

***Bbs7* Cas9-KO Strategy**

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Design Date: 2020-7-22

Project Overview

Project Name

Bbs7

Project type

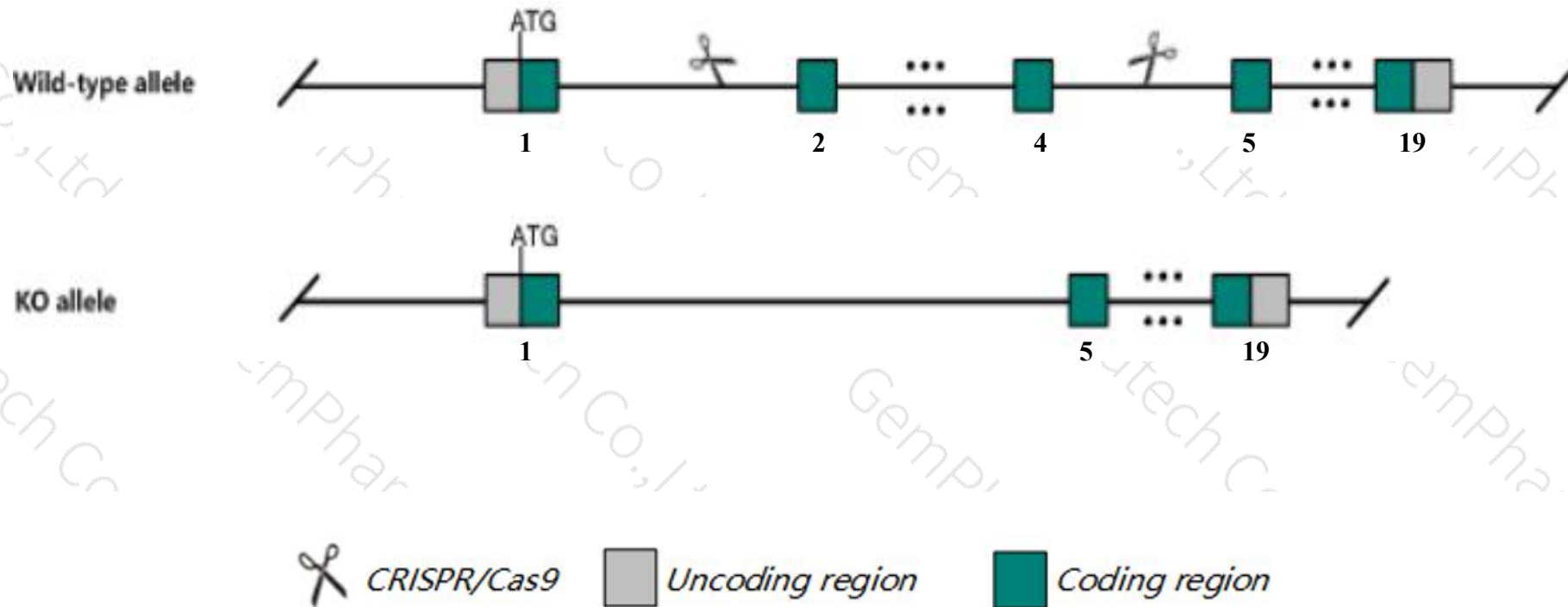
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Bbs7* gene. The schematic diagram is as follows:



- The *Bbs7* gene has 6 transcripts. According to the structure of *Bbs7* gene, exon2-exon4 of *Bbs7*-203(ENSMUST00000108156.8) transcript is recommended as the knockout region. The region contains 305bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Bbs7* 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.

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit partial preweaning lethality, retinal degeneration, obesity, ventriculomegaly, abnormal brain ependyma motile cilium morphology, and male infertility characterized by abnormal sperm flagellar axoneme structures.
- The *Bbs7* gene is located on the Chr3. 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)

Bbs7 Bardet-Biedl syndrome 7 (human) [*Mus musculus* (house mouse)]

Gene ID: 71492, updated on 26-Jun-2020

Summary

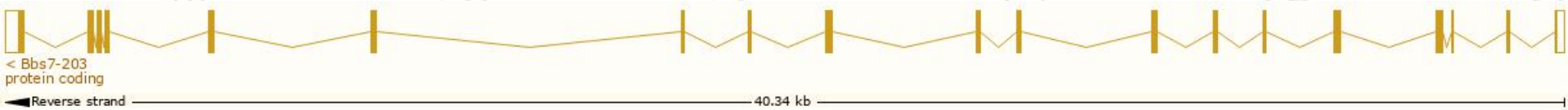
Official Symbol	Bbs7 provided by MGI
Official Full Name	Bardet-Biedl syndrome 7 (human) provided by MGI
Primary source	MGI:MGI:1918742
See related	Ensembl:ENSMUSG00000037325
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	8430406N16Rik
Expression	Broad expression in testis adult (RPKM 9.6), CNS E18 (RPKM 4.4) and 18 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

