Cyp2e1 Cas9-CKO Strategy

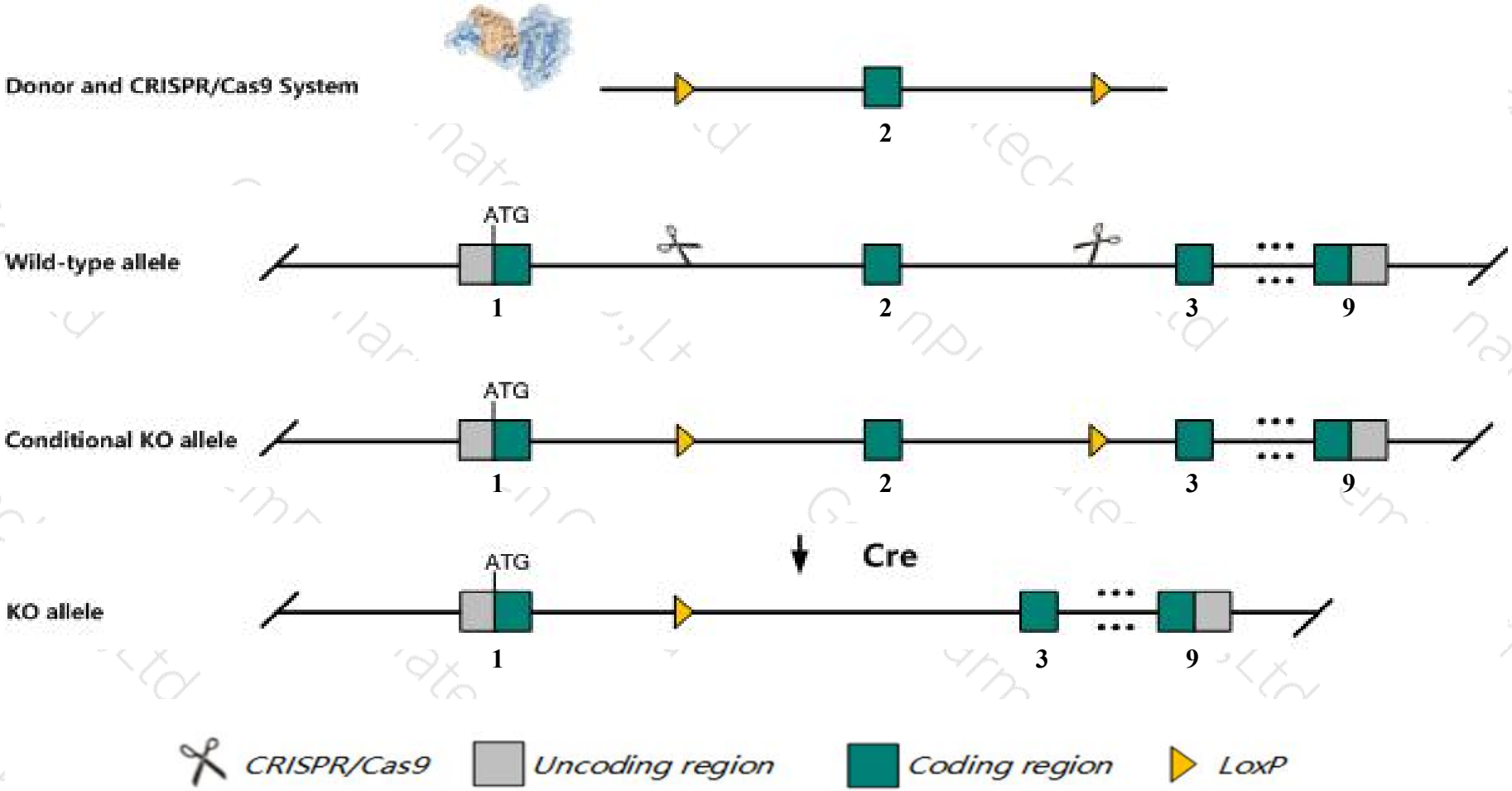
Designer: Lixin Lv

Project Overview

Project Name	***Cyp2e1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cyp2e1* gene. The schematic diagram is as follows:



