

Baz1a Cas9-KO Strategy

Designer: Miaomiao Cui

Reviewer: Lingyan Wu

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Project Overview

Project Name

Baz1a

Project type

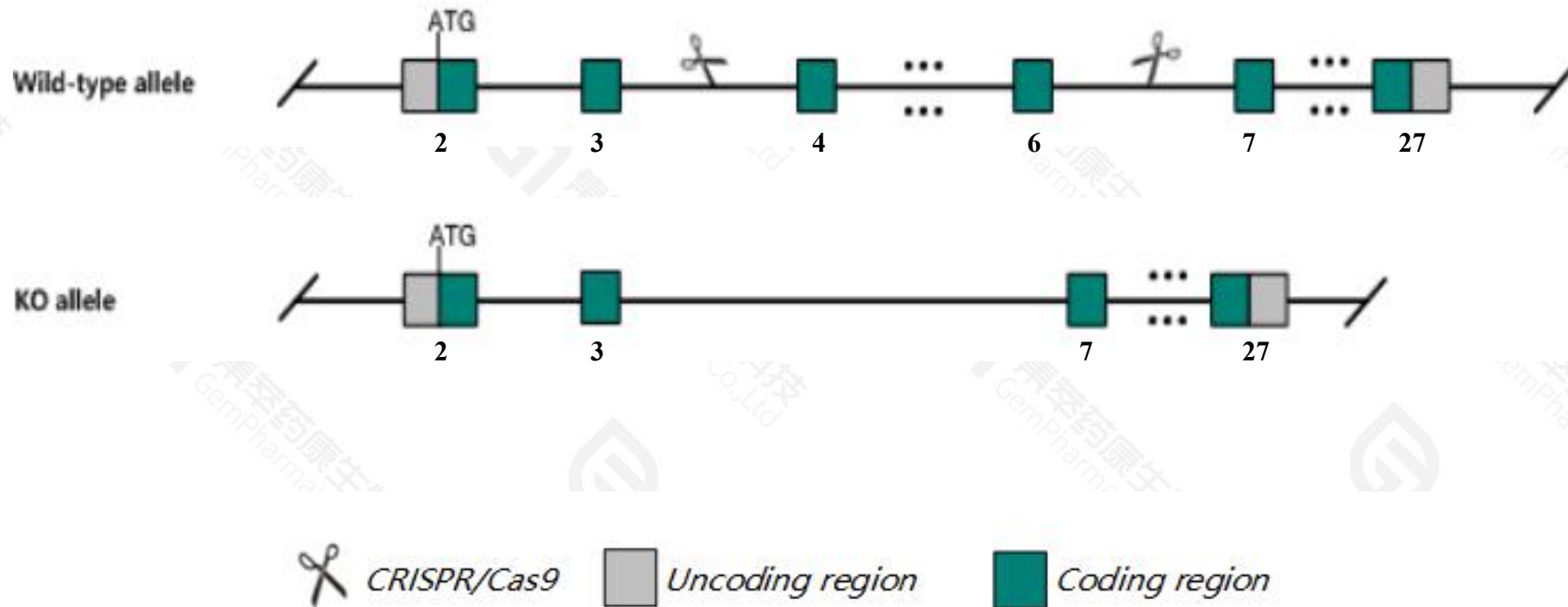
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Baz1a* gene. The schematic diagram is as follows:



- The *Baz1a* gene has 8 transcripts. According to the structure of *Baz1a* gene, exon4-exon6 of *Baz1a*-205(ENSMUST00000173433.8) transcript is recommended as the knockout region. The region contains 334bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Baz1a* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, mice homozygous for a knock-out allele are viable and able to repair meiotic double-strand breaks but exhibit teratospermia, oligospermia, asthenospermia, and male infertility due to impaired spermiogenesis.
- Transcript *Baz1a*-204&207&208 may not be affected.
- The *Baz1a* gene is located on the Chr12. 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Baz1a bromodomain adjacent to zinc finger domain 1A [Mus musculus (house mouse)]

Gene ID: 217578, updated on 17-Dec-2020

Summary



Official Symbol Baz1a provided by [MGI](#)

Official Full Name bromodomain adjacent to zinc finger domain 1A provided by [MGI](#)

