

Ttc7 Cas9-CKO Strategy

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Reviewer:	
Design Date:	2019-12-23

Project Overview

Project Name

Ttc7

Project type

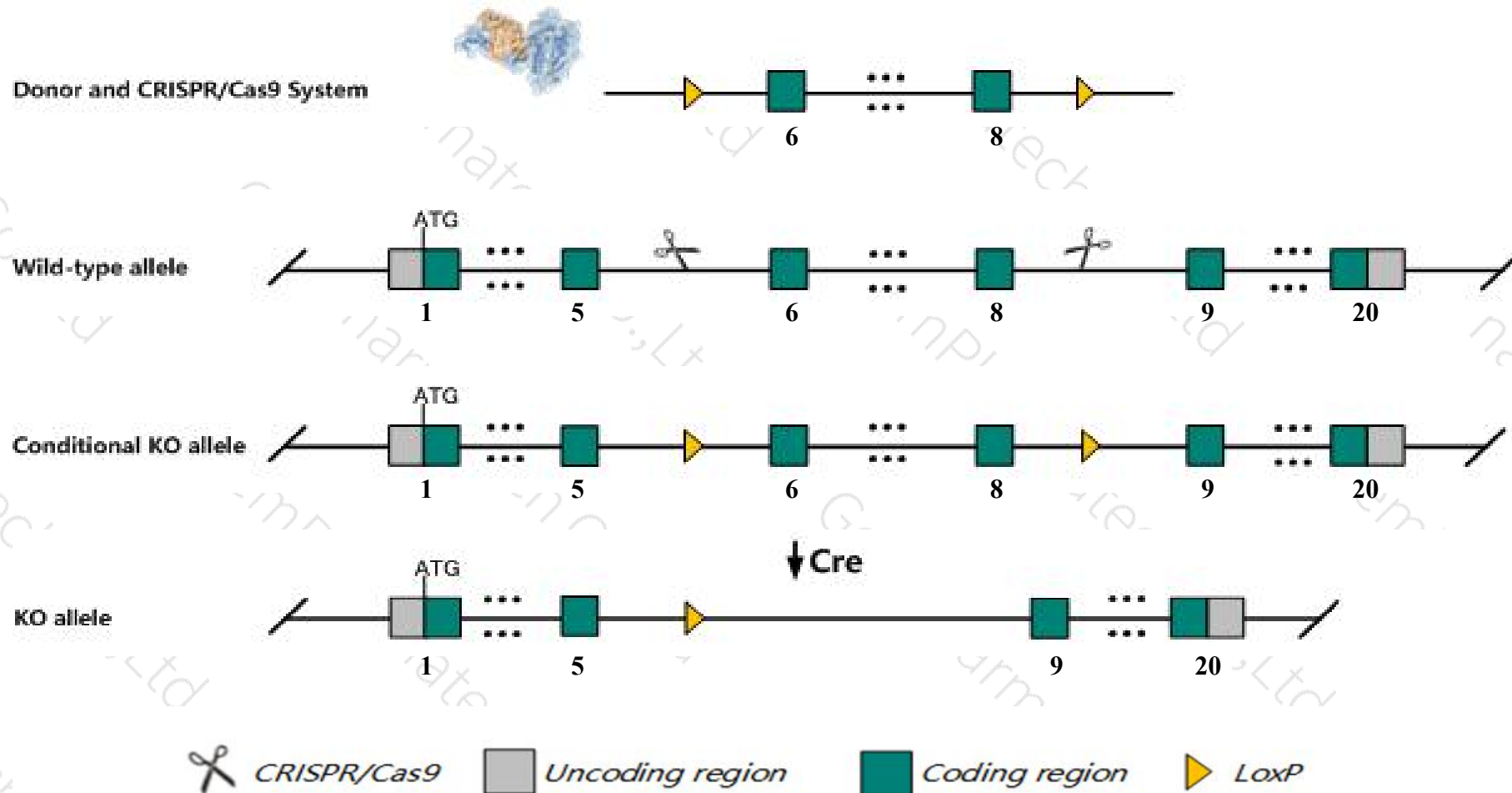
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ttc7* gene. The schematic diagram is as follows:



