

***Rcbtb2* Cas9-KO Strategy**

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Project Overview

Project Name

Rcbtb2

Project type

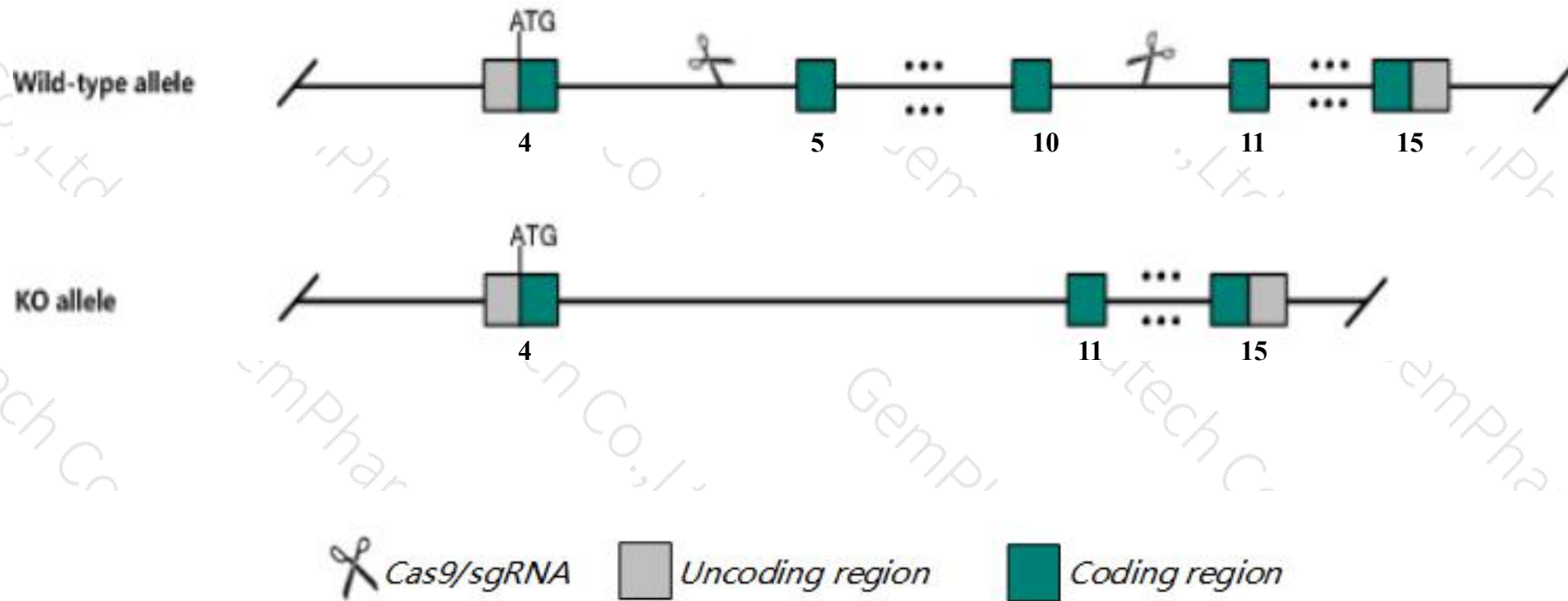
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rcbtb2* gene. The schematic diagram is as follows:



- The *Rcbtb2* gene has 26 transcripts. According to the structure of *Rcbtb2* gene, exon5-exon10 of *Rcbtb2*-209(ENSMUST00000164822.7) transcript is recommended as the knockout region. The region contains 884bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rcbtb2* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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 *Rcbtb2* gene is located on the Chr14. 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)

Rcbtb2 regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2 [Mus musculus (house mouse)]

Gene ID: 105670, updated on 13-Mar-2020

Summary



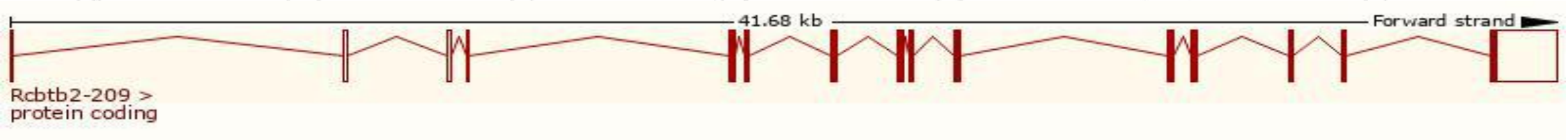
Official Symbol	Rcbtb2 provided by MGI
Official Full Name	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2 provided by MGI
Primary source	MGI:MGI:1917200
See related	Ensembl:ENSMUSG00000022106
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2610028E02Rik, 2810420M18Rik, AI448345, AW240694, Chc1l, RC/BTB2
Expression	Ubiquitous expression in thymus adult (RPKM 22.6), CNS E11.5 (RPKM 17.4) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

