

Nt5c1a Cas9-CKO Strategy

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Design Date: 2020-5-20

Project Overview

Project Name

Nt5c1a

Project type

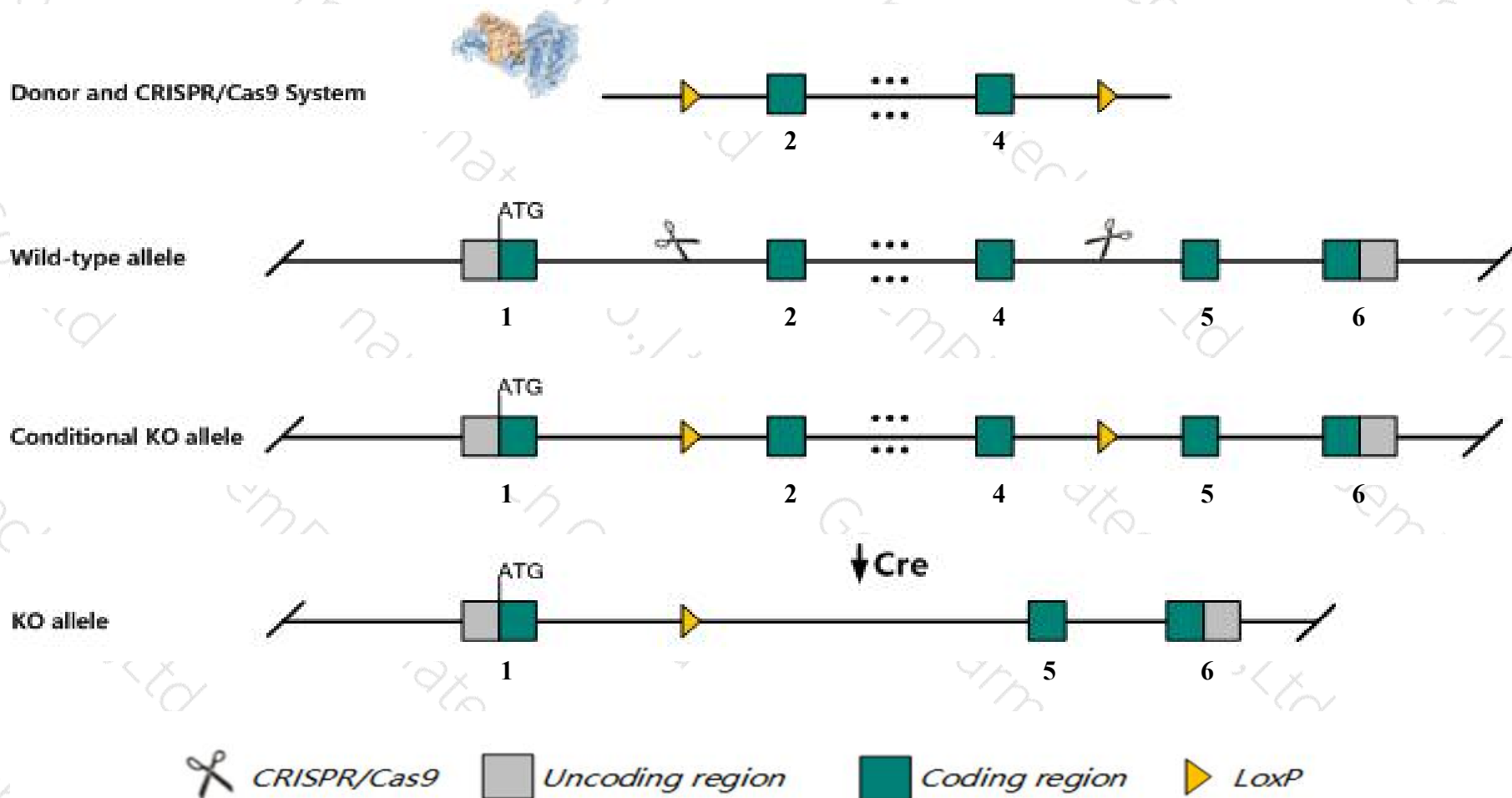
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Nt5c1a* gene. The schematic diagram is as follows:



- The *Nt5c1a* gene has 1 transcript. According to the structure of *Nt5c1a* gene, exon2-exon4 of *Nt5c1a-201* (ENSMUST00000068262.5) transcript is recommended as the knockout region. The region contains 421bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Nt5c1a* 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, mice homozygous for a null allele exhibit reduced adenosine levels in muscles post-electrical stimulation.
- The *Nt5c1a* gene is located on the Chr4. 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)

Nt5c1a 5'-nucleotidase, cytosolic 1A [Mus musculus (house mouse)]

