Hells Cas9-CKO Strategy

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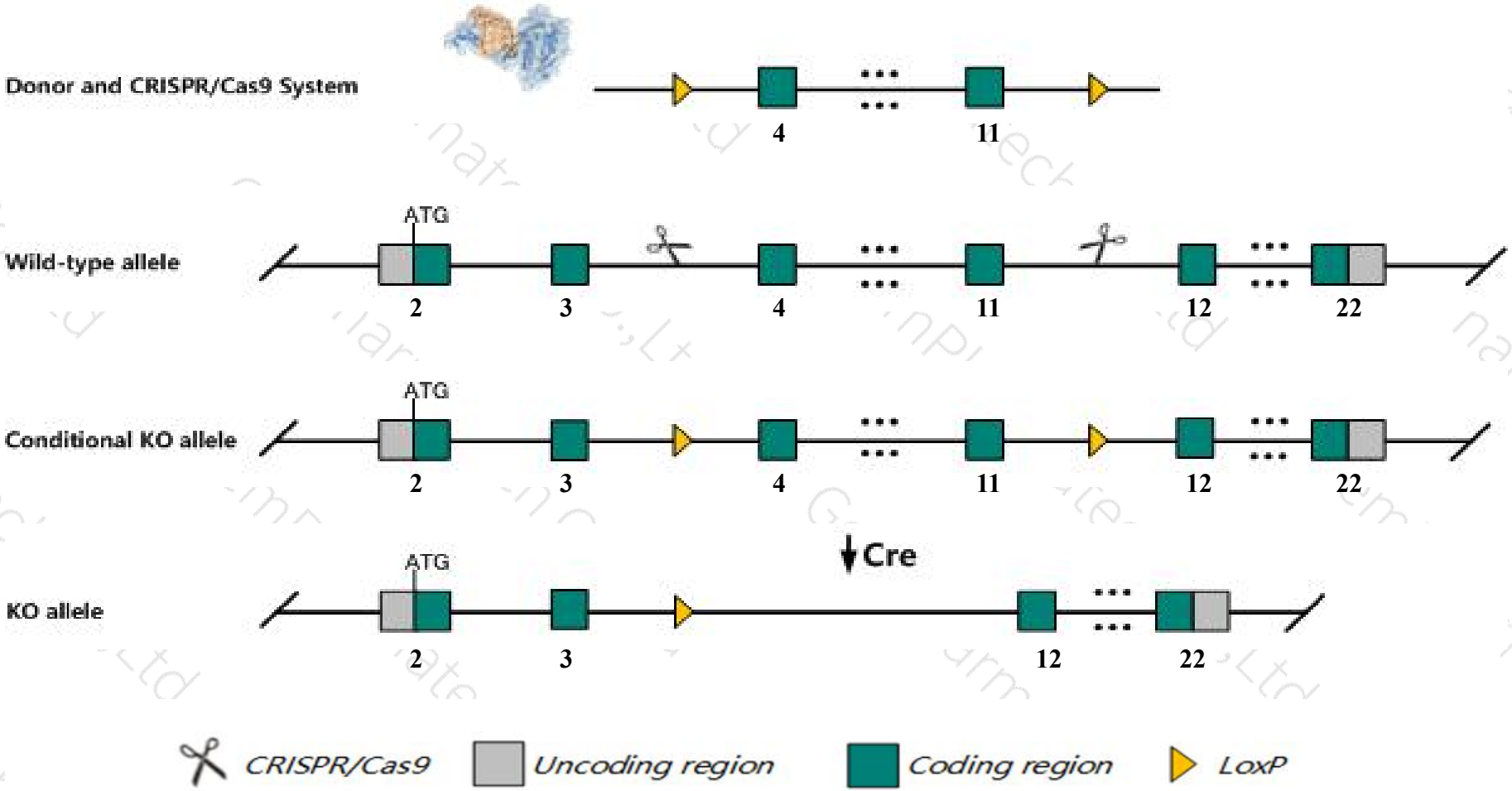
Project Overview

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

Conditional Knockout strategy

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



Technical routes

- The *Hells* gene has 6 transcripts. According to the structure of *Hells* gene, exon4-exon11 of *Hells-201* (ENSMUST00000025965.11) transcript is recommended as the knockout region.The region contains 950bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Hells* 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,Homozygotes for a null allele show DNA hypomethylation, delayed growth, multiorgan and skeletal defects, premature graying, alopecia, low fat deposition, kyphosis, cachexia and early death. Homozygotes for another null allele show neonatal death, low birth weight, lymphoid defects and renal lesions.

