

Batf2 Cas9-KO Strategy

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Reviewer:

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Design Date:

2020/2/17

Project Overview

Project Name

Batf2

Project type

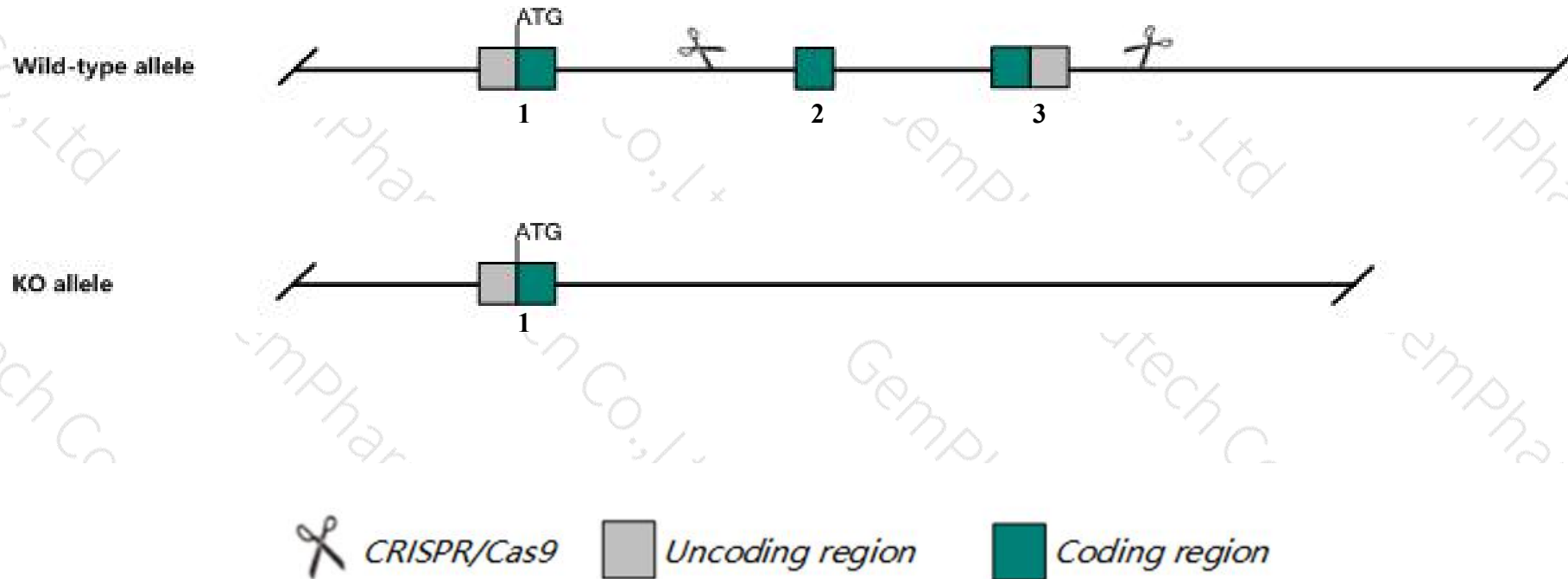
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Batf2* gene. The schematic diagram is as follows:



- The *Batf2* gene has 7 transcripts. According to the structure of *Batf2* gene, exon2-exon3 of *Batf2-201* (ENSMUST00000045042.7) transcript is recommended as the knockout region. The region contains most of coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Batf2* gene. The brief process is as follows: CRISPR/Cas9 system we

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit increased susceptibility to parasitic infection induced morbidity/mortality.
- The *Batf2* gene is located on the Chr19. 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.

Gene information (NCBI)

Batf2 basic leucine zipper transcription factor, ATF-like 2 [*Mus musculus* (house mouse)]

Gene ID: 74481, updated on 24-Oct-2019

Summary

Official Symbol Batf2 provided by [MGI](#)
Official Full Name basic leucine zipper transcription factor, ATF-like 2 provided by [MGI](#)
Primary source [MGI:MGI:1921731](#)
See related [Ensembl:ENSMUSG00000039699](#)
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 B-ATF-2
Expression Biased expression in large intestine adult (RPKM 36.2), duodenum adult (RPKM 28.4) and 8 other tissues [See more](#)
Orthologs [human](#) [all](#)

Genomic context

Location: 19; 19 A

See Batf2 in [Genome Data Viewer](#)

Exon count: 3

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	19	NC_000085.6 (6164391..6172476)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	19	NC_000085.5 (6164458..6172476)