Gene ID: 230718, updated on 13-Mar-2020

Summary



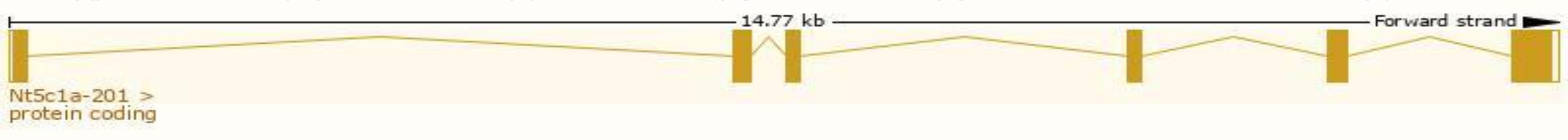
Official Symbol	Nt5c1a provided by MGI
Official Full Name	5'-nucleotidase, cytosolic 1A provided by MGI
Primary source	MGI:MGI:2155700
See related	Ensembl:ENSMUSG00000054958
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Cn1a, Gm49
Expression	Biased expression in heart adult (RPKM 8.9), adrenal adult (RPKM 7.9) and 5 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

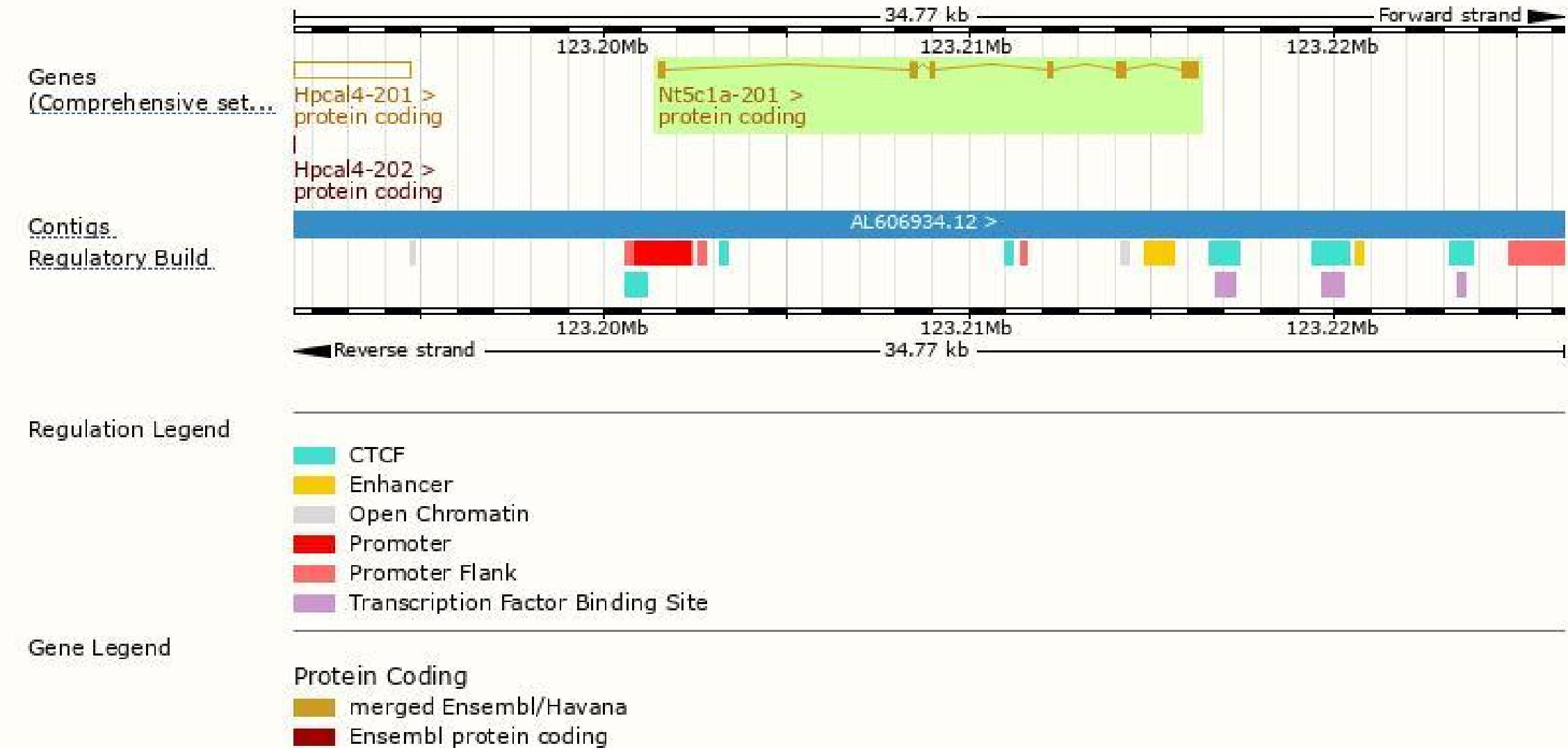
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nt5c1a-201	ENSMUST00000068262.5	1220	365aa	Protein coding	CCDS3887.1	A3KFX0	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1