Primary source [MGI:MGI:1309478](#)

See related [Ensembl:ENSMUSG00000035021](#)

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 Acf, Acf1, B930060C03, BC065123, Gtl, Gtl5, Wcrf18, Wcrf180, cbp146

Expression Broad expression in testis adult (RPKM 10.5), liver E14 (RPKM 10.0) and 22 other tissues [See more](#)

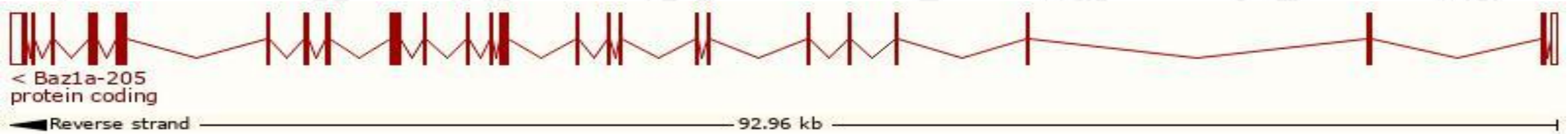
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

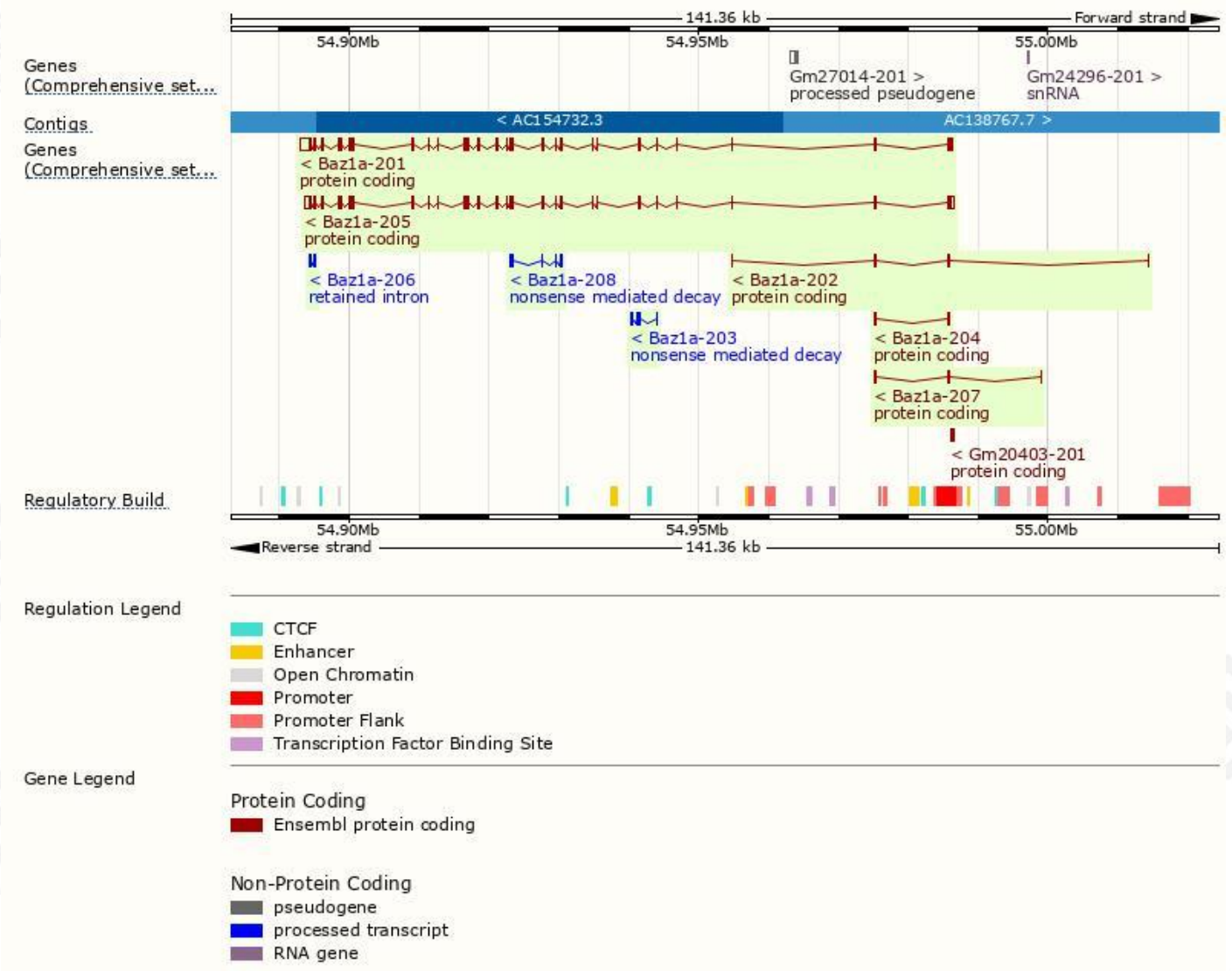
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Baz1a-205	ENSMUST00000173433.8	5788	1552aa	Protein coding	CCDS56838		TSL:5 , GENCODE basic , APPRIS P2 ,
Baz1a-201	ENSMUST00000038926.13	6188	1555aa	Protein coding	-		TSL:5 , GENCODE basic , APPRIS ALT2 ,
Baz1a-202	ENSMUST00000172875.8	589	172aa	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Baz1a-204	ENSMUST00000173177.2	418	86aa	Protein coding	-		CDS 3' incomplete , TSL:2 ,
Baz1a-207	ENSMUST00000173529.2	411	81aa	Protein coding	-		CDS 3' incomplete , TSL:2 ,
Baz1a-203	ENSMUST00000173176.2	592	91aa	Nonsense mediated decay	-		CDS 5' incomplete , TSL:3 ,
Baz1a-208	ENSMUST00000174225.2	557	79aa	Nonsense mediated decay	-		CDS 5' incomplete , TSL:2 ,
Baz1a-206	ENSMUST00000173453.2	526	No protein	Retained intron	-		TSL:2 ,

