

Orc1 Cas9-KO Strategy

Designer: QiongZhou

Project Overview

Project Name

Orc1

Project type

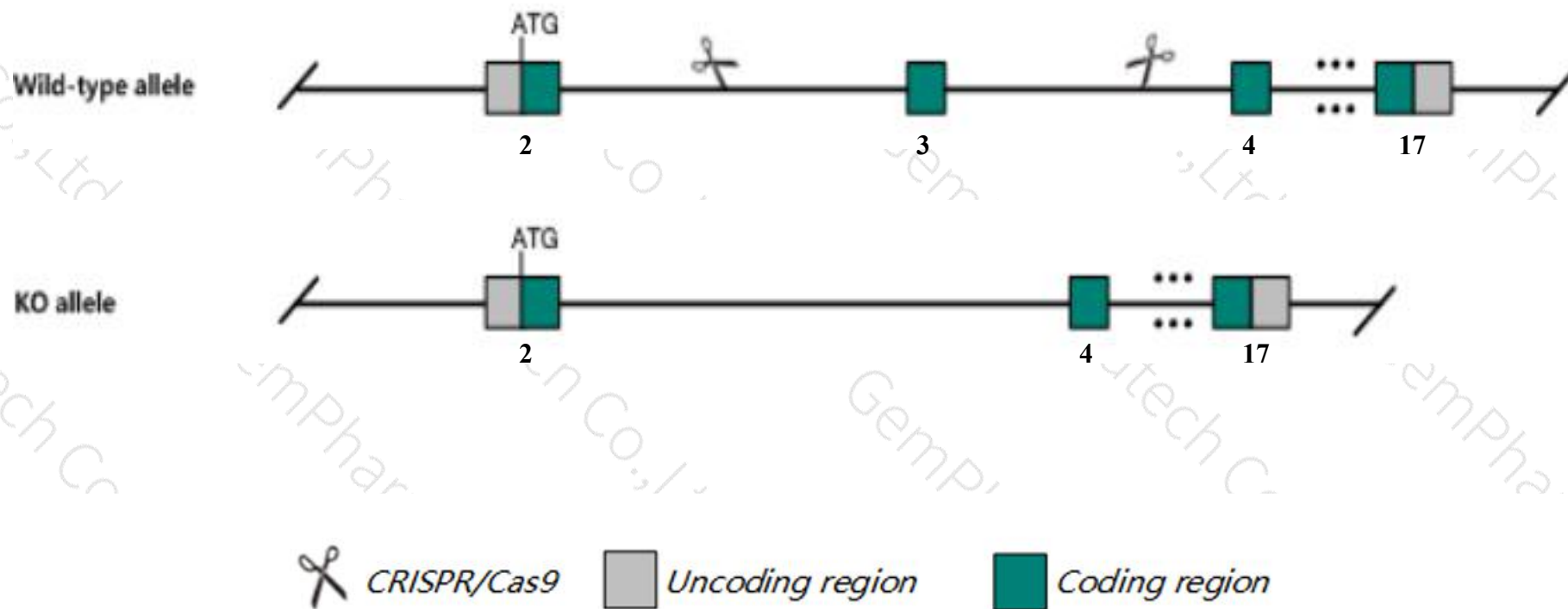
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Orc1* gene. The schematic diagram is as follows:



- The *Orc1* gene has 5 transcripts. According to the structure of *Orc1* gene, exon3 of *Orc1-201* (ENSMUST00000102744.3) transcript is recommended as the knockout region. The region contains 125bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Orc1* gene. The brief process is as follows: CRISPR/Cas9 system v

- The *Orc1* 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)

Orc1 origin recognition complex, subunit 1 [Mus musculus (house mouse)]

Gene ID: 18392, updated on 13-Mar-2020

Summary



Official Symbol Orc1 provided by [MGI](#)

Official Full Name origin recognition complex, subunit 1 provided by [MGI](#)

Primary source [MGI:MGI:1328337](#)

