Slc15a2 Cas9-KO Strategy

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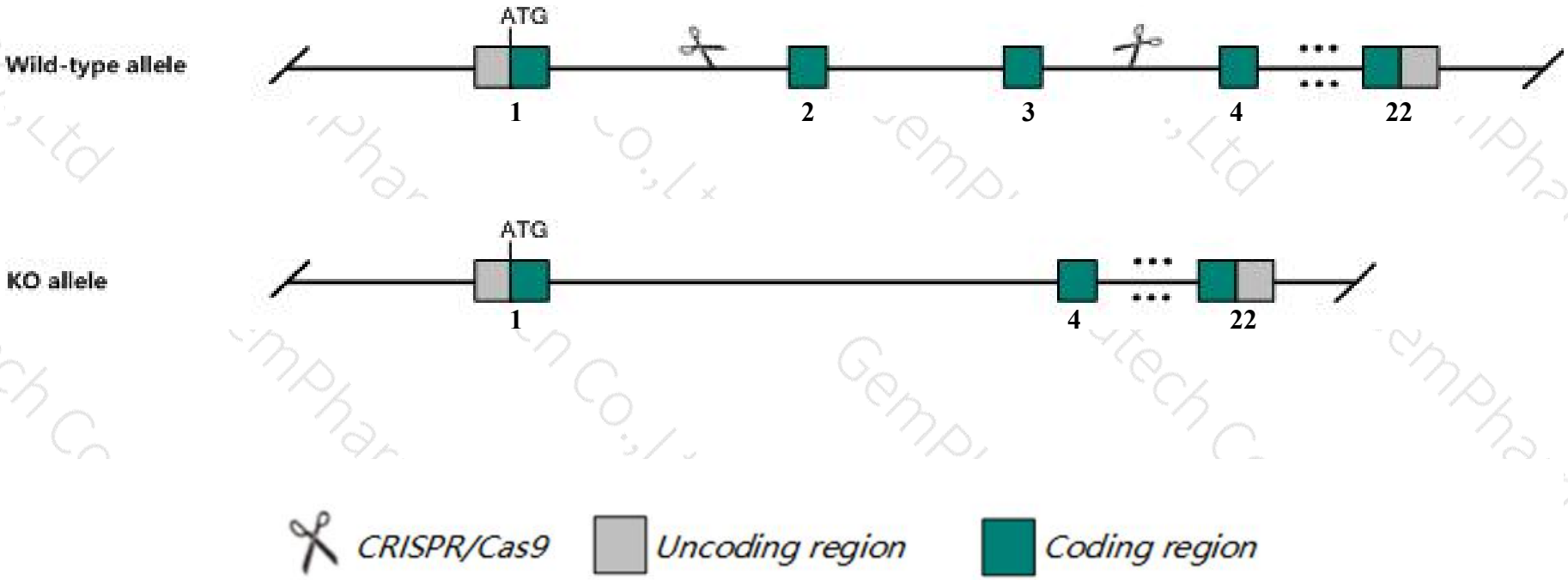
Project Overview

Project Name	***Slc15a2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc15a2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Slc15a2* gene has 14 transcripts. According to the structure of *Slc15a2* gene, exon2-exon3 of *Slc15a2-201* (ENSMUST00000023616.9) transcript is recommended as the knockout region.The region contains 230bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Slc15a2* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

- According to the existing MGI data,Homozygous mutant mice have impairments of dipeptide transportion, however, show no gross defects.
- Transcript *Slc15a2*-202&203&204&206&209&210&211&214 may not be affected.
- The *Slc15a2* gene is located on the Chr16. 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）

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Slc15a2 solute carrier family 15 (H+/peptide transporter), member 2 [*Mus musculus* (house mouse)]

Gene ID: 57738, updated on 12-Aug-2019

Summary

Official Symbol	Slc15a2 provided by MGI
Official Full Name	solute carrier family 15 (H+/peptide transporter), member 2 provided by MGI
Primary source	MGI:MGI:1890457
See related	Ensembl:ENSMUSG00000022899
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	Pept2; C78862; 8430408C16Rik
Expression	Broad expression in kidney adult (RPKM 7.8), frontal lobe adult (RPKM 3.5) and 17 other tissues See more
Orthologs	human all

