Ptpdc1 Cas9-CKO Strategy

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Project Overview

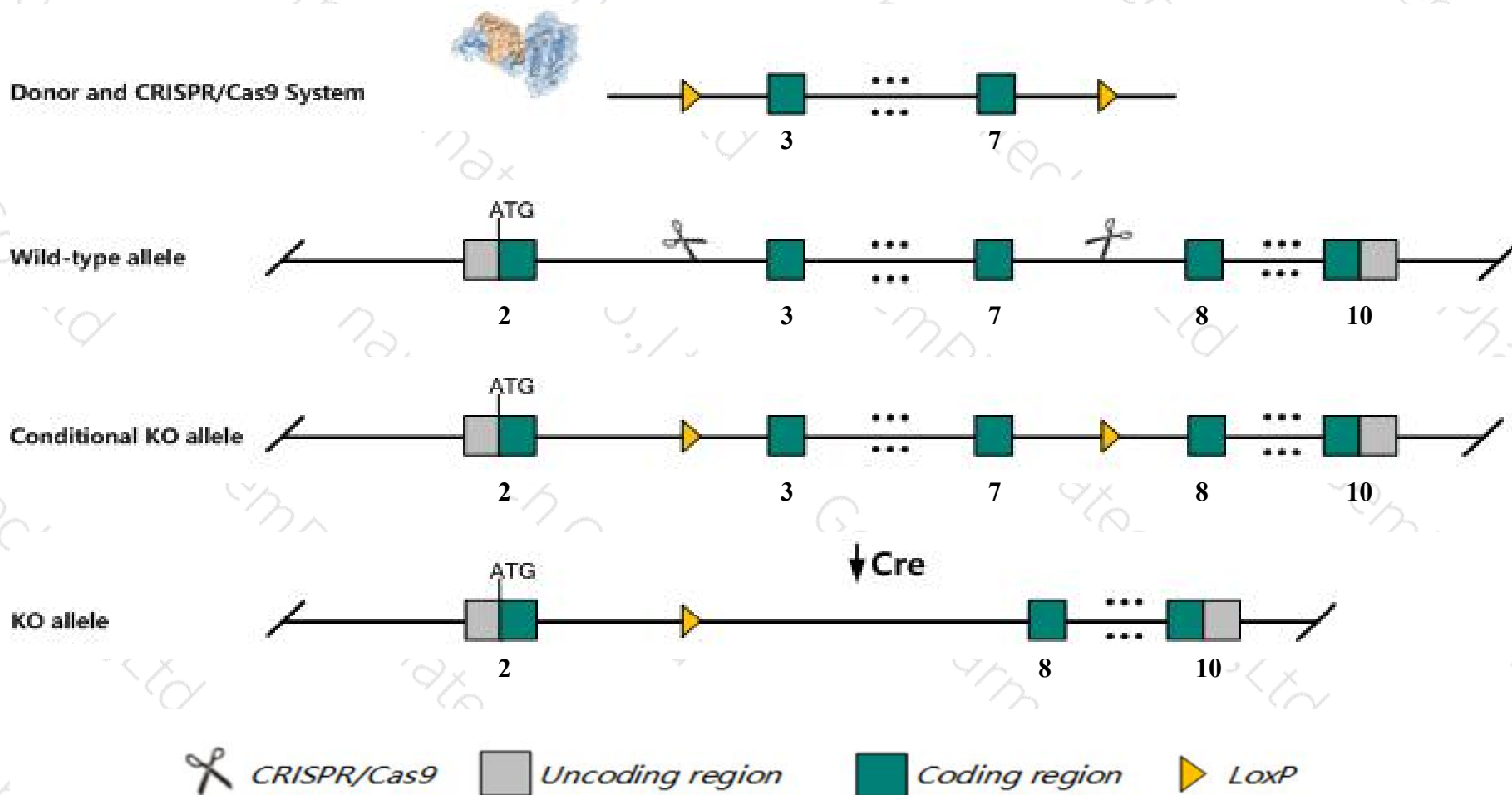|	
Project Name	***Ptpdc1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6J**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ptpdc1* gene. The schematic diagram is as follows:

Technical routes

➢ The *Ptpdc1* gene has 5 transcripts. According to the structure of *Ptpdc1* gene, exon3-exon7 of *Ptpdc1-201* (ENSMUST00000035824.10) transcript is recommended as the knockout region.The region contains 1757bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Ptpdc1* gene. The brief process is as follows:CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6J 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/6J 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,homozygous knockout mice are viable, fertile and do not exhibit growth defects. a high throughput screen detected small testes.

