Fignl1 Cas9-CKO Strategy

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Project Overview

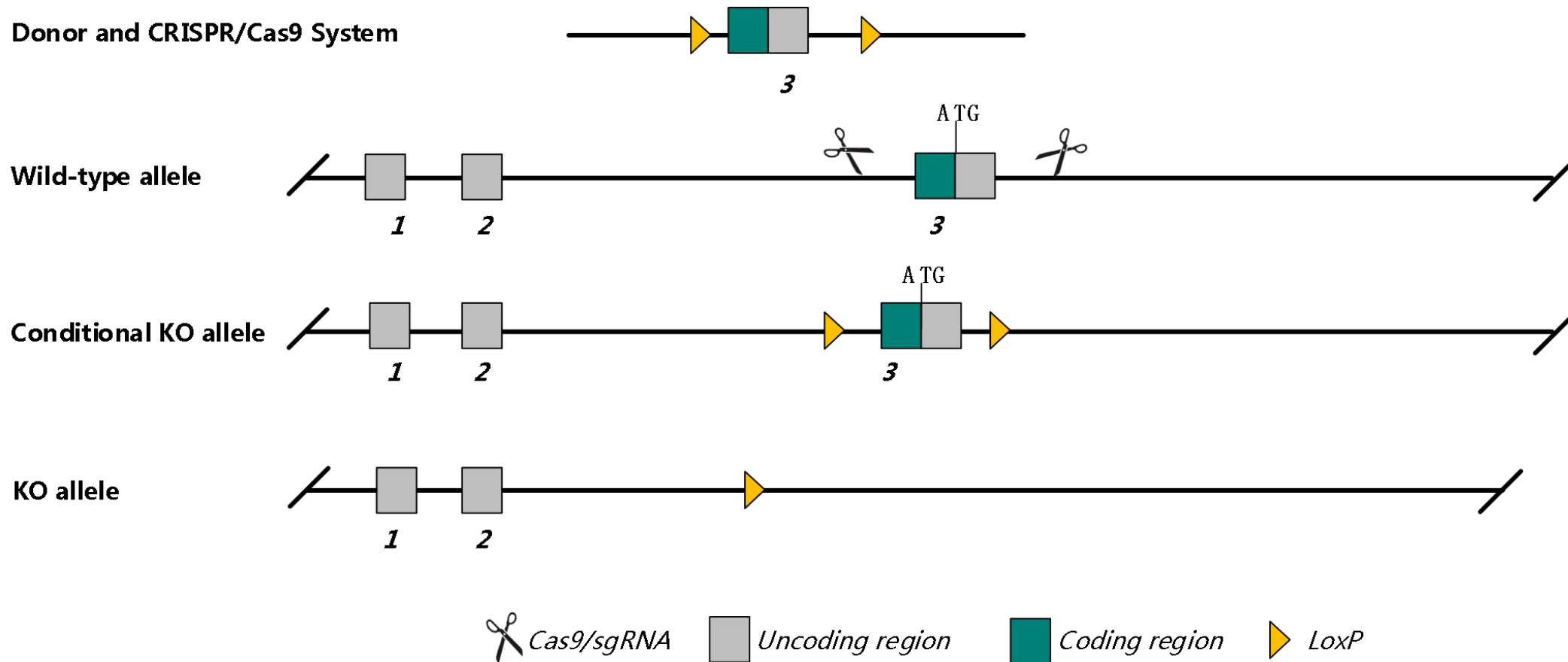|	
Project Name	*Fignl1*
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fignl1* gene. The schematic diagram is as follows:

Cas9/sgRNA   Uncoding region   Coding region   LoxP

Technical routes

➤ The *Fignl1* gene has 7 transcripts. According to the structure of *Fignl1* gene, exon3 of *Fignl1-207* (ENSMUST00000171938.1) transcript is recommended as the knockout region.The region contains all 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 *Fignl1* 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

➢ The *Fignl1* gene is located on the Chr11. 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.

