

Maz Cas9-CKO Strategy

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Project Overview

Project Name

Maz

Project type

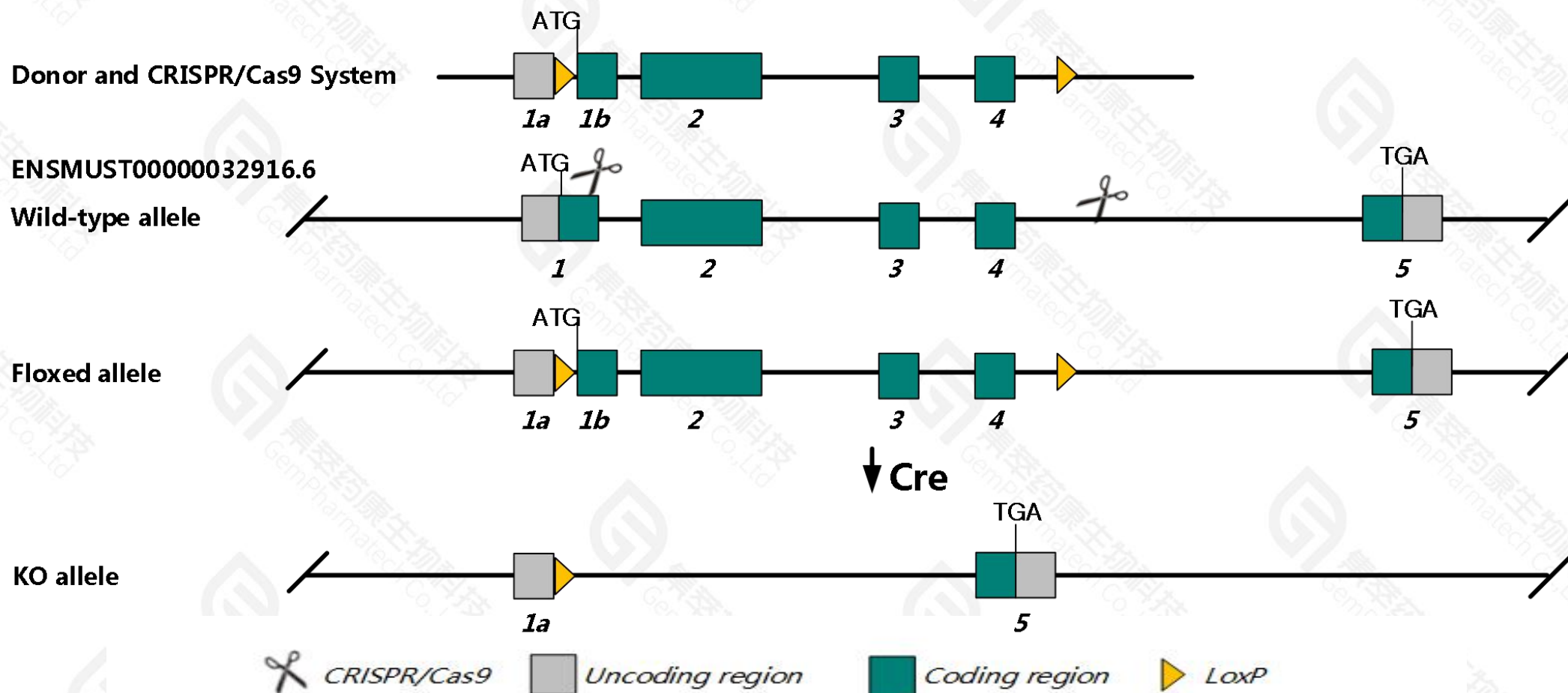
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- The *Maz* gene has 6 transcripts. According to the structure of *Maz* gene, exon1-exon4 of *Maz-201*(ENSMUST00000032916.6) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Maz* 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.