Technical routes

- The *Cyp2e1* gene has 4 transcripts. According to the structure of *Cyp2e1* gene, exon2 of *Cyp2e1-201* (ENSMUST00000026552.8) transcript is recommended as the knockout region.The region contains 160bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Cyp2e1* 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

- According to the existing MGI data,Mice homozygous for a null allele exhibit altered responses to xenobiotics including decreased urethane-induced tumors and allylnitrile- or acetamenophen-associated mortality but increased allylnitrile-induced vestibular function loss.

- The *Cyp2e1* gene is located on the Chr7. 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）

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Cyp2e1 cytochrome P450, family 2, subfamily e, polypeptide 1 [Mus musculus (house mouse)]

Gene ID: 13106, updated on 19-Mar-2019

Summary

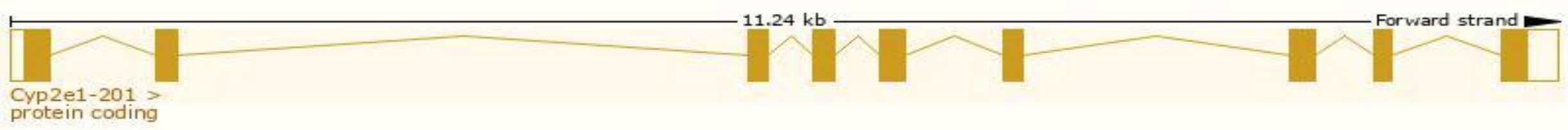
Official Symbol	Cyp2e1 provided by MGI
Official Full Name	cytochrome P450, family 2, subfamily e, polypeptide 1 provided by MGI
Primary source	MGI:MGI:88607
See related	Ensembl:ENSMUSG00000025479
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	CYPIIE1, Cyp2e
Expression	Biased expression in liver adult (RPKM 981.7), subcutaneous fat pad adult (RPKM 122.6) and 2 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

