Tonsl Cas9-CKO Strategy

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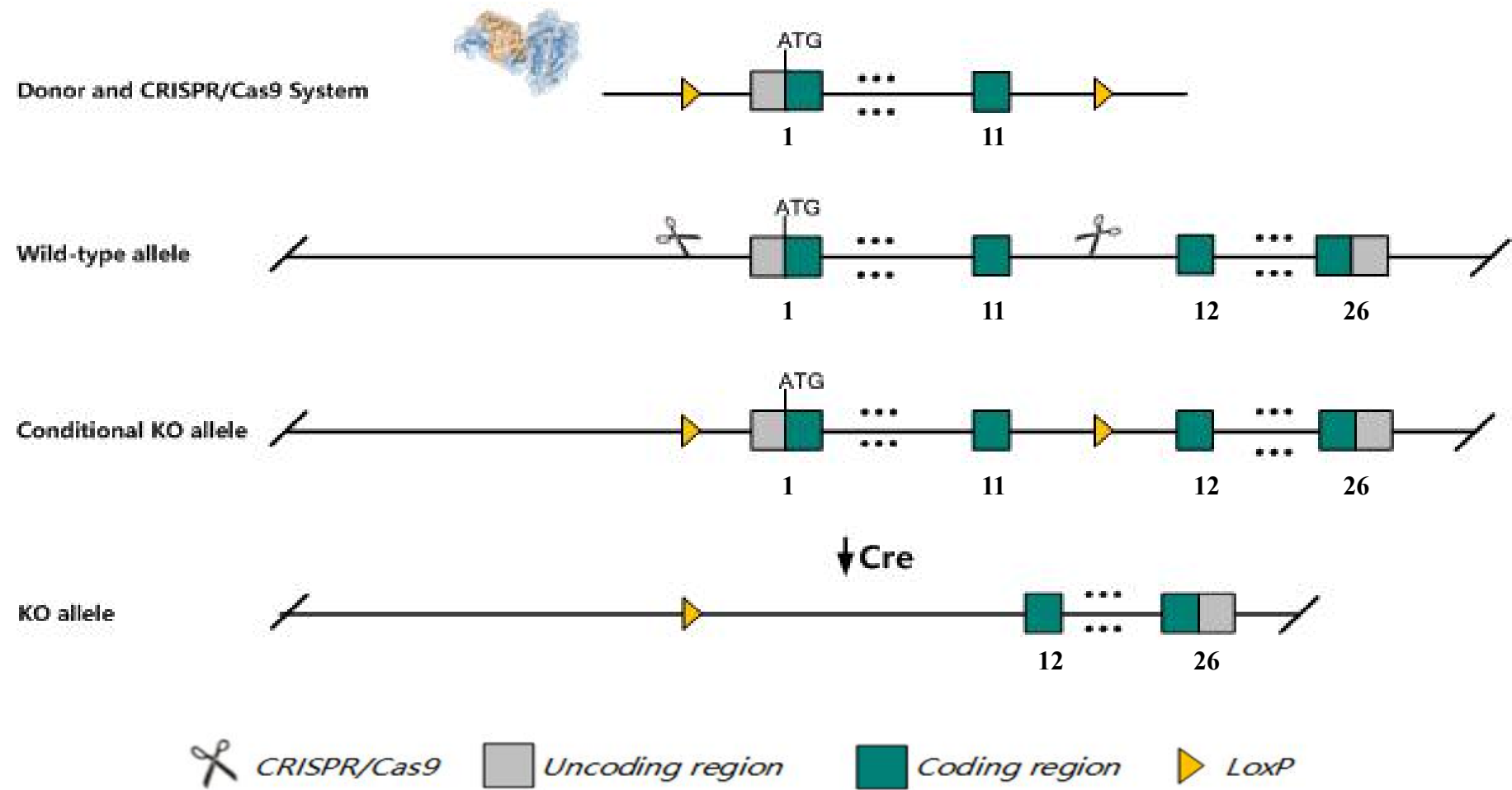|	
Project Name	*Tonsl*
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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

Technical routes

The *Tonsl* gene has 8 transcripts. According to the structure of *Tonsl* gene, exon1-exon11 of *Tonsl-206*(ENSMUST00000168185.8) transcript is recommended as the knockout region.The region contains start codon ATG.Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Tonsl* 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.

