Spg7 Cas9-CKO Strategy

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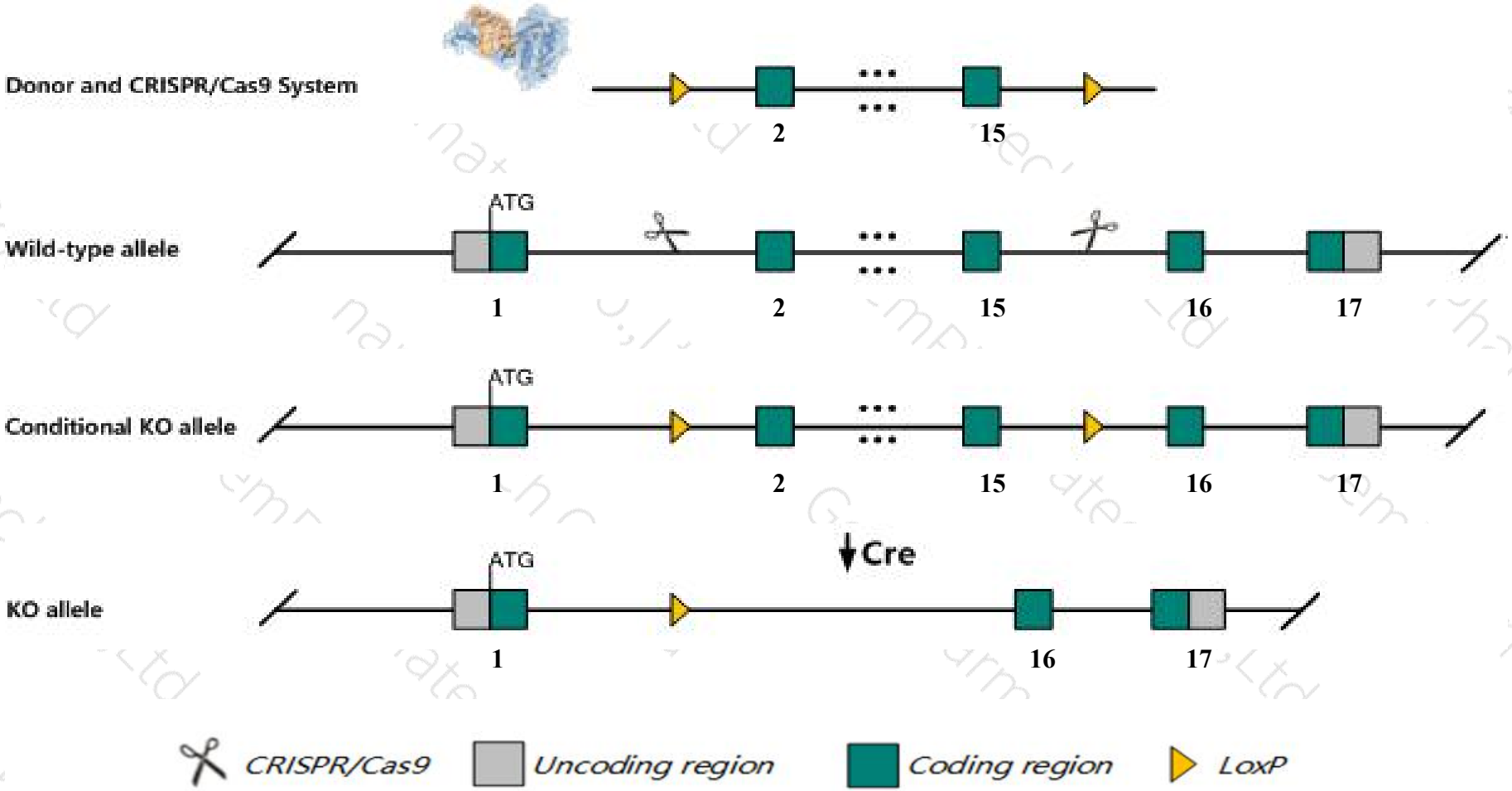
Project Overview

Project Name	***Spg7***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Spg7* gene. The schematic diagram is as follows:



Technical routes

- The *Spg7* gene has 13 transcripts. According to the structure of *Spg7* gene, exon2-exon15 of *Spg7-209* (ENSMUST00000149248.8) transcript is recommended as the knockout region.The region contains most of the coding sequence.Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Spg7* 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.