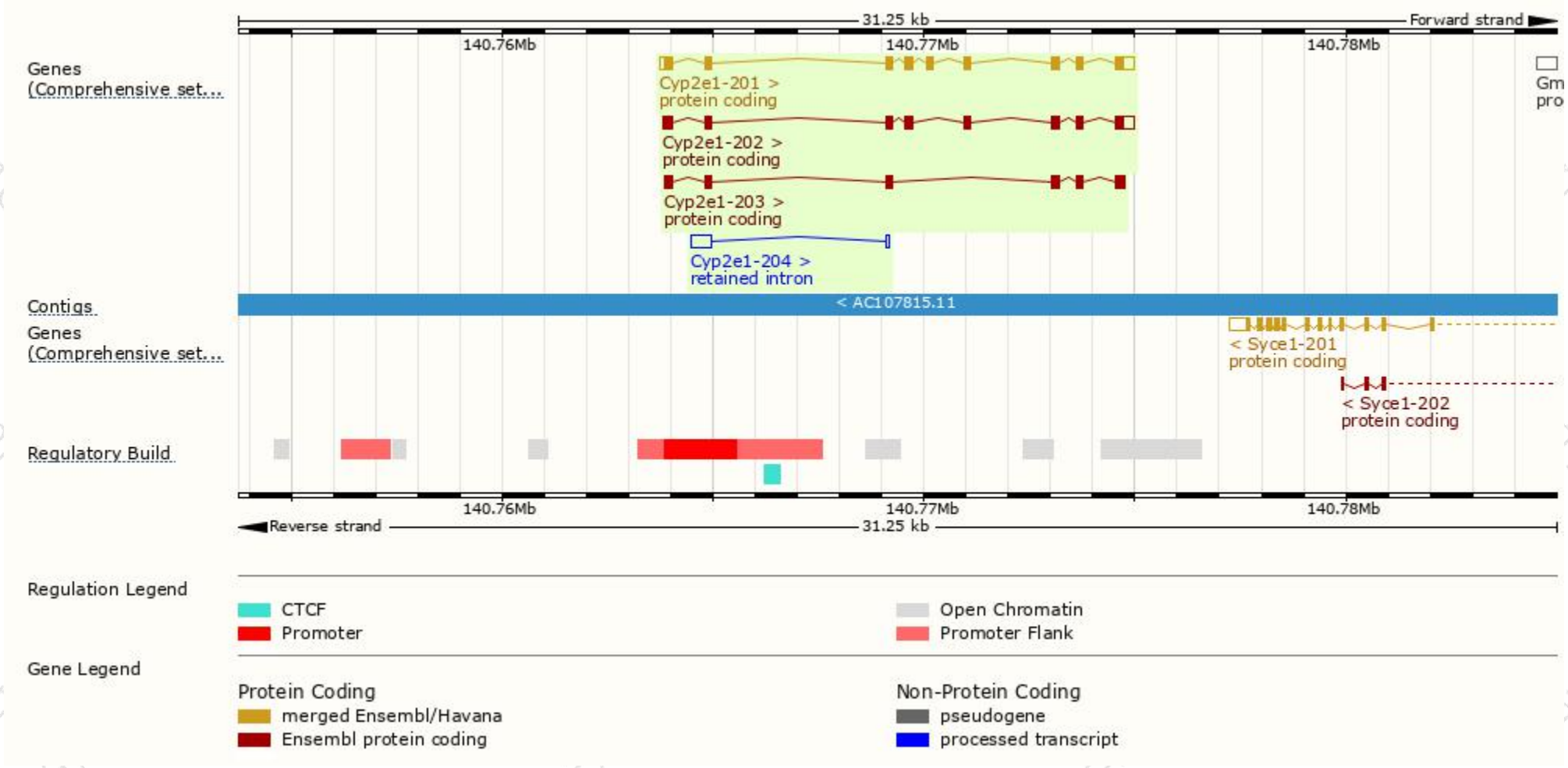
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cyp2e1-201	ENSMUST00000026552.8	1833	493aa	Protein coding	CCDS21985	Q05421	TSL:1 GENCODE basic APPRIS P1
Cyp2e1-202	ENSMUST00000209253.1	1582	434aa	Protein coding	-	A0A1B0GSV7	TSL:5 GENCODE basic
Cyp2e1-203	ENSMUST00000210235.1	1012	333aa	Protein coding	-	Q0PGA1	TSL:1 GENCODE basic
Cyp2e1-204	ENSMUST00000210403.1	569	No protein	Retained intron	-	-	TSL:2

