

Mindy1 Cas9-CKO Strategy

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Reviewer:

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Design Date:

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Project Overview

Project Name

Mindy1

Project type

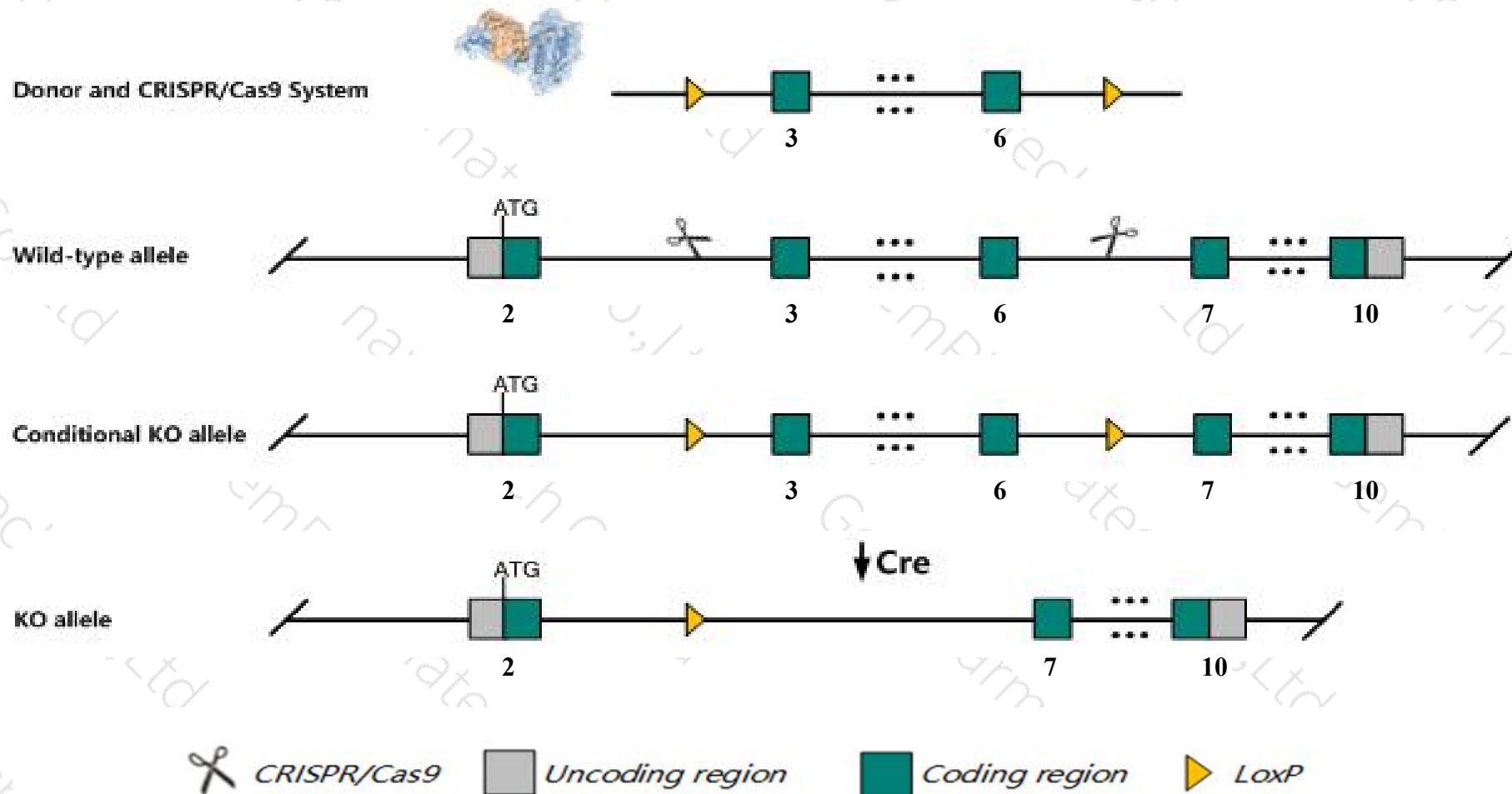
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mindy1* gene. The schematic diagram is as follows:



Technical routes

- The *Mindy1* gene has 12 transcripts. According to the structure of *Mindy1* gene, exon3-exon6 of *Mindy1*-202 (ENSMUST00000107187.8) transcript is recommended as the knockout region. The region contains 385bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mindy1* 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.