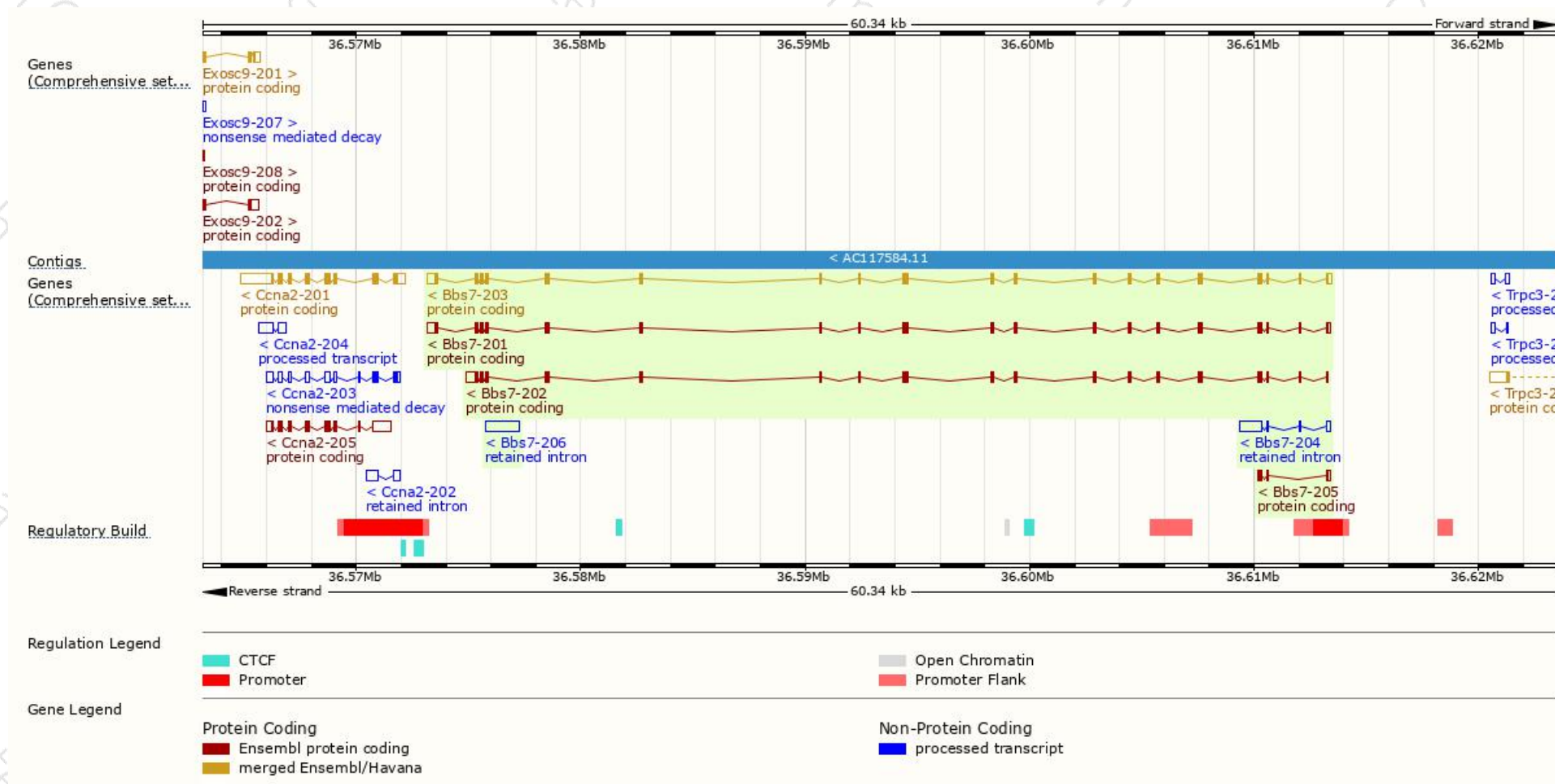
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Bbs7-205	ENSMUST00000142333.1	377	91aa	Protein coding	-	D3YXR1	CDS 3' incomplete TSL:2
Bbs7-202	ENSMUST00000108155.7	2437	673aa	Protein coding	-	E9Q0R0	TSL:5 GENCODE basic
Bbs7-203	ENSMUST00000108156.8	2687	715aa	Protein coding	CCDS17314	Q8K2G4	TSL:1 GENCODE basic APPRIS P2
Bbs7-201	ENSMUST00000040148.10	2599	715aa	Protein coding	-	Q8K2G4	TSL:1 GENCODE basic APPRIS ALT1
Bbs7-206	ENSMUST00000199136.1	1509	No protein	Retained intron	-	-	TSL:NA
Bbs7-204	ENSMUST00000129671.1	1288	No protein	Retained intron	-	-	TSL:1

