

Bag3 Cas9-KO Strategy

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Project Overview

Project Name

Bag3

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Bag3* gene. The schematic diagram is as follows:



- The *Bag3* gene has 1 transcript. According to the structure of *Bag3* gene, the predicted promoter region and exon1-4 of *Bag3*-201 (ENSMUST00000033136.8) transcript is recommended as the knockout region. The region contains the predicted promoter sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Bag3* gene. The brief process is as follows: gRNA was transcribed in vitro. Cas9 and gRNA 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 gene trap allele exhibit postnatal lethality, growth retardation, cardiomyocyte and skeletal myocyte degeneration, and pulmonary edema. Mice homozygous for a null allele also exhibit postnatal lethality and growth retardation but lack the myocyte degeneration phenotype.
- The *Bag3* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Bag3 BCL2-associated athanogene 3 [*Mus musculus* (house mouse)]

Gene ID: 29810, updated on 30-Sep-2018

Summary

Official Symbol Bag3 provided by [MGI](#)

Official Full Name BCL2-associated athanogene 3 provided by [MGI](#)

Primary source [MGI:MGI:1352493](#)

See related [Ensembl:ENSMUSG00000030847](#) [Vega:OTTMUSG00000058717](#)

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 Bis; mg638; AA407278

Expression Broad expression in adrenal adult (RPKM 127.9), heart adult (RPKM 49.8) and 16 other tissues [See more](#)

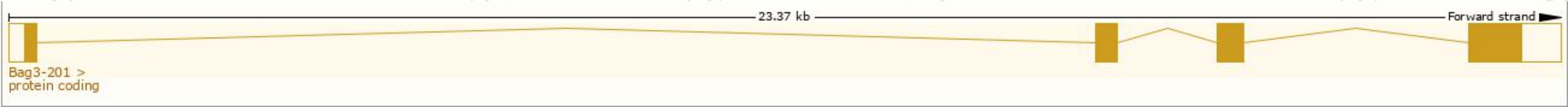
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

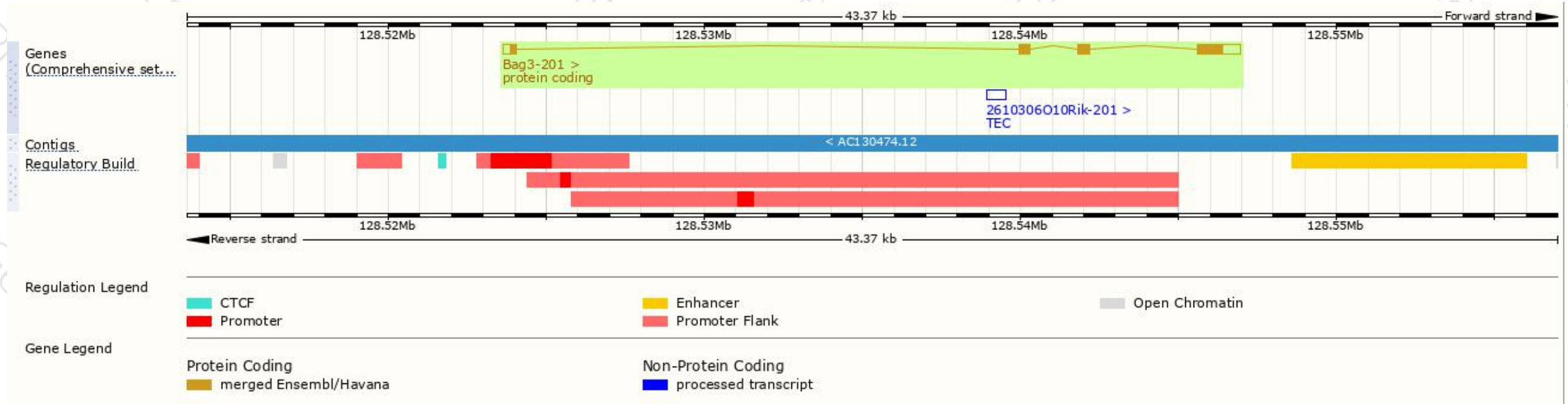
The gene has 1 transcript, and all transcripts are shown below:

Name ▲	Transcript ID ▲	bp ▲	Protein ▲	Biotype ▲	CCDS ▲	UniProt ▲	Flags ▲
Bag3-201	ENSMUST00000033136.8	2562	577aa	Protein coding	CCDS21898	Q9JLV1	TSL:1 Gencode basic APPRIS P1

