Cyp1a1 Cas9-KO Strategy

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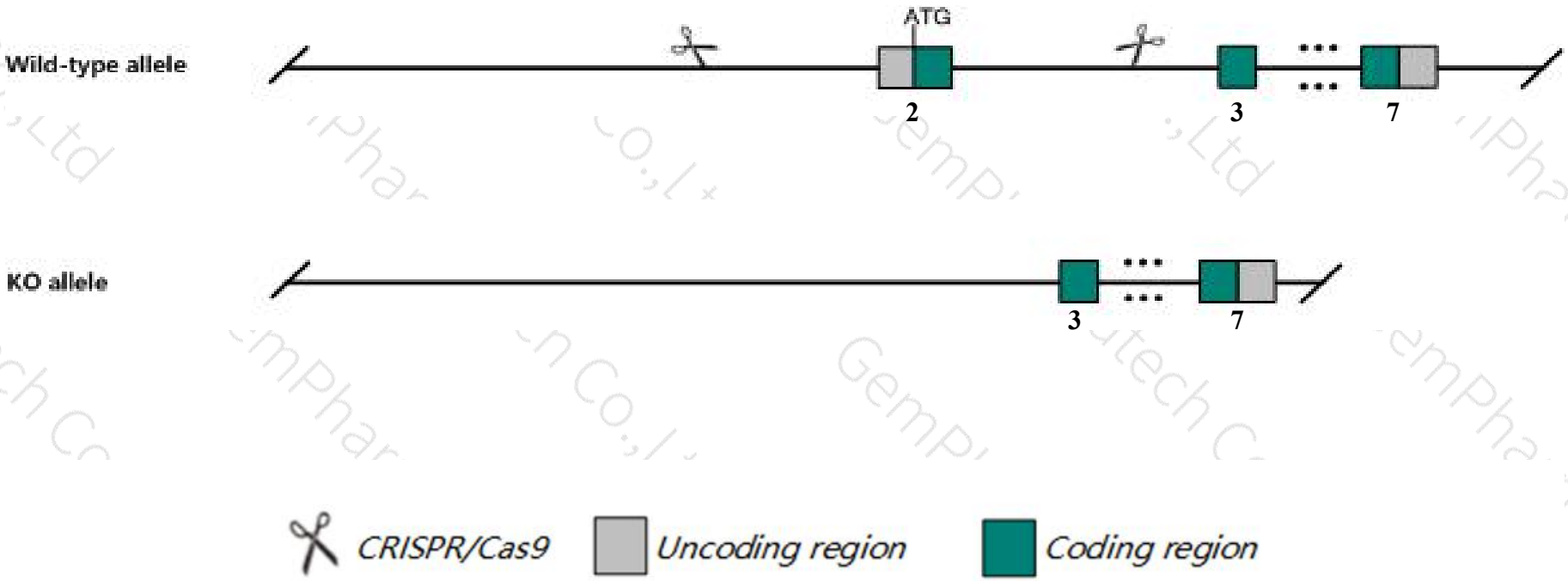
Project Overview

Project Name	***Cyp1a1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cyp1a1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Cyp1a1* gene has 2 transcripts. According to the structure of *Cyp1a1* gene, exon2 of *Cyp1a1-202* (ENSMUST00000216433.1) transcript is recommended as the knockout region.The region contains start codon ATG. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Cyp1a1* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

- According to the existing MGI data,Mice homozygous for a null allele display resitance to some signs of TCDD induced toxicity but do not display any gross abnormalities in the abscence of treatment.

- The *Cyp1a1* gene is located on the Chr9. 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）

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Cyp1a1 cytochrome P450, family 1, subfamily a, polypeptide 1 [Mus musculus (house mouse)]

Gene ID: 13076, updated on 19-Mar-2019

Summary

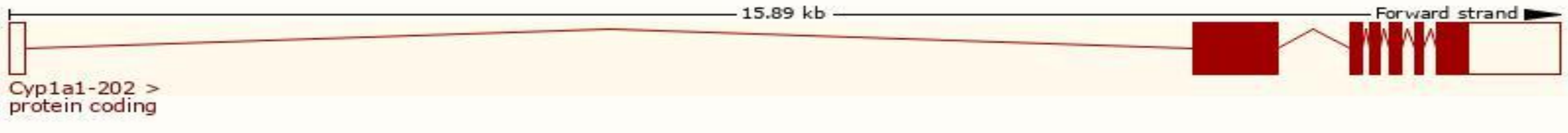
Official Symbol	Cyp1a1 provided by MGI
Official Full Name	cytochrome P450, family 1, subfamily a, polypeptide 1 provided by MGI
Primary source	MGI:MGI:88588
See related	Ensembl:ENSMUSG00000032315
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AHH, AHRR, CP11, CYPIA1, P450-1
Expression	Biased expression in liver adult (RPKM 18.0), lung adult (RPKM 13.7) and 2 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

