Yme1l1 Cas9-KO Strategy

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Project Overview

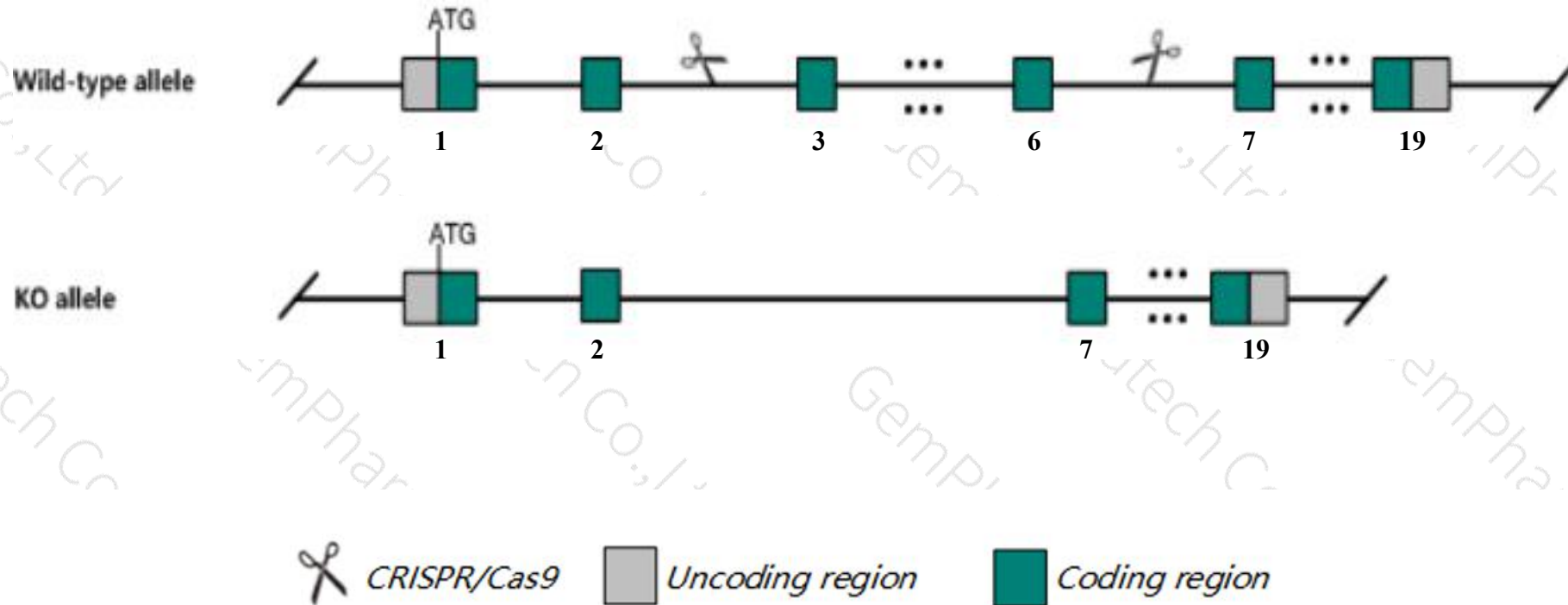|	
Project Name	***Yme1l1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Yme1l1* gene. The schematic diagram is as follows:

➤ The *Yme1l1* gene has 6 transcripts. According to the structure of *Yme1l1* gene, exon3-exon6 of *Yme1l1-201* (ENSMUST00000028117.3) transcript is recommended as the knockout region.The region contains 523bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Yme1l1* gene. The brief process is as follows: CRISPR/Cas9 syster

➢ According to the existing MGI data,Homozygous null embryos die prior to E13.5, and show a developmental delay from E8.5 to E12.5.

➢ The knockout region is near to the N-terminal of *Mastl* gene,this strategy may influence the regulatory function of the N-terminal of *Mastl* gene.

➢ Transcript *Yme1l1*-203&206 may not be affected.