Notice

- According to the existing MGI data,homozygous null mice exhibit impaired motor skills, putativley associated with axonal degeneration in the central and peripheral nervous systems.
- The KO region deletes most of the coding sequence, but does not result in frameshift.
- The *Spg7* gene is located on the Chr8. 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）

集萃药康 GemPharmatech

Spg7 SPG7, paraplegin matrix AAA peptidase subunit [Mus musculus (house mouse)]

Gene ID: 234847, updated on 19-Mar-2019

Summary

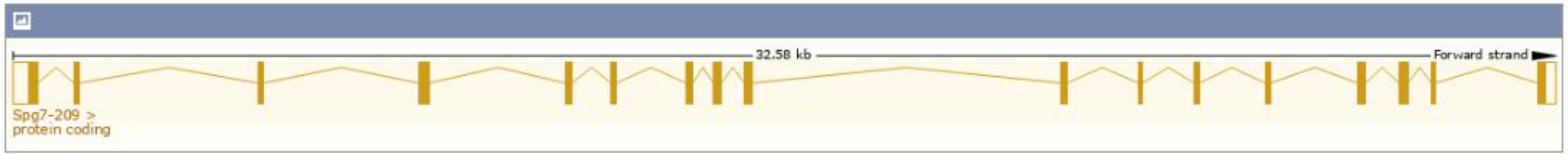
Official Symbol	Spg7 provided by MGI
Official Full Name	SPG7, paraplegin matrix AAA peptidase subunit provided byMGI
Primary source	MGI:MGI:2385906
See related	Ensembl:ENSMUSG00000000738
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI452278, AU015315, Cmar, PGN
Expression	Ubiquitous expression in adrenal adult (RPKM 106.3), duodenum adult (RPKM 72.3) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 13 transcripts,all transcripts are shown below:

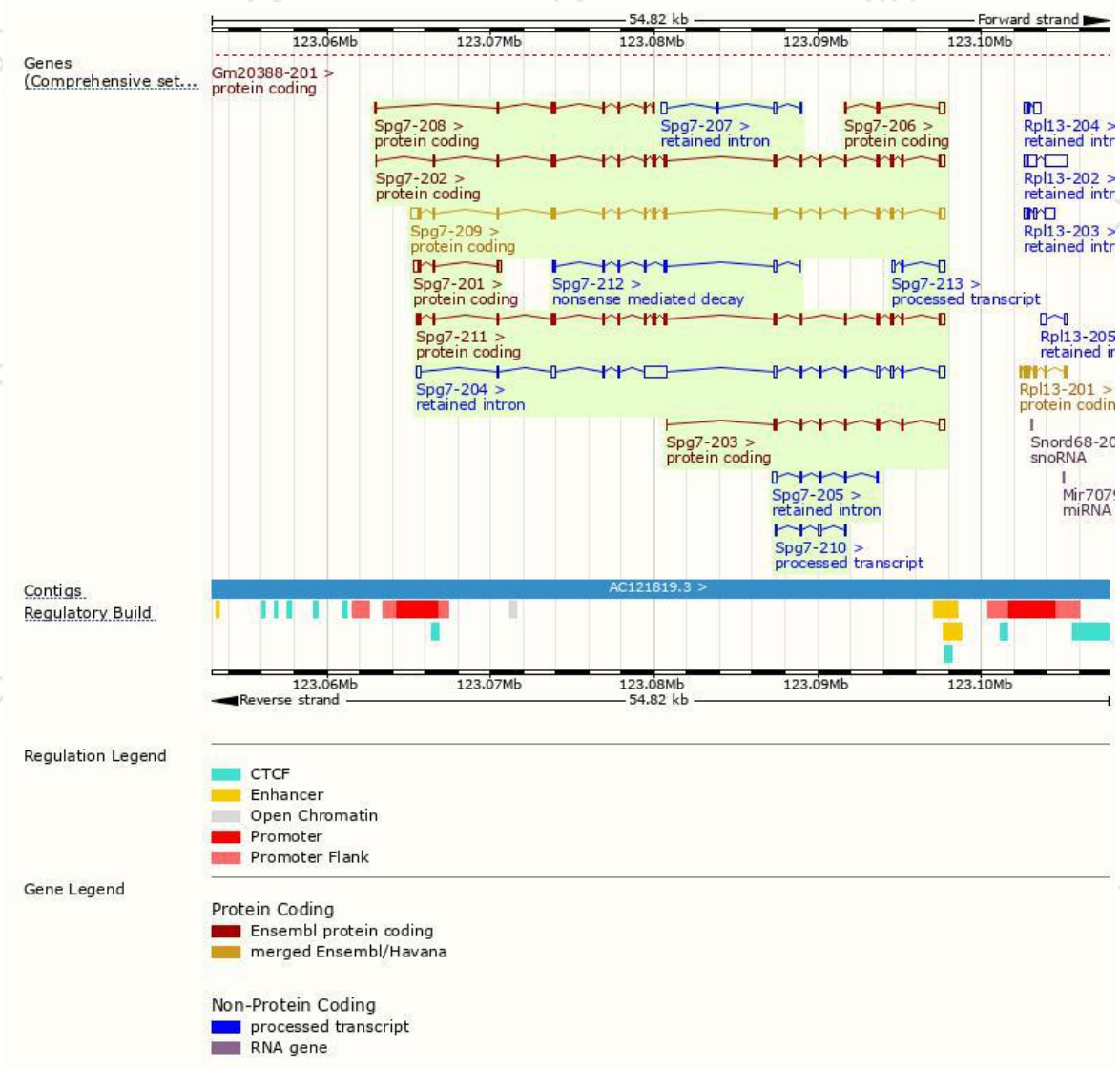
