

***Batf* Cas9-CKO Strategy**

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Project Overview

Project Name

Batf

Project type

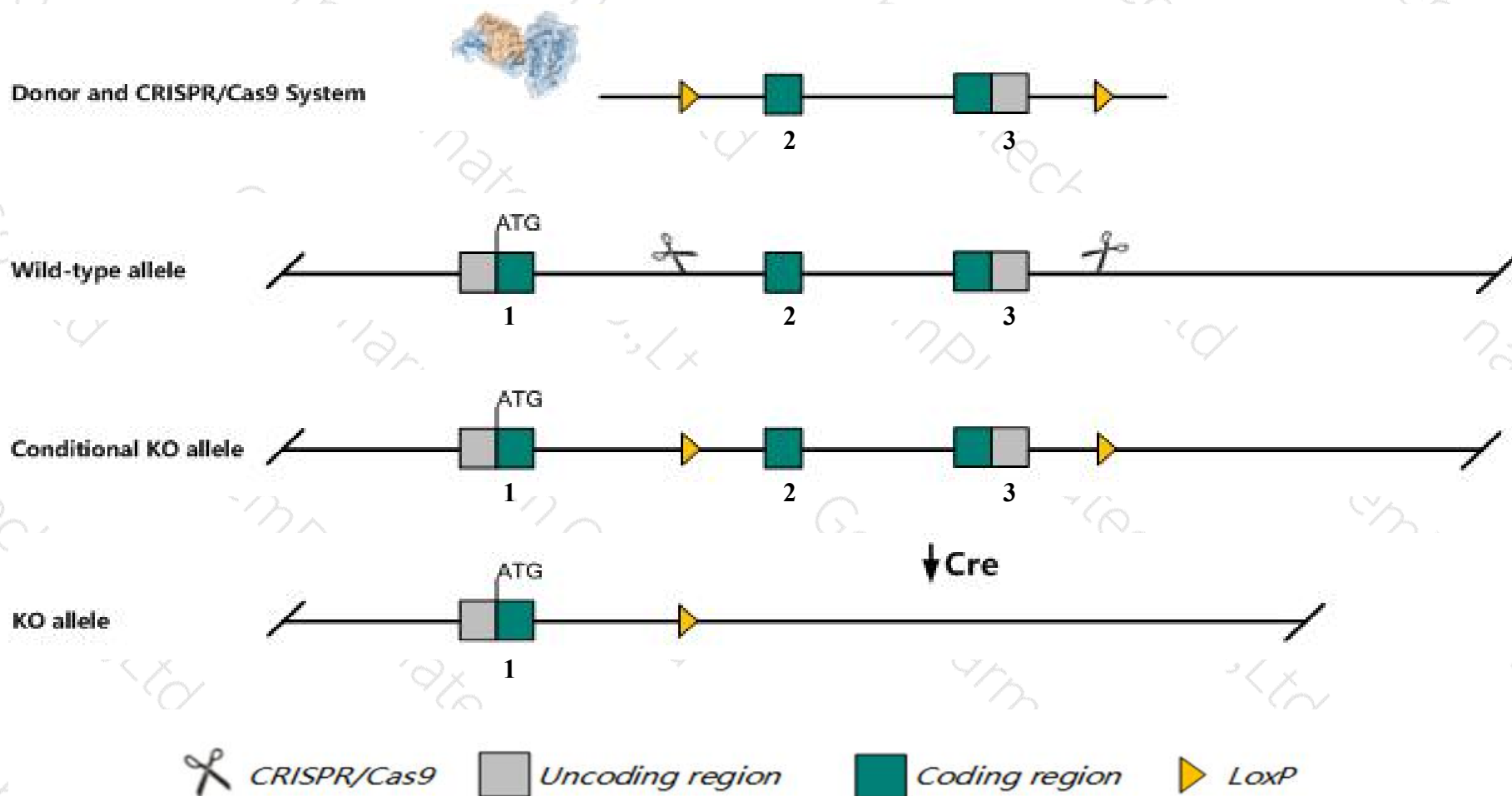
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- The *Batf* gene has 2 transcripts. According to the structure of *Batf* gene, exon2-exon3 of *Batf*-201 (ENSMUST00000040536.5) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Batf* 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, Homozygote null mice are defective in generation of Th17 T cells.
- The *Batf* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

