Foxi1 Cas9-KO Strategy

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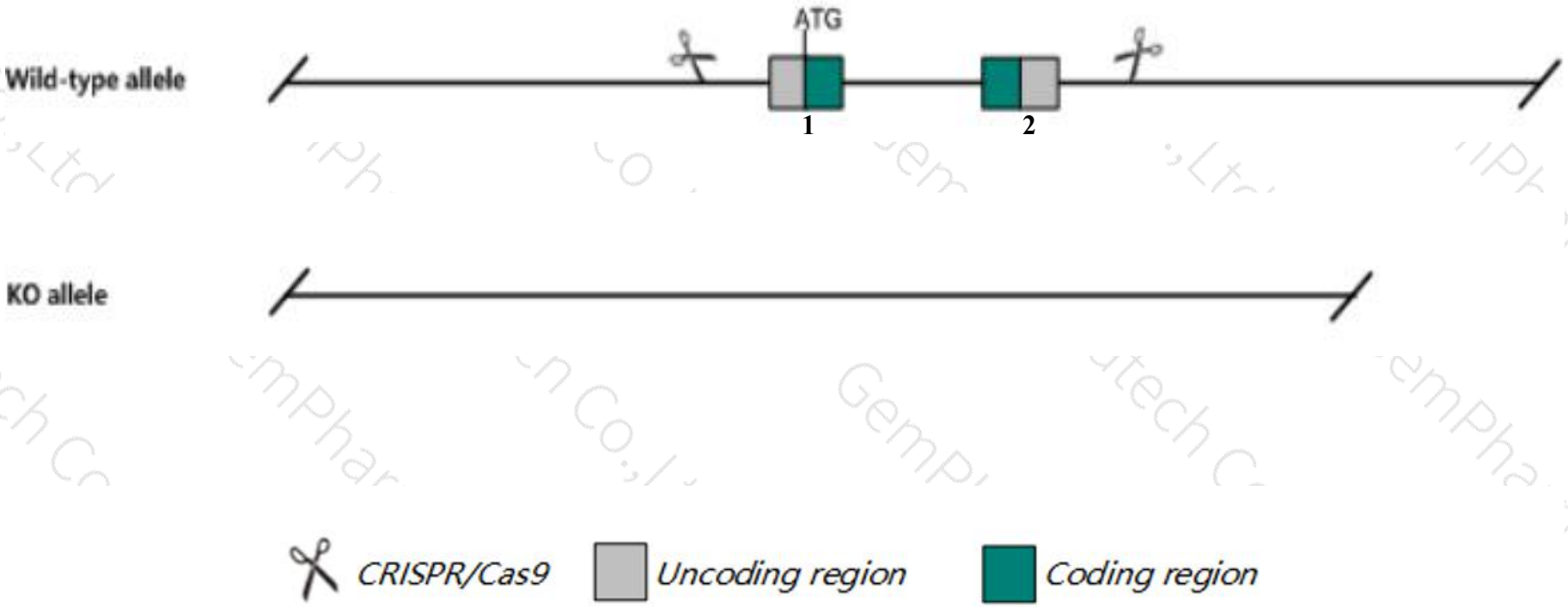