- The *Hells* gene is located on the Chr19. 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）

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Hells helicase, lymphoid specific [Mus musculus (house mouse)]

Gene ID: 15201, updated on 31-Jan-2019

Summary

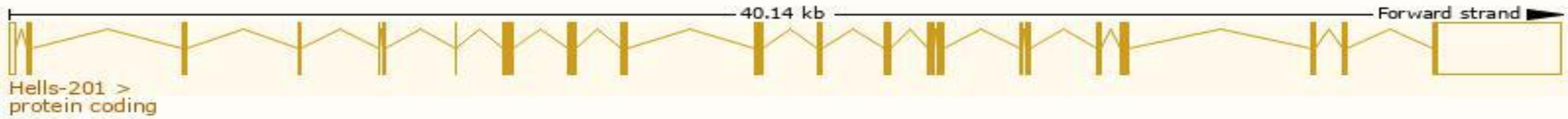
Official Symbol	Hells provided by MGI
Official Full Name	helicase, lymphoid specific provided by MGI
Primary source	MGI:MGI:106209
See related	Ensembl:ENSMUSG00000025001
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI323785, E130115I21Rik, LSH, Lysh, PASG, YFK8
Expression	Biased expression in CNS E11.5 (RPKM 12.2), liver E14 (RPKM 8.5) and 10 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

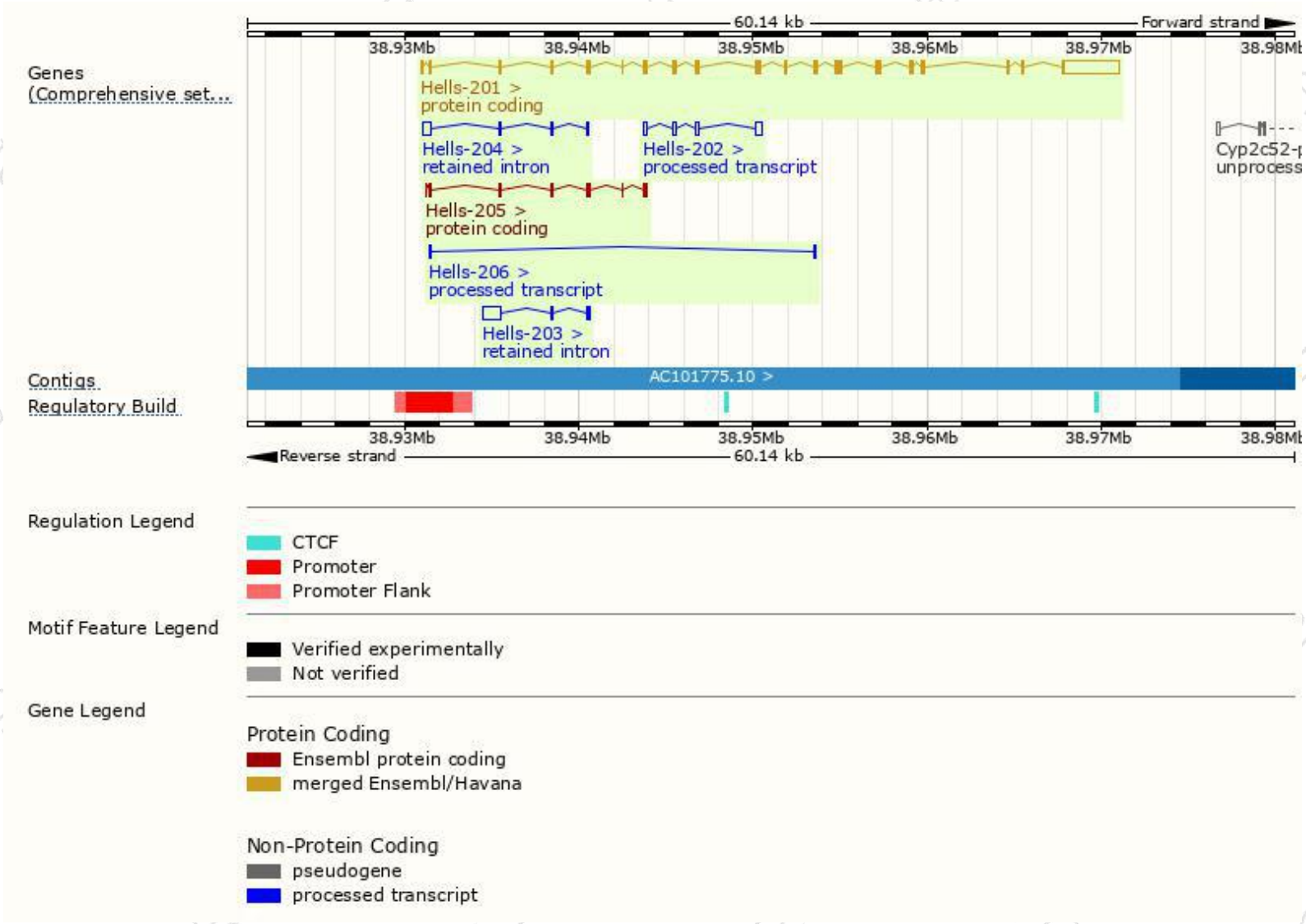
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hells-201	ENSMUST00000025965.11	5868	821aa	Protein coding	CCDS29789	Q60848	TSL:1 GENCODE basic APPRIS P1
Hells-205	ENSMUST00000145051.1	689	209aa	Protein coding	-	D3Z414	CDS 3' incomplete TSL:3
Hells-202	ENSMUST00000127968.1	868	No protein	Processed transcript	-	-	TSL:2
Hells-206	ENSMUST00000155465.1	190	No protein	Processed transcript	-	-	TSL:5
Hells-203	ENSMUST00000128949.1	1128	No protein	Retained intron	-	-	TSL:3
Hells-204	ENSMUST00000138292.7	693	No protein	Retained intron	-	-	TSL:5

