

Grip1 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Grip1

Project type

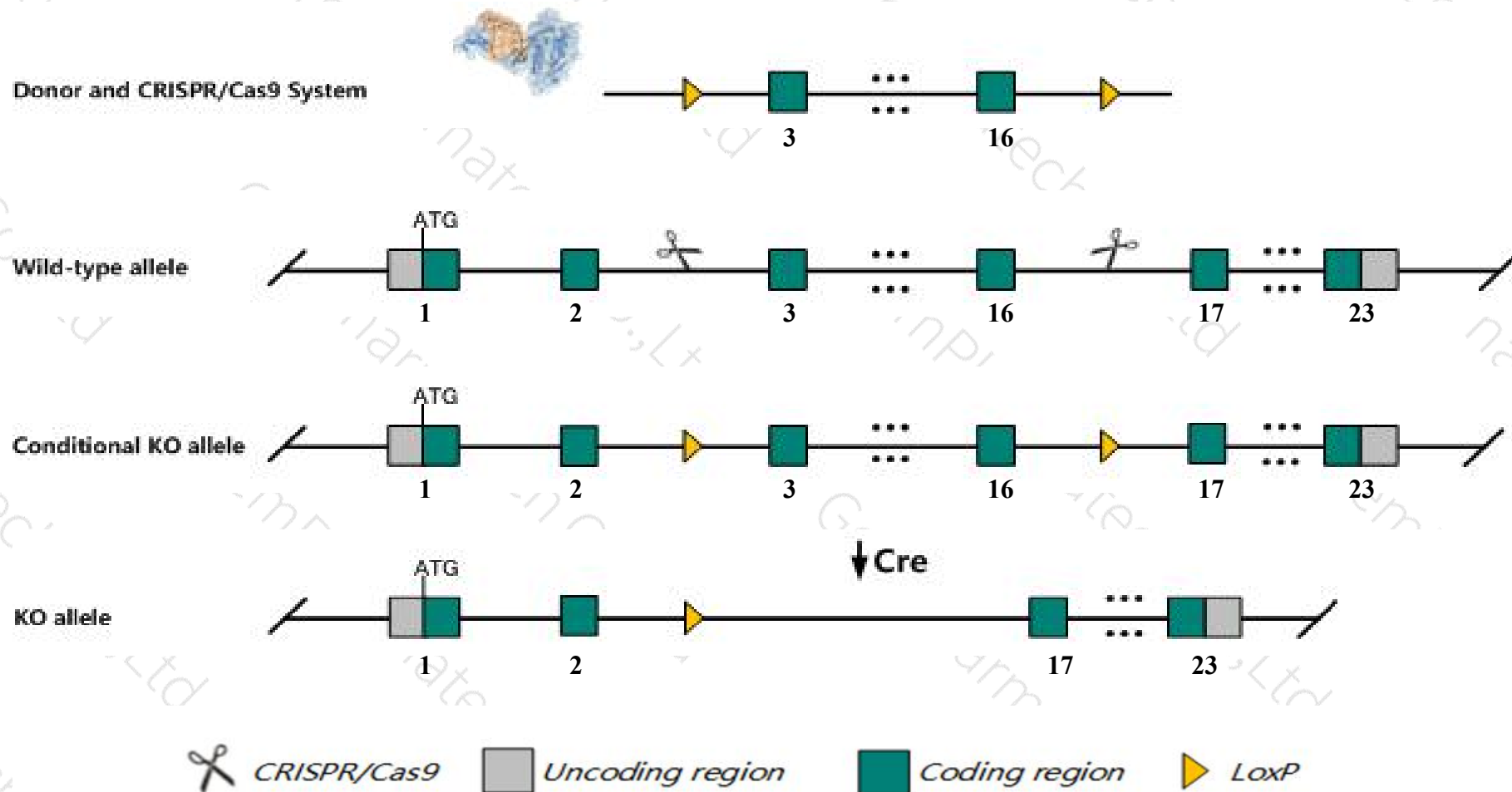
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Grip1* gene. The schematic diagram is as follows:



Technical routes

- The *Grip1* gene has 16 transcripts. According to the structure of *Grip1* gene, exon3-exon16 of *Grip1*-201 (ENSMUST00000041962.15) transcript is recommended as the knockout region. The region contains 1834bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Grip1* 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, Homozygous ablation of gene function results in embryonic lethality and blistering skin lesions.
- The *Grip1* gene is located on the Chr10. 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)

Grip1 glutamate receptor interacting protein 1 [*Mus musculus* (house mouse)]

