

# *Cyp11b2* Cas9-KO Strategy

Designer: Xueting Zhang

Reviewer: Yanhua Shen

Date: 2020-4-8

# Project Overview



**Project Name**

*Cyp11b2*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cyp11b2* gene. The schematic diagram is as follows:



# Technical routes

- The *Cyp11b2* gene has 2 transcripts. According to the structure of *Cyp11b2* gene, exon3-exon9 of *Cyp11b2-201* (ENSMUST00000167634.1) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cyp11b2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a null allele exhibit some postnatal lethality, altered blood chemistry, hypotension, and abnormal adrenal cortex morphology.
- The N-terminal of *Cyp11b2* gene will remain several amino acids, it may remain the partial function of *Cyp11b2* gene.
- The *Cyp11b2* gene is located on the Chr15. 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)

## Cyp11b2 cytochrome P450, family 11, subfamily b, polypeptide 2 [Mus musculus (house mouse)]

Gene ID: 13072, updated on 13-Mar-2020

### Summary



**Official Symbol** Cyp11b2 provided by [MGI](#)

**Official Full Name** cytochrome P450, family 11, subfamily b, polypeptide 2 provided by [MGI](#)

**Primary source** [MGI:MGI:88584](#)

**See related** [Ensembl:ENSMUSG00000022589](#)

**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** ALDOS, Cpn2, Cyp11b, Cyp11b-2

**Expression** Restricted expression toward adrenal adult (RPKM 151.7)[See more](#)

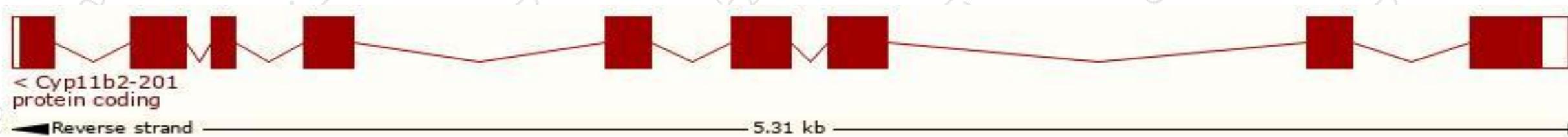
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

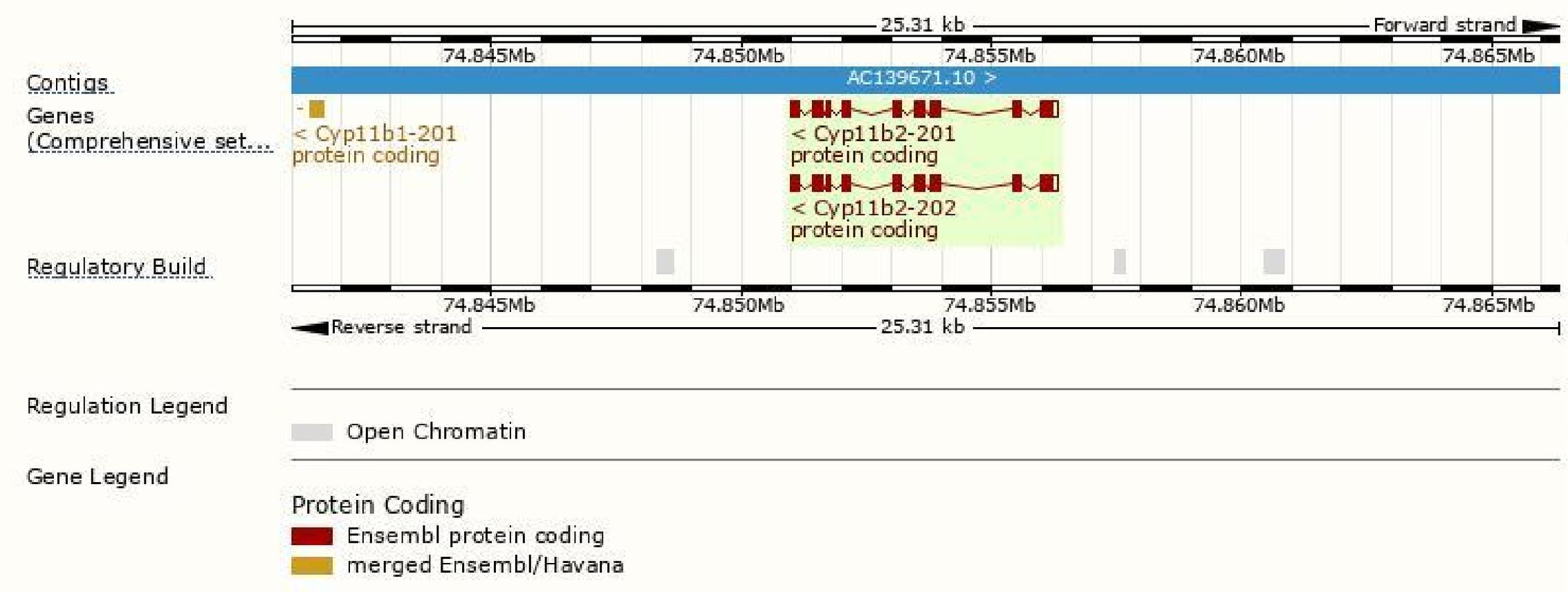
The gene has 2 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cyp11b2-201	<a href="#">ENSMUST00000167634.1</a>	1625	<a href="#">502aa</a>	Protein coding	<a href="#">CCDS27536</a>	<a href="#">G3UWE4</a>	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 P2
Cyp11b2-202	<a href="#">ENSMUST00000238900.1</a>	1625	<a href="#">500aa</a>	Protein coding	-	<a href="#">P15539</a>	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 ALT2

