Cfh Cas9-CKO Strategy

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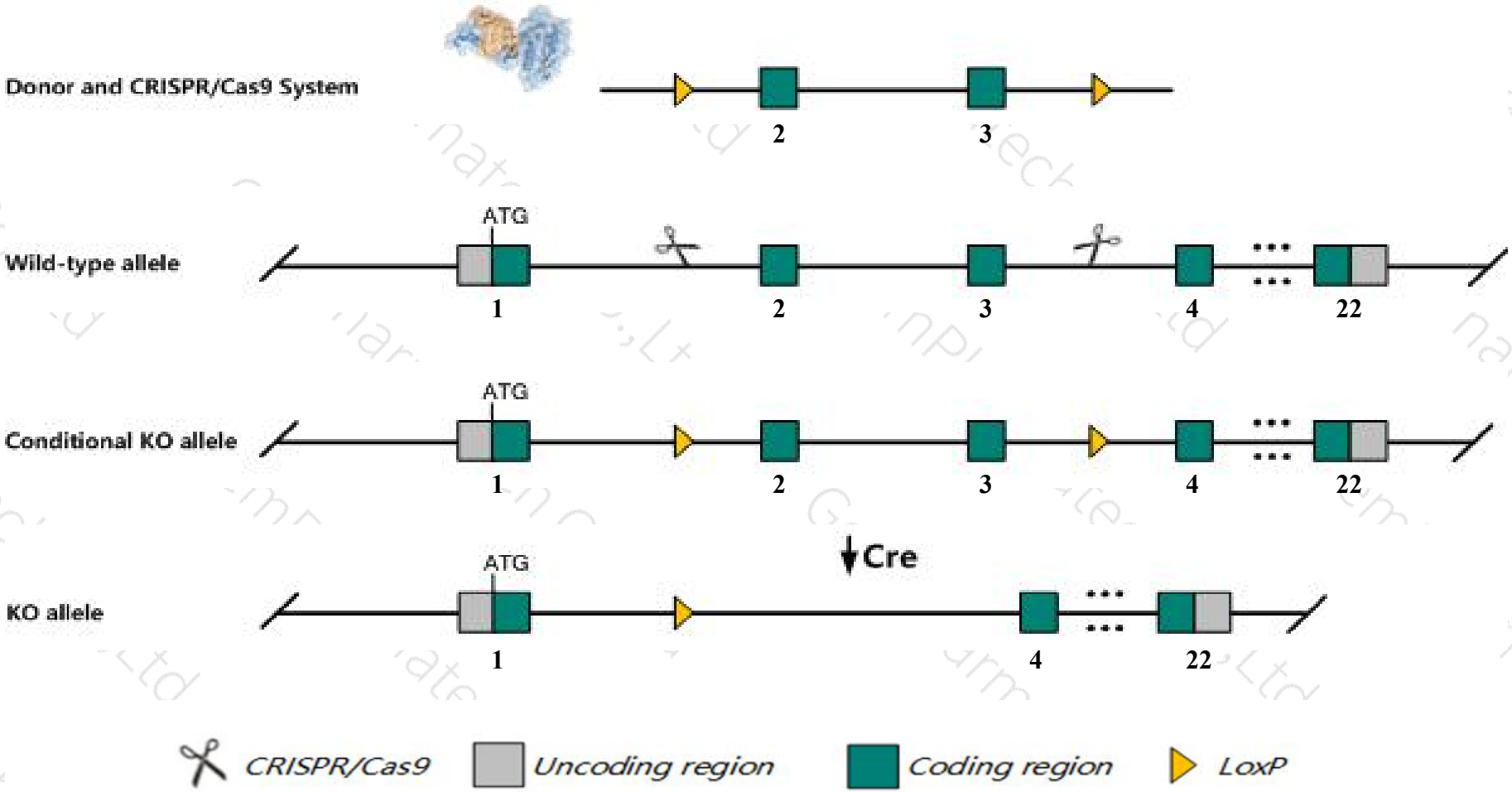
Project Overview

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

Conditional Knockout strategy

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



Technical routes

- The *Cfh* gene has 8 transcripts. According to the structure of *Cfh* gene, exon2-exon3 of *Cfh-202* (ENSMUST00000111976.8) transcript is recommended as the knockout region.The region contains 292bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Cfh* 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,Homozygous mutation of this gene results in markedly reduced serum C3, abnormal renal histology, spontaneous membranoproliferative glomerulonephritis (MPGN), hematuria, proteinuria, and increased mortality at 8 months of age.

