Birc5 Cas9-CKO Strategy

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Project Overview

Project Name	***Birc5***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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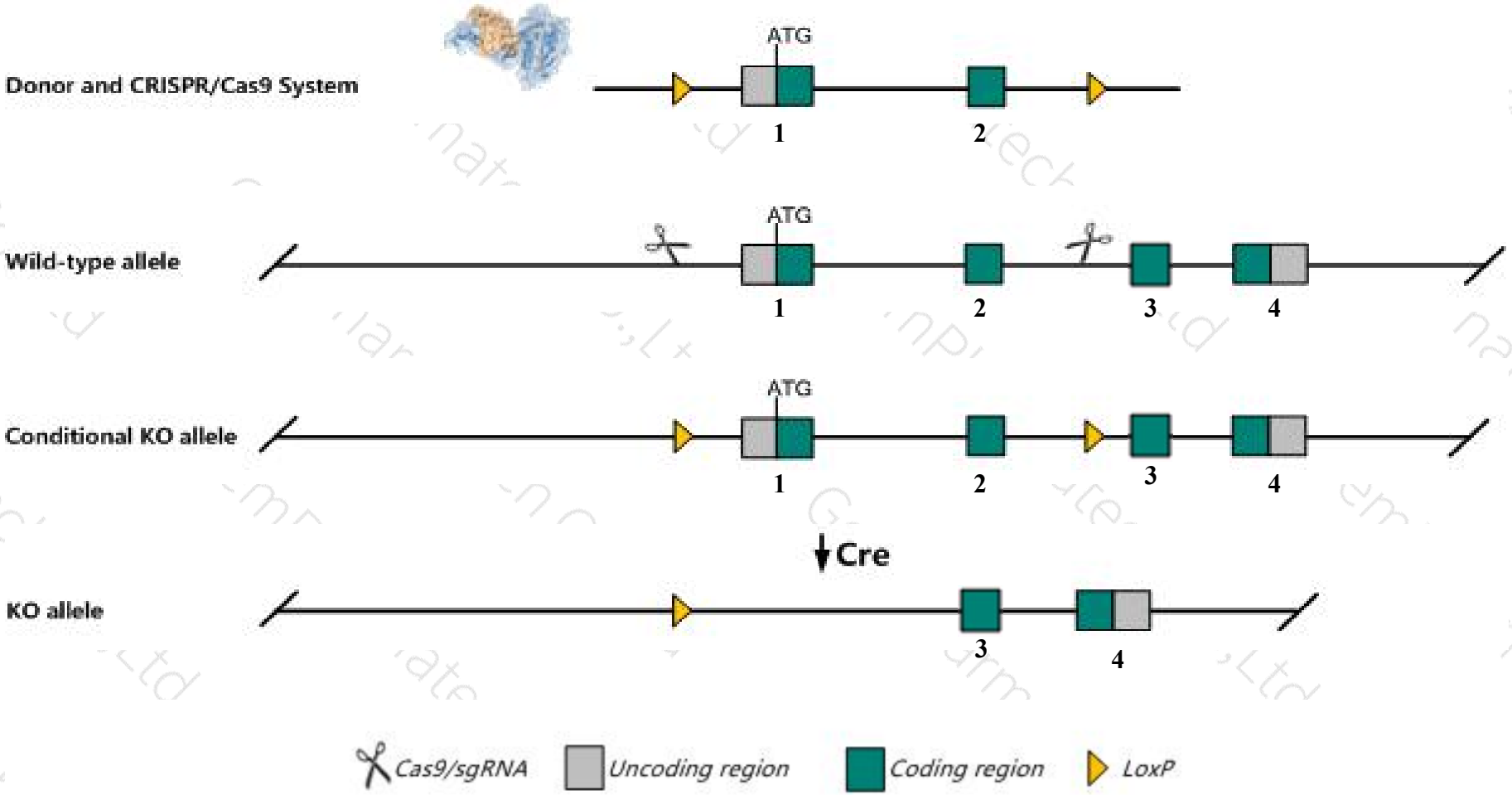
This model will use CRISPR/Cas9 technology to edit the *Birc5* gene. The schematic diagram is as follows:



Technical routes

- The *Birc5* gene has 2 transcripts. According to the structure of *Birc5* gene, exon1-exon2 of *Birc5-201* (ENSMUST00000081387.10) transcript is recommended as the knockout region.The region contains start codon ATG. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Birc5* 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.

Notice

➢ According to the existing MGI data,Homozygous null mutants die during early embryonic development.

