Wiz Cas9-CKO Strategy

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Project Overview

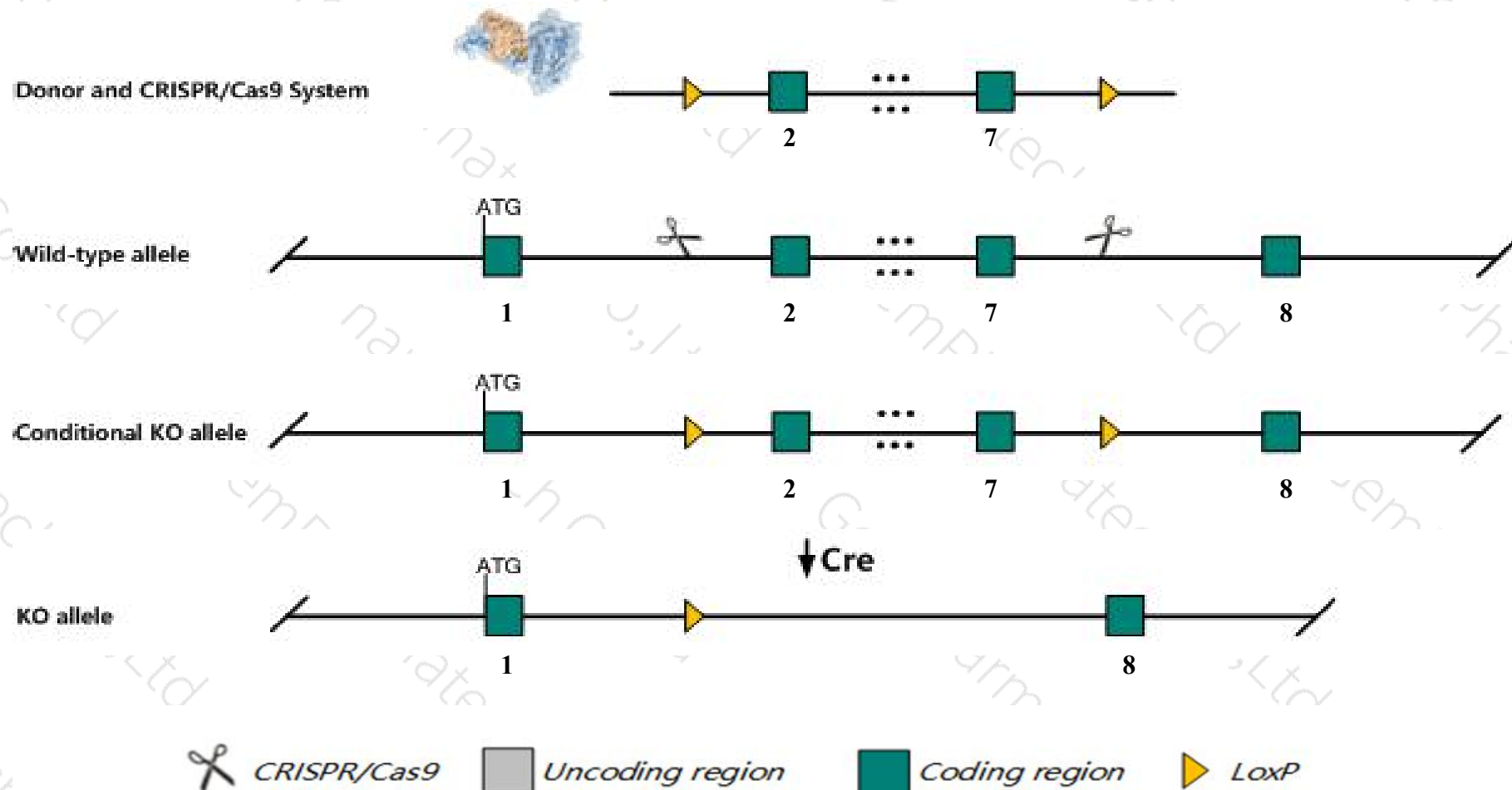|	
Project Name	*Wiz*
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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

Technical routes

➤ The *Wiz* gene has 14 transcripts. According to the structure of *Wiz* gene, exon2-exon7 of *Wiz-201*(ENSMUST00000064694.13) transcript is recommended as the knockout region.The region contains 2524bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Wiz* 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 mutant mice die prenatally.