- The *Ttc7* gene has 10 transcripts. According to the structure of *Ttc7* gene, exon6-exon8 of *Ttc7-201* (ENSMUST00000041110.11) transcript is recommended as the knockout region. The region contains 301bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ttc7* 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 spontaneous mutation exhibit reduced growth, sparse hair, thickened, scaly skin, increased numbers of splenic B cells, macrophages, and erythroid cells, elevated IgE, glomerulonephritis, and forestomach papillomas.
- Transcript *Ttc7*-203/206/210 lncRNA may be unaffected.
- The *Ttc7* gene is located on the Chr17. 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)

Ttc7 tetratricopeptide repeat domain 7 [*Mus musculus* (house mouse)]

Gene ID: 225049, updated on 18-Nov-2019

Summary



Official Symbol Ttc7 provided by MGI

Official Full Name tetratricopeptide repeat domain 7 provided by MGI

Primary source [MGI:MGI:1920999](#)

See related [Ensembl:ENSMUSG00000036918](#)

Gene type protein coding

RefSeq status VALIDATED

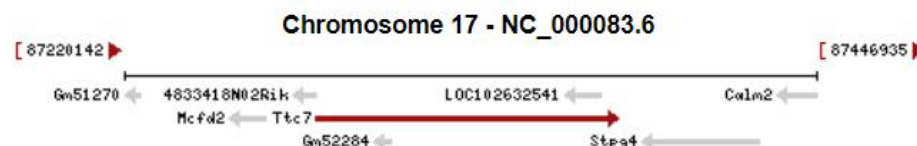
Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as fsn; hea; Ttc7a; 1110035E02Rik; 1700007L07Rik

Expression Broad expression in duodenum adult (RPKM 23.6), spleen adult (RPKM 20.7) and 24 other tissues [See more](#)

Orthologs [human](#) [all](#)

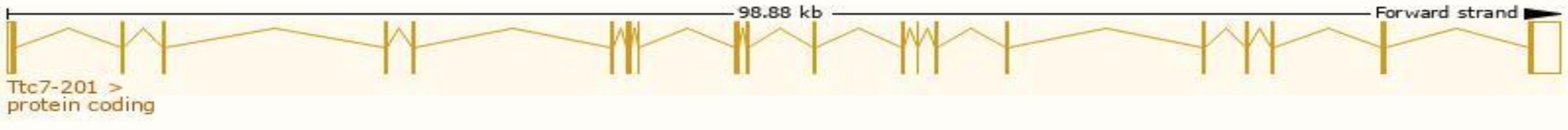


Transcript information (Ensembl)

