GemPharmatech™

Por Cas9-CKO Strategy

Designer: Qian Chen

Reviewer: Xueting Zhang

Design Date: 2023-9-19

Overview

Target Gene Name

- Por

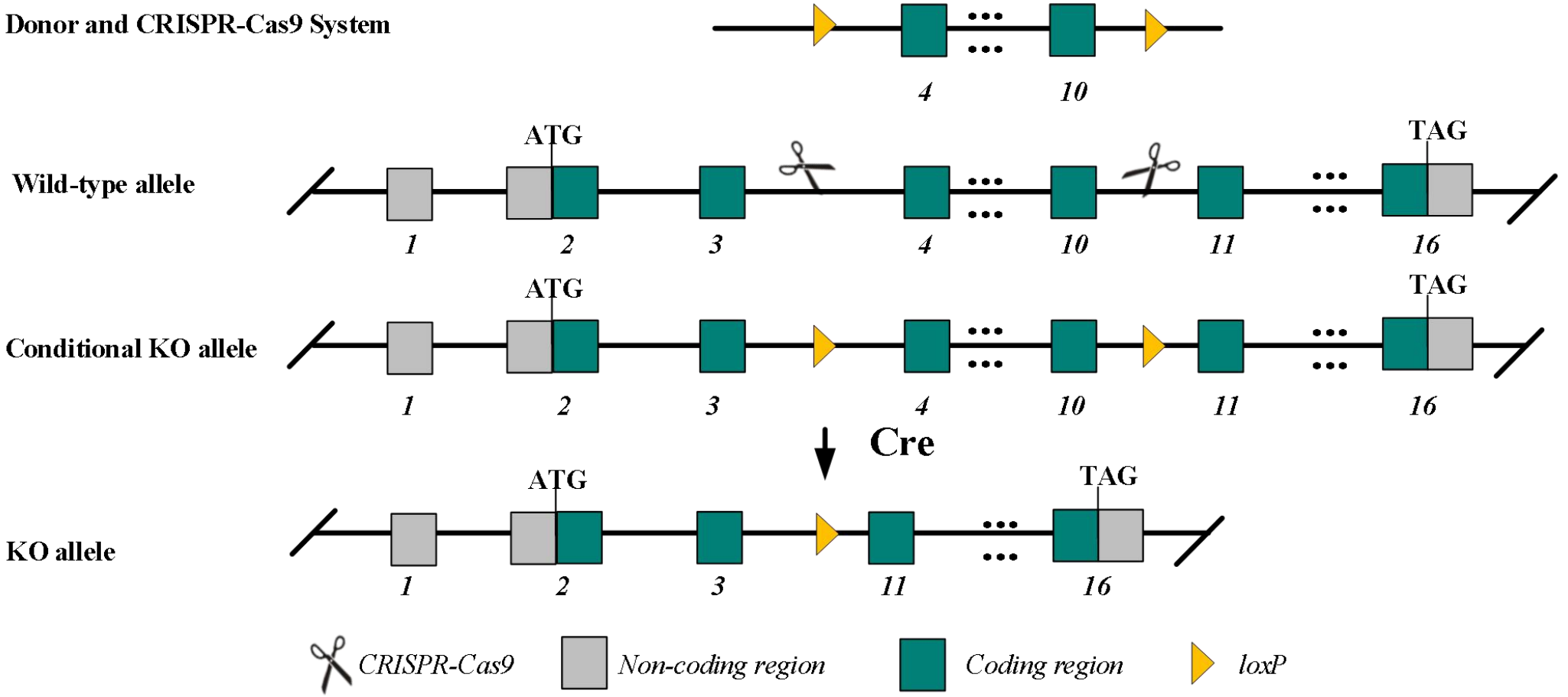
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Por* gene.

Technical Information

- The *Por* gene has 9 transcripts. According to the structure of *Por* gene, exon 4-exon 10 of *Por*-201 (ENSMUST00000005651.13) transcript is recommended as the knockout region. The region contains 829 bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Por* 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- 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.