Gene ID: 74053, updated on 12-Aug-2019

Summary

Official Symbol Grip1 provided by [MGI](#)

Official Full Name glutamate receptor interacting protein 1 provided by [MGI](#)

Primary source [MGI:MGI:1921303](#)

See related [Ensembl:ENSMUSG00000034813](#)

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 eb; GRIP; 4931400F03Rik

Summary This gene encodes a protein containing multiple PDZ (post synaptic density protein, Drosophila disc large tumor suppressor, and zonula occludens-1 protein) domains. The encoded protein acts as a mediator between cytoskeletal and membrane proteins, particularly in neuronal cells, and facilitates complex formation at the cell membrane. Mutation of this gene can cause embryonic lethality resulting from defects of the dermo-epidermal junction. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Mar 2013]

Expression Biased expression in testis adult (RPKM 9.5), CNS E18 (RPKM 3.2) and 8 other tissues [See more](#)

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

Transcript information (Ensembl)

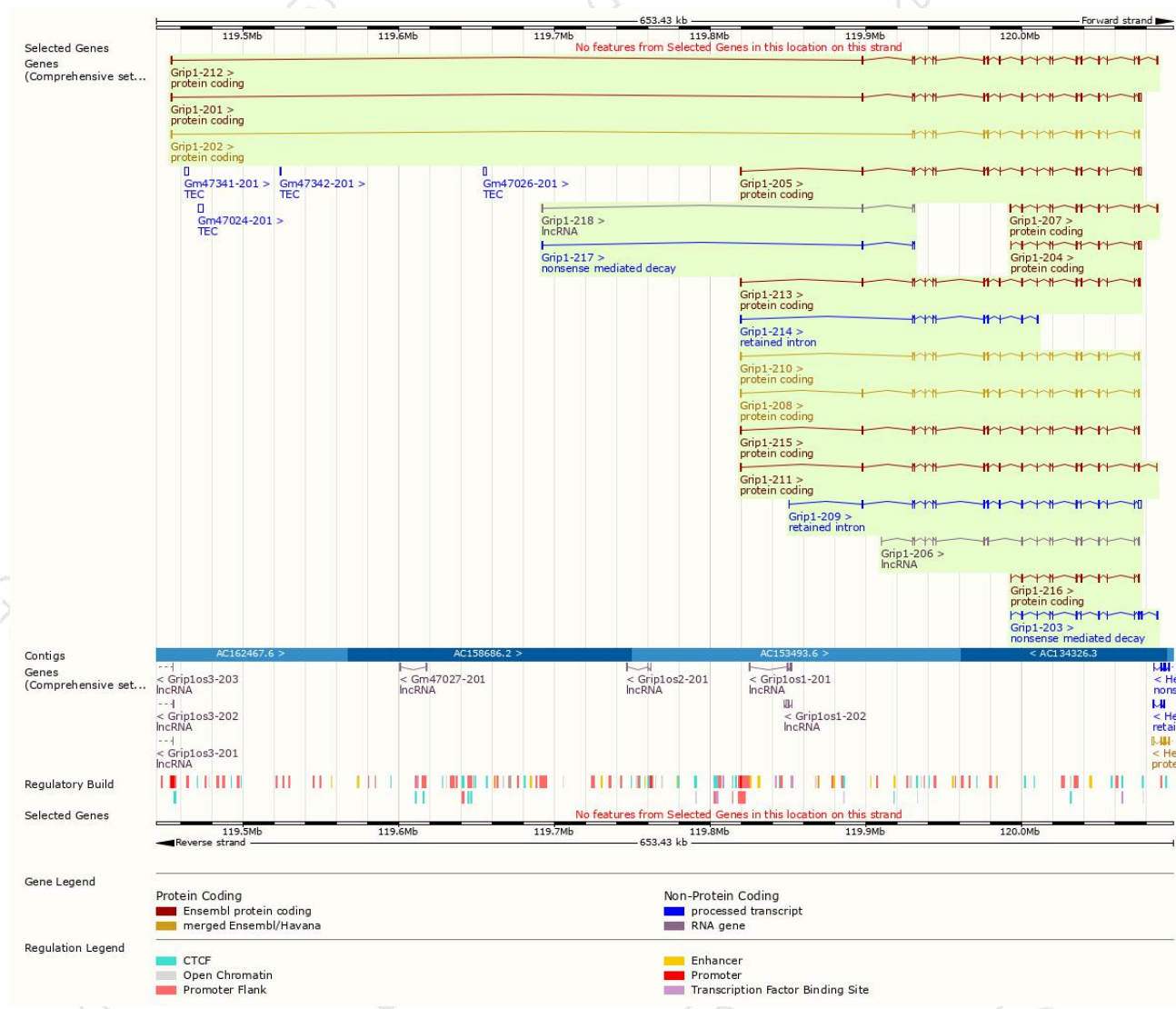
The gene has 16 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Grip1-201	ENSMUST00000041962.15	5343	1061aa	Protein coding	CCDS70112	H7BX09	TSL:1 GENCODE basic APPRIS ALT2
Grip1-205	ENSMUST000000105262.8	4996	1060aa	Protein coding	CCDS70113	H7BX90	TSL:1 GENCODE basic APPRIS ALT2
Grip1-212	ENSMUST000000147356.8	4145	1113aa	Protein coding	CCDS70111	Q6GQT7	TSL:1 GENCODE basic APPRIS ALT2
Grip1-202	ENSMUST00000077871.13	3720	1034aa	Protein coding	CCDS36071	Q925T6	TSL:1 GENCODE basic APPRIS ALT2
Grip1-204	ENSMUST000000105261.8	3608	632aa	Protein coding	CCDS70114	Q925T6	TSL:1 GENCODE basic
Grip1-208	ENSMUST000000136410.7	3532	1127aa	Protein coding	CCDS24202	Q925T6	TSL:1 GENCODE basic APPRIS P3
Grip1-210	ENSMUST000000144825.7	3250	1033aa	Protein coding	CCDS36072	Q925T6	TSL:1 GENCODE basic APPRIS ALT2
Grip1-213	ENSMUST000000147454.7	4520	1112aa	Protein coding	-	D3YZL8	TSL:5 GENCODE basic APPRIS ALT2
Grip1-211	ENSMUST000000144959.7	3462	1112aa	Protein coding	-	D3Z6T4	TSL:5 GENCODE basic APPRIS ALT2
Grip1-215	ENSMUST000000148954.7	3293	1075aa	Protein coding	-	D3YWY4	TSL:5 GENCODE basic APPRIS ALT2
Grip1-207	ENSMUST000000130387.7	2780	697aa	Protein coding	-	D3Z066	TSL:5 GENCODE basic
Grip1-216	ENSMUST000000154238.7	2482	712aa	Protein coding	-	D3Z6R6	TSL:5 GENCODE basic
Grip1-203	ENSMUST000000081260.2	2361	631aa	Nonsense mediated decay	-	Q6X4T6	TSL:1
Grip1-206	ENSMUST000000127787.1	2979	No protein	Processed transcript	-	-	TSL:5
Grip1-209	ENSMUST000000139352.7	5451	No protein	Retained intron	-	-	TSL:2
Grip1-214	ENSMUST000000147598.7	2054	No protein	Retained intron	-	-	TSL:2