➢ Gm36550-201 will be deleted.

➢ The *Ptpdc1* gene is located on the Chr13. 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）

Ptpdc1 protein tyrosine phosphatase domain containing 1 [Mus musculus (house mouse)]

Gene ID: 218232, updated on 13-Mar-2020

▲ Summary

|	
Official Symbol	Ptpdc1 provided by MGI
Official Full Name	protein tyrosine phosphatase domain containing 1 provided by MGI
Primary source	MGI:MGI:2145430
See related	Ensembl:ENSMUSG00000038042
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI843923, AW456874, Naa-1, Ptpcd1
Summary	The protein encoded by this gene is a centrosomal mitotic phosphatase. This protein has been implicated in centrosomal duplication and cytokinesis. In addition, knockdown of expression levels in non-cycling cells results in extra long cilia, suggesting that this protein may function in regulating cilia length independent of a function in cell cycle control. Alternative splicing results in multiple transcript variants encoding different isoforms. [provided by RefSeq, Sep 2014]
Expression	Biased expression in testis adult (RPKM 13.7), frontal lobe adult (RPKM 4.4) and 13 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
Ptpdc1-201	ENSMUST00000035824.10	4402	747aa	Protein coding	CCDS26495	Q6NZK8	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
Ptpdc1-203	ENSMUST00000222028.1	3164	808aa	Protein coding	-	Q6NZK8	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 ALT2
