

Tlr3 Cas9-CKO Strategy

Designer:

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Project Overview

Project Name

Tlr3

Project type

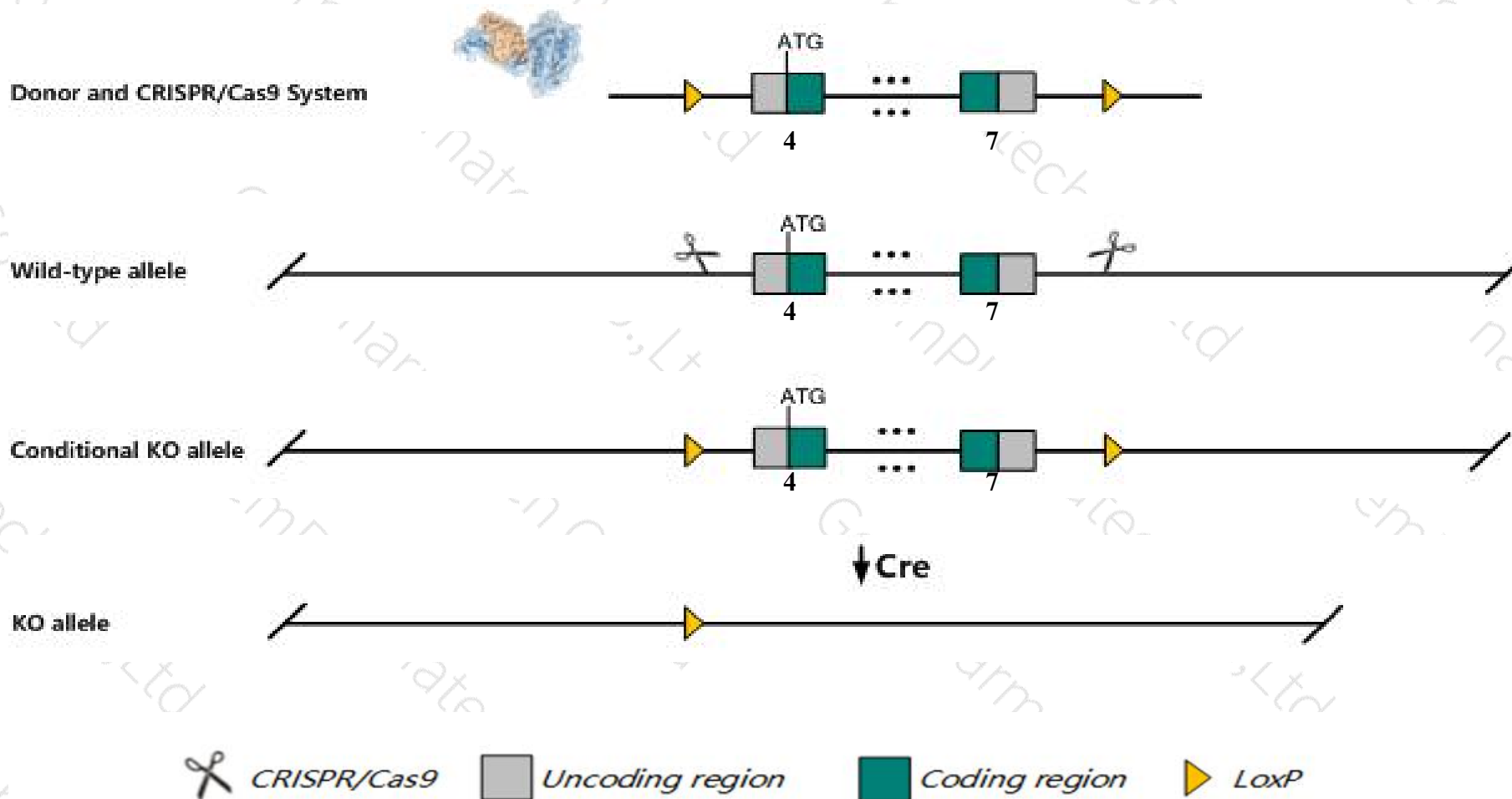
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tlr3* gene. The schematic diagram is as follows:



Technical routes

- The *Tlr3* gene has 9 transcripts. According to the structure of *Tlr3* gene, exon4-exon7 of *Tlr3-201* (ENSMUST00000034056.11) 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 *Tlr3* 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.