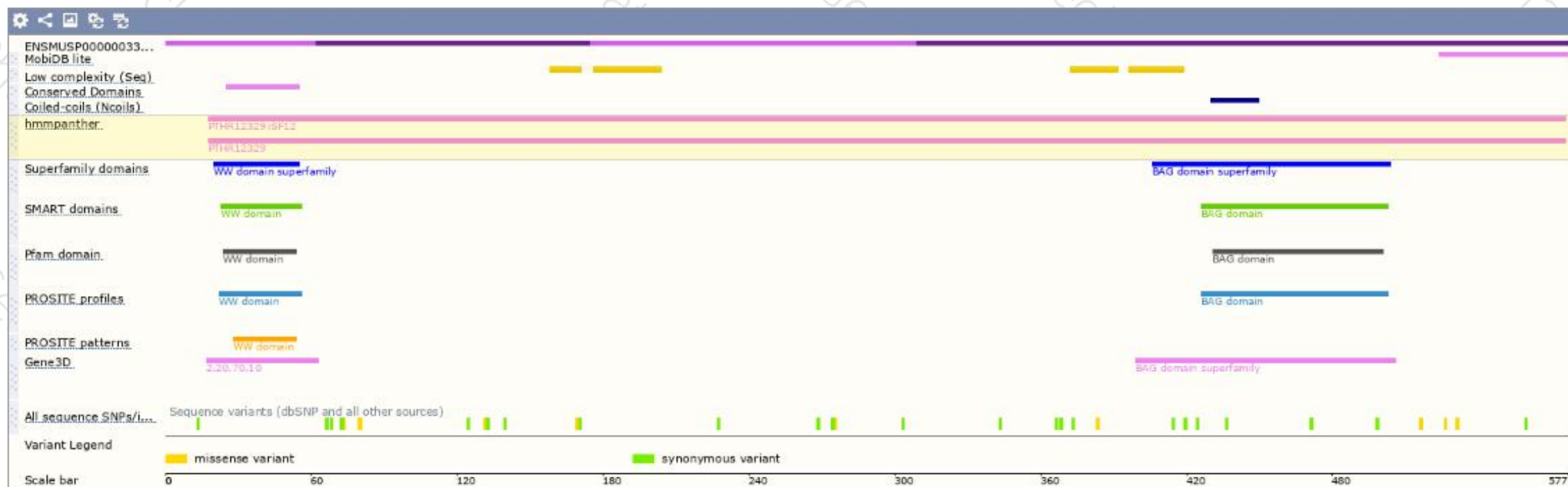
The strategy is based on the design of *Bag3-201* transcript, The transcription is shown below



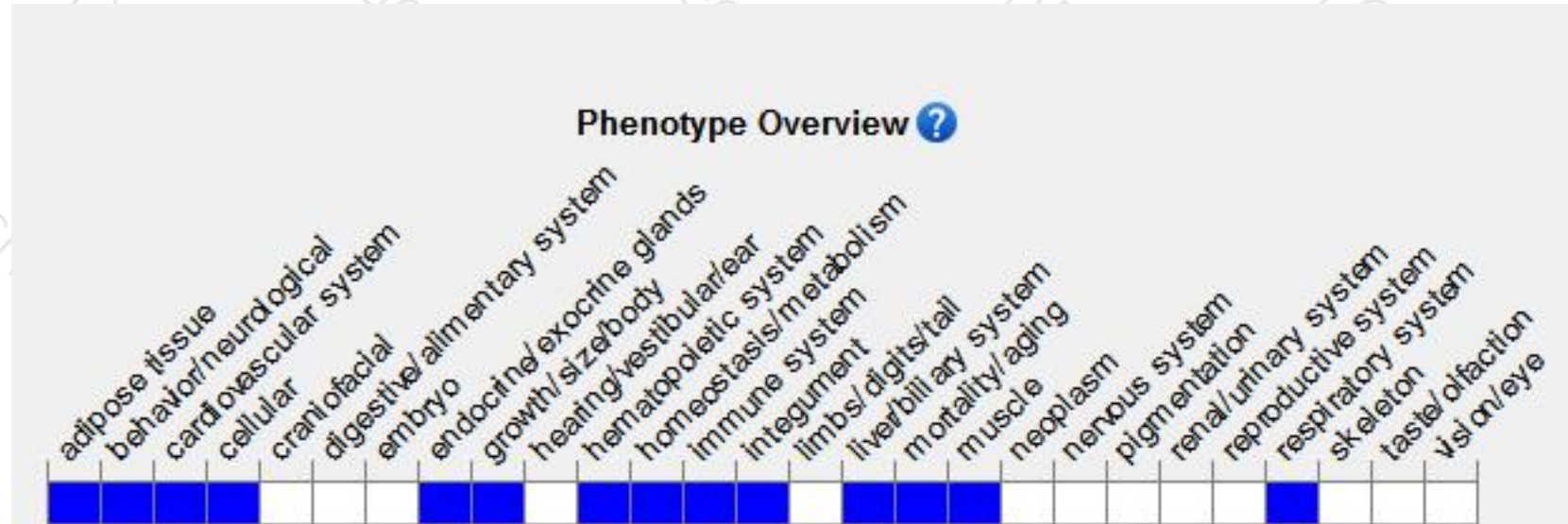
Genomic location distribution



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 gene trap allele exhibit postnatal lethality, growth retardation, cardiomyocyte and skeletal myocyte degeneration, and pulmonary edema. Mice homozygous for a null allele also exhibit postnatal lethality and growth retardation but lack the myocyte degeneration phenotype.

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

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