

Fmo1 Cas9-CKO Strategy

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Design Date:	2020-5-15

Project Overview

Project Name

Fmo1

Project type

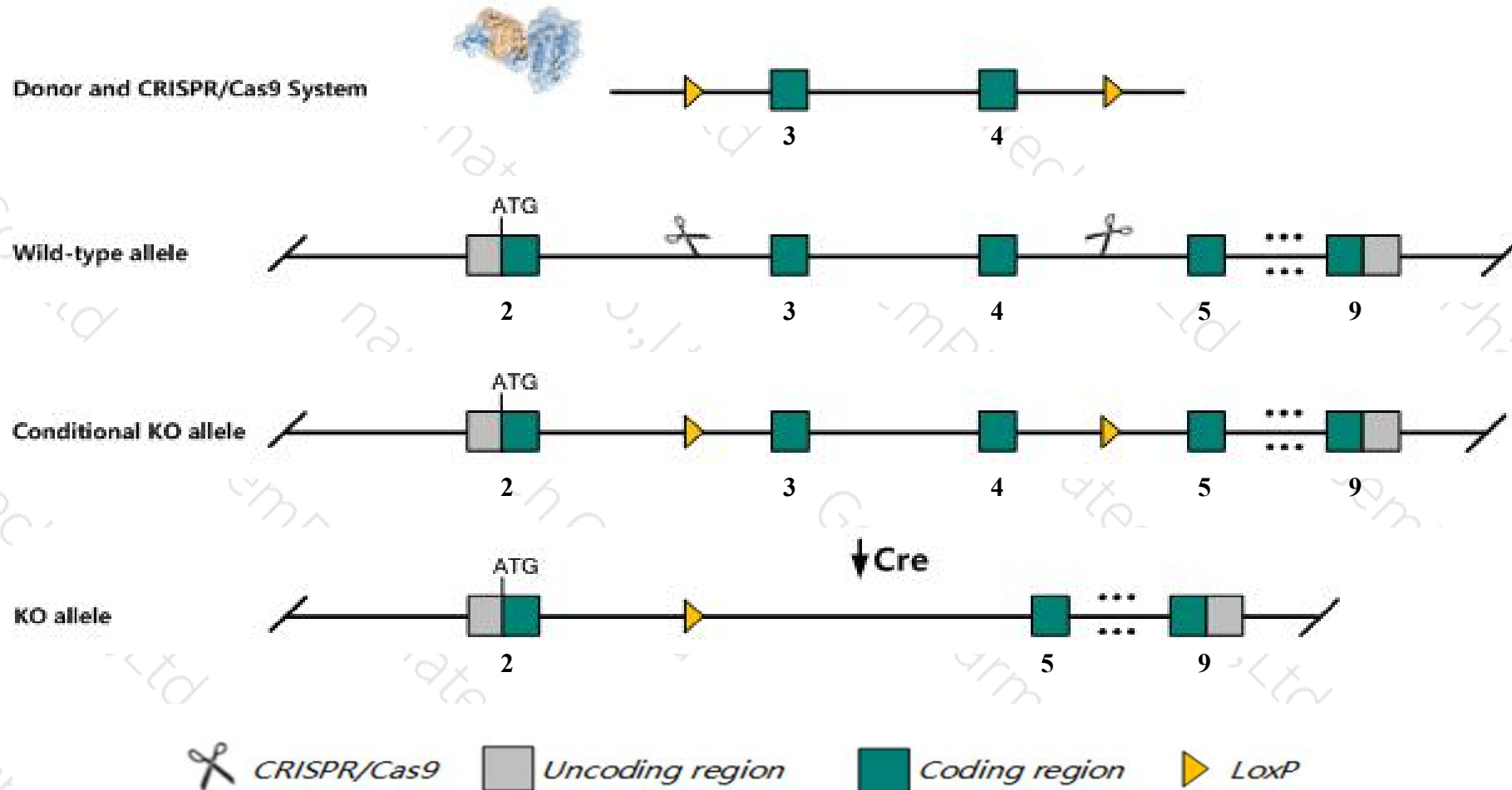
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fmo1* gene. The schematic diagram is as follows:



- The *Fmo1* gene has 8 transcripts. According to the structure of *Fmo1* gene, exon3-exon4 of *Fmo1-201* (ENSMUST00000046049.13) transcript is recommended as the knockout region. The region contains 352bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fmo1* 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.

