Trim62 Cas9-CKO Strategy

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Project Overview

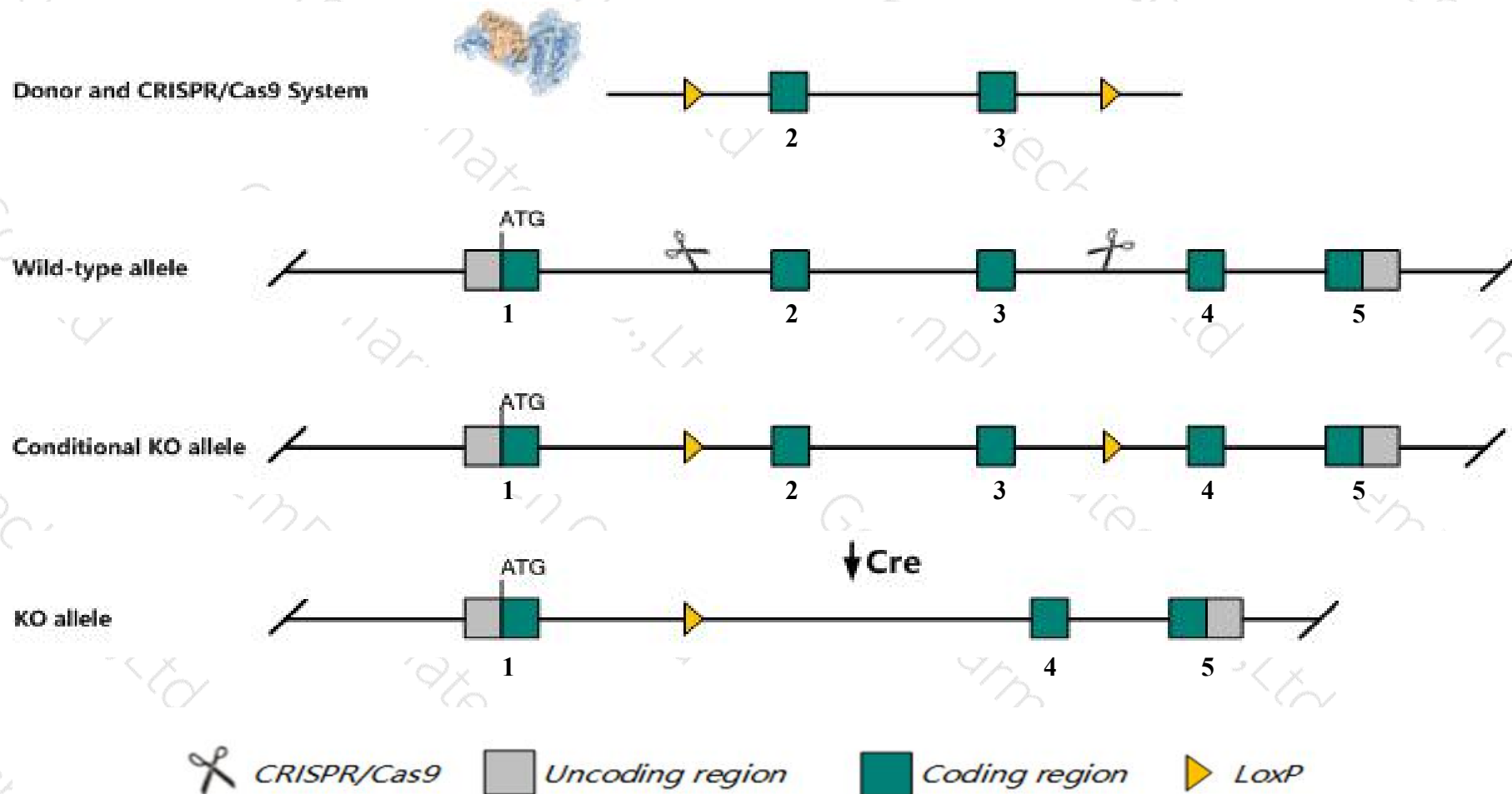|	
Project Name	***Trim62***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Trim62* gene. The schematic diagram is as follows:

Technical routes

➤ The *Trim62* gene has 2 transcripts. According to the structure of *Trim62* gene, exon2-exon3 of *Trim62-201* (ENSMUST00000035667.8) transcript is recommended as the knockout region.The region contains Ens 353bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Trim62* 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 heterozygous or homozygous for a targeted allele exhibit increased tumorigenesis.

