

Cntn1 Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Cntn1

Project type

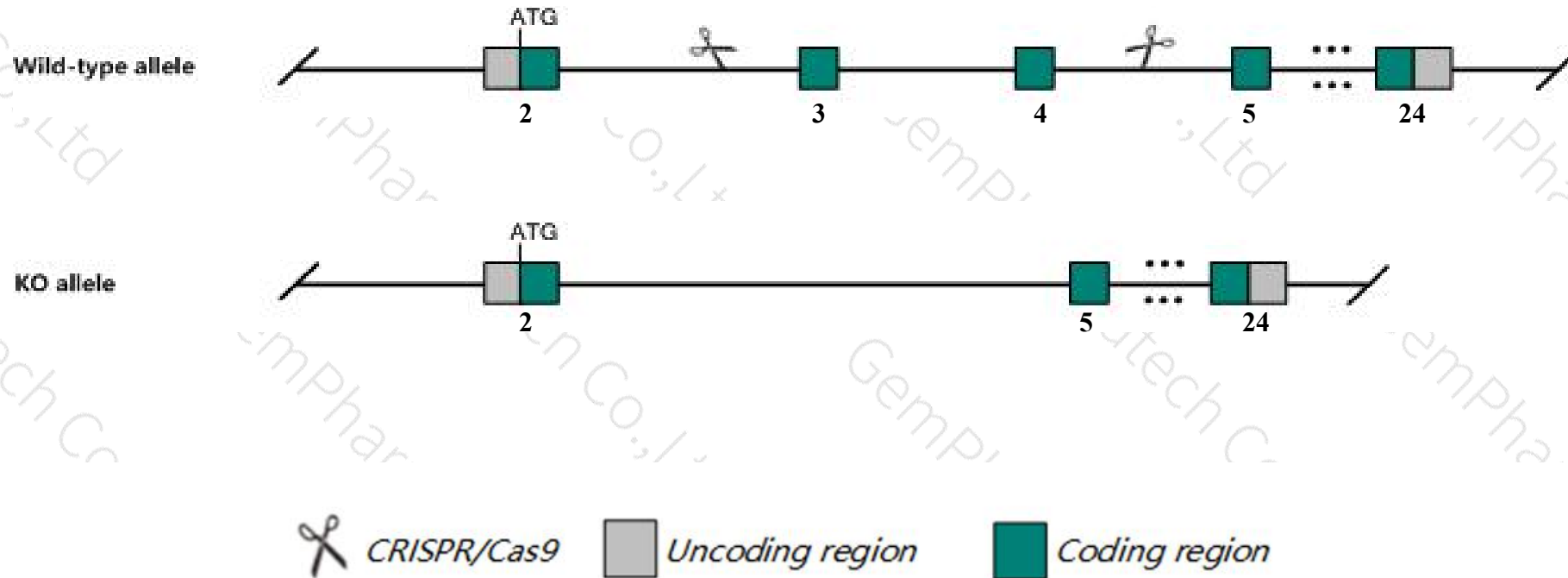
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cntn1* gene. The schematic diagram is as follows:



- The *Cntn1* gene has 4 transcripts. According to the structure of *Cntn1* gene, exon3-exon4 of *Cntn1-204* (ENSMUST00000169825.7) transcript is recommended as the knockout region. The region contains 166bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cntn1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mutations of this gene result in growth retardation, progressive ataxia and death prior to weaning. A targeted null mutation, but not a spontaneous mutation, causes a small cerebellum with abnormalities of the molecular layer and abnormal Purkinje cell axon morphology.
- The *Cntn1* gene is located on the Chr15. 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)

Cntn1 contactin 1 [Mus musculus (house mouse)]

