

Yme1l1 Cas9-CKO Strategy

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Project Overview

Project Name

Yme1l1

Project type

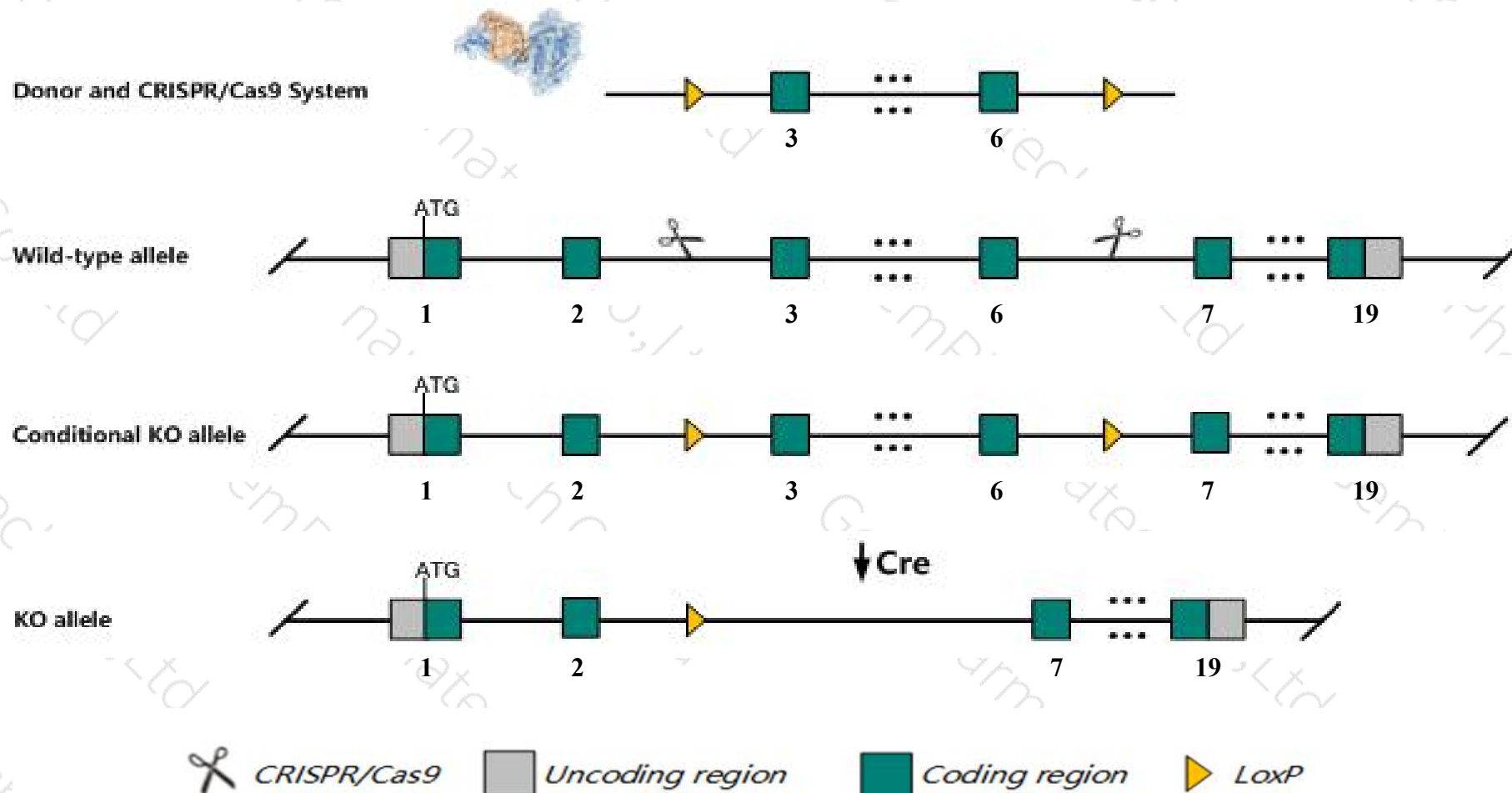
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Yme111* gene. The schematic diagram is as follows:



Technical routes

- The *Yme111* gene has 6 transcripts. According to the structure of *Yme111* gene, exon3-exon6 of *Yme111-201* (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 *Yme111* 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.

