

***Baz2a* Cas9-CKO Strategy**

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Reviewer:

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Project Overview

Project Name

Baz2a

Project type

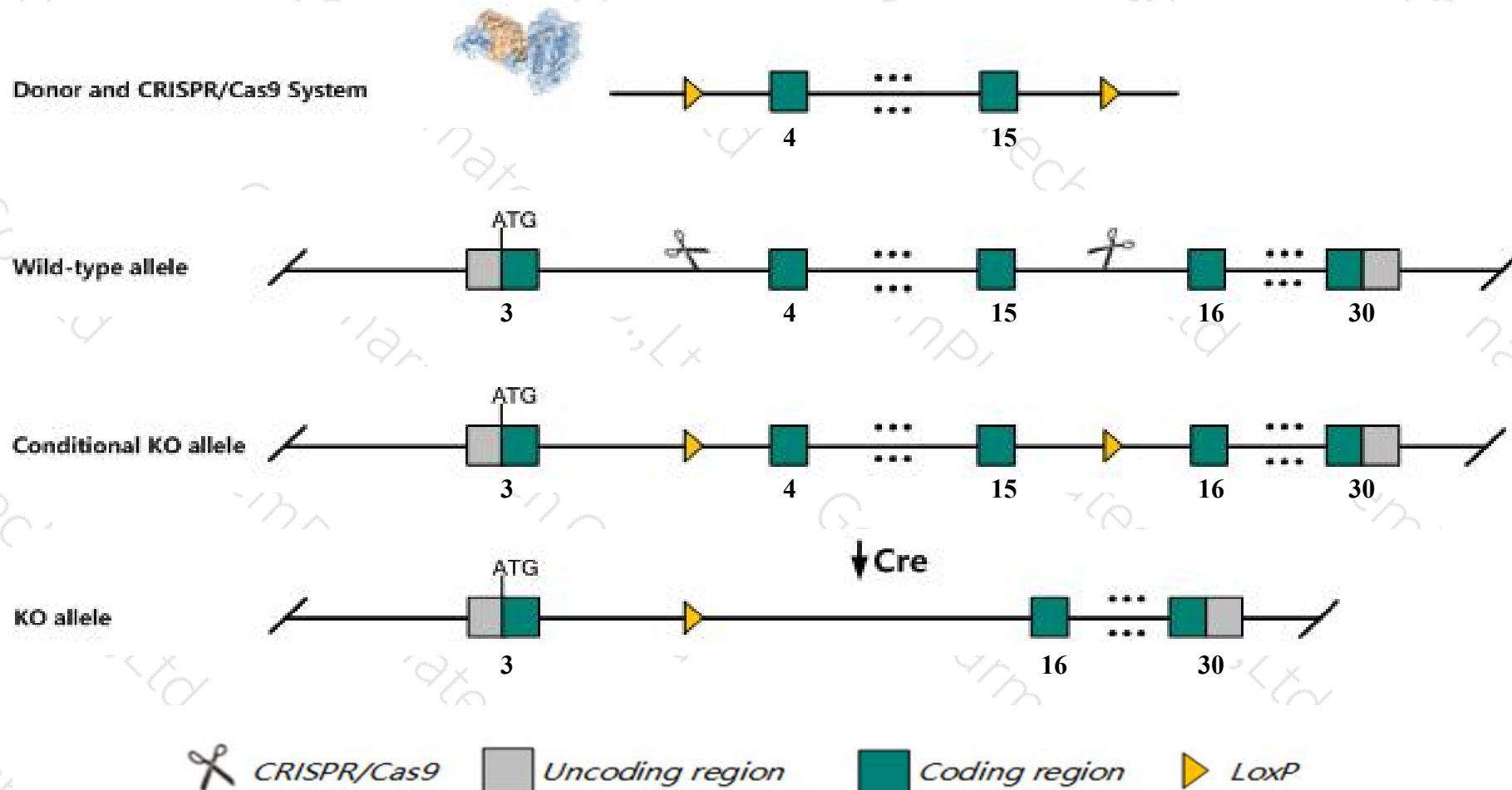
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Baz2a* gene. The schematic diagram is as follows:



