

***Bag6* Cas9-KO Strategy**

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Project Overview

Project Name

Bag6

Project type

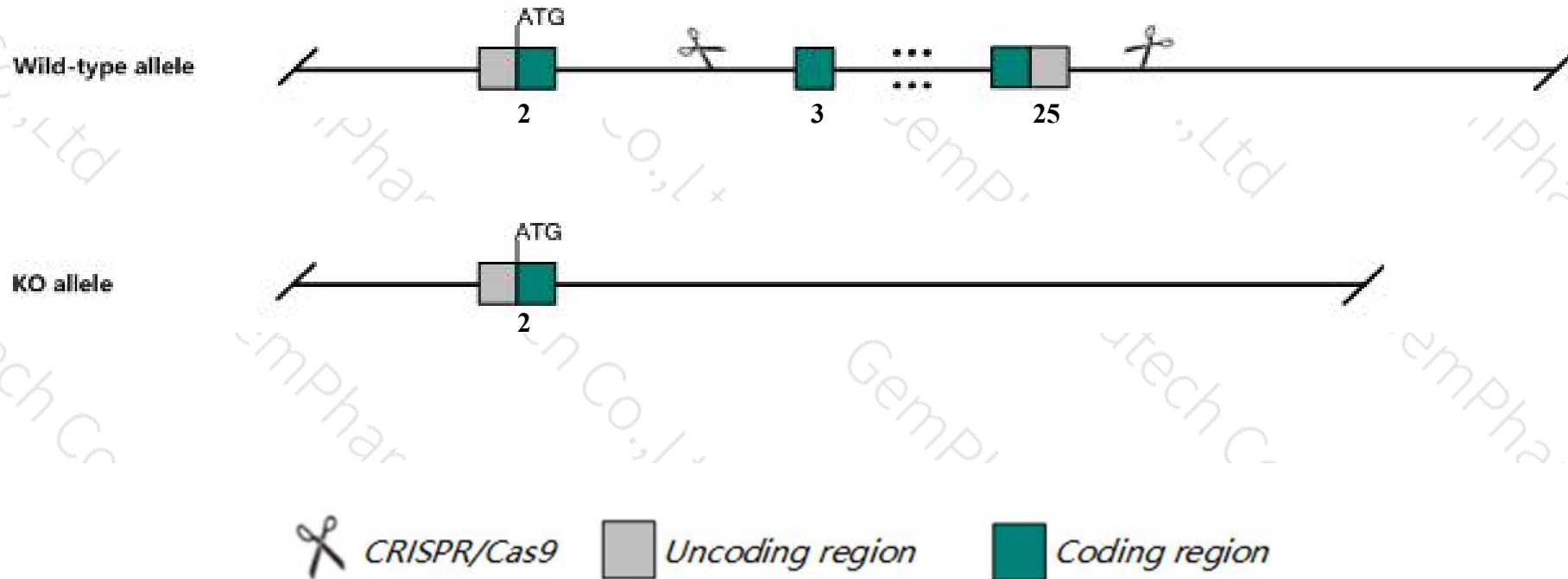
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Bag6* gene. The schematic diagram is as follows:



- The *Bag6* gene has 16 transcripts. According to the structure of *Bag6* gene, exon3-exon25 of *Bag6-201* (ENSMUST00000025250.13) 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 *Bag6* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Targeted disruption of this gene results in either embryonic lethality following abnormal brain development or neonatal death associated with severe developmental defects in the lung and kidney. These developmental defects are associated with widespread aberrant apoptosis and proliferation.
- The knockout region is about 1.4 kb away from the C-terminus of the *Prrc2a* gene, which may affect the regulation of the C-terminus of the gene.
- The *Bag6* gene is located on the Chr17. 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)

Bag6 BCL2-associated athanogene 6 [*Mus musculus* (house mouse)]

