

Gnaq Cas9-CKO Strategy

Designer:

Daohua Xu

Reviewer:

Huimin Su

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Project Overview

Project Name

Gnaq

Project type

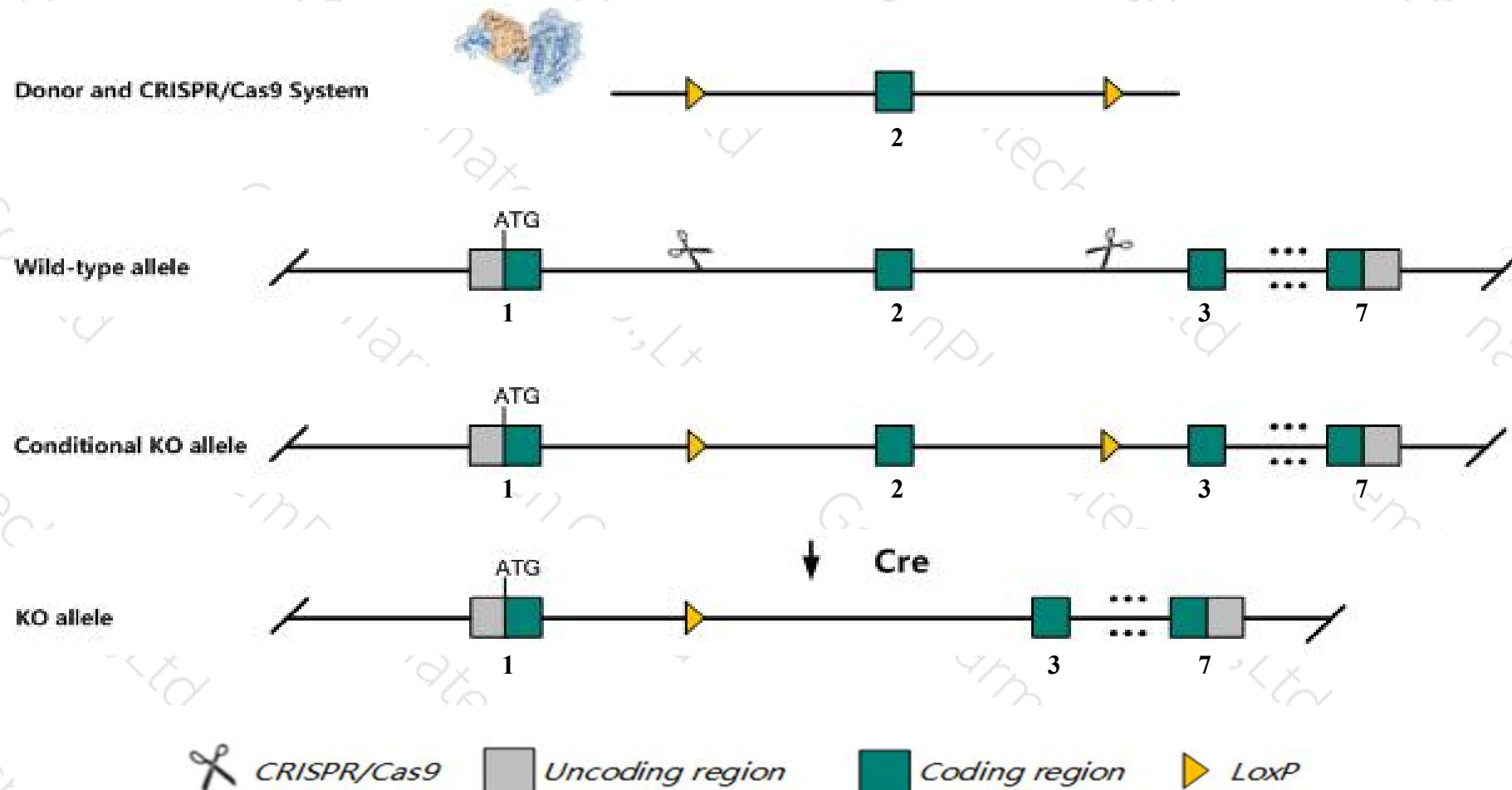
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- The *Gnaq* gene has 3 transcripts. According to the structure of *Gnaq* gene, exon2 of *Gnaq-201* (ENSMUST00000025541.5) transcript is recommended as the knockout region. The region contains 185bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Gnaq* 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, Mutant mice exhibit pigmentation anomalies affecting the ears, tail and footpads.
- The *Gnaq* 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)