Genomic context

Location: 16; 16 B3

See Slc15a2 in Genome Data Viewer

Exon count: 24

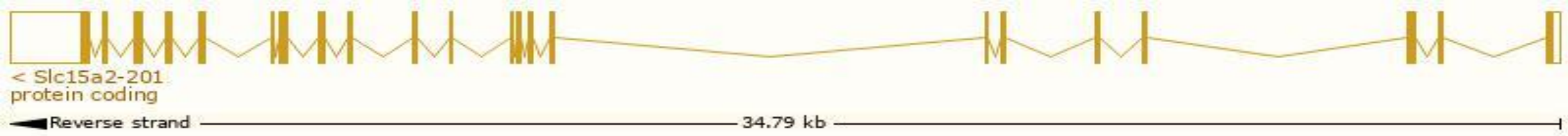
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	16	NC_000082.6 (36750161..36785158, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	16	NC_000082.5 (36750250..36785048, complement)

Transcript information（Ensembl）

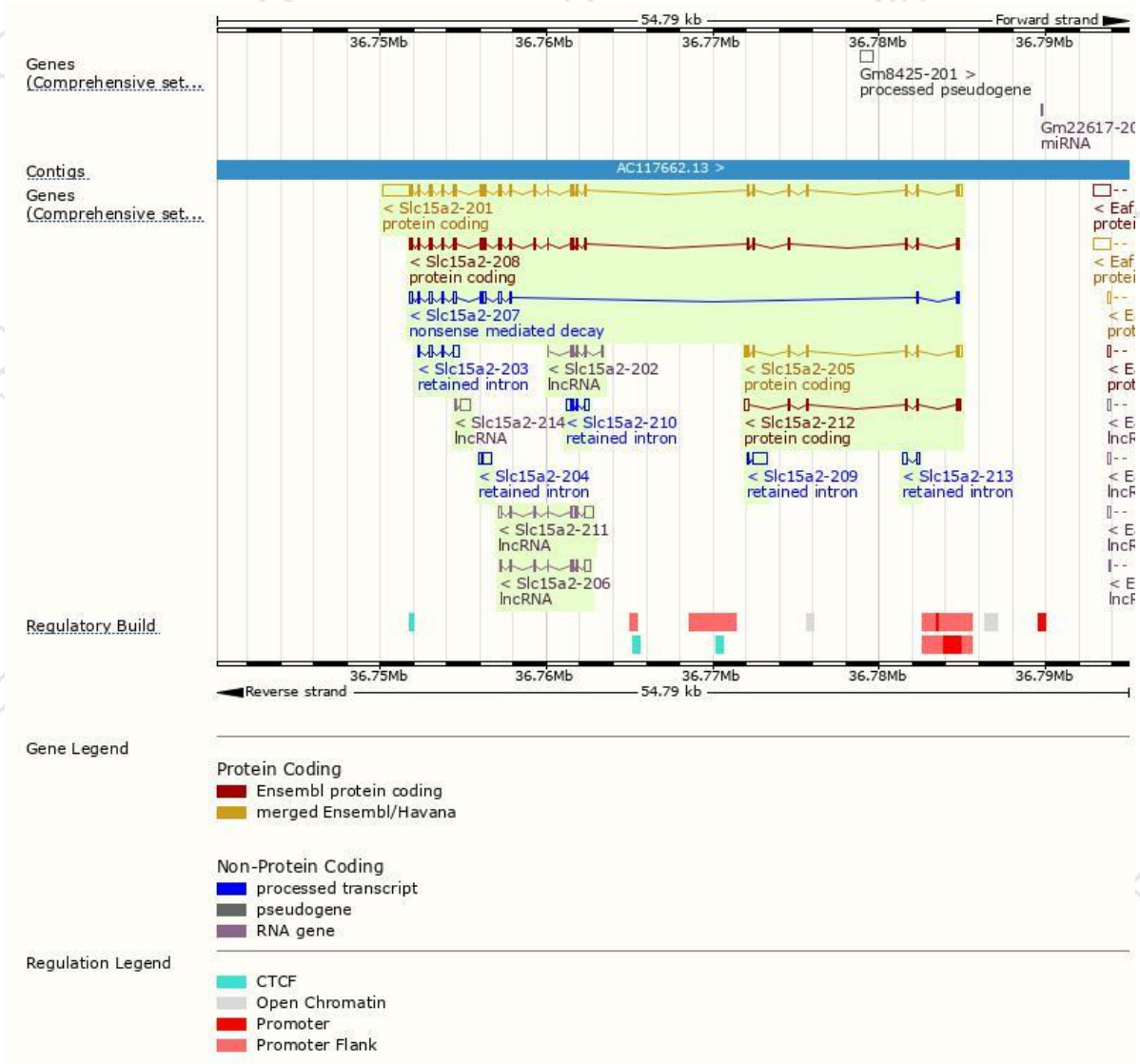
The gene has 14 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc15a2-201	ENSMUST00000023616.9	3994	740aa	Protein coding	CCDS28156	E9QMN8	TSL:1 GENCODE basic APPRIS P2
Slc15a2-205	ENSMUST00000164579.7	1068	259aa	Protein coding	CCDS49842	E9Q329	TSL:1 GENCODE basic
Slc15a2-208	ENSMUST00000165531.7	2158	709aa	Protein coding	-	E9PYQ9	TSL:5 GENCODE basic APPRIS ALT2
Slc15a2-212	ENSMUST00000168279.1	958	189aa	Protein coding	-	G3XA51	TSL:3 GENCODE basic
Slc15a2-207	ENSMUST00000165380.7	1292	84aa	Nonsense mediated decay	-	E9Q0L2	TSL:5
Slc15a2-209	ENSMUST00000166399.1	928	No protein	Retained intron	-	-	TSL:2
Slc15a2-210	ENSMUST00000167909.1	729	No protein	Retained intron	-	-	TSL:2
Slc15a2-204	ENSMUST00000163964.1	679	No protein	Retained intron	-	-	TSL:3
Slc15a2-203	ENSMUST00000163471.1	622	No protein	Retained intron	-	-	TSL:3
Slc15a2-213	ENSMUST00000169644.1	516	No protein	Retained intron	-	-	TSL:3
Slc15a2-211	ENSMUST00000167941.7	1170	No protein	lncRNA	-	-	TSL:5
Slc15a2-206	ENSMUST00000164770.7	874	No protein	lncRNA	-	-	TSL:5
Slc15a2-214	ENSMUST00000172382.1	694	No protein	lncRNA	-	-	TSL:3
Slc15a2-202	ENSMUST00000100308.9	430	No protein	lncRNA	-	-	TSL:3