➢ The *Cfh* gene is located on the Chr1. 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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Cfh complement component factor h [Mus musculus (house mouse)]

Gene ID: 12628, updated on 19-Mar-2019

Summary

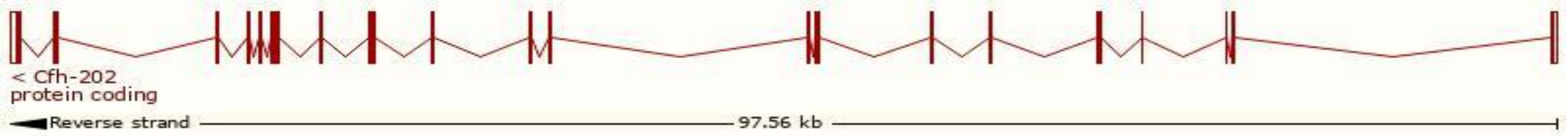
Official Symbol	Cfh provided by MGI
Official Full Name	complement component factor h provided byMGI
Primary source	MGI:MGI:88385
See related	Ensembl:ENSMUSG00000026365
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Mud-1, NOM, Sas-1, Sas1
Expression	Biased expression in liver E18 (RPKM 75.9), liver adult (RPKM 32.7) and 10 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

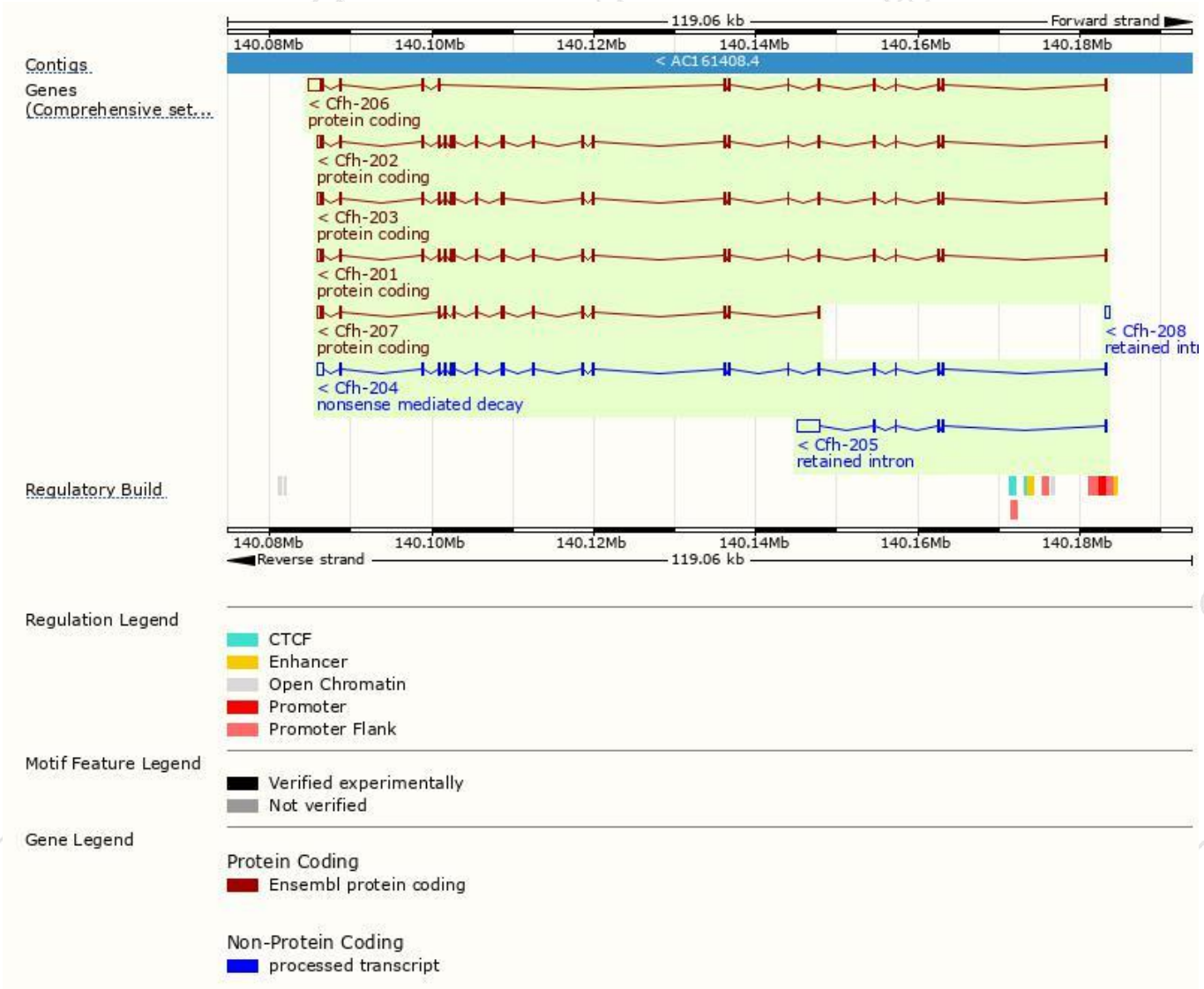
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cfh-202	ENSMUST00000111976.8	4365	1252aa	Protein coding	CCDS48388	E9Q8I0	TSL:1 GENCODE basic APPRIS P2
Cfh-201	ENSMUST00000066859.12	4361	1234aa	Protein coding	-	P06909	TSL:1 GENCODE basic APPRIS ALT2
Cfh-203	ENSMUST00000111977.7	4100	1195aa	Protein coding	-	E9Q8H9	TSL:1 GENCODE basic APPRIS ALT2
Cfh-206	ENSMUST00000192880.5	3746	707aa	Protein coding	-	A0A0A6YVP8	TSL:5 GENCODE basic
Cfh-207	ENSMUST00000192919.5	2976	837aa	Protein coding	-	A0A0A6YWP4	CDS 5' incomplete TSL:5
Cfh-204	ENSMUST00000123238.1	4300	1110aa	Nonsense mediated decay	-	D6RGQ0	TSL:1
Cfh-205	ENSMUST00000148225.1	3415	No protein	Retained intron	-	-	TSL:1
Cfh-208	ENSMUST00000194688.1	631	No protein	Retained intron	-	-	TSL:NA

