Sec63 Cas9-CKO Strategy

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Project Overview

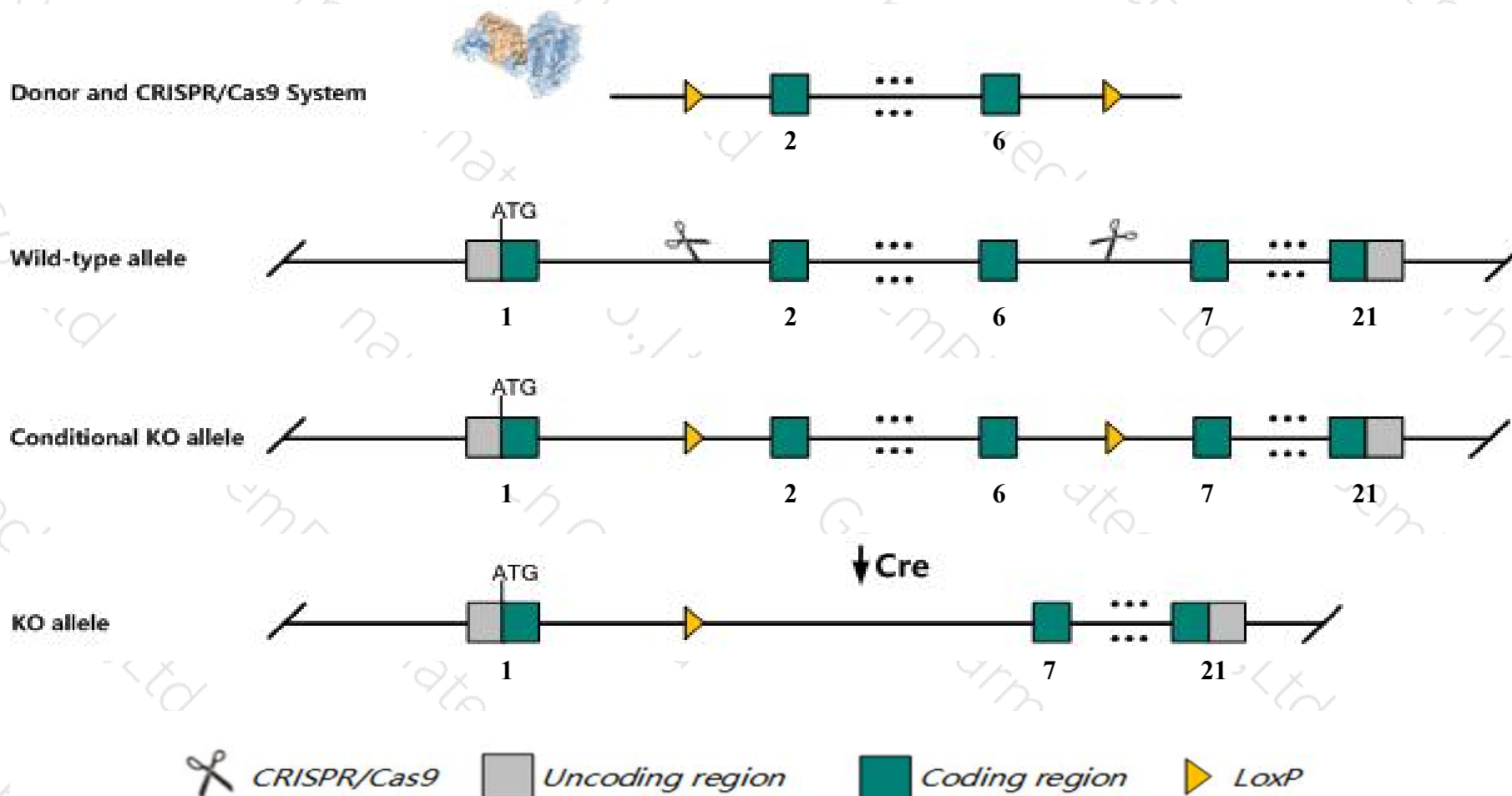|	
Project Name	*Sec63*
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sec63* gene. The schematic diagram is as follows:

Technical routes

➤ The *Sec63* gene has 5 transcripts. According to the structure of *Sec63* gene, exon2-exon6 of *Sec63-201*(ENSMUST00000019937.4) transcript is recommended as the knockout region.The region contains Ens 449bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Sec63* 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 knock-out allele exhibit early embryonic lethality. Mice homozygous for a conditional allele activated in the kidneys or ubiquitously develop polycystic kidney and liver phenotypes, respectively.