➢ The *Wiz* gene is located on the Chr17. 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）

Wiz widely-interspaced zinc finger motifs [Mus musculus (house mouse)]

Gene ID: 22404, updated on 13-Mar-2020
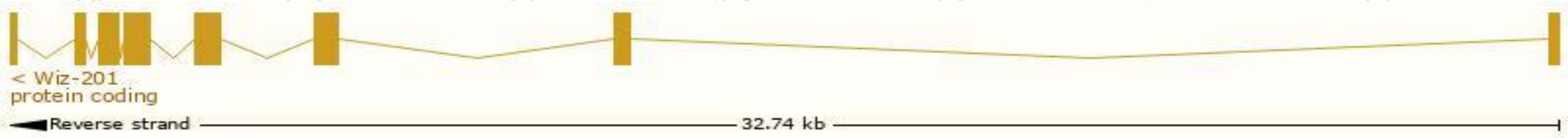
▲ Summary

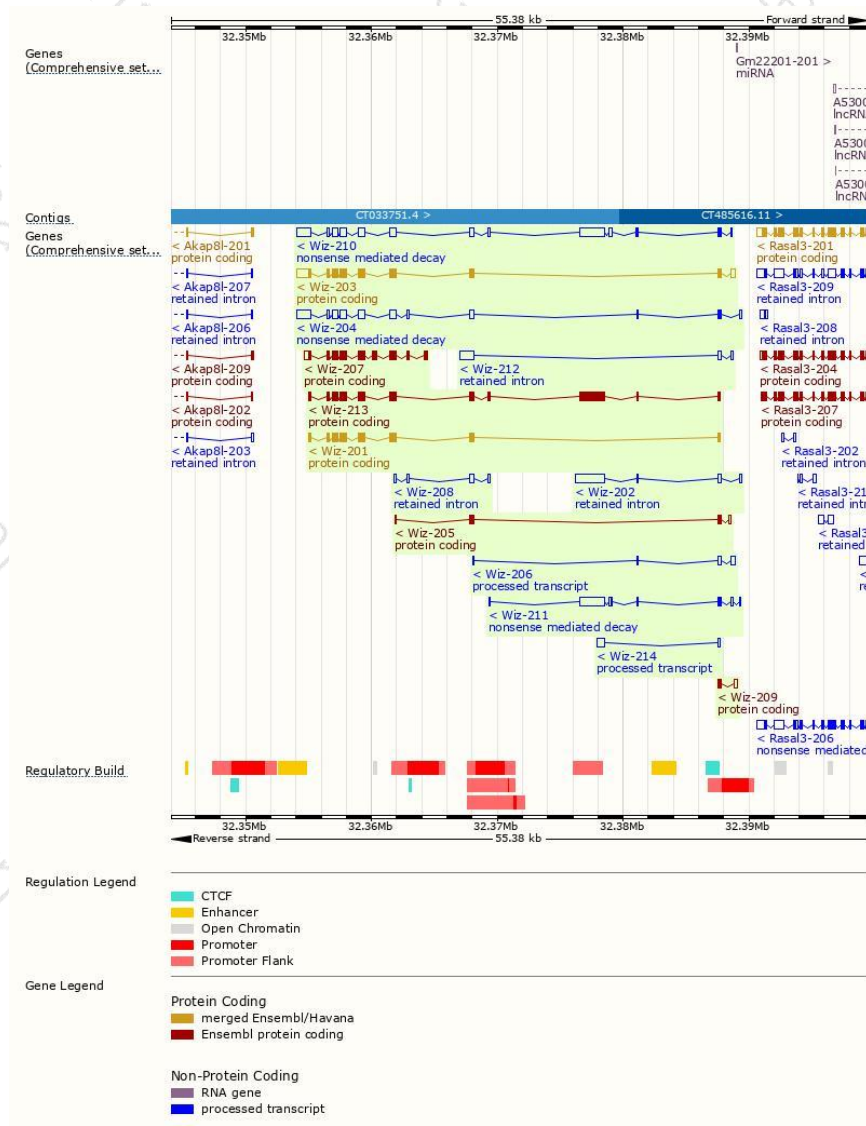|	
Official Symbol	Wiz provided by MGI
Official Full Name	widely-interspaced zinc finger motifs provided by MGI
Primary source	MGI:MGI:1332638
See related	Ensembl:ENSMUSG00000024050
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Expression	Ubiquitous expression in whole brain E14.5 (RPKM 12.4), CNS E14 (RPKM 11.2) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 14 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Wiz-203	ENSMUST00000087703.11	4175	955aa	Protein coding	CCDS28616	G5E8J8	TSL:1 GENCODE basic
Wiz-201	ENSMUST00000064694.13	2871	956aa	Protein coding	CCDS28617	O88286	TSL:1 GENCODE basic
Wiz-213	ENSMUST00000236409.1	5058	1685aa	Protein coding	-	A0A494BAG6	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
Wiz-207	ENSMUST00000169488.9	3578	1059aa	Protein coding	-	F6ZBR8	TSL:5 GENCODE basic
Wiz-205	ENSMUST00000165912.7	773	189aa	Protein coding	-	E9Q1G2	CDS 3' incomplete TSL:3
Wiz-209	ENSMUST00000170603.2	544	62aa	Protein coding	-	E9Q5R9	CDS 3' incomplete TSL:3
Wiz-210	ENSMUST00000170617.7	6426	87aa	Nonsense mediated decay	-	E9Q5W4	TSL:5
Wiz-204	ENSMUST00000163107.8	4316	88aa	Nonsense mediated decay	-	E9PZC6	TSL:1
Wiz-211	ENSMUST00000171728.2	2958	119aa	Nonsense mediated decay	-	E9Q869	TSL:5
Wiz-206	ENSMUST00000169280.7	742	No protein	Processed transcript	-	-	TSL:2
Wiz-214	ENSMUST00000238144.1	721	No protein	Processed transcript	-	-	
Wiz-202	ENSMUST00000087699.10	2781	No protein	Retained intron	-	-	TSL:2
Wiz-212	ENSMUST00000172216.7	1485	No protein	Retained intron	-	-	TSL:2
Wiz-208	ENSMUST00000169741.1	812	No protein	Retained intron	-	-	TSL:3