- According to the existing MGI data, Homozygotes for a null allele show alterations in innate immunity against different viruses, viral pathogenesis, anxiety, hippocampal synaptic plasticity, memory retention and neurogenesis. Homozygotes for another null allele show altered ds-RNA responses in dendritic and aorta smooth muscle cells.
- The *Tlr3* 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 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)

Tlr3 toll-like receptor 3 [Mus musculus (house mouse)]

Gene ID: 142980, updated on 9-Apr-2019

Summary

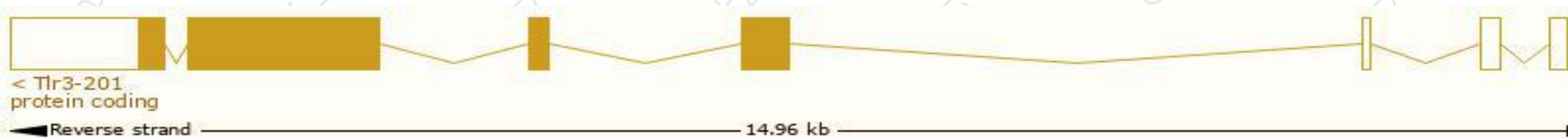
Official Symbol	Tlr3 provided by MGI
Official Full Name	toll-like receptor 3 provided by MGI
Primary source	MGI:MGI:2156367
See related	Ensembl:ENSMUSG000000031639
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI957183
Expression	Broad expression in bladder adult (RPKM 3.5), large intestine adult (RPKM 1.7) and 25 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

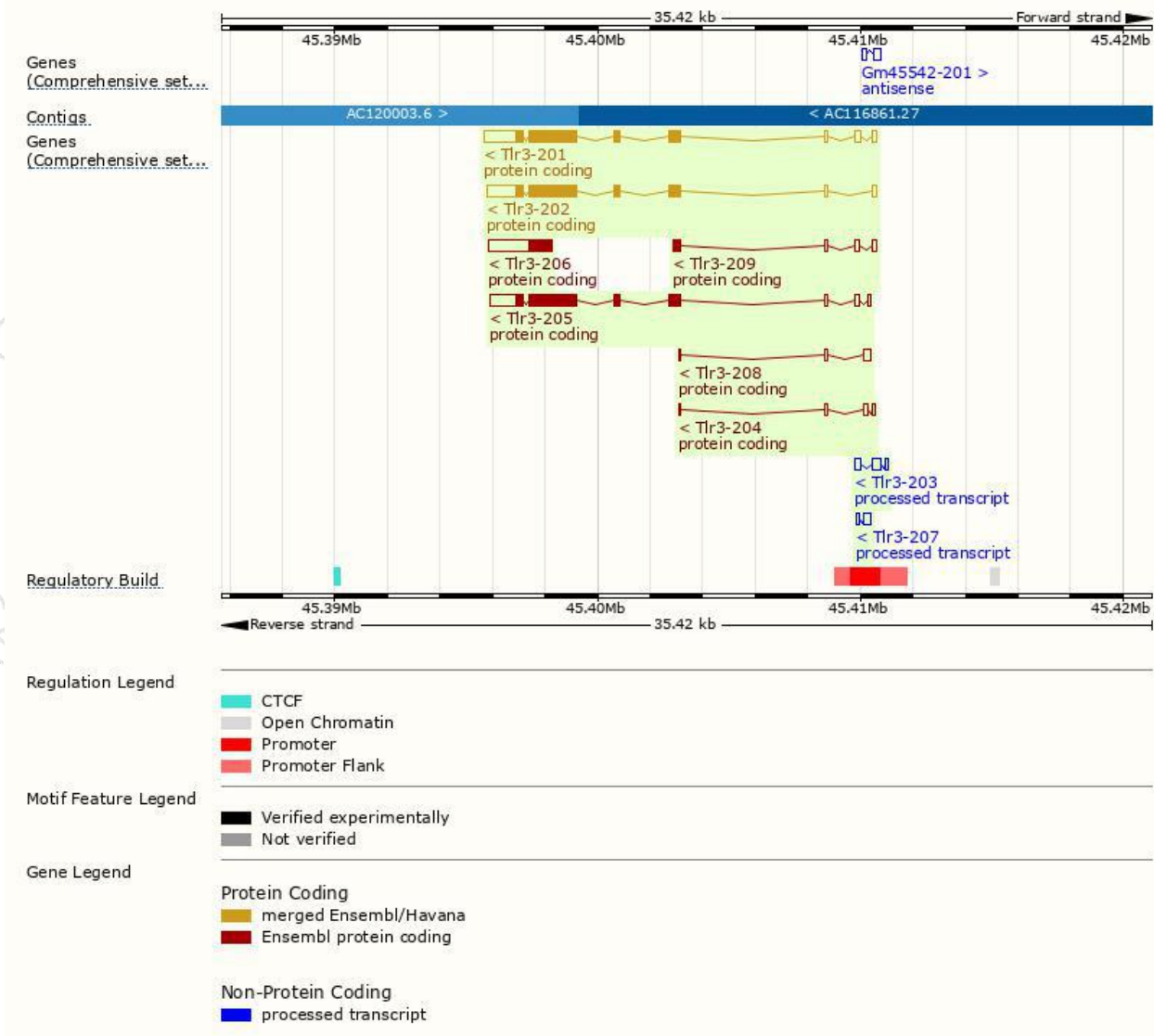
The gene has 9 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tlr3-209	ENSMUST00000211370.1	707	93aa	Protein coding	-	A0A1B0GSY9	CDS 3' incomplete TSL:2
Tlr3-208	ENSMUST00000210996.1	382	15aa	Protein coding	-	A0A1B0GTA2	CDS 3' incomplete TSL:2
Tlr3-207	ENSMUST00000210354.1	393	No protein	lncRNA	-	-	TSL:2
Tlr3-206	ENSMUST00000210013.1	2417	306aa	Protein coding	-	A0A1B0GS40	CDS 5' incomplete TSL:NA
Tlr3-205	ENSMUST00000209772.1	4096	905aa	Protein coding	CCDS22278	Q99MB1	TSL:1 GENCODE basic APPRIS P1
Tlr3-204	ENSMUST00000209651.1	387	7aa	Protein coding	-	A0A1Y7VI41	CDS 3' incomplete TSL:5
Tlr3-203	ENSMUST00000209269.1	649	No protein	lncRNA	-	-	TSL:3
Tlr3-202	ENSMUST00000167106.2	4093	905aa	Protein coding	CCDS22278	Q99MB1	TSL:1 GENCODE basic APPRIS P1
Tlr3-201	ENSMUST00000034056.11	4407	905aa	Protein coding	CCDS22278	Q99MB1	TSL:1 GENCODE basic APPRIS P1

