

Cop1 Cas9-CKO Strategy

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Project Overview

Project Name

Cop1

Project type

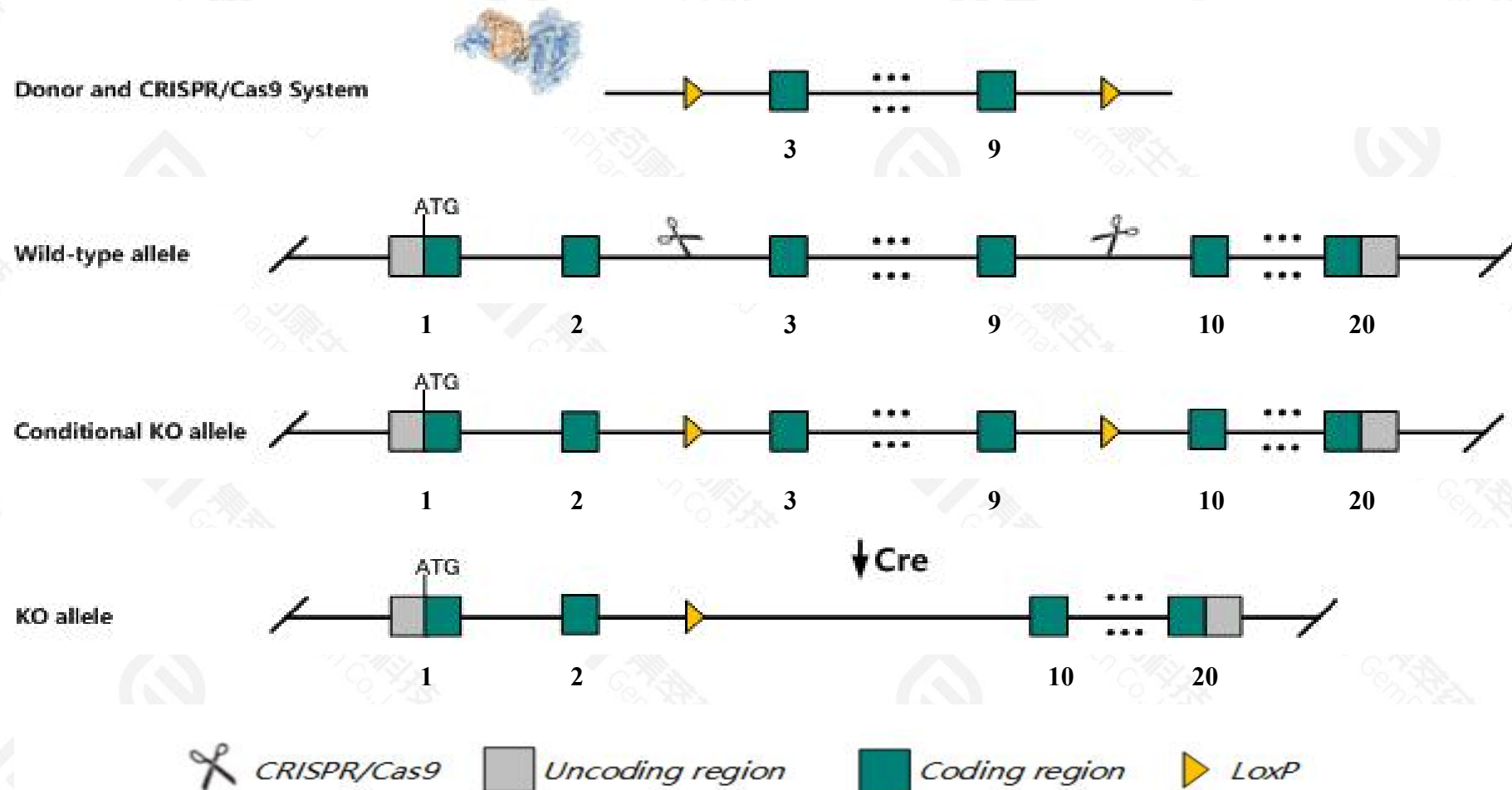
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cop1* gene. The schematic diagram is as follows:



- The *Cop1* gene has 13 transcripts. According to the structure of *Cop1* gene, exon3-exon9 of *Cop1-201*(ENSMUST00000076894.11) transcript is recommended as the knockout region. The region contains 559bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cop1* 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.