Fignl1 fidgetin-like 1 [Mus musculus (house mouse)]

Gene ID: 60530, updated on 31-Jan-2019

▲ Summary

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Official Symbol	Fignl1 provided by MGI
Official Full Name	fidgetin-like 1 provided by MGI
Primary source	MGI:MGI:1890648
See related	Ensembl:ENSMUSG00000035455
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
Expression	Biased expression in liver E14 (RPKM 22.0), liver E14.5 (RPKM 18.3) and 9 other tissuesSee more
Orthologs	human all

Transcript information　Ensembl

The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fignl1-207	ENSMUST00000171938.1	2974	683aa	Protein coding	CCDS24438	Q8BPY9	TSL:1 GENCODE basic APPRIS P1
Fignl1-201	ENSMUST00000047689.10	2961	683aa	Protein coding	CCDS24438	Q8BPY9	TSL:1 GENCODE basic APPRIS P1
Fignl1-206	ENSMUST00000171080.7	2844	683aa	Protein coding	CCDS24438	Q8BPY9	TSL:2 GENCODE basic APPRIS P1
Fignl1-202	ENSMUST00000109664.1	2807	683aa	Protein coding	CCDS24438	Q8BPY9	TSL:1 GENCODE basic APPRIS P1
Fignl1-204	ENSMUST00000150714.1	421	119aa	Protein coding	-	Q5SWU3	CDS 3' incomplete TSL:2
Fignl1-205	ENSMUST00000152345.7	2092	No protein	Processed transcript	-	-	TSL:1
Fignl1-203	ENSMUST00000123815.1	770	No protein	Processed transcript	-	-	TSL:3

The strategy is based on the design of *Fignl1-207* transcript,The transcription is shown below