➢ The *Yme1l1* gene is located on the Chr2. 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）

Yme1l1 YME1-like 1 (S. cerevisiae) [*Mus musculus* (house mouse)]

Gene ID: 27377, updated on 13-Aug-2019

Summary

Official Symbol	Yme1l1 provided by MGI
Official Full Name	YME1-like 1 (S. cerevisiae) provided by MGI
Primary source	MGI:MGI:1351651
See related	Ensembl:ENSMUSG00000026775
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	Ftsh; FtsH1
Expression	Broad expression in placenta adult (RPKM 18.6), CNS E11.5 (RPKM 15.0) and 21 other tissues See more
Orthologs	human all

Genomic context

Location: 2; 2 A3

See Yme1l1 in Genome Data Viewer

Exon count: 20

| Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	2	NC_000068.7 (23155442..23199260)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	2	NC_000068.6 (23012066..23054156)

Transcript information（Ensembl）

The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Yme1l1-201	ENSMUST00000028117.3	4707	715aa	Protein coding	CCDS15728	O88967	TSL:1 GENCODE basic APPRIS P1
Yme1l1-202	ENSMUST00000125004.7	2769	No protein	Processed transcript	-	-	TSL:2
Yme1l1-203	ENSMUST00000134342.1	869	No protein	Processed transcript	-	-	TSL:3
Yme1l1-205	ENSMUST00000148616.1	662	No protein	Processed transcript	-	-	TSL:5
Yme1l1-206	ENSMUST00000149240.1	628	No protein	Processed transcript	-	-	TSL:2
Yme1l1-204	ENSMUST00000147750.1	563	No protein	Processed transcript	-	-	TSL:3