- According to the existing MGI data, mice homozygous for a conditional allele activated in prostate epithelial cells exhibit prostate gland hyperplasia and prostate intraepithelial neoplasia due to increased cell proliferation.
- Transcript *Cop1-202* may not be affected.
- The *Cop1* 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)

Cop1 COP1, E3 ubiquitin ligase [Mus musculus (house mouse)]

Gene ID: 26374, updated on 17-Dec-2020

Summary



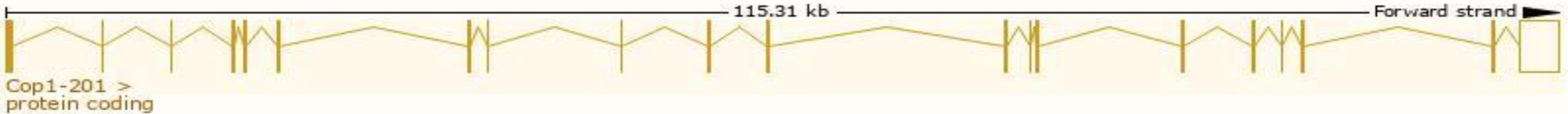
Official Symbol	Cop1 provided by MGI
Official Full Name	COP1, E3 ubiquitin ligase provided by MGI
Primary source	MGI:MGI:1347046
See related	Ensembl:ENSMUSG00000040782
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI316802, C80879, Co, Rfwd, Rfwd2
Expression	Ubiquitous expression in CNS E14 (RPKM 4.0), whole brain E14.5 (RPKM 4.0) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

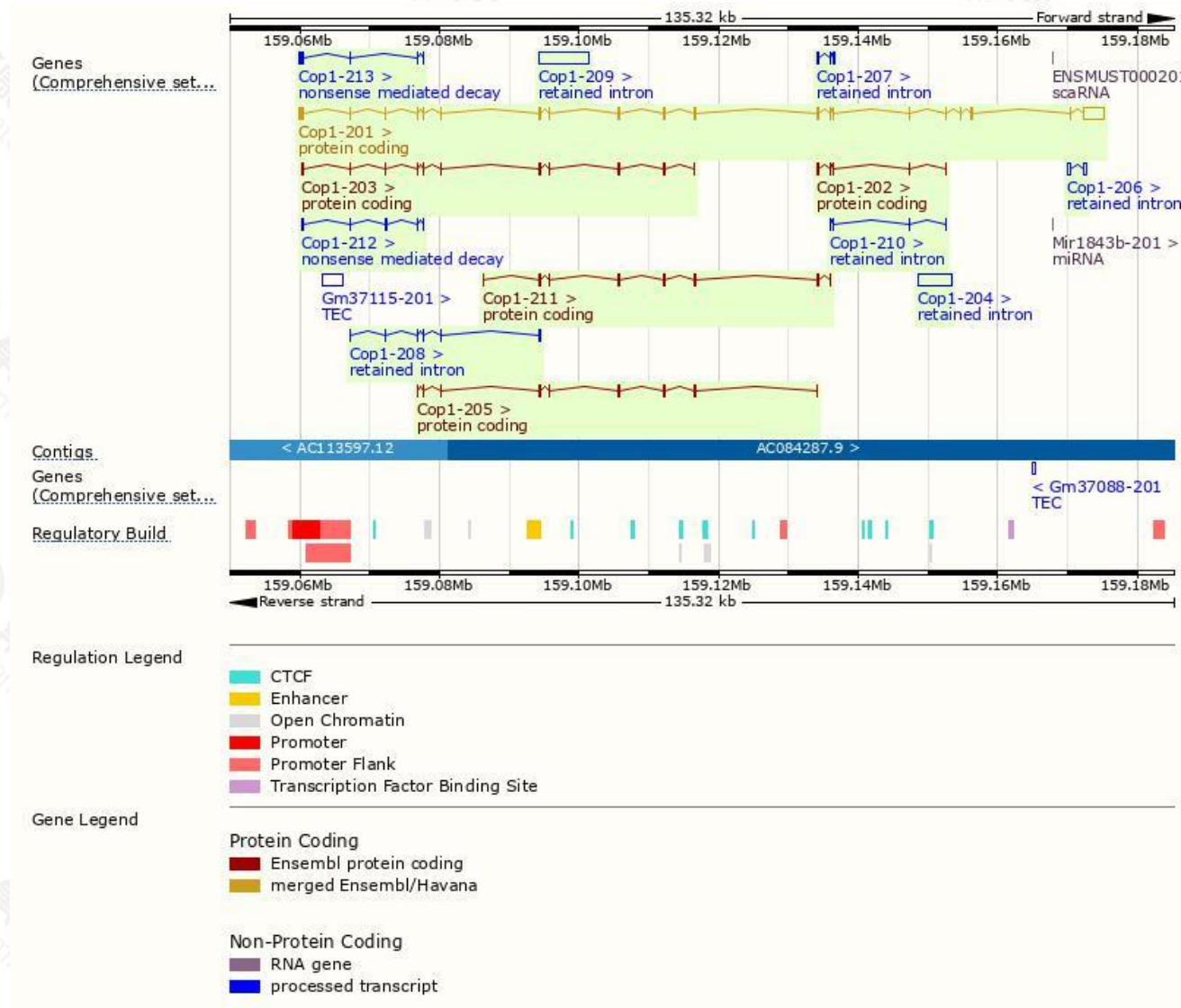
The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cop1-201	ENSMUST00000076894.11	5116	733aa	Protein coding	CCDS35745		TSL:1 , GENCODE basic , APPRIS P1 ,
Cop1-203	ENSMUST00000192215.6	1040	346aa	Protein coding	-		CDS 5' and 3' incomplete , TSL:5 ,
Cop1-211	ENSMUST00000195044.2	745	202aa	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Cop1-205	ENSMUST00000192762.6	680	227aa	Protein coding	-		CDS 5' and 3' incomplete , TSL:5 ,
Cop1-202	ENSMUST00000192044.2	464	155aa	Protein coding	-		CDS 5' and 3' incomplete , TSL:3 ,
Cop1-213	ENSMUST00000195800.6	753	159aa	Nonsense mediated decay	-		TSL:3 ,
Cop1-212	ENSMUST00000195554.6	545	60aa	Nonsense mediated decay	-		CDS 5' incomplete , TSL:3 ,
Cop1-209	ENSMUST00000194713.2	6999	No protein	Retained intron	-		TSL:NA ,
Cop1-204	ENSMUST00000192597.2	4961	No protein	Retained intron	-		TSL:NA ,
Cop1-206	ENSMUST00000192841.2	776	No protein	Retained intron	-		TSL:2 ,
Cop1-208	ENSMUST00000194049.2	655	No protein	Retained intron	-		TSL:5 ,
Cop1-210	ENSMUST00000194798.2	473	No protein	Retained intron	-		TSL:3 ,
Cop1-207	ENSMUST00000193776.2	392	No protein	Retained intron	-		TSL:2 ,