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit fetal and postnatal lethality, kidney agenesis, and impacts fertility in rare surviving mice. Mice heterozygous for this allele exhibit fetal lethality and abnormal bladder function and architecture.
- The flox region is about 3 kb away from the 5th end of the *Prmt2* gene, which may affect the regulation of this gene.
- The *Maz* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Maz MYC-associated zinc finger protein (purine-binding transcription factor) [Mus musculus (house mouse)]

Gene ID: 17188, updated on 17-Feb-2021

Summary



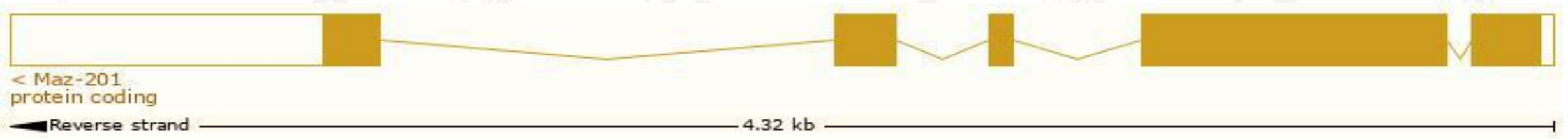
Official Symbol	Maz provided by MGI
Official Full Name	MYC-associated zinc finger protein (purine-binding transcription factor) provided by MGI
Primary source	MGI:MGI:1338823
See related	Ensembl:ENSMUSG00000030678
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	MAZI, PU, PUR1, Pur, Pur-1, SAF, SAF-1, SAF-2
Expression	Ubiquitous expression in thymus adult (RPKM 242.4), adrenal adult (RPKM 140.7) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

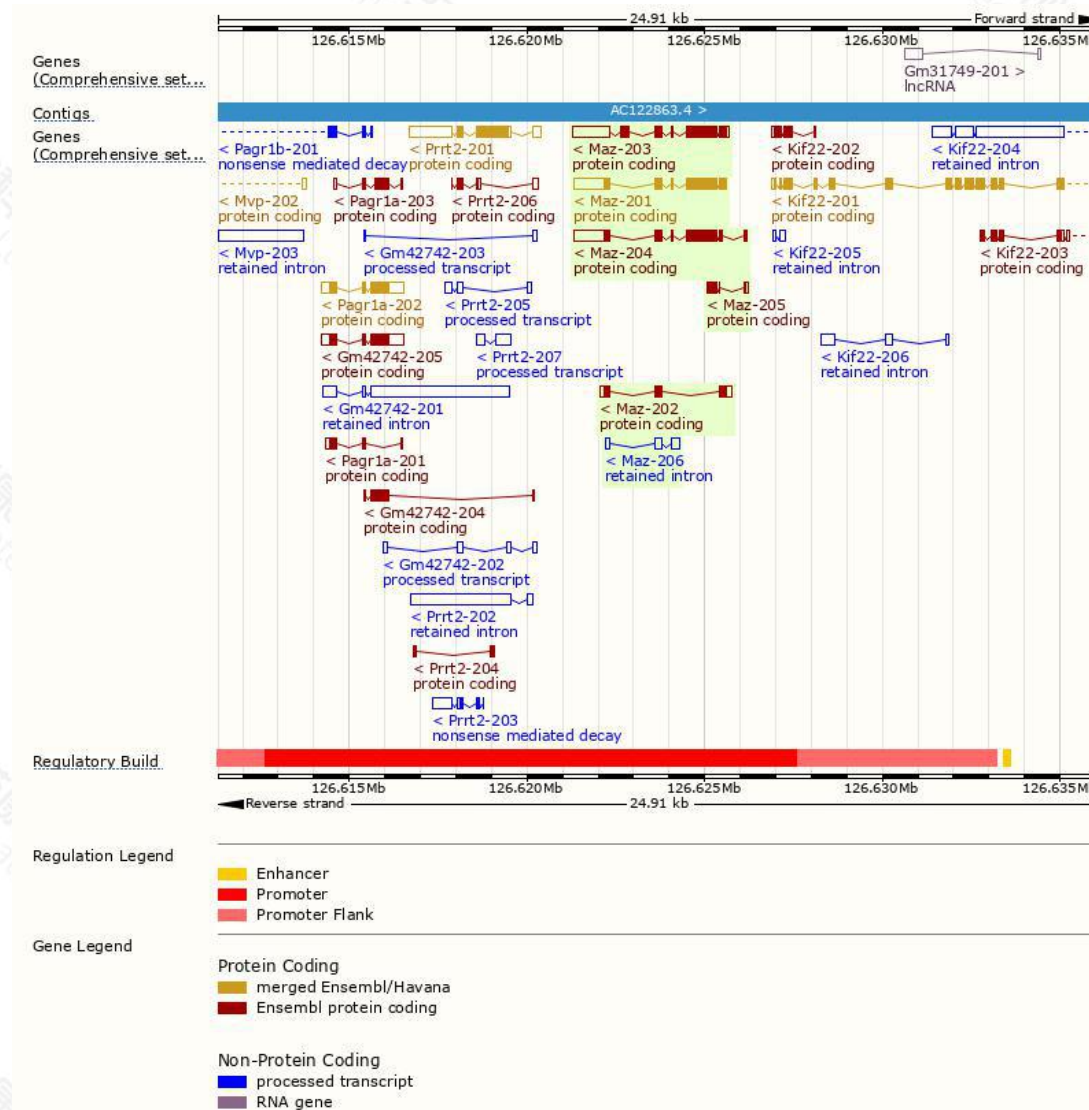
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Maz-201	ENSMUST00000032916.6	2347	477aa	Protein coding	CCDS40137		TSL:1 , GENCODE basic ,
Maz-203	ENSMUST00000205568.2	2650	493aa	Protein coding	-		TSL:5 , GENCODE basic , APPRIS P1 ,
Maz-204	ENSMUST00000206254.2	2282	454aa	Protein coding	-		TSL:5 , GENCODE basic ,
Maz-202	ENSMUST00000205461.2	796	172aa	Protein coding	-		TSL:5 , GENCODE basic ,
Maz-205	ENSMUST00000206291.2	379	109aa	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Maz-206	ENSMUST00000206953.2	548	No protein	Retained intron	-		TSL:1 ,