Notice

- The *Fmo1* gene is located on the Chr1. 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)

Fmo1 flavin containing monooxygenase 1 [Mus musculus (house mouse)]

Gene ID: 14261, updated on 13-Mar-2020

Summary



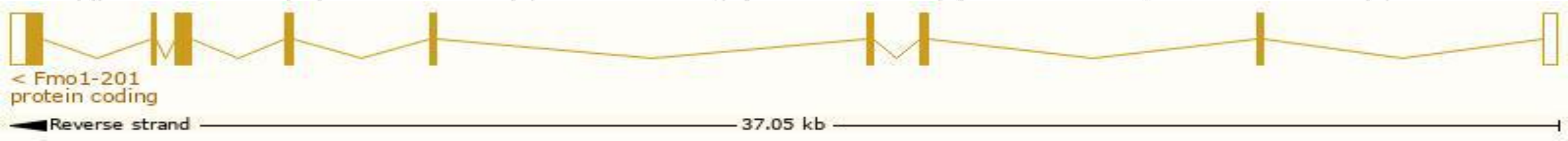
Official Symbol	Fmo1 provided by MGI
Official Full Name	flavin containing monooxygenase 1 provided by MGI
Primary source	MGI:MGI:1310002
See related	Ensembl:ENSMUSG00000040181
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Expression	Biased expression in kidney adult (RPKM 131.1), placenta adult (RPKM 107.8) and 9 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

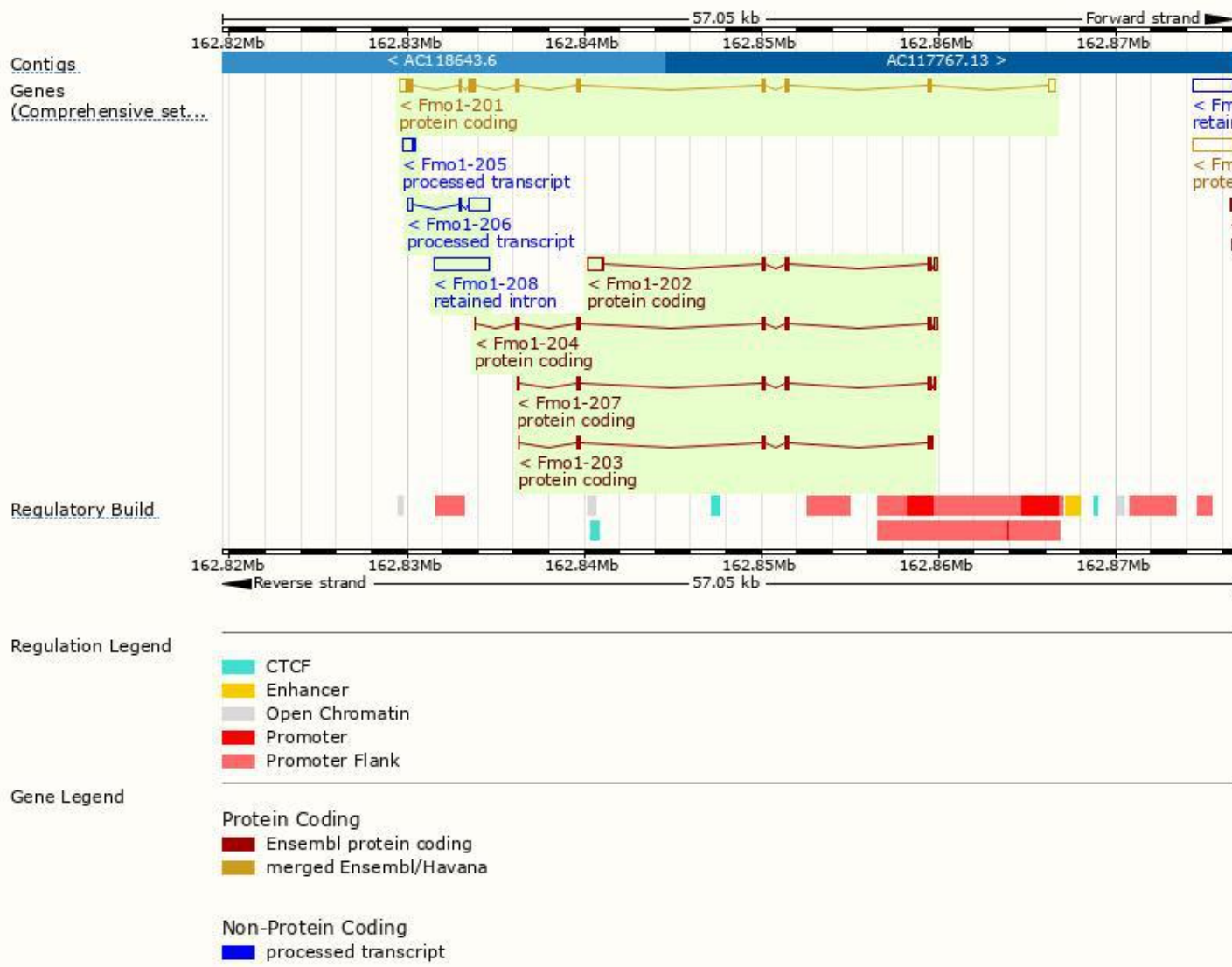
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fmo1-201	ENSMUST0000046049.13	2388	532aa	Protein coding	CCDS15424	P50285	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
Fmo1-202	ENSMUST00000111518.2	1506	182aa	Protein coding	-	Q8C9C1	TSL:1 GENCODE basic
Fmo1-204	ENSMUST00000134098.7	1077	303aa	Protein coding	-	Q3UNX7	CDS 3' incomplete TSL:1
Fmo1-203	ENSMUST00000131058.7	821	221aa	Protein coding	-	D3Z0T2	CDS 3' incomplete TSL:2
Fmo1-207	ENSMUST00000193078.5	750	229aa	Protein coding	-	A0A0A6YVP9	CDS 3' incomplete TSL:5
Fmo1-206	ENSMUST00000143902.1	1481	No protein	Processed transcript	-	-	TSL:2
Fmo1-205	ENSMUST00000136120.1	584	No protein	Processed transcript	-	-	TSL:3
Fmo1-208	ENSMUST00000193766.1	3106	No protein	Retained intron	-	-	TSL:NA

