Brip1 Cas9-CKO Strategy

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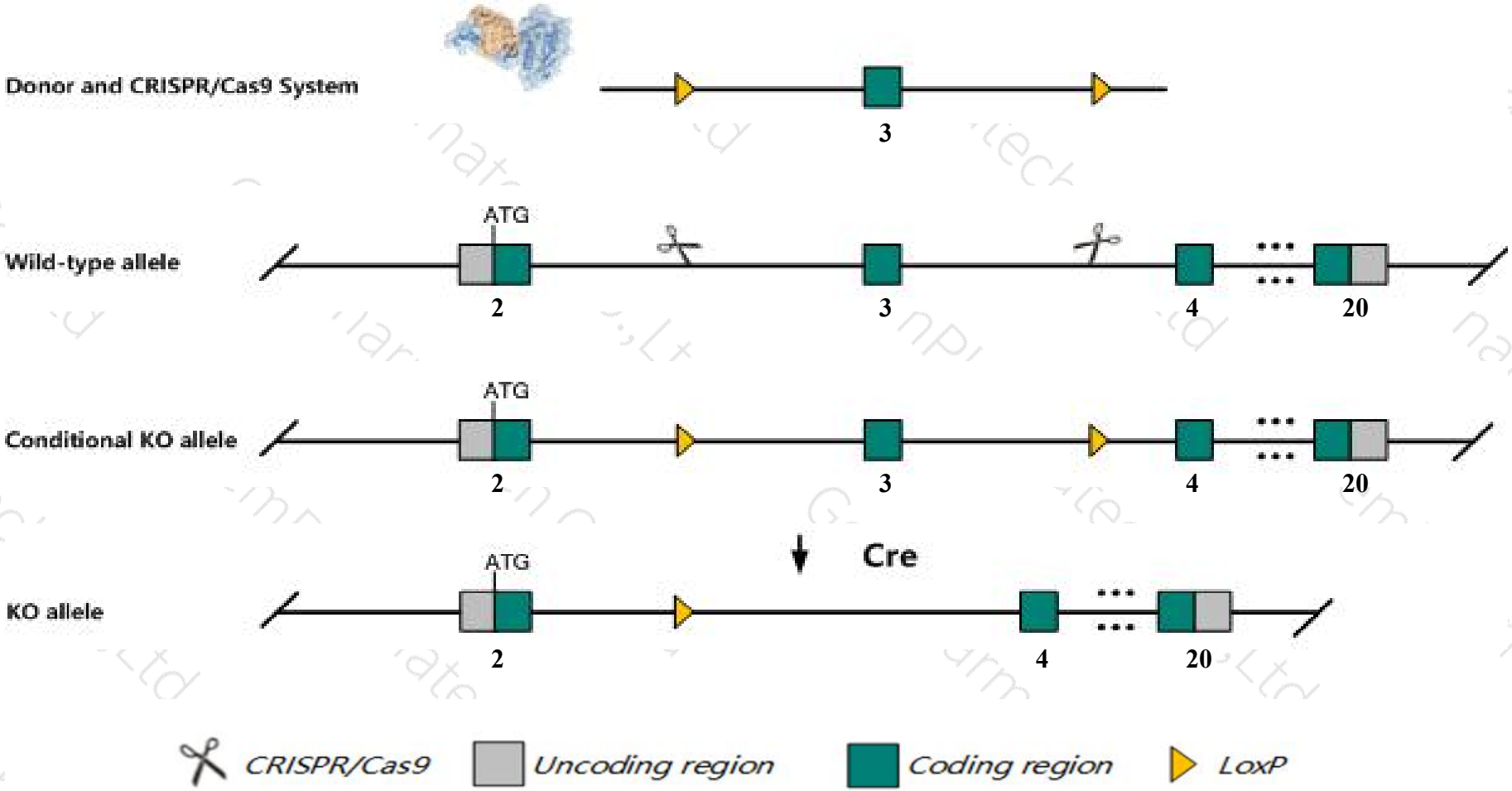
Project Overview

Project Name	***Brip1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Brip1* gene. The schematic diagram is as follows:



Technical routes

- The *Brip1* gene has 3 transcripts. According to the structure of *Brip1* gene, exon3 of *Brip1-201* (ENSMUST00000044423.3) transcript is recommended as the knockout region.The region contains 112bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Brip1* 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,Mice homozygous for a gene trapped allele exhibit gonadal atrophy, subfertility, germ cell attrition, epithelial tumor predisposition, increased cellular sensitivity to interstrand crosslink-inducing agents, hypersensitivity to replication inhibitors, and predisposition to lymphoma.