- Transcript *Mindy1-207* may not be affected.
- The *Mindy1* gene is located on the Chr3. 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)

Mindy1 MINDY lysine 48 deubiquitinase 1 [Mus musculus (house mouse)]

Gene ID: 75007, updated on 13-Mar-2020

Summary



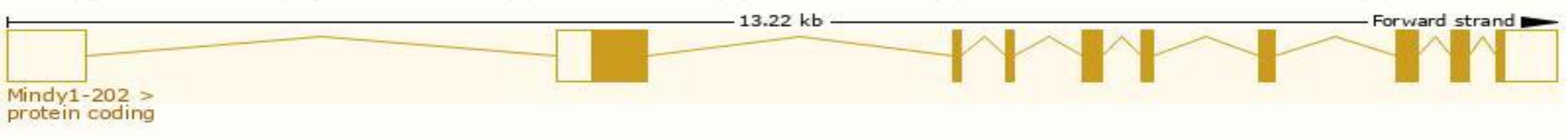
Official Symbol	Mindy1 provided by MGI
Official Full Name	MINDY lysine 48 deubiquitinase 1 provided by MGI
Primary source	MGI:MGI:1922257
See related	Ensembl:ENSMUSG00000038712
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1810005H09Rik, 4930504E06Rik, AA562754, AA960384, AW561904, Fam63a, cl-40, mKIAA1390, ni
Expression	Ubiquitous expression in adrenal adult (RPKM 42.0), ovary adult (RPKM 32.3) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