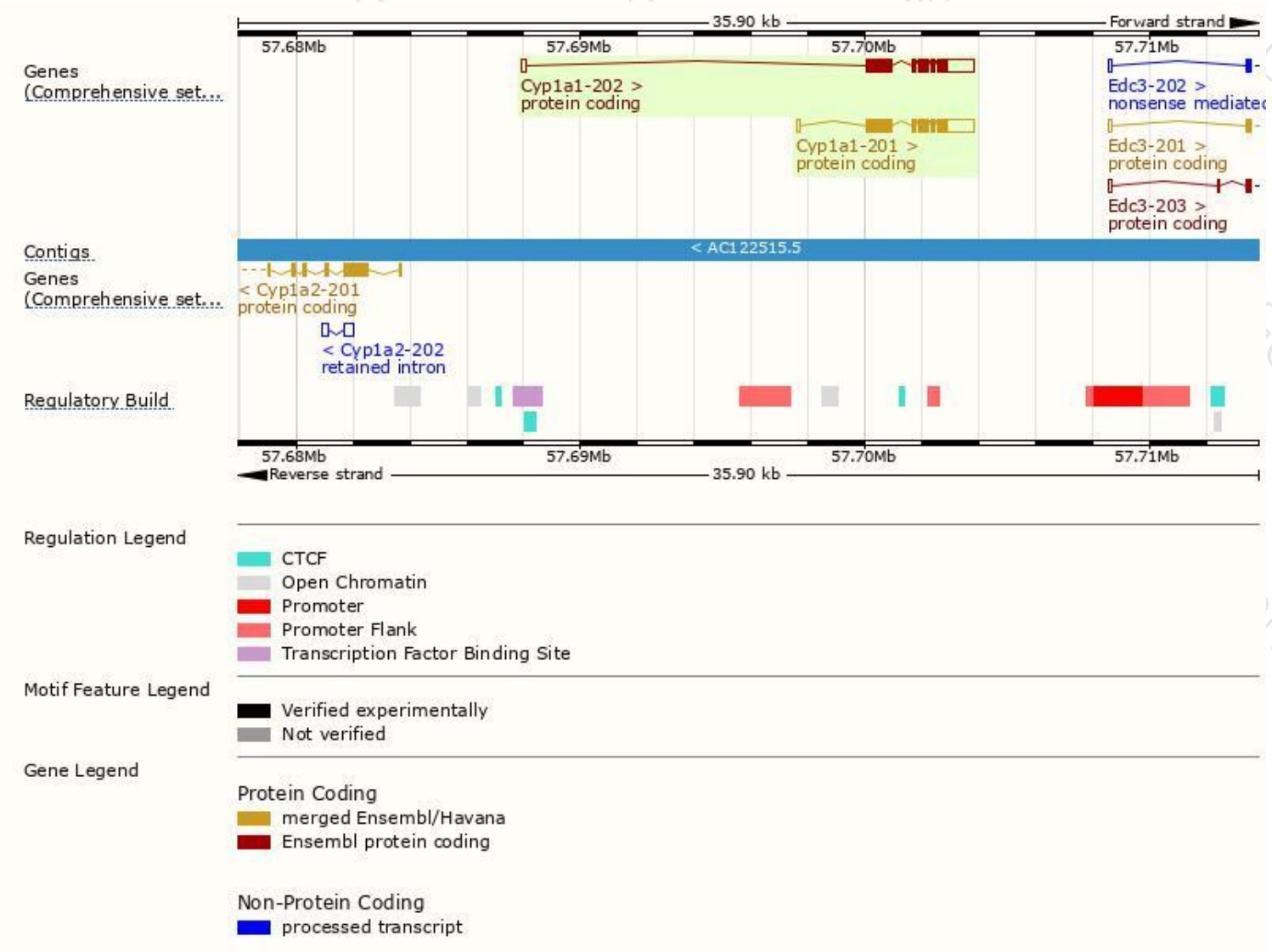
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cyp1a1-202	ENSMUST00000216433.1	2697	524aa	Protein coding	CCDS23230	P00184 Q05A20	TSL:1 GENCODE basic APPRIS P1
Cyp1a1-201	ENSMUST00000034865.5	2621	524aa	Protein coding	CCDS23230	P00184 Q05A20	TSL:1 GENCODE basic APPRIS P1