➢ The *Trim62* gene is located on the Chr4. 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）

Trim62 tripartite motif-containing 62 [Mus musculus (house mouse)]

Gene ID: 67525, updated on 31-Jan-2019

▲ Summary

|	
Official Symbol	Trim62 provided by MGI
Official Full Name	tripartite motif-containing 62 provided by MGI
Primary source	MGI:MGI:1914775
See related	Ensembl:ENSMUSG00000041000
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	6330414G21Rik, AI450348, Dear1
Expression	Broad expression in cerebellum adult (RPKM 21.1), ovary adult (RPKM 7.9) and 19 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 2 transcripts,all transcripts are shown below:

| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags		
Trim62-201	ENSMUST00000035667.8	3752	475aa	Protein coding	CCDS18677	Q80V85	TSL:1	GENCODE basic	APPRIS P1
Trim62-202	ENSMUST00000147852.1	2722	145aa	Nonsense mediated decay	-	D6RJM1		TSL:1	

The strategy is based on the design of *Trim62-201* transcript,The transcription is shown below

27.74 kb

Forward strand

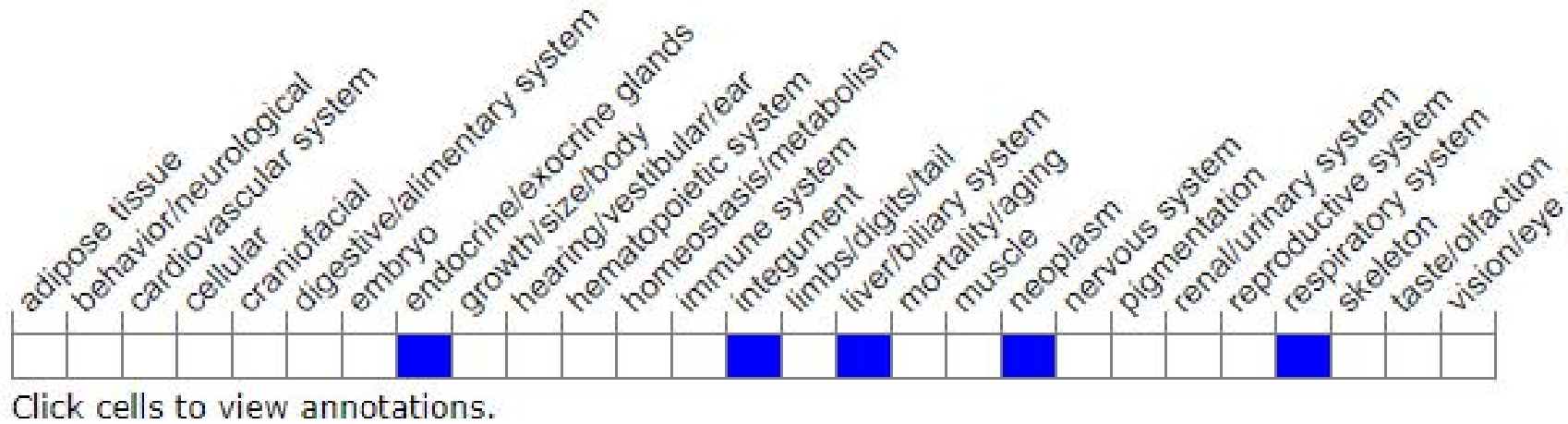Trim62-201 >
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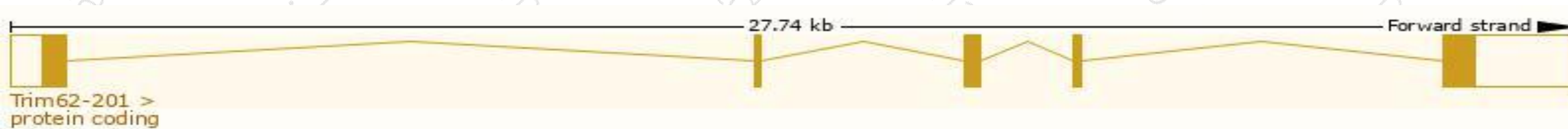
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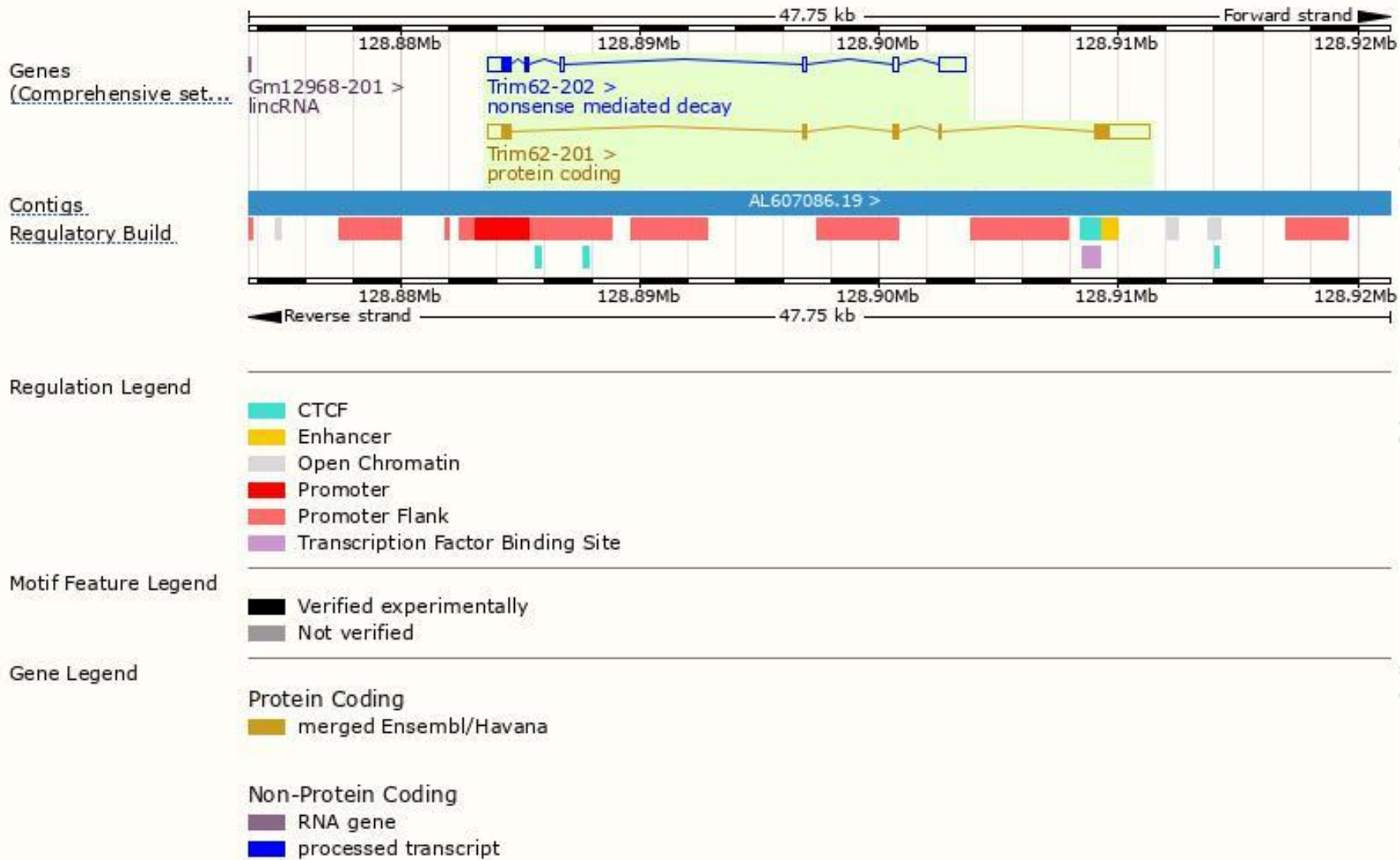
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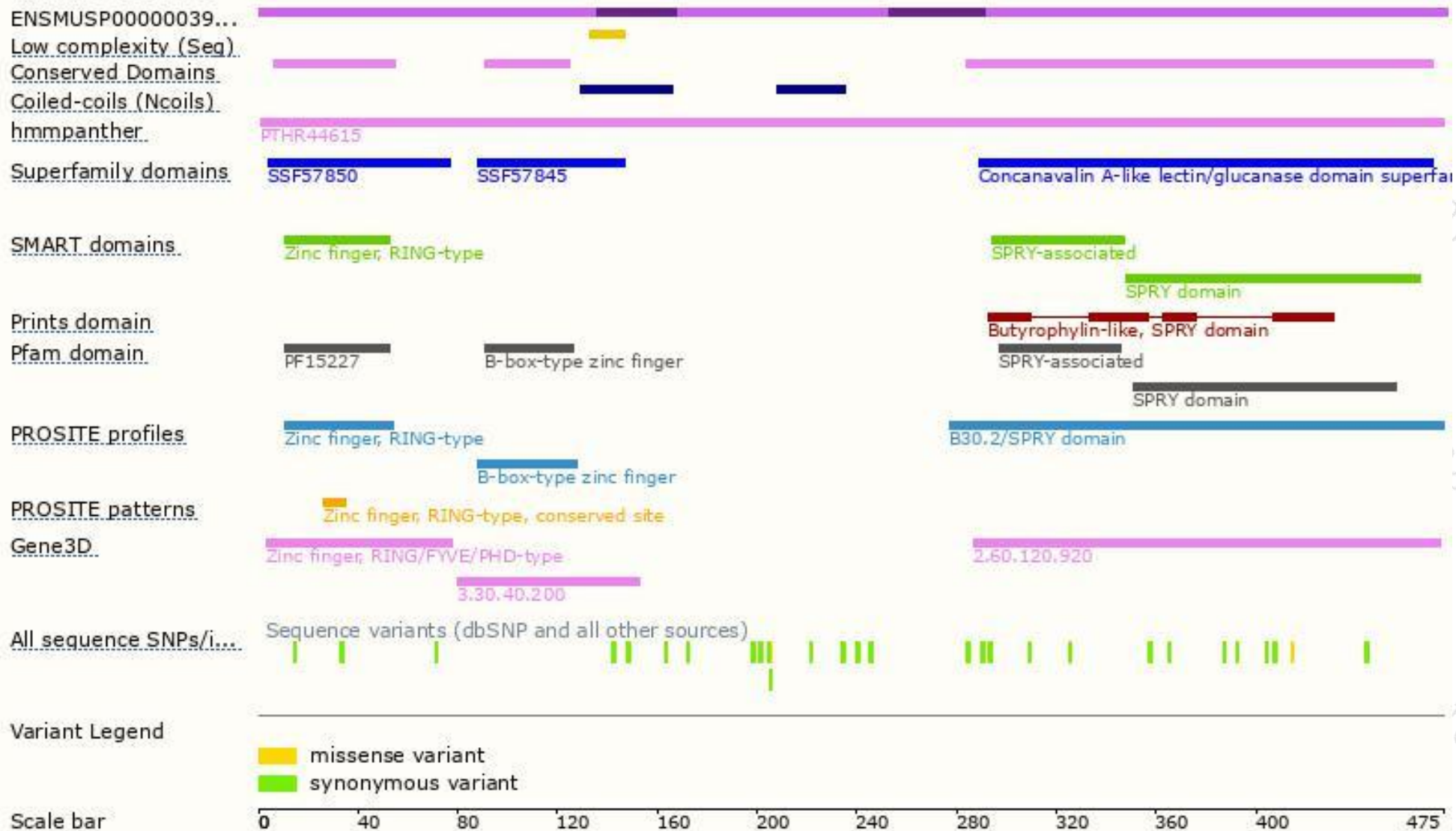
Mouse phenotype description(MGI)

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 heterozygous or homozygous for a targeted allele exhibit increased tumorigenesis.

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