Ptpdc1-205	ENSMUST00000238995.1	2962	795aa	Protein coding	-	-	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
Ptpdc1-204	ENSMUST00000223025.1	1873	92aa	Nonsense mediated decay	-	A0A1Y7VLX3	TSL:1
Ptpdc1-202	ENSMUST00000221887.1	1072	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Ptpdc1-201* transcript,the transcription is shown below:
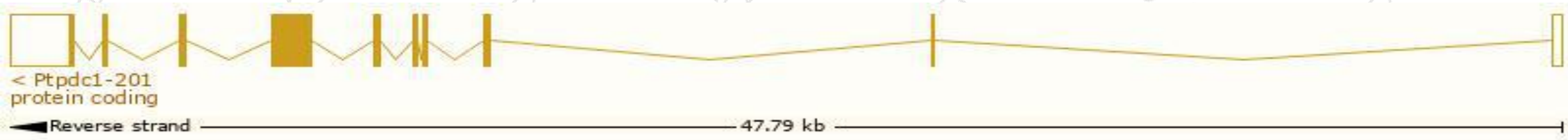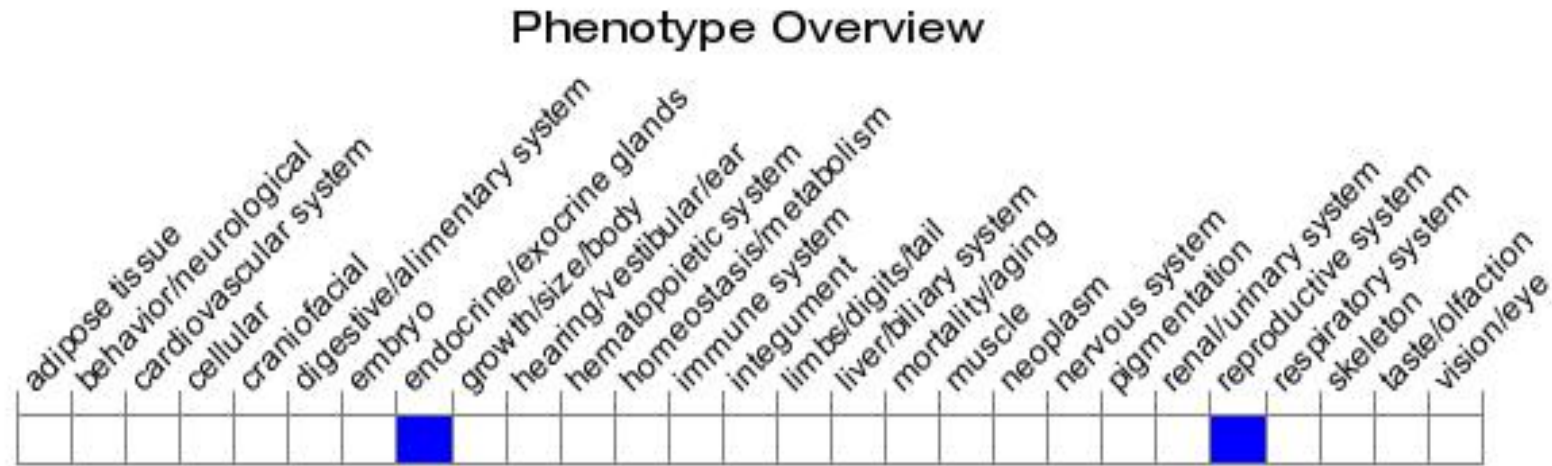
Genomic location distribution
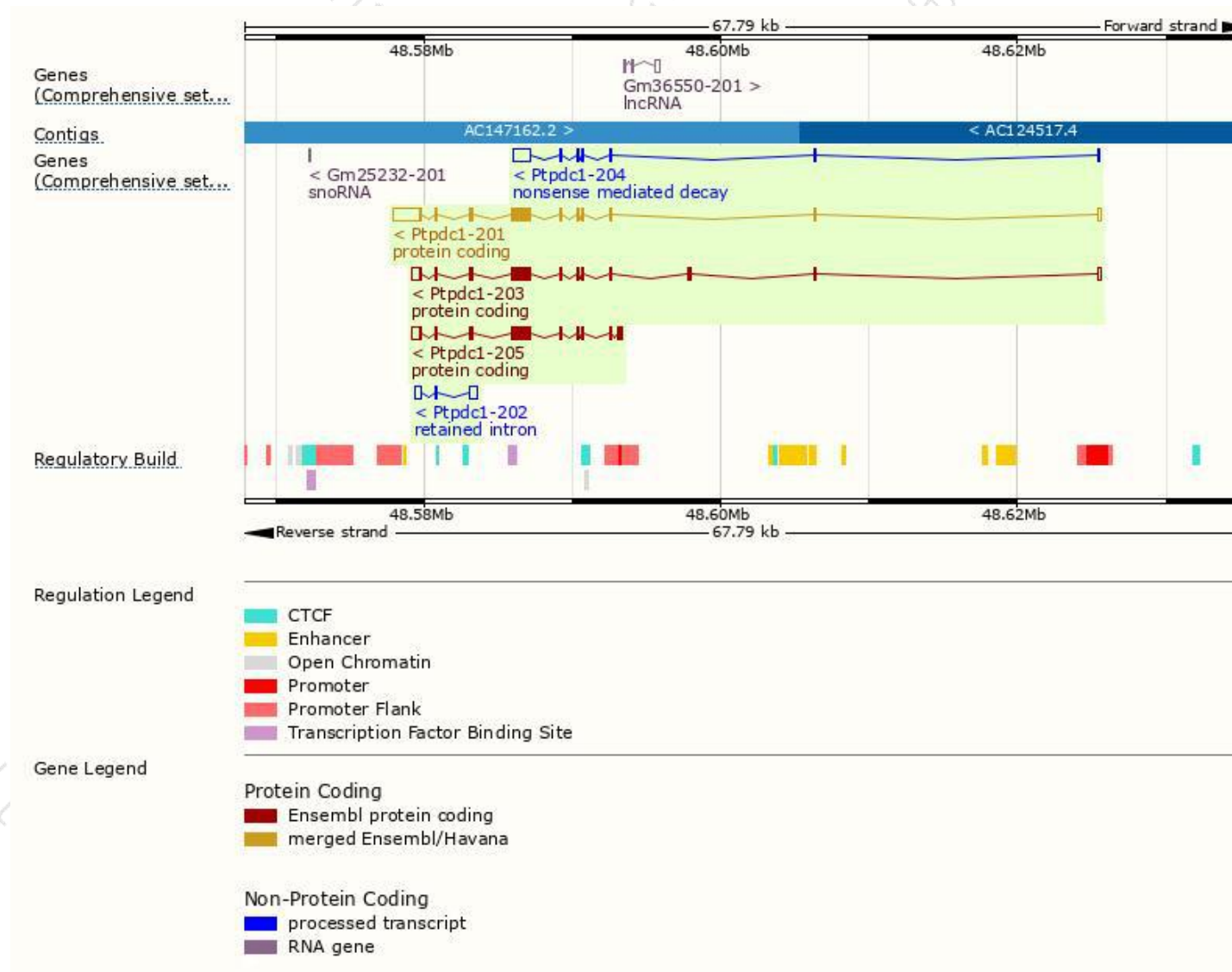
Protein domain
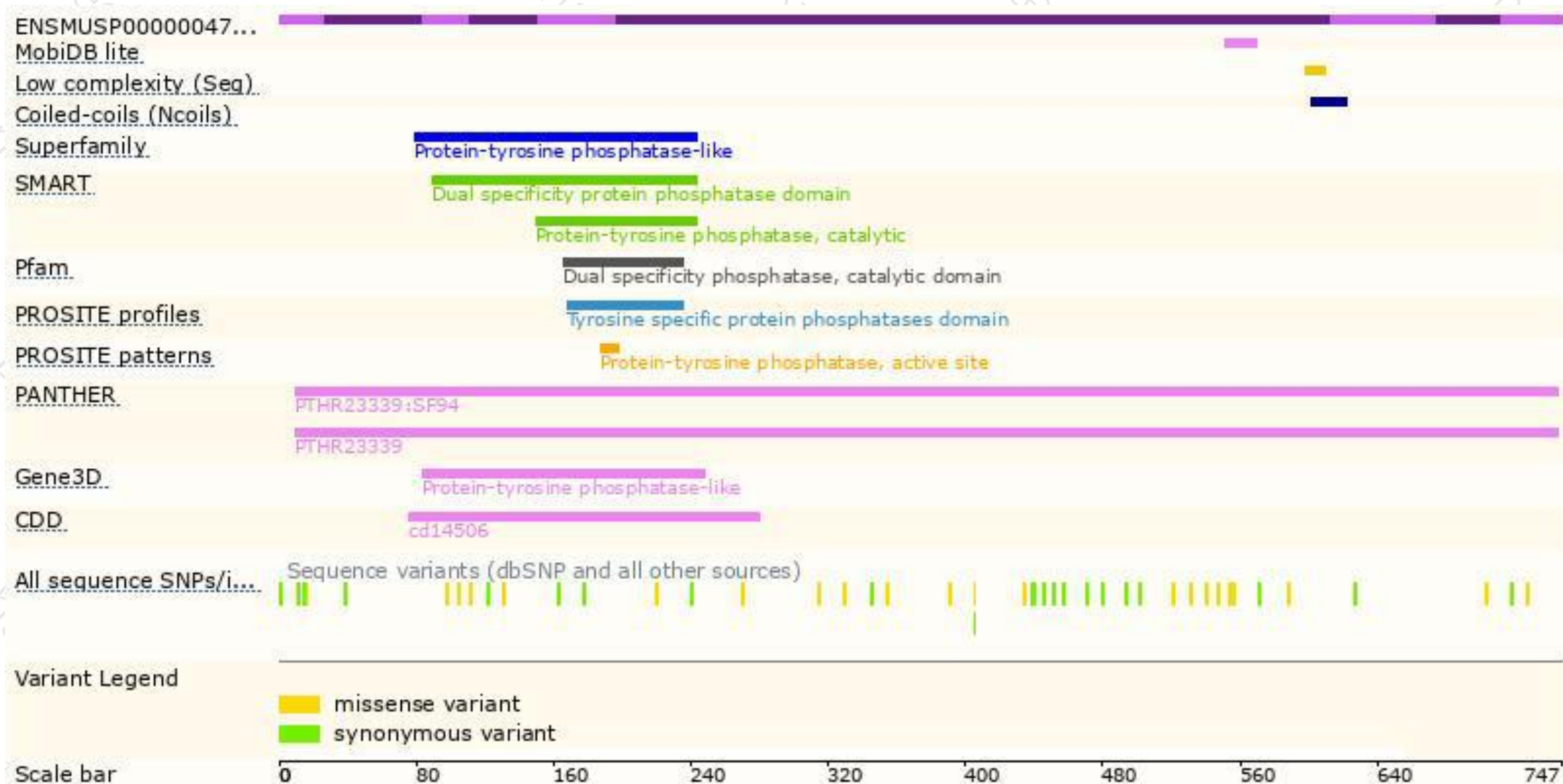
Mouse phenotype description(MGI)

Phenotype Overview

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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