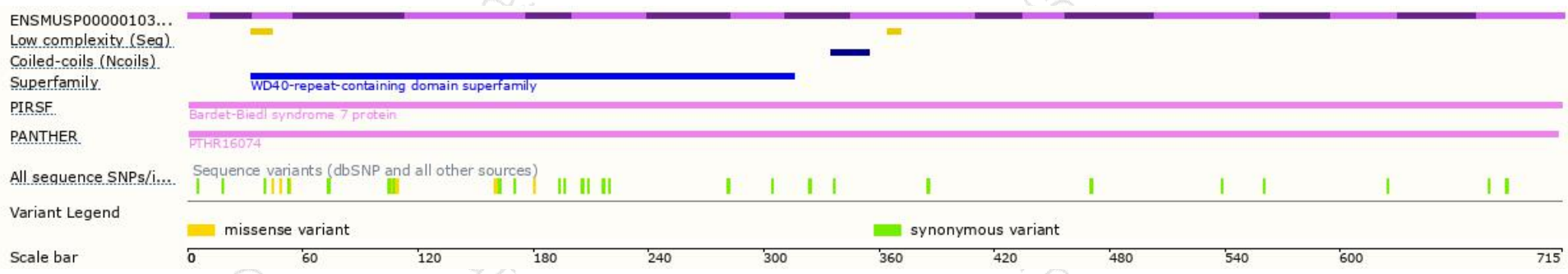
The strategy is based on the design of *Bbs7-203* transcript,the transcription is shown below:



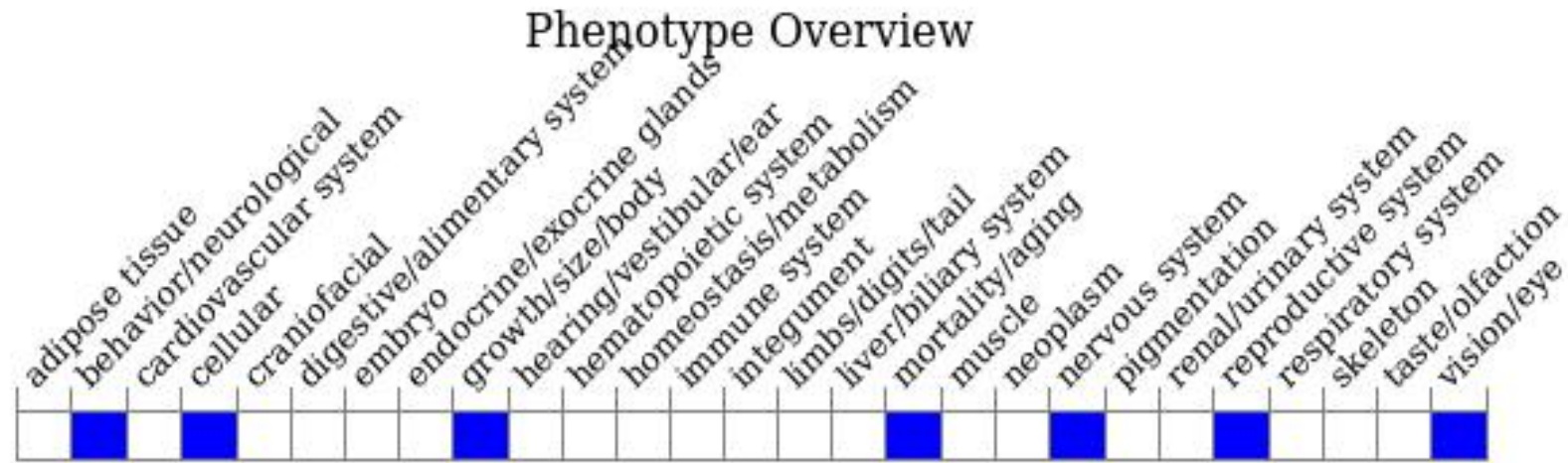
Genomic location distribution



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, mice homozygous for a knock-out allele exhibit partial preweaning lethality, retinal degeneration, obesity, ventriculomegaly, abnormal brain ependyma motile cilium morphology, and male infertility characterized by abnormal sperm flagellar axoneme structures.

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

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