

Nr2e1 Cas9-CKO Strategy

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Design Date: 2019-9-12
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Project Overview

Project Name

Nr2e1

Project type

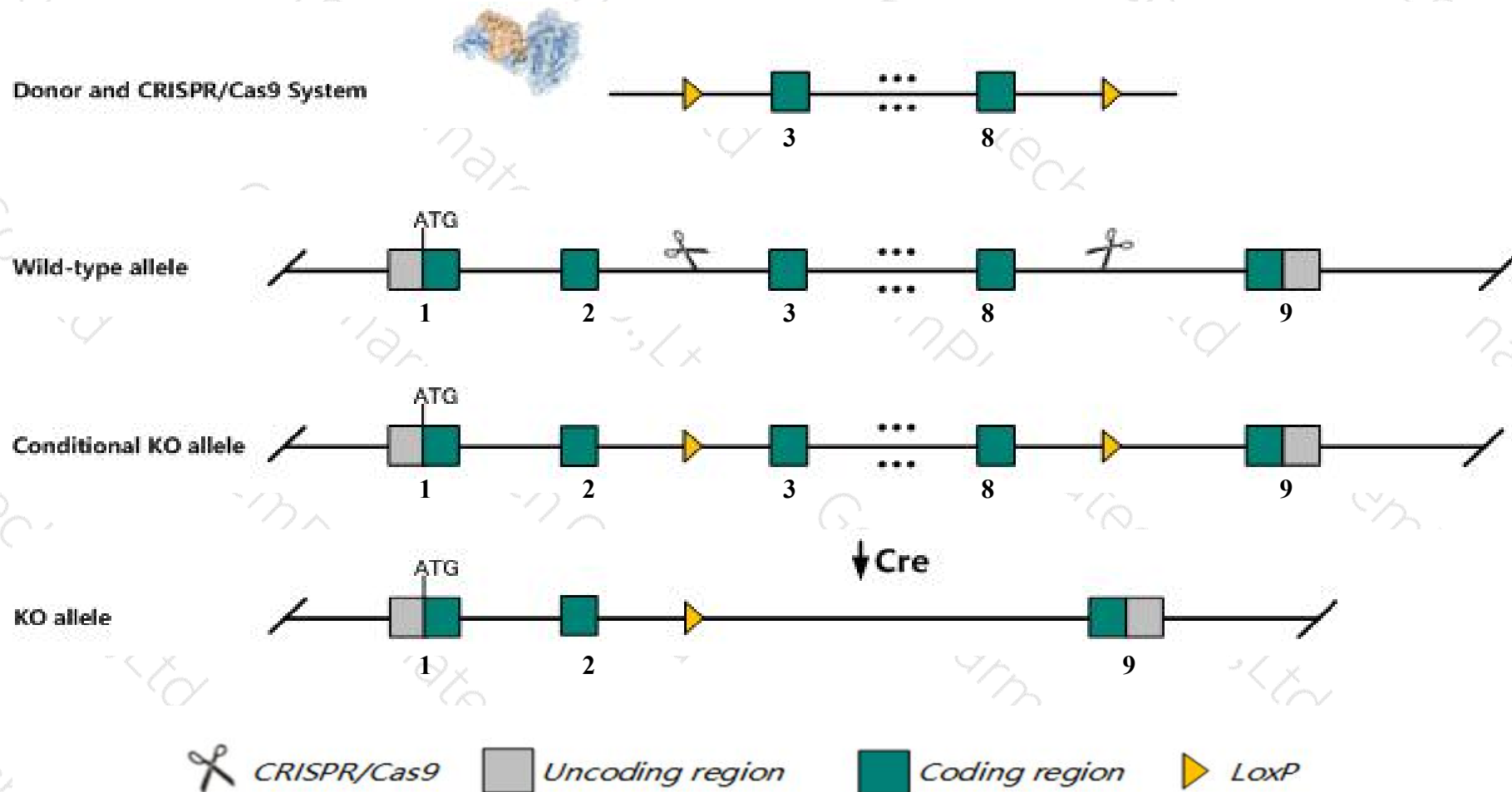
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Nr2e1* gene. The schematic diagram is as follows:



Technical routes

- The *Nr2e1* gene has 4 transcripts. According to the structure of *Nr2e1* gene, exon3-exon8 of *Nr2e1*-201 (ENSMUST00000019938.10) transcript is recommended as the knockout region. The region contains 824bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Nr2e1* 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.

- According to the existing MGI data, Homozygotes have small brains, hypoplasia of cerebrum and olfactory lobes, thin optic layers, reduced retinal vessels and hydrocephaly on some genetic backgrounds. Mutants do poorly in sensorimotor tests, are aggressive and females lack maternal behavior.
- The *Nr2e1* gene is located on the Chr10. 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)

Nr2e1 nuclear receptor subfamily 2, group E, member 1 [Mus musculus (house mouse)]

Gene ID: 21907, updated on 2-Apr-2019

Summary



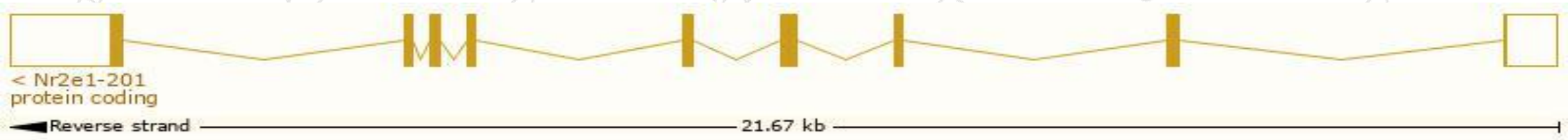
Official Symbol	Nr2e1 provided by MGI
Official Full Name	nuclear receptor subfamily 2, group E, member 1 provided by MGI
Primary source	MGI:MGI:1100526
See related	Ensembl:ENSMUSG00000019803
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Mtl1, MtlI, TLL, Tlx, XTLL, fierce, frc, tailless
Expression	Biased expression in CNS E11.5 (RPKM 10.9), CNS E14 (RPKM 9.7) and 4 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

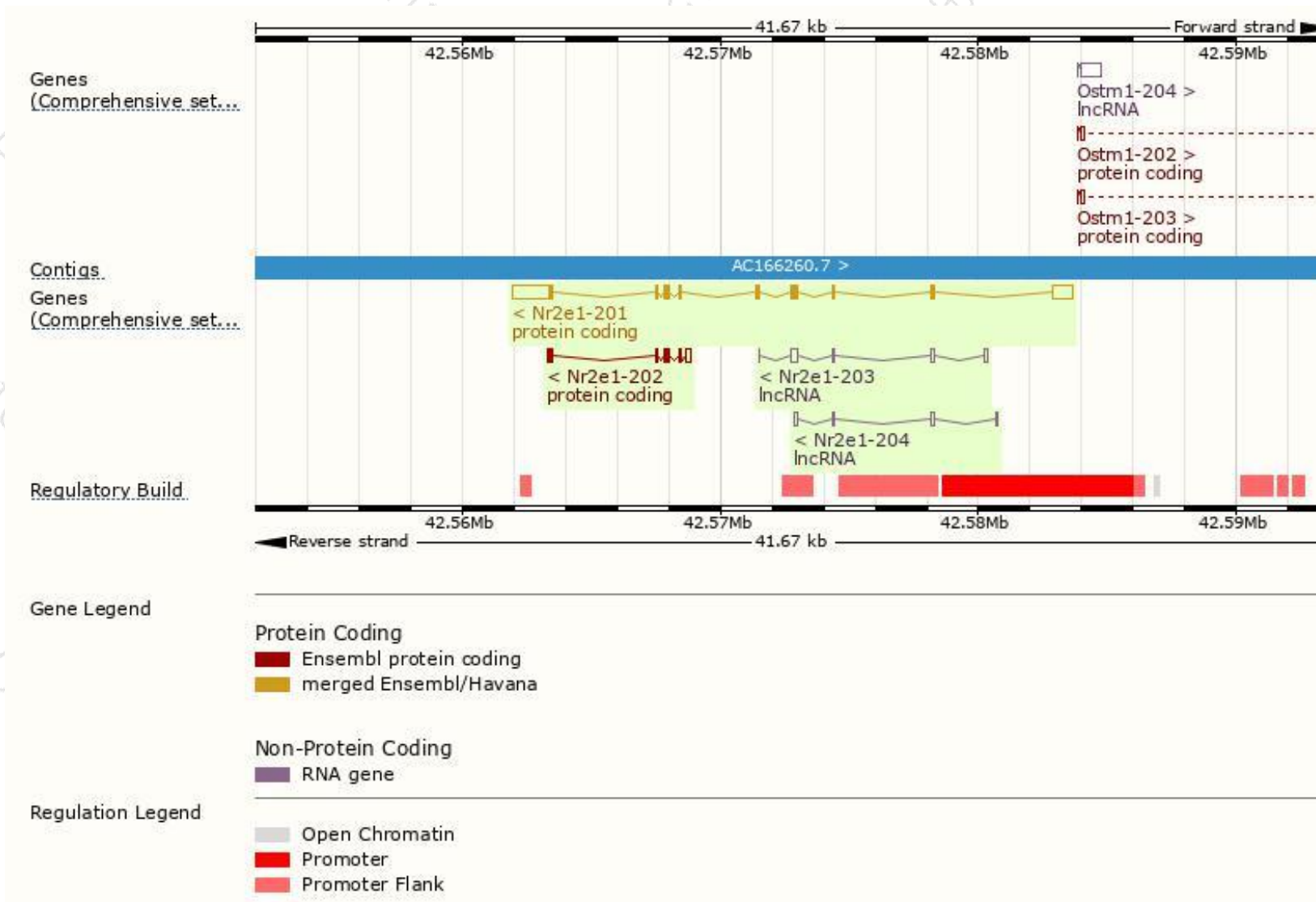
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nr2e1-201	ENSMUST00000019938.10	3285	385aa	Protein coding	CCDS23813	Q64104 Q78ZM1	TSL:1 GENCODE basic APPRIS P1
Nr2e1-202	ENSMUST00000105498.2	780	173aa	Protein coding	-	Q3UXE8	TSL:1 GENCODE basic
Nr2e1-203	ENSMUST00000126848.1	654	No protein	lncRNA	-	-	TSL:3
Nr2e1-204	ENSMUST00000143891.1	464	No protein	lncRNA	-	-	TSL:5

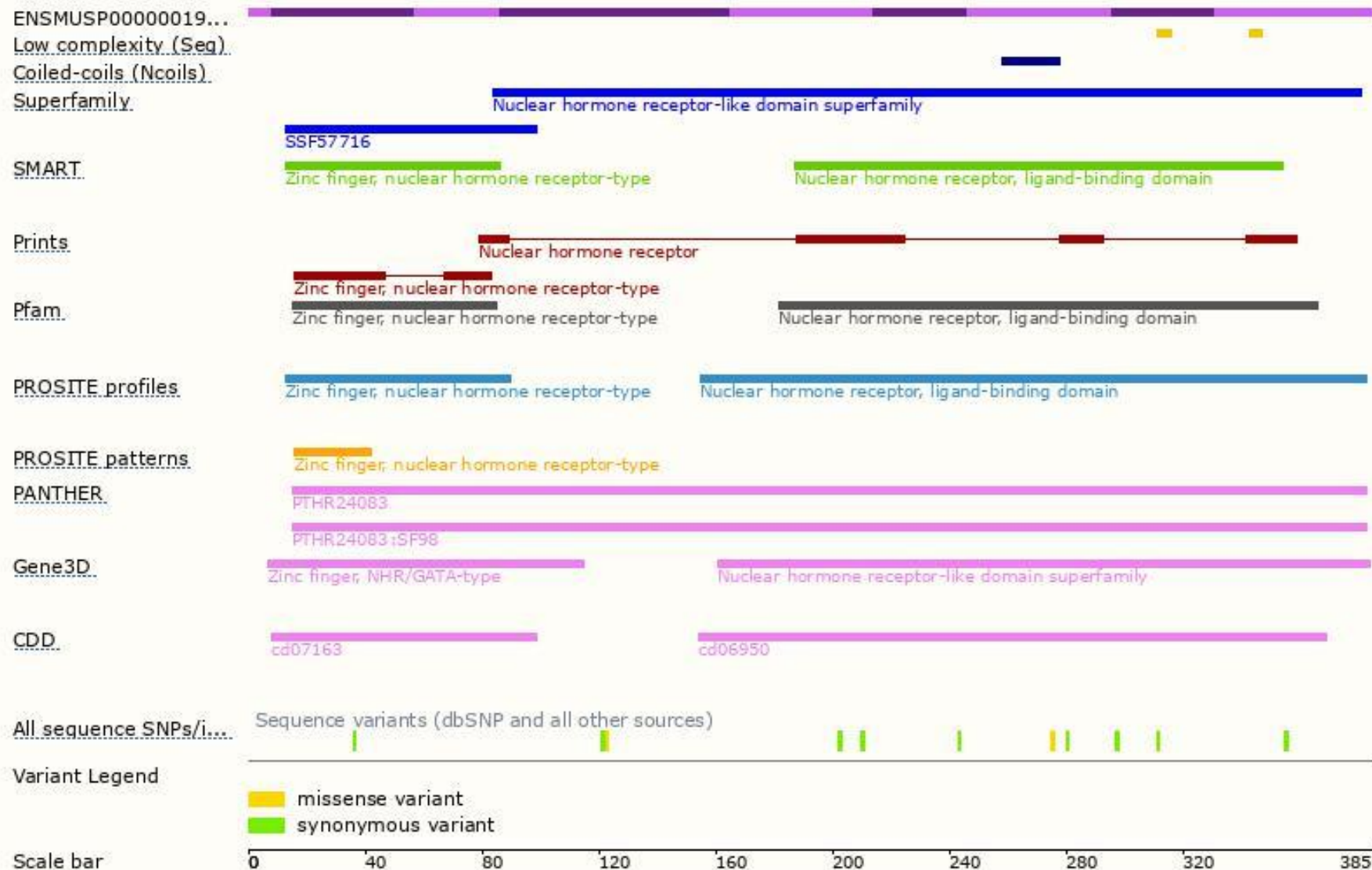
The strategy is based on the design of *Nr2e1-201* transcript,The transcription is shown below



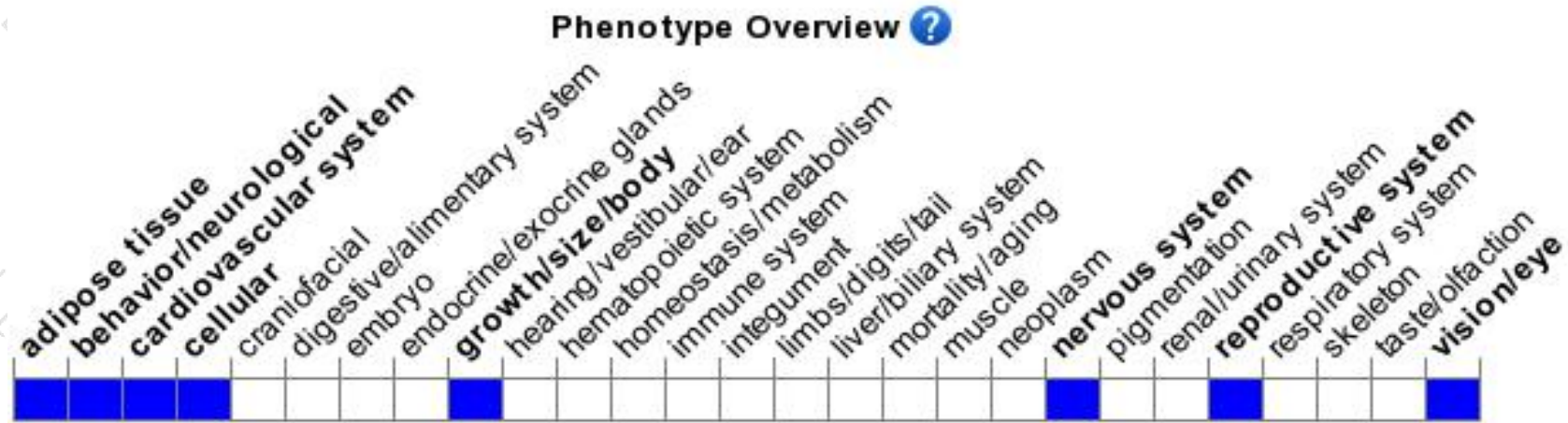
Genomic location distribution



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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