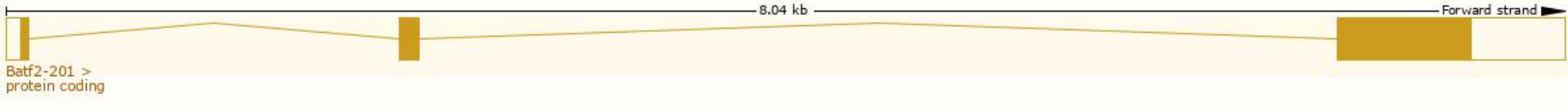


Transcript information (Ensembl)

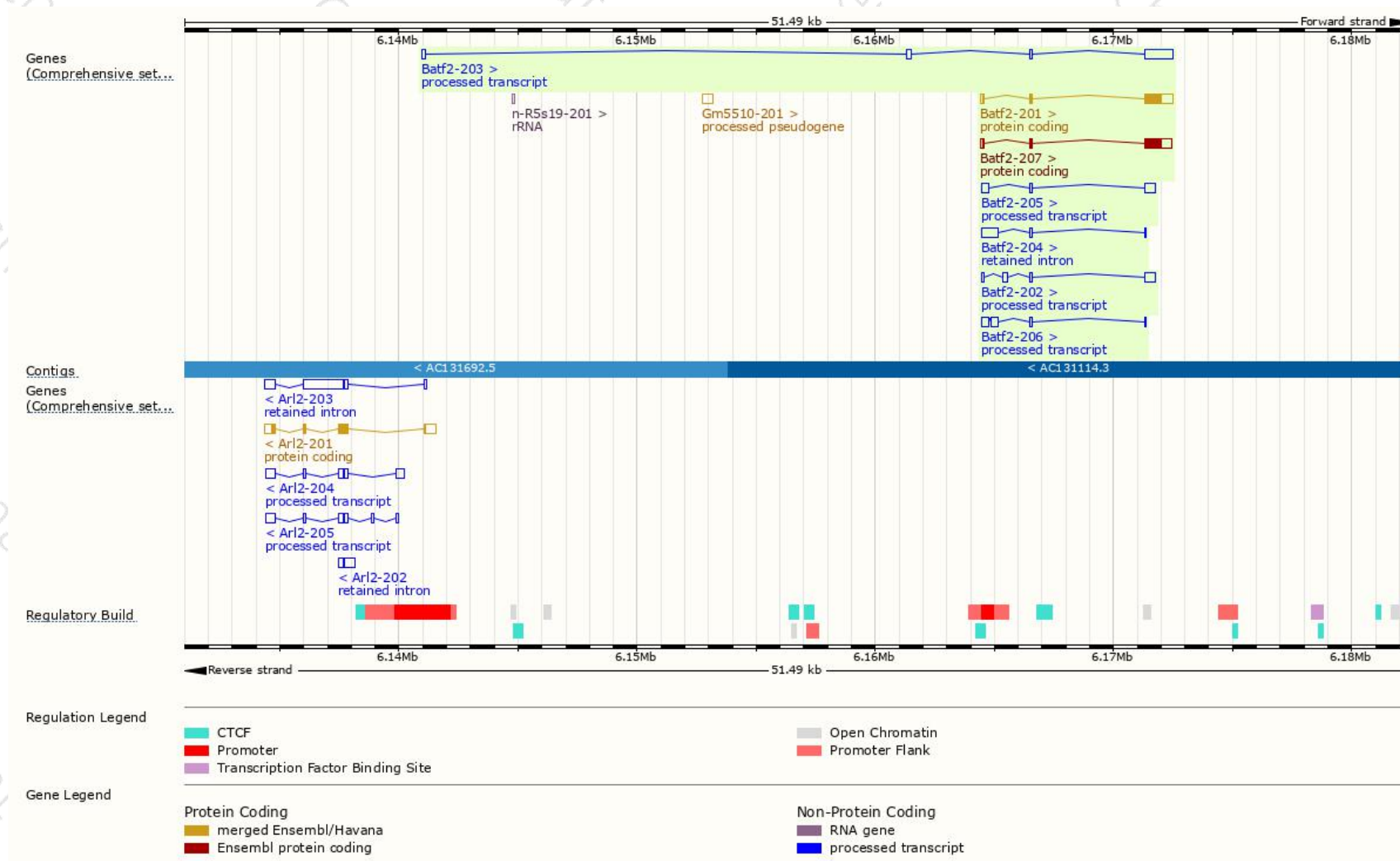
The gene has 7 transcripts, and the transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Batf2-201	ENSMUST00000045042.7	1391	277aa	Protein coding	CCDS29497	Q8R1H8	TSL:1 GENCODE basic APPRIS P1
Batf2-207	ENSMUST00000237511.1	1382	276aa	Protein coding	-	Q8R1H8	GENCODE basic
Batf2-203	ENSMUST00000134150.7	1584	No protein	Processed transcript	-	-	TSL:1
Batf2-205	ENSMUST00000139326.7	865	No protein	Processed transcript	-	-	TSL:3
Batf2-202	ENSMUST00000132750.7	857	No protein	Processed transcript	-	-	TSL:3
Batf2-206	ENSMUST00000141858.1	722	No protein	Processed transcript	-	-	TSL:3
Batf2-204	ENSMUST00000135461.7	882	No protein	Retained intron	-	-	TSL:5

