Ylpm1 Cas9-KO *Strategy*

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Project Overview

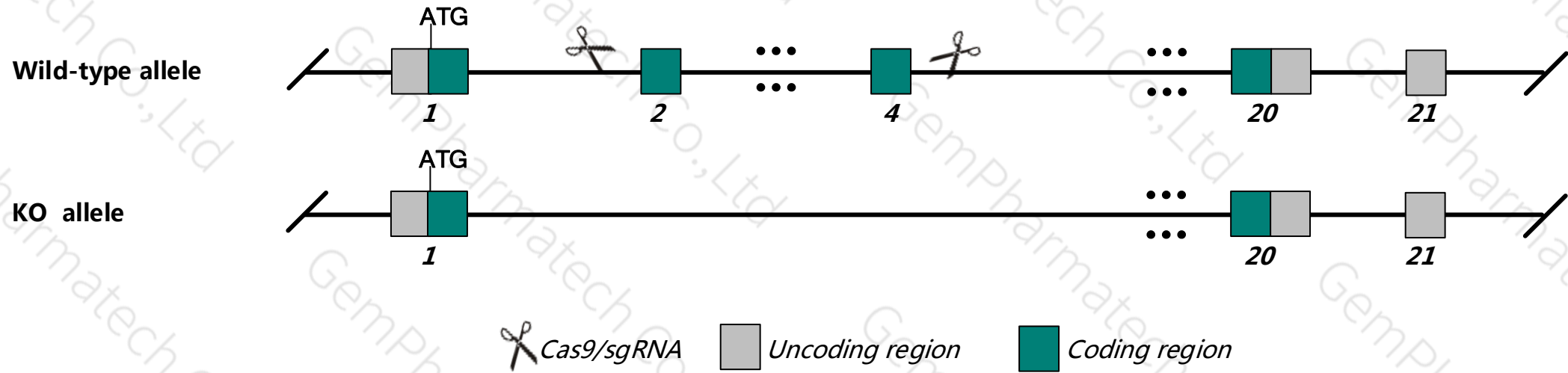|	
Project Name	*Ylpm1*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ylpm1* gene. The schematic diagram is as follows:

Technical routes

- The *Ylpm1* gene has 8 transcript.According to the structure of *Ylpm1* gene, exon2-4 of *Ylpm1*-201 (ENSMUST00000021670.14) transcript is recommended as the knockout region.The region contains 1400bp coding sequence.Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Ylpm1* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA 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.

Notice

➤ The *Ylpm1* gene is located on the Chr12. 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）

Ylpm1   YLP motif containing 1 [*Mus musculus* (house mouse)]