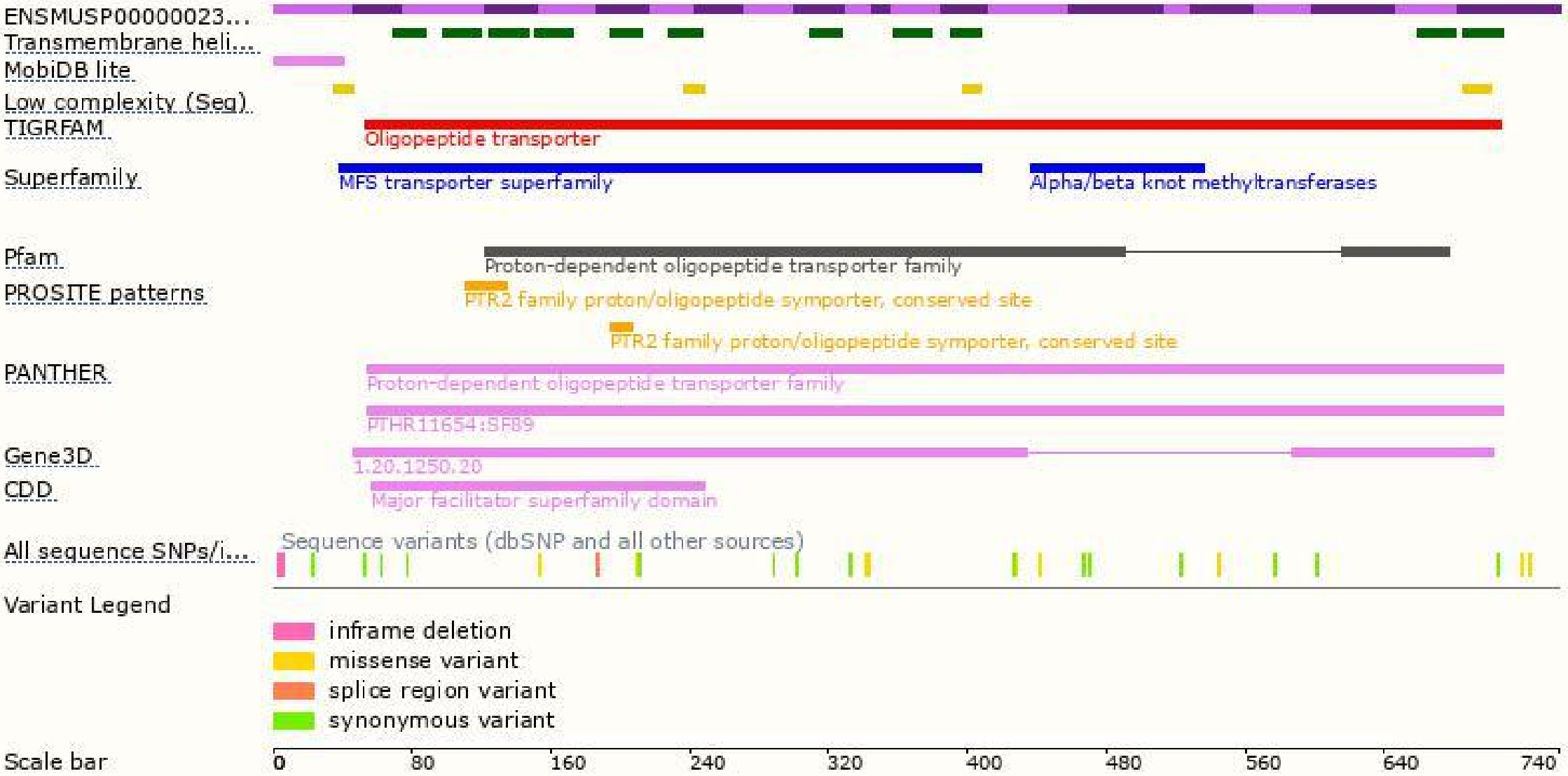
The strategy is based on the design of *Slc15a2-201* transcript,The transcription is shown below