Gene ID: 224727, updated on 30-Aug-2019

Summary

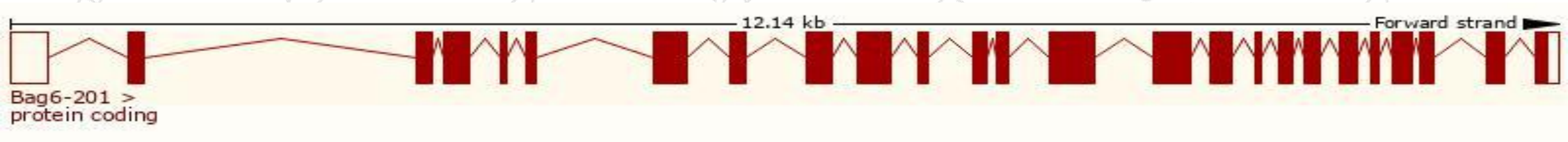
Official Symbol	Bag6 provided by MGI
Official Full Name	BCL2-associated athanogene 6 provided by MGI
Primary source	MGI:MGI:1919439
See related	Ensembl:ENSMUSG00000024392
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	G3; Bat3; BAG-6; Scythe; AA408914; D17H6S52E; 2410045D21Rik
Expression	Ubiquitous expression in testis adult (RPKM 225.5), adrenal adult (RPKM 122.8) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

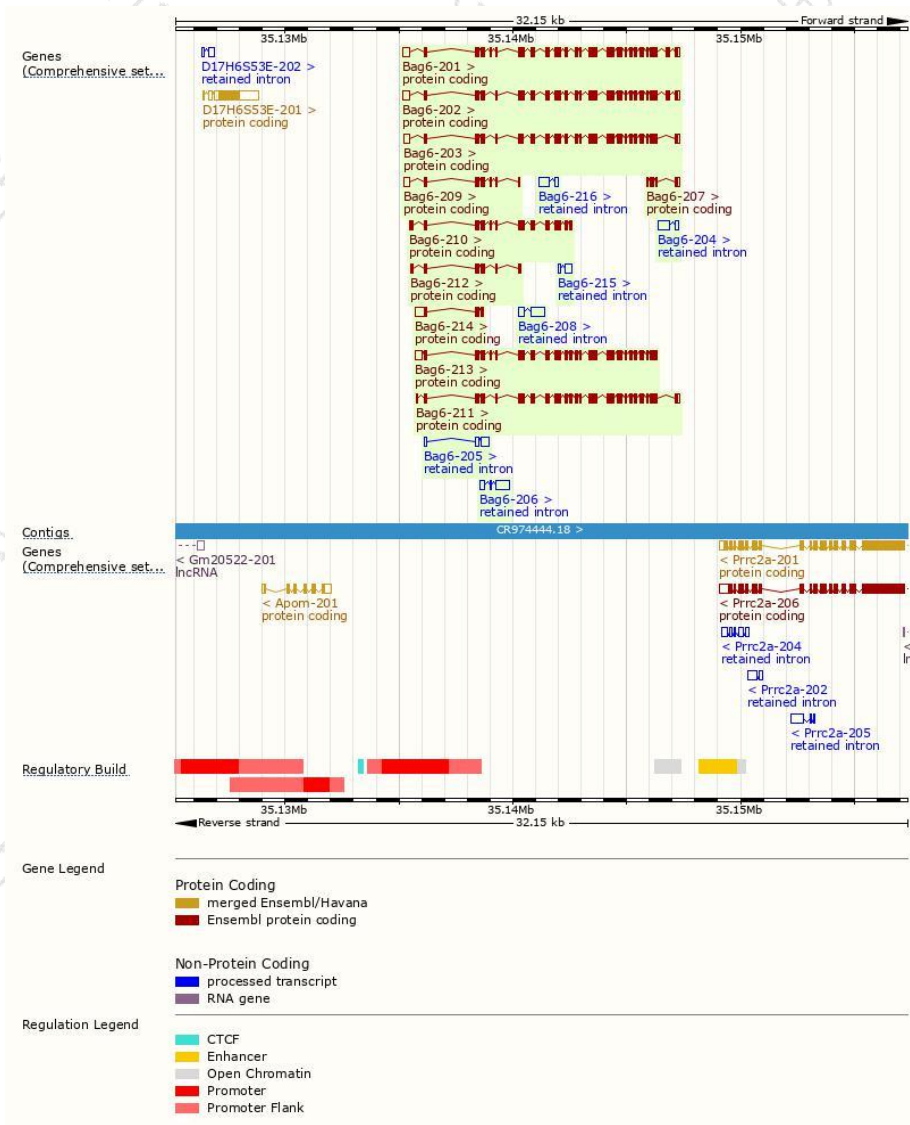
The gene has 16 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Bag6-201	ENSMUST00000025250.13	3858	1154aa	Protein coding	CCDS28688	Q9Z1R2	TSL:5 GENCODE basic APPRIS P3
Bag6-202	ENSMUST00000166426.8	3787	1136aa	Protein coding	CCDS57073	Q3UF95	TSL:1 GENCODE basic APPRIS ALT2
Bag6-211	ENSMUST00000173550.7	3536	1122aa	Protein coding	CCDS57072	G3UZF6	TSL:1 GENCODE basic
Bag6-213	ENSMUST00000174281.8	3611	1107aa	Protein coding	-	A0A1B0GX81	CDS 3' incomplete TSL:1
Bag6-203	ENSMUST00000172571.7	3599	1082aa	Protein coding	-	G3UYQ2	TSL:5 GENCODE basic
Bag6-210	ENSMUST00000173535.7	1722	563aa	Protein coding	-	G3UXT8	CDS 3' incomplete TSL:1
Bag6-209	ENSMUST00000173491.7	886	209aa	Protein coding	-	G3UYZ0	CDS 3' incomplete TSL:5
Bag6-212	ENSMUST00000173952.7	770	253aa	Protein coding	-	G3V013	CDS 3' incomplete TSL:2
Bag6-214	ENSMUST00000174478.7	756	115aa	Protein coding	-	S4R183	CDS 3' incomplete TSL:2
Bag6-207	ENSMUST00000172993.1	444	120aa	Protein coding	-	S4R224	CDS 5' incomplete TSL:2
Bag6-206	ENSMUST00000172925.1	880	No protein	Retained intron	-	-	TSL:3
Bag6-208	ENSMUST00000173351.1	831	No protein	Retained intron	-	-	TSL:3
Bag6-204	ENSMUST00000172882.1	683	No protein	Retained intron	-	-	TSL:2
Bag6-216	ENSMUST00000174797.1	622	No protein	Retained intron	-	-	TSL:1
Bag6-205	ENSMUST00000172889.1	611	No protein	Retained intron	-	-	TSL:2
Bag6-215	ENSMUST00000174613.1	402	No protein	Retained intron	-	-	TSL:2