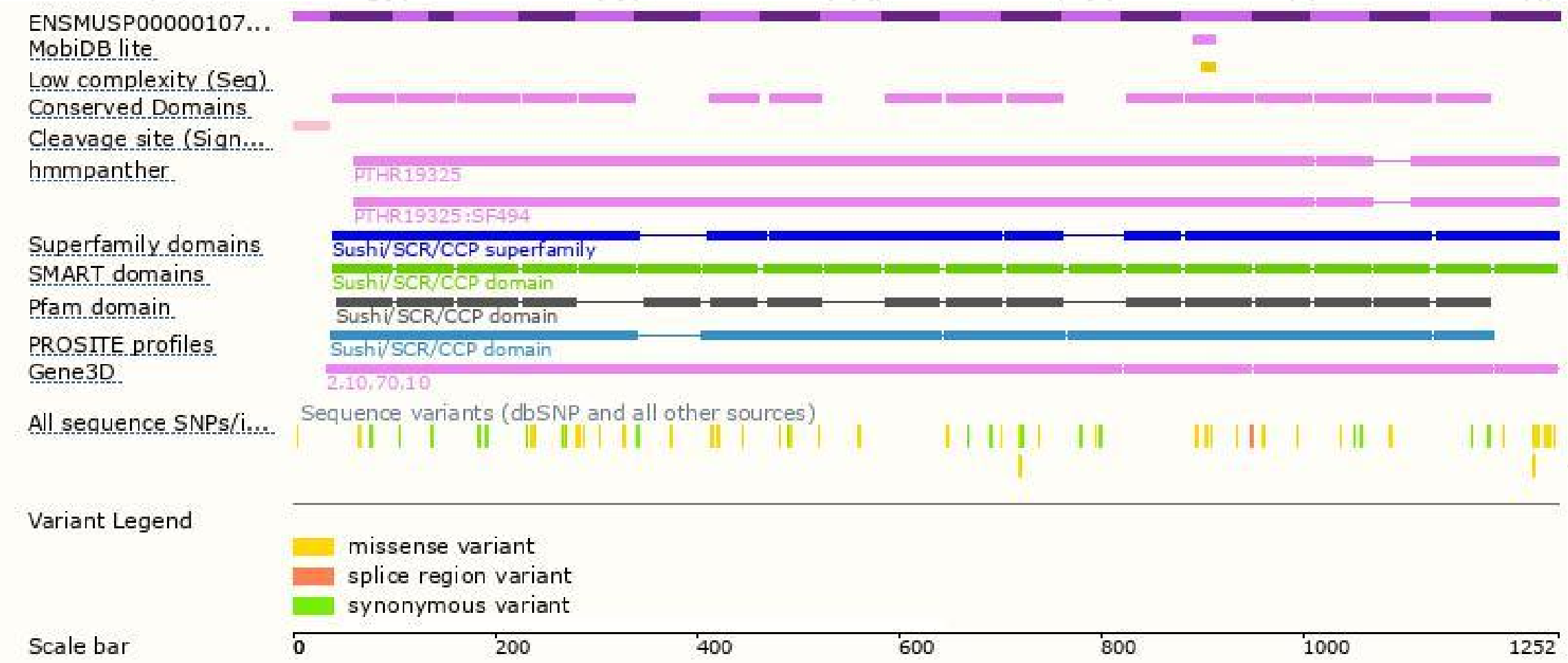
The strategy is based on the design of *Cfh-202* transcript,The transcription is shown below



