

# ***Rbbp4 Cas9-KO Strategy***

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<b>Design Date:</b>	<b>2020-5-6</b>

# Project Overview

**Project Name**

***Rbbp4***

**Project type**

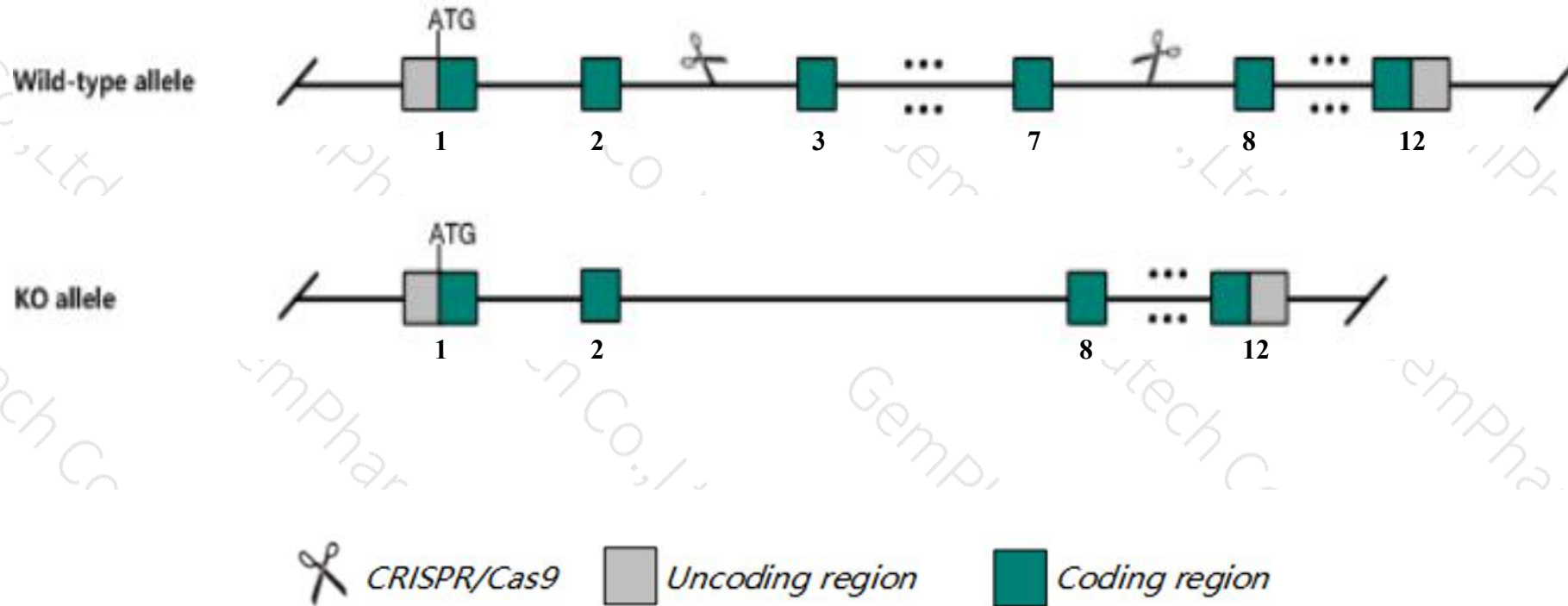
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rbbp4* gene. The schematic diagram is as follows:



- The *Rbbp4* gene has 4 transcripts. According to the structure of *Rbbp4* gene, exon3-exon7 of *Rbbp4-201* (ENSMUST00000102598.3) transcript is recommended as the knockout region. The region contains 724bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rbbp4* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for a knock-out allele show complete embryonic lethality between implantation and somite formation. cultured blastocysts fail to form typical outgrowth colonies.
- The *Rbbp4* gene is located on the Chr4. 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)

## Rbbp4 retinoblastoma binding protein 4, chromatin remodeling factor [Mus musculus (house mouse)]

Gene ID: 19646, updated on 13-Mar-2020

### Summary



**Official Symbol** Rbbp4 provided by [MGI](#)

**Official Full Name** retinoblastoma binding protein 4, chromatin remodeling factor provided by [MGI](#)

**Primary source** [MGI:MGI:1194912](#)

**See related** [Ensembl:ENSMUSG00000057236](#)

**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** RBAP48, mRbAp48

**Expression** Ubiquitous expression in CNS E11.5 (RPKM 70.9), liver E14 (RPKM 42.3) and 25 other tissues [See more](#)

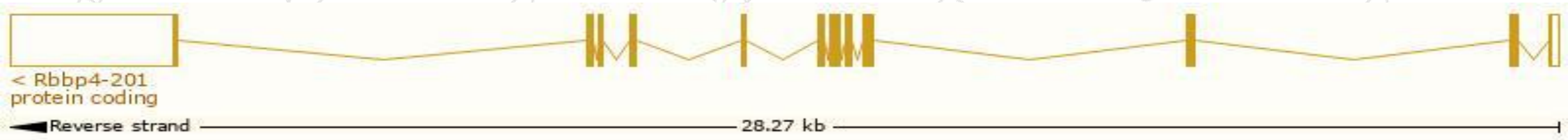
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