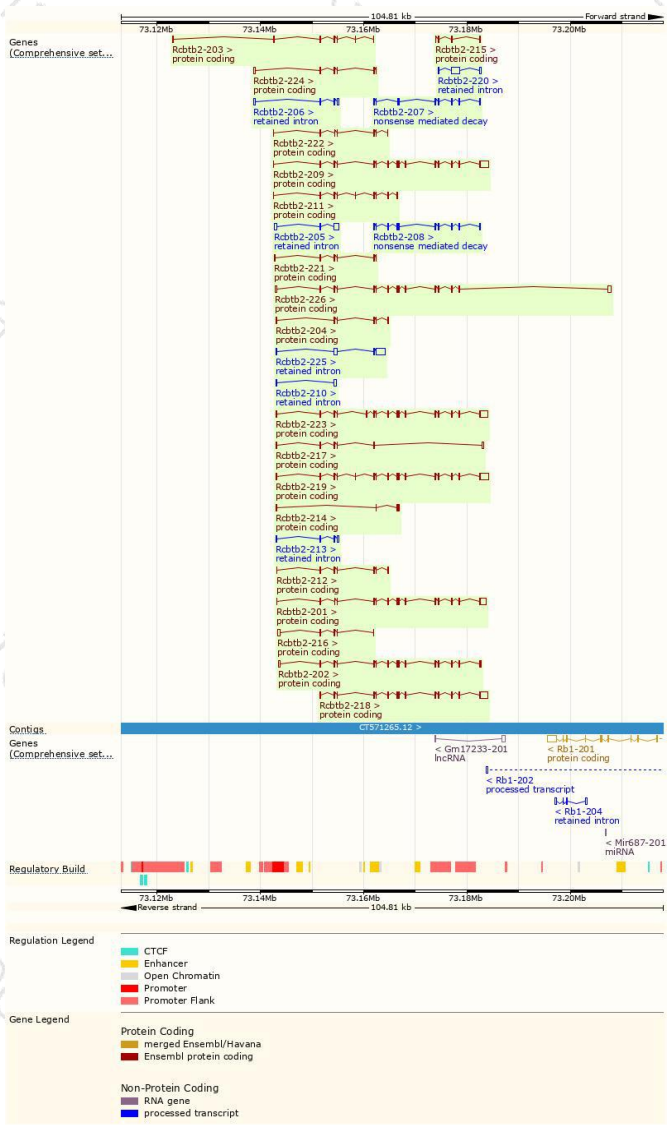
The gene has 26 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rcbtb2-209	ENSMUST00000164822.7	3531	551aa	Protein coding	CCDS27266	Q99IJ7	TSL:1 GENCODE basic APPRIS P2
Rcbtb2-218	ENSMUST00000169479.7	3351	551aa	Protein coding	CCDS27266	Q99IJ7	TSL:1 GENCODE basic APPRIS P2
Rcbtb2-201	ENSMUST00000022702.12	2971	551aa	Protein coding	CCDS27266	Q99IJ7	TSL:5 GENCODE basic APPRIS P2
Rcbtb2-202	ENSMUST00000110952.9	2176	551aa	Protein coding	CCDS27266	Q99IJ7	TSL:1 GENCODE basic APPRIS P2
Rcbtb2-219	ENSMUST00000169513.7	3622	527aa	Protein coding	-	Q99IJ7	TSL:1 GENCODE basic APPRIS ALT2
Rcbtb2-223	ENSMUST00000170677.7	3573	527aa	Protein coding	-	Q99IJ7	TSL:1 GENCODE basic APPRIS ALT2
Rcbtb2-226	ENSMUST00000171767.7	2692	517aa	Protein coding	-	E9Q3B1	TSL:1 GENCODE basic
Rcbtb2-217	ENSMUST00000167401.7	868	72aa	Protein coding	-	E9Q5U1	TSL:5 GENCODE basic
Rcbtb2-211	ENSMUST00000165429.7	837	157aa	Protein coding	-	E9Q3W8	CDS 3' incomplete TSL:5
Rcbtb2-204	ENSMUST00000163533.7	762	149aa	Protein coding	-	E9QA48	CDS 3' incomplete TSL:3
Rcbtb2-212	ENSMUST00000165567.7	749	172aa	Protein coding	-	E9Q7J4	CDS 3' incomplete TSL:5
Rcbtb2-224	ENSMUST00000171070.7	741	69aa	Protein coding	-	E9PY30	CDS 3' incomplete TSL:5
Rcbtb2-216	ENSMUST00000167021.7	702	24aa	Protein coding	-	E9Q213	CDS 3' incomplete TSL:5
Rcbtb2-222	ENSMUST00000170370.7	637	128aa	Protein coding	-	E9QAL7	CDS 3' incomplete TSL:3
Rcbtb2-221	ENSMUST00000170368.7	559	86aa	Protein coding	-	E9PZR2	CDS 3' incomplete TSL:5
Rcbtb2-203	ENSMUST00000163399.7	528	5aa	Protein coding	-	-	CDS 3' incomplete TSL:3
Rcbtb2-214	ENSMUST00000165727.7	465	90aa	Protein coding	-	E9QA84	CDS 3' incomplete TSL:3
Rcbtb2-215	ENSMUST00000166875.1	357	119aa	Protein coding	-	F6QHR6	CDS 5' and 3' incomplete TSL:1
Rcbtb2-208	ENSMUST00000164298.7	1471	292aa	Nonsense mediated decay	-	F6ZTZ2	CDS 5' incomplete TSL:5
Rcbtb2-207	ENSMUST00000163797.1	1255	219aa	Nonsense mediated decay	-	F6X7I4	CDS 5' incomplete TSL:5
Rcbtb2-225	ENSMUST00000171163.1	2674	No protein	Retained intron	-	-	TSL:1
Rcbtb2-220	ENSMUST00000170278.1	1859	No protein	Retained intron	-	-	TSL:1
Rcbtb2-205	ENSMUST00000163546.7	1462	No protein	Retained intron	-	-	TSL:1
Rcbtb2-206	ENSMUST00000163650.7	892	No protein	Retained intron	-	-	TSL:3
Rcbtb2-210	ENSMUST00000165334.1	649	No protein	Retained intron	-	-	TSL:3
Rcbtb2-213	ENSMUST00000165646.7	591	No protein	Retained intron	-	-	TSL:2

