Bag2 Cas9-KO Strategy

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Date:2020-02-24

Project Overview

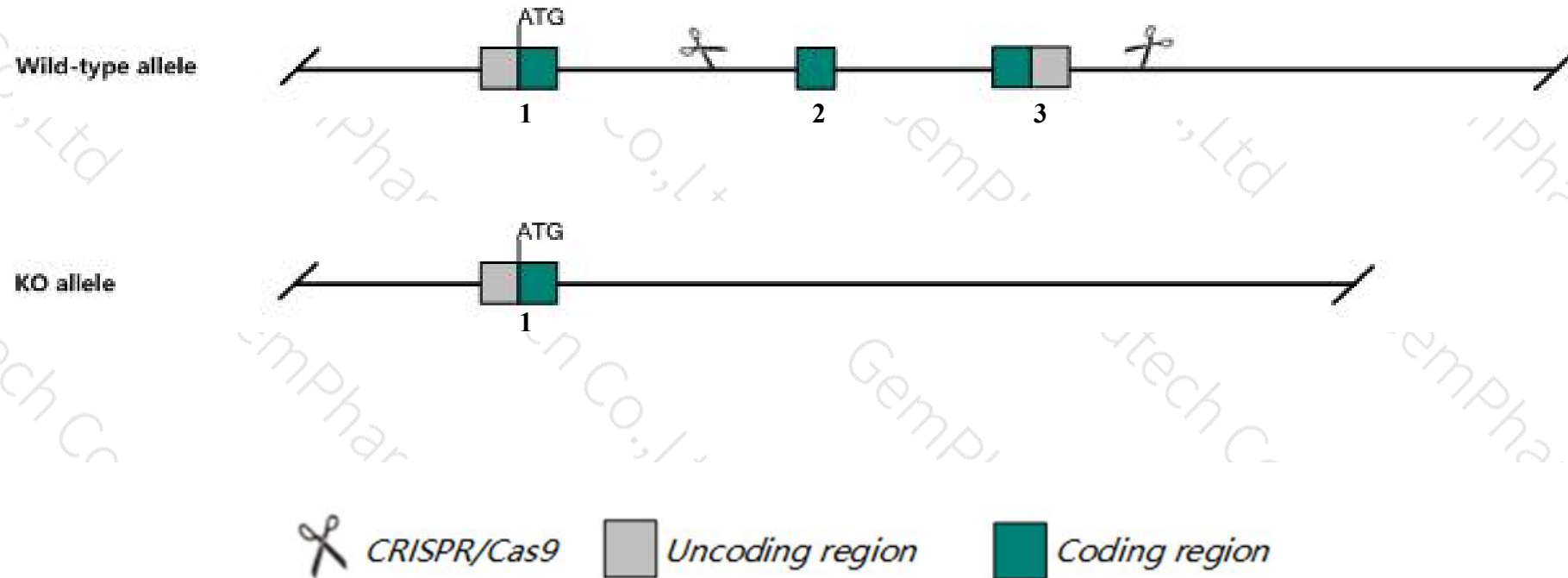|	
Project Name	*Bag2*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Bag2* gene. The schematic diagram is as follows:

Technical routes

➢ The *Bag2* gene has 4 transcripts. According to the structure of *Bag2* gene, exon2-exon3 of *Bag2-201*

  (ENSMUST00000044691.8) 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 *Bag2* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ *Gm37905* gene will be deleted.

➢ Transcript *Bag2*-204 may not be affected.

➢ The *Bag2* gene is located on the Chr1. 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）

Bag2 BCL2-associated athanogene 2 [*Mus musculus* (house mouse)]

Gene ID: 213539, updated on 12-Nov-2019

▲ Summary

Official Symbol	Bag2 provided by MGI
Official Full Name	BCL2-associated athanogene 2 provided by MGI
Primary source	MGI:MGI:1891254
See related	Ensembl:ENSMUSG00000042215
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	BC016230; 2610042A13Rik
Expression	Ubiquitous expression in bladder adult (RPKM 26.9), placenta adult (RPKM 26.6) and 28 other tissues See more
Orthologs	human all