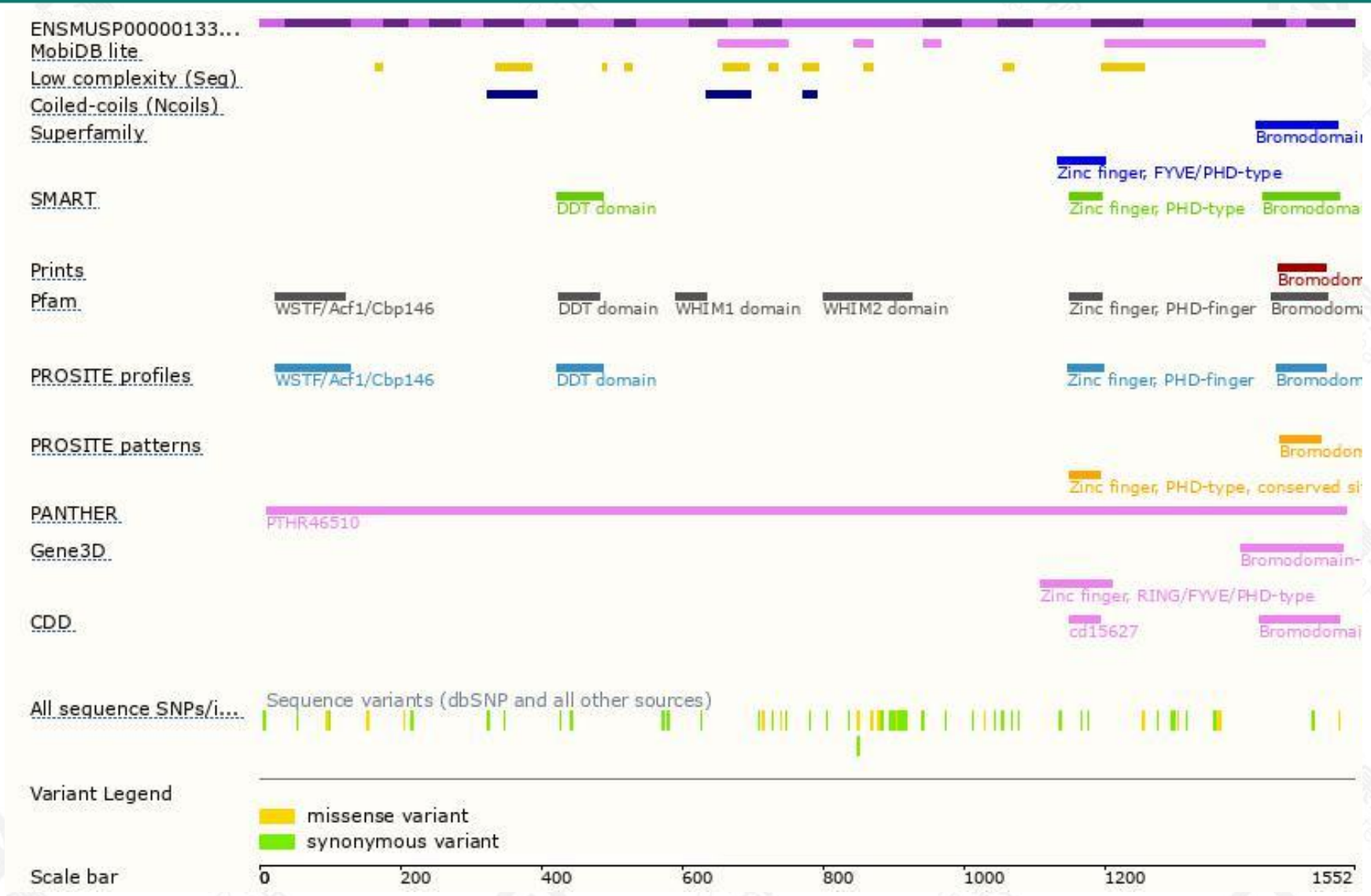
The strategy is based on the design of *Baz1a-205* transcript,the transcription is shown below:



