Agtpbp1 Cas9-CKO Strategy

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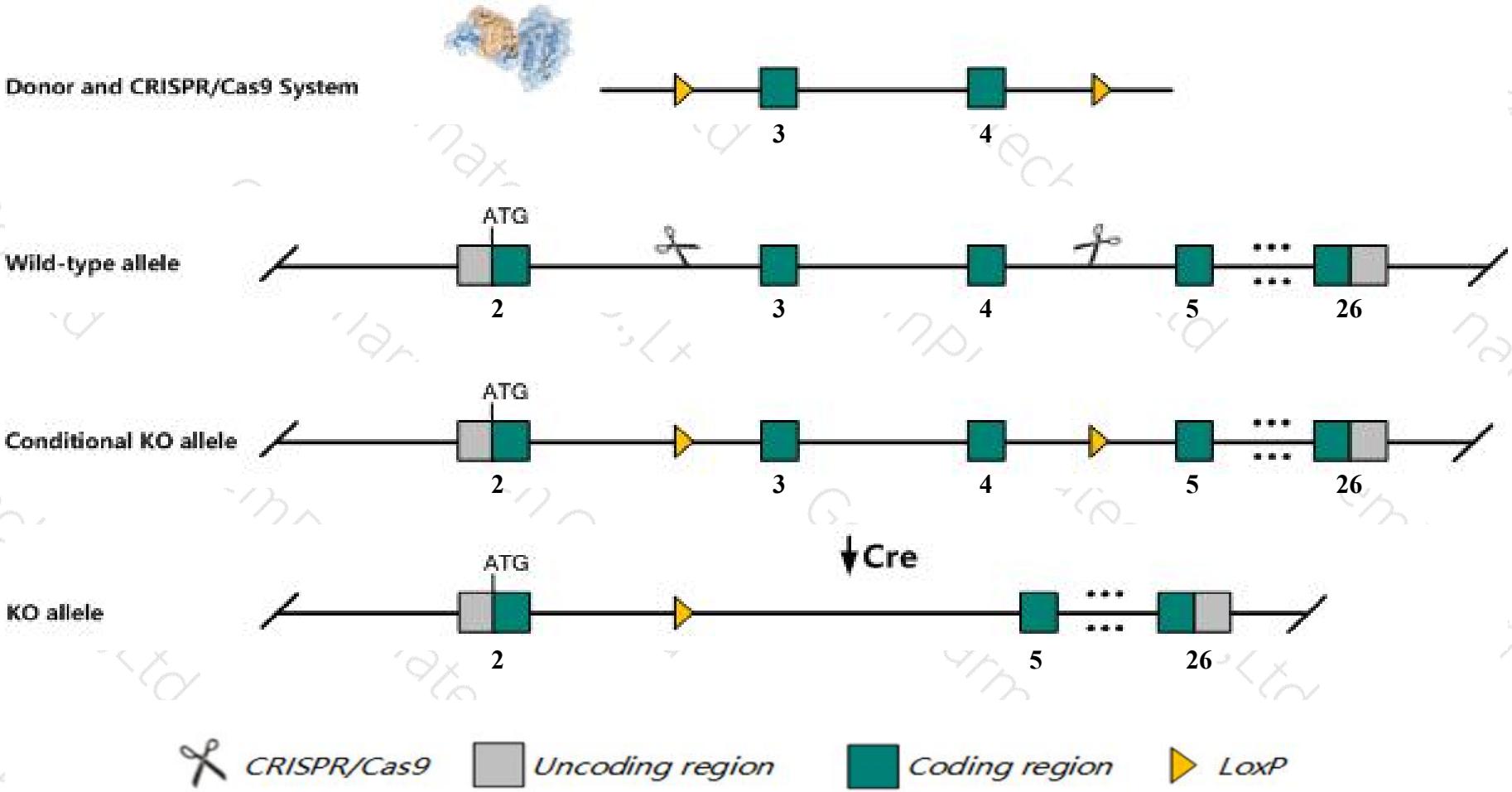
Project Overview

Project Name	***Agtpbp1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Agtpbp1* gene. The schematic diagram is as follows:



Technical routes

- The *Agtpbp1* gene has 24 transcripts. According to the structure of *Agtpbp1* gene, exon3-exon4 of *Agtpbp1-201* (ENSMUST00000022040.13) transcript is recommended as the knockout region.The region contains 193bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Agtpbp1* 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,Homozygotes show moderate ataxia due to degeneration of Purkinje cells of the cerebellum. Also, there is gradual degeneration of retina photoreceptor cells, olfactory bulb mitral cells and some thalamic neurons. Males have abnormal sperm and are sterile.
- The transcripts of 204, 217, 223 are incomplete and effects are unknown.
- The 203, 211, 215, 224 transcripts were not affected.
- The *Agtpbp1* gene is located on the Chr13. 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

Agtpbp1 ATP/GTP binding protein 1 [*Mus musculus* (house mouse)]

Gene ID: 67269, updated on 14-Oct-2019

Summary

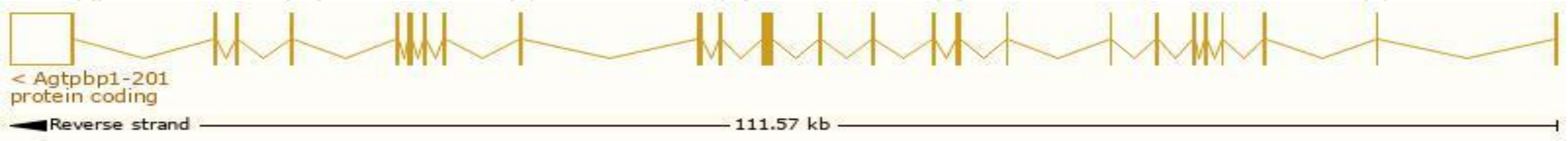
Official Symbol	Agtpbp1 provided by MGI
Official Full Name	ATP/GTP binding protein 1 provided by MGI
Primary source	MGI:MGI:2159437
See related	Ensembl:ENSMUSG00000021557
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	pcd; CCP1; Nna1; atms; nmf243; 1700020N17Rik; 2310001G17Rik; 2900054O13Rik; 4930445M19Rik; 5730402G09Rik
Expression	Broad expression in cerebellum adult (RPKM 16.1), cortex adult (RPKM 14.6) and 21 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

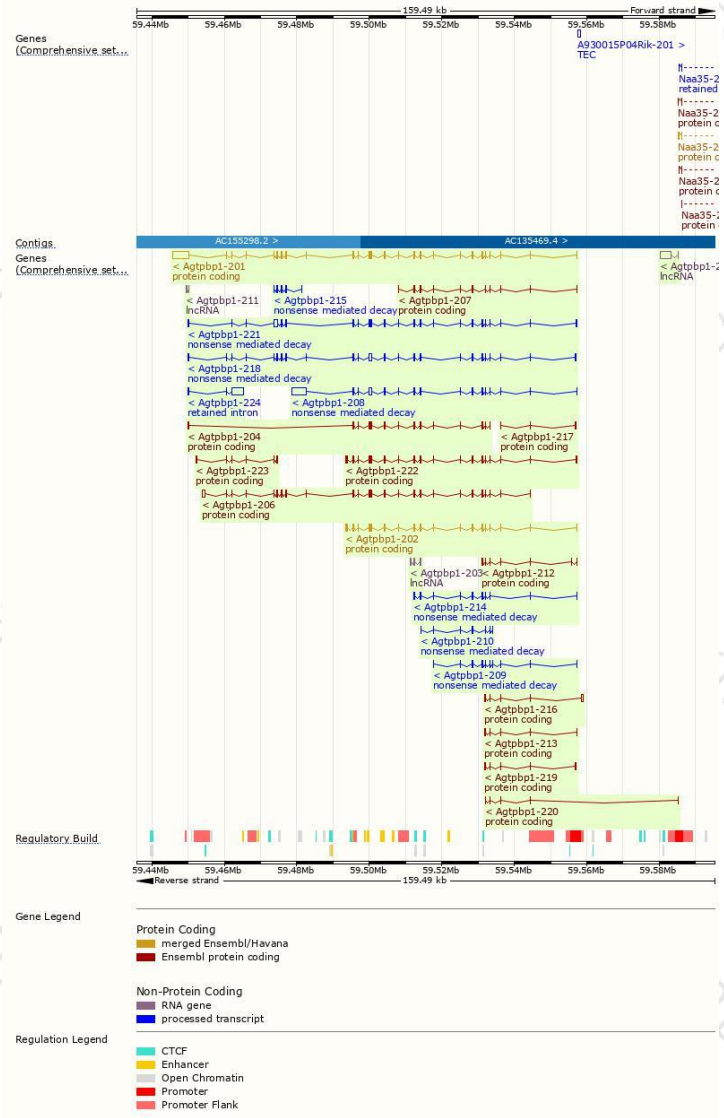
The gene has 24 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Agtpbp1-201	ENSMUST00000022040.13	8174	1218aa	Protein coding	CCDS36686	Q641K1	TSL:1 GENCODE basic APPRIS P3
Agtpbp1-206	ENSMUST00000164215.7	4331	1174aa	Protein coding	CCDS70470	Q641K1	TSL:1 GENCODE basic APPRIS ALT2
Agtpbp1-222	ENSMUST00000171606.8	3037	789aa	Protein coding	CCDS36687	Q641K1	TSL:1 GENCODE basic
Agtpbp1-202	ENSMUST00000109830.8	2879	789aa	Protein coding	CCDS36687	Q641K1	TSL:1 GENCODE basic
Agtpbp1-204	ENSMUST00000163149.8	2293	685aa	Protein coding	-	F6ZCF0	CDS 5' incomplete TSL:5
Agtpbp1-207	ENSMUST00000165370.8	1086	332aa	Protein coding	-	E9PX07	CDS 3' incomplete TSL:3
Agtpbp1-223	ENSMUST00000224397.1	844	226aa	Protein coding	-	A0A286YDV2	CDS 5' incomplete
Agtpbp1-216	ENSMUST00000168821.7	721	99aa	Protein coding	-	Q8C1R2	TSL:1 GENCODE basic
Agtpbp1-219	ENSMUST00000170378.7	653	99aa	Protein coding	-	Q8C1R2	TSL:3 GENCODE basic
Agtpbp1-212	ENSMUST00000166585.7	600	103aa	Protein coding	-	E9Q3T5	CDS 3' incomplete TSL:5
Agtpbp1-213	ENSMUST00000167096.7	508	99aa	Protein coding	-	Q8C1R2	TSL:1 GENCODE basic
Agtpbp1-217	ENSMUST00000169434.1	453	51aa	Protein coding	-	E9Q2R5	CDS 3' incomplete TSL:2
Agtpbp1-220	ENSMUST00000170520.7	379	86aa	Protein coding	-	E9Q878	CDS 3' incomplete TSL:5
Agtpbp1-208	ENSMUST00000165477.8	6290	246aa	Nonsense mediated decay	-	E9PXA7	TSL:2
Agtpbp1-221	ENSMUST00000170555.7	4601	795aa	Nonsense mediated decay	-	Q641K1	TSL:2
Agtpbp1-218	ENSMUST00000169745.7	4143	246aa	Nonsense mediated decay	-	E9PXA7	TSL:1
Agtpbp1-214	ENSMUST00000167593.7	1024	42aa	Nonsense mediated decay	-	E9PYF9	TSL:1
Agtpbp1-209	ENSMUST00000165598.7	921	71aa	Nonsense mediated decay	-	E9Q352	TSL:5
Agtpbp1-215	ENSMUST00000168141.1	680	98aa	Nonsense mediated decay	-	A0A286YDY7	CDS 5' incomplete TSL:5
Agtpbp1-210	ENSMUST00000165851.7	654	33aa	Nonsense mediated decay	-	A0A286YCK8	CDS 5' incomplete TSL:2
Agtpbp1-224	ENSMUST00000225133.1	3874	No protein	Retained intron	-	-	
Agtpbp1-205	ENSMUST00000163284.1	3158	No protein	lncRNA	-	-	TSL:1
Agtpbp1-203	ENSMUST00000151827.2	400	No protein	lncRNA	-	-	TSL:3
Agtpbp1-211	ENSMUST00000166276.1	278	No protein	lncRNA	-	-	TSL:3

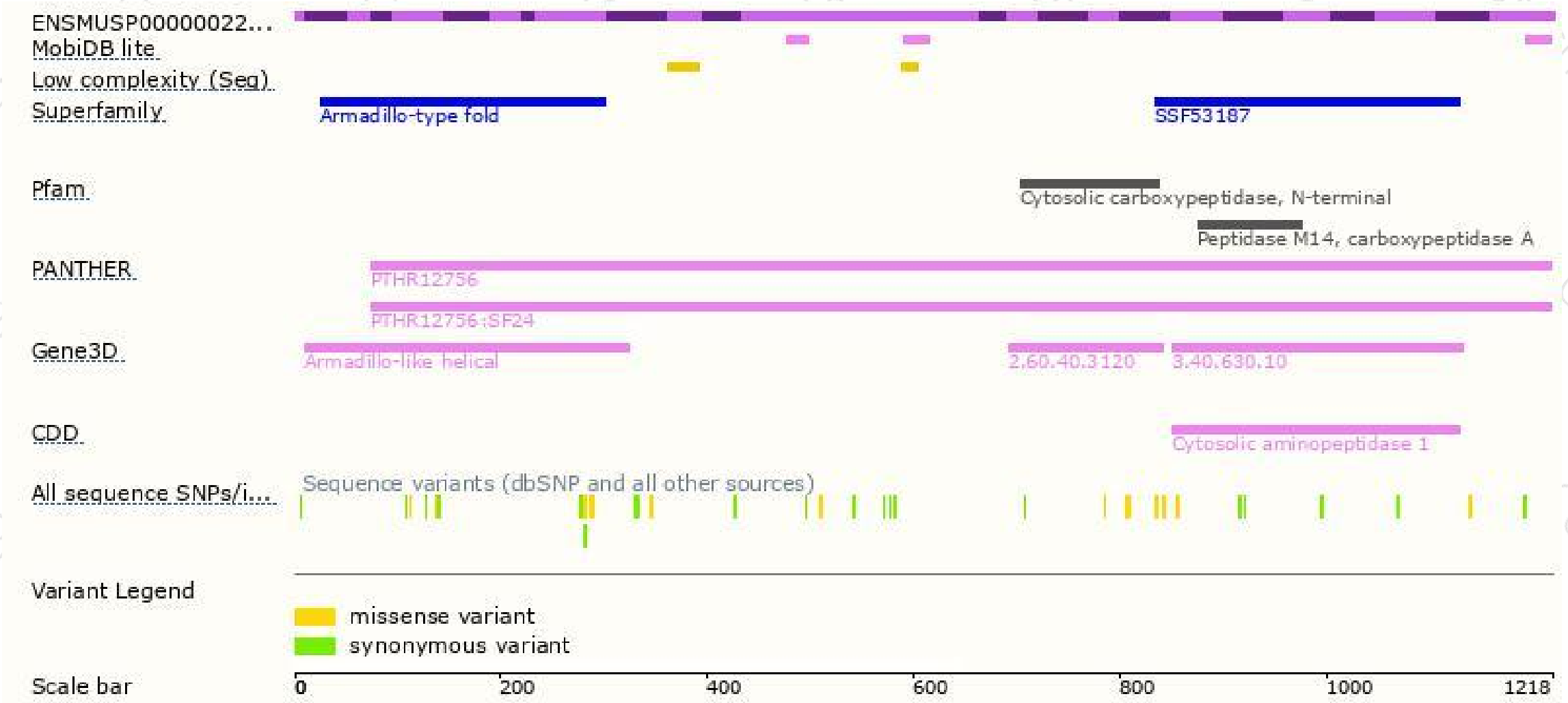
The strategy is based on the design of *Agtpbp1-201* transcript,The transcription is shown below



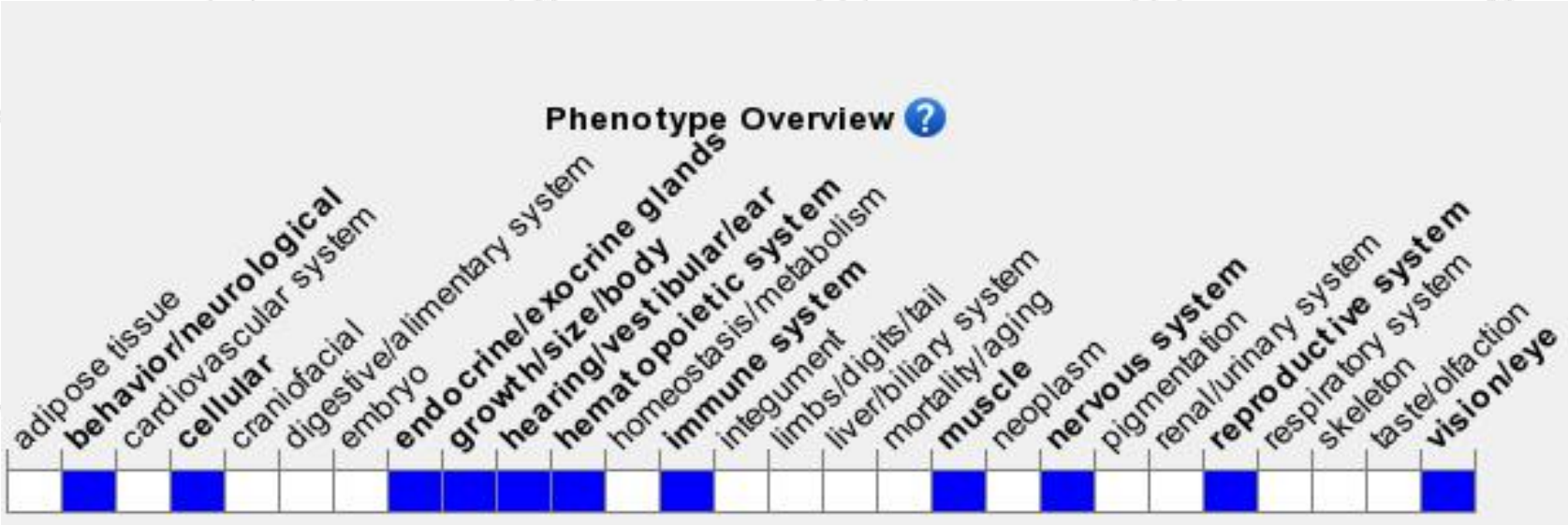
Genomic location distribution



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/).

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

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