▲ Genomic context

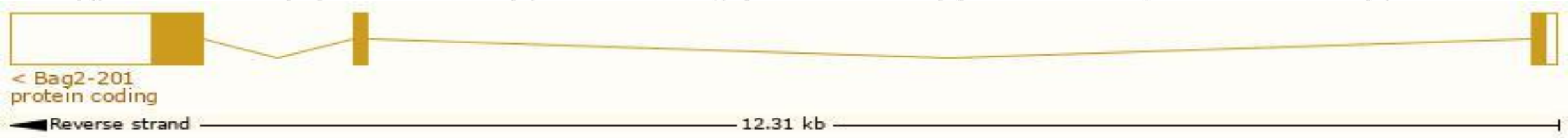**Location:** 1; 1 B

See Bag2 in Genome Data Viewer

Exon count: 4

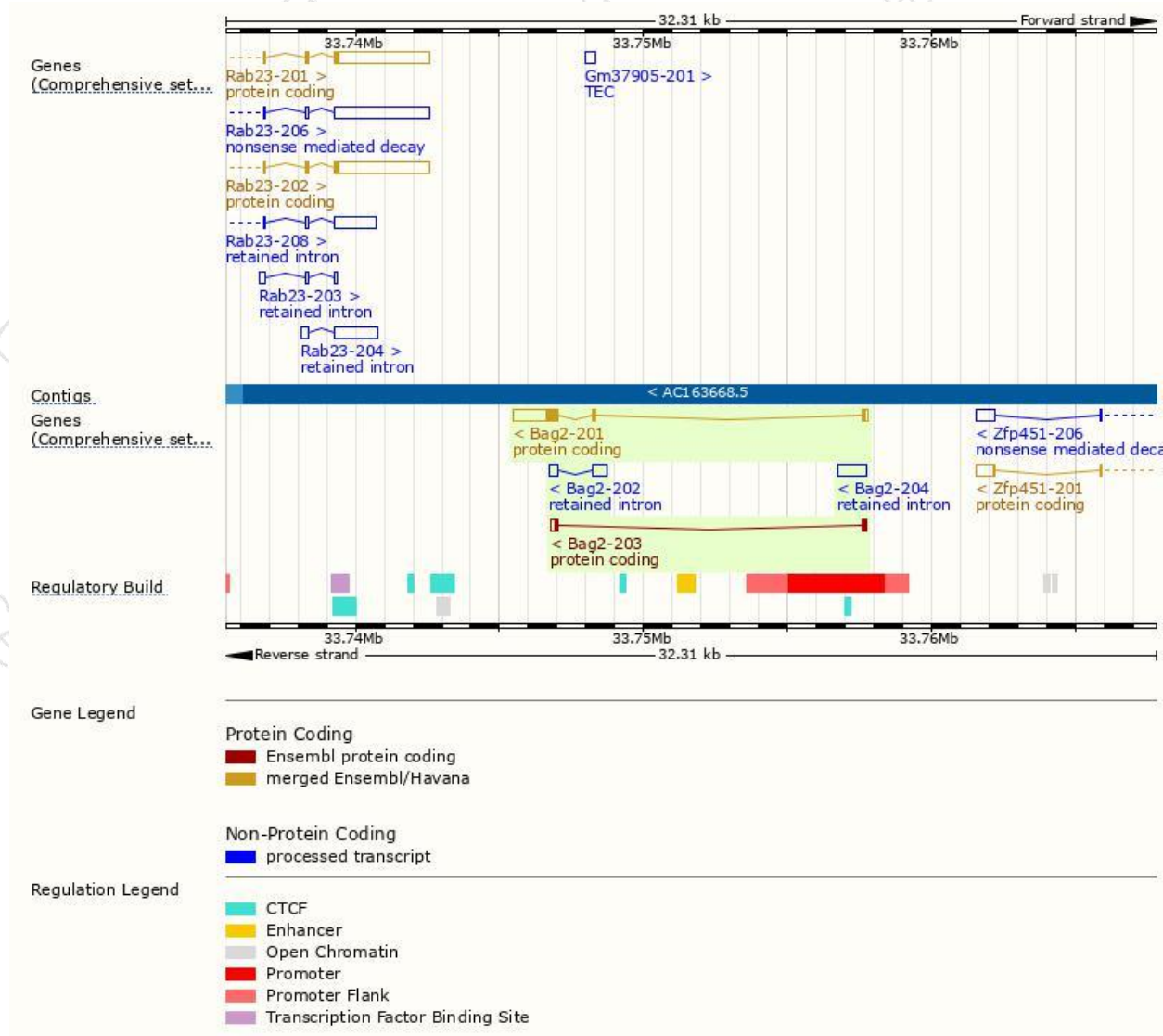| Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	1	NC_000067.6 (33745484..33757750, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	1	NC_000067.5 (33802329..33814595, complement)