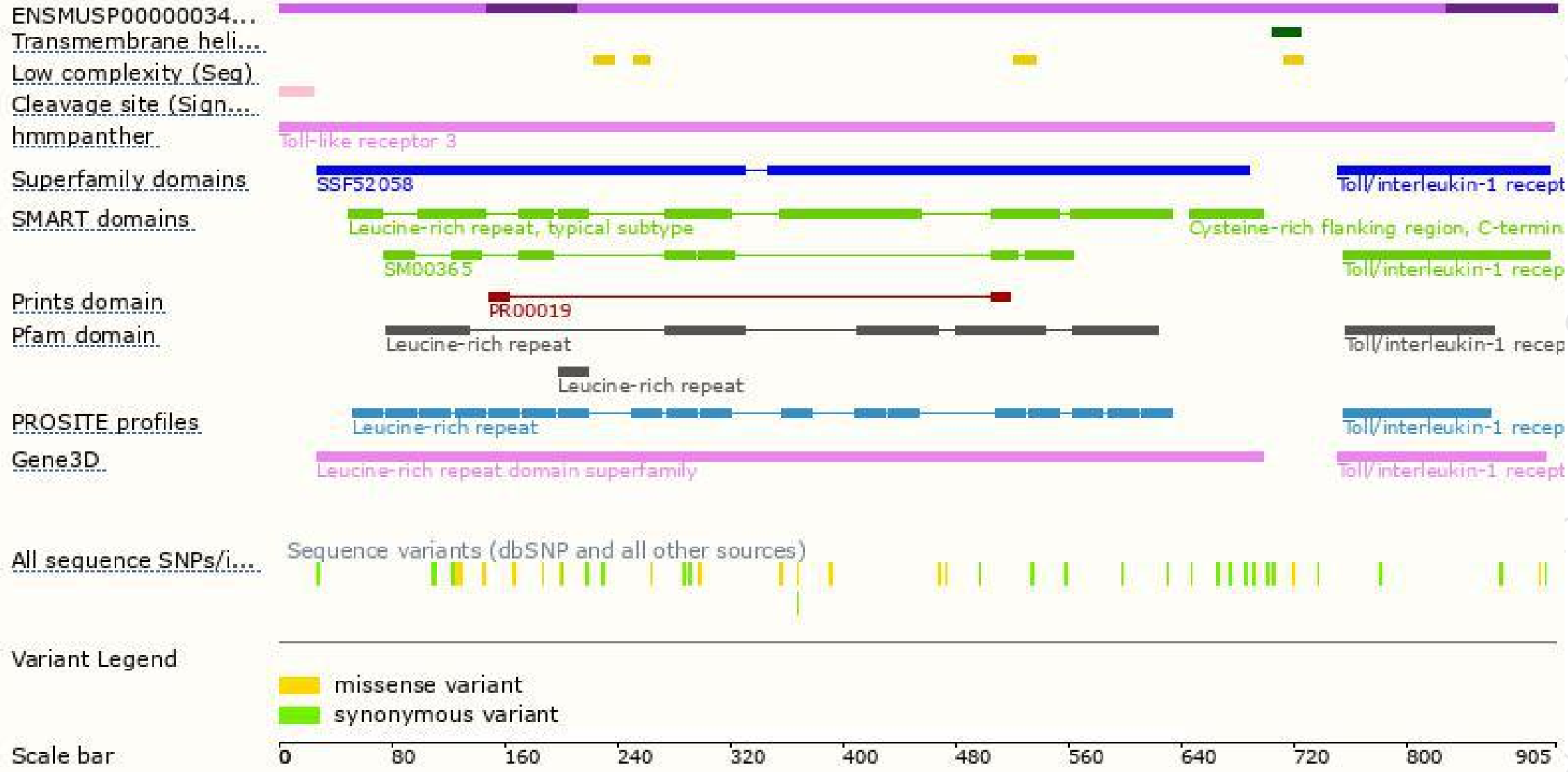
The strategy is based on the design of *Tlr3-201* transcript, The transcription is shown below