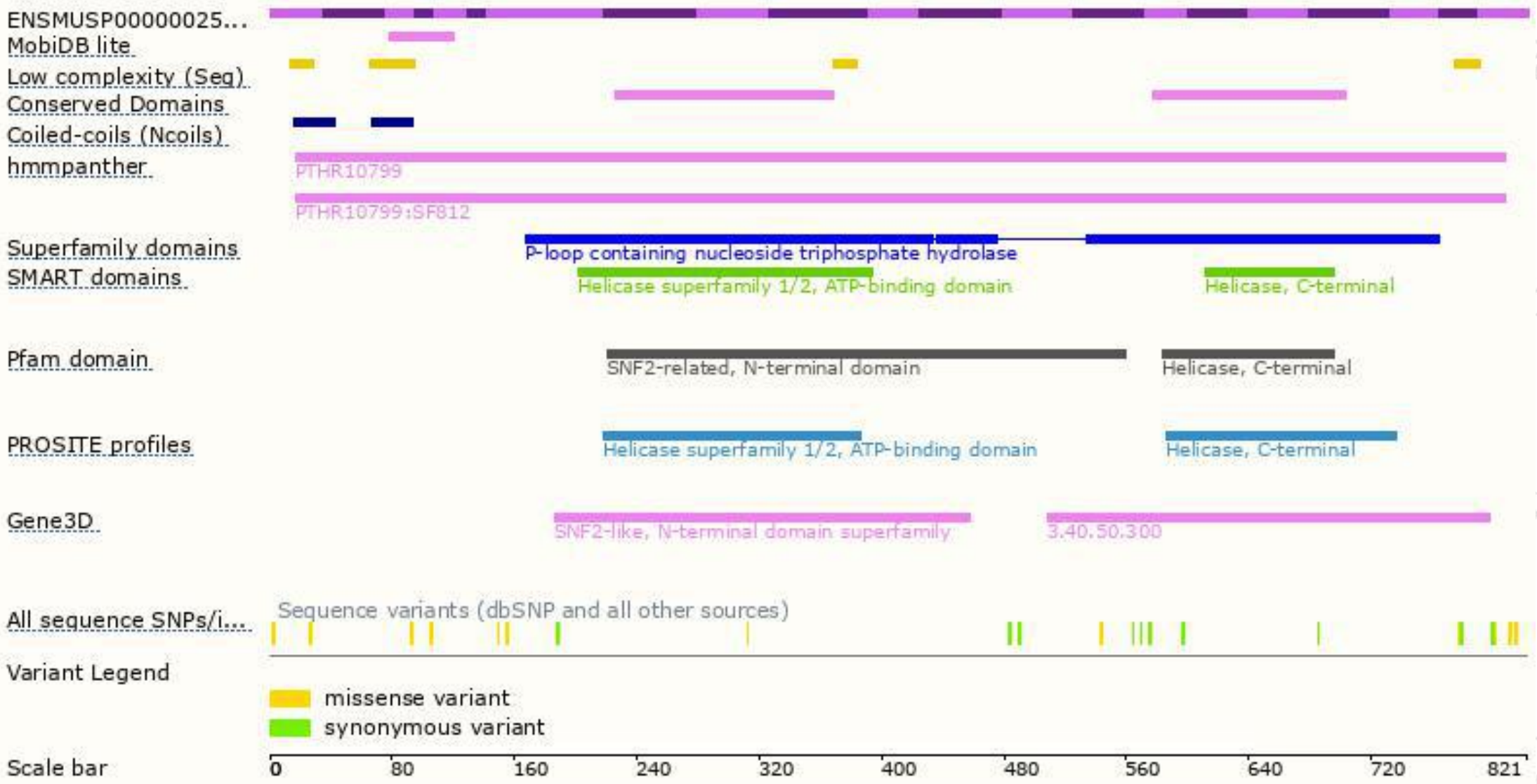
The strategy is based on the design of *Hells-201* transcript,The transcription is shown below



