

Arhgap18 Cas9-KO Strategy

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Reviewer: Yanhua Shen

Design Date: 2019-9-2

Project Overview

Project Name

Arhgap18

Project type

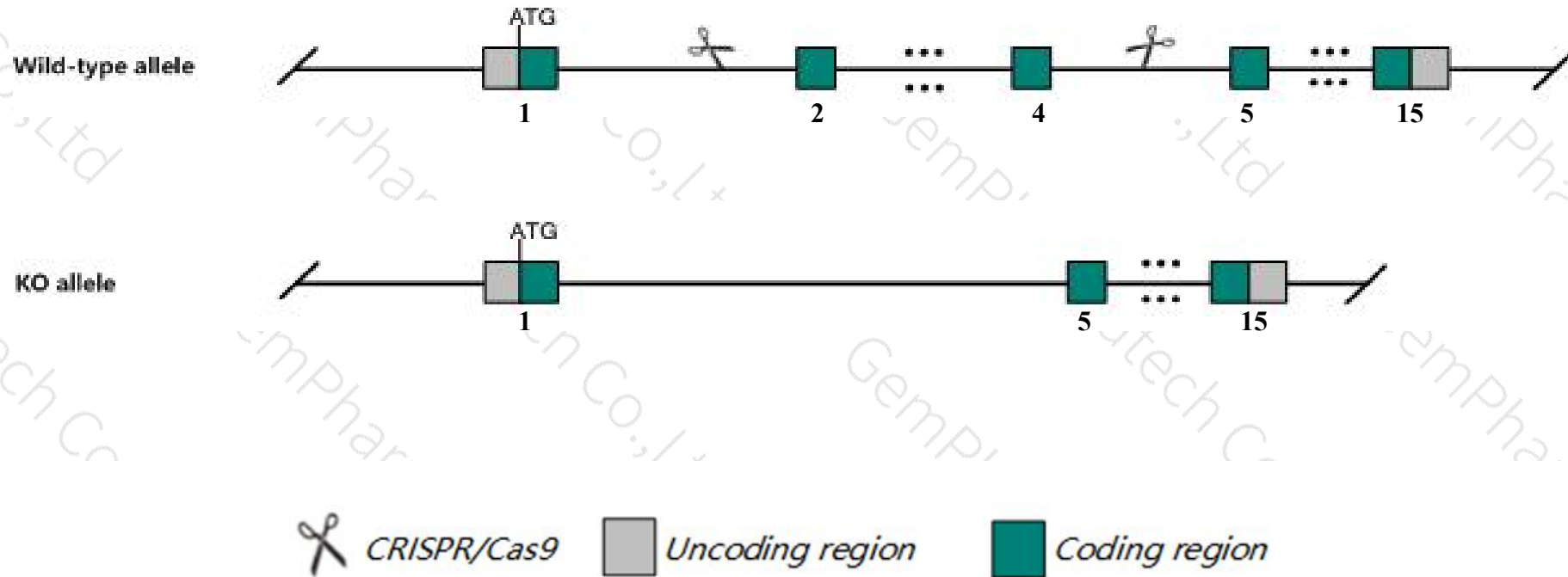
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Arhgap18* gene. The schematic diagram is as follows:



- The *Arhgap18* gene has 5 transcripts. According to the structure of *Arhgap18* gene, exon2-exon4 of *Arhgap18-201* (ENSMUST00000039557.8) transcript is recommended as the knockout region. The region contains 497bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Arhgap18* gene. The brief process is as follows: CRISPR/Cas9 sys

- Transcript *Arhgap18*-203&205 may not be affected.
- The *Arhgap18* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Arhgap18 Rho GTPase activating protein 18 [*Mus musculus* (house mouse)]

