

***Bbs1* Cas9-CKO Strategy**

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Project Overview

Project Name

Bbs1

Project type

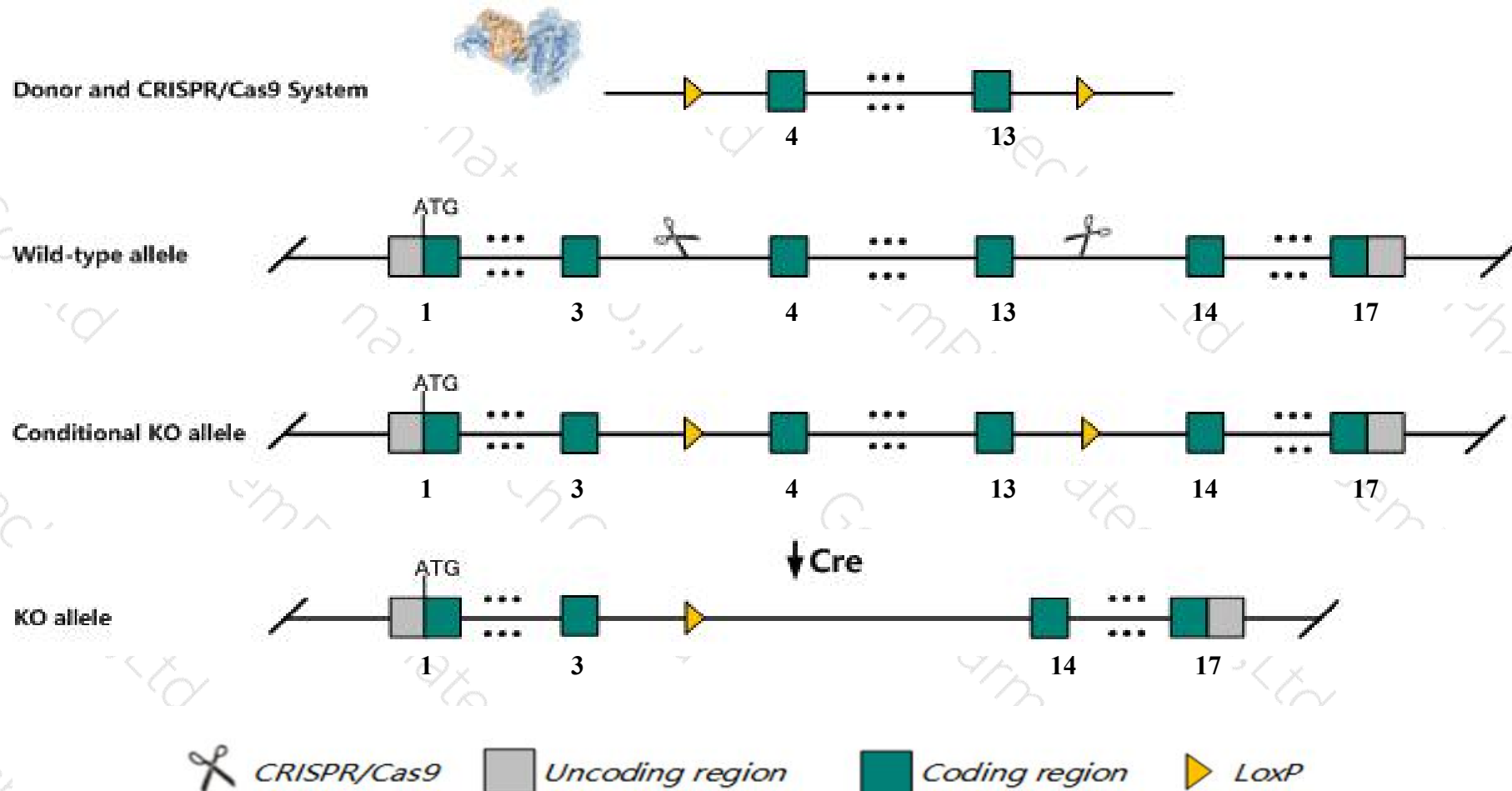
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Bbs1* gene. The schematic diagram is as follows:



Technical routes

- The *Bbs1* gene has 8 transcripts. According to the structure of *Bbs1* gene, exon4-exon13 of *Bbs1-201*(ENSMUST00000053506.7) transcript is recommended as the knockout region. The region contains 1180bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Bbs1* 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, homozygous null mice display partial embryonic lethality, low body weight before weaning, obesity after weaning, retinal degeneration, and abnormal olfactory epithelium and neurons.
- The KO region is close to *Gm25334* gene. Knockout the region may affect the function of *Gm25334* gene.
- The *Bbs1* gene is located on the Chr19. 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)

Bbs1 Bardet-Biedl syndrome 1 (human) [*Mus musculus* (house mouse)]