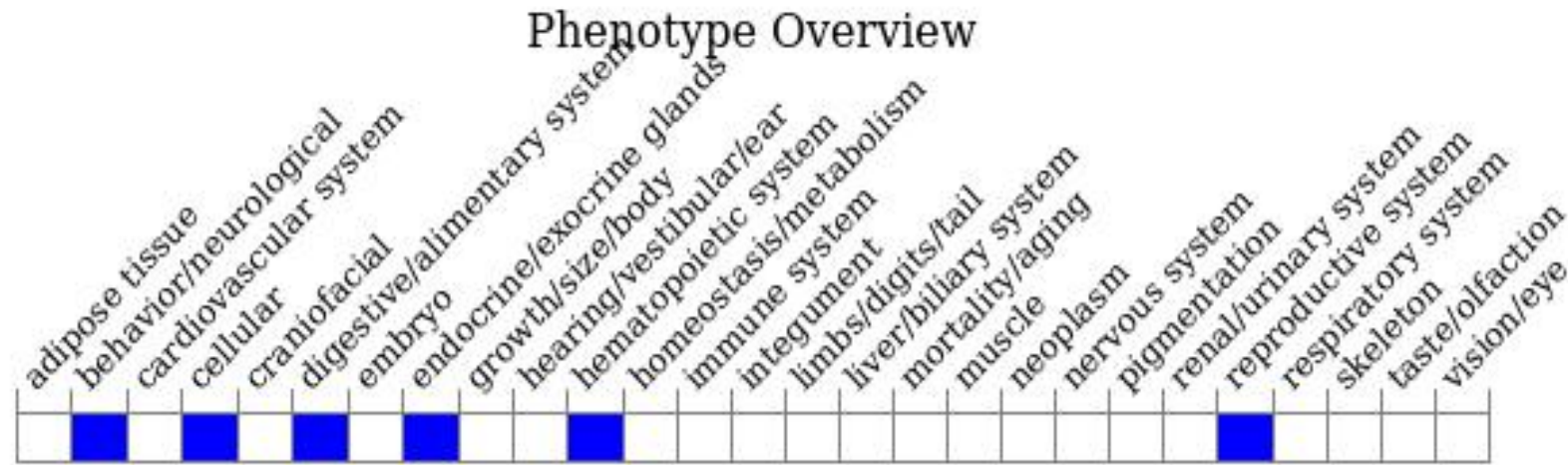
Genomic location distribution



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 are viable and able to repair meiotic double-strand breaks but exhibit teratospermia, oligospermia, asthenospermia, and male infertility due to impaired spermiogenesis.

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

