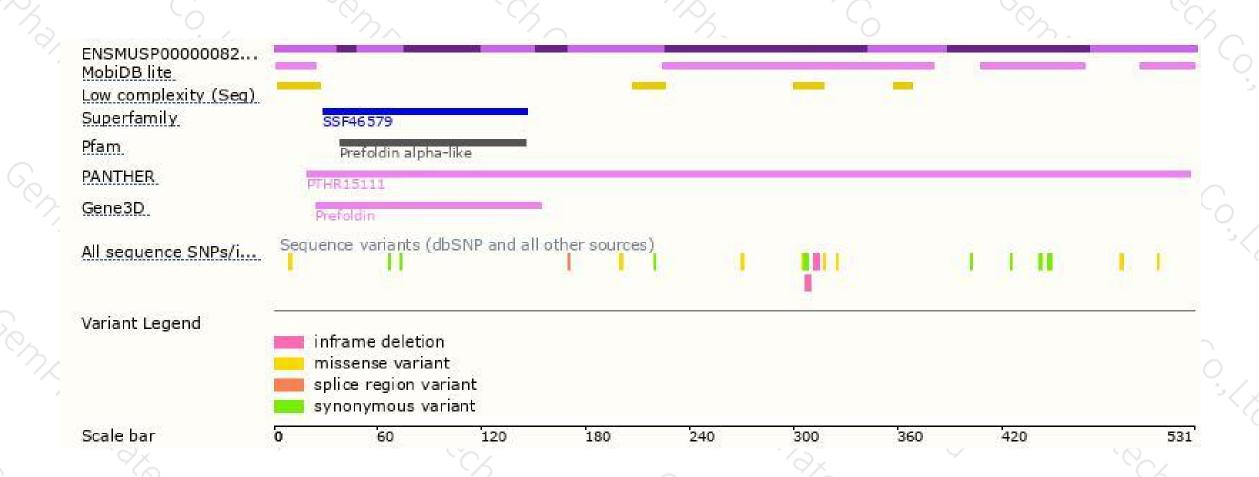
### Genomic location distribution





### Protein domain







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





