

***Man2b2* Cas9-KO Strategy**

Designer: Daohua Xu

Reviewer: Huimin Su

Design Date: 2020-5-12

Project Overview

Project Name

Man2b2

Project type

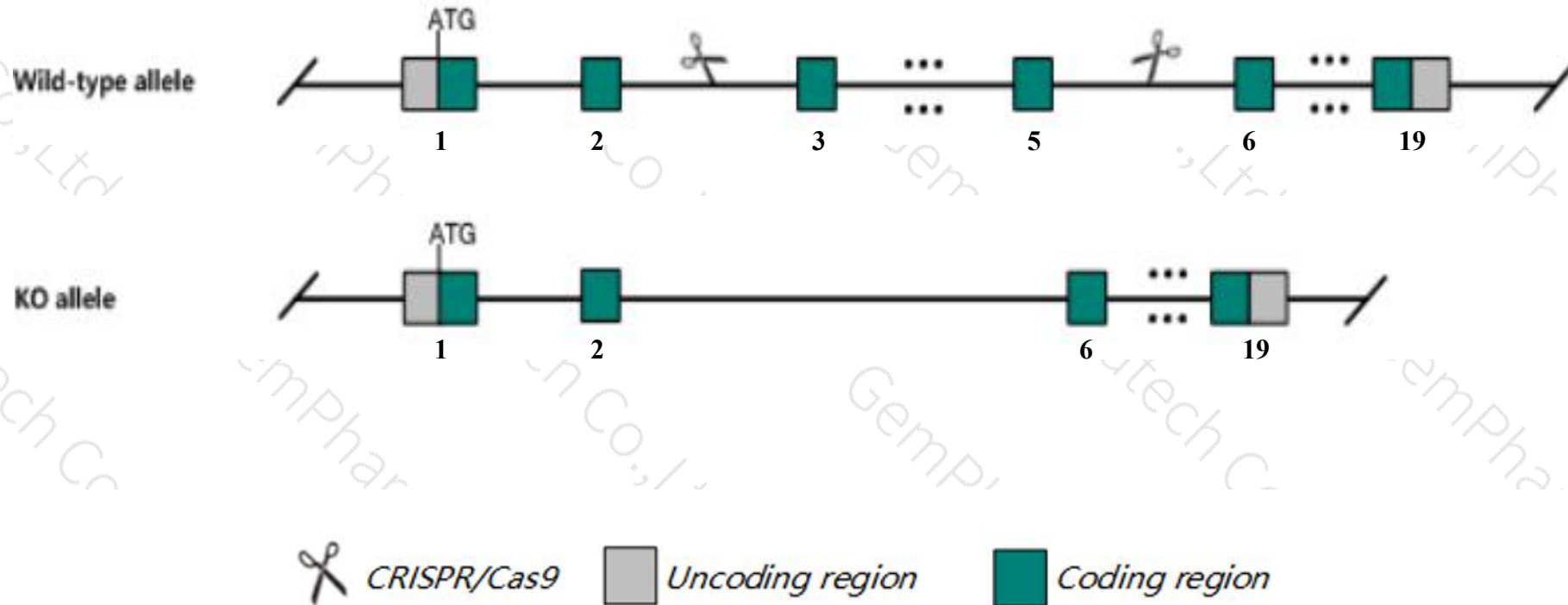
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Man2b2* gene. The schematic diagram is as follows:



- The *Man2b2* gene has 3 transcripts. According to the structure of *Man2b2* gene, exon3-exon5 of *Man2b2-201* (ENSMUST00000031002.9) transcript is recommended as the knockout region. The region contains 395bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Man2b2* gene. The brief process is as follows: CRISPR/Cas9 system

- Transcript *Man2b2-202* and *Man2b2-203* may not be affected.
- The *Man2b2* gene is located on the Chr5. 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)

Man2b2 mannosidase 2, alpha B2 [Mus musculus (house mouse)]

Gene ID: 17160, updated on 13-Mar-2020

Summary



Official Symbol Man2b2 provided by [MGI](#)

Official Full Name mannosidase 2, alpha B2 provided by [MGI](#)

Primary source [MGI:MGI:1195262](#)

See related [Ensembl:ENSMUSG00000029119](#)

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 mKIAA0935

Expression Ubiquitous expression in testis adult (RPKM 75.3), ovary adult (RPKM 58.0) and 27 other tissues [See more](#)

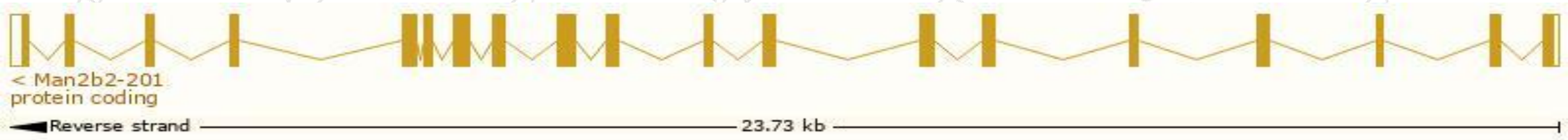
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

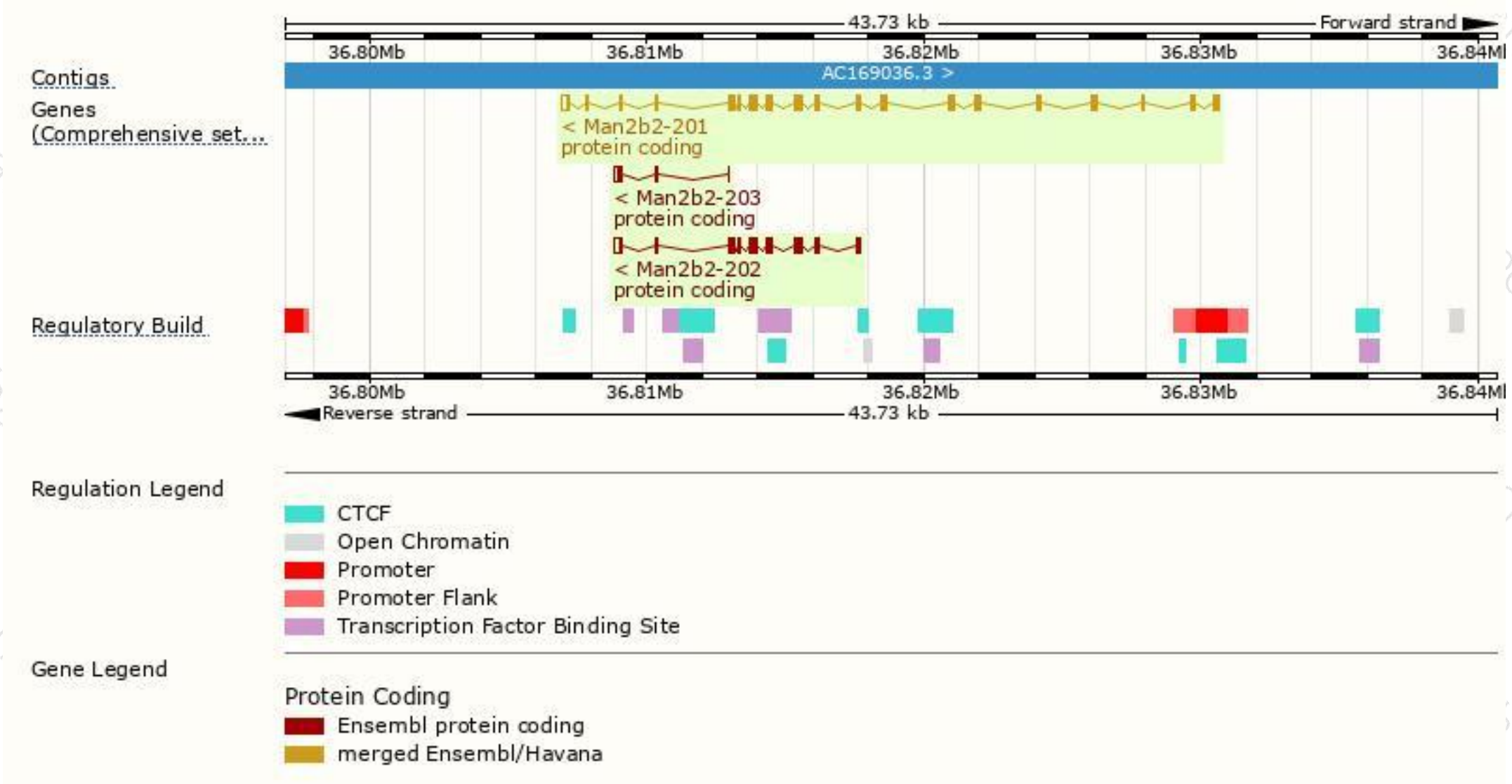
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Man2b2-201	ENSMUST00000031002.9	3330	1018aa	Protein coding	CCDS19243	O54782	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
Man2b2-202	ENSMUST00000124711.1	1725	494aa	Protein coding	-	F6TMZ3	CDS 5' incomplete TSL:1
Man2b2-203	ENSMUST00000147893.1	445	104aa	Protein coding	-	F6Z025	CDS 5' incomplete TSL:5

The strategy is based on the design of *Man2b2-201* transcript,The transcription is shown below



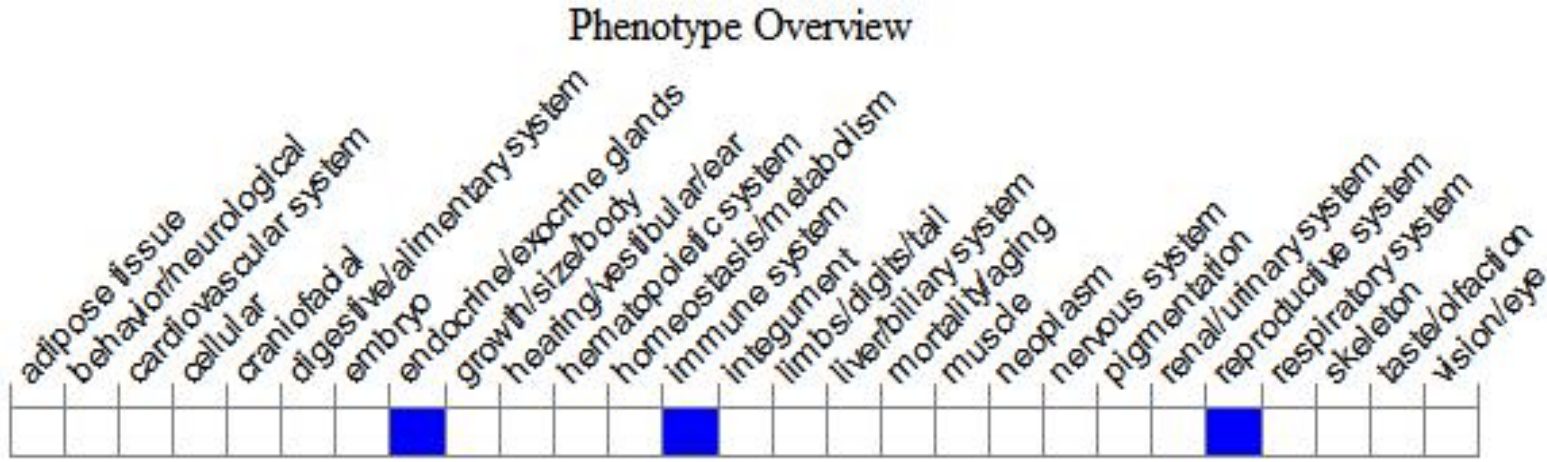
Genomic location distribution



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