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

Gene ID: 53314, updated on 9-Mar-2019

Summary



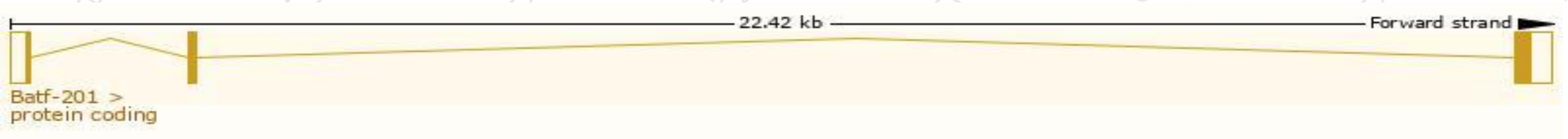
Official Symbol	Batf provided by MGI
Official Full Name	basic leucine zipper transcription factor, ATF-like provided by MGI
Primary source	MGI:MGI:1859147
See related	Ensembl:ENSMUSG000000034266
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	B-ATF, SFA-2
Expression	Broad expression in spleen adult (RPKM 6.8), thymus adult (RPKM 3.8) and 21 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

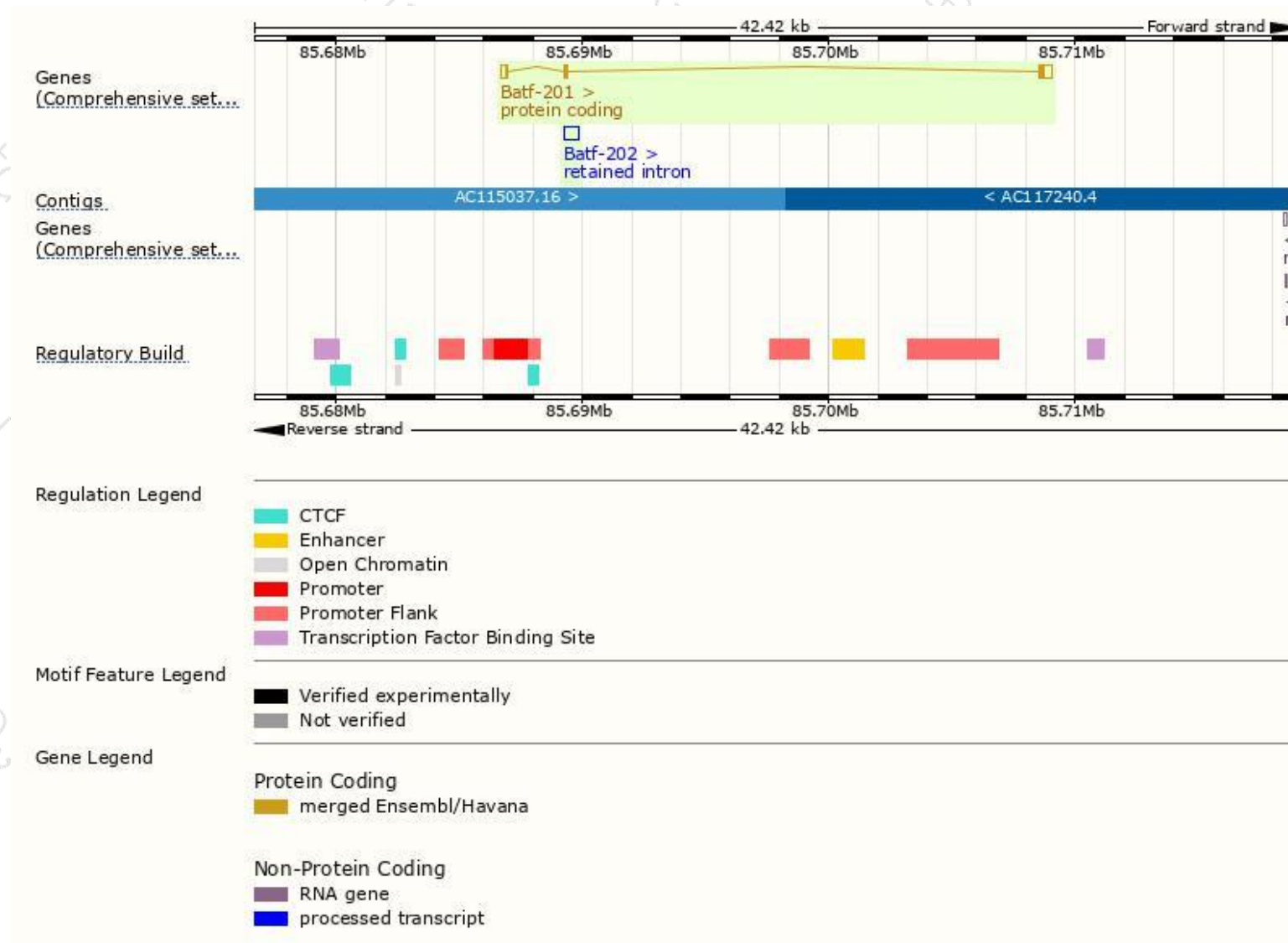
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Batf-201	ENSMUST00000040536.5	955	125aa	Protein coding	CCDS26061	O35284	TSL:1 GENCODE basic APPRIS P1
Batf-202	ENSMUST00000222781.1	532	No protein	Retained intron	-	-	TSL:NA