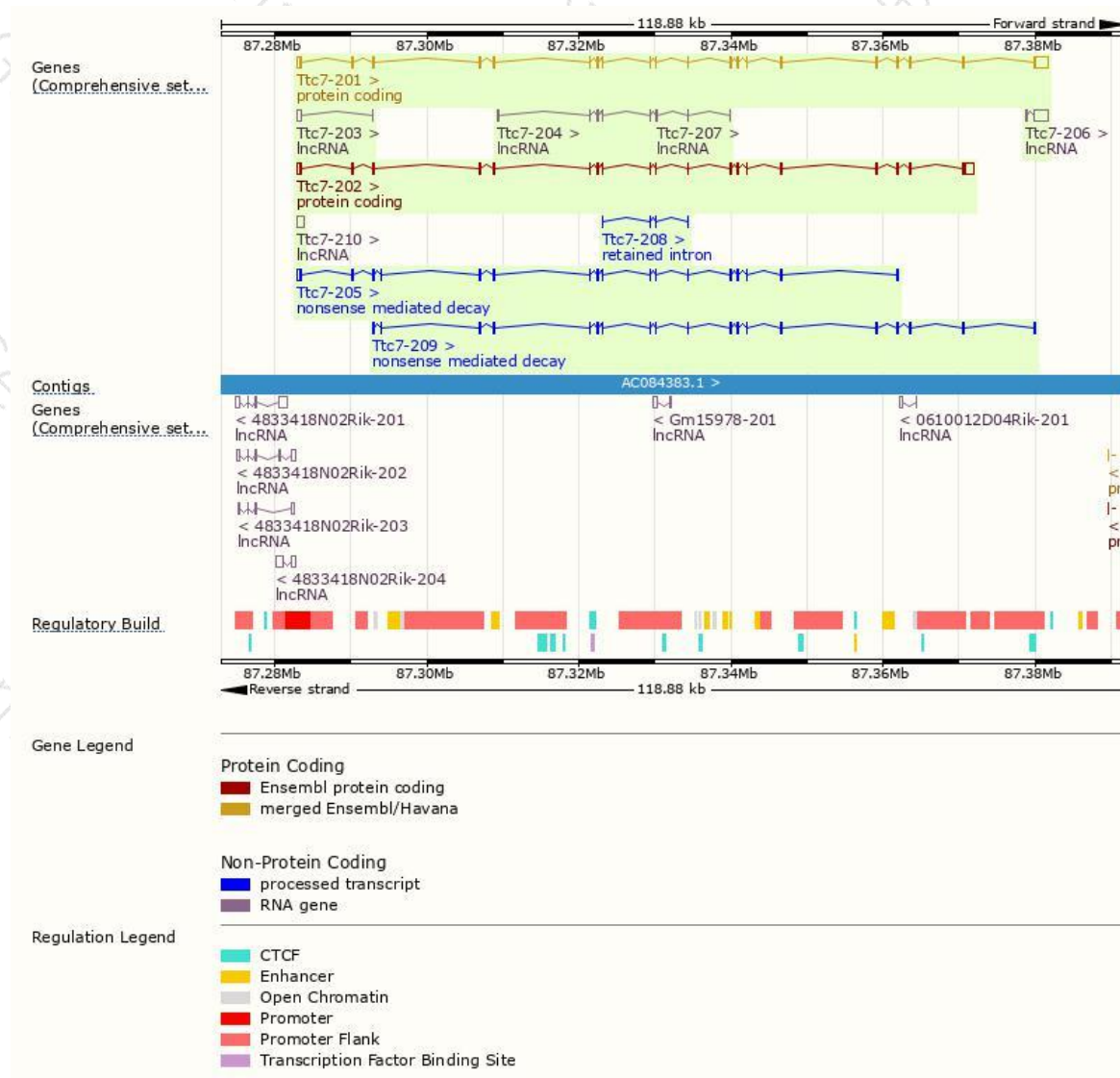
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ttc7-201	ENSMUST00000041110.11	4614	858aa	Protein coding	CCDS29016	Q8BGB2	TSL:1 GENCODE basic APPRIS P1
Ttc7-202	ENSMUST00000125875.7	3917	822aa	Protein coding	-	D3Z0R8	TSL:2 GENCODE basic
Ttc7-209	ENSMUST00000154255.7	2304	93aa	Nonsense mediated decay	-	F6ZVR4	CDS 5' incomplete TSL:5
Ttc7-205	ENSMUST00000144204.7	2209	210aa	Nonsense mediated decay	-	D6RG81	TSL:5
Ttc7-208	ENSMUST00000153014.1	349	No protein	Retained intron	-	-	TSL:5
Ttc7-206	ENSMUST00000148126.1	2028	No protein	lncRNA	-	-	TSL:2
Ttc7-210	ENSMUST00000234468.1	868	No protein	lncRNA	-	-	-
Ttc7-204	ENSMUST00000127970.7	670	No protein	lncRNA	-	-	TSL:3
Ttc7-203	ENSMUST00000126497.1	637	No protein	lncRNA	-	-	TSL:3
Ttc7-207	ENSMUST00000148554.1	219	No protein	lncRNA	-	-	TSL:5