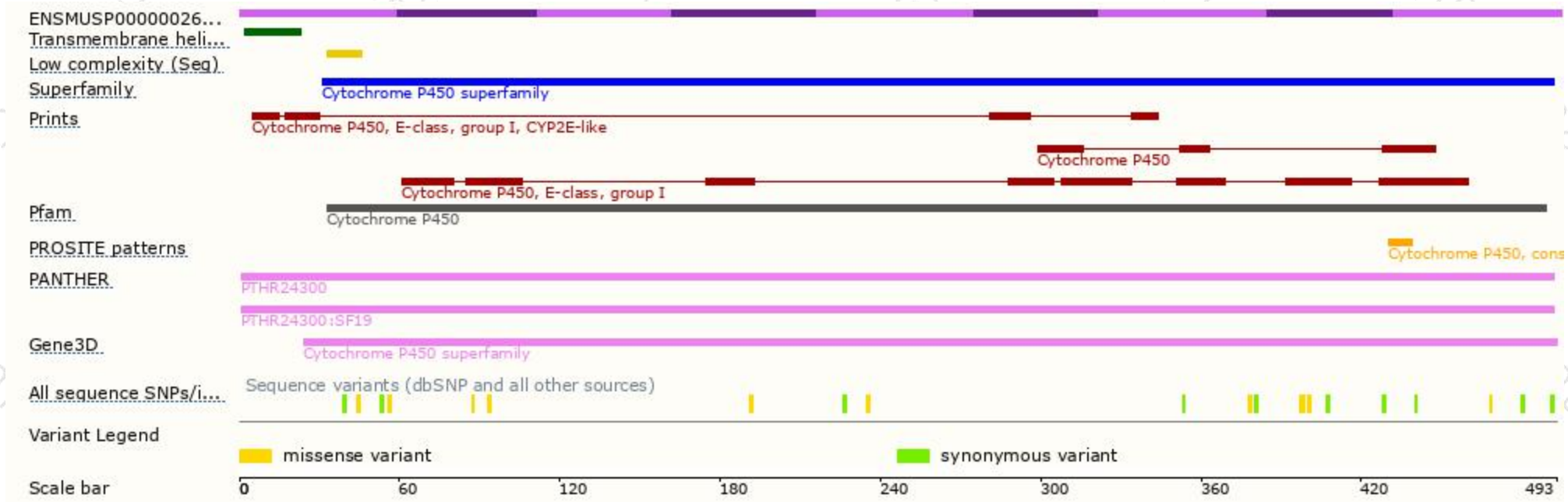
The strategy is based on the design of *Cyp2e1-201* transcript,The transcription is shown below



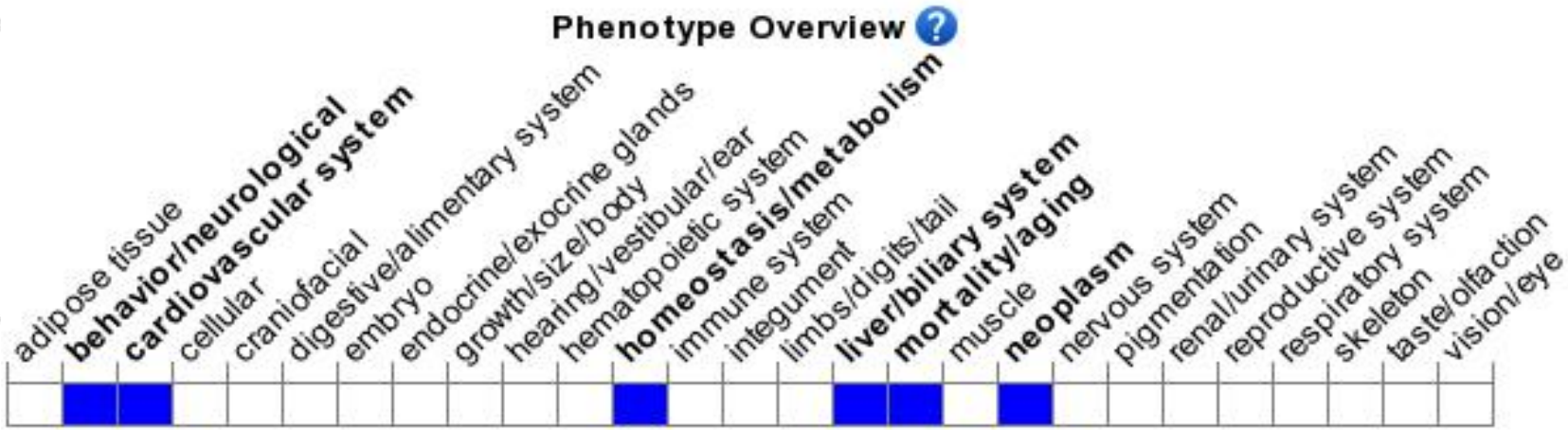
Genomic location distribution



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/).

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

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