Gnaq guanine nucleotide binding protein, alpha q polypeptide [Mus musculus (house mouse)]

Gene ID: 14682, updated on 10-Feb-2019

Summary



Official Symbol	Gnaq provided by MGI
Official Full Name	guanine nucleotide binding protein, alpha q polypeptide provided by MGI
Primary source	MGI:MGI:95776
See related	Ensembl:ENSMUSG00000024639
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	1110005L02Rik, 6230401I02Rik, AA408290, AW060788, Dsk1, Dsk10, Galphaq, Gq, Gql
Expression	Ubiquitous expression in CNS E18 (RPKM 21.9), CNS E14 (RPKM 19.1) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

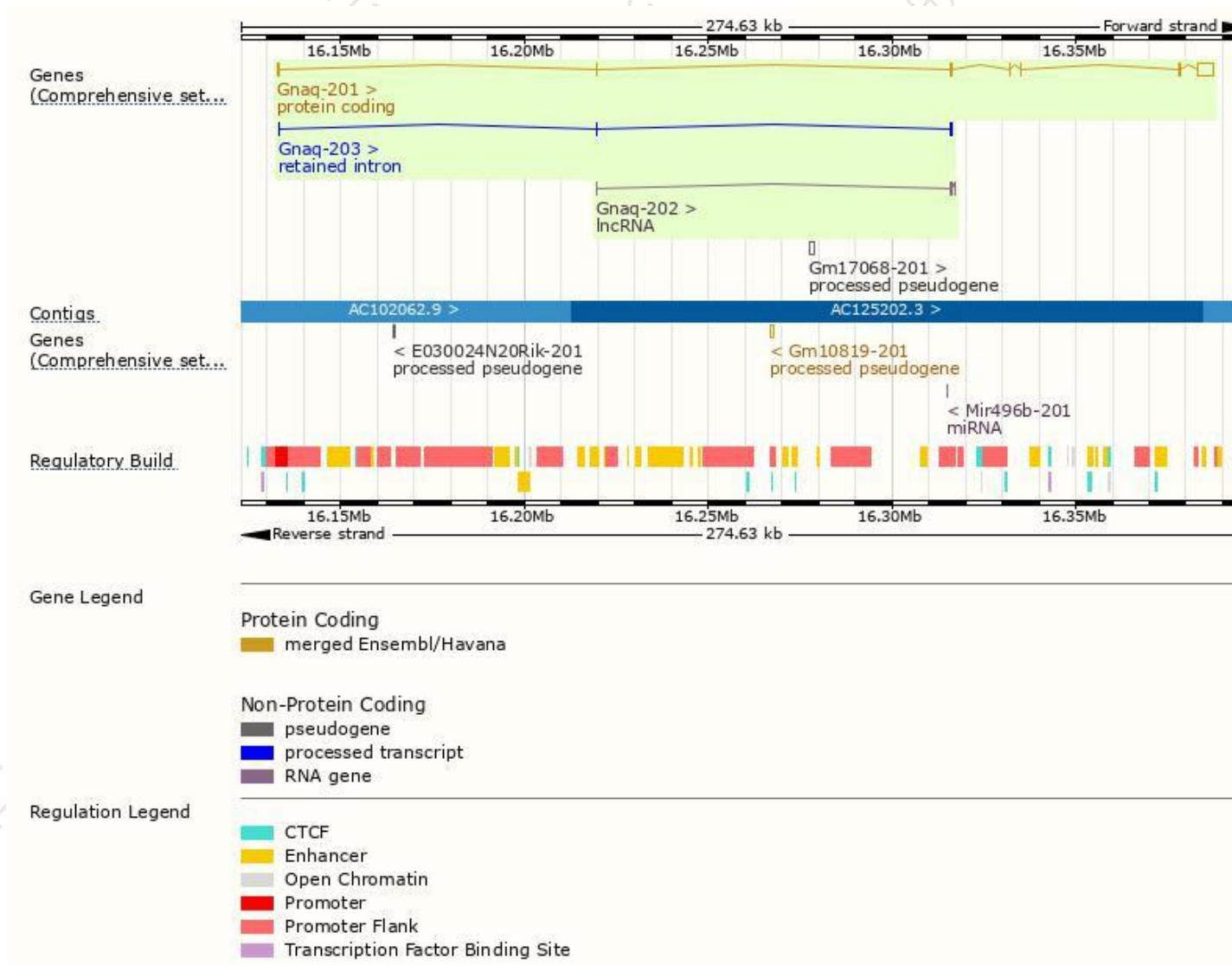
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Gnaq-201	ENSMUST00000025541.5	5644	359aa	Protein coding	CCDS29684	P21279 Q3UHH5	TSL:1 GENCODE basic APPRIS P1
Gnaq-203	ENSMUST00000170229.1	862	No protein	Retained intron	-	-	TSL:2
Gnaq-202	ENSMUST00000167656.1	481	No protein	lncRNA	-	-	TSL:3

