

# *Nin* Cas9-CKO Strategy

Designer:Xiaojing Li

Reviewer:JiaYu

Design Date:2020-2-14

# Project Overview

---

**Project Name**

*Nin*

---

**Project type**

**Cas9-CKO**

---

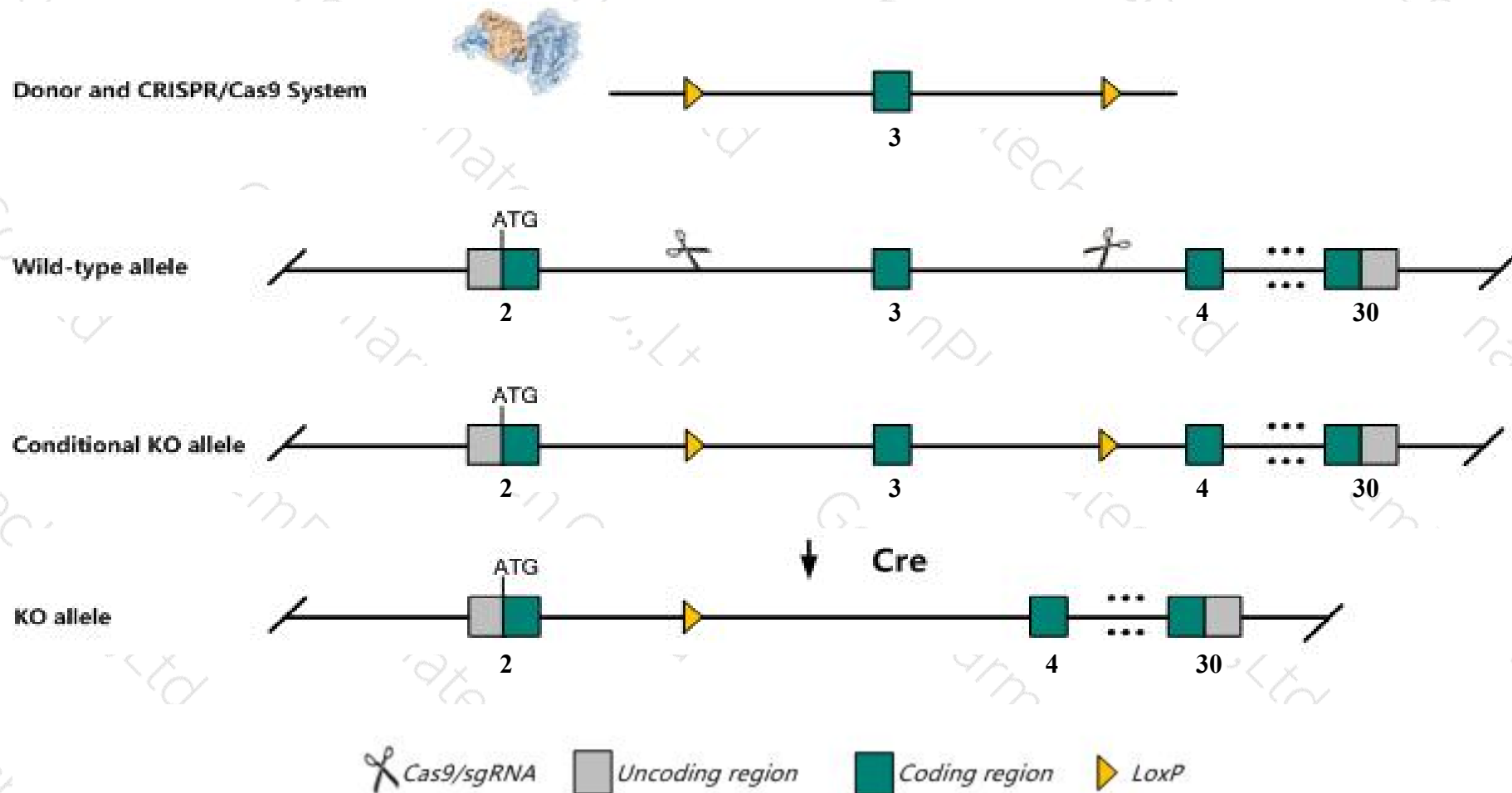
**Strain background**

**C57BL/6J**

---

# Conditional Knockout strategy

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



# Technical routes

- The *Nin* gene has 17 transcripts. According to the structure of *Nin* gene, exon3 of *Nin-211* (ENSMUST00000222237.1) transcript is recommended as the knockout region. The region contains 82bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Nin* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed. Cas9, sgRNA and Donor were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.
- The flox mice was 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, mice homozygous for a knock-out allele exhibit partial pre- and postnatal lethality, thinner skin, delayed skin barrier formation, impaired skin barrier function, impaired differentiation of suprabasal cells, and defects in mitotic spindle orientation, desmosome assembly and lamellar body secretion.
- The *Nin* gene is located on the Chr12. 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)

