Tusc3 Cas9-CKO Strategy

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Project Overview

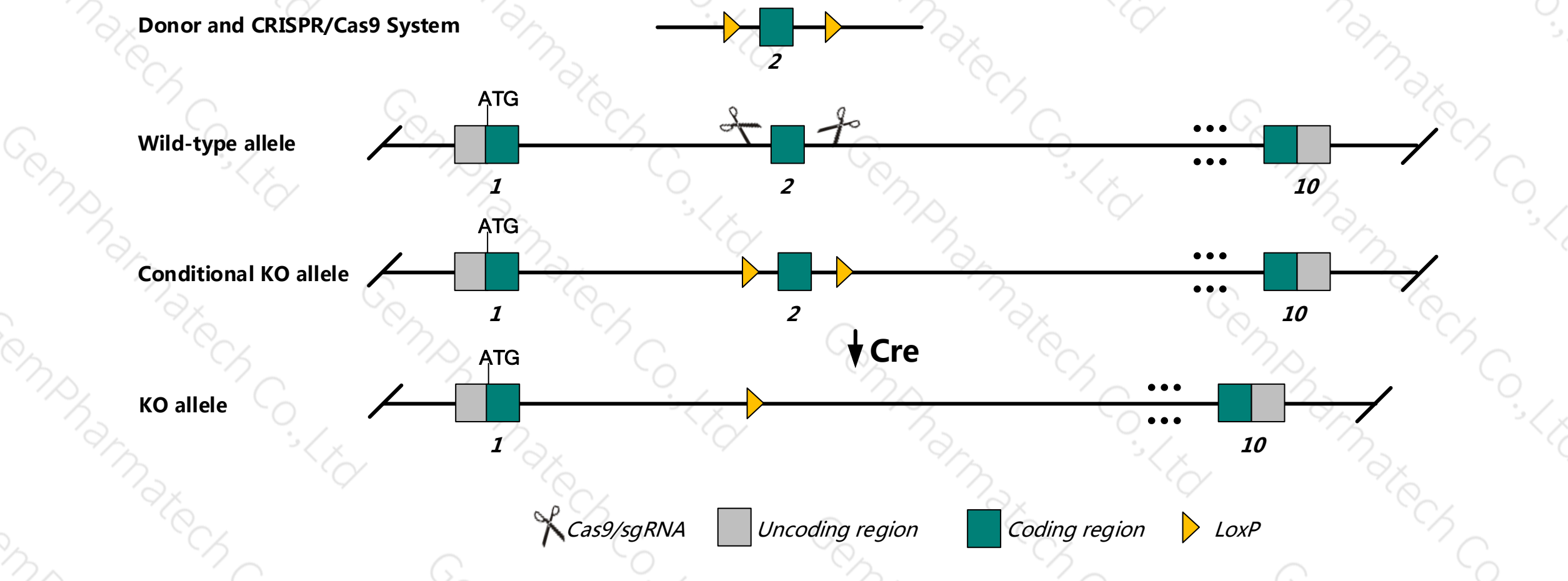|	
Project Name	*Tusc3*
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tusc3* gene. The schematic diagram is as follows:

Technical routes

➢ The *Tusc3* gene has 6 transcripts.According to the structure of *Tusc3* gene, exon2 of *Tusc3*-201 （ENSMUST00000167992.7） transcript is recommended as the knockout region.The region contains 170bp coding sequence.Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Tusc3* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed.Cas9, sgRNA 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 was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues or cell types.

Notice

➢ The *Tusc3* gene is located on the Chr8. 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 gene transcription and translation processes, all risks cannot be predicted under existing information.

Gene information （NCBI）

Tusc3   tumor suppressor candidate 3 [*Mus musculus* (house mouse)]

Gene ID: 80286, updated on 2-Oct-2018

▲ **Summary**

|	
Official Symbol	Tusc3 provided by MGI
Official Full Name	tumor suppressor candidate 3 provided by MGI
Primary source	MGI:MGI:1933134
See related	Ensembl:ENSMUSG00000039530 Vega:OTTMUSG00000061049
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	N33; AU022242; BC003311
Annotation information	Annotation category: suggests misassembly
Expression	Ubiquitous expression in CNS E18 (RPKM 43.6), whole brain E14.5 (RPKM 27.6) and 27 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