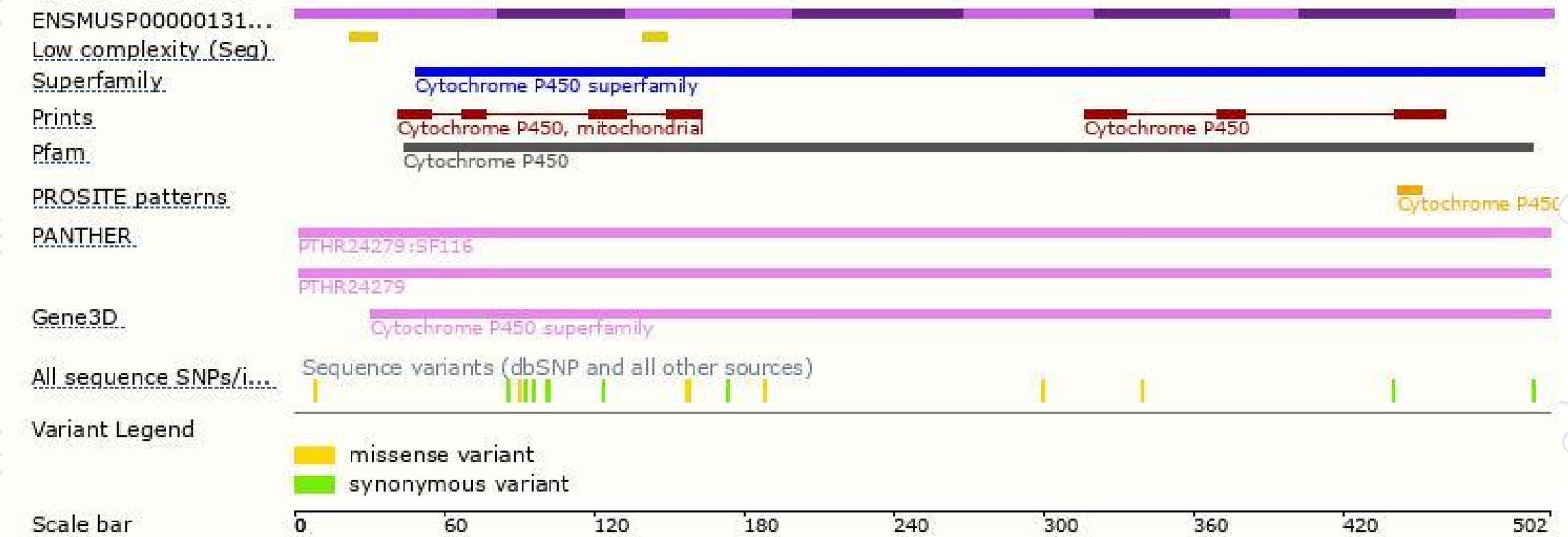
The strategy is based on the design of *Cyp11b2-201* transcript, The transcription is shown below



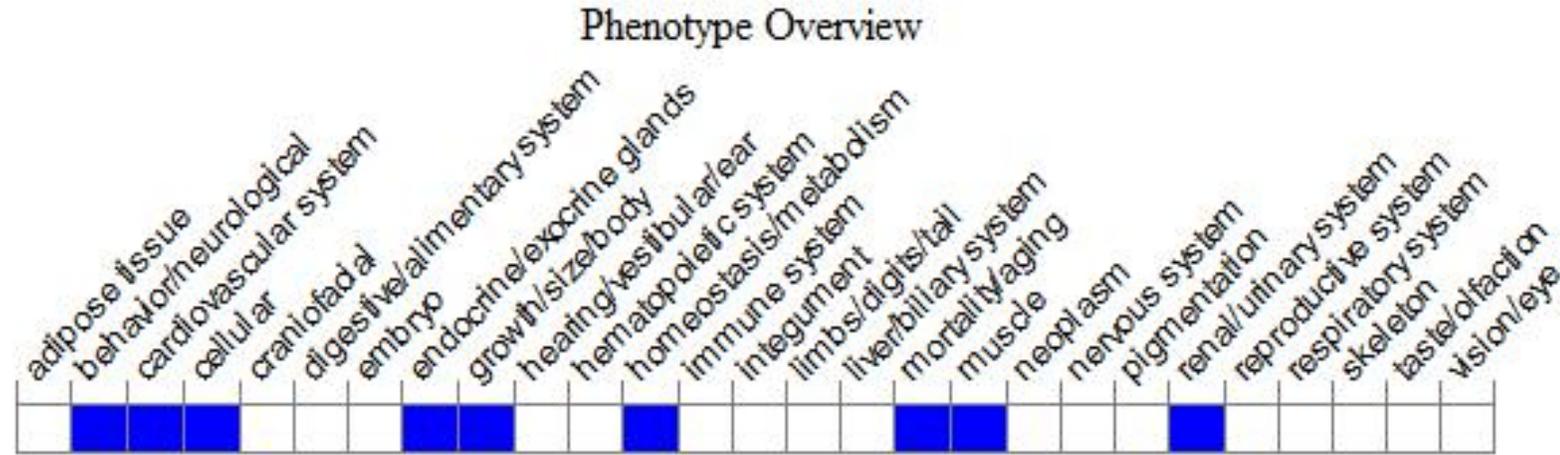
# Genomic location distribution



# 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, Mice homozygous for a null allele exhibit some postnatal lethality, altered blood chemistry, hypotension, and abnormal adrenal cortex morphology.

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

Tel: 400-9660890

