

***Man2b2* Cas9-CKO Strategy**

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Project Overview

Project Name

Man2b2

Project type

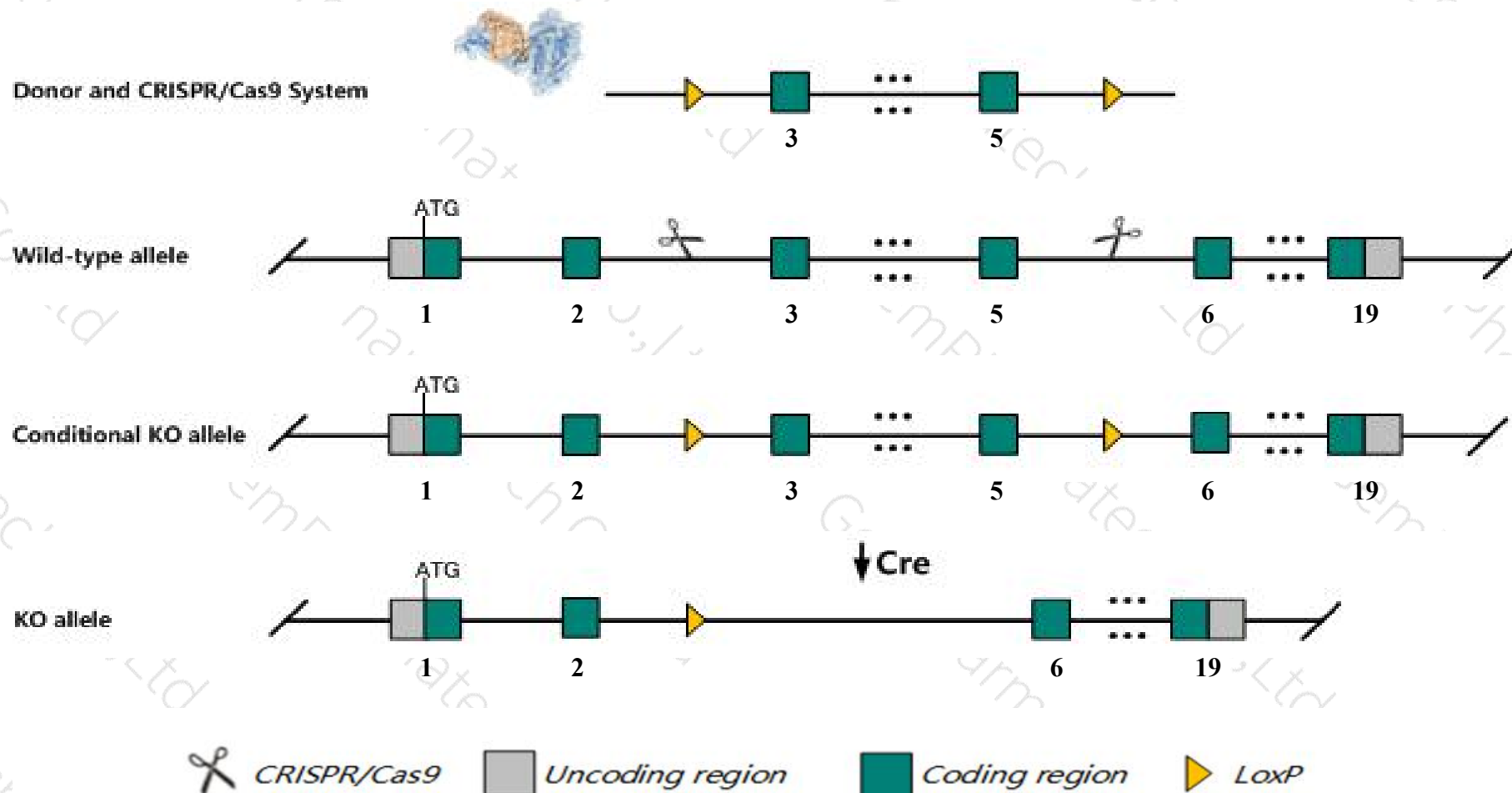
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional 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 and Donor 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.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological 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](#)

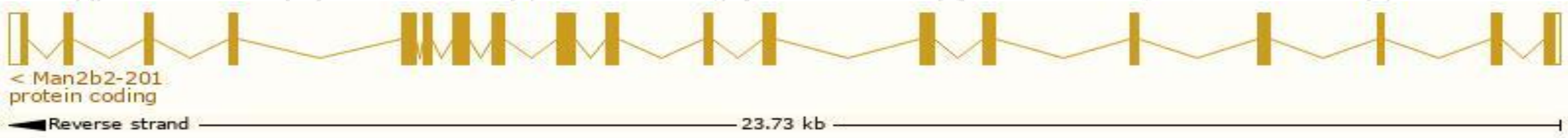
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