Gene ID: 73910, updated on 12-Aug-2019

Summary

- Official Symbol** Arhgap18 provided by [MGI](#)
- Official Full Name** Rho GTPase activating protein 18 provided by [MGI](#)
- Primary source** [MGI:MGI:1921160](#)
- See related** [Ensembl:ENSMUSG00000039031](#)
- Gene type** protein coding
- RefSeq status** PROVISIONAL
- Organism** [Mus musculus](#)
- Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
- Also known as** AI314906; AI843501; 4833419J07Rik
- Expression** Ubiquitous expression in placenta adult (RPKM 9.0), bladder adult (RPKM 3.7) and 25 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 10; 10 A4

See Arhgap18 in [Genome Data Viewer](#)

Exon count: 16

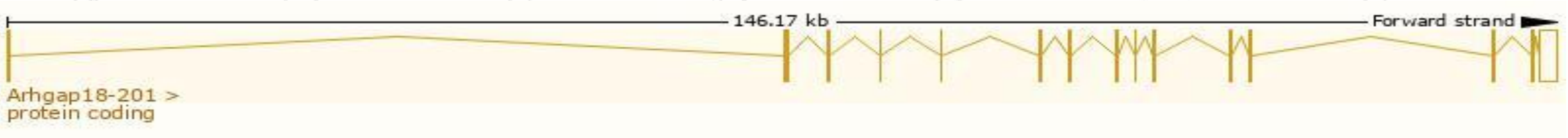
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	10	NC_000076.6 (26772408..26918648)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	10	NC_000076.5 (26492318..26638454)

Transcript information (Ensembl)

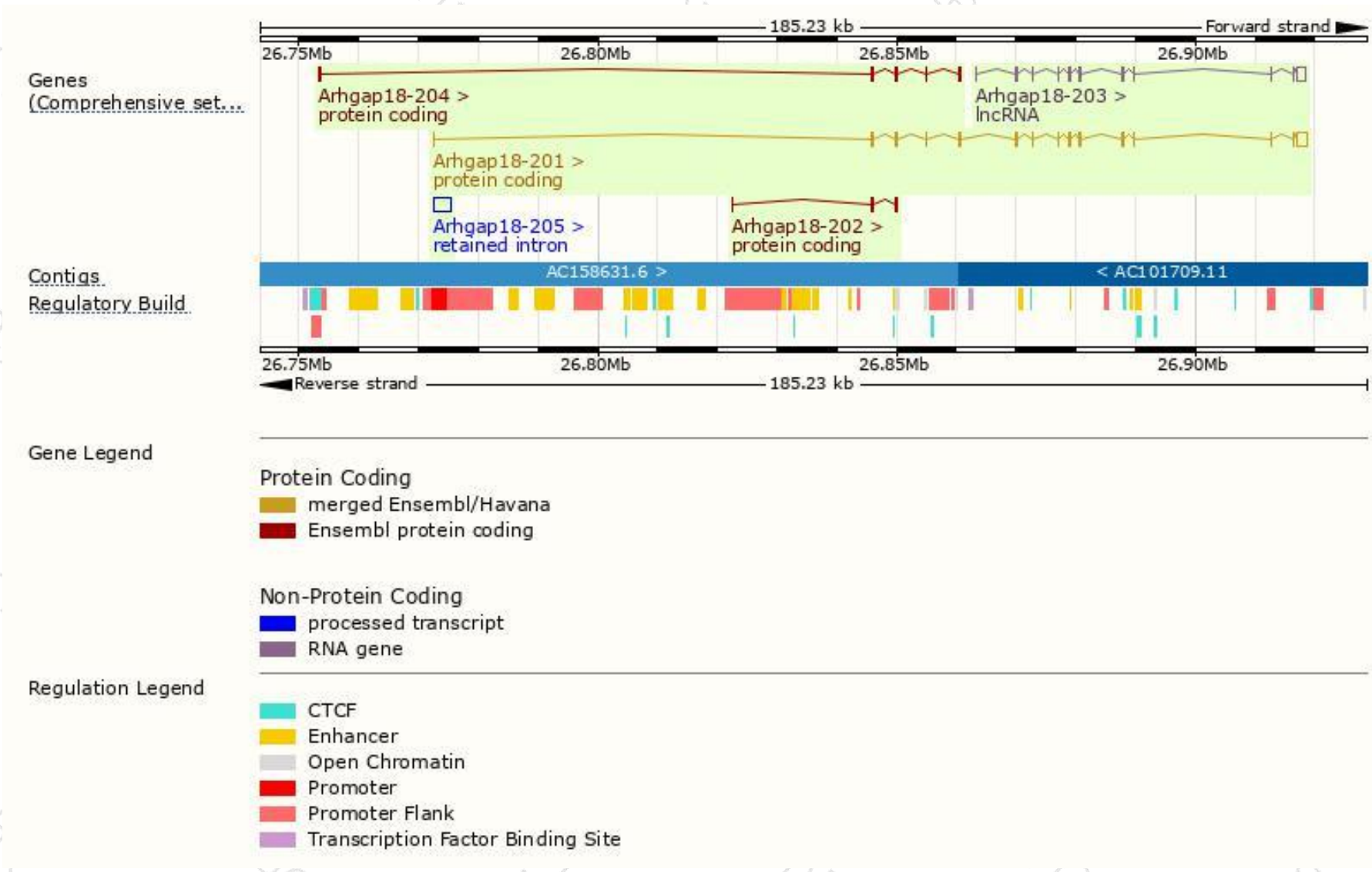
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Arhgap18-201	ENSMUST00000039557.8	3651	663aa	Protein coding	CCDS23757	Q8K0Q5	TSL:1 GENCODE basic APPRIS P1
Arhgap18-204	ENSMUST00000176060.7	755	190aa	Protein coding	-	H3BJL1	CDS 3' incomplete TSL:3
Arhgap18-202	ENSMUST00000135866.1	374	73aa	Protein coding	-	H3BLG9	CDS 3' incomplete TSL:2
Arhgap18-205	ENSMUST00000220012.1	2868	No protein	Retained intron	-	-	TSL:NA
Arhgap18-203	ENSMUST00000142284.1	2669	No protein	lncRNA	-	-	TSL:1