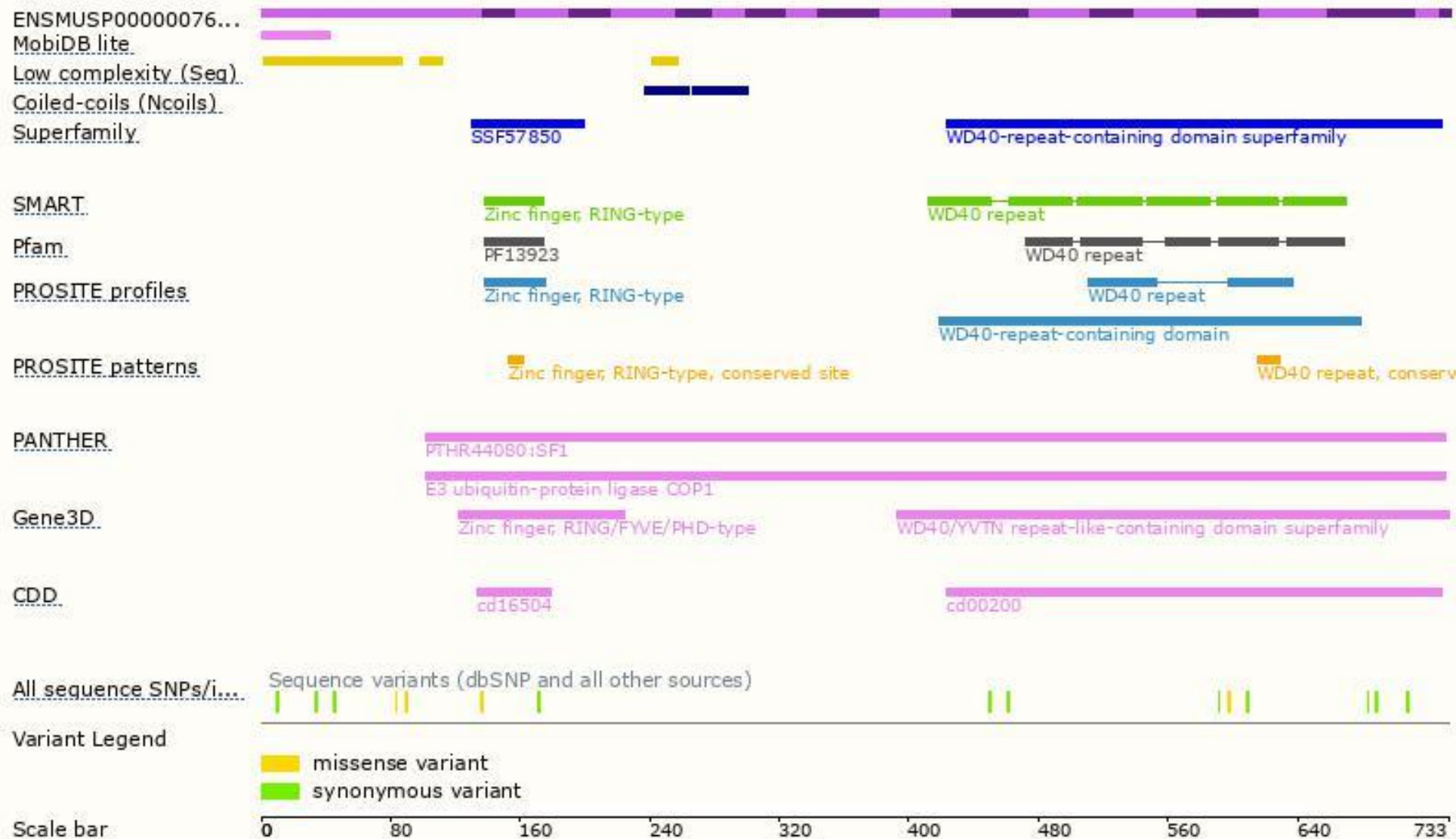
The strategy is based on the design of *Cop1-201* transcript,the transcription is shown below:



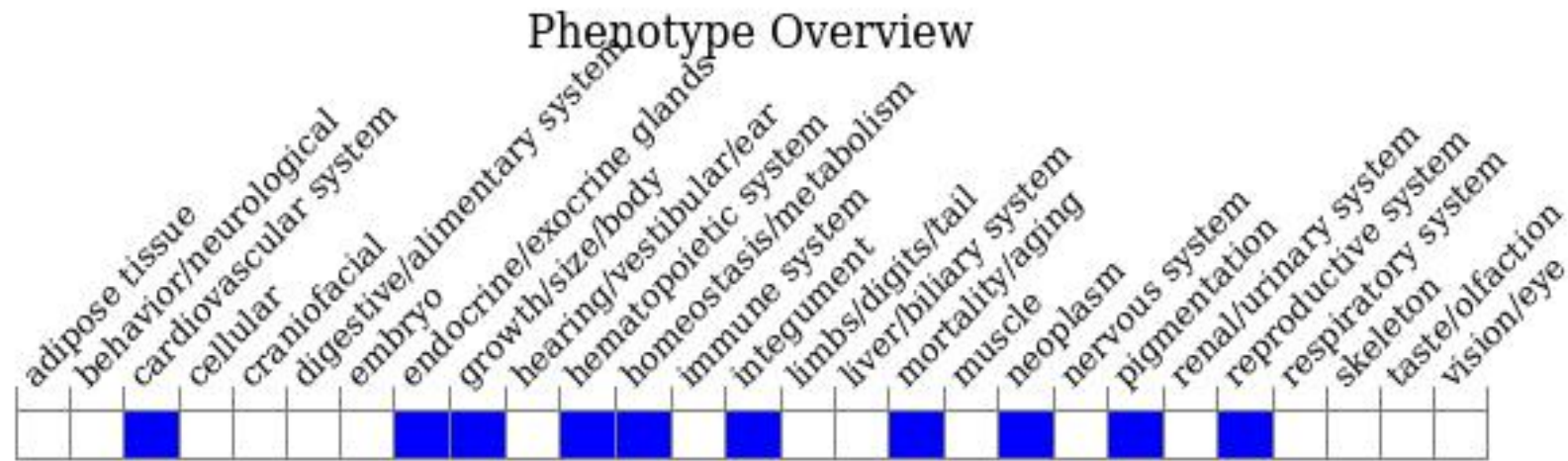
Genomic location distribution



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 conditional allele activated in prostate epithelial cells exhibit prostate gland hyperplasia and prostate intraepithelial neoplasia due to increased cell proliferation.

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