

***Bicral* Cas9-KO Strategy**

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Project Overview

Project Name

Bicral

Project type

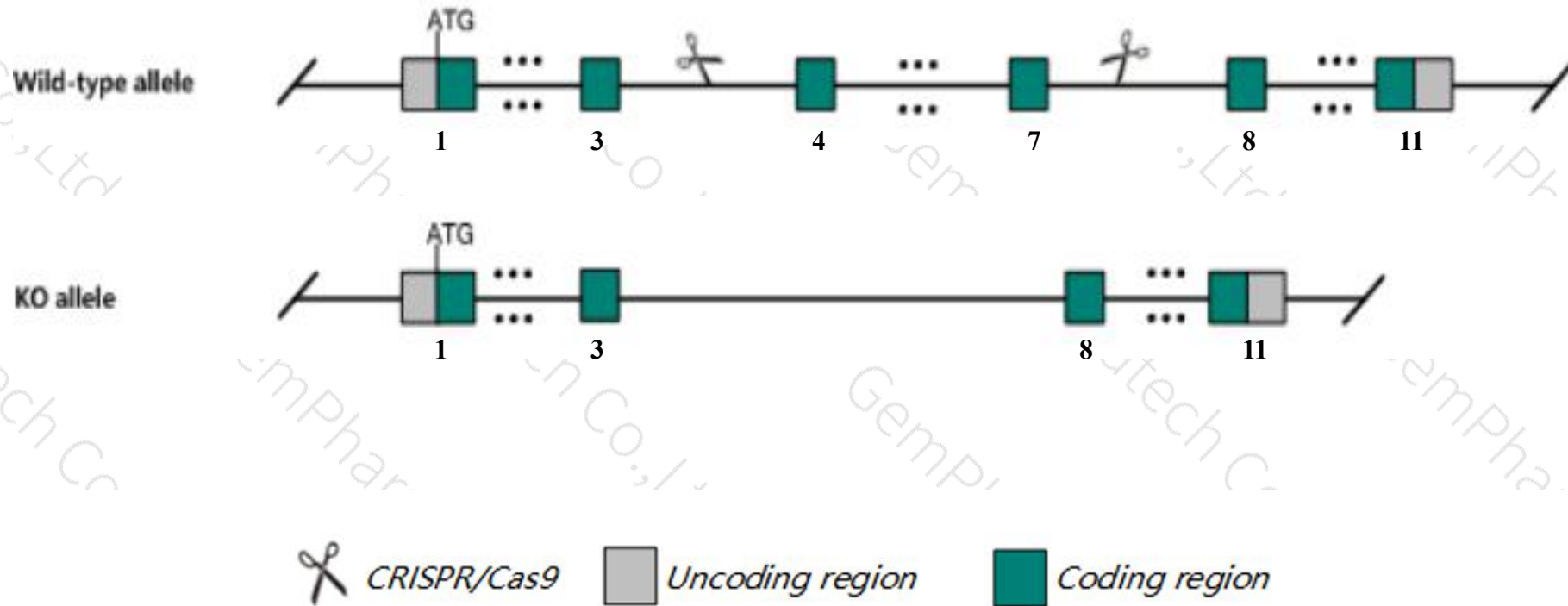
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Bicral* gene has 4 transcripts. According to the structure of *Bicral* gene, exon4-exon7 of *Bicral-201*(ENSMUST00000040624.6) transcript is recommended as the knockout region. The region contains 1940bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Bicral* 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 gene trapped allele display abnormal embryo turning, embryonic growth retardation, cardiac hypertrophy, and complete embryonic lethality during organogenesis.
- The effect on transcript *Bicral*-203 is unknown.
- The *Bicral* gene is located on the Chr17. 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)

Bicral BRD4 interacting chromatin remodeling complex associated protein like [Mus musculus (house mouse)]

Gene ID: 210982, updated on 13-Mar-2020

Summary



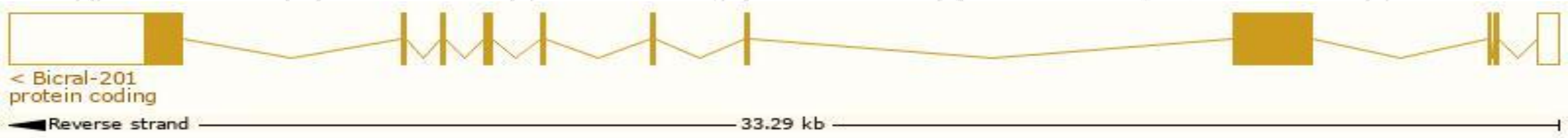
Official Symbol	Bicral provided by MGI
Official Full Name	BRD4 interacting chromatin remodeling complex associated protein like provided by MGI
Primary source	MGI:MGI:2673855
See related	Ensembl:ENSMUSG00000036568
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Gltscr1l, mKIAA0240
Expression	Ubiquitous expression in frontal lobe adult (RPKM 3.2), cerebellum adult (RPKM 3.2) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