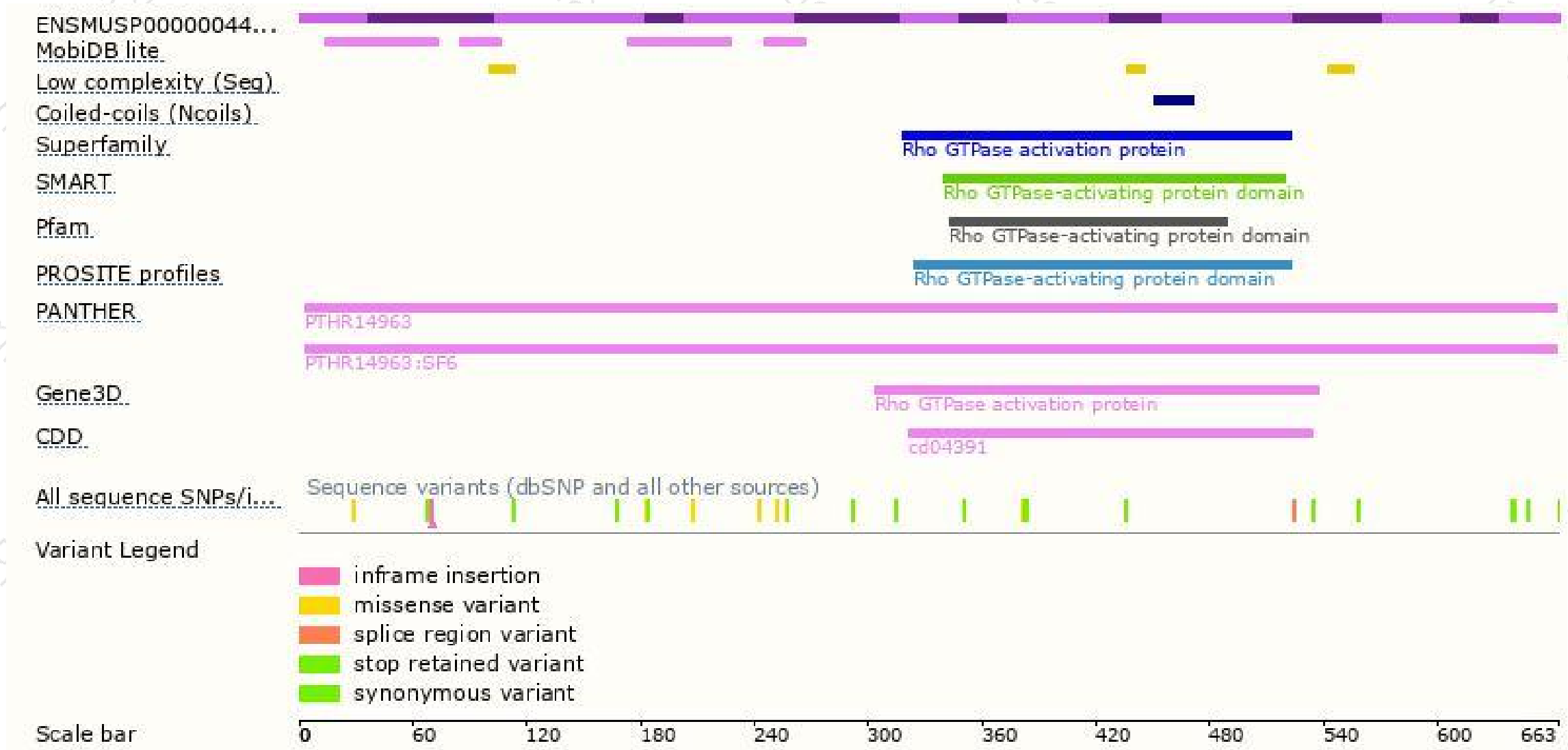
The strategy is based on the design of *Arhgap18-201* transcript,The transcription is shown below