➢ The *Brip1* gene is located on the Chr11. 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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Brip1 BRCA1 interacting protein C-terminal helicase 1 [Mus musculus (house mouse)]

Gene ID: 237911, updated on 31-Jan-2019

Summary

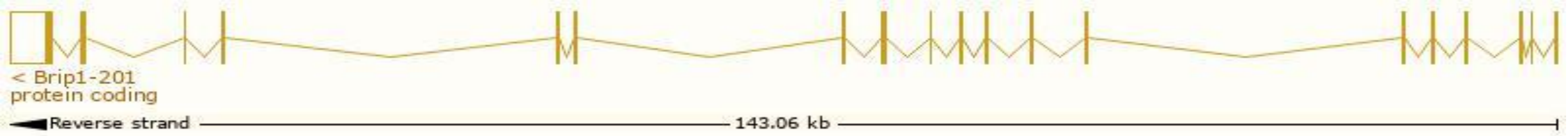
Official Symbol	Brip1 provided by MGI
Official Full Name	BRCA1 interacting protein C-terminal helicase 1 provided by MGI
Primary source	MGI:MGI:2442836
See related	Ensembl:ENSMUSG00000034329
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	3110009N10Rik, 8030460J03Rik, Bach1, FACJ, Fancj, OF
Summary	This gene encodes a member of the DEAH subfamily of DEAD box helicases. A similar protein in humans is both a DNA-dependent ATPase and a 5-prime-to-3-prime DNA helicase, and plays a role in the repair of DNA double stranded breaks through interaction with the breast cancer-associated tumor suppressor BRCA1. [provided by RefSeq, Feb 2011]
Expression	Biased expression in CNS E11.5 (RPKM 1.7), liver E14 (RPKM 1.5) and 13 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

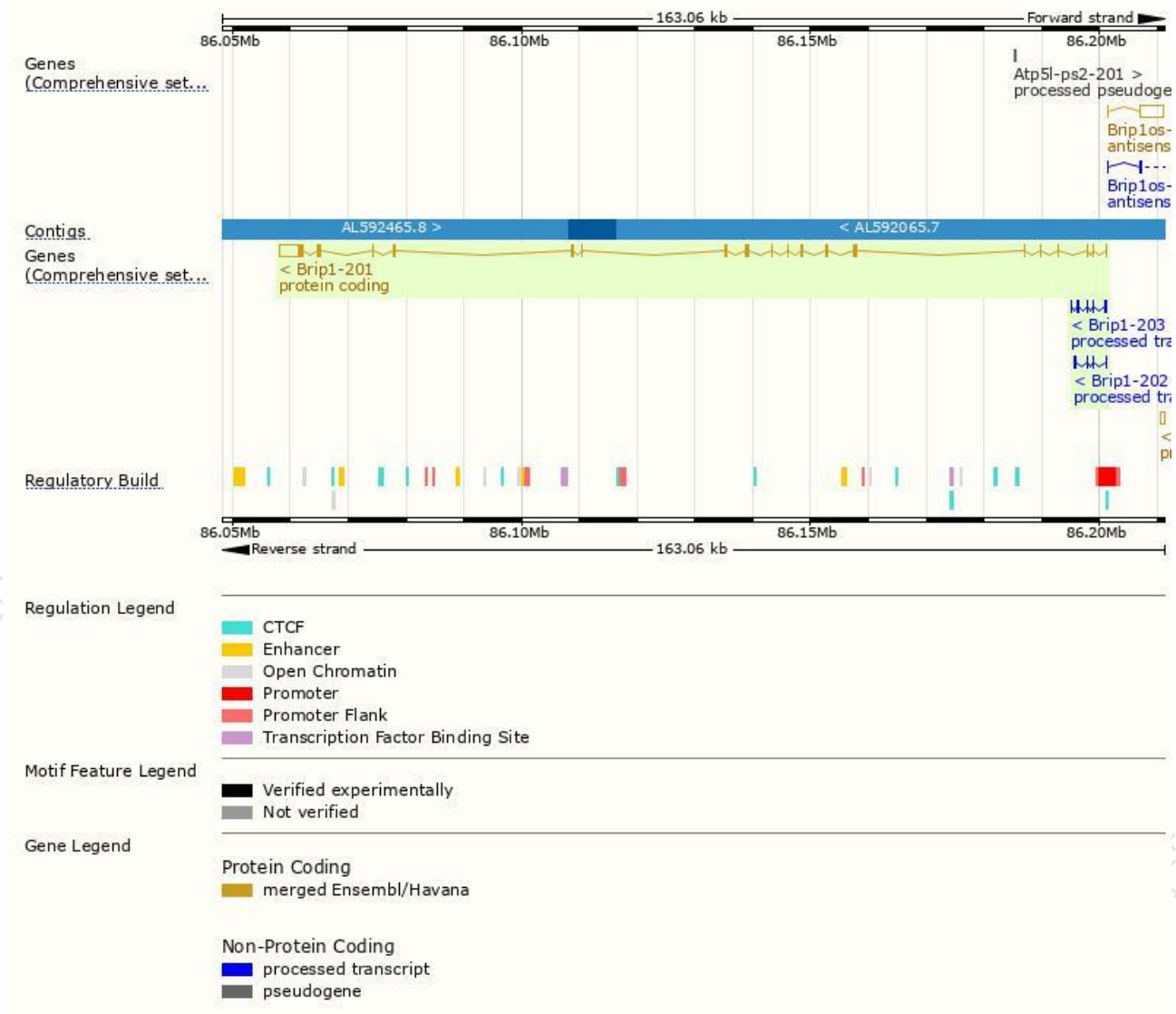
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Brip1-201	ENSMUST00000044423.3	6931	1174aa	Protein coding	CCDS25197	Q5SXJ3	TSL:1 GENCODE basic APPRIS P1
Brip1-202	ENSMUST00000123366.1	600	No protein	Processed transcript	-	-	TSL:3
Brip1-203	ENSMUST00000149748.7	507	No protein	Processed transcript	-	-	TSL:1