Gene ID: 52028, updated on 25-Sep-2020

Summary

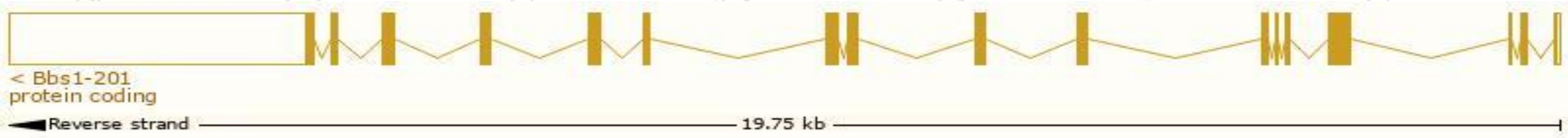
Official Symbol	Bbs1 provided by MGI
Official Full Name	Bardet-Biedl syndrome 1 (human) provided by MGI
Primary source	MGI:MGI:1277215
See related	Ensembl:ENSMUSG000000006464
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI451249; D19Ert609; D19Ert609e
Expression	Broad expression in frontal lobe adult (RPKM 5.9), cortex adult (RPKM 5.0) and 25 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

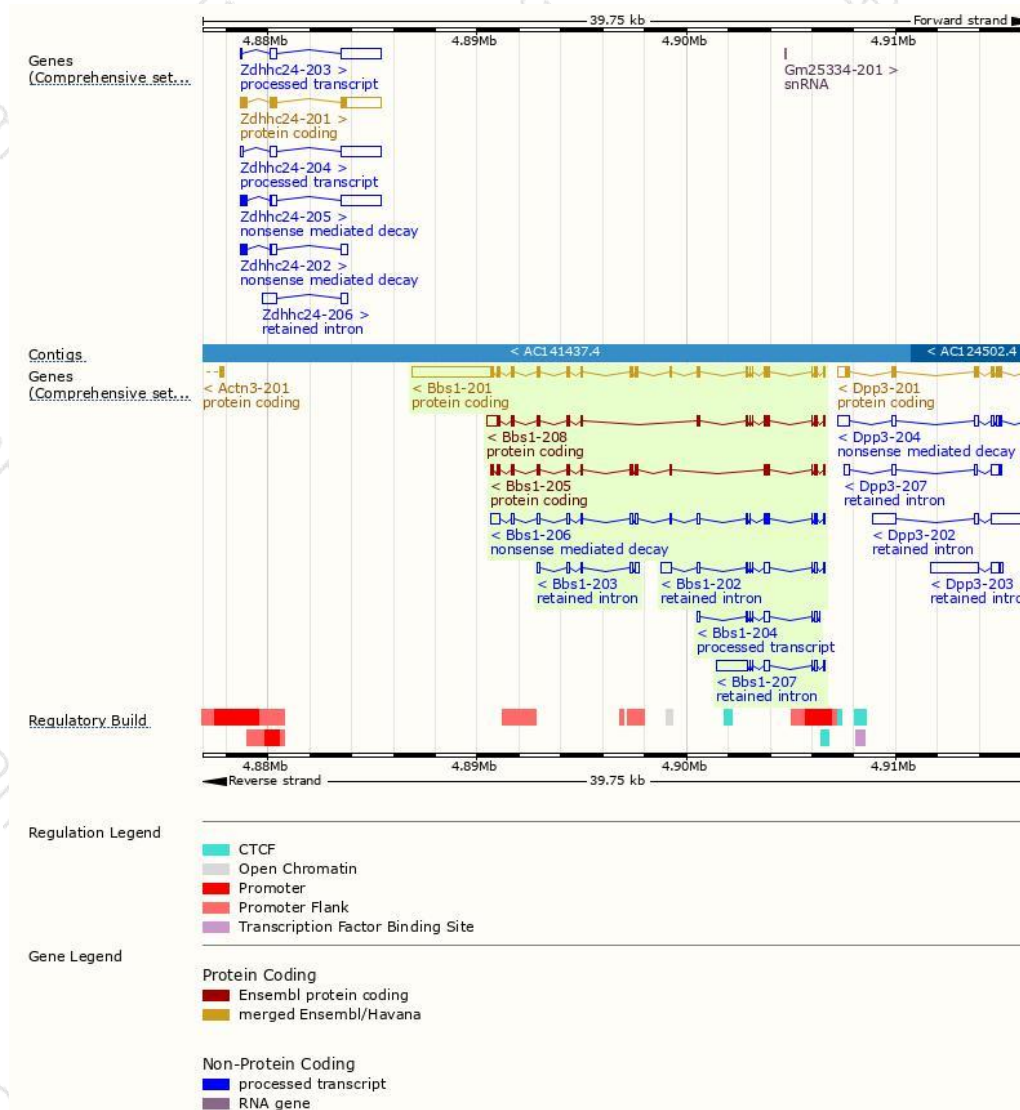
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Bbs1-201	ENSMUST00000053506.7	5602	593aa	Protein coding	CCDS29442	Q3V3N7	TSL:1 GENCODE basic APPRIS P1
Bbs1-208	ENSMUST00000238170.1	1841	452aa	Protein coding	-	A0A494B9Z5	GENCODE basic
Bbs1-205	ENSMUST00000237085.1	1549	496aa	Protein coding	-	A0A494B8X5	GENCODE basic
Bbs1-206	ENSMUST00000237362.1	1993	164aa	Nonsense mediated decay	-	A0A494B9R9	
Bbs1-204	ENSMUST00000236538.1	643	No protein	Processed transcript	-	-	
Bbs1-207	ENSMUST00000237638.1	2019	No protein	Retained intron	-	-	
Bbs1-202	ENSMUST00000235498.1	1244	No protein	Retained intron	-	-	
Bbs1-203	ENSMUST00000236150.1	667	No protein	Retained intron	-	-	

