

Celsr3 Cas9-CKO Strategy

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Reviewer:

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Design Date:

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Project Overview

Project Name

Celsr3

Project type

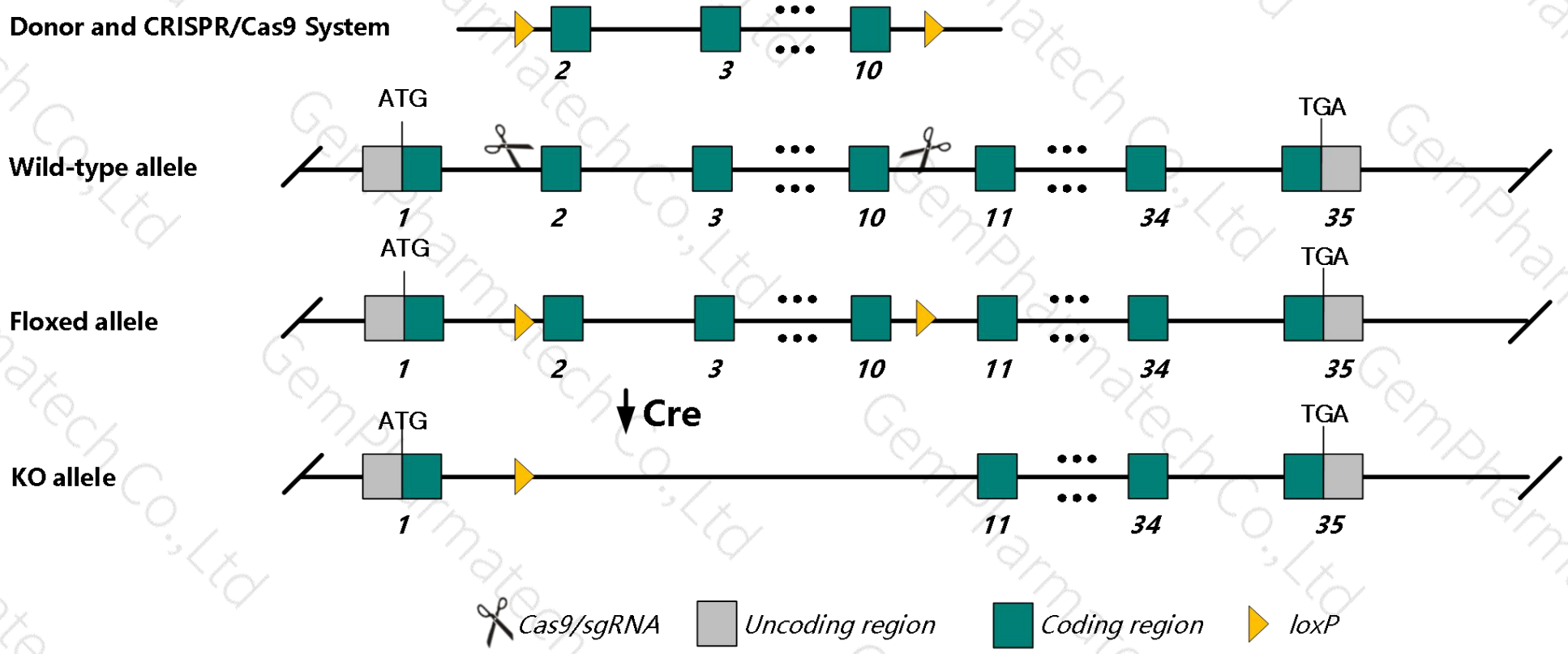
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Celsr3* gene. The schematic diagram is as follows:



- The *Celsr3* gene has 7 transcripts. According to the structure of *Celsr3* gene, exon2-exon10 of *Celsr3-201* (ENSMUST00000024238.10) transcript is recommended as the knockout region. The region contains 1880bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Celsr3* gene. The brief process is as follows: gRNA was transcribed in vitro, donor was constructed. Cas9, gRNA 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, Mice homozygous for a null allele exhibit neonatal lethality, abnormal nervous system development, and abnormal respiratory system development.
- Transcript *Celsr3-204/205/206* may not be affected. The size of intron10 for 3'-loxP site insertion is 558bp. The KO region is close to 5'UTR region of the *Gm35025* gene. Knockout the region may affect the regulatory function of *Gm35025* gene.
- The *Celsr3* gene is located on the Chr9. 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)

Celsr3 cadherin, EGF LAG seven-pass G-type receptor 3 [*Mus musculus* (house mouse)]

Gene ID: 107934, updated on 14-Aug-2019

Summary



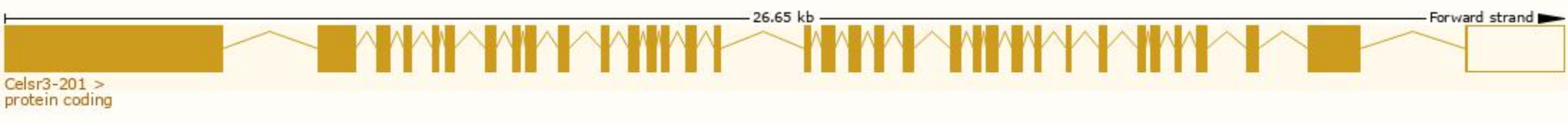
Official Symbol	Celsr3 provided by MGI
Official Full Name	cadherin, EGF LAG seven-pass G-type receptor 3 provided by MGI
Primary source	MGI:MGI:1858236
See related	Ensembl:ENSMUSG00000023473
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Fmi1; Adgrc3; flamingo; mKIAA0812
Expression	Biased expression in whole brain E14.5 (RPKM 20.1), CNS E18 (RPKM 16.6) and 6 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

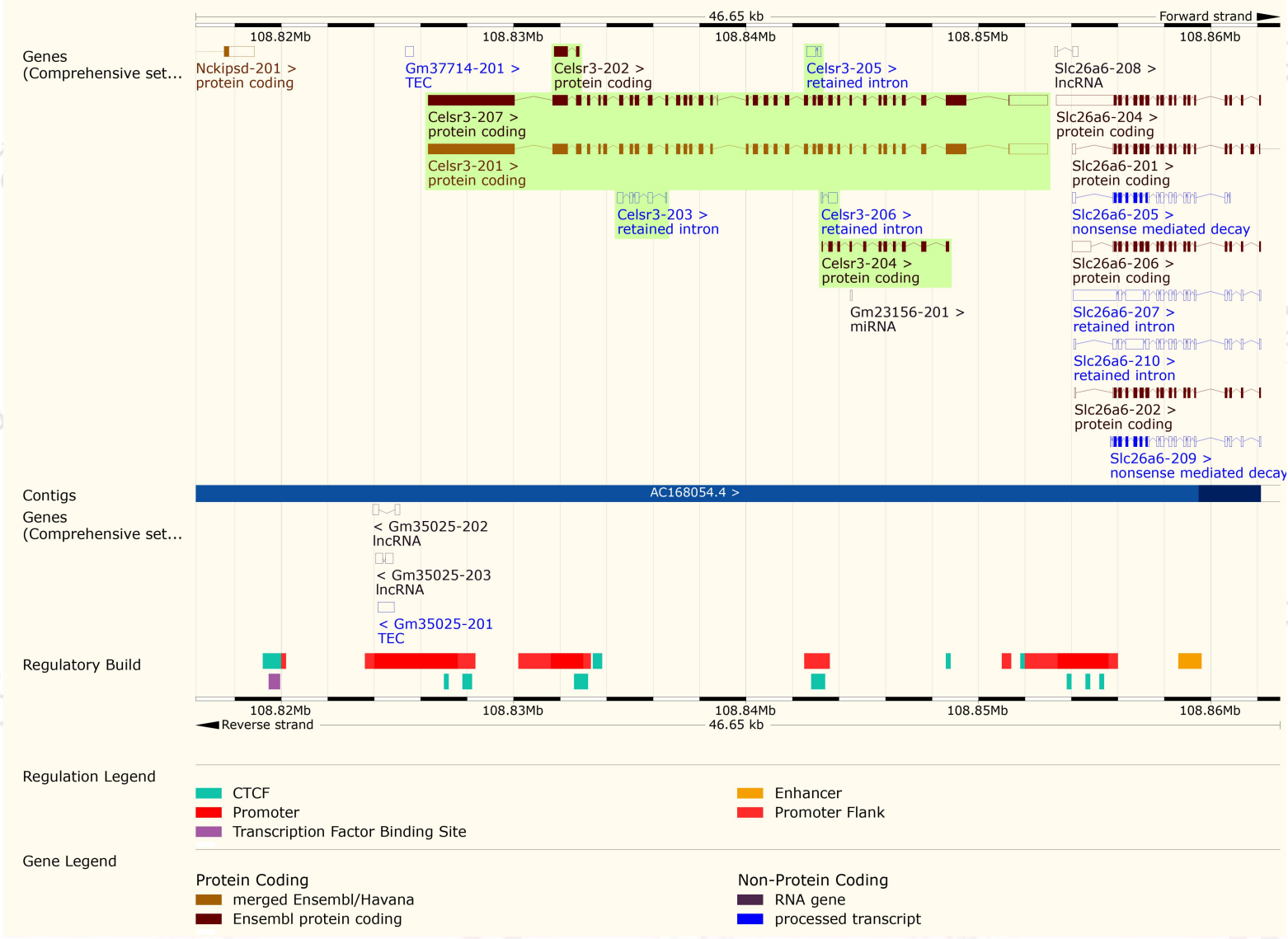
The gene has 7 transcripts,all transcripts are shown below:

Name ▲	Transcript ID ▲	bp ▲	Protein ▲	Translation ID ▲	Biotype ▲	CCDS ▲	UniProt ▲	Flags ▲
Celsr3-201	ENSMUST00000024238.10	11547	3301aa	ENSMUSP00000024238.5	Protein coding	-	Q91ZI0	TSL:1 GENCODE basic APPRIS ALT2
Celsr3-202	ENSMUST00000192235.1	722	240aa	ENSMUSP00000141429.1	Protein coding	-	A0A0A6YW76	CDS 5' and 3' incomplete TSL:3
Celsr3-203	ENSMUST00000193726.1	767	No protein	-	Retained intron	-	-	TSL:5
Celsr3-204	ENSMUST00000194079.1	1418	472aa	ENSMUSP00000141789.1	Protein coding	-	A0A0A6YX12	CDS 5' and 3' incomplete TSL:1
Celsr3-205	ENSMUST00000195255.1	524	No protein	-	Retained intron	-	-	TSL:2
Celsr3-206	ENSMUST00000195857.1	443	No protein	-	Retained intron	-	-	TSL:2
Celsr3-207	ENSMUST00000213524.2	11571	3309aa	ENSMUSP00000150759.1	Protein coding	-	A0A1L1SUG9	TSL:1 GENCODE basic APPRIS P5

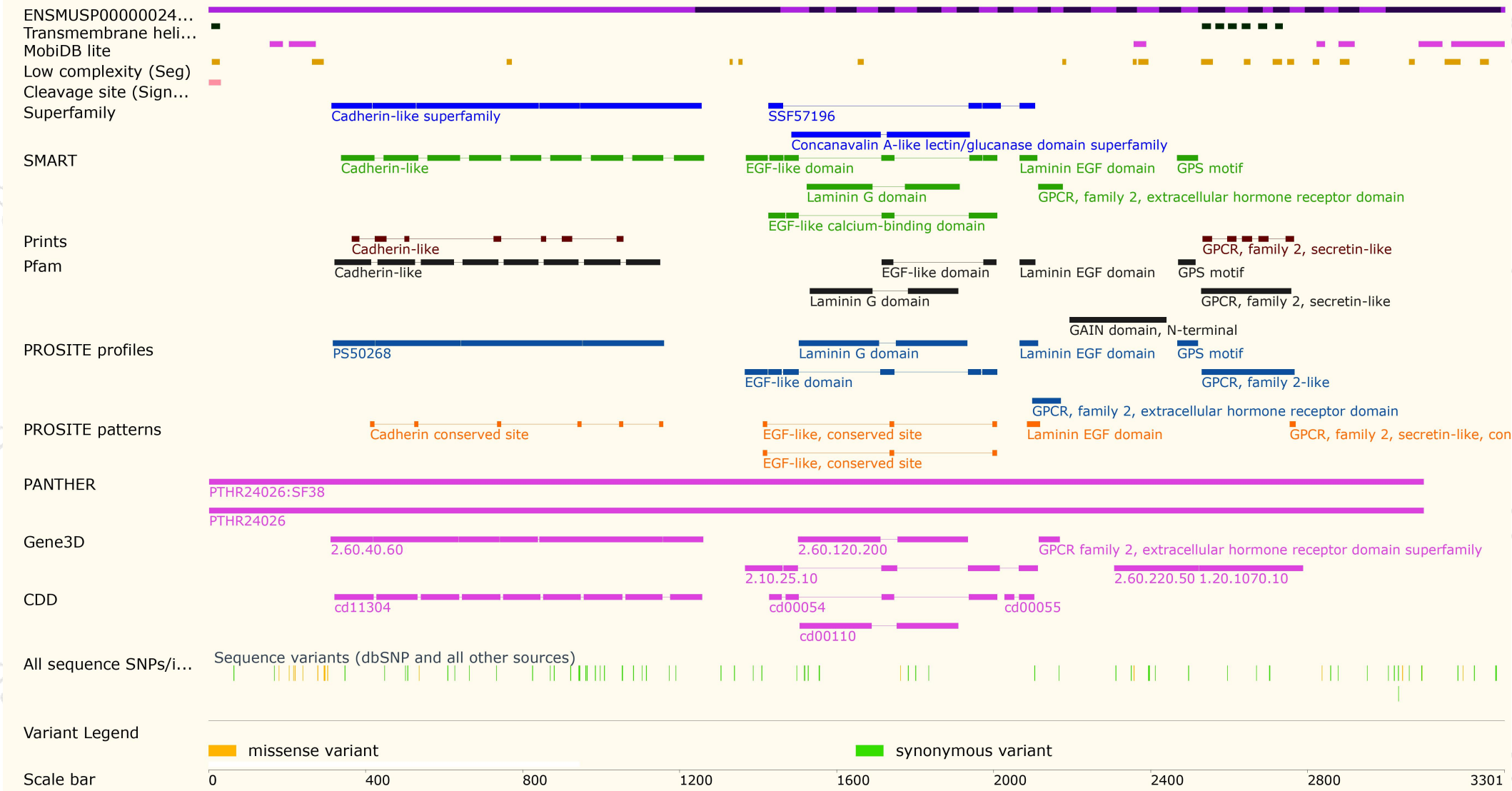
The strategy is based on the design of *Celsr3-201* transcript,The transcription is shown below



Genomic location distribution

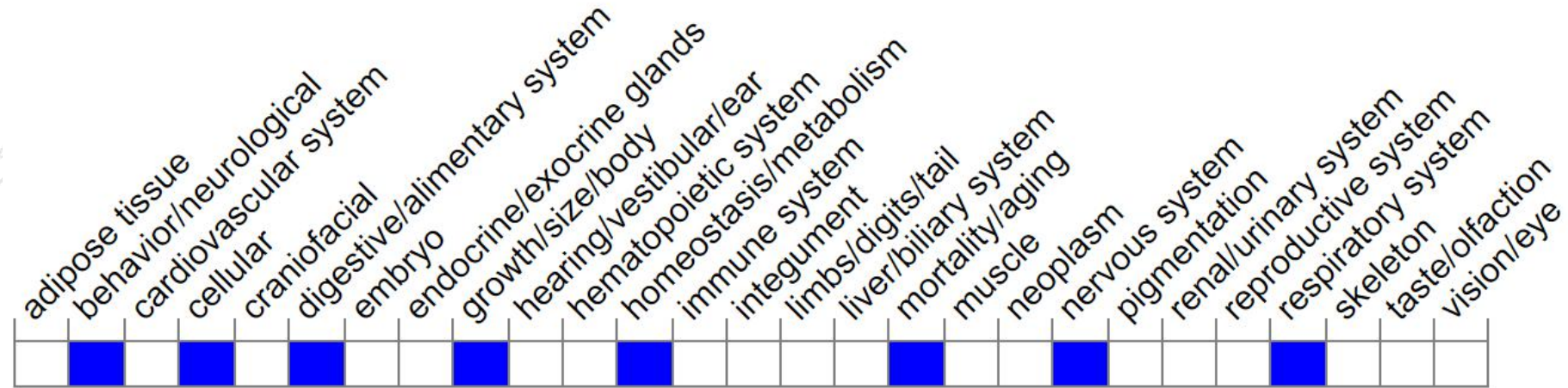


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview ?



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).

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

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