Gene Information

Por cytochrome p450 oxidoreductase [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 18984, updated on 7-Sep-2023

Summary

Official Symbol	Por provided by MGI
Official Full Name	cytochrome p450 oxidoreductase provided by MGI
Primary source	MGI:MGI:97744
See related	Ensembl:ENSMUSG00000005514 AllianceGenome:MGI:97744
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	CPR; CYPOR; P450R; 4933424M13Rik
Summary	Enables oxidoreductase activity. Predicted to be involved in several processes, including cellular organofluorine metabolic process; negative regulation of hydrolase activity; and positive regulation of steroid biosynthetic process. Predicted to be located in membrane and mitochondrion. Predicted to be active in cytosol. Is expressed in several structures, including alimentary system; limb; metanephros; nervous system; and sensory organ. Human ortholog(s) of this gene implicated in congenital adrenal hyperplasia and cytochrome P450 oxidoreductase deficiency. Orthologous to human POR (cytochrome p450 oxidoreductase). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in adrenal adult (RPKM 159.7), lung adult (RPKM 143.3) and 27 other tissues See more
Orthologs	human all

NEW **Try the new Gene table**

Try the new Transcript table

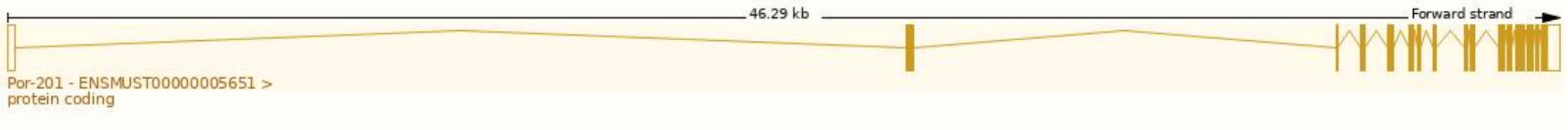
Source: https://www.ncbi.nlm.nih.gov/

Transcript Information

The gene has 9 transcripts,all transcripts are shown below:

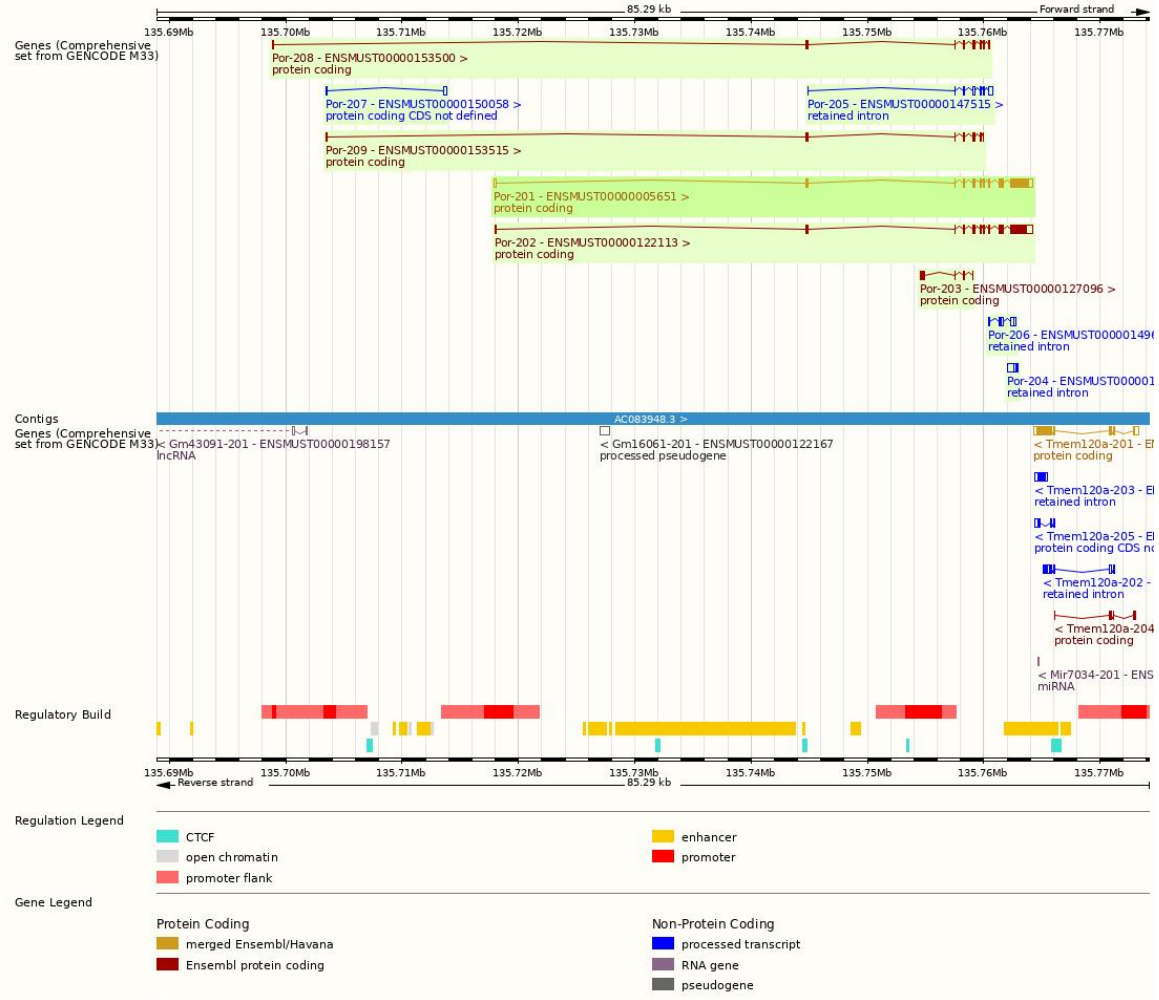
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000005651.13	Por-201	2636	678aa	Protein coding	CCDS39318	P37040	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1
ENSMUST00000122113.8	Por-202	2606	649aa	Protein coding		Q05DV1	GENCODE basic TSL:2
ENSMUST00000153500.8	Por-208	918	273aa	Protein coding		E9Q997	TSL:3 CDS 3' incomplete
ENSMUST00000153515.8	Por-209	747	219aa	Protein coding		E9PVT9	TSL:3 CDS 3' incomplete
ENSMUST00000127096.2	Por-203	505	168aa	Protein coding		F6R7H8	TSL:5 CDS 5' and 3' incomplete
ENSMUST00000150058.2	Por-207	344	No protein	Protein coding CDS not defined		-	TSL:3
ENSMUST00000147515.2	Por-205	918	No protein	Retained intron		-	TSL:2
ENSMUST00000132084.2	Por-204	674	No protein	Retained intron		-	TSL:2
ENSMUST00000149684.2	Por-206	673	No protein	Retained intron		-	TSL:2