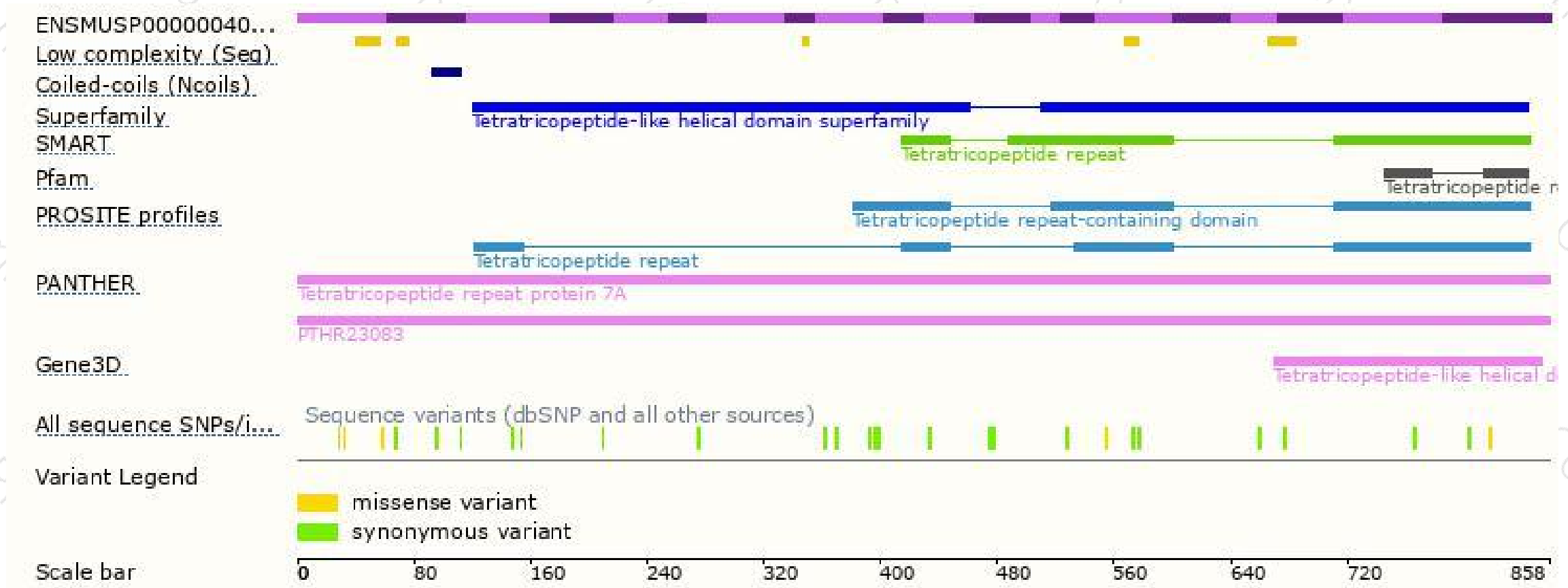
The strategy is based on the design of *Ttc7-201* transcript,The transcription is shown below



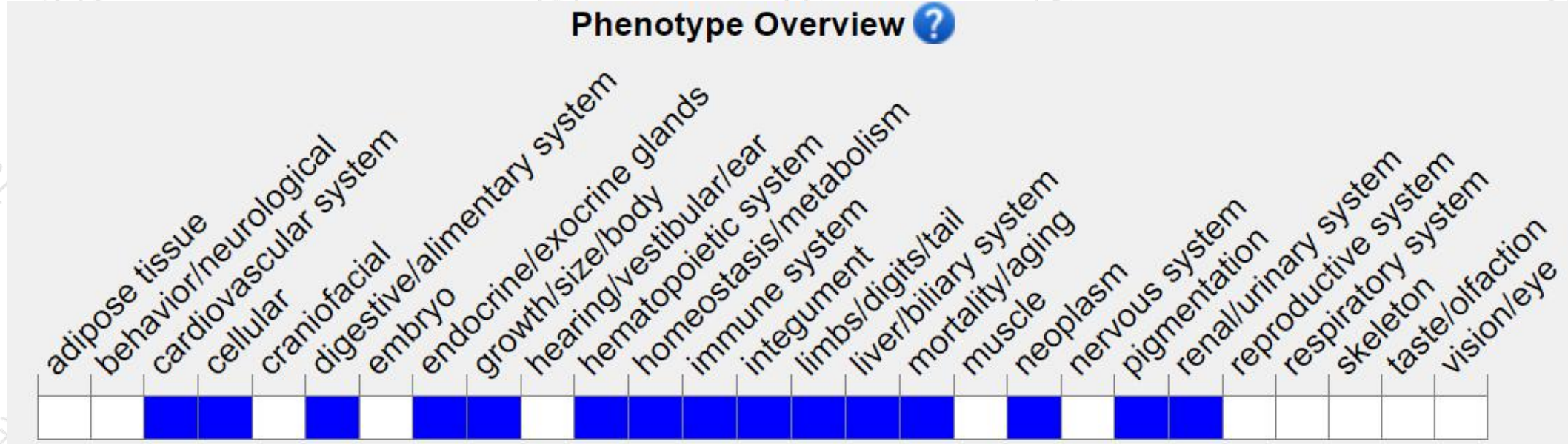
Genomic location distribution



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 spontaneous mutation exhibit reduced growth, sparse hair, thickened, scaly skin, increased numbers of splenic B cells, macrophages, and erythroid cells, elevated IgE, glomerulonephritis, and forestomach papillomas.

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

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