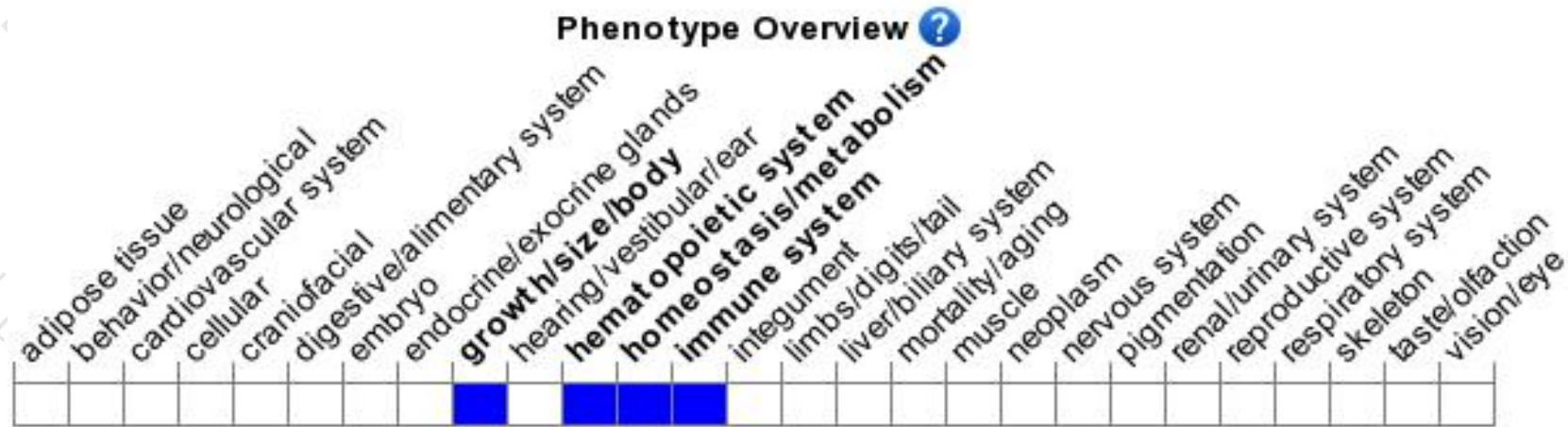
Genomic location distribution



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/>).

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

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