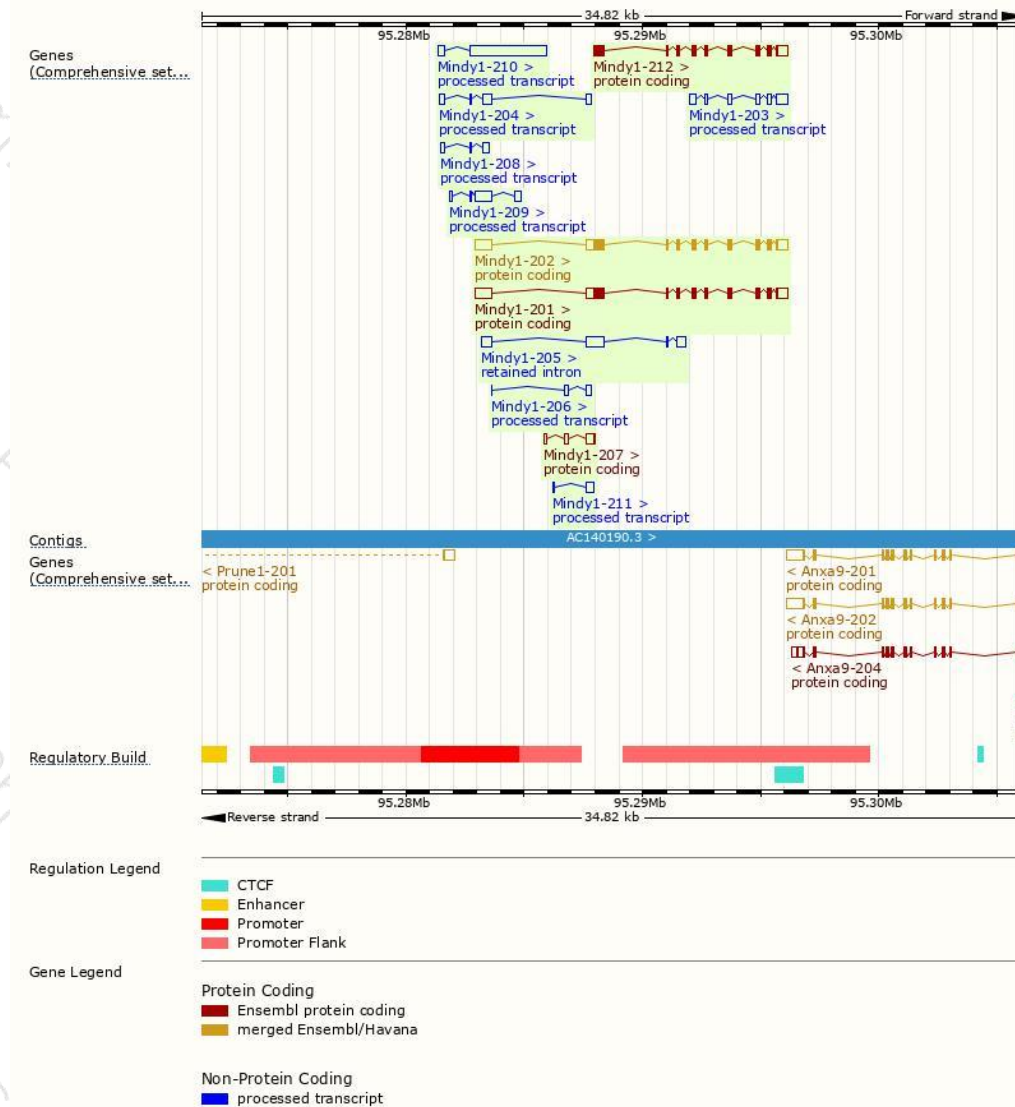
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mindy1-202	ENSMUST00000107187.8	2827	468aa	Protein coding	CCDS57233	B7ZMR0_Q76LS9	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
Mindy1-201	ENSMUST00000039537.13	2800	459aa	Protein coding	CCDS17611	Q76LS9	TSL:1 GENCODE basic
Mindy1-212	ENSMUST00000168223.1	1812	459aa	Protein coding	CCDS17611	Q76LS9	TSL:5 GENCODE basic
Mindy1-207	ENSMUST00000143498.1	641	22aa	Protein coding	-	A0A0G2JDK1	CDS 3' incomplete TSL:2
Mindy1-210	ENSMUST00000152640.1	3548	No protein	Processed transcript	-	-	TSL:1
Mindy1-203	ENSMUST00000133762.1	1373	No protein	Processed transcript	-	-	TSL:5
Mindy1-209	ENSMUST00000149568.1	1128	No protein	Processed transcript	-	-	TSL:2
Mindy1-204	ENSMUST00000135249.7	844	No protein	Processed transcript	-	-	TSL:3
Mindy1-208	ENSMUST00000147963.7	486	No protein	Processed transcript	-	-	TSL:3
Mindy1-211	ENSMUST00000153928.1	402	No protein	Processed transcript	-	-	TSL:3
Mindy1-206	ENSMUST00000137743.7	393	No protein	Processed transcript	-	-	TSL:1
Mindy1-205	ENSMUST00000135264.1	1553	No protein	Retained intron	-	-	TSL:1