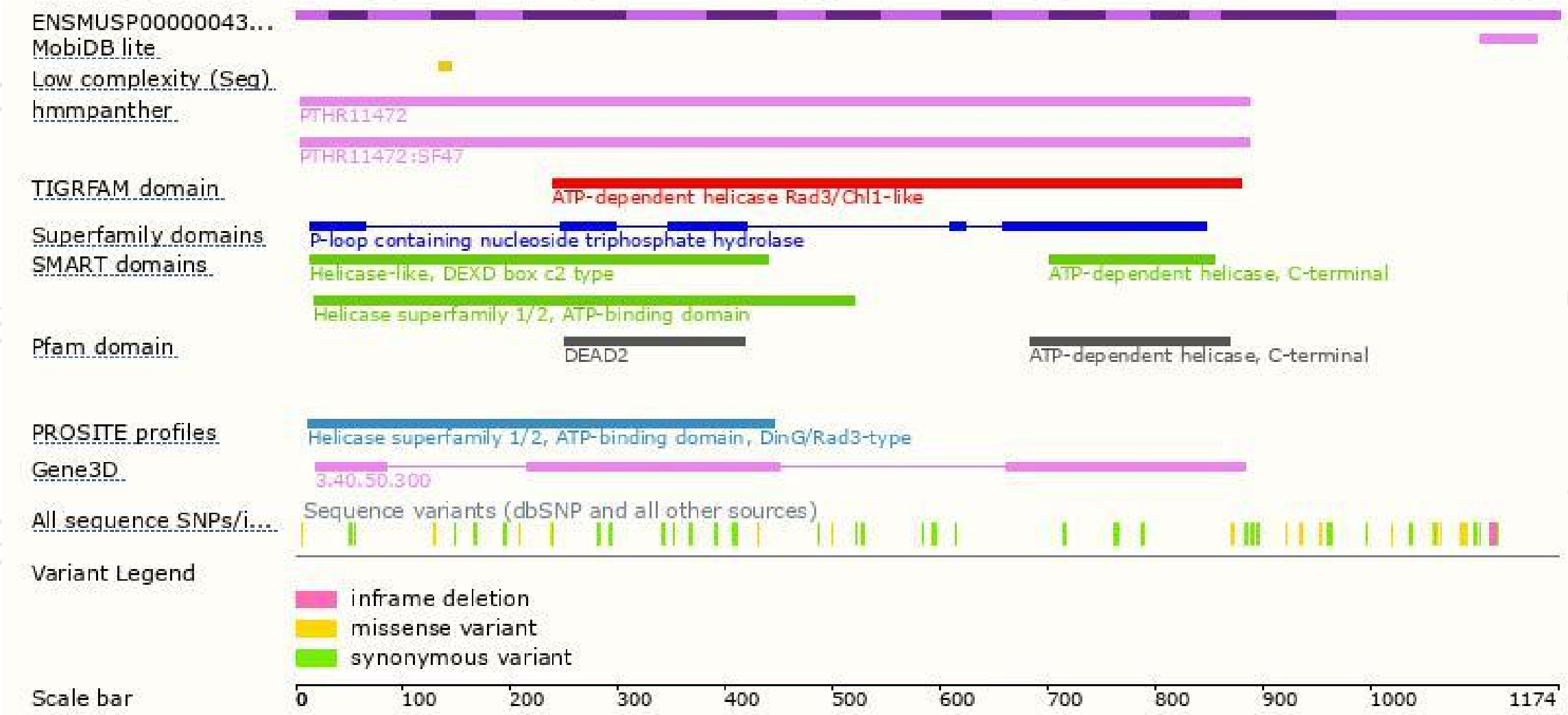
The strategy is based on the design of *Brip1-201* transcript,The transcription is shown below