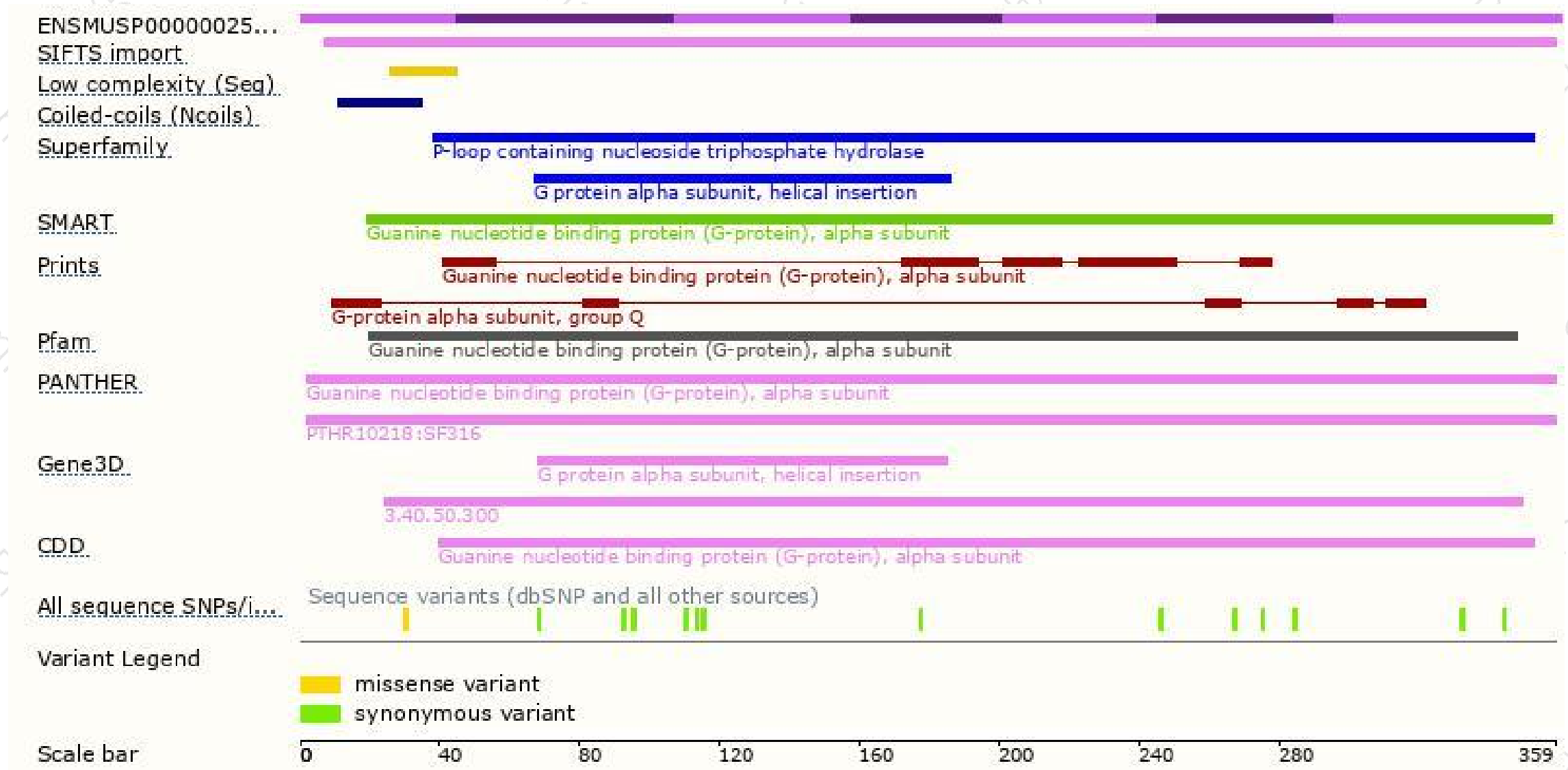
The strategy is based on the design of *Gnaq-201* transcript,The transcription is shown below