The *Tonsl* gene is located on the Chr15. 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.

Transcript *Tonsl*-203 may not be affected.

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

Tonsl tonsoku-like, DNA repair protein [Mus musculus (house mouse)]

Gene ID: 72749, updated on 17-Dec-2020

▲ Summary

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Official Symbol	Tonsl provided by MGI
Official Full Name	tonsoku-like, DNA repair protein provided by MGI
Primary source	MGI:MGI:1919999
See related	Ensembl:ENSMUSG00000059323
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	2810439M11Rik, Nfkb, Nfkbil2
Expression	Ubiquitous expression in duodenum adult (RPKM 12.6), large intestine adult (RPKM 12.1) and 26 other tissues See more
Orthologs	human all

Transcript information　Ensembl

The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tonsl-206	ENSMUST00000168185.8	4235	1363aa	Protein coding	CCDS27580		TSL:1 , GENCODE basic , APPRIS P1 ,
Tonsl-203	ENSMUST00000165163.8	743	86aa	Protein coding	-		CDS 5' incomplete , TSL:3 ,
Tonsl-205	ENSMUST00000166974.2	471	64aa	Protein coding	-		CDS 3' incomplete , TSL:2 ,
Tonsl-204	ENSMUST00000165190.2	2932	417aa	Nonsense mediated decay	-		TSL:1 ,
Tonsl-208	ENSMUST00000171478.2	713	No protein	Processed transcript	-		TSL:3 ,
Tonsl-202	ENSMUST00000163990.2	502	No protein	Retained intron	-		TSL:2 ,
Tonsl-201	ENSMUST00000163161.2	491	No protein	Retained intron	-		TSL:3 ,
Tonsl-207	ENSMUST00000168432.2	420	No protein	Retained intron	-		TSL:3 ,

The strategy is based on the design of *Tonsl-206* transcript,the transcription is shown below:

< Tonsl-206
protein coding

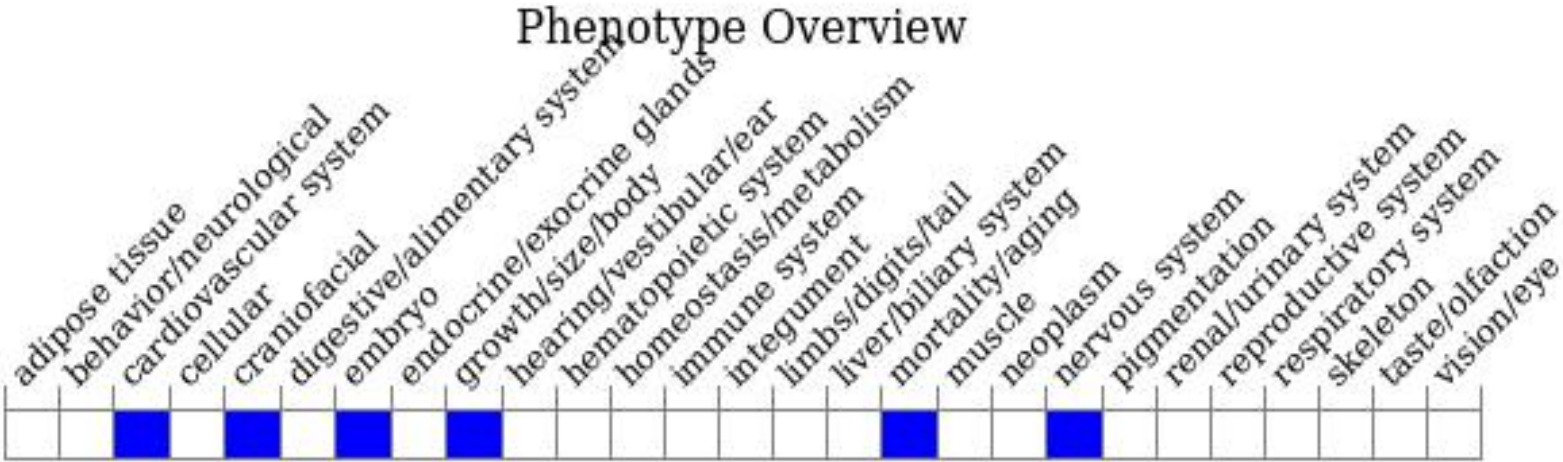◄ Reverse strand ──────────── 13.72 kb ────────────
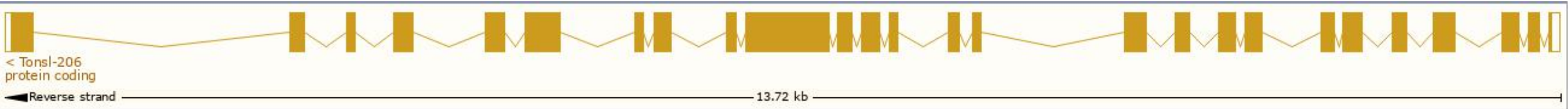
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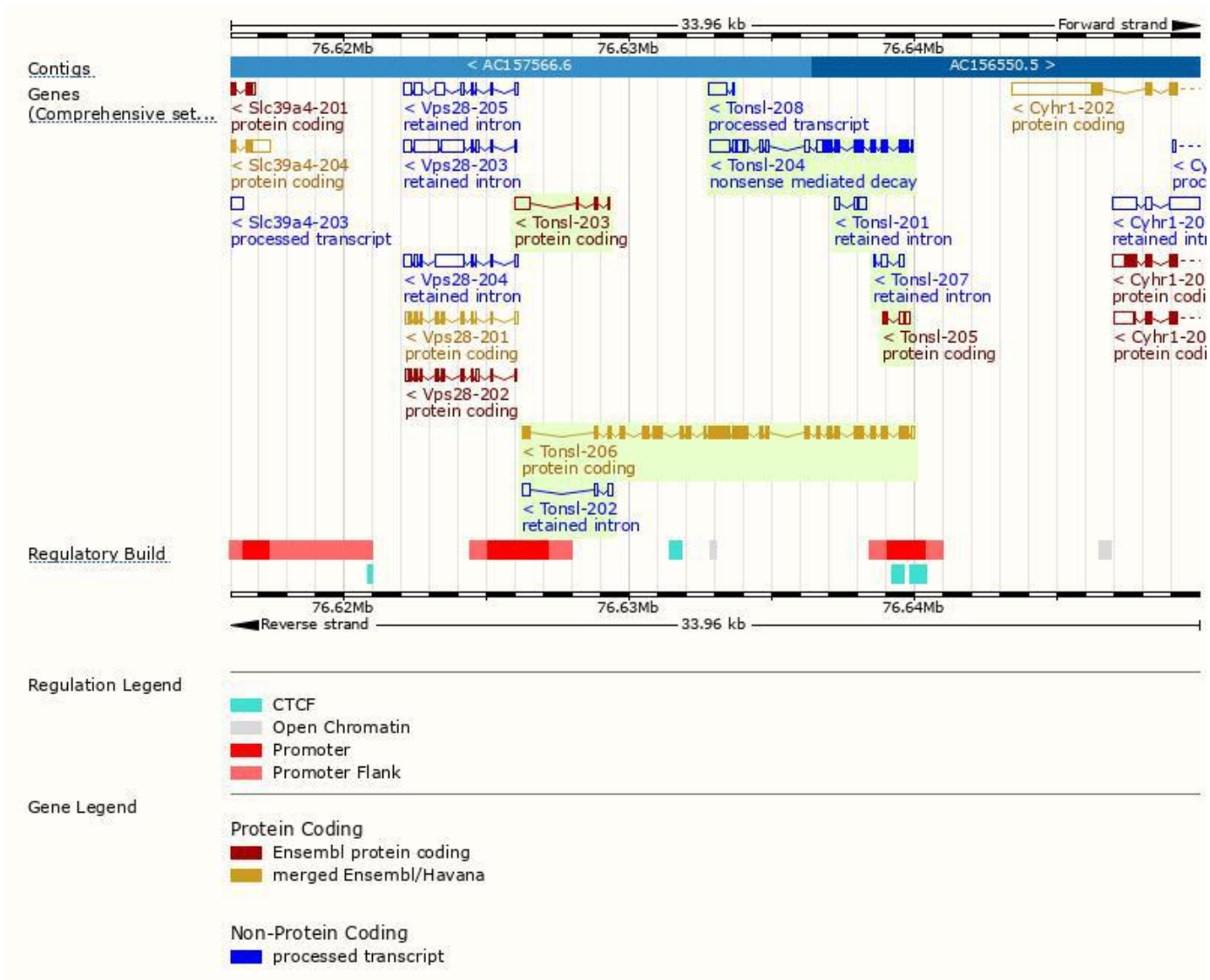