Gene ID: 12805, updated on 7-Apr-2019

Summary



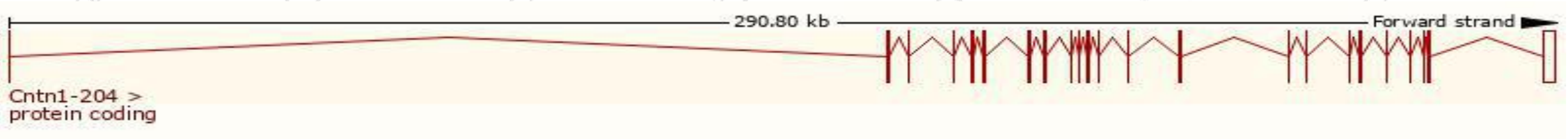
Official Symbol	Cntn1 provided by MGI
Official Full Name	contactin 1 provided by MGI
Primary source	MGI:MGI:105980
See related	Ensembl:ENSMUSG00000055022
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AW495098, CNTN, F3cam, usl
Expression	Biased expression in cerebellum adult (RPKM 20.9), cortex adult (RPKM 17.7) and 4 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

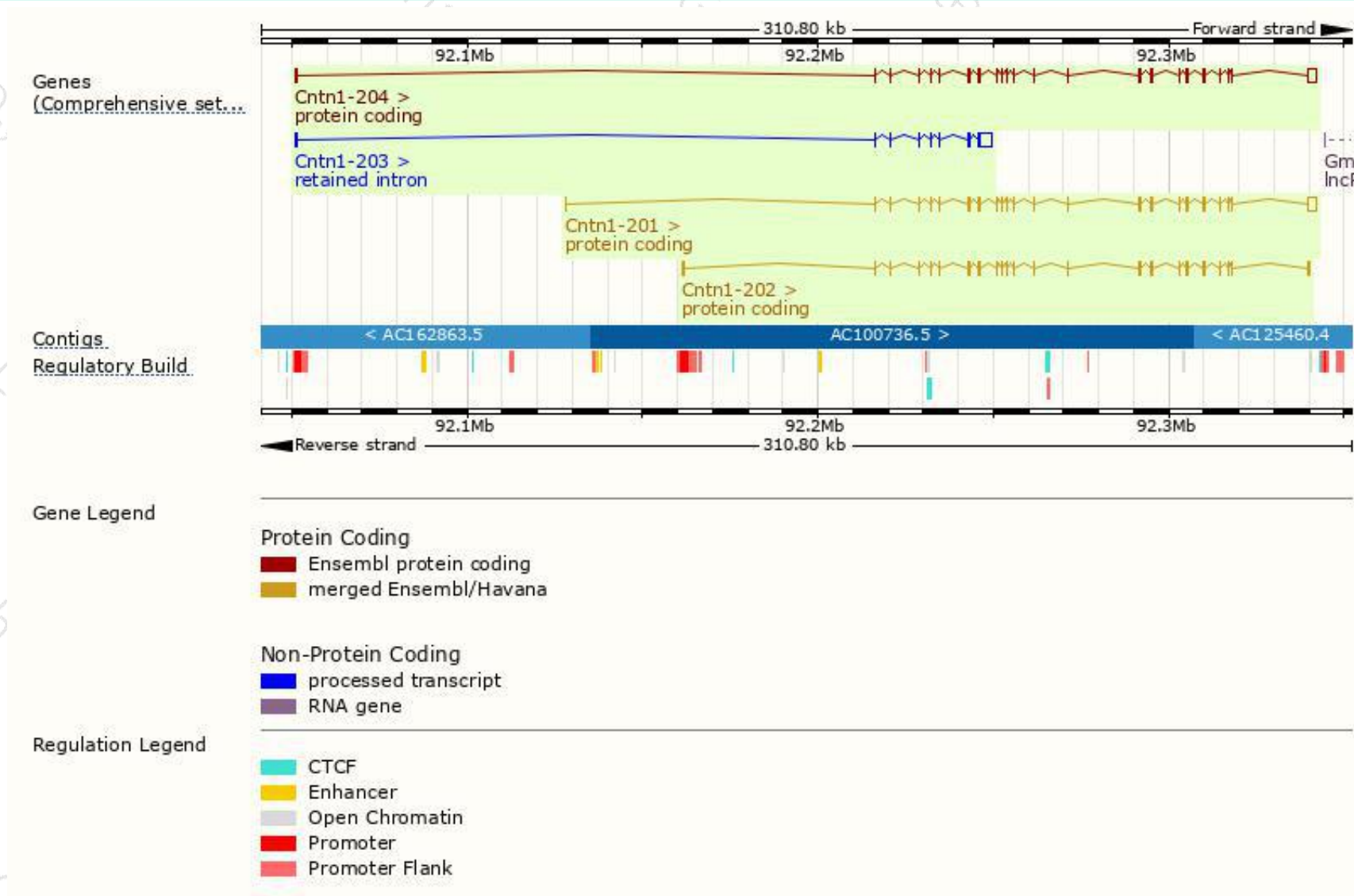
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cntn1-204	ENSMUST00000169825.7	5671	1020aa	Protein coding	CCDS27763	P12960	TSL:5 GENCODE basic APPRIS P1
Cntn1-201	ENSMUST00000000109.10	5646	1020aa	Protein coding	CCDS27763	P12960	TSL:1 GENCODE basic APPRIS P1
Cntn1-202	ENSMUST00000068378.5	3964	1020aa	Protein coding	CCDS27763	P12960	TSL:1 GENCODE basic APPRIS P1
Cntn1-203	ENSMUST00000141187.7	4524	No protein	Retained intron	-	-	TSL:1

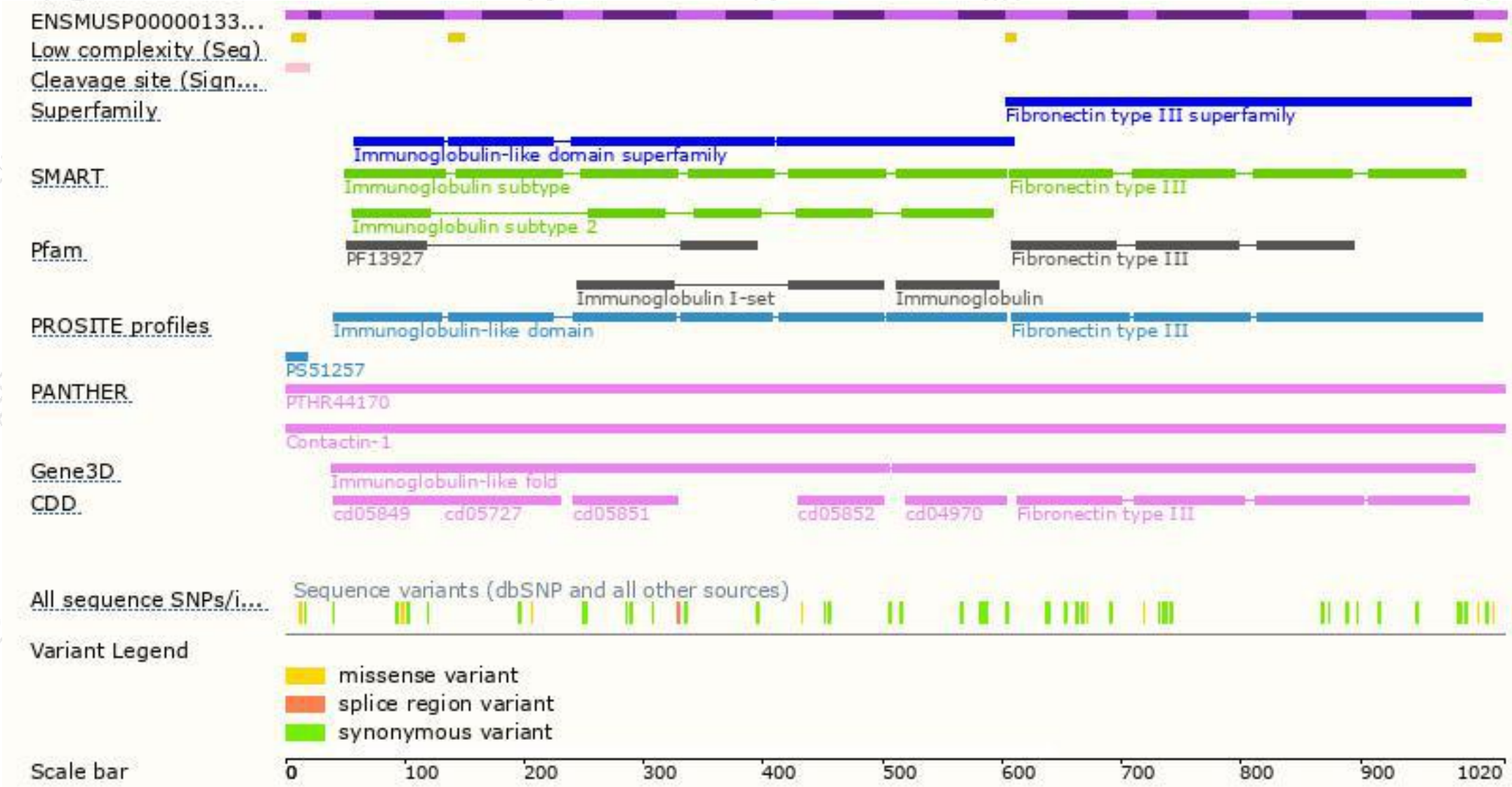
The strategy is based on the design of *Cntn1-204* transcript,The transcription is shown below



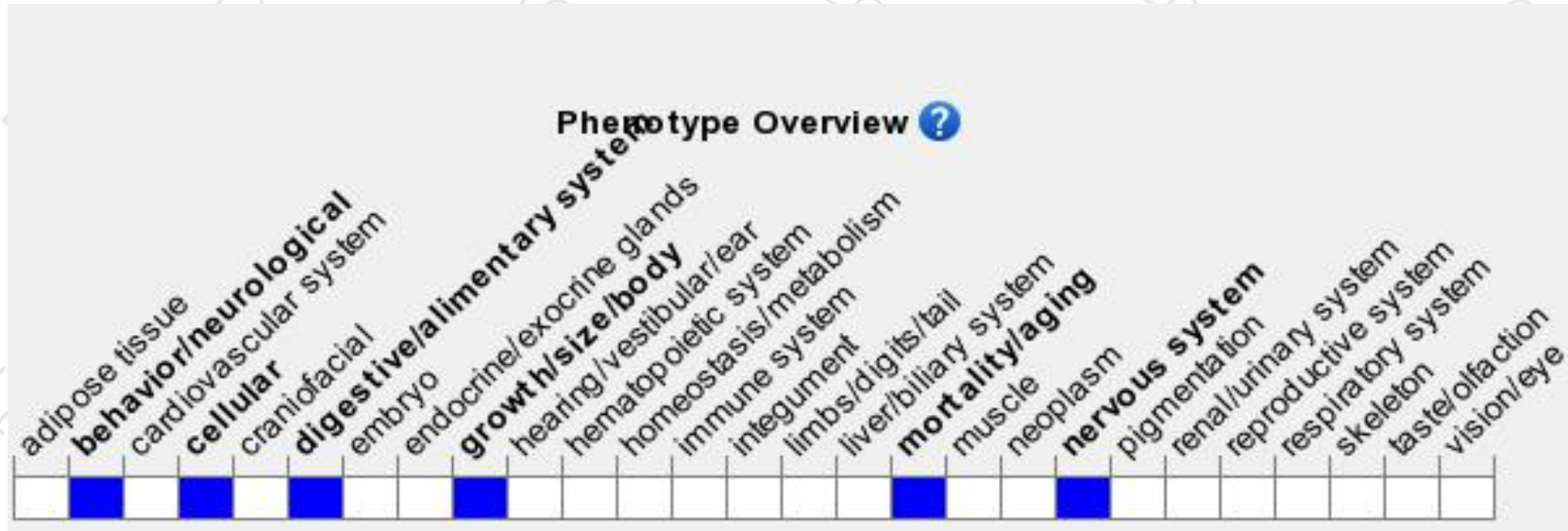
Genomic location distribution



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, Mutations of this gene result in growth retardation, progressive ataxia and death prior to weaning. A targeted null mutation, but not a spontaneous mutation, causes a small cerebellum with abnormalities of the molecular layer and abnormal Purkinje cell axon morphology.

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

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