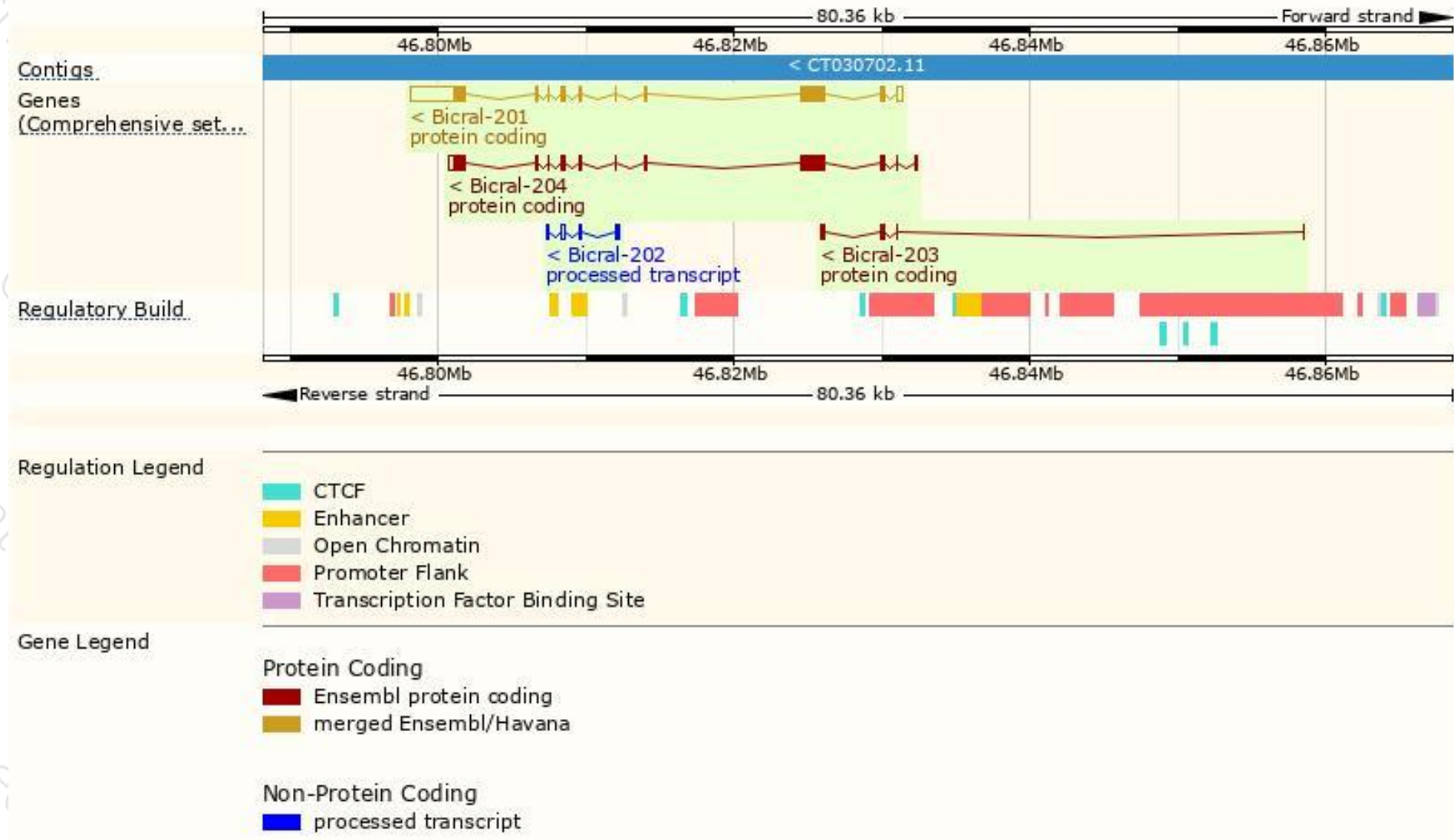
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Bicral-201	ENSMUST00000040624.6	6575	1074aa	Protein coding	CCDS50126	B2RX81 Q8CHH5	TSL:1 GENCODE basic APPRIS P1
Bicral-204	ENSMUST00000233537.1	3685	1074aa	Protein coding	CCDS50126	B2RX81 Q8CHH5	GENCODE basic APPRIS P1
Bicral-203	ENSMUST00000233455.1	540	162aa	Protein coding	-	A0A3B2W406	CDS 3' incomplete
Bicral-202	ENSMUST00000233142.1	566	No protein	Processed transcript	-	-	