See related [Ensembl:ENSMUSG00000028587](#)

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 AA545195, MmORC1, Orc1l

Expression Broad expression in liver E14 (RPKM 4.8), liver E14.5 (RPKM 4.6) and 16 other tissues [See more](#)

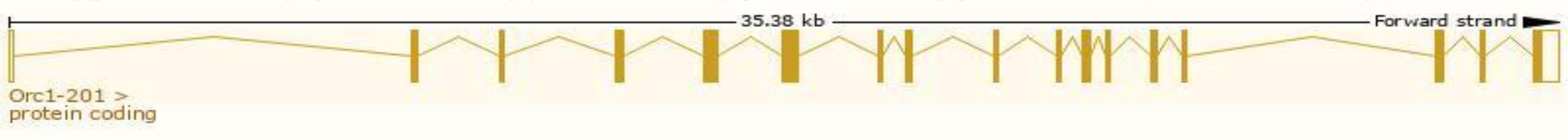
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

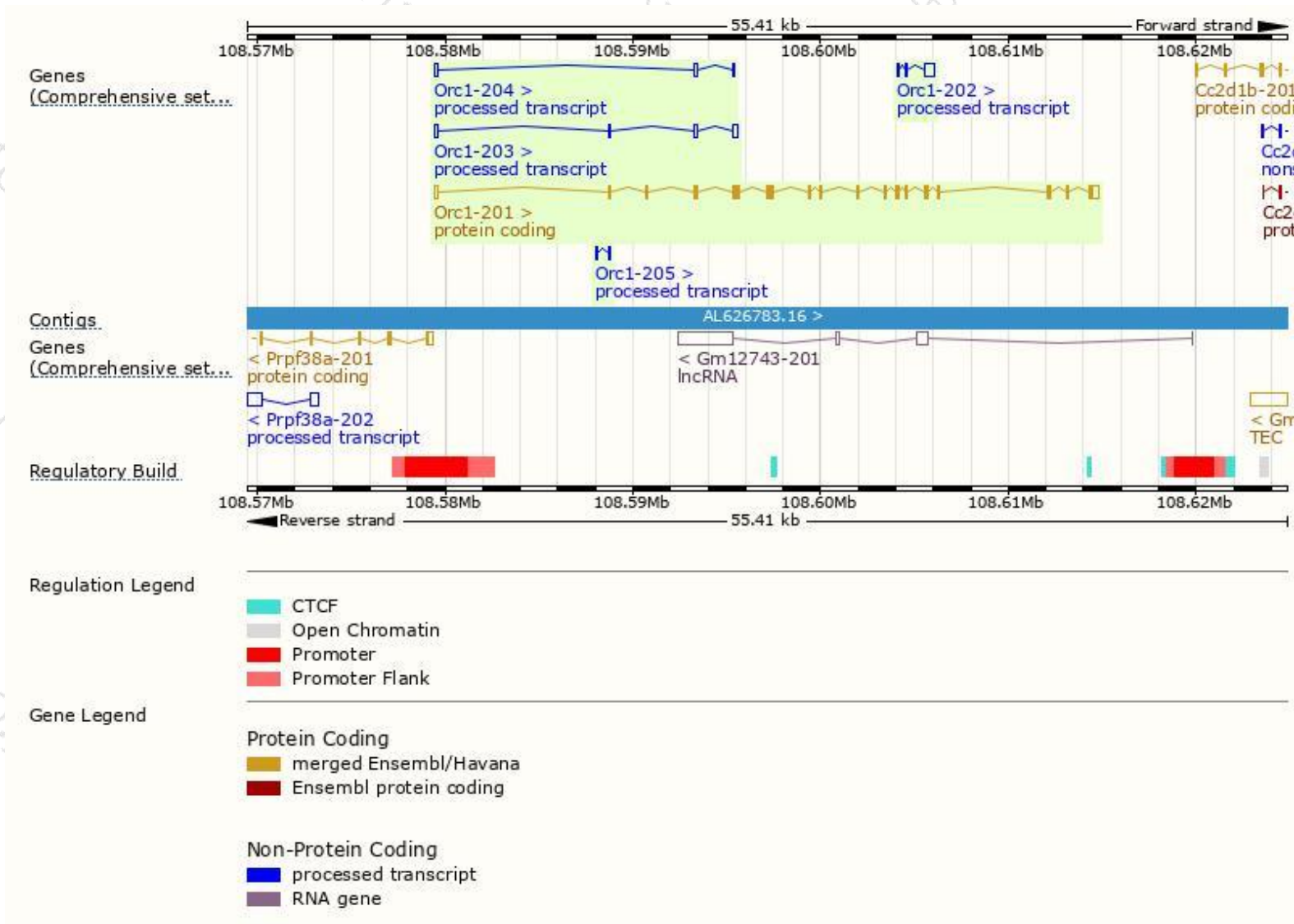
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Orc1-201	ENSMUST00000102744.3	3014	840aa	Protein coding	CCDS18453	Q9Z1N2	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
Orc1-203	ENSMUST00000130162.1	679	No protein	Processed transcript	-	-	TSL:2
Orc1-202	ENSMUST00000129931.1	670	No protein	Processed transcript	-	-	TSL:3
Orc1-204	ENSMUST00000139772.7	443	No protein	Processed transcript	-	-	TSL:3
Orc1-205	ENSMUST00000143497.1	173	No protein	Processed transcript	-	-	TSL:5

