

Btrc Cas9-CKO Strategy

Designer:

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Design Date:

2018/6/4

Project Overview

Project Name

Btrc

Project type

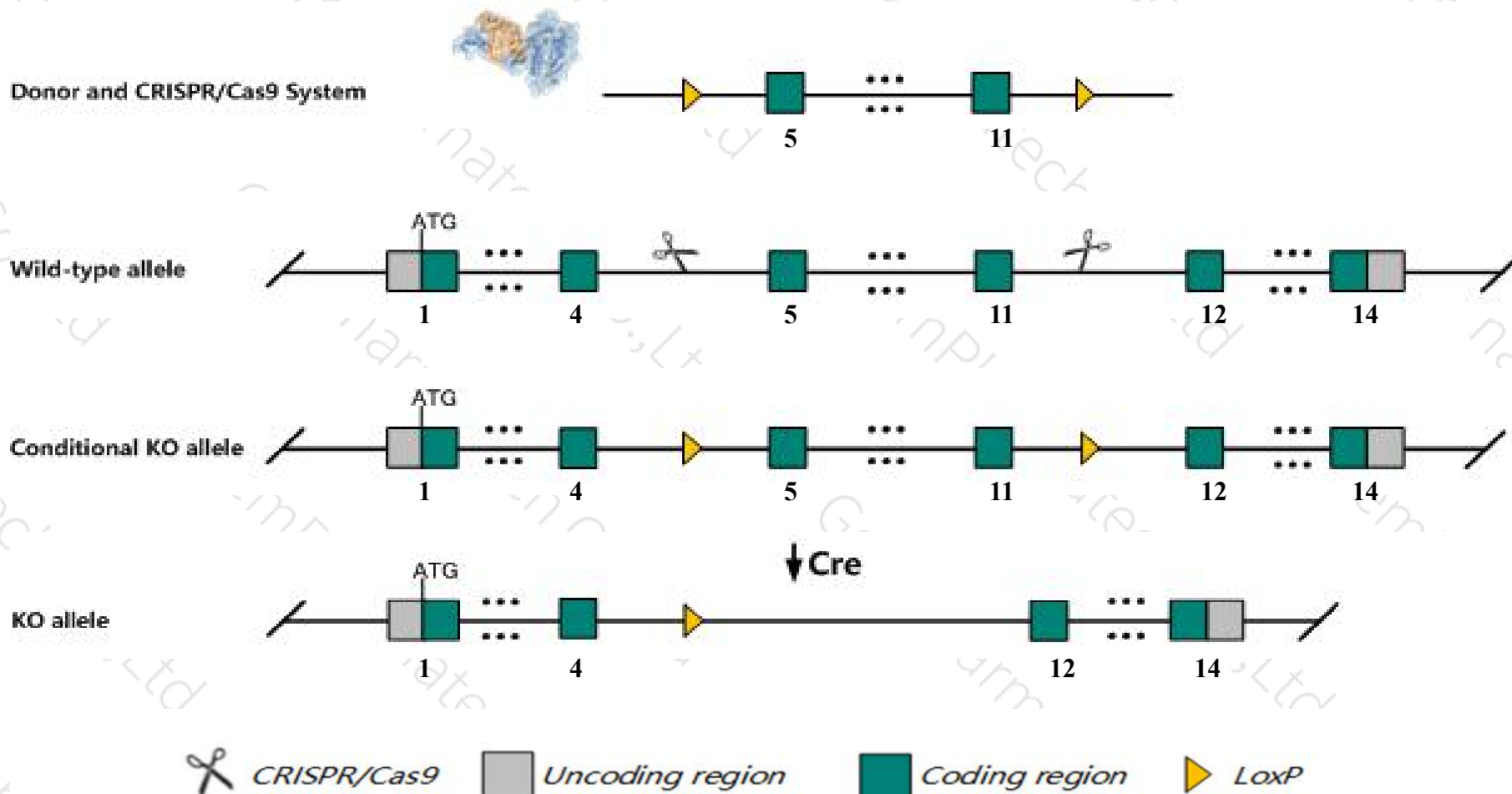
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



Technical routes

- The *Btrc* gene has 11 transcripts. According to the structure of *Btrc* gene, exon5-exon11 of *Btrc-201* (ENSMUST00000065601.12) transcript is recommended as the knockout region. The region contains 1142bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Btrc* 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, Embryonic fibroblasts from homozygotes show an increase in polyploidy and apoptosis and decreased cell proliferation. In a second allele, homozygous mutation results in reduced male fertility and abnormal male meiosis with oligozoospermia.
- The *Btrc* 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)