Technical routes

- The *Baz2a* gene has 8 transcripts. According to the structure of *Baz2a* gene, exon4-exon15 of *Baz2a*-208 (ENSMUST00000220049.1) transcript is recommended as the knockout region. The region contains 2585bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Baz2a* 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 *Baz2a* gene is located on the Chr10. 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)

Baz2a bromodomain adjacent to zinc finger domain, 2A [Mus musculus (house mouse)]

Gene ID: 116848, updated on 31-Jan-2019

Summary



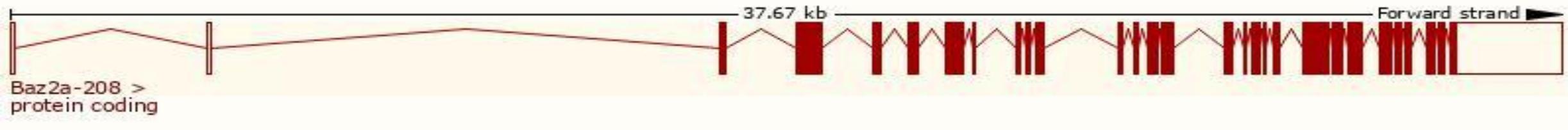
Official Symbol	Baz2a provided by MGI
Official Full Name	bromodomain adjacent to zinc finger domain, 2A provided by MGI
Primary source	MGI:MGI:2151152
See related	Ensembl:ENSMUSG00000040054
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AA415431, C030005G16Rik, C78388, Tip5, Walp3, mKIAA0314
Expression	Ubiquitous expression in thymus adult (RPKM 35.9), testis adult (RPKM 35.5) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

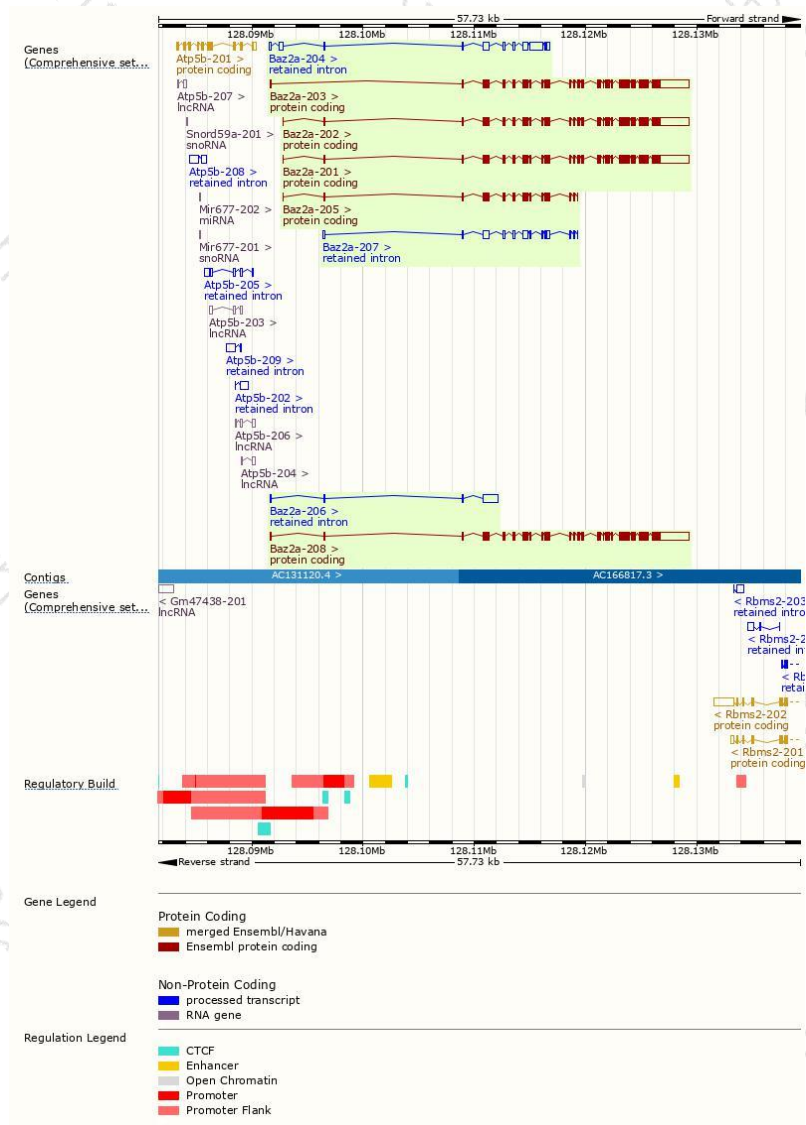
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Baz2a-208	ENSMUST00000220049.1	8443	1887aa	Protein coding	CCDS36088	F8VPM0	TSL:5 GENCODE basic APPRIS P2
Baz2a-201	ENSMUST00000045621.8	8369	1887aa	Protein coding	CCDS36088	F8VPM0	TSL:5 GENCODE basic APPRIS P2
Baz2a-203	ENSMUST00000217851.1	8385	1890aa	Protein coding	-	A0A1W2P6X9	TSL:5 GENCODE basic APPRIS ALT2
Baz2a-202	ENSMUST00000170054.8	8372	1888aa	Protein coding	-	E9Q374	TSL:5 GENCODE basic APPRIS ALT2
Baz2a-205	ENSMUST00000219072.1	2446	763aa	Protein coding	-	A0A1W2P6L0	CDS 3' incomplete TSL:1
Baz2a-204	ENSMUST00000218772.1	3721	No protein	Retained intron	-	-	TSL:5
Baz2a-207	ENSMUST00000219980.1	2455	No protein	Retained intron	-	-	TSL:1
Baz2a-206	ENSMUST00000219082.1	1782	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Baz2a-208* transcript,The transcription is shown below