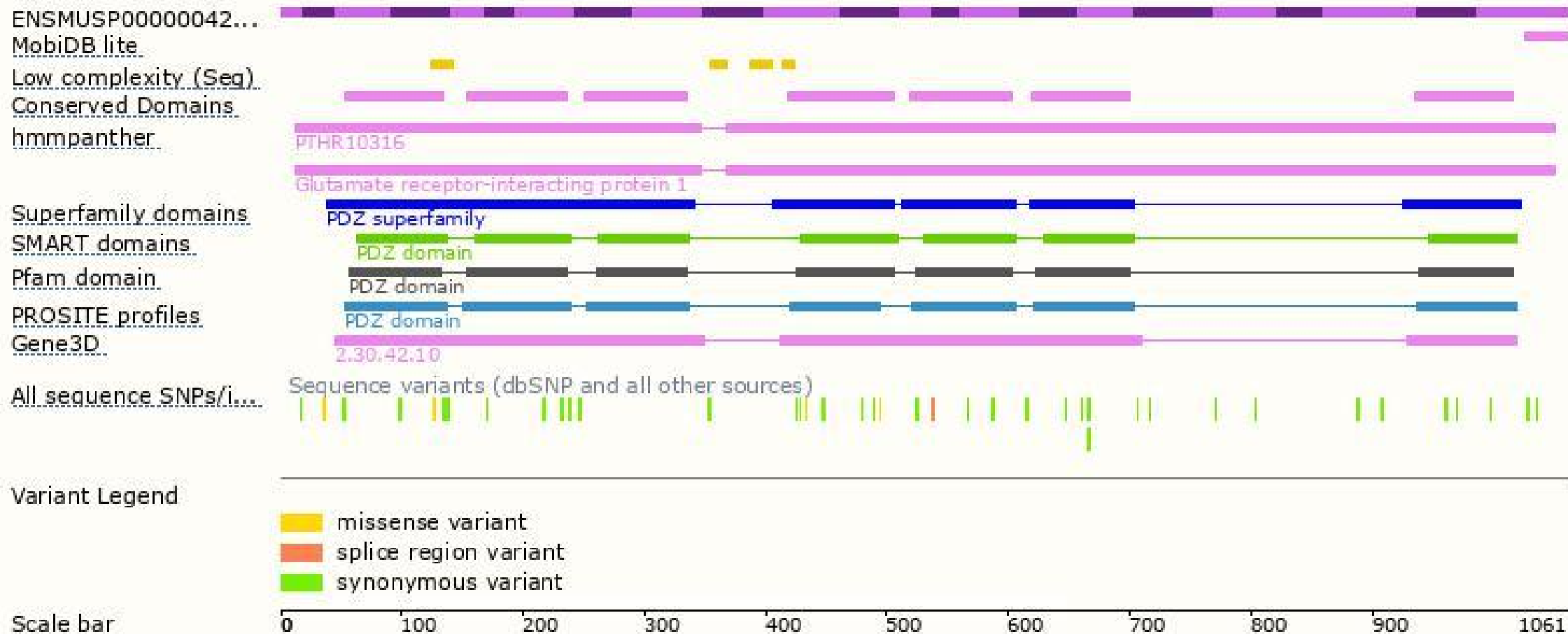
The strategy is based on the design of *Grip1-201* transcript,The transcription is shown below



