

Pcdh15 Cas9-KO Strategy

Designer: Xueting Zhang

Reviewer: Yanhua Shen

Date: 2019-11-26

Project Overview

Project Name

Pcdh15

Project type

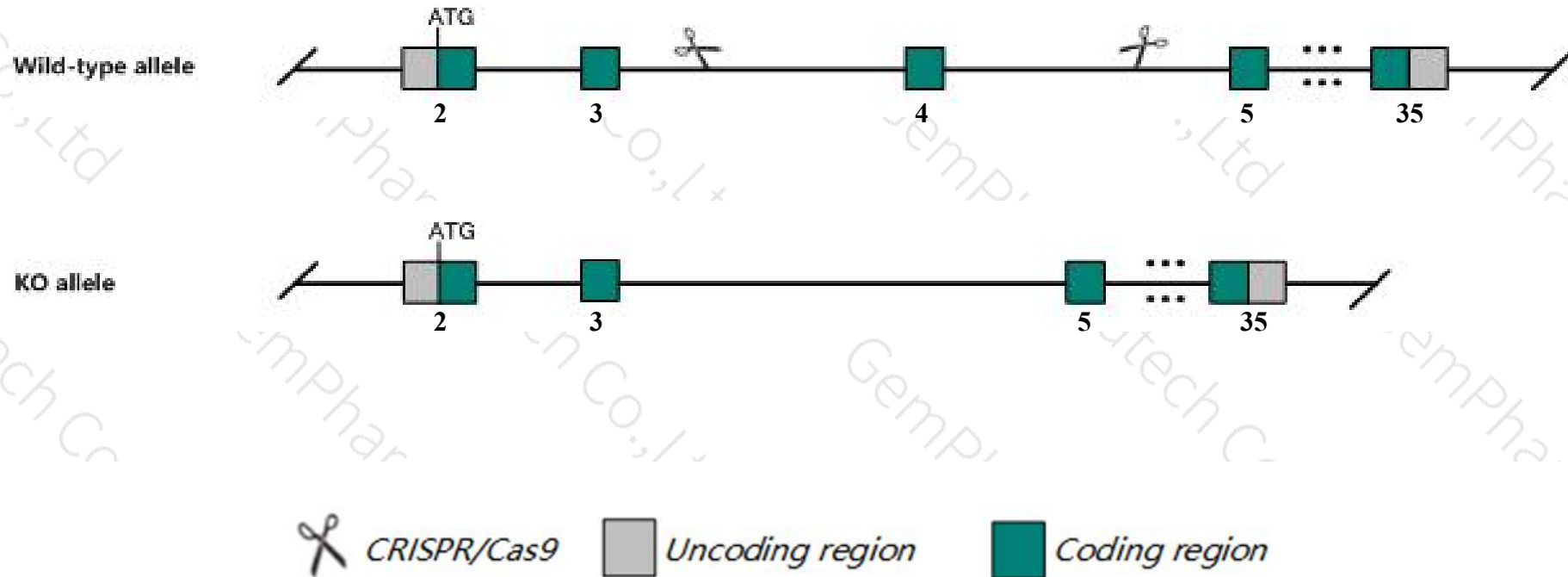
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pcdh15* gene. The schematic diagram is as follows:



- The *Pcdh15* gene has 41 transcripts. According to the structure of *Pcdh15* gene, exon4 of *Pcdh15*-234 (ENSMUST00000191854.5) transcript is recommended as the knockout region. The region contains 161bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pcdh15* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygotes for severe mutations exhibit circling, head-tossing, hyperactivity, impaired swimming and profound deafness. Mice have defects in cochlea and degeneration of hair cells, spiral ganglion cells and saccular macula. Females are poor mothers.
- The effect on transcript *Pcdh15*-207&221&239 is unknown.
- The *Pcdh15* 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)

Pcdh15 protocadherin 15 [*Mus musculus* (house mouse)]

Gene ID: 11994, updated on 1-Oct-2019

Summary

- Official Symbol** Pcdh15 provided by [MGI](#)
- Official Full Name** protocadherin 15 provided by [MGI](#)
- Primary source** [MGI:MGI:1891428](#)
- See related** [Ensembl:ENSMUSG00000052613](#)
- 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** av; roda; Ush1f; nmf19; Gm9815; BB078305
- Expression** Biased expression in frontal lobe adult (RPKM 1.4), CNS E18 (RPKM 1.1) and 9 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 10 B5.3; 10 37.43 cM See Pcdh15 in [Genome Data Viewer](#)

Exon count: 52

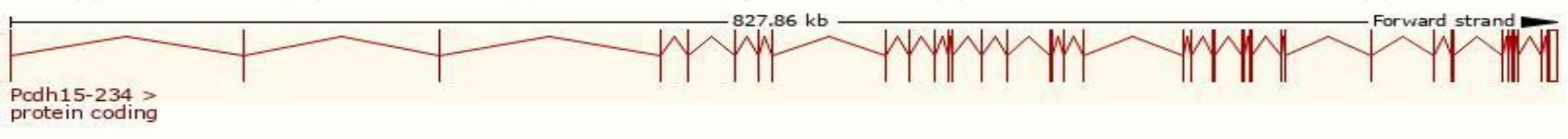
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	10	NC_000076.6 (73096277..74649831)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	10	NC_000076.5 (73284615..74112482)

Transcript information (Ensembl)

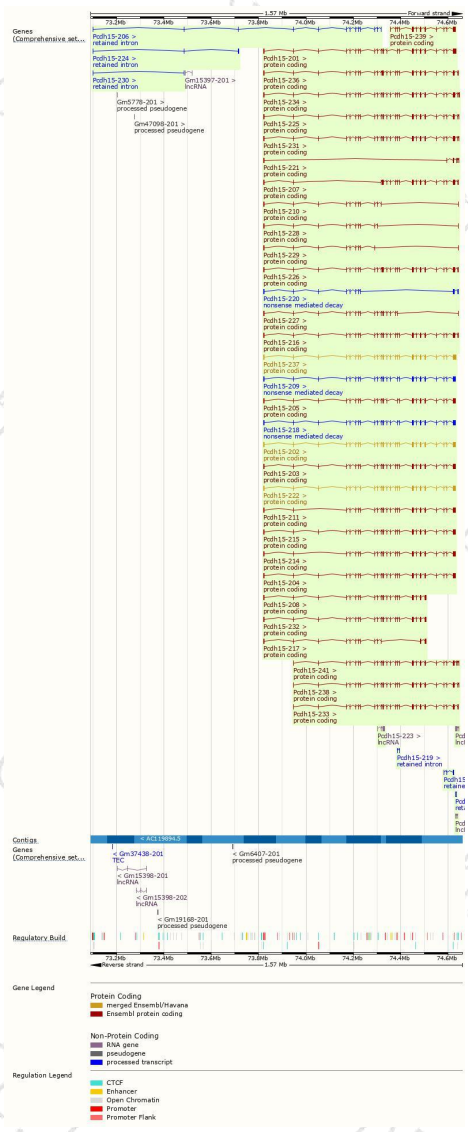
The gene has 41 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pcdh15-234	ENSMUST00000191854.5	9104	1817aa	Protein coding	CCDS56712	Q99P-J1	TSL5 GENCODE basic APPRIS ALT2
Pcdh15-237	ENSMUST00000193361.5	7081	1543aa	Protein coding	CCDS56934	Q99P-J1	TSL5 GENCODE basic APPRIS P3
Pcdh15-203	ENSMUST00000105424.0	6932	1928aa	Protein coding	CCDS56715	Q99P-J1	TSL5 GENCODE basic APPRIS ALT2
Pcdh15-215	ENSMUST00000131321.8	6926	1926aa	Protein coding	CCDS56718	Q99P-J1	TSL1 GENCODE basic APPRIS ALT2
Pcdh15-205	ENSMUST00000092420.12	6917	1833aa	Protein coding	CCDS48584	Q99P-J1	TSL1 GENCODE basic APPRIS ALT2
Pcdh15-211	ENSMUST00000126920.9	6866	1916aa	Protein coding	CCDS56720	Q99P-J1	TSL5 GENCODE basic APPRIS ALT2
Pcdh15-214	ENSMUST00000129404.9	6857	1813aa	Protein coding	CCDS56721	Q99P-J1	TSL5 GENCODE basic APPRIS ALT2
Pcdh15-222	ENSMUST00000147189.8	6806	1896aa	Protein coding	CCDS48595	Q99P-J1	TSL1 GENCODE basic APPRIS ALT2
Pcdh15-204	ENSMUST00000105426.9	6802	1936aa	Protein coding	CCDS56716	Q99P-J1	TSL5 GENCODE basic APPRIS ALT2
Pcdh15-209	ENSMUST00000105429.9	6719	1867aa	Protein coding	CCDS56719	Q99P-J1	TSL5 GENCODE basic
Pcdh15-218	ENSMUST00000131728.8	6522	1518aa	Protein coding	CCDS56719	Q99P-J1	TSL5 GENCODE basic APPRIS ALT2
Pcdh15-236	ENSMUST00000151118.8	6287	1705aa	Protein coding	CCDS58211	Q99P-J1	TSL5 GENCODE basic APPRIS ALT2
Pcdh15-231	ENSMUST00000177307.7	5696	1892aa	Protein coding	CCDS56719	Q99P-J1	TSL5 GENCODE basic APPRIS ALT2
Pcdh15-232	ENSMUST00000177420.0	4878	1176aa	Protein coding	CCDS56712	Q99P-J1	TSL-1 GENCODE basic
Pcdh15-208	ENSMUST00000125009.8	4869	1171aa	Protein coding	CCDS56714	Q99P-J1	TSL-1 GENCODE basic
Pcdh15-201	ENSMUST00000064562.13	8830	1865aa	Protein coding	-	EQG159	TSL-5 GENCODE basic
Pcdh15-238	ENSMUST00000193174.5	9396	1783aa	Protein coding	-	ADA0A5Y117	TSL5 GENCODE basic APPRIS ALT2
Pcdh15-225	ENSMUST00000149977.8	8843	1675aa	Protein coding	-	ADA140T883	TSL5 GENCODE basic APPRIS ALT2
Pcdh15-233	ENSMUST00000161708.5	5346	1781aa	Protein coding	-	Q99P-J1	TSL5 GENCODE basic APPRIS ALT2
Pcdh15-207	ENSMUST00000124046.7	5336	1129aa	Protein coding	-	Q99P-J1	TSL5 GENCODE basic
Pcdh15-241	ENSMUST00000195531.5	5241	1714aa	Protein coding	-	ADA0A6YX83	TSL5 GENCODE basic APPRIS ALT2
Pcdh15-239	ENSMUST00000195735.5	5054	1677aa	Protein coding	-	Q99P-J1	TSL5 GENCODE basic APPRIS ALT2
Pcdh15-239	ENSMUST00000194511.1	4715	1333aa	Protein coding	-	ADA0A6YX83	CDS 9 incomplete TSL-5
Pcdh15-227	ENSMUST00000152055.8	3660	881aa	Protein coding	-	Q99P-J1	TSL-1 GENCODE basic
Pcdh15-217	ENSMUST00000134009.8	3300	850aa	Protein coding	-	Q99P-J1	TSL-1 GENCODE basic
Pcdh15-219	ENSMUST00000125517.0	3074	719aa	Protein coding	-	Q99P-J1	TSL-1 GENCODE basic
Pcdh15-228	ENSMUST00000152819.8	2887	850aa	Protein coding	-	Q99P-J1	TSL-1 GENCODE basic
Pcdh15-229	ENSMUST00000155701.8	2754	736aa	Protein coding	-	Q99P-J1	TSL-1 GENCODE basic
Pcdh15-221	ENSMUST00000146682.7	1891	415aa	Protein coding	-	Q99P-J1	TSL-1 GENCODE basic
Pcdh15-209	ENSMUST00000125055.8	8852	884aa	Nonsense mediated decay	-	Q99P-J1	TSL-5
Pcdh15-218	ENSMUST00000136096.8	6846	884aa	Nonsense mediated decay	-	Q99P-J1	TSL-2
Pcdh15-220	ENSMUST00000144302.8	3315	328aa	Nonsense mediated decay	-	Q99P-J1	TSL-2
Pcdh15-246	ENSMUST00000194729.1	9272	No protein	Retained intron	-	-	TSL-NA
Pcdh15-224	ENSMUST00000148922.1	2712	No protein	Retained intron	-	-	TSL-1
Pcdh15-206	ENSMUST00000133398.8	2436	No protein	Retained intron	-	-	TSL-1
Pcdh15-230	ENSMUST00000196996.1	1024	No protein	Retained intron	-	-	TSL-1
Pcdh15-213	ENSMUST00000128843.1	691	No protein	Retained intron	-	-	TSL-5
Pcdh15-219	ENSMUST00000139106.2	462	No protein	Retained intron	-	-	TSL-2
Pcdh15-212	ENSMUST00000127928.6	3404	No protein	lncRNA	-	-	TSL-1
Pcdh15-223	ENSMUST00000147455.1	2841	No protein	lncRNA	-	-	TSL-1
Pcdh15-235	ENSMUST00000192370.1	556	No protein	lncRNA	-	-	TSL-3

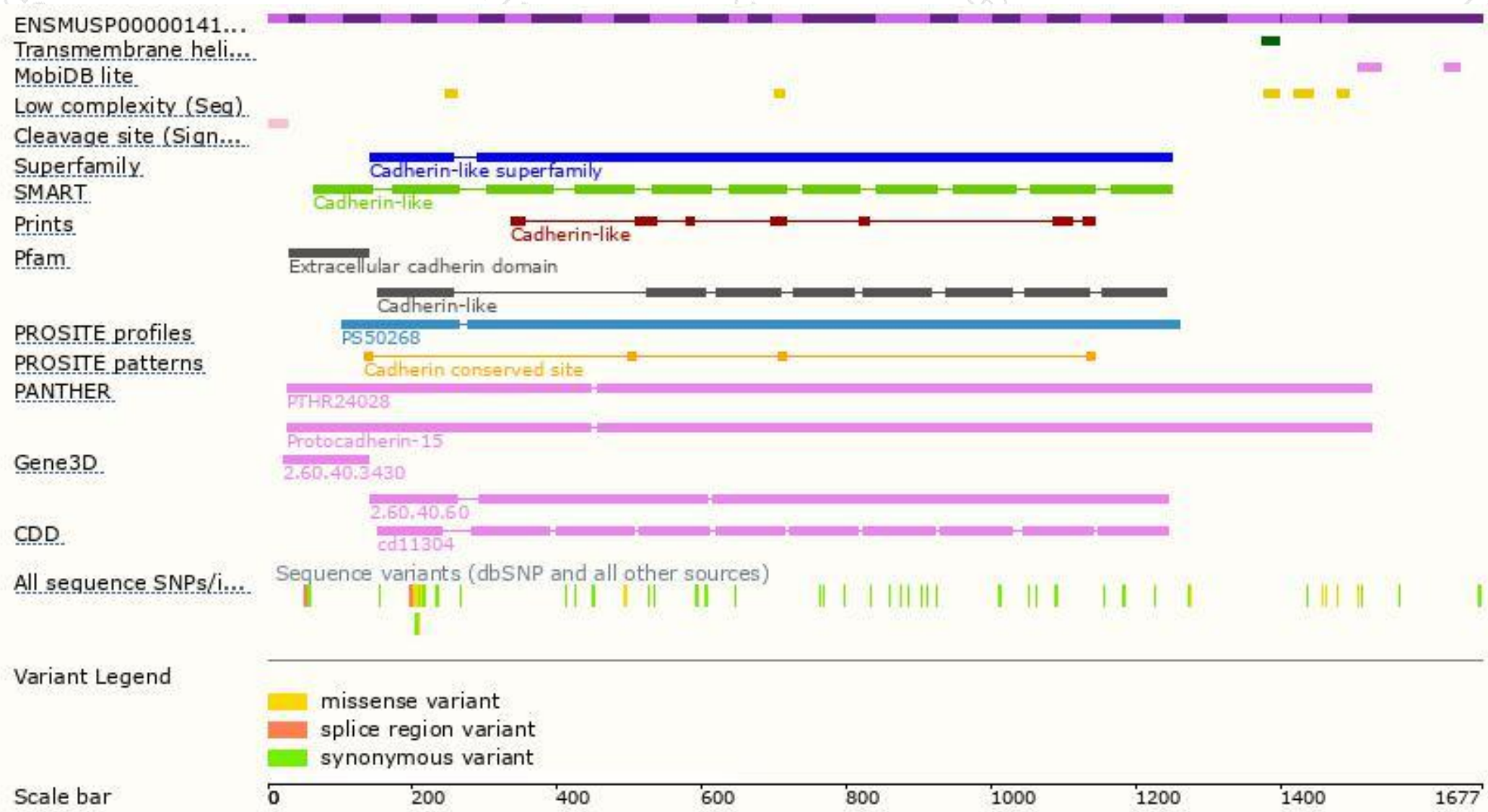
The strategy is based on the design of *Pcdh15-234* transcript,The transcription is shown below



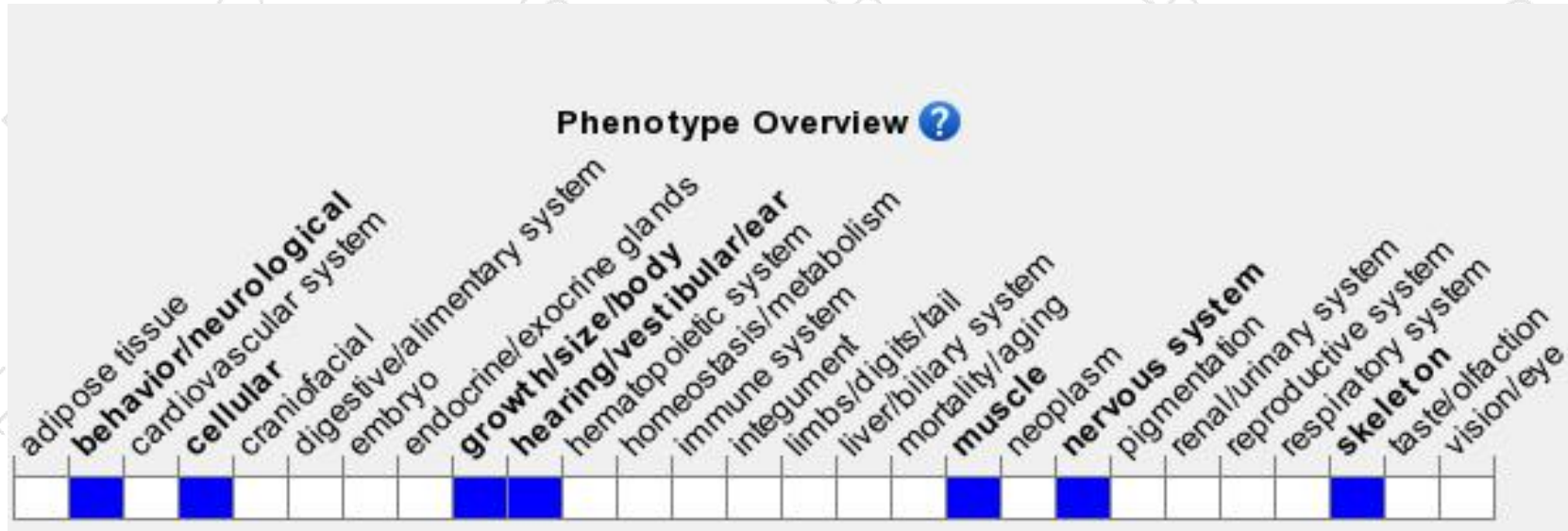
Genomic location distribution



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, Homozygotes for severe mutations exhibit circling, head-tossing, hyperactivity, impaired swimming and profound deafness. Mice have defects in cochlea and degeneration of hair cells, spiral ganglion cells and saccular macula. Females are poor mothers.

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

Tel: 400-9660890