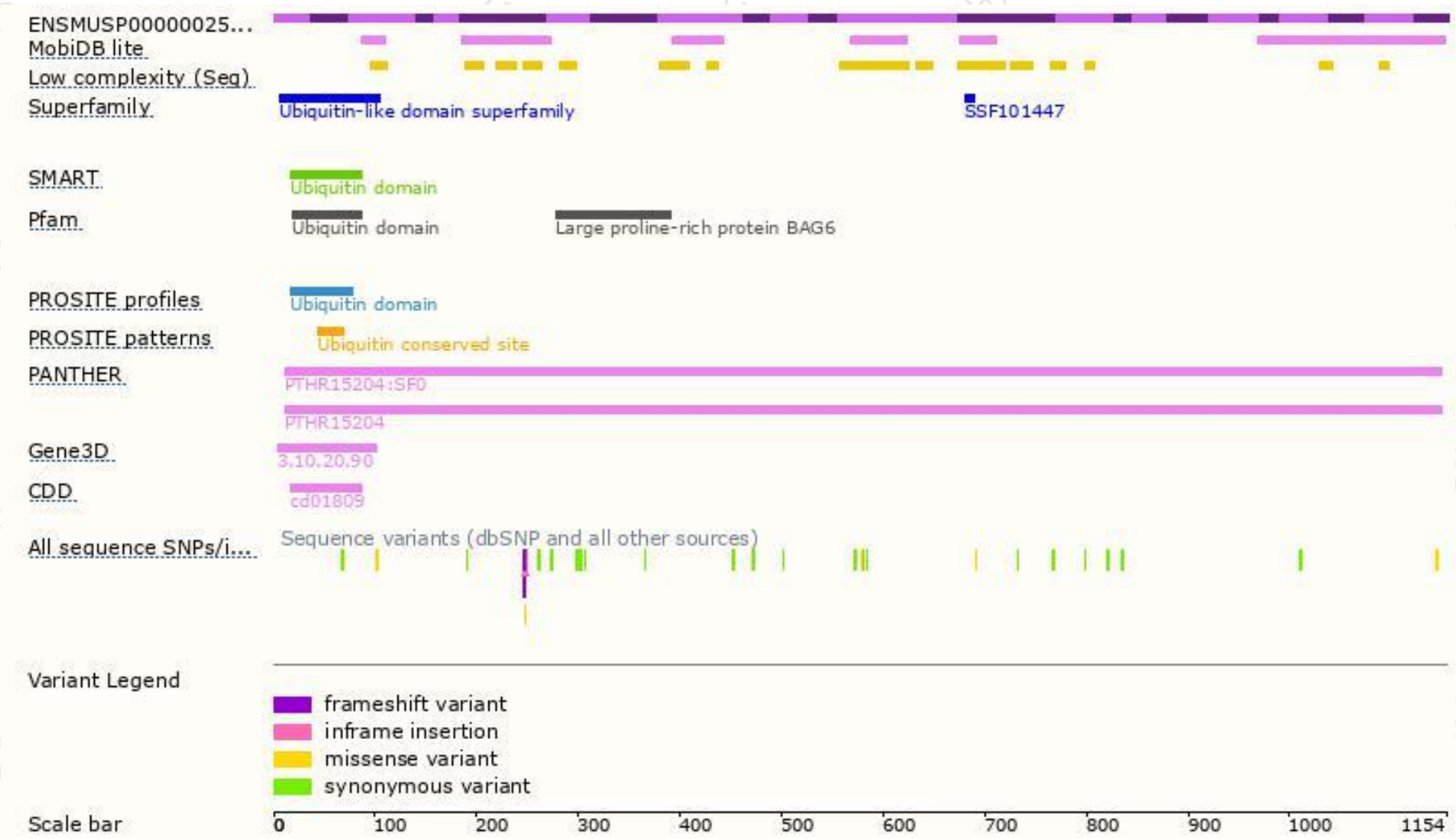
The strategy is based on the design of *Bag6-201* transcript,The transcription is shown below



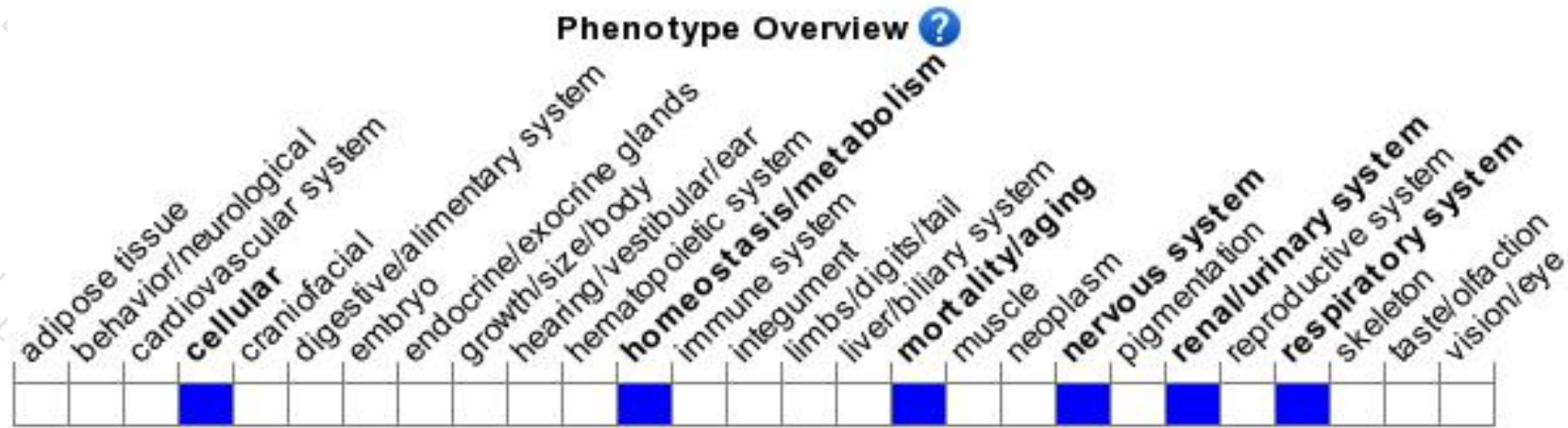
Genomic location distribution



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/>).

According to the existing MGI data, Targeted disruption of this gene results in either embryonic lethality following abnormal brain development or neonatal death associated with severe developmental defects in the lung and kidney. These developmental defects are associated with widespread aberrant apoptosis and proliferation.

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

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