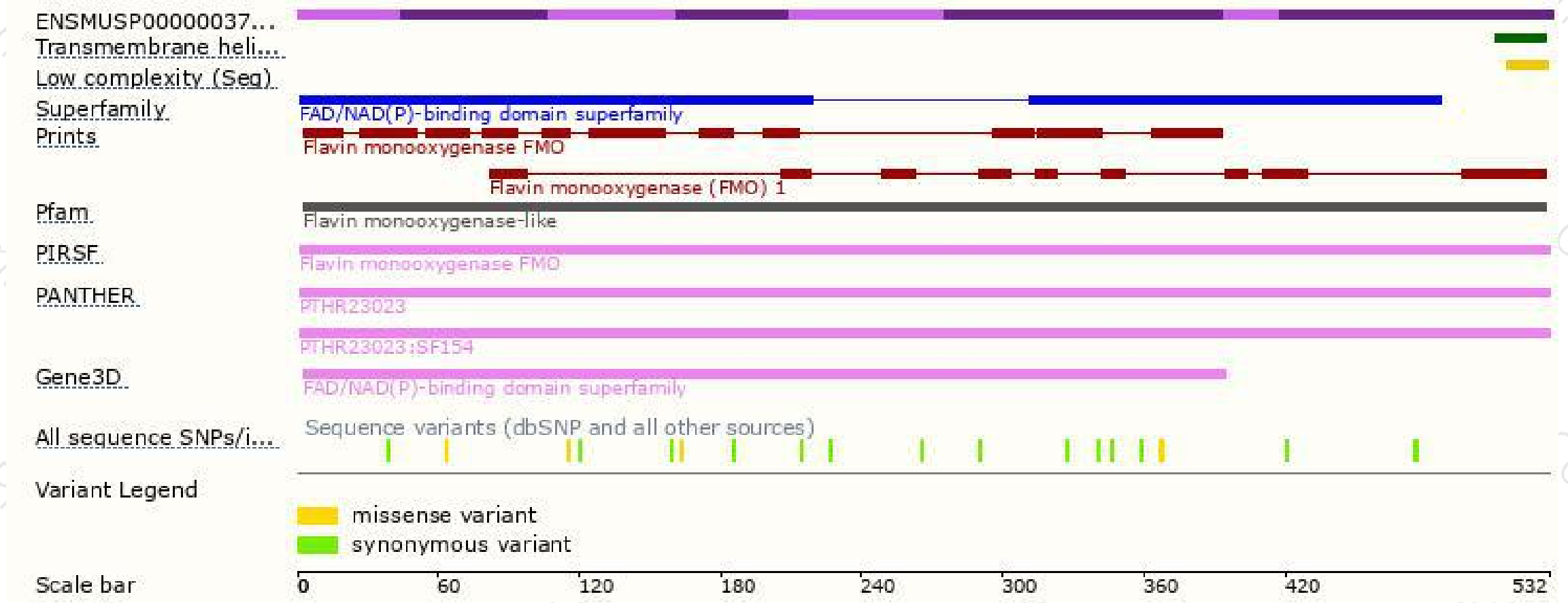
The strategy is based on the design of *Fmo1-201* transcript,the transcription is shown below



Genomic location distribution



Protein domain



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

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