< Fignl1-207
protein coding

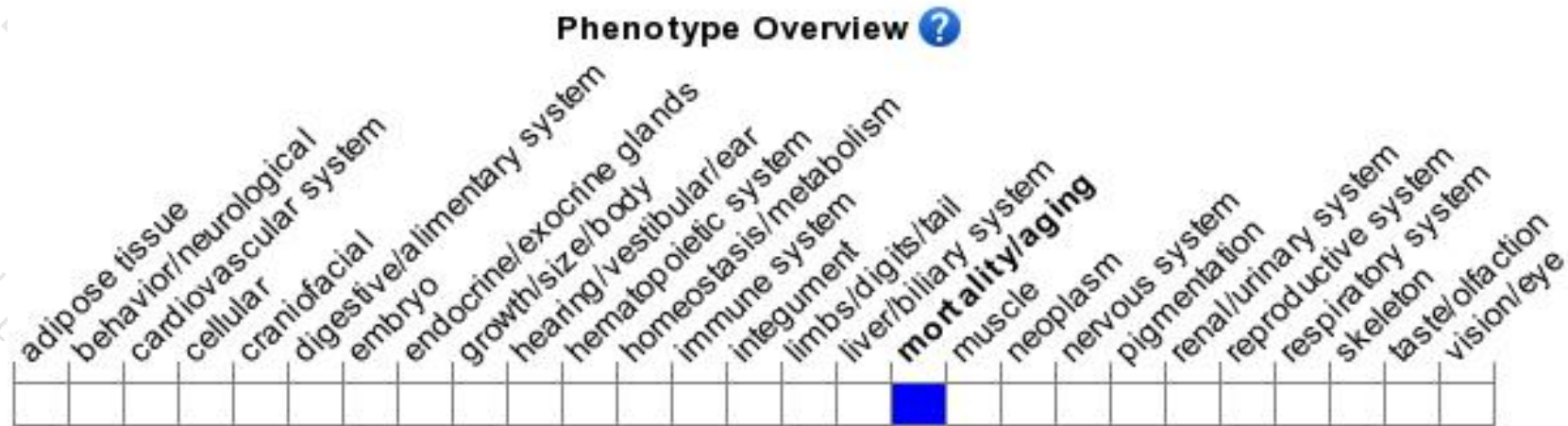◄ Reverse strand

8.68 kb
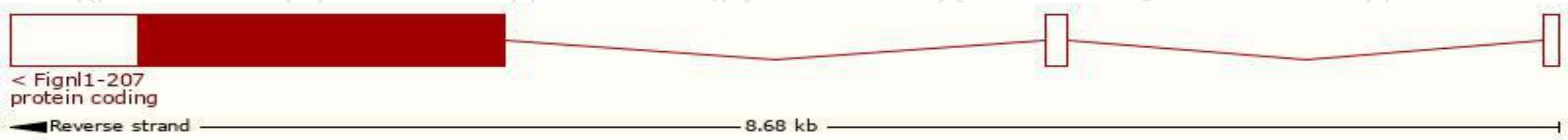
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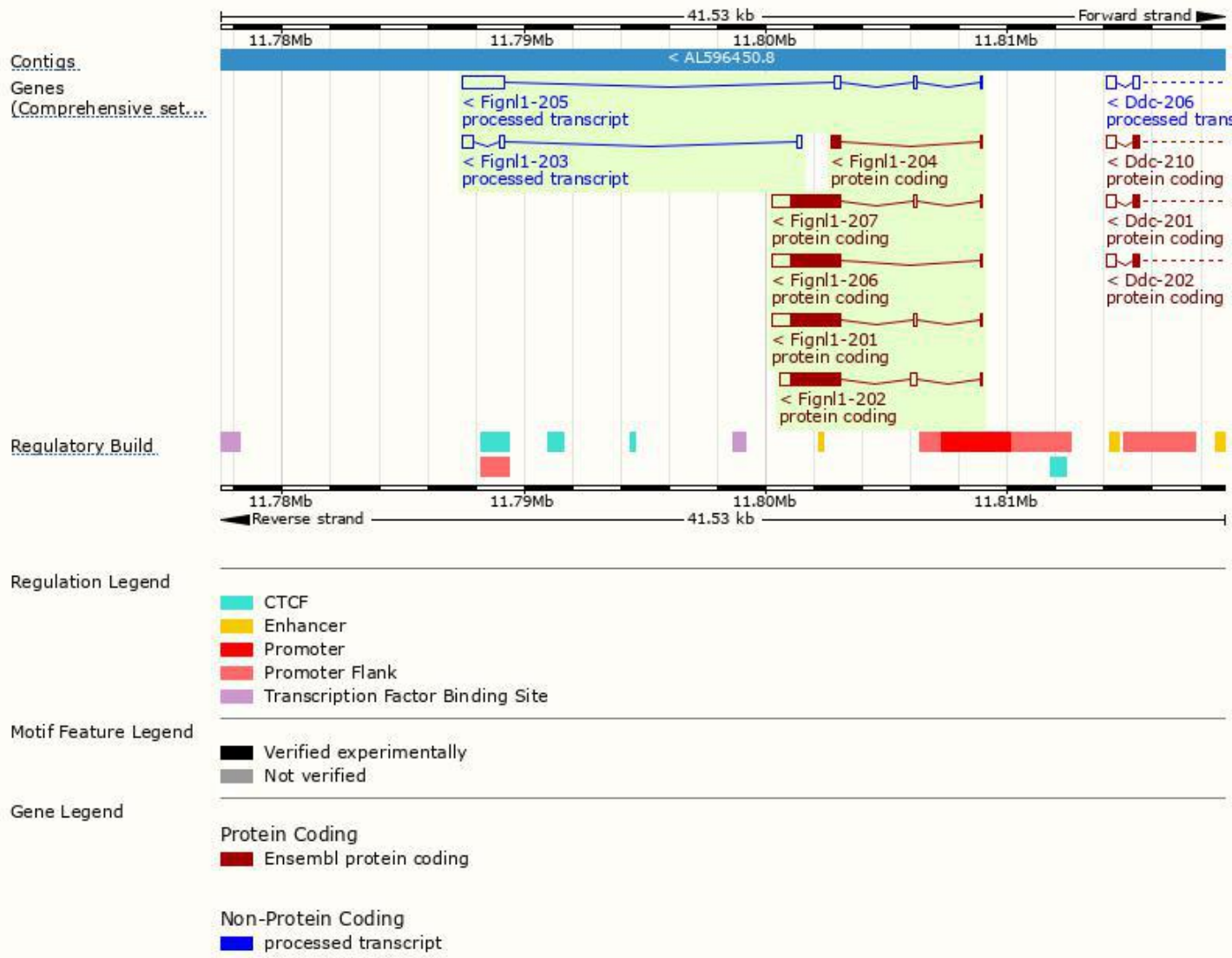