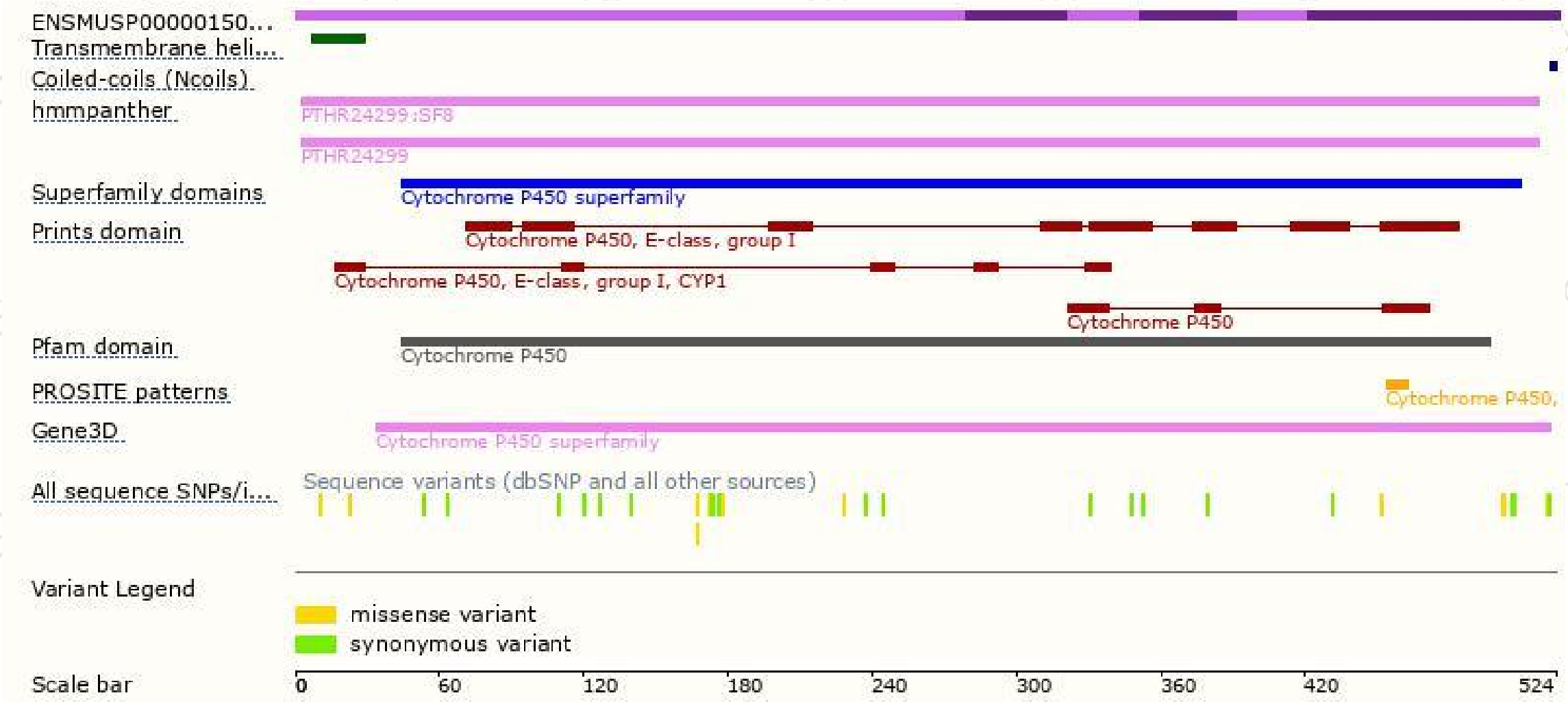
The strategy is based on the design of *Cyp1a1-202* transcript,The transcription is shown below



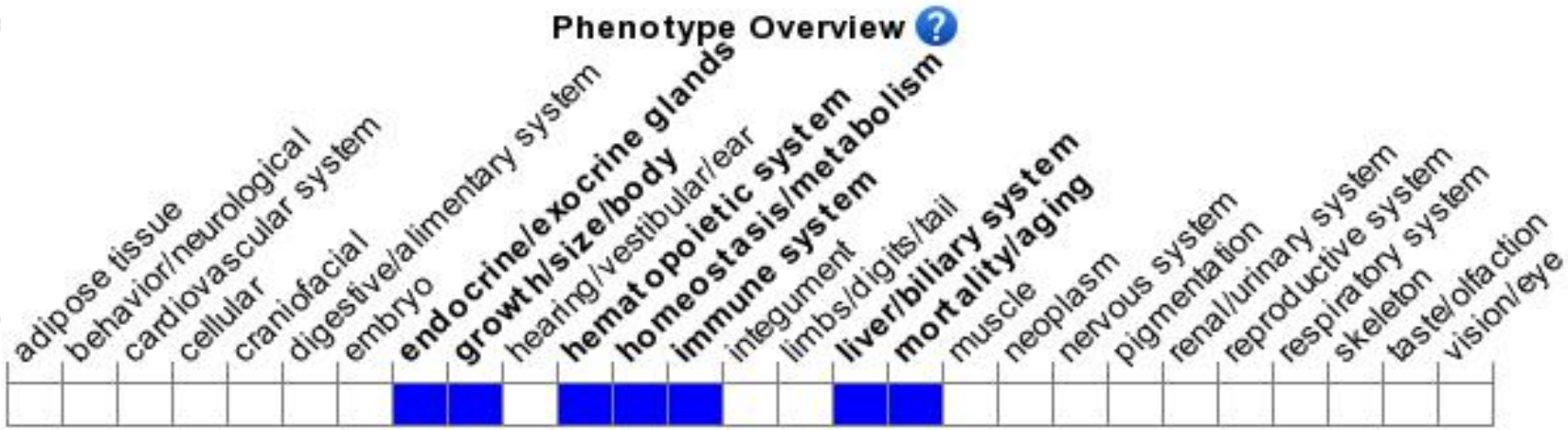
Genomic location distribution



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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