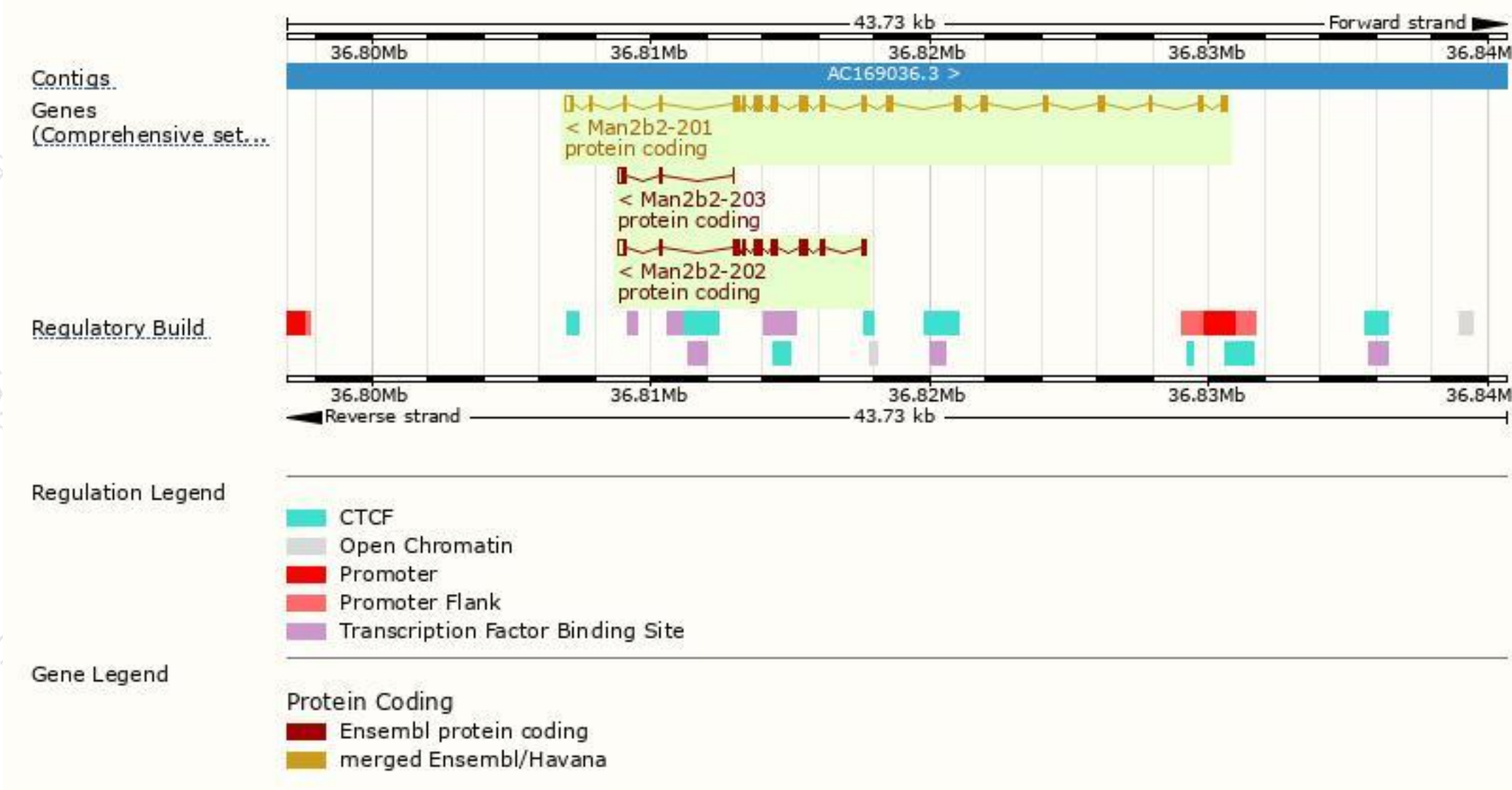
The gene has 3 transcripts,all transcripts are shown below:

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

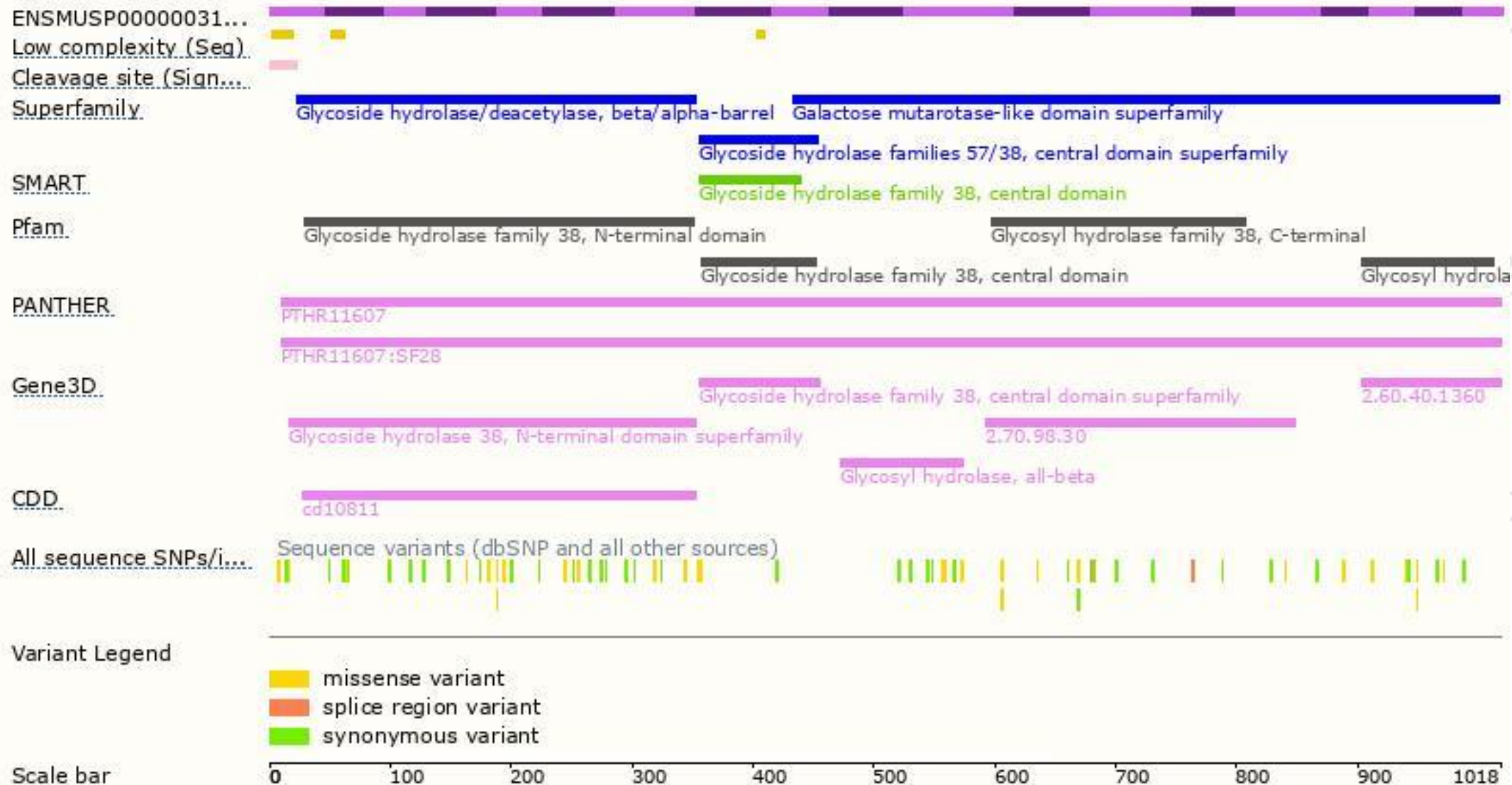
The strategy is based on the design of *Man2b2-201* transcript,The transcription is shown below



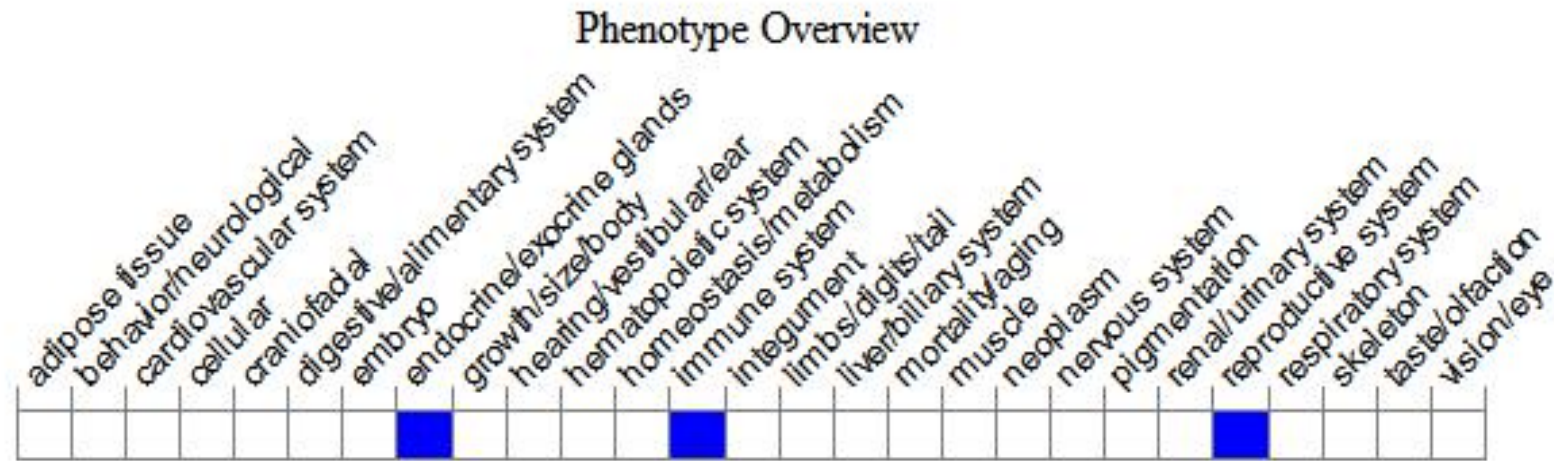
Genomic location distribution



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.

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