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



Genomic location distribution



Protein domain

ENSMUSP00000040...

MobiDB lite

Low complexity (Seg)

Conserved Domains

Coiled-coils (Ncoils)

hmmpanther

Superfamily domains

SMART domains

Prints domain

Pfam domain

PROSITE profiles

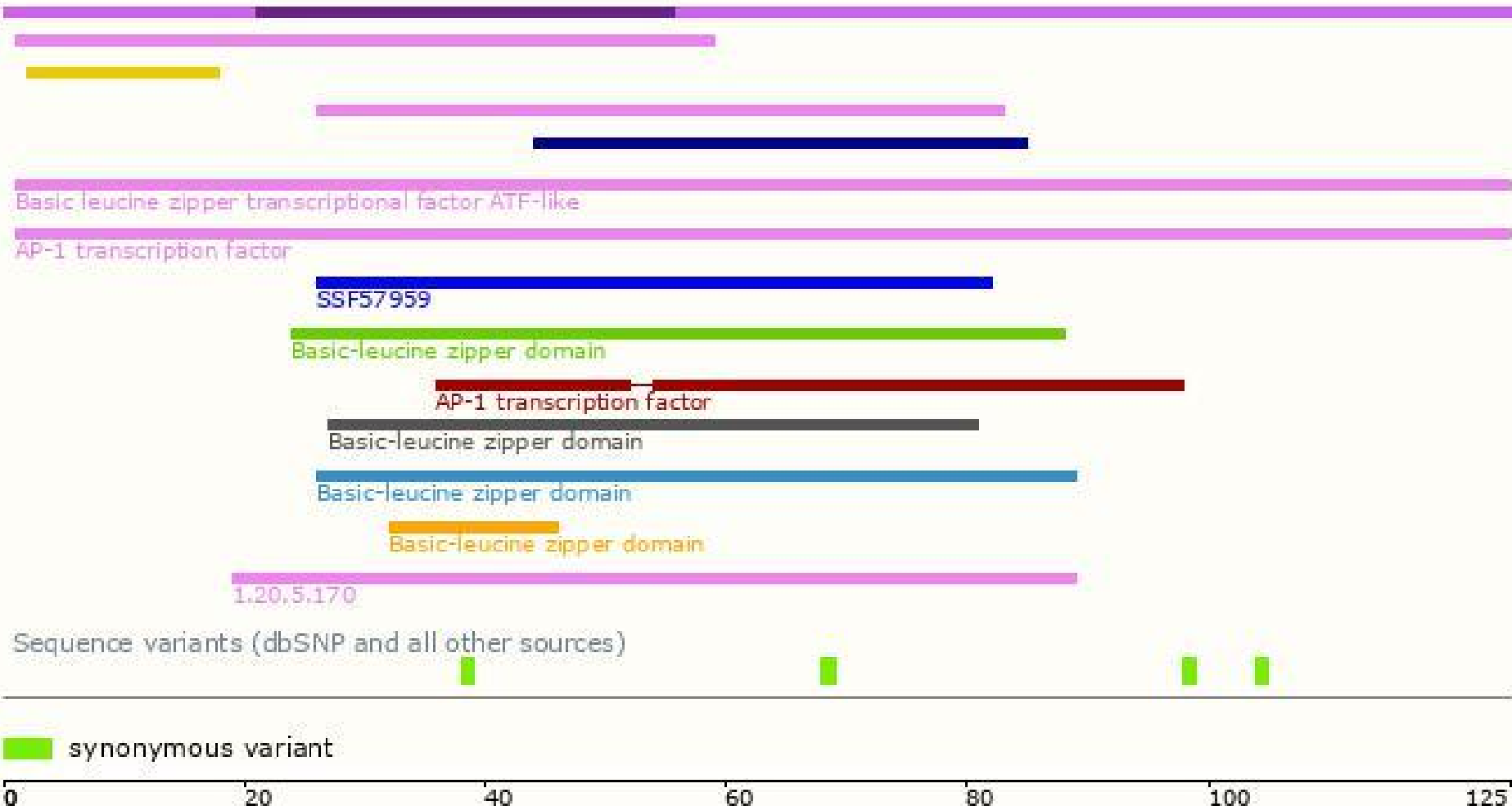