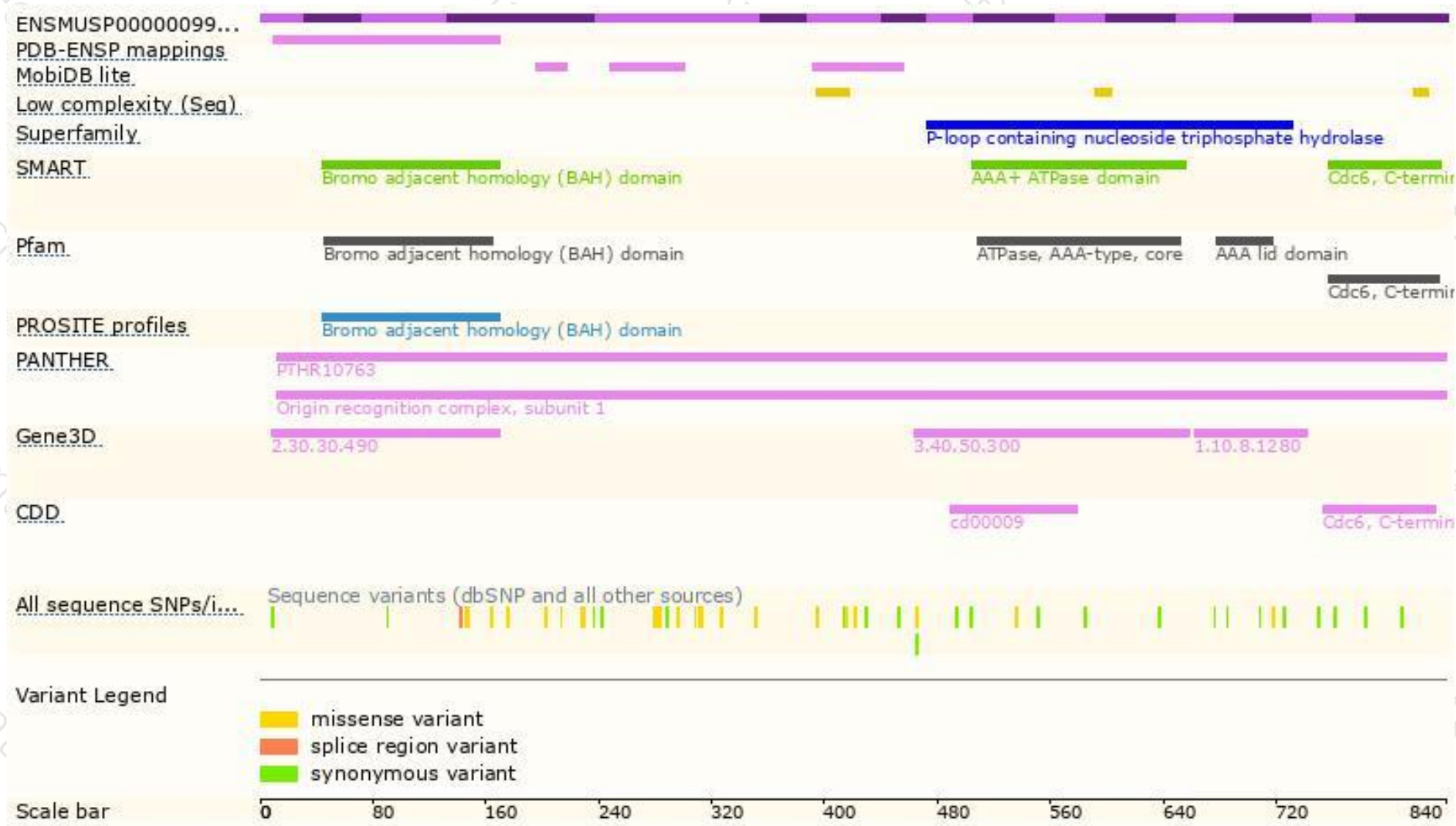
The strategy is based on the design of *Orc1-201* transcript,the transcription is shown below:



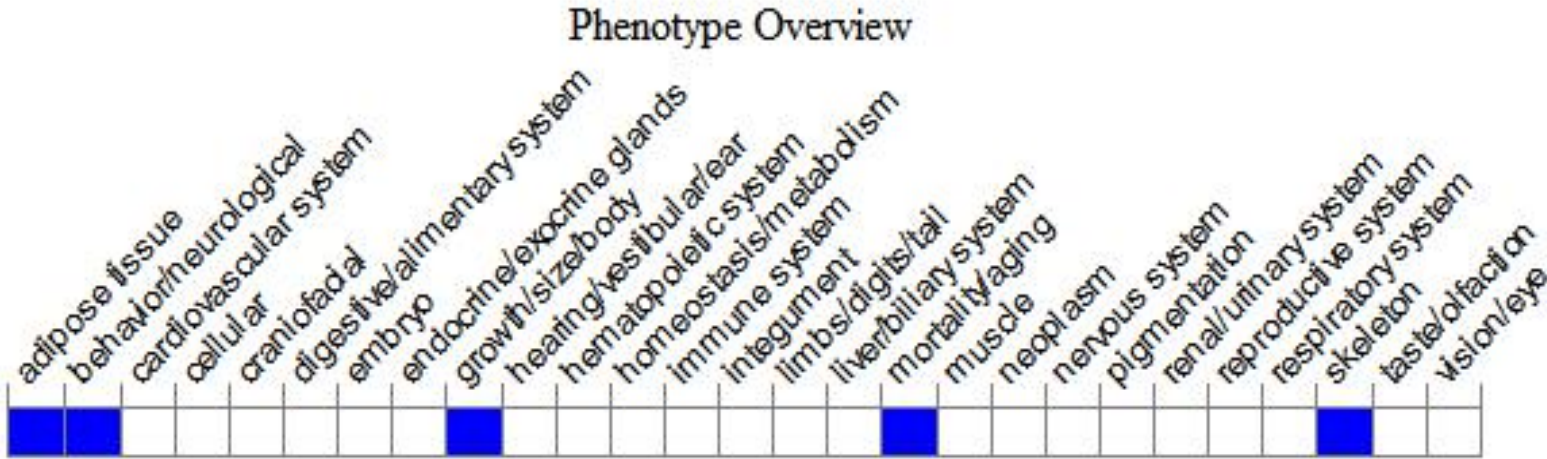
Genomic location distribution



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/>).

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

Tel: 400-9660890