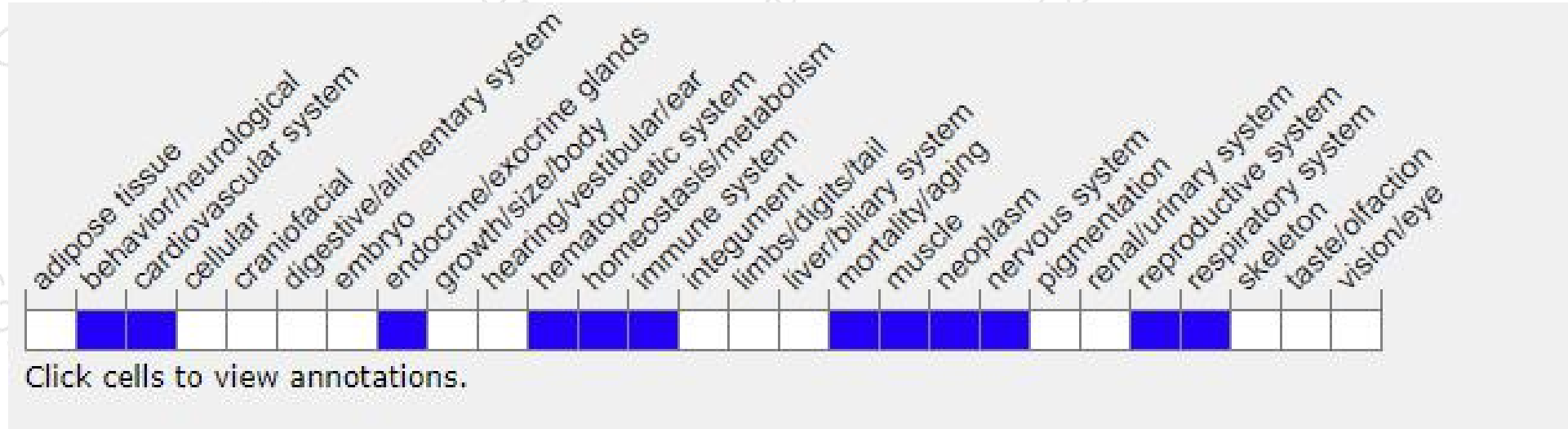
Genomic location distribution



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/>).

According to the existing MGI data, Homozygotes for a null allele show alterations in innate immunity against different viruses, viral pathogenesis, anxiety, hippocampal synaptic plasticity, memory retention and neurogenesis. Homozygotes for another null allele show altered ds-RNA responses in dendritic and aorta smooth muscle cells.

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

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