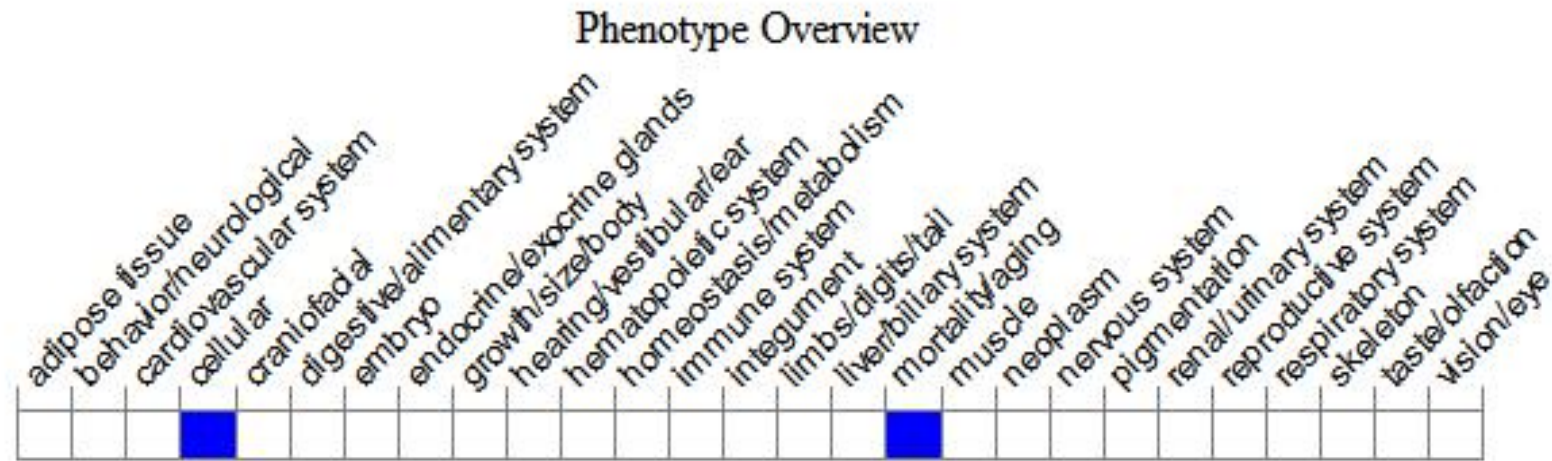The strategy is based on the design of *Wiz-201* transcript,the transcription is shown below:

< Wiz-201
protein coding

◀ Reverse strand

32.74 kb

Genomic location distribution

Protein domain

ENSMUSP00000069...
MobiDB lite
Low complexity (Seg)
Superfamily — Zinc finger C2H2 superfamily
SMART — Zinc finger C2H2-type
PROSITE profiles — Zinc finger C2H2-type
PROSITE patterns — Zinc finger C2H2-type
PANTHER — PTHR24396:SF22 / PTHR24396

All sequence SNPs/i... — Sequence variants (dbSNP and all other sources)

Variant Legend
- frameshift variant
- missense variant
- synonymous variant

Scale bar: 0 80 160 240 320 400 480 560 640 720 800 956

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 mutant mice die prenatally.

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