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Spg7-209	ENSMUST00000149248.8	2896	781aa	Protein coding	CCDS40508	Q3ULF4	TSL:1 GENCODE basic APPRIS P2
Spg7-211	ENSMUST00000153285.8	2481	744aa	Protein coding	-	D3YXB7	TSL:5 GENCODE basic APPRIS ALT2
Spg7-202	ENSMUST00000125975.7	2408	676aa	Protein coding	-	D3YZN4	TSL:5 GENCODE basic APPRIS ALT2
Spg7-203	ENSMUST00000128234.7	1080	253aa	Protein coding	-	F6W695	CDS 5' incomplete TSL:3
Spg7-201	ENSMUST00000108868.10	845	145aa	Protein coding	-	A0A1I7Q4C2	TSL:2 GENCODE basic
Spg7-208	ENSMUST00000142541.7	809	230aa	Protein coding	-	D3Z342	CDS 3' incomplete TSL:5
Spg7-206	ENSMUST00000135991.1	592	90aa	Protein coding	-	F6VTG4	CDS 5' incomplete TSL:5
Spg7-212	ENSMUST00000153492.7	883	209aa	Nonsense mediated decay	-	G3UX97	CDS 5' incomplete TSL:5
Spg7-204	ENSMUST00000128803.7	3385	No protein	Retained intron	-	-	TSL:5
Spg7-207	ENSMUST00000142150.1	693	No protein	Retained intron	-	-	TSL:3
Spg7-205	ENSMUST00000130787.7	613	No protein	Retained intron	-	-	TSL:3
Spg7-213	ENSMUST00000212364.1	669	No protein	lncRNA	-	-	TSL:3
Spg7-210	ENSMUST00000152972.1	390	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Spg7-209* transcript,The transcription is shown below

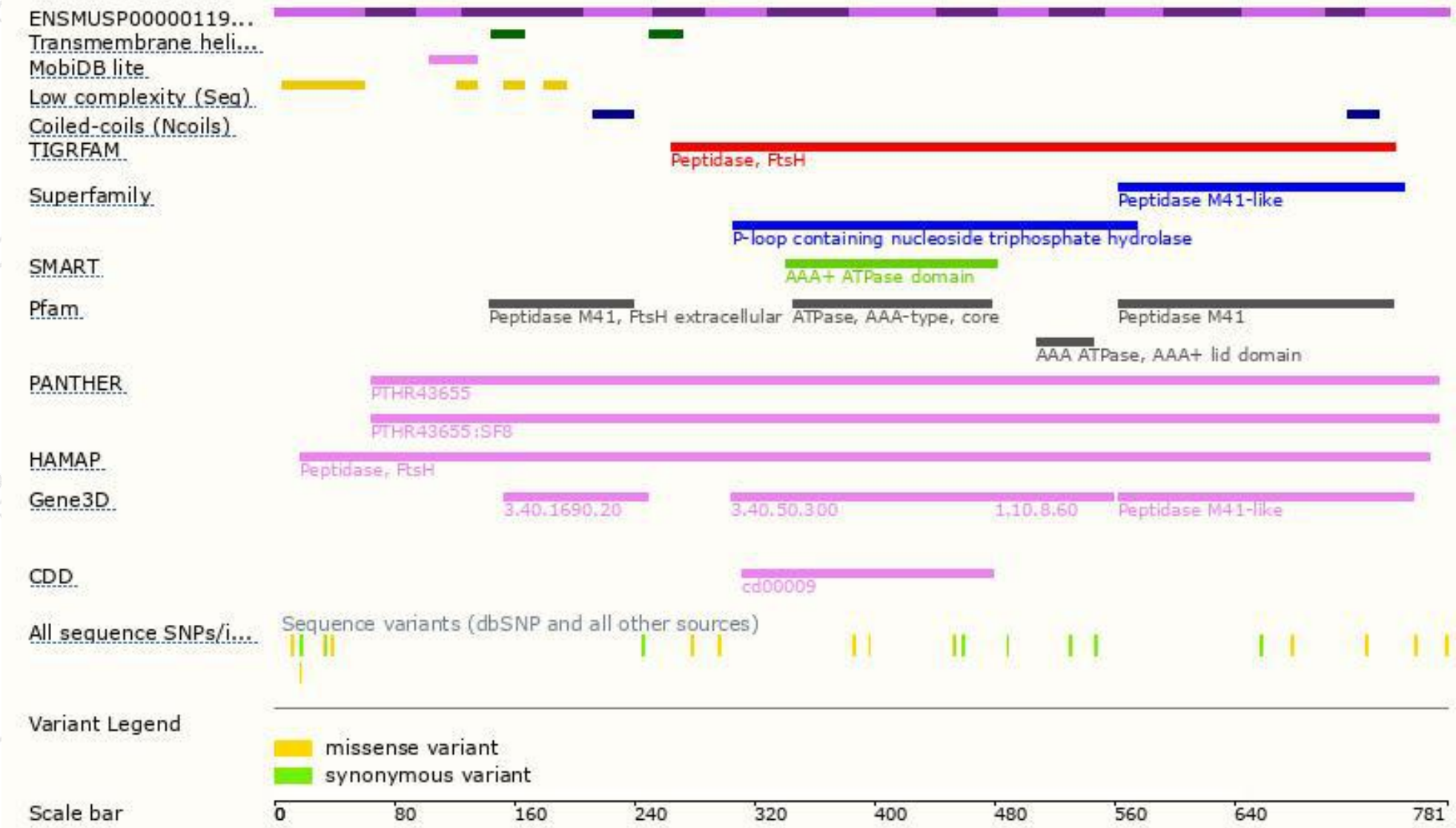


Statistics **Exons:** 17, **Coding exons:** 17, **Transcript length:** 2,896 bps, **Translation length:** 781 residues

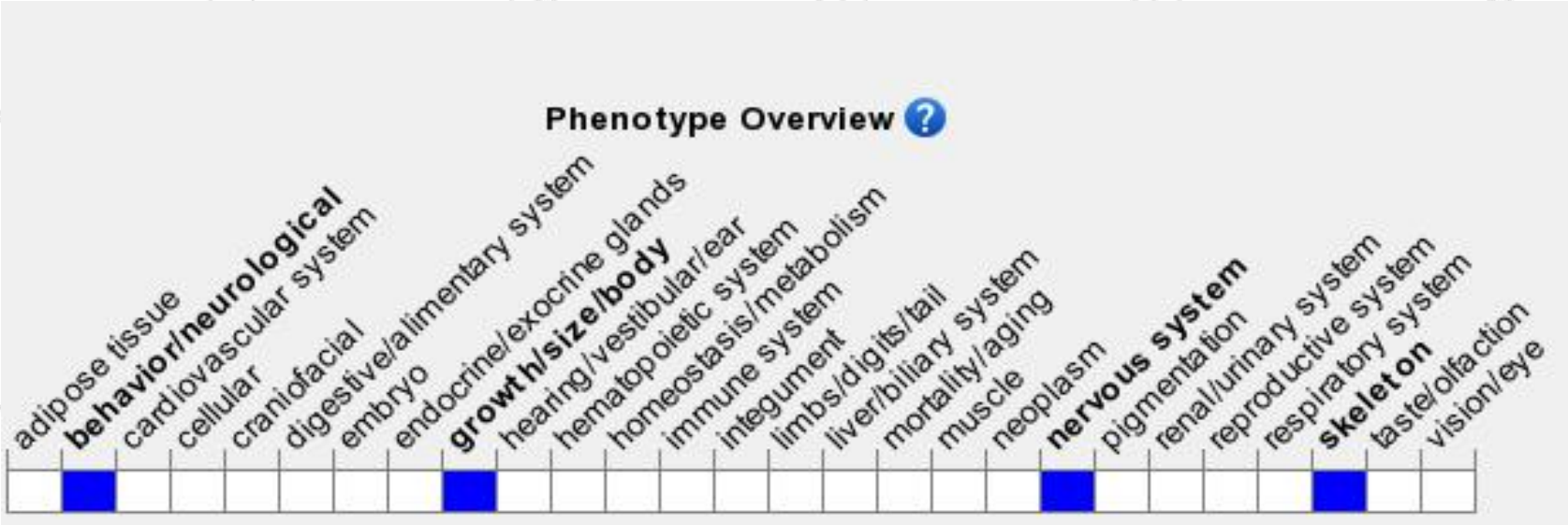
Genomic location distribution



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/).

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

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