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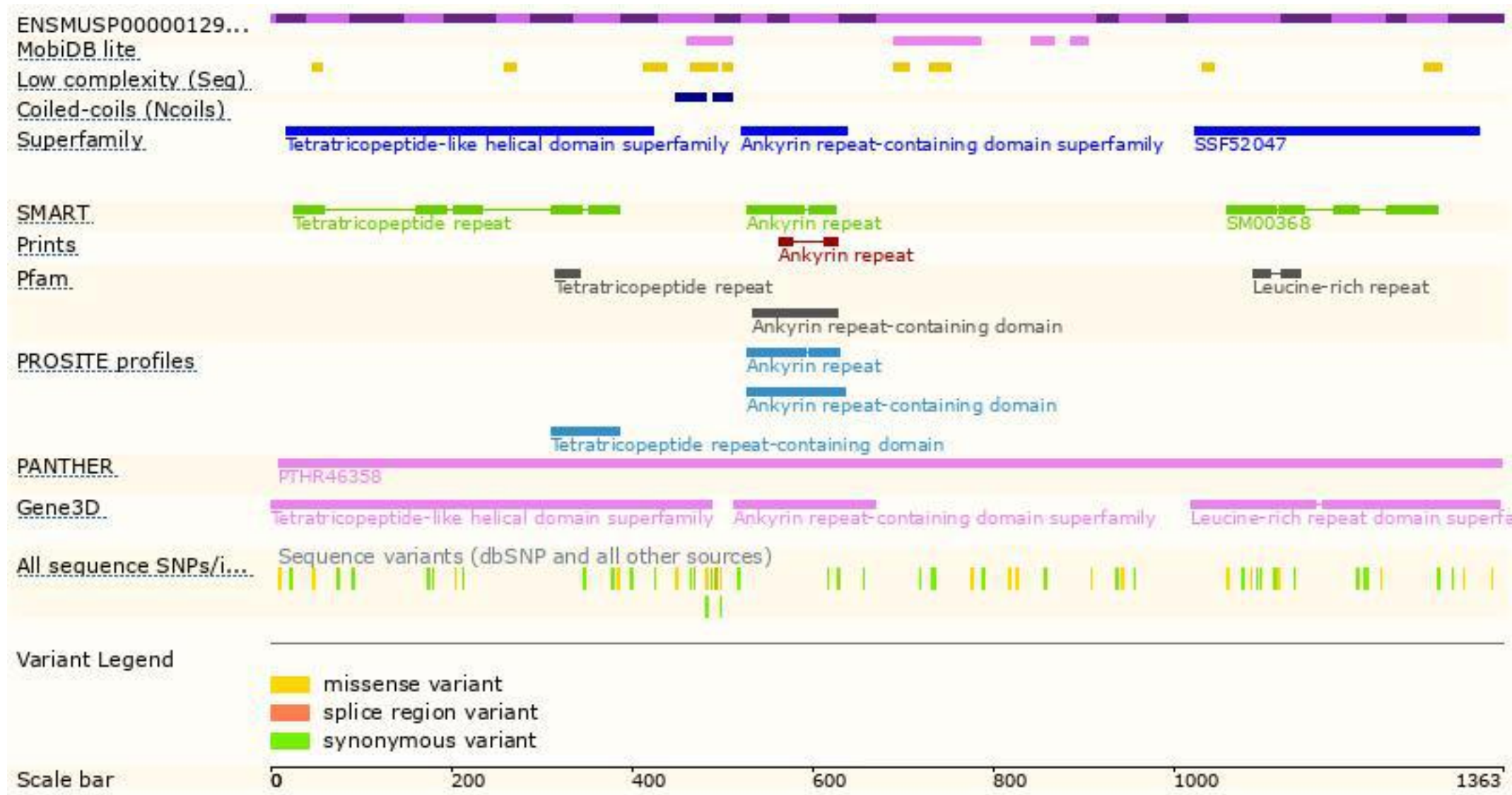
Mouse phenotype description(MGI)

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

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