PROSITE patterns

Gene3D

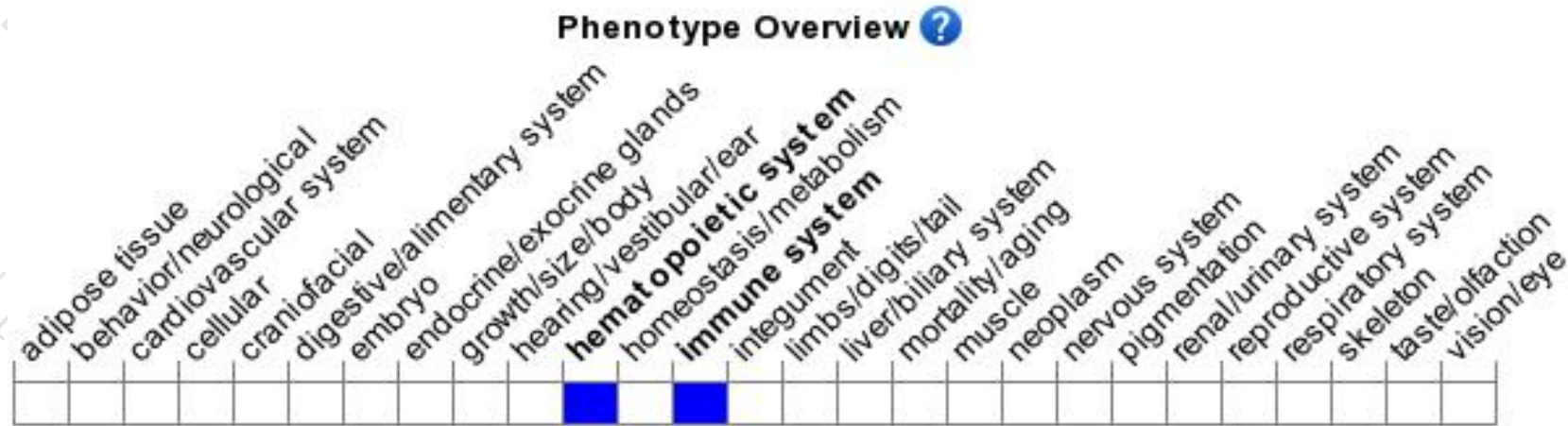
All sequence SNPs/i...

Variant Legend

Scale bar



Mouse phenotype description(MGI)



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

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

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