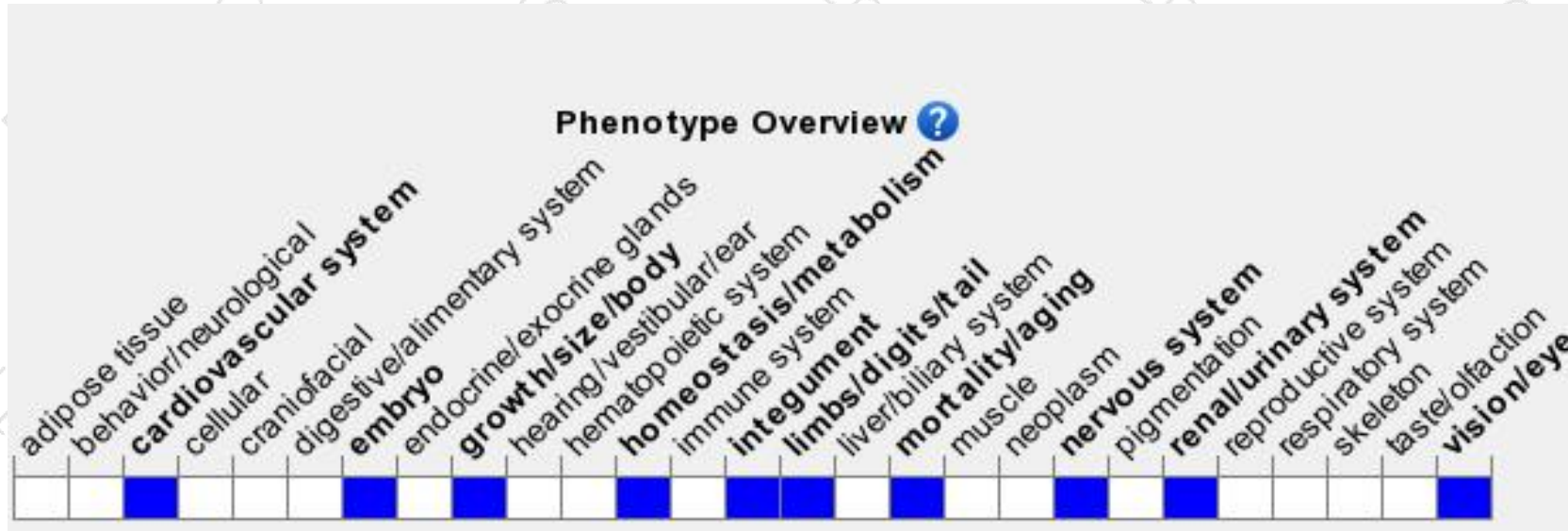
Genomic location distribution



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, Homozygous ablation of gene function results in embryonic lethality and blistering skin lesions.

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

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