

Mybpc2 Cas9-KO Strategy

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Project Overview

Project Name

Mybpc2

Project type

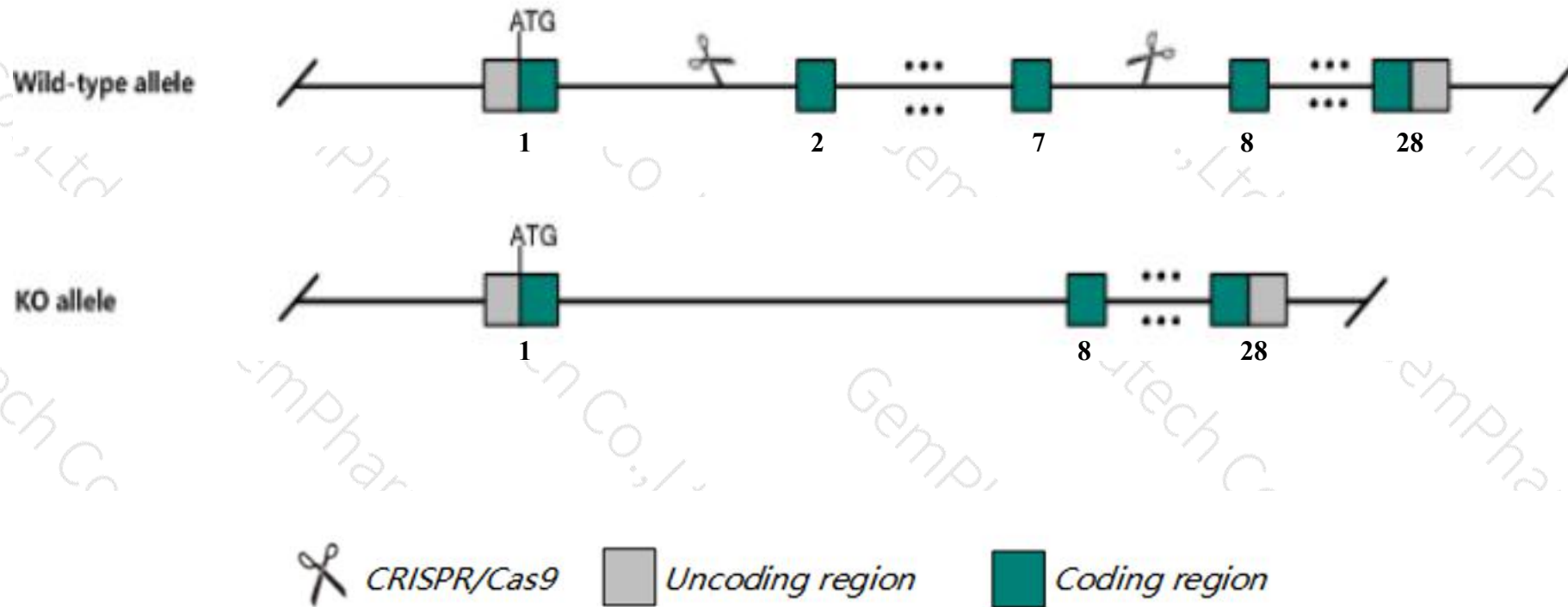
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mybpc2* gene. The schematic diagram is as follows:



- The *Mybpc2* gene has 2 transcripts. According to the structure of *Mybpc2* gene, exon2-exon7 of *Mybpc2-201* (ENSMUST00000165208.3) transcript is recommended as the knockout region. The region contains 541bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mybpc2* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Mybpc2* gene is located on the Chr7. 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)

Mybpc2 myosin binding protein C, fast-type [Mus musculus (house mouse)]

Gene ID: 233199, updated on 13-Mar-2020

Summary



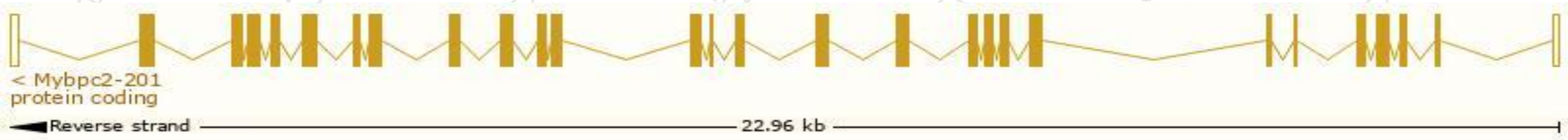
Official Symbol	Mybpc2 provided by MGI
Official Full Name	myosin binding protein C, fast-type provided by MGI
Primary source	MGI:MGI:1336170
See related	Ensembl:ENSMUSG000000038670
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Expression	Biased expression in mammary gland adult (RPKM 39.2) and heart adult (RPKM 2.0) See more
Orthologs	human all