Btrc beta-transducin repeat containing protein [Mus musculus (house mouse)]

Gene ID: 12234, updated on 12-Feb-2019

Summary



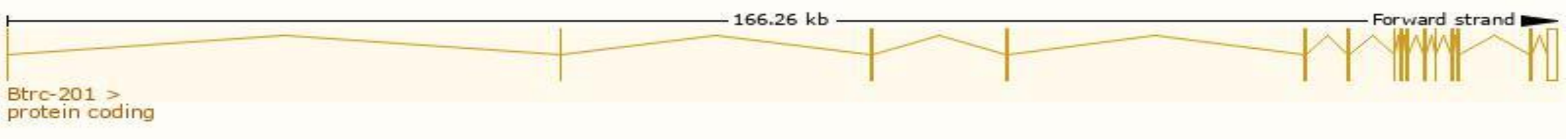
Official Symbol	Btrc provided by MGI
Official Full Name	beta-transducin repeat containing protein provided by MGI
Primary source	MGI:MGI:1338871
See related	Ensembl:ENSMUSG00000025217
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Beta-Trcp1, E3RS-1kappaB, E3RS1kappaB, FWD1, Fbw1a, HOS, SCF b-TRCP, Slimb, b-TrCP, beta-TrCP
Expression	Ubiquitous expression in frontal lobe adult (RPKM 10.9), CNS E18 (RPKM 10.0) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Btrc-201	ENSMUST00000065601.12	2978	605aa	Protein coding	CCDS29860	Q3ULA2	TSL:1 GENCODE basic APPRIS P3
Btrc-202	ENSMUST00000111936.3	2064	569aa	Protein coding	CCDS38002	Q3ULA2	TSL:1 GENCODE basic APPRIS ALT 1
Btrc-206	ENSMUST00000224102.1	3037	150aa	Protein coding	-	A0A286YE08	GENCODE basic
Btrc-209	ENSMUST00000224478.1	2194	506aa	Protein coding	-	A0A286YDT6	GENCODE basic
Btrc-204	ENSMUST00000223764.1	438	111aa	Protein coding	-	A0A286YCS1	CDS 3' incomplete
Btrc-203	ENSMUST00000223684.1	361	54aa	Protein coding	-	A0A286YCD6	CDS 3' incomplete
Btrc-207	ENSMUST00000224318.1	338	34aa	Protein coding	-	A0A286YDI3	CDS 3' incomplete
Btrc-205	ENSMUST00000224053.1	4720	No protein	Processed transcript	-	-	
Btrc-210	ENSMUST00000225662.1	4502	No protein	Retained intron	-	-	
Btrc-208	ENSMUST00000224439.1	3493	No protein	Retained intron	-	-	
Btrc-211	ENSMUST00000225898.1	515	No protein	Retained intron	-	-	