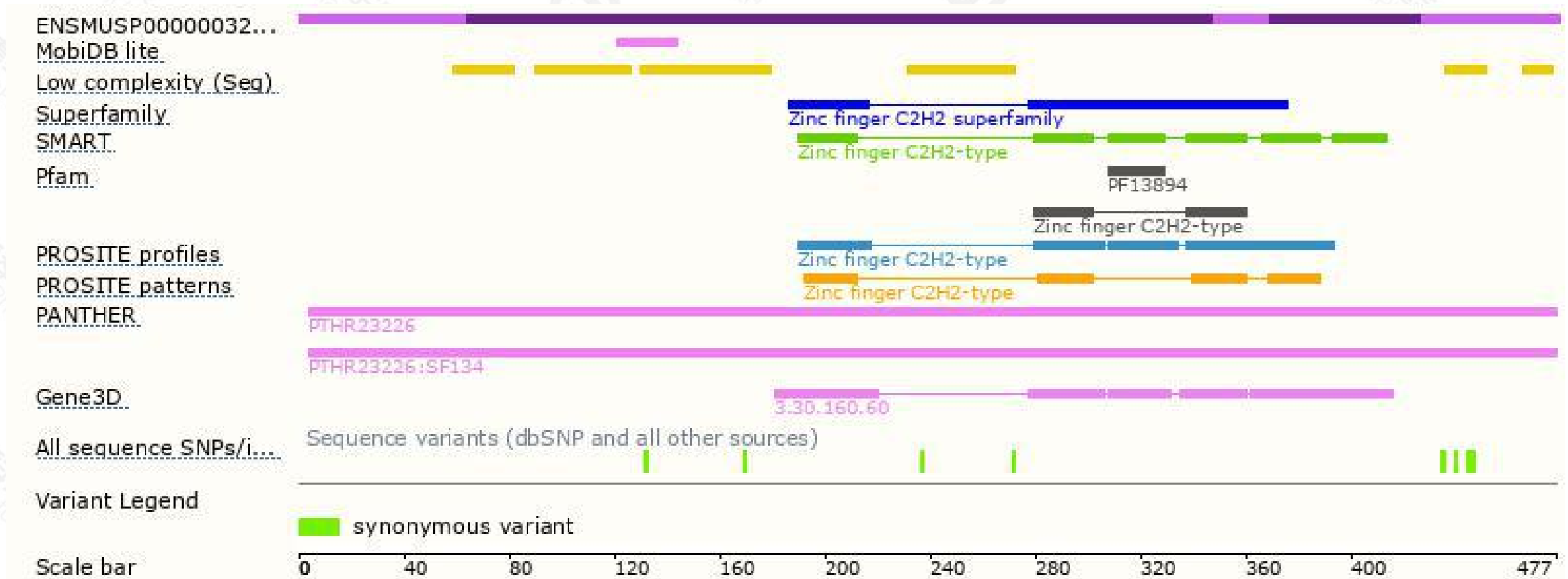
The strategy is based on the design of *Maz-201* transcript,the transcription is shown below:



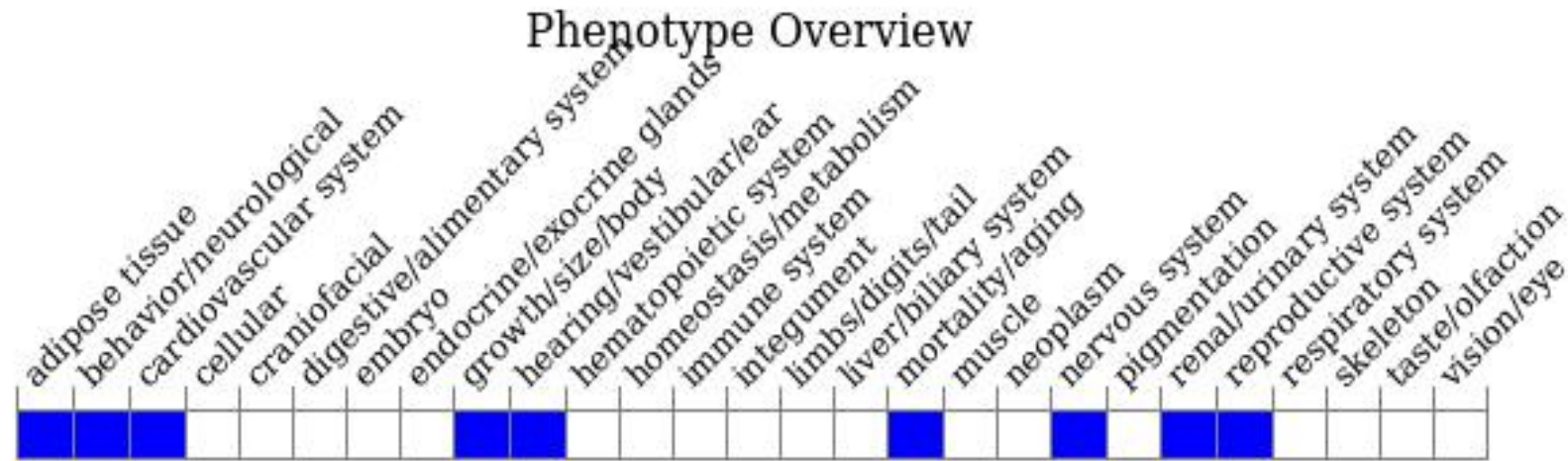
Genomic location distribution



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/>).

According to the existing MGI data, mice homozygous for a knock-out allele exhibit fetal and postnatal lethality, kidney agenesis, and impacts fertility in rare surviving mice. Mice heterozygous for this allele exhibit fetal lethality and abnormal bladder function and architecture.

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