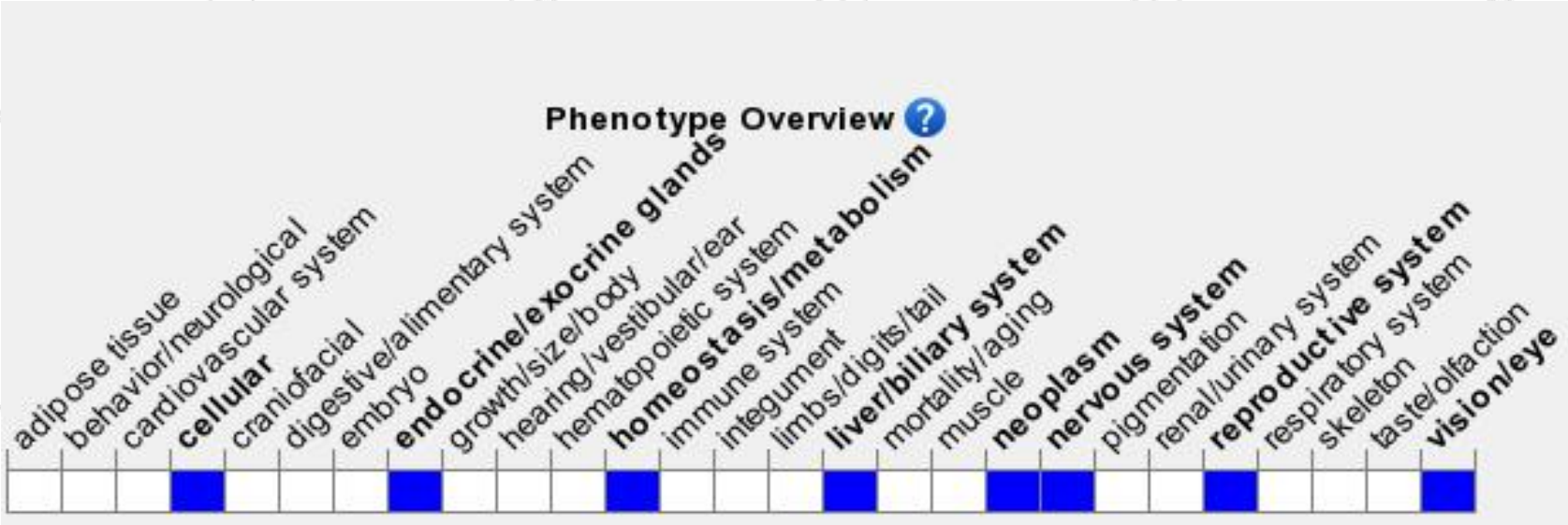
Genomic location distribution



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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