- 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 floxed 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological 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

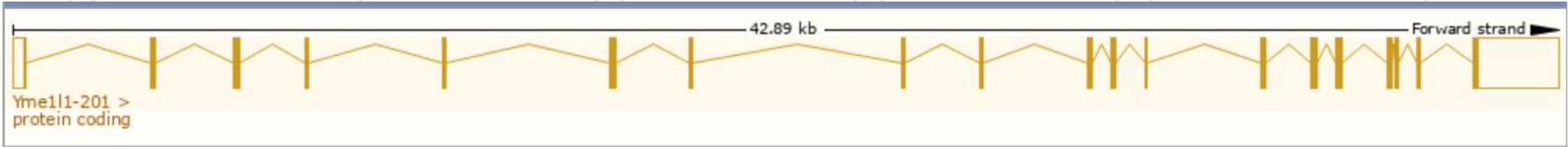
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	2	NC_000068.7 (23155442..23199260)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	2	NC_000068.6 (23012066..23054156)

Transcript information (Ensembl)

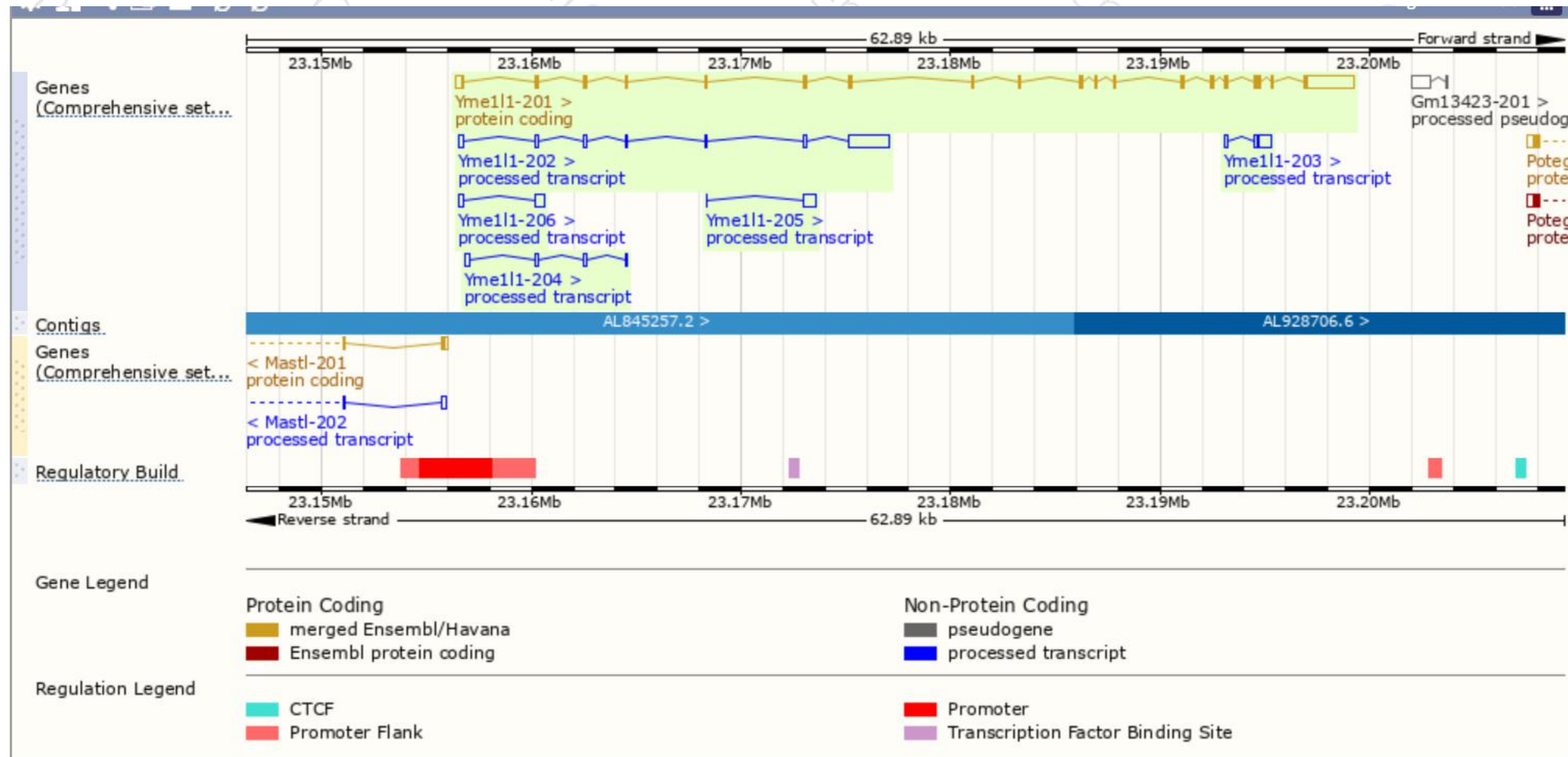
The gene has 6 transcripts,all transcripts are shown below:

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



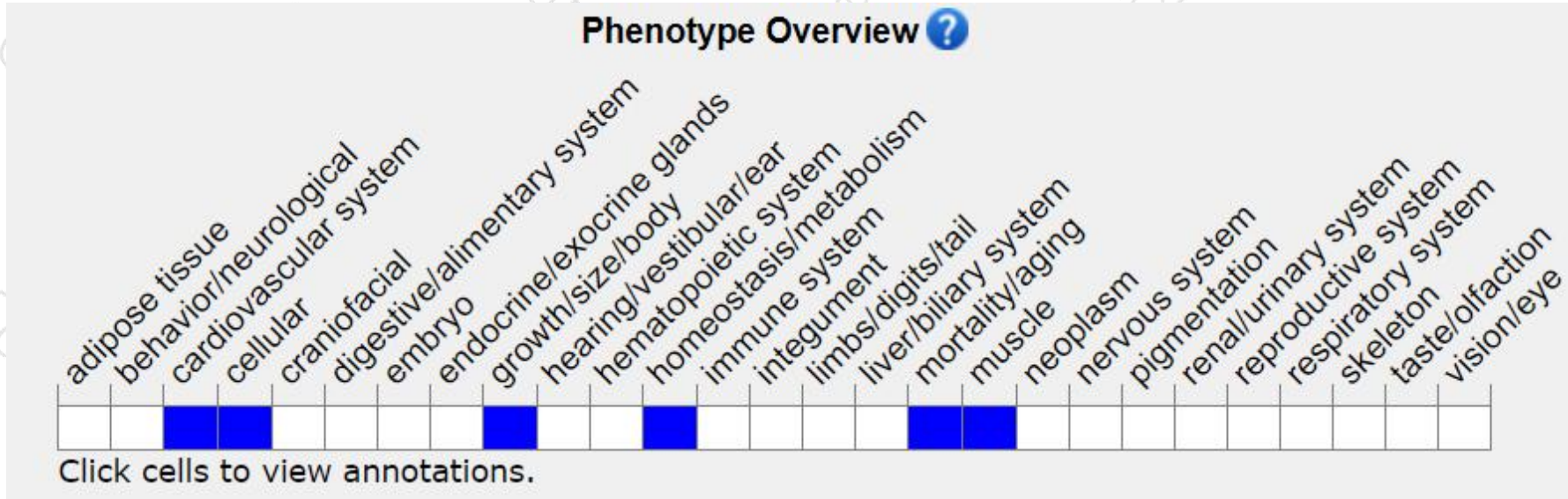
Genomic location distribution



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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