The strategy is based on the design of *Yme1l1-201* transcript,The transcription is shown below
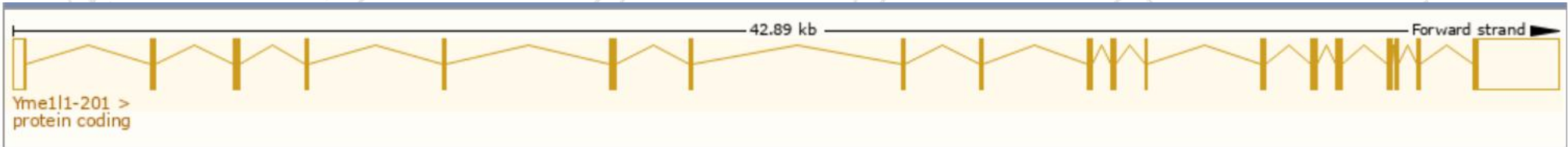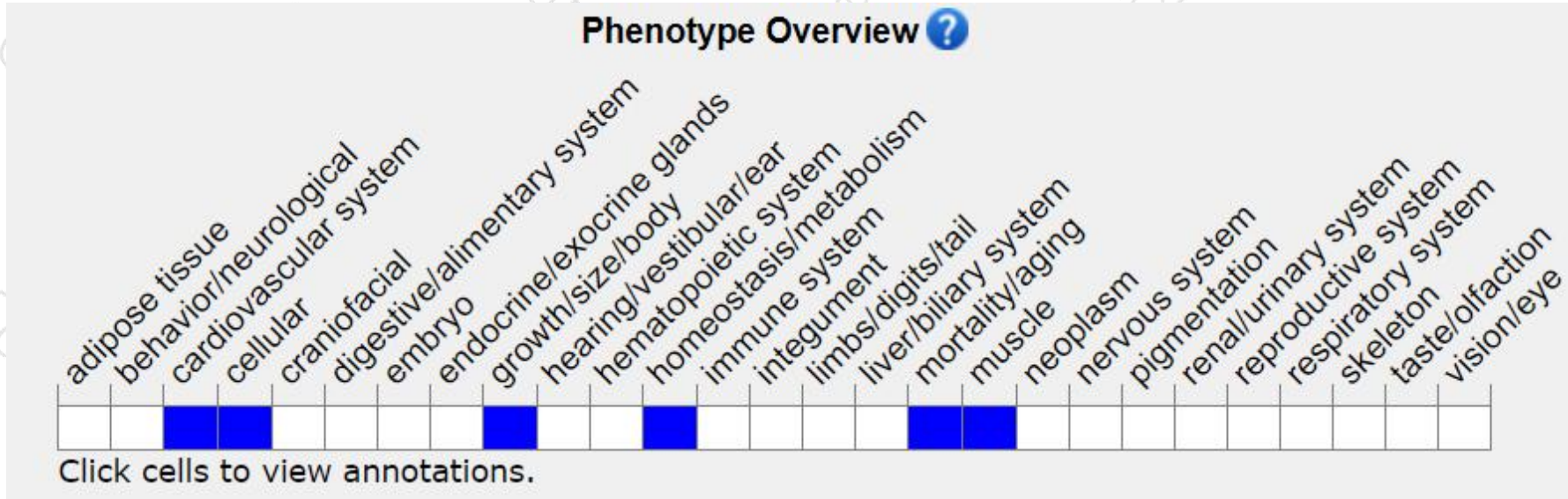
Genomic location distribution
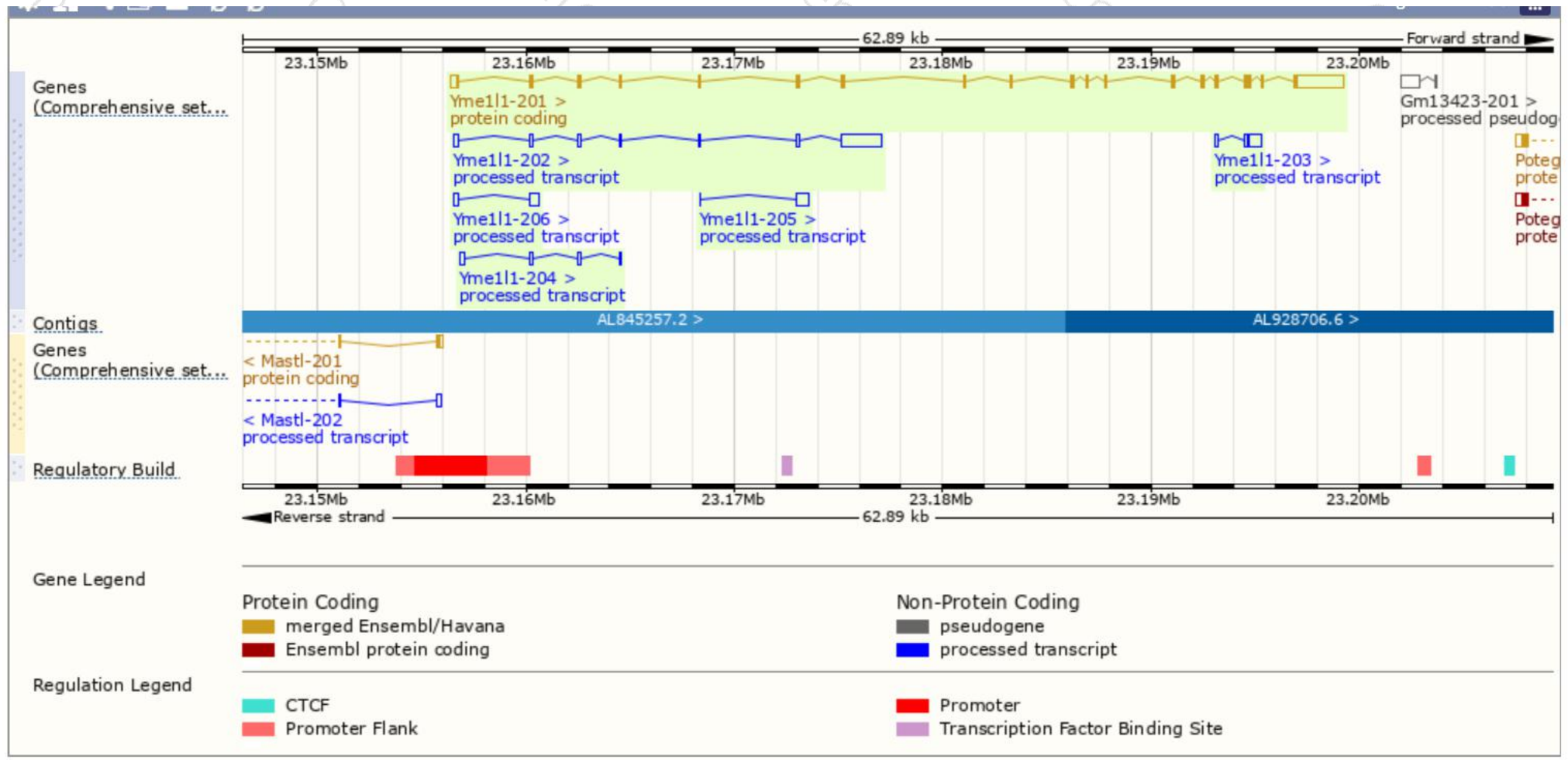
Protein domain

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,Homozygous null embryos die prior to E13.5, and show a developmental delay from E8.5 to E12.5.

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