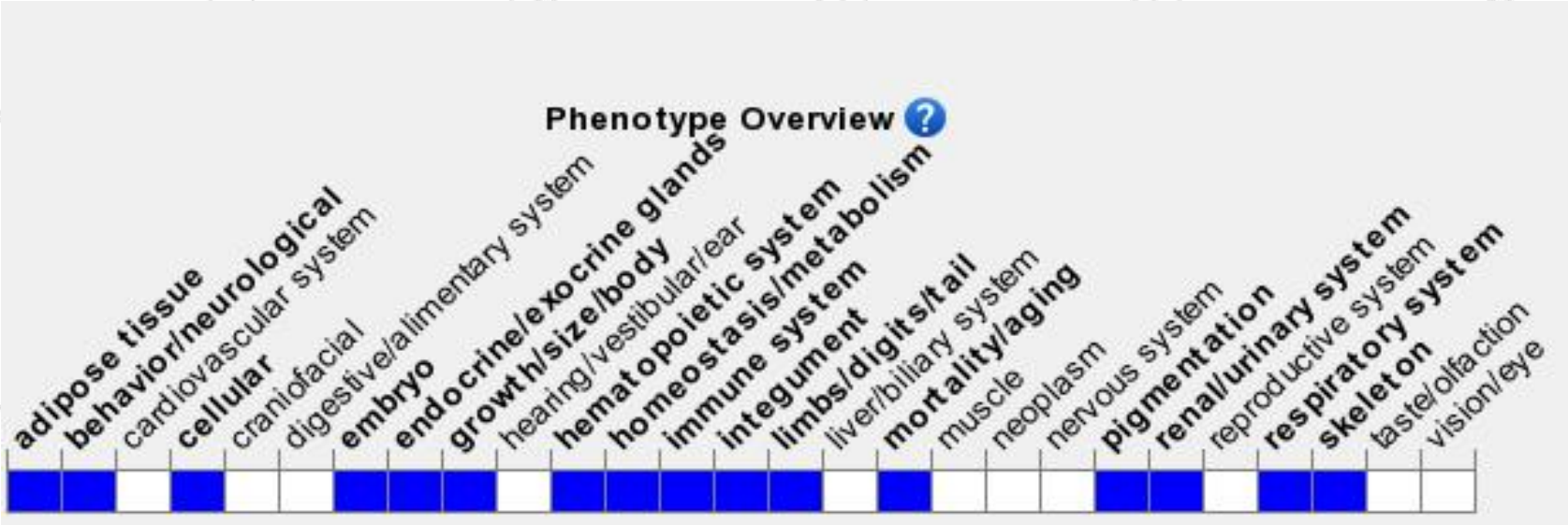
Genomic location distribution



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/).

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

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