➢ The *Birc5* gene is located on the Chr11. 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）

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Birc5 baculoviral IAP repeat-containing 5 [*Mus musculus* (house mouse)]

Gene ID: 11799, updated on 12-Aug-2019

Summary

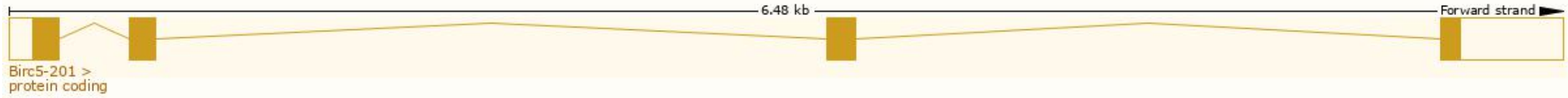
Official Symbol	Birc5 provided by MGI
Official Full Name	baculoviral IAP repeat-containing 5 provided by MGI
Primary source	MGI:MGI:1203517
See related	Ensembl:ENSMUSG00000017716
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Api4; TIAP; AAC-11; survivin40
Summary	This gene is a member of the inhibitor of apoptosis (IAP) gene family, which encode negative regulatory proteins that prevent apoptotic cell death. IAP family members usually contain multiple baculovirus IAP repeat (BIR) domains, but this gene encodes proteins with only a single BIR domain. The encoded proteins also lack a C-terminus RING finger domain. In humans, gene expression is high during fetal development and in most tumors yet low in adult tissues. Antisense transcripts have been identified in human that regulate this gene's expression. At least three transcript variants encoding distinct isoforms have been found for this gene, although at least one of these transcript variants is a nonsense-mediated decay (NMD) candidate. [provided by RefSeq, Jul 2008]
Expression	Biased expression in liver E14 (RPKM 37.4), liver E14.5 (RPKM 32.6) and 13 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

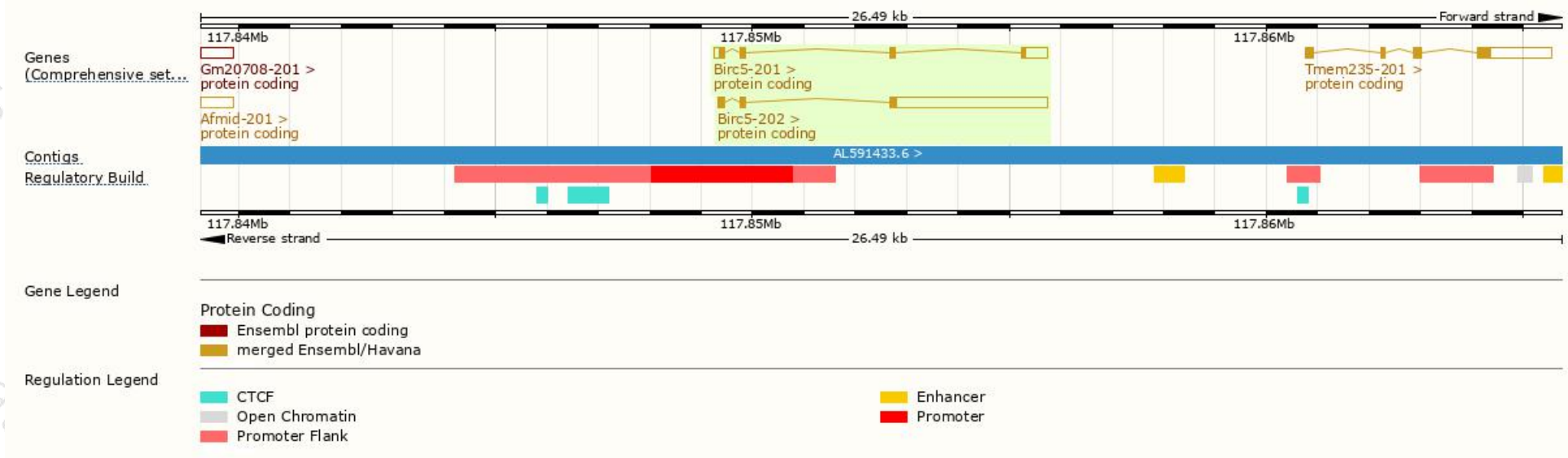
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Birc5-202	ENSMUST00000093906.4	3334	121aa	Protein coding	CCDS25695	O70201	TSL:1 GENCODE basic
Birc5-201	ENSMUST00000081387.10	947	140aa	Protein coding	CCDS25694	O70201 Q549P2	TSL:1 GENCODE basic APPRIS P1