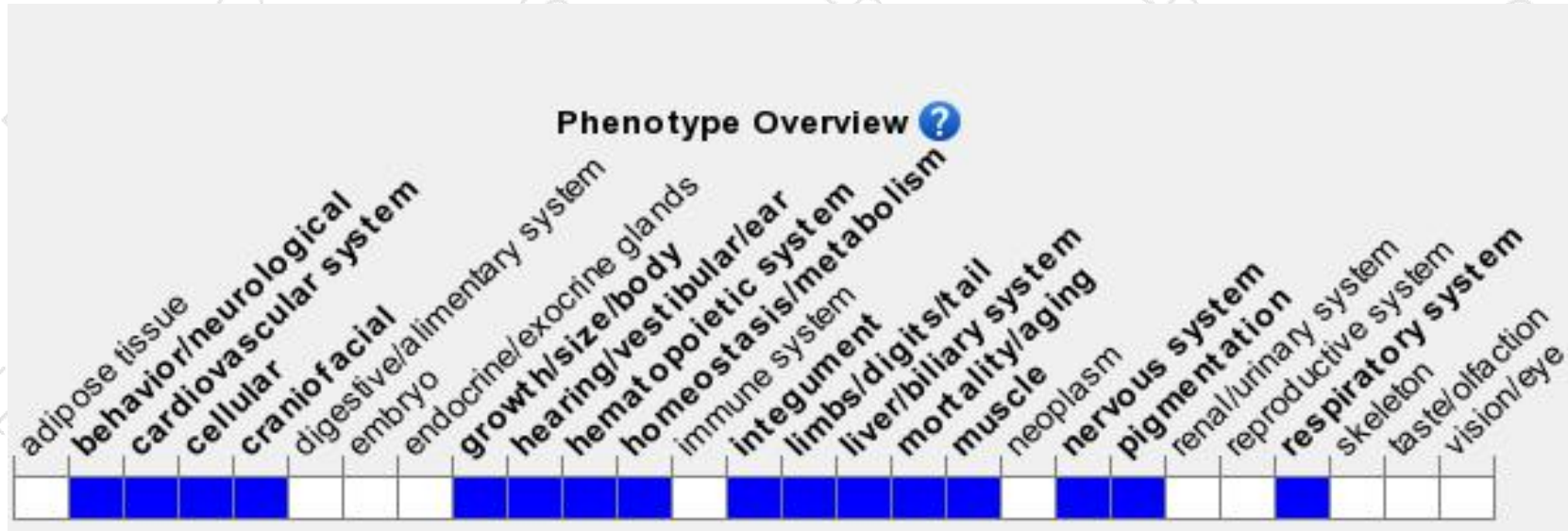
Genomic location distribution



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, Mutant mice exhibit pigmentation anomalies affecting the ears, tail and footpads.

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

Tel: 400-9660890