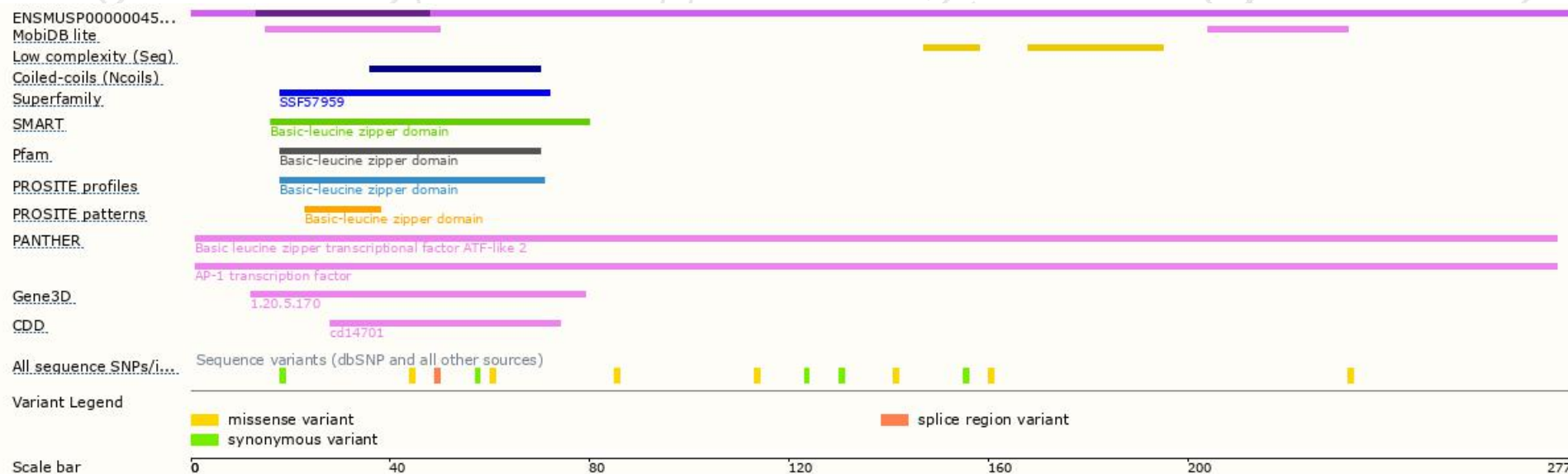
The strategy is based on the design of *Batf2-201* transcript, The transcription is shown below



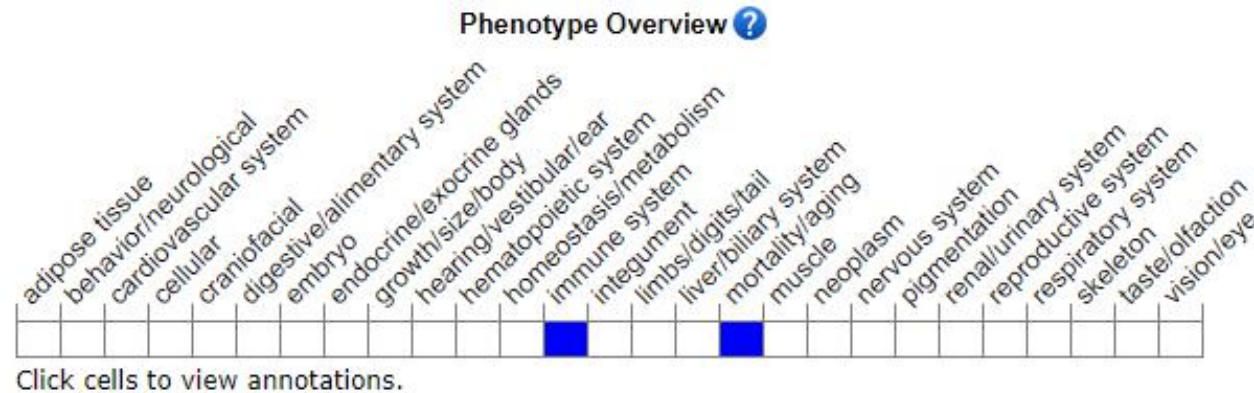
Genomic location distribution



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/>).

Mice homozygous for a knock-out allele exhibit increased susceptibility to parasitic infection induced morbidity/mortality.

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

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