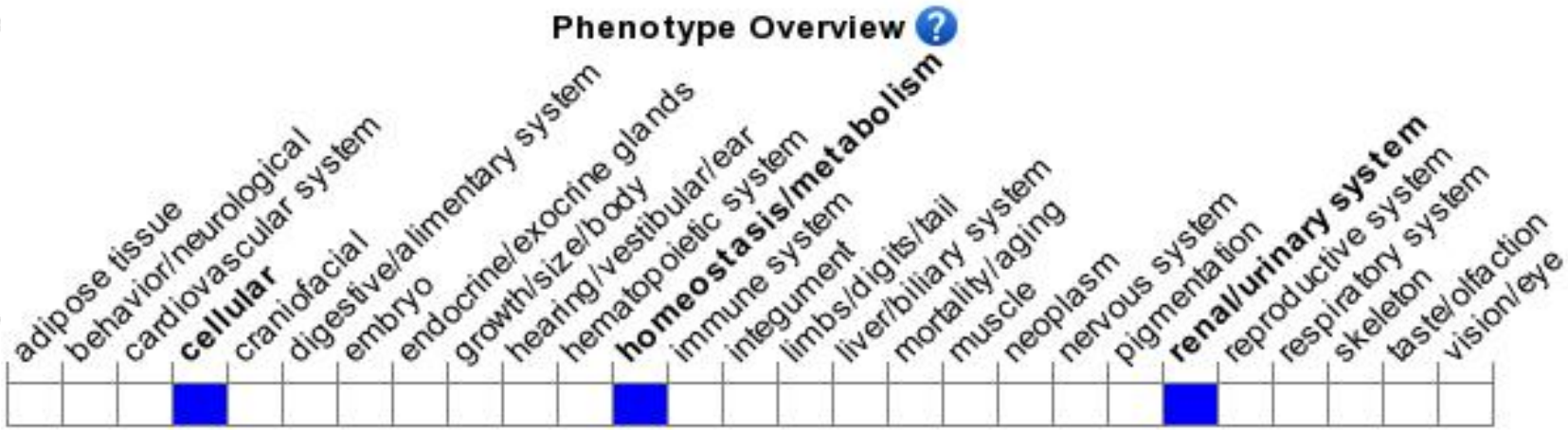
Genomic location distribution



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,Homozygous mutant mice have impairments of dipeptide transportion, however, show no gross defects.

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

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