## Nin ninein [ *Mus musculus* (house mouse) ]

Gene ID: 18080, updated on 10-Oct-2019

### Summary

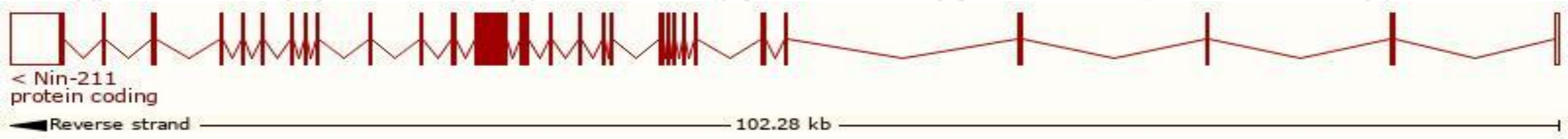
Official Symbol	Nin provided by <a href="#">MGI</a>
Official Full Name	ninein provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:105108</a>
See related	<a href="#">Ensembl:ENSMUSG000000021068</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI385615; AU024711; mKIAA1565; 3110068G20Rik
Expression	Ubiquitous expression in CNS E18 (RPKM 5.4), CNS E14 (RPKM 4.0) and 23 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

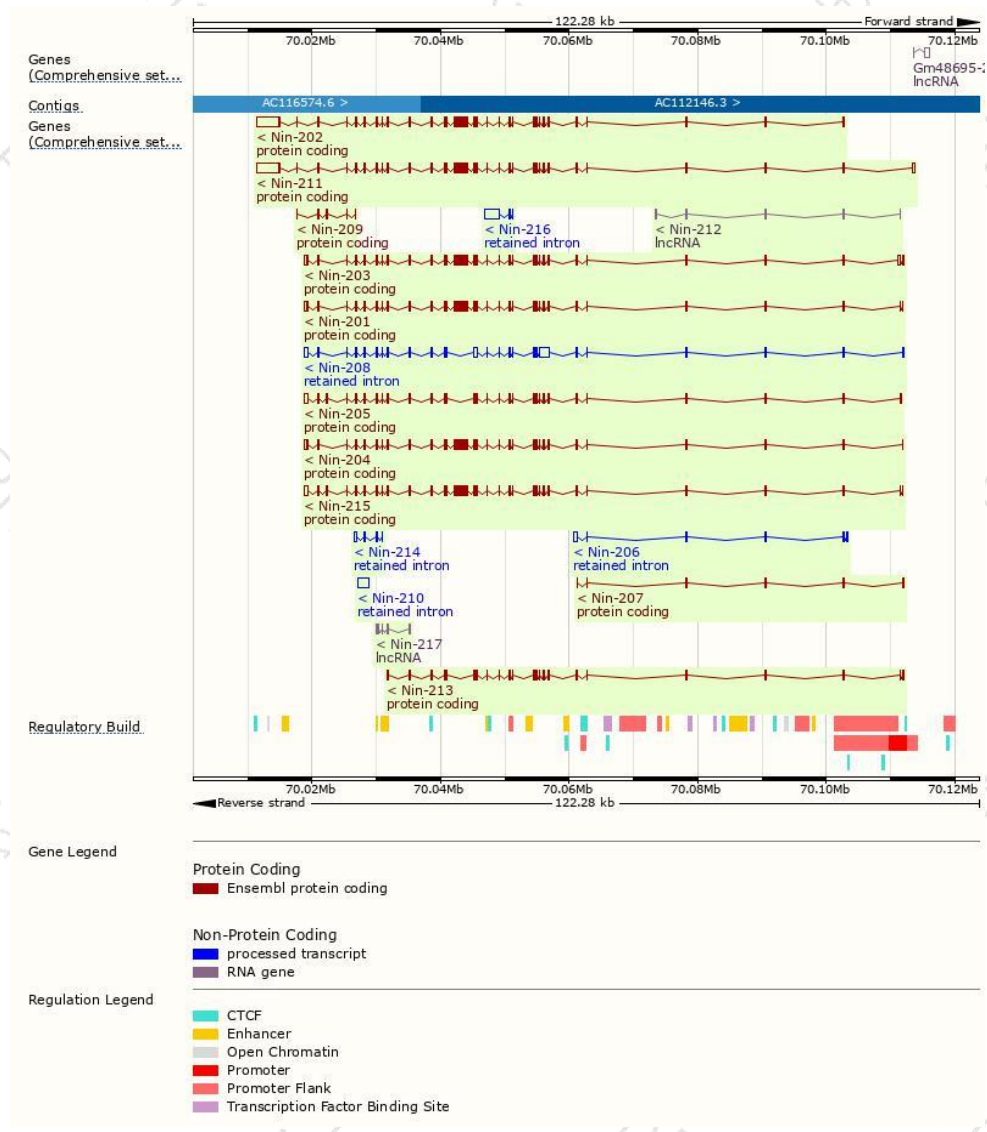
The gene has 17 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nin-211	<a href="#">ENSMUST00000222237.1</a>	9919	<a href="#">2113aa</a>	Protein coding	<a href="#">CCDS36468</a>	<a href="#">Q61043</a>	TSL:5 GENCODE basic APPRIS P4
Nin-202	<a href="#">ENSMUST00000085314.10</a>	9675	<a href="#">2113aa</a>	Protein coding	<a href="#">CCDS36468</a>	<a href="#">Q61043</a>	TSL:1 GENCODE basic APPRIS P4
Nin-203	<a href="#">ENSMUST00000095666.12</a>	7183	<a href="#">2035aa</a>	Protein coding	<a href="#">CCDS36469</a>	<a href="#">Q61043</a>	TSL:5 GENCODE basic APPRIS ALT2
Nin-201	<a href="#">ENSMUST00000021468.13</a>	6708	<a href="#">2035aa</a>	Protein coding	<a href="#">CCDS36469</a>	<a href="#">Q61043</a>	TSL:1 GENCODE basic APPRIS ALT2
Nin-204	<a href="#">ENSMUST00000169074.1</a>	6636	<a href="#">2035aa</a>	Protein coding	<a href="#">CCDS36469</a>	<a href="#">Q61043</a>	TSL:1 GENCODE basic APPRIS ALT2
Nin-215	<a href="#">ENSMUST00000223257.1</a>	6744	<a href="#">1979aa</a>	Protein coding	-	<a href="#">A0A1Y7VNC5</a>	TSL:1 GENCODE basic APPRIS ALT2
Nin-205	<a href="#">ENSMUST00000220689.1</a>	4723	<a href="#">1272aa</a>	Protein coding	-	<a href="#">Q61043</a>	TSL:1 GENCODE basic APPRIS ALT2
Nin-213	<a href="#">ENSMUST00000222835.1</a>	3181	<a href="#">996aa</a>	Protein coding	-	<a href="#">A0A1Y7VJC3</a>	CDS 3' incomplete TSL:1
Nin-207	<a href="#">ENSMUST00000221275.1</a>	729	<a href="#">178aa</a>	Protein coding	-	<a href="#">A0A1Y7VIQ3</a>	CDS 3' incomplete TSL:3
Nin-209	<a href="#">ENSMUST00000221579.1</a>	521	<a href="#">80aa</a>	Protein coding	-	<a href="#">A0A1Y7VJS5</a>	CDS 5' incomplete TSL:3
Nin-208	<a href="#">ENSMUST00000221486.1</a>	5655	No protein	Retained intron	-	-	TSL:2
Nin-216	<a href="#">ENSMUST00000223316.1</a>	2490	No protein	Retained intron	-	-	TSL:1
Nin-210	<a href="#">ENSMUST00000222137.1</a>	1650	No protein	Retained intron	-	-	TSL:NA
Nin-206	<a href="#">ENSMUST00000221141.1</a>	1397	No protein	Retained intron	-	-	TSL:1
Nin-214	<a href="#">ENSMUST00000223048.1</a>	656	No protein	Retained intron	-	-	TSL:2
Nin-212	<a href="#">ENSMUST00000222466.1</a>	846	No protein	lncRNA	-	-	TSL:3
Nin-217	<a href="#">ENSMUST00000223469.1</a>	488	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Nin-211* transcript,The transcription is shown below

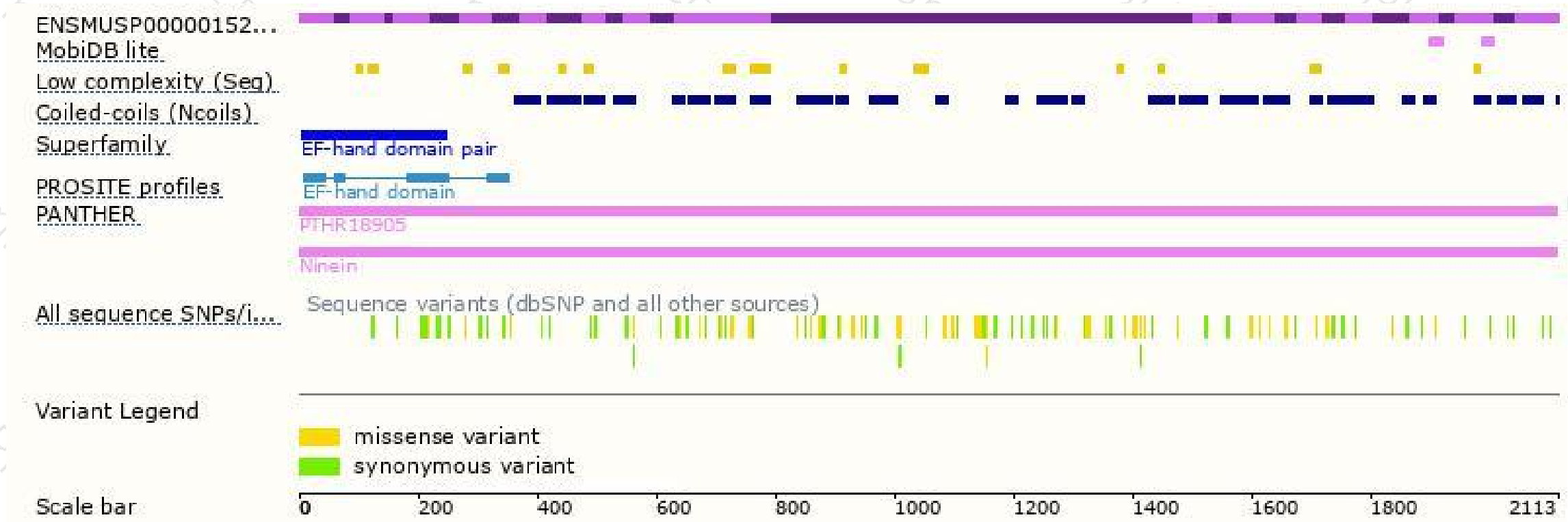


# Genomic location distribution

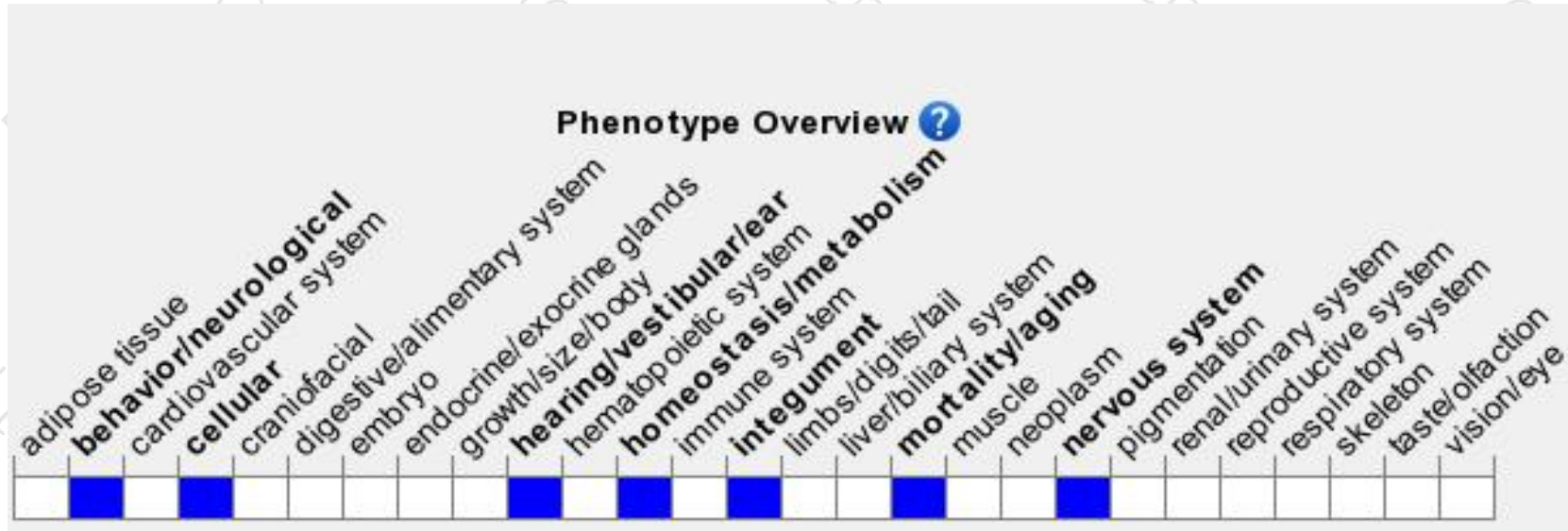




# Protein domain



# 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.

Tel: 025-5864 1534