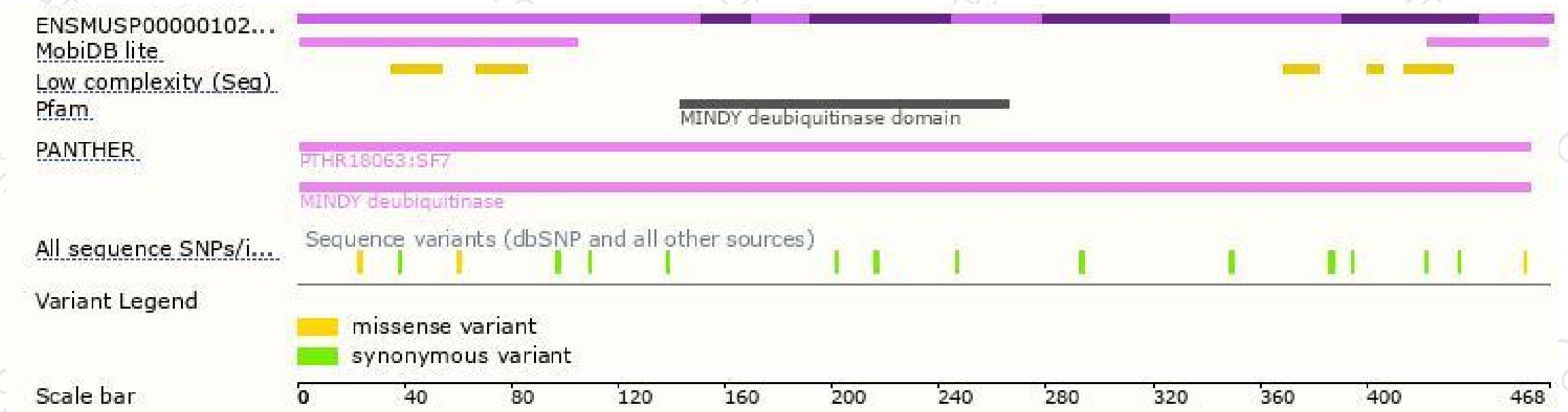
The strategy is based on the design of *Mindy1-202* transcript,The transcription is shown below



Genomic location distribution

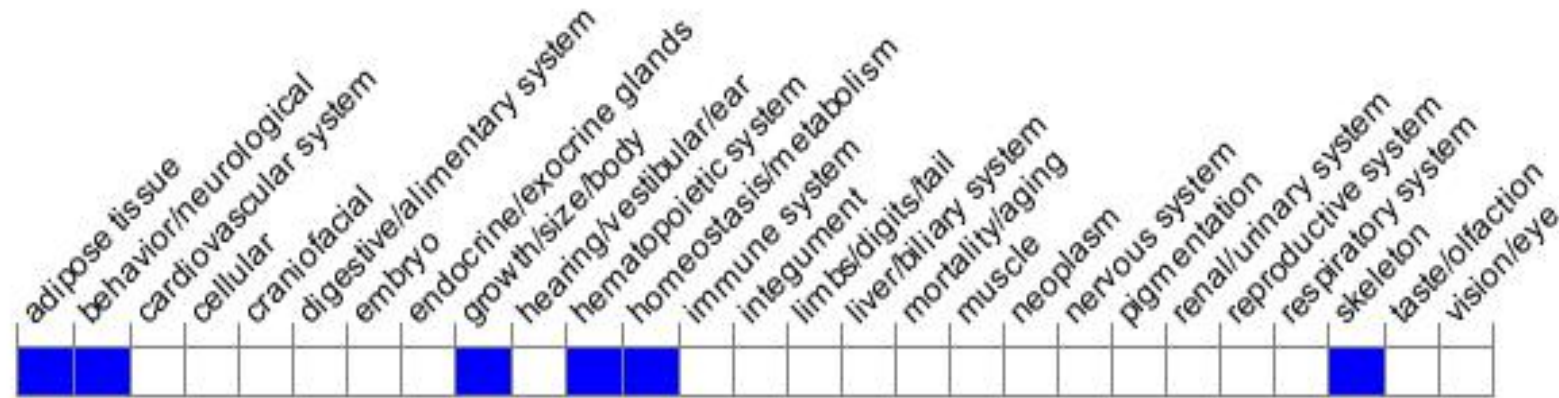


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).

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

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