➢ The *Sec63* gene is located on the Chr10. 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.

Sec63 SEC63-like (S. cerevisiae) [Mus musculus (house mouse)]

Gene ID: 140740, updated on 3-Feb-2019

▲ Summary

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Official Symbol	Sec63 provided by MGI
Official Full Name	SEC63-like (S. cerevisiae) provided by MGI
Primary source	MGI:MGI:2155302
See related	Ensembl:ENSMUSG00000019802
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	5730478J10Rik, AI649014, AW319215
Expression	Ubiquitous expression in CNS E11.5 (RPKM 15.6), bladder adult (RPKM 13.9) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sec63-201	ENSMUST00000019937.4	6032	760aa	Protein coding	CCDS23815	Q8VHE0	TSL:1 GENCODE basic APPRIS P1
Sec63-205	ENSMUST00000155410.7	5206	No protein	Retained intron	-	-	TSL:2
Sec63-204	ENSMUST00000144228.1	4137	No protein	Retained intron	-	-	TSL:2
Sec63-202	ENSMUST00000105496.1	752	No protein	lncRNA	-	-	TSL:3
Sec63-203	ENSMUST00000124613.7	699	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Sec63-201* transcript,the transcription is shown below:
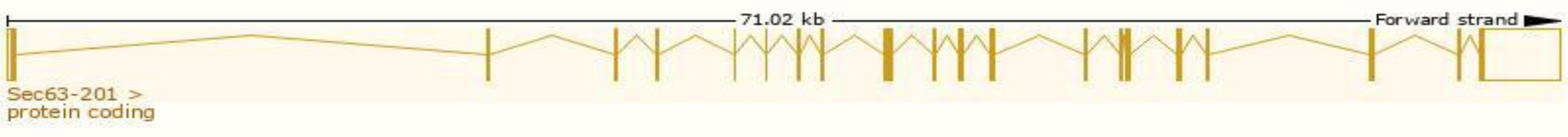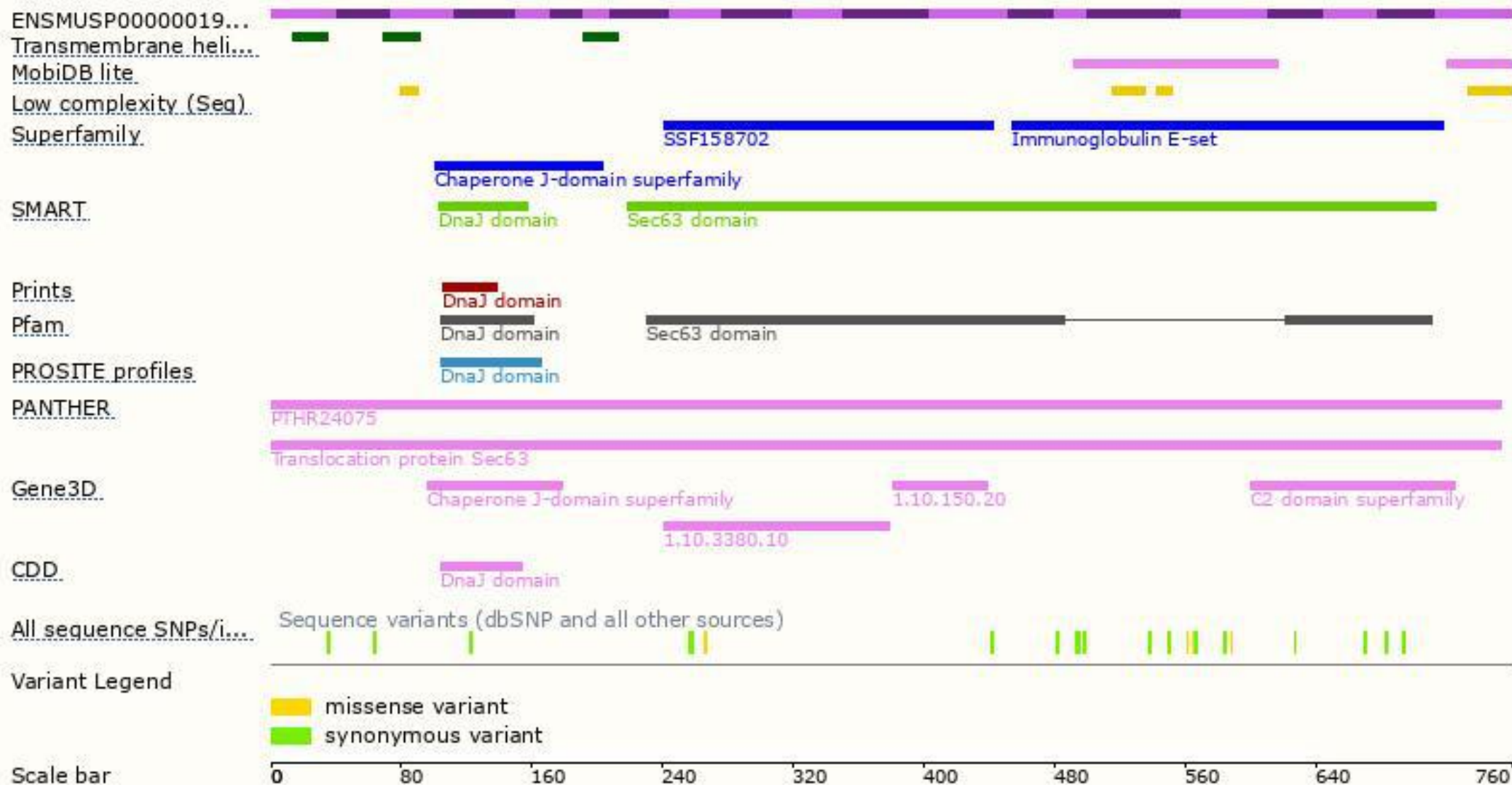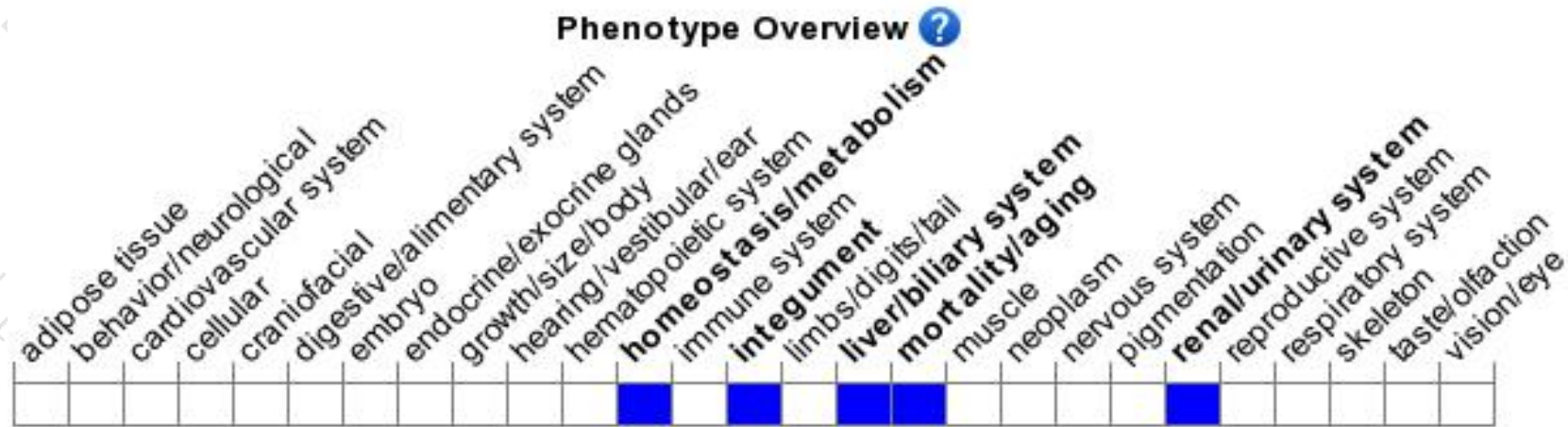
Genomic location distribution
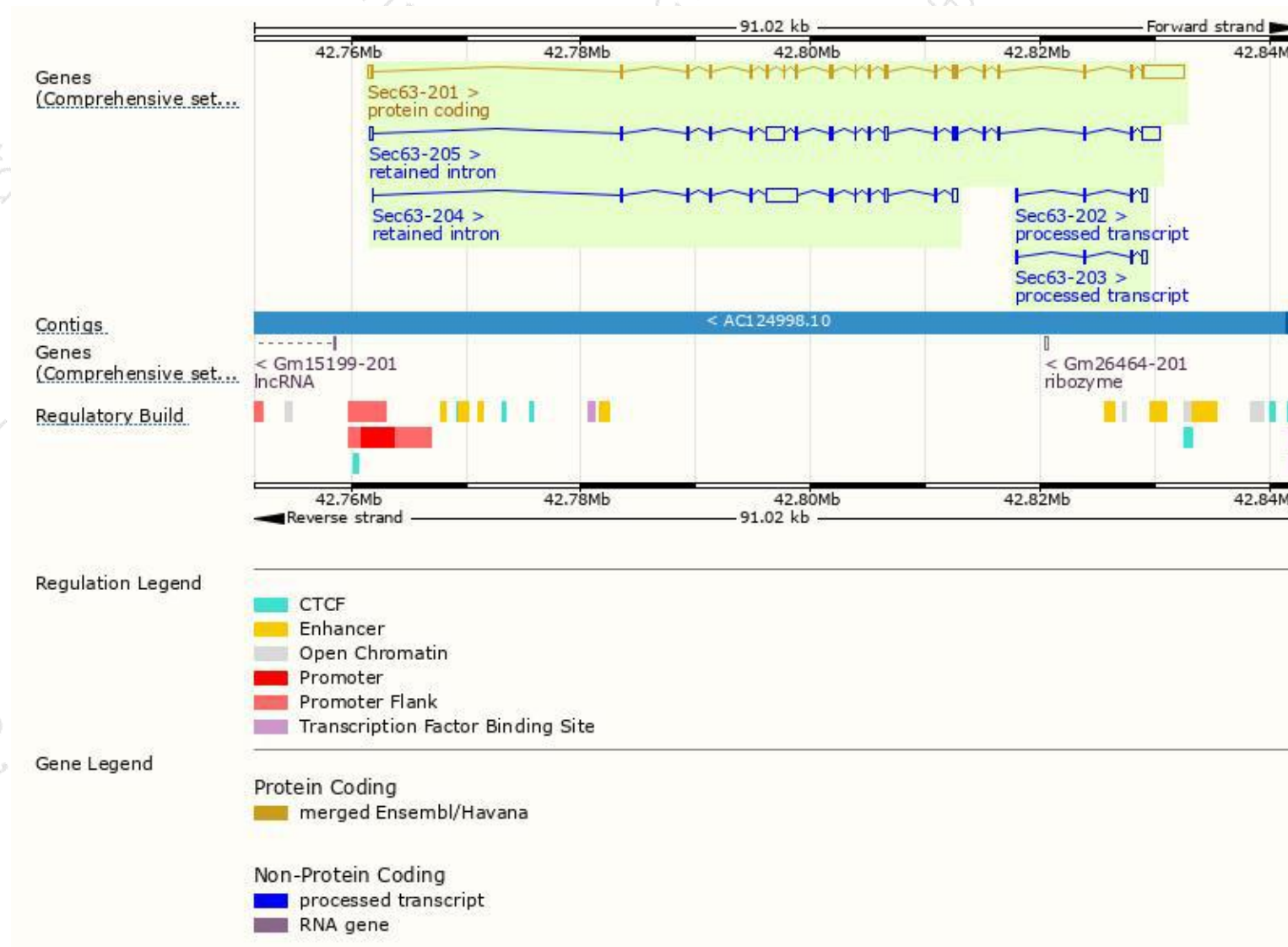
Protein domain

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 knock-out allele exhibit early embryonic lethality. Mice homozygous for a conditional allele activated in the kidneys or ubiquitously develop polycystic kidney and liver phenotypes, respectively.

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