Transcript information（Ensembl）

The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Bag2-201	ENSMUST00000044691.8	1860	210aa	Protein coding	CCDS14864	Q91YN9	TSL:1 GENCODE basic APPRIS P1
Bag2-203	ENSMUST00000187602.1	378	57aa	Protein coding	-	A0A087WNX9	TSL:2 GENCODE basic
Bag2-204	ENSMUST00000189741.1	955	No protein	Retained intron	-	-	TSL:NA
Bag2-202	ENSMUST00000155484.1	781	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Bag2-201* transcript,The transcription is shown below

< Bag2-201
protein coding

◄ Reverse strand

12.31 kb

Genomic location distribution

Protein domain

ENSMUSP00000042...
SIFTS import
Coiled-coils (Ncoils)
SMART
BAG domain
PROSITE profiles
BAG domain
PANTHER
BAG family molecular chaperone regulator 2
Gene3D
1.20.58.890

All sequence SNPs/i...   Sequence variants (dbSNP and all other sources)

Variant Legend

- missense variant
- splice region variant
- synonymous variant

Scale bar   0   20   40   60   80   100   120   140   160   180   210
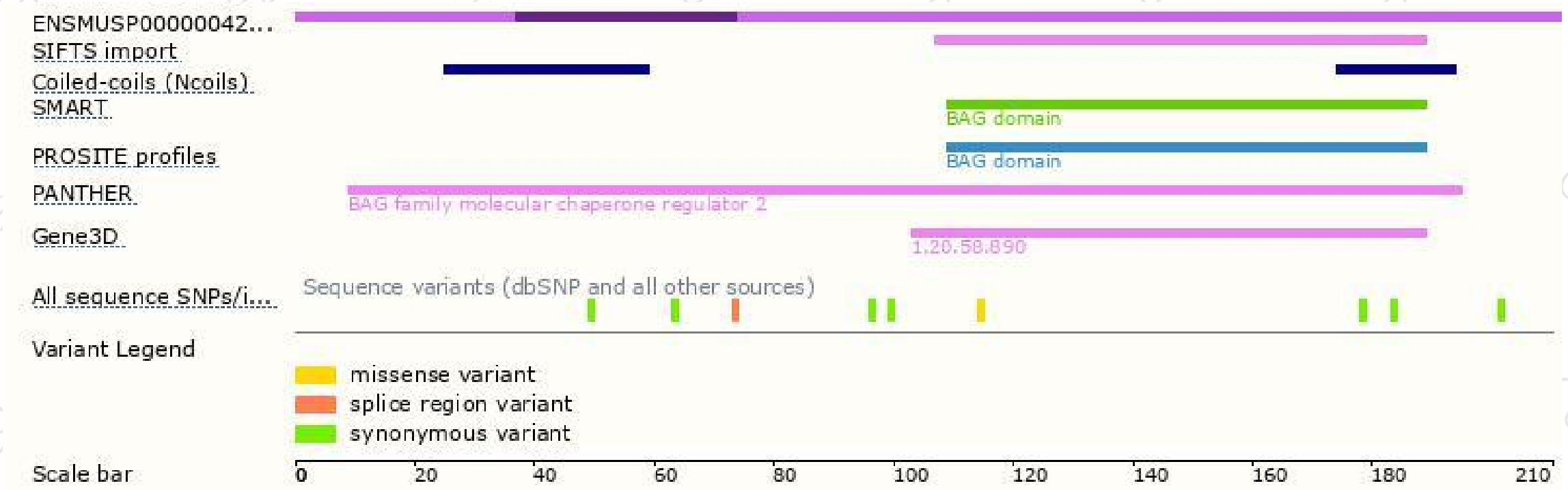
If you have any questions, you are welcome to inquire.
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