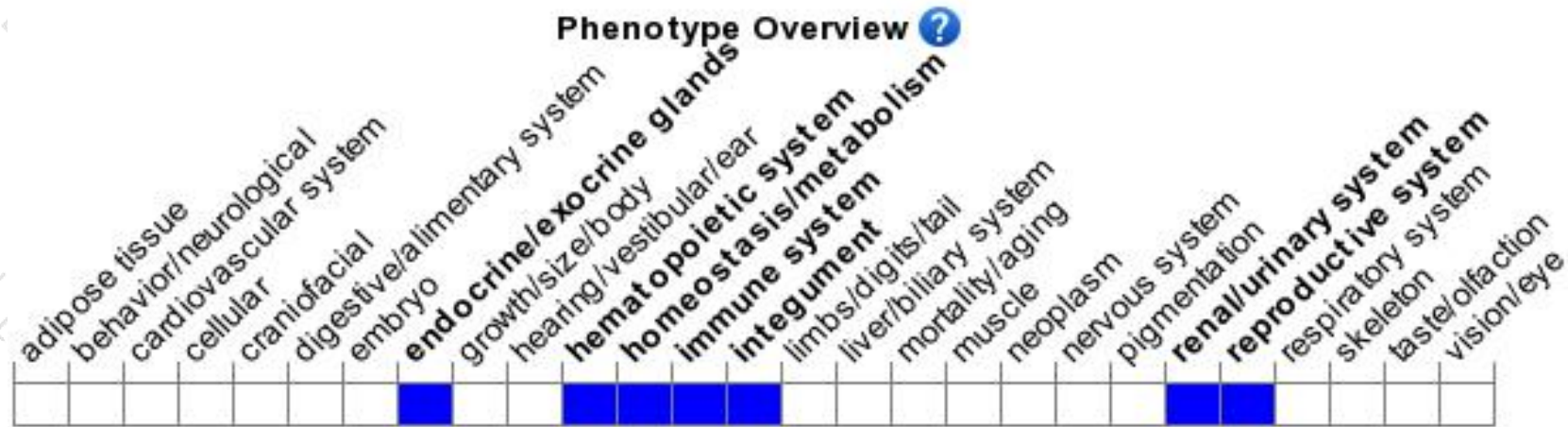
Genomic location distribution



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/>).

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

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