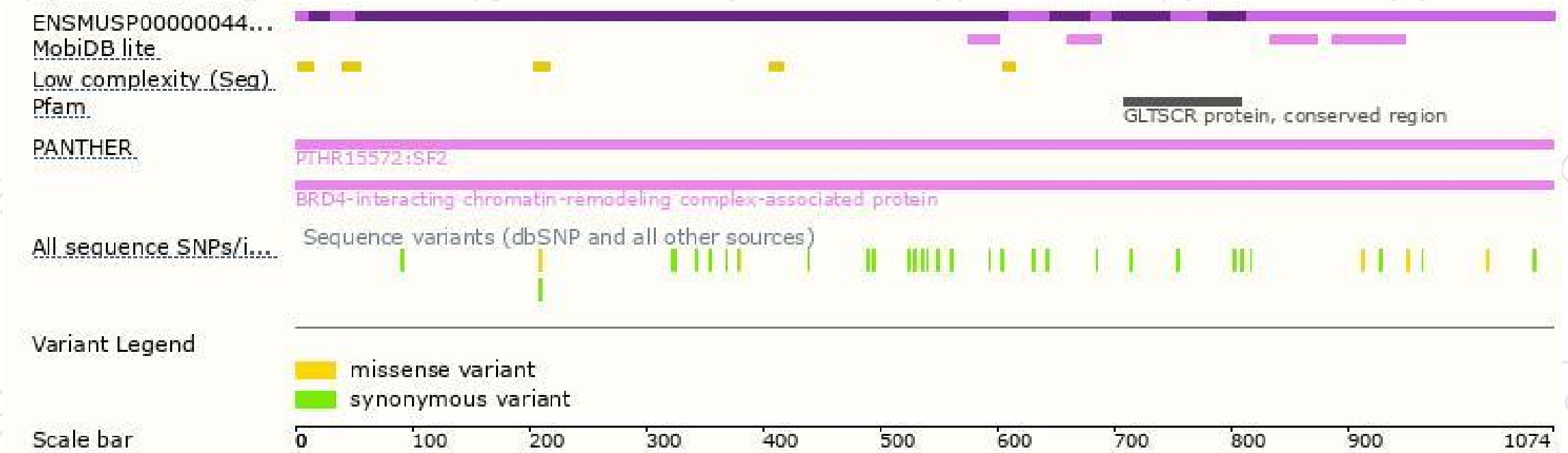
The strategy is based on the design of *Bicral-201* transcript,the transcription is shown below:



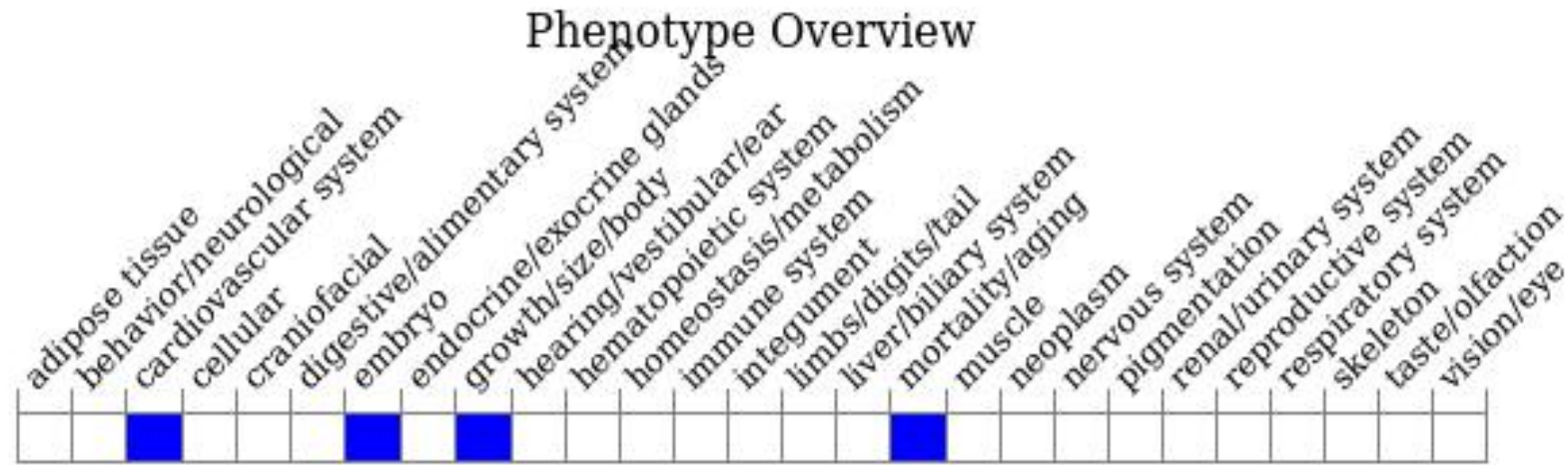
Genomic location distribution



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, mice homozygous for a gene trapped allele display abnormal embryo turning, embryonic growth retardation, cardiac hypertrophy, and complete embryonic lethality during organogenesis.

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

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