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



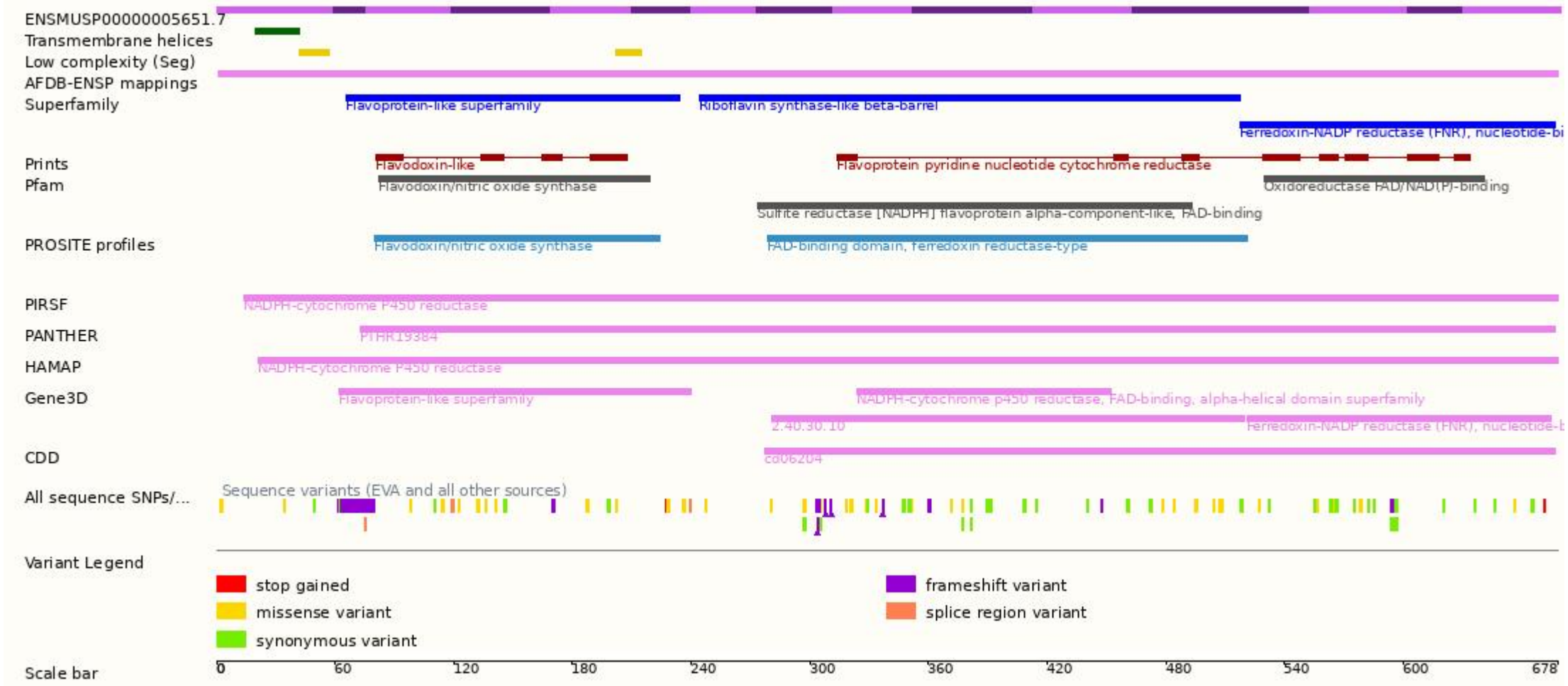
Source: https://www.ensembl.org

Genomic Information



Source: : https://www.ensembl.org

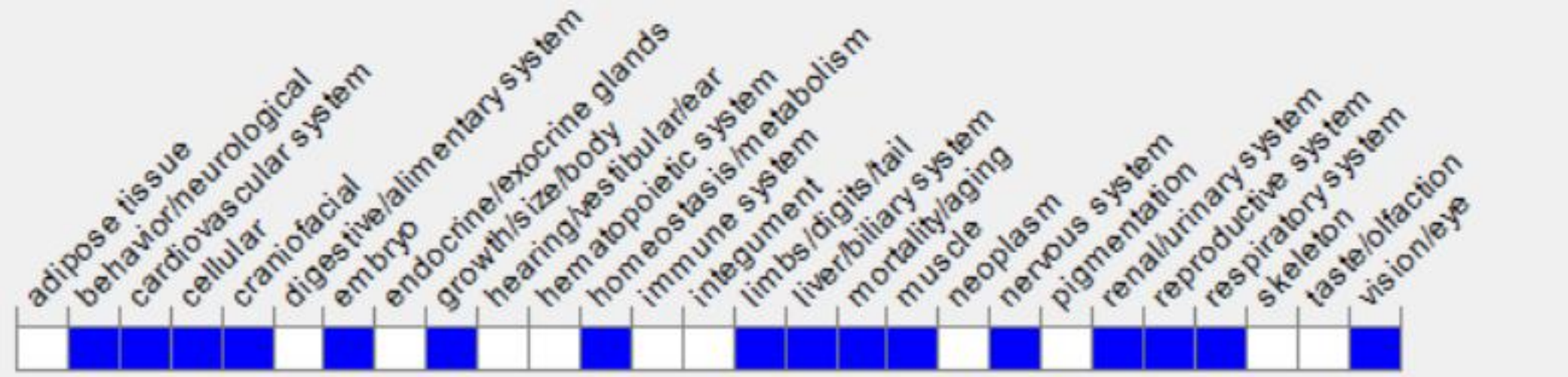
Protein Information



GemPharmatech™

Source: : https://www.ensembl.org

Mouse Phenotype Information (MGI)



- Homozygotes for targeted null mutations exhibit defects of the neural tube, eye, heart, and limbs, retarded growth, and prenatal lethality. Liver-specific knockouts exhibit increased liver weight, hepatic lipidosis, and impaired drug metabolism.

Source: https://www.informatics.jax.org

Important Information

- Homozygotes for targeted null mutations exhibit defects of the neural tube, eye, heart, and limbs, retarded growth, and prenatal lethality. Liver-specific knockouts exhibit increased liver weight, hepatic lipidosis, and impaired drug metabolism.
- After cross cre, 76 amino acids remained at the N-terminus of this strategy, with unknown effects.
- The effect of the knock-out region on the *Por*-203 , *Por*-208 and *Por*-209 transcripts is unknown.
- *Por* is located on Chr5. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 the existing technology level.