The gene has 6 transcripts, and all transcripts are shown below ：

| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	RefSeq	Flags
Tusc3-201	ENSMUST00000167992.7	1511	347aa	Protein coding	CCDS85529	Q8BTV1	NM_030254 NP_084530	TSL:1 GENCODE basic APPRIS P1
Tusc3-203	ENSMUST00000209440.1	1535	347aa	Protein coding	-	Q8BTV1	-	TSL:1 GENCODE basic APPRIS P1
Tusc3-202	ENSMUST00000169034.1	1262	105aa	Protein coding	-	Q99J74	-	TSL:1 GENCODE basic
Tusc3-205	ENSMUST00000210890.1	588	196aa	Protein coding	-	A0A1B0GRW4	-	CDS 5' and 3' incomplete TSL:3
Tusc3-206	ENSMUST00000211241.1	1264	105aa	Nonsense mediated decay	-	Q99J74	-	TSL:5
Tusc3-204	ENSMUST00000209970.1	2667	No protein	Retained intron	-	-	-	TSL:1

The strategy is based on the design of *Tusc3-201* transcript,The transcription is shown below
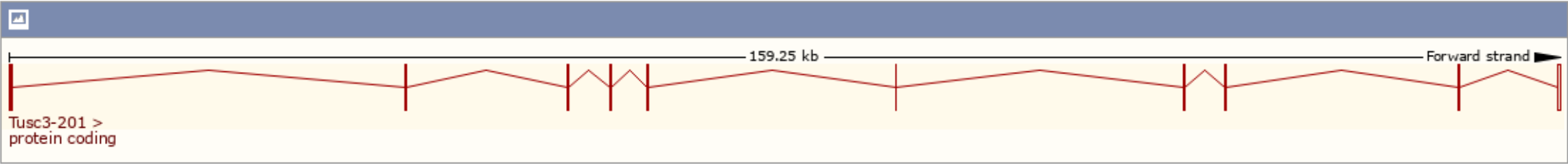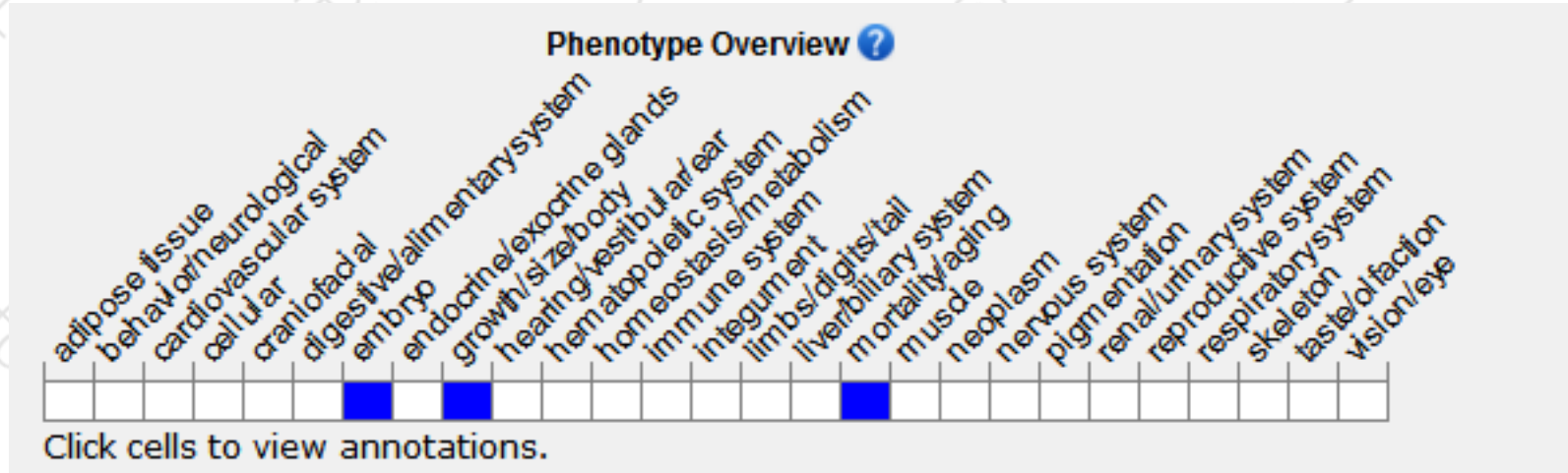
Genomic location distribution
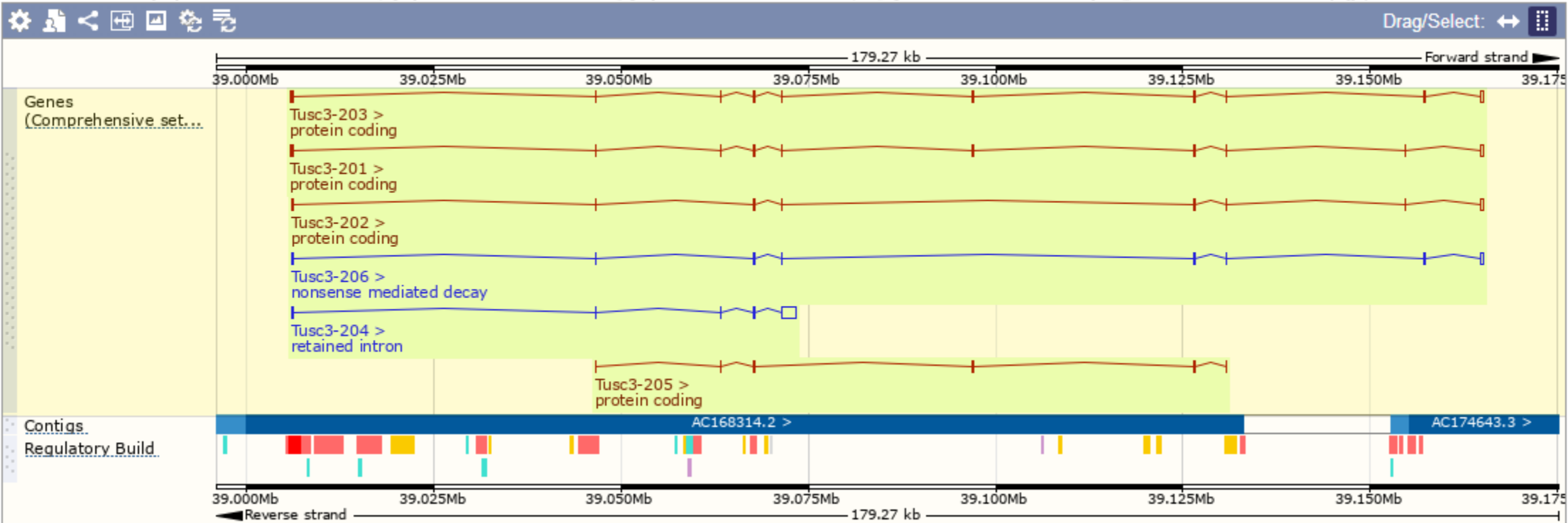
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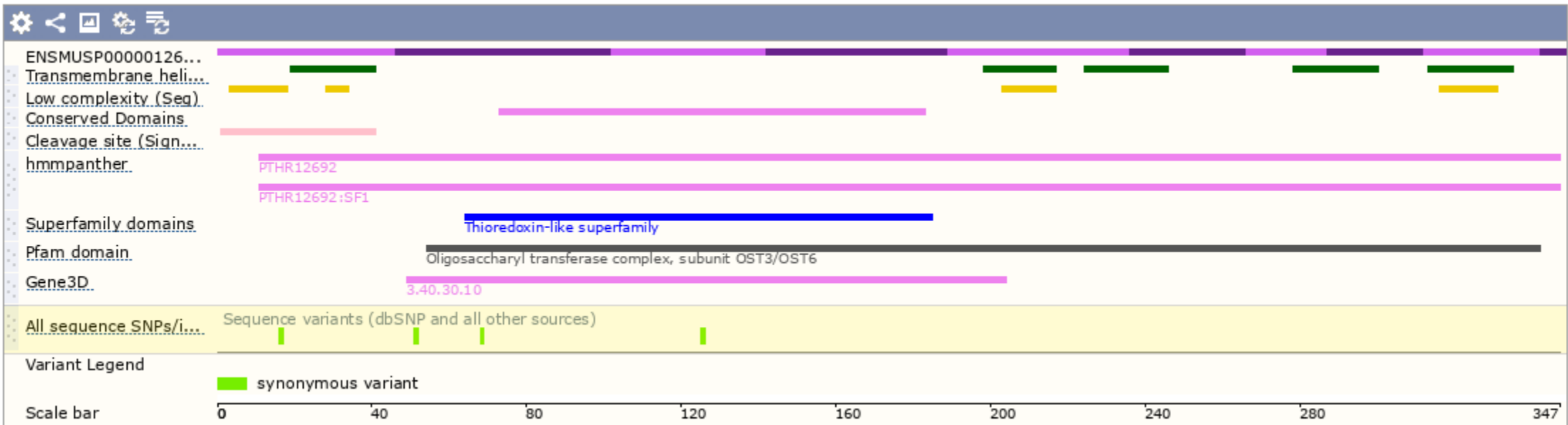
Mouse phenotype description(MGI)

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

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