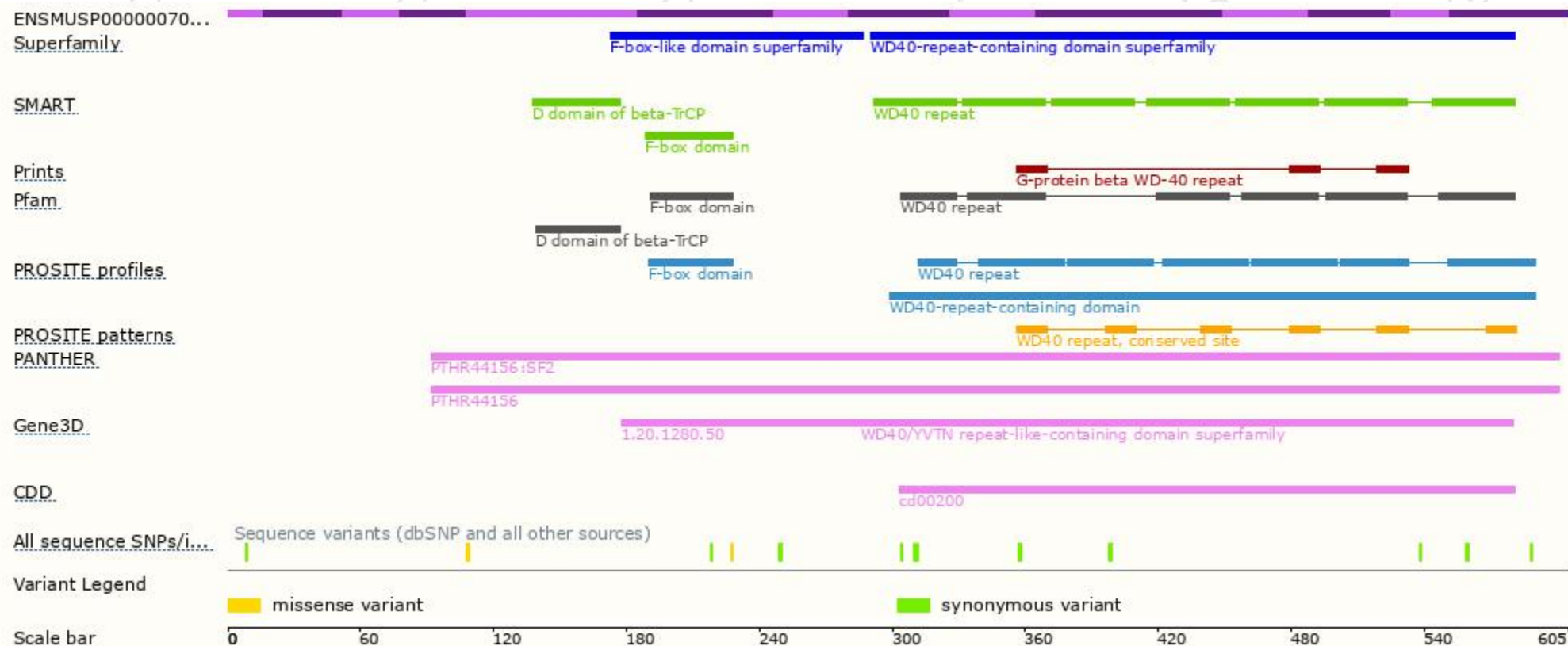
The strategy is based on the design of *Btrc-201* transcript,The transcription is shown below



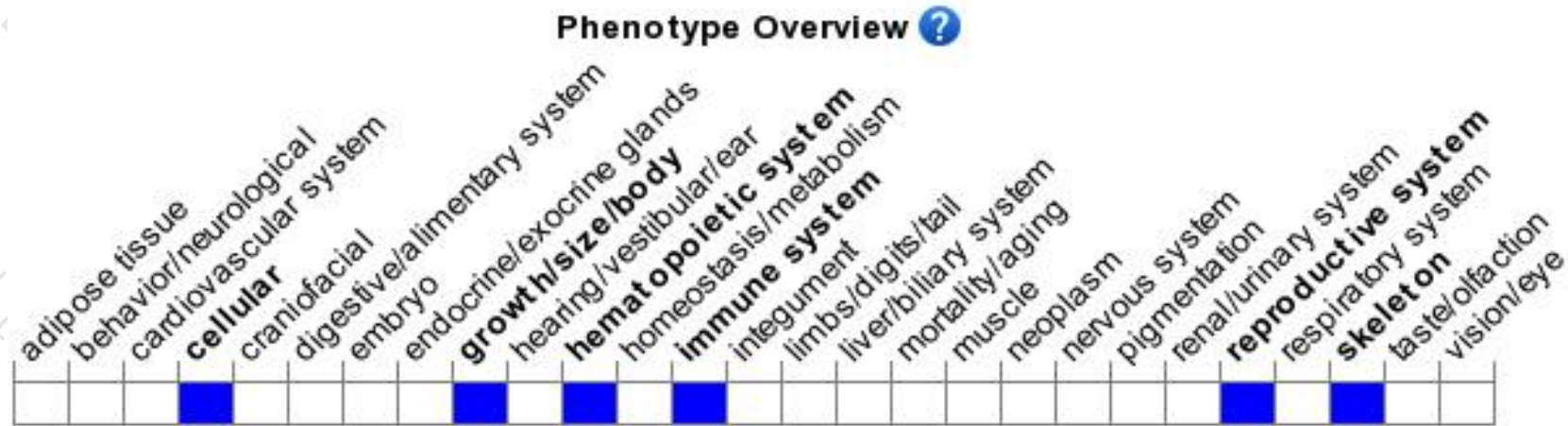
Genomic location distribution



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, Embryonic fibroblasts from homozygotes show an increase in polyploidy and apoptosis and decreased cell proliferation. In a second allele, homozygous mutation results in reduced male fertility and abnormal male meiosis with oligozoospermia.

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

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