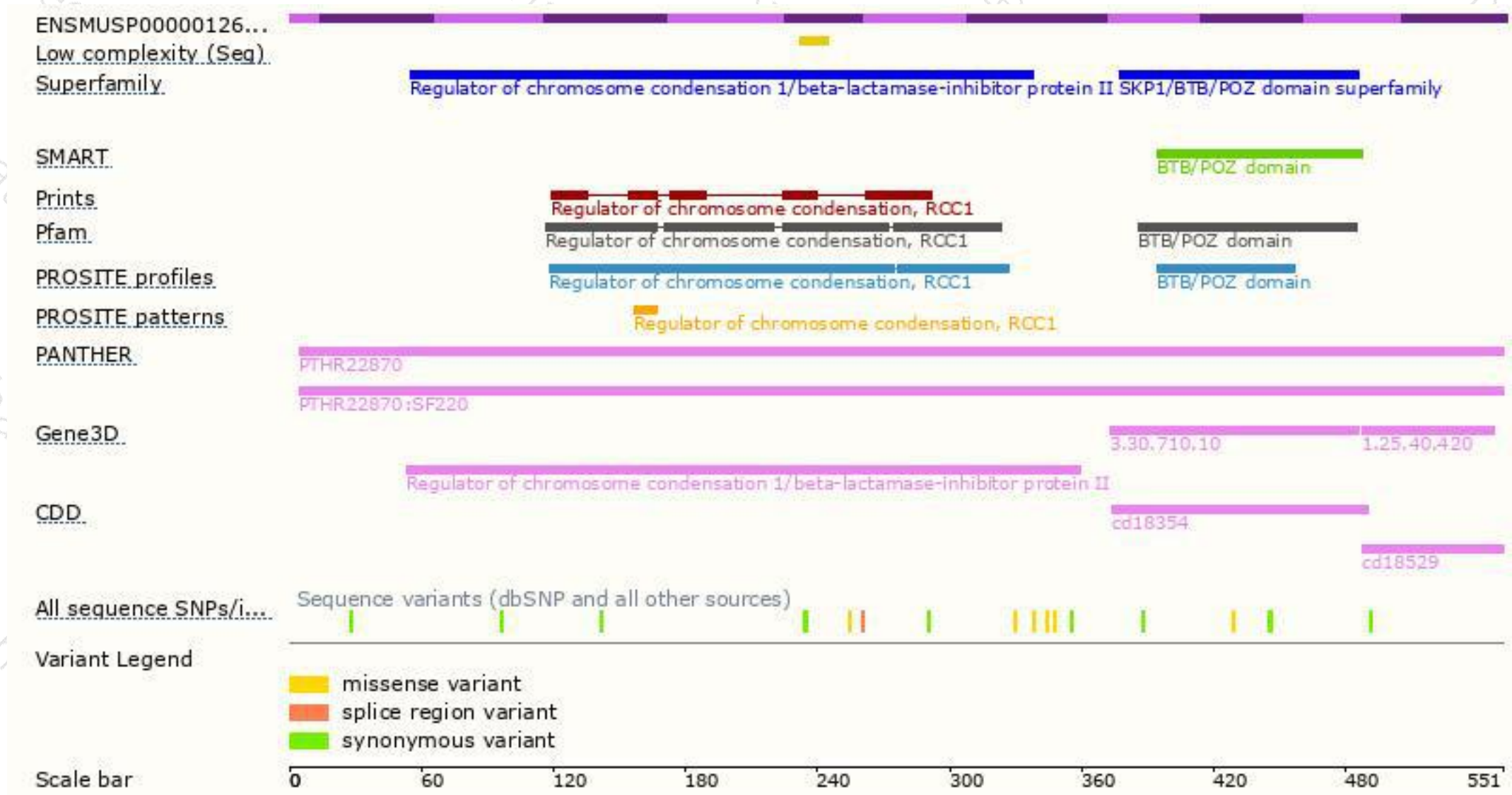
The strategy is based on the design of *Rcbtb2-209* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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