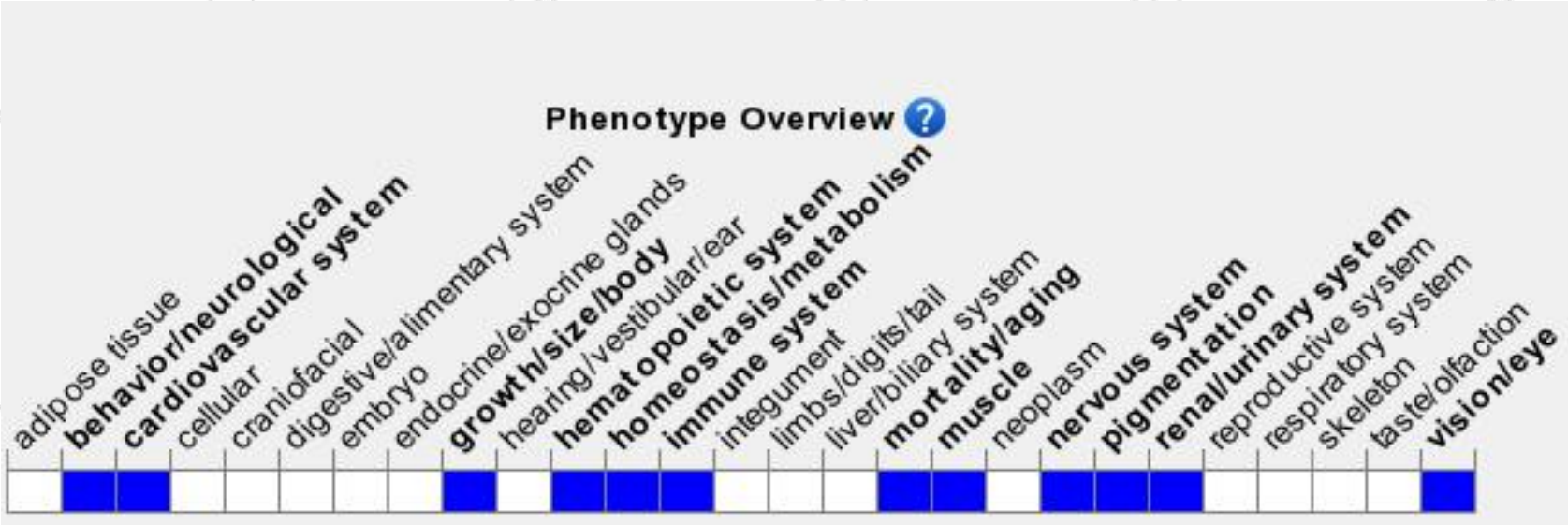
Genomic location distribution



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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