Transcript information (Ensembl)

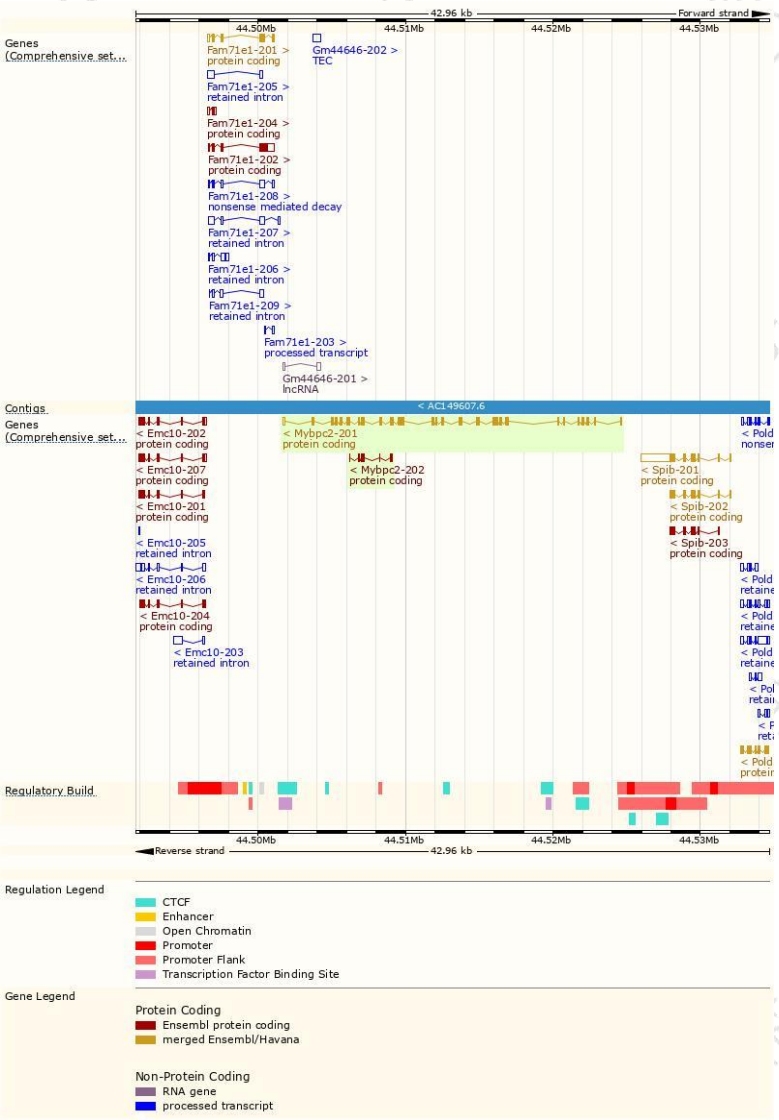
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mybpc2-201	ENSMUST00000165208.3	3611	1136aa	Protein coding	CCDS52233	Q5XKE0	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
Mybpc2-202	ENSMUST00000207516.1	464	155aa	Protein coding	-	A0A140LI70	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5

The strategy is based on the design of *Mybpc2-201* transcript,the transcription is shown below:



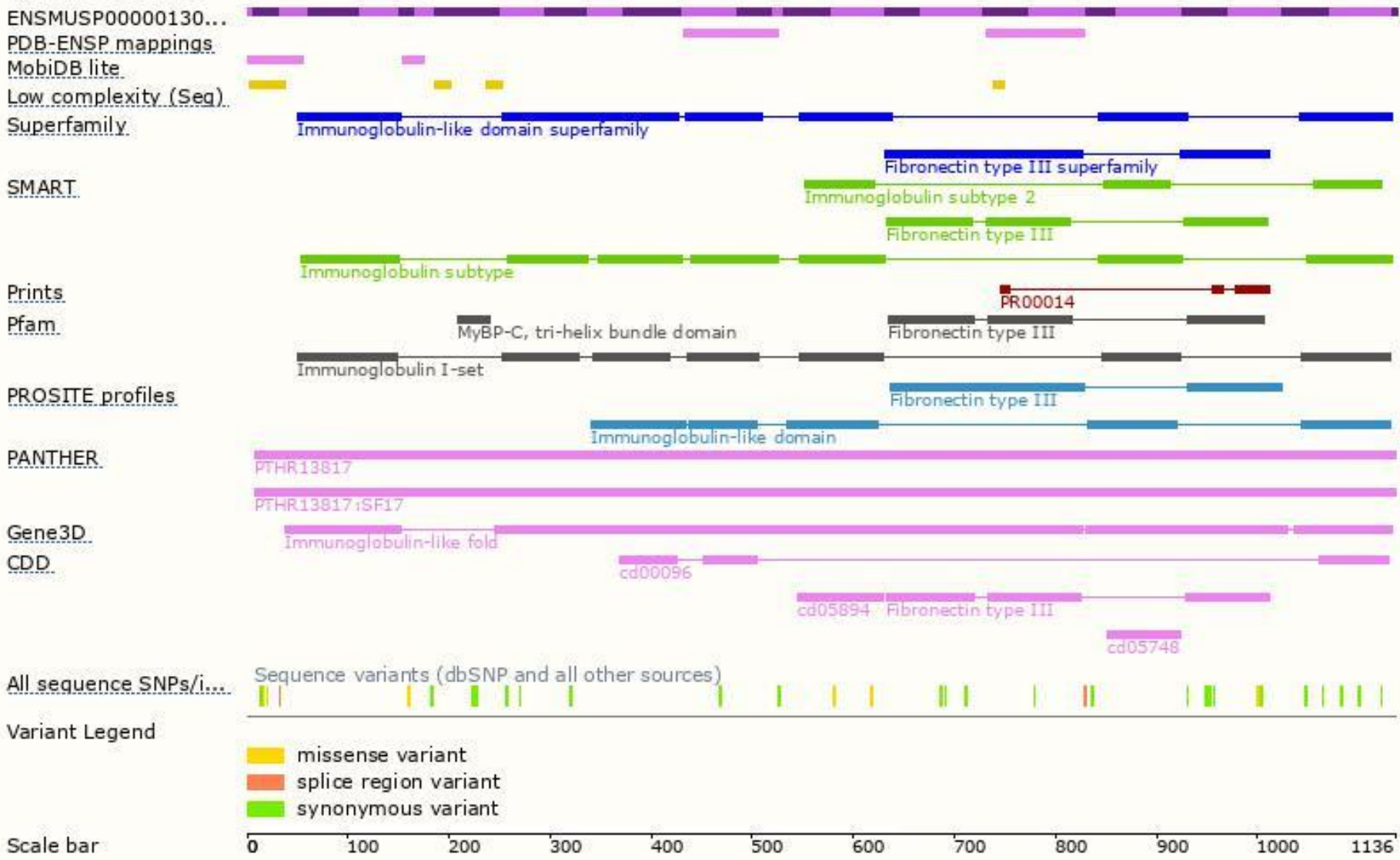
Genomic location distribution



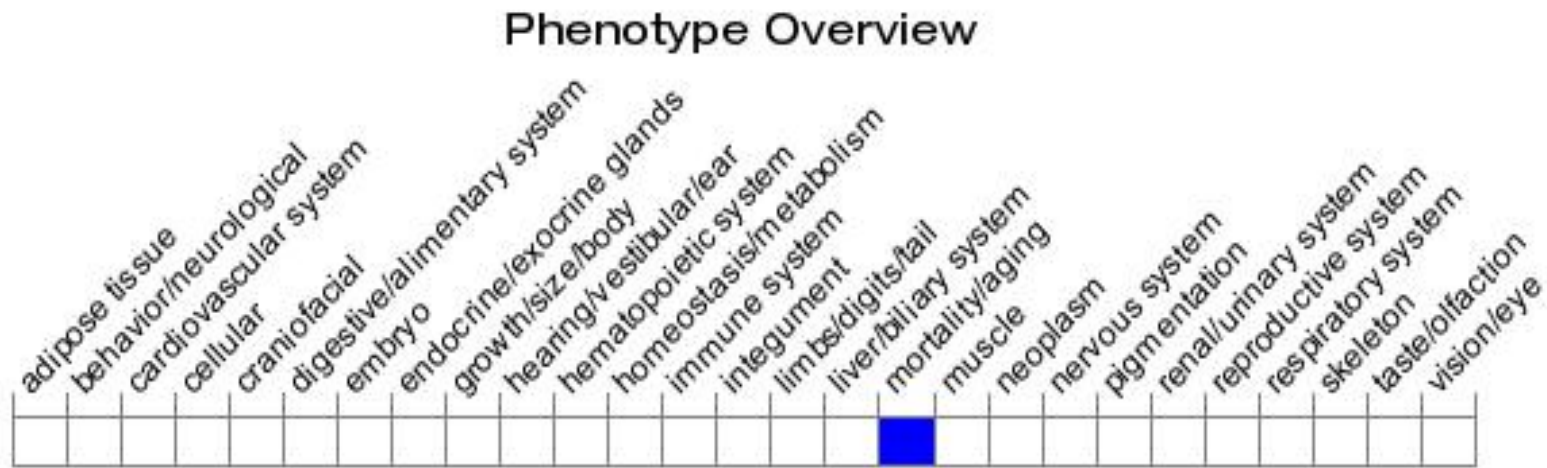
Protein domain



集萃药康
GemPharmatech



Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).

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

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