Gene ID: 56531, updated on 18-Apr-2019

▲ Summary

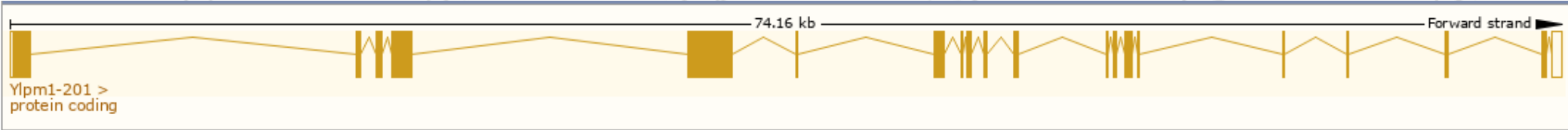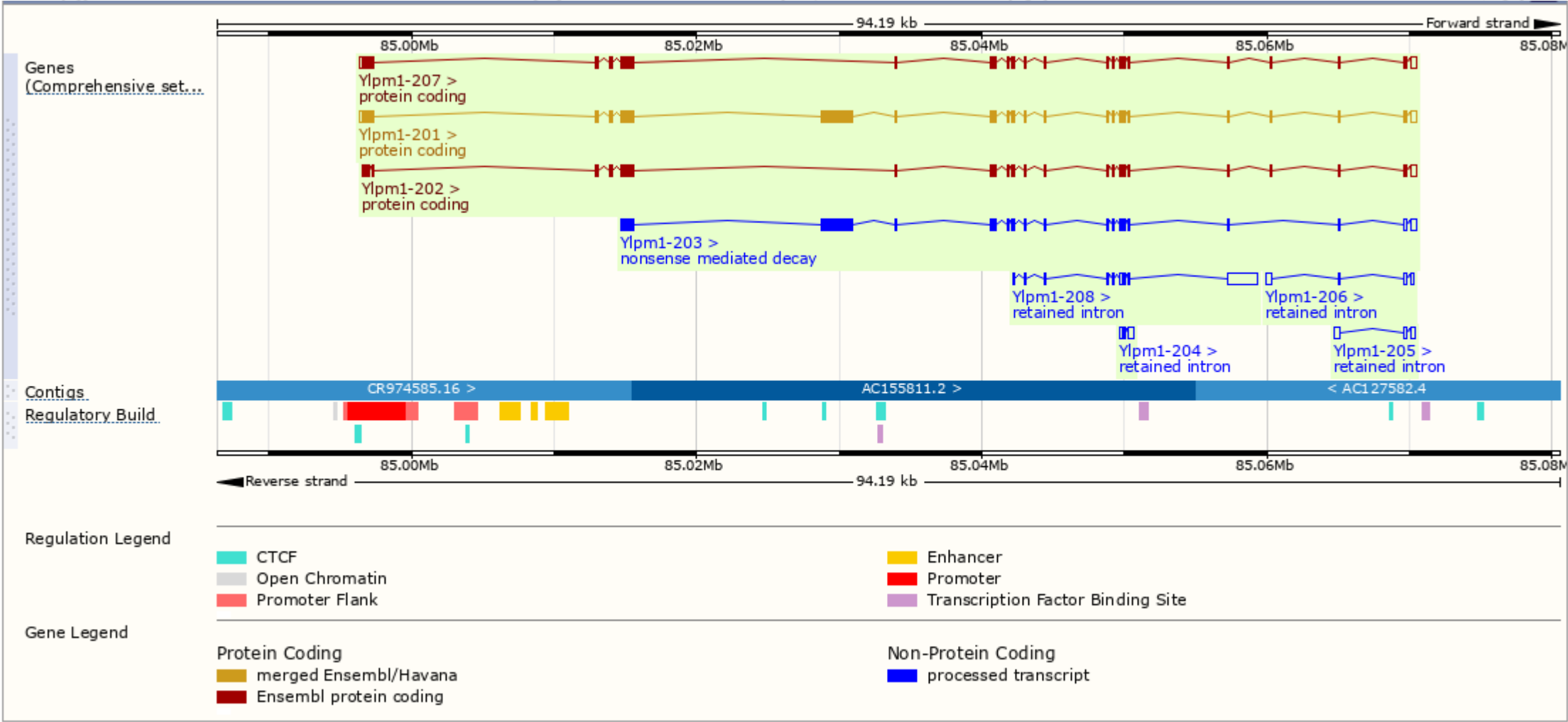|	
Official Symbol	Ylpm1 provided by MGI
Official Full Name	YLP motif containing 1 provided by MGI
Primary source	MGI:MGI:1926195
See related	Ensembl:ENSMUSG00000021244
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	ZAP; Zap3; A930013E17Rik
Expression	Ubiquitous expression in testis adult (RPKM 14.2), CNS E11.5 (RPKM 12.5) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

The gene has 8 transcripts, and all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags		
Ylpm1-201	ENSMUST00000021670.14	7003	2139aa	Protein coding	CCDS49114	D3YWX2	TSL:5	GENCODE basic	APPRIS P2
Ylpm1-207	ENSMUST00000168977.7	4893	1433aa	Protein coding	-	E9Q803	TSL:5	GENCODE basic	APPRIS ALT2
Ylpm1-202	ENSMUST00000101202.9	4605	1386aa	Protein coding	-	Q9R0I7	TSL:5	GENCODE basic	APPRIS ALT2
Ylpm1-203	ENSMUST00000164558.7	5416	1577aa	Nonsense mediated decay	-	F6YTL8	CDS 5' incomplete	TSL:5	
Ylpm1-208	ENSMUST00000169150.7	3002	No protein	Retained intron	-	-	TSL:1		
Ylpm1-205	ENSMUST00000166605.1	915	No protein	Retained intron	-	-	TSL:1		
Ylpm1-206	ENSMUST00000167838.7	812	No protein	Retained intron	-	-	TSL:3		
Ylpm1-204	ENSMUST00000165803.1	596	No protein	Retained intron	-	-	TSL:3		