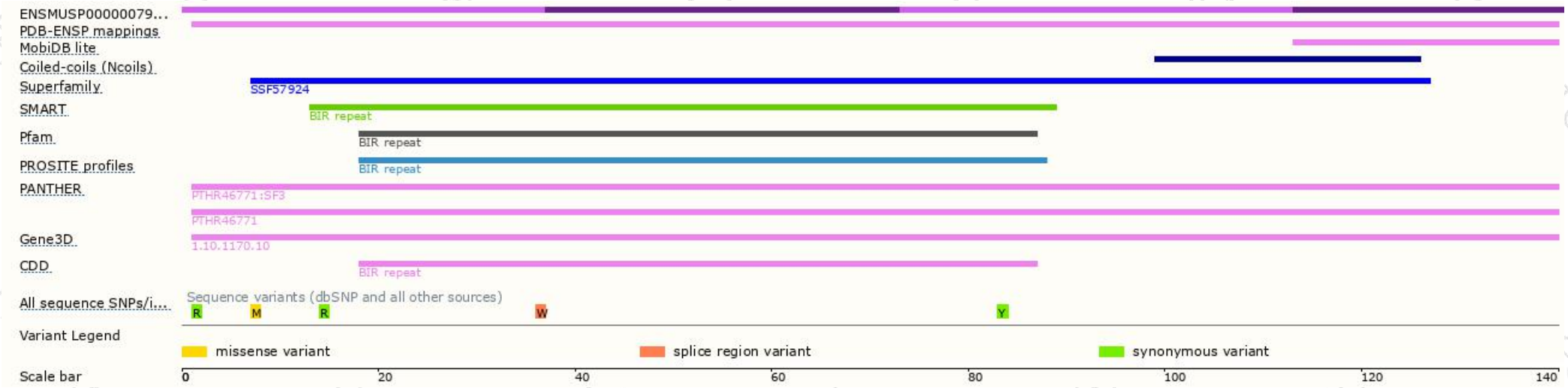
The strategy is based on the design of *Birc5-201* transcript,The transcription is shown below



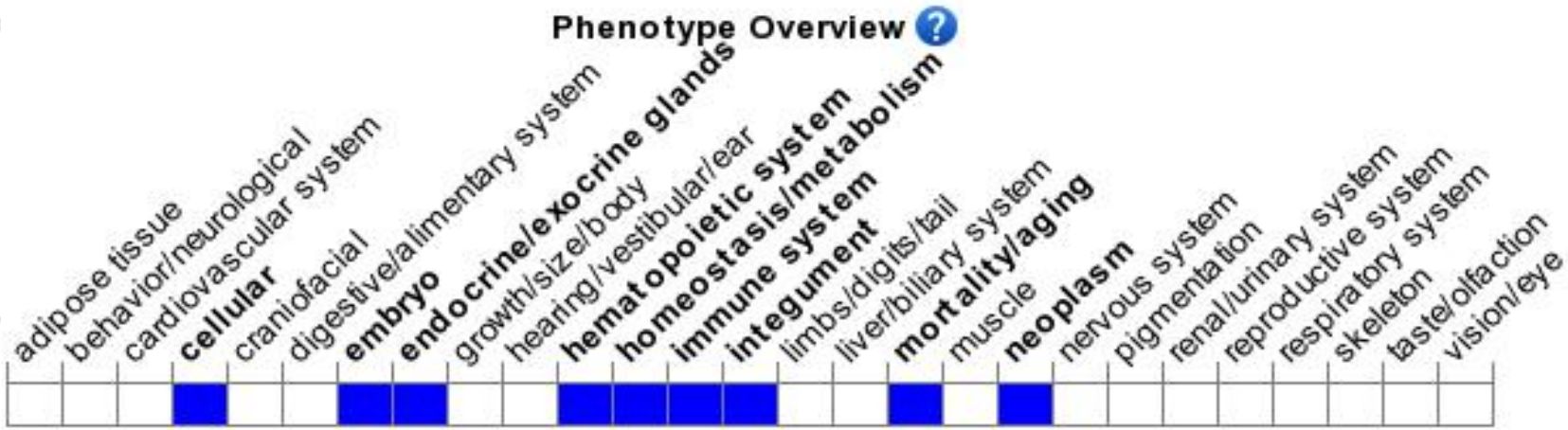
Genomic location distribution



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 mutants die during early embryonic development.

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

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