Protein domain
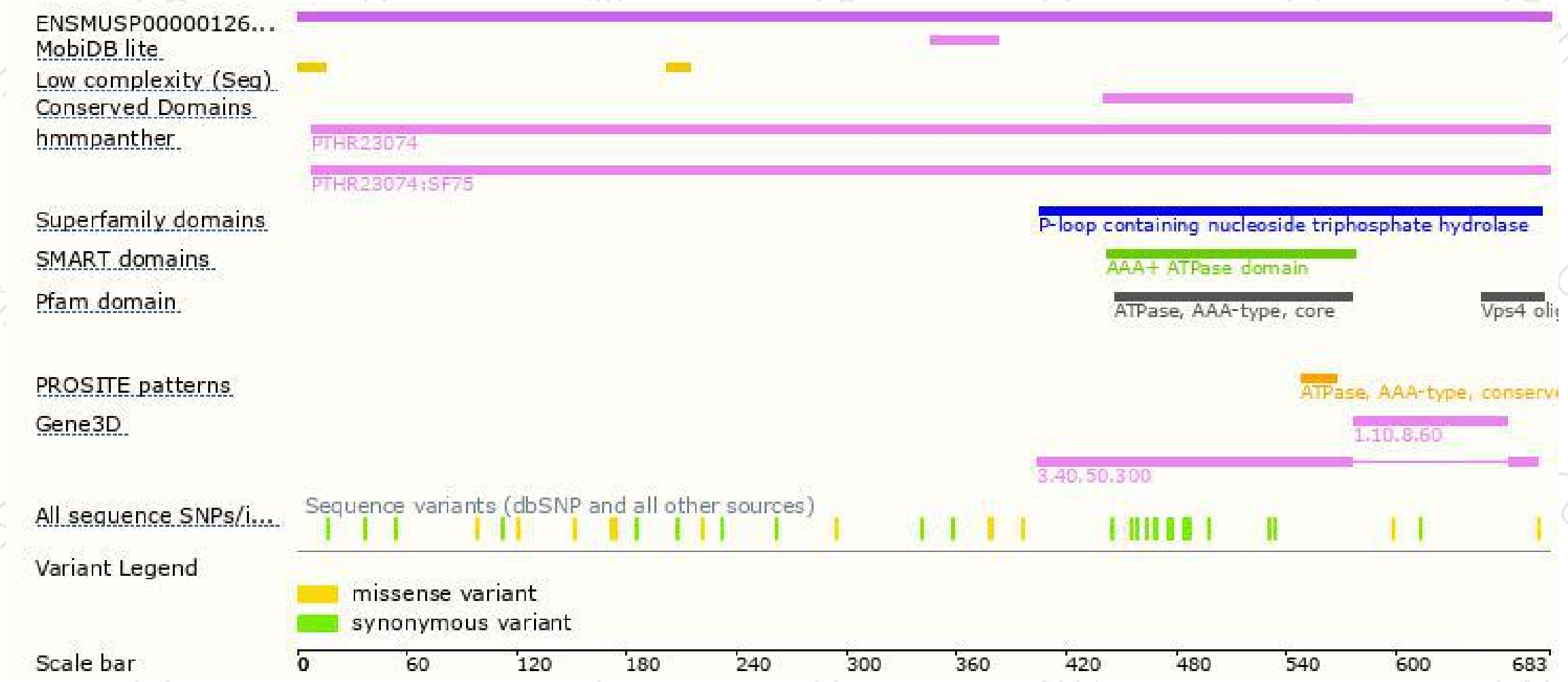
Mouse phenotype description(MGI)

Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

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