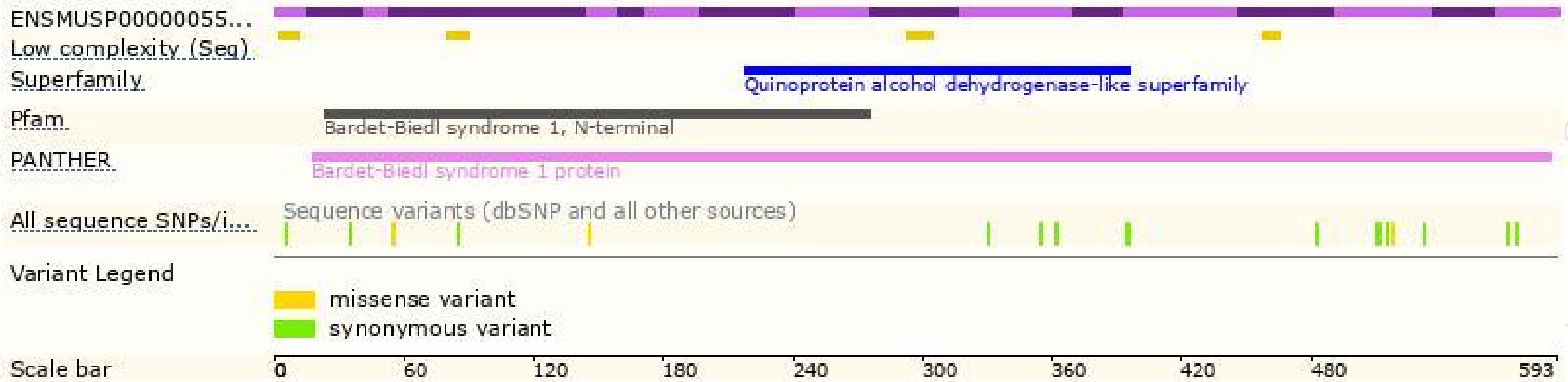
The strategy is based on the design of *Bbs1-201* transcript,the transcription is shown below:



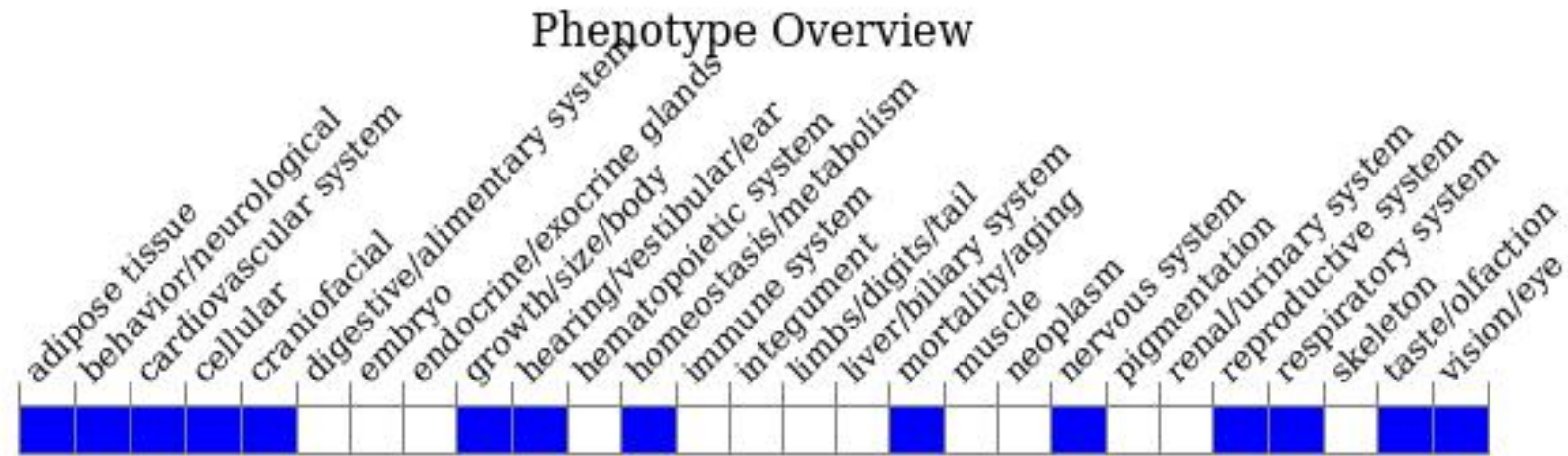
Genomic location distribution



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, homozygous null mice display partial embryonic lethality, low body weight before weaning, obesity after weaning, retinal degeneration, and abnormal olfactory epithelium and neurons.

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

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