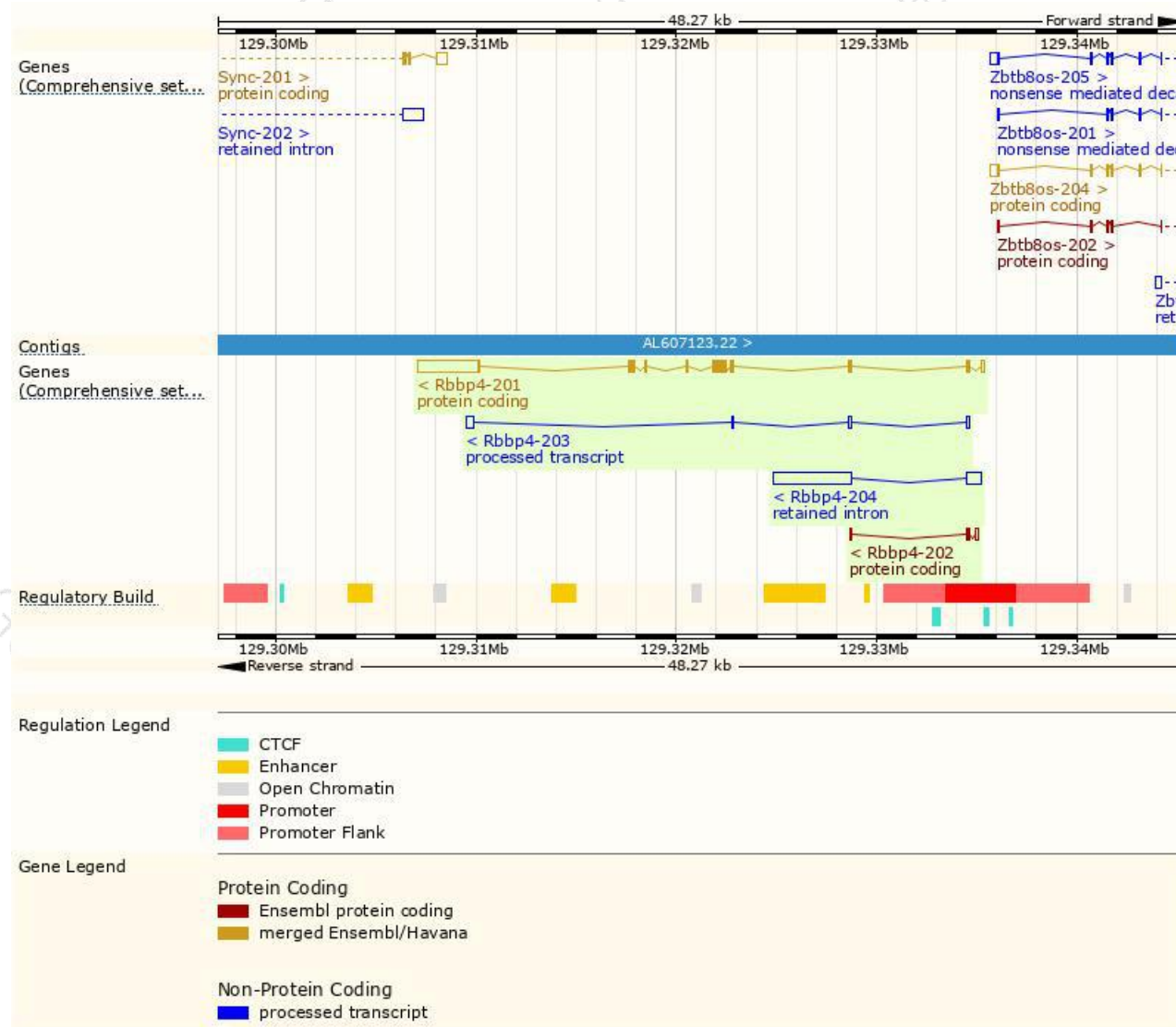
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rbbp4-201	<a href="#">ENSMUST00000102598.3</a>	4407	<a href="#">425aa</a>	Protein coding	<a href="#">CCDS18688</a>	<a href="#">Q60972</a>	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Rbbp4-202	<a href="#">ENSMUST00000135585.1</a>	392	<a href="#">48aa</a>	Protein coding	-	<a href="#">A8Y5E8</a>	CDS 3' incomplete TSL:3
Rbbp4-203	<a href="#">ENSMUST00000140291.1</a>	722	No protein	Processed transcript	-	-	TSL:5
Rbbp4-204	<a href="#">ENSMUST00000147183.1</a>	4663	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Rbbp4-201* transcript,the transcription is shown below:

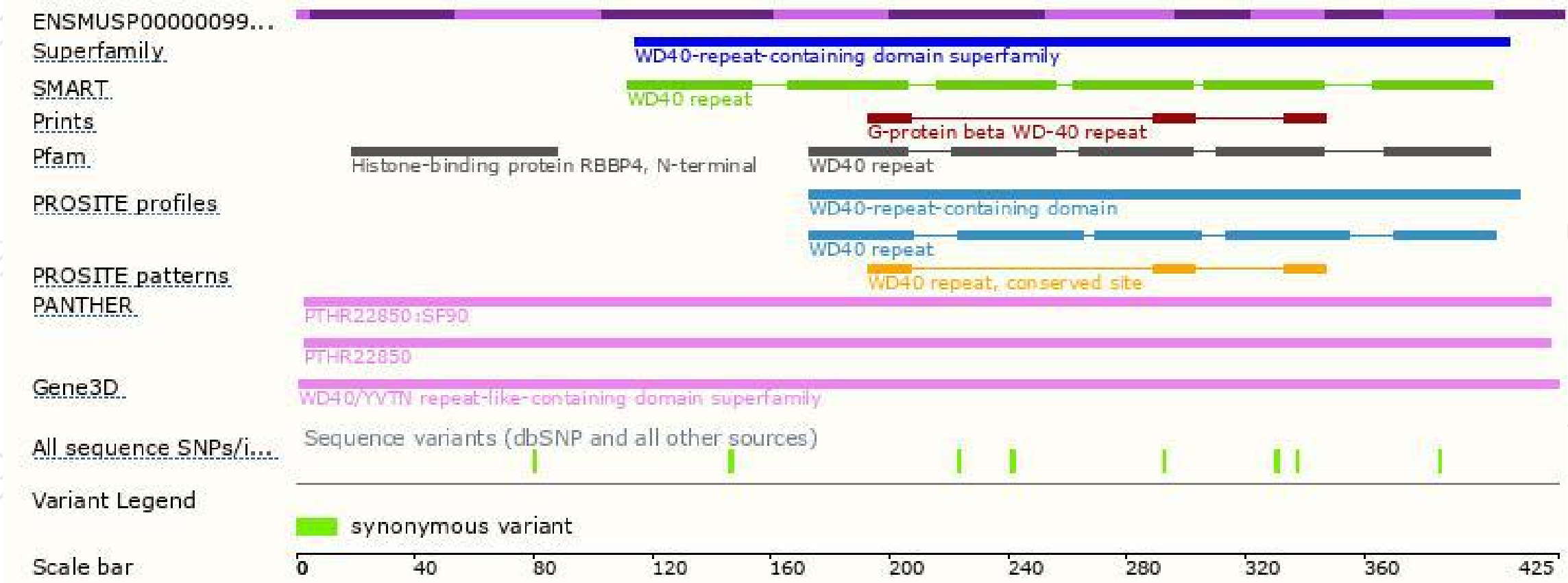


# Genomic location distribution

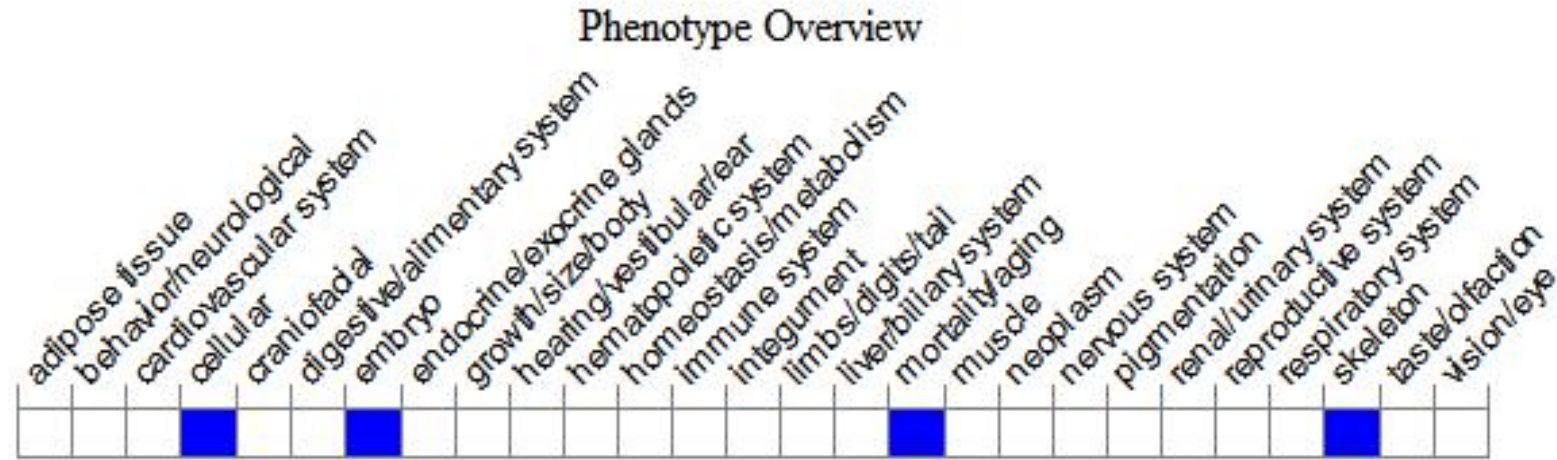




# Protein domain



# 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 knock-out allele show complete embryonic lethality between implantation and somite formation. Cultured blastocysts fail to form typical outgrowth colonies.

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

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