The strategy is based on the design of *Ylpm1*-201 transcript,The transcription is shown below
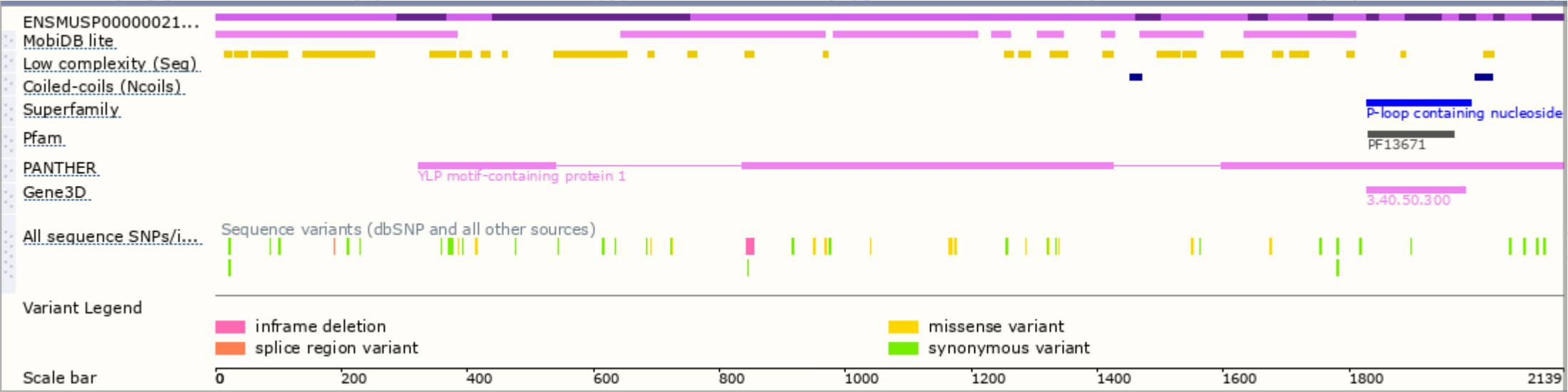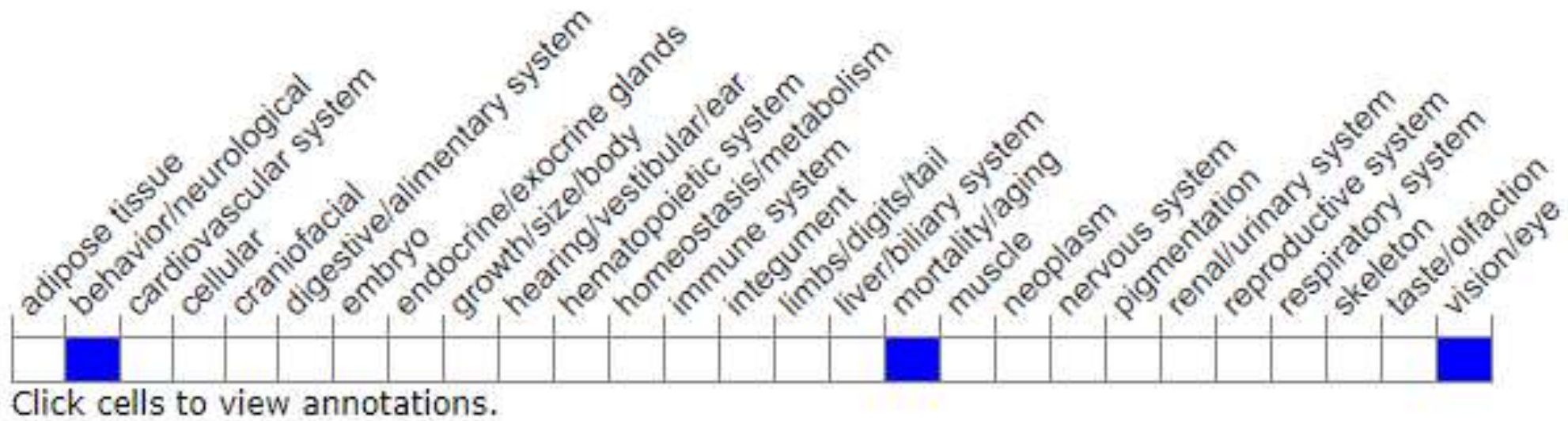
Genomic location distribution

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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