Brap Cas9-KO Strategy

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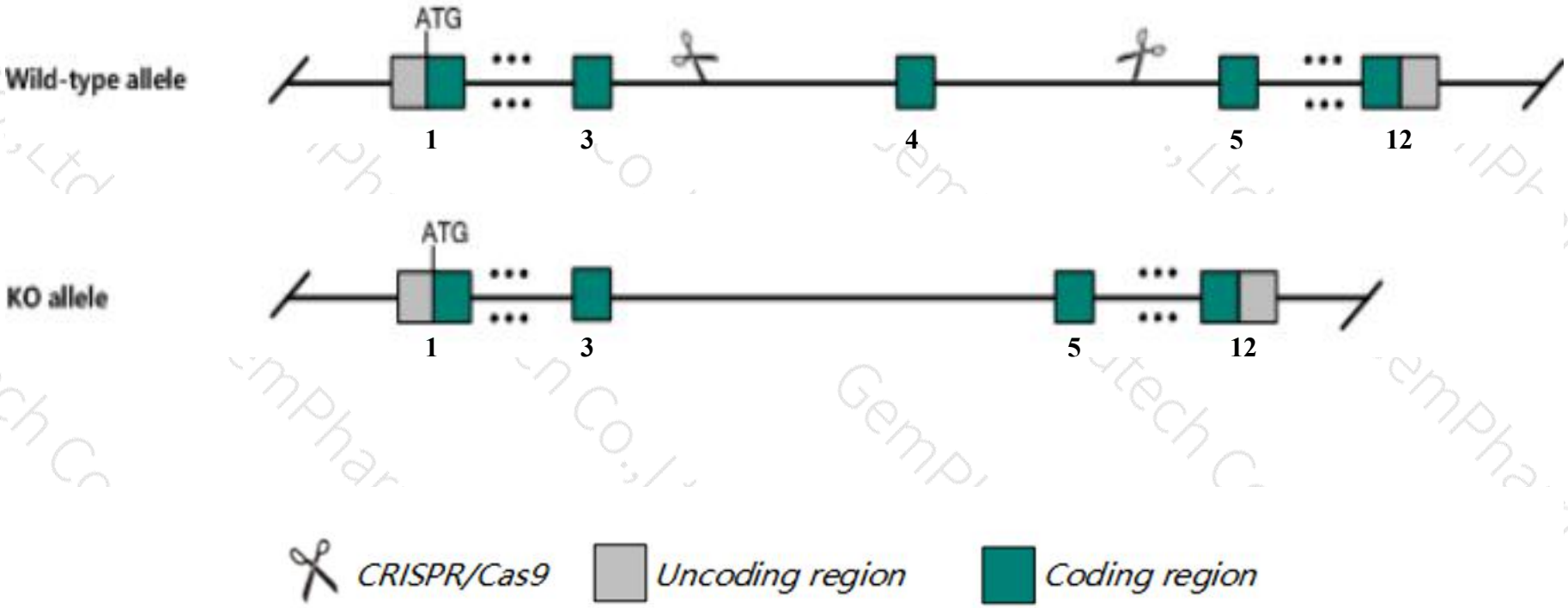
Project Overview

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

Knockout strategy

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



Technical routes

➢ The *Brap* gene has 9 transcripts. According to the structure of *Brap* gene, exon4 of *Brap-201*(ENSMUST00000031414.14) transcript is recommended as the knockout region.The region contains 190bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Brap* gene. The brief process is as follows: CRISPR/Cas9 system 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.

Notice

➢ According to the existing MGI data,mice homozygous for a knock-out allele exhibit embryonic lethality during organogenesis and subtle defects in cell cycle-dependent nuclear movement in neural progenitors.

➢ The *Brap* gene is located on the Chr5. 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）

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Brap BRCA1 associated protein [*Mus musculus* (house mouse)]

Gene ID: 72399, updated on 26-Jun-2020

Summary

Official Symbol	Brap provided by MGI
Official Full Name	BRCA1 associated protein provided by MGI
Primary source	MGI:MGI:1919649
See related	Ensembl:ENSMUSG00000029458
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	IMP; BRAP2; 3010002G07Rik
Expression	Ubiquitous expression in testis adult (RPKM 46.8), liver adult (RPKM 15.7) and 28 other tissues See more
Orthologs	human all

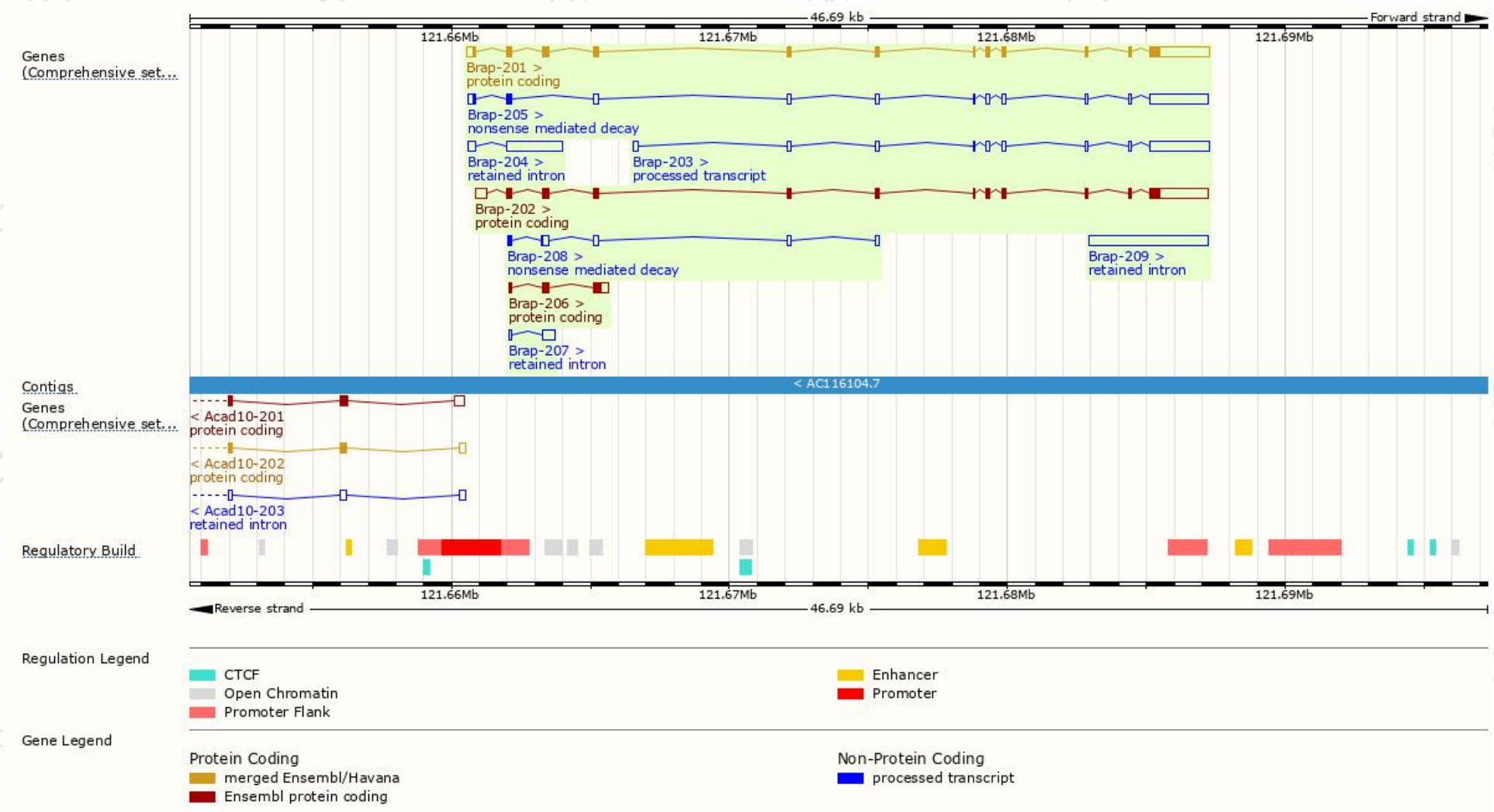
Transcript information（Ensembl）

The gene has 9 transcripts,all transcripts are shown below:

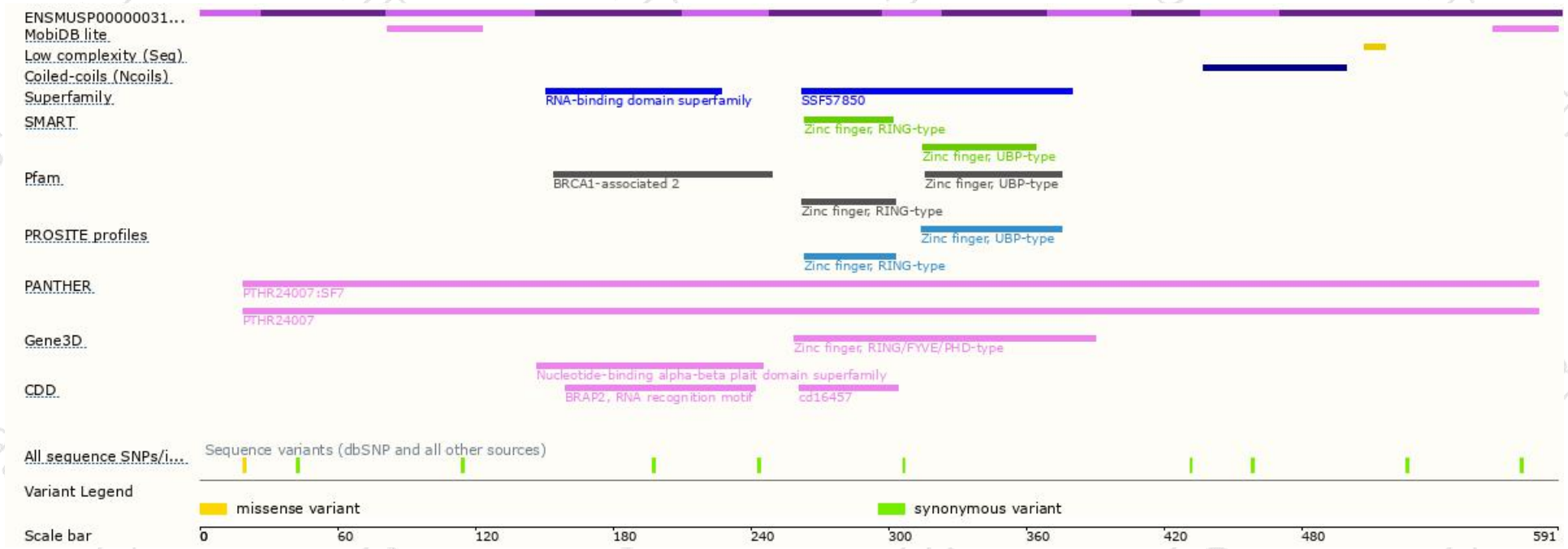
Name	Transcript ID	bp	Protein ▲	Biotype	CCDS	UniProt	Flags
Brap-208	ENSMUST00000195952.4	827	57aa	Nonsense mediated decay	-	A0A0G2JFY1	CDS 5' incomplete TSL:3
Brap-205	ENSMUST00000140996.5	3524	83aa	Nonsense mediated decay	-	D6RG84	TSL:1
Brap-206	ENSMUST00000142701.2	851	199aa	Protein coding	-	A0A0G2JF68	CDS 5' incomplete TSL:1
Brap-202	ENSMUST00000111765.7	3861	561aa	Protein coding	CCDS80389	Q99MP8	TSL:1 GENCODE basic
Brap-201	ENSMUST00000031414.14	3744	591aa	Protein coding	CCDS19640	Q99MP8	TSL:1 GENCODE basic APPRIS P1
Brap-203	ENSMUST00000127703.2	3094	No protein	Processed transcript	-	-	TSL:1
Brap-209	ENSMUST00000196897.1	4318	No protein	Retained intron	-	-	TSL:NA
Brap-204	ENSMUST00000132491.1	2222	No protein	Retained intron	-	-	TSL:2
Brap-207	ENSMUST00000148052.1	492	No protein	Retained intron	-	-	TSL:3

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

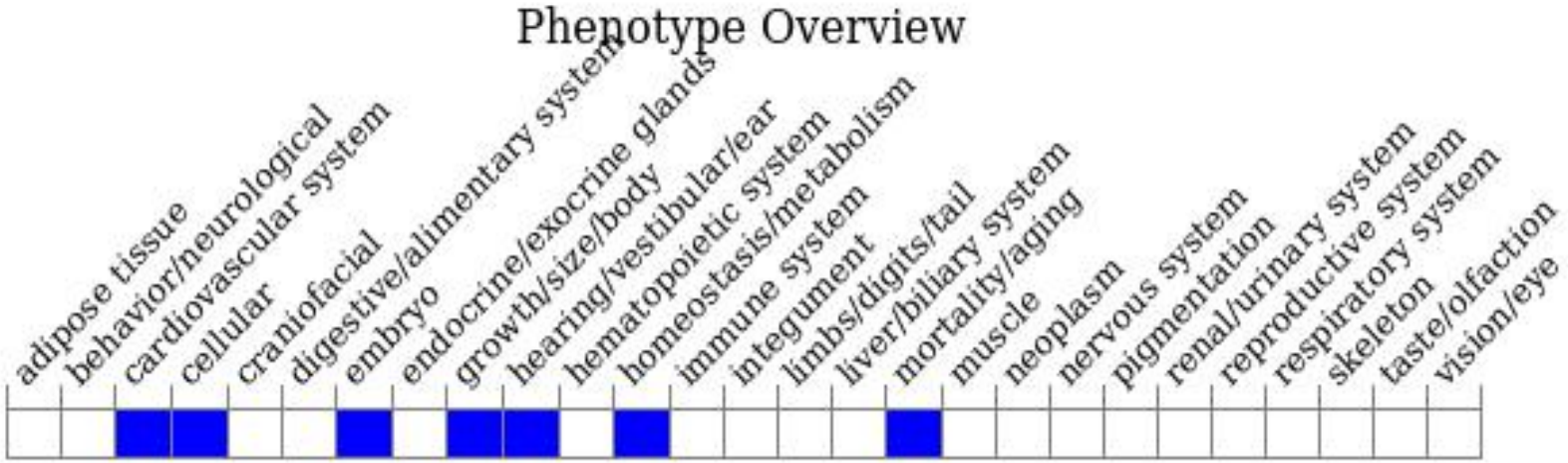
Genomic location distribution



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/).

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

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