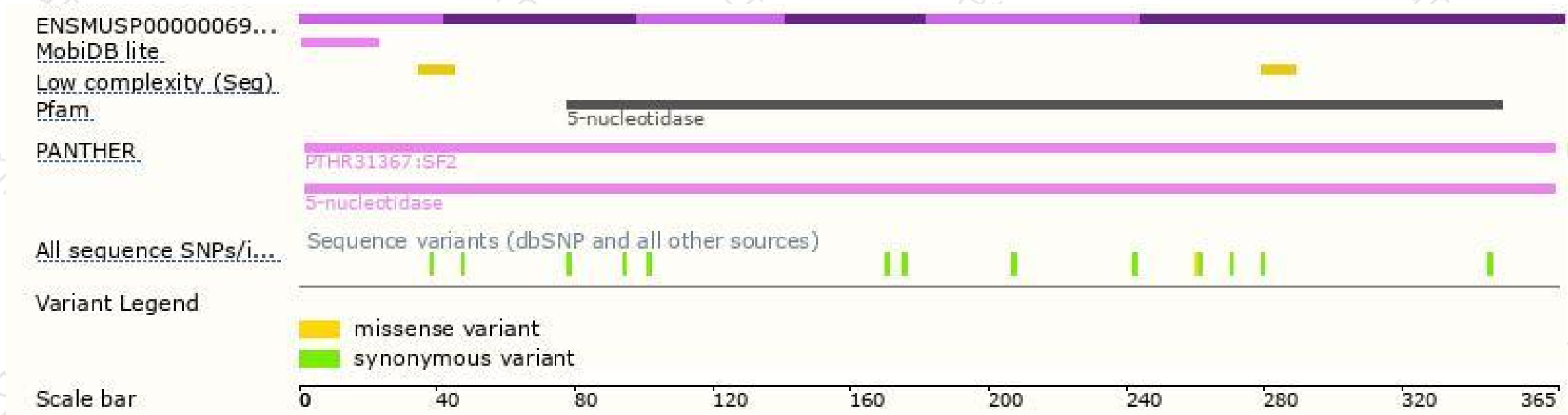
The strategy is based on the design of *Nt5c1a-201* transcript, The transcription is shown below



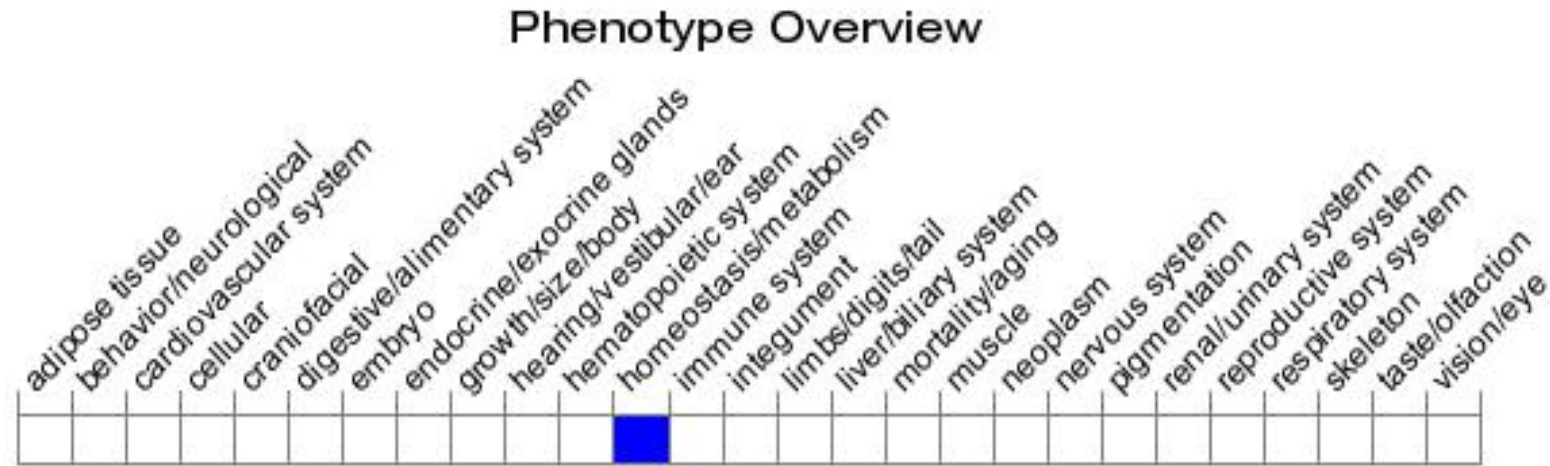
Genomic location distribution



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, Mice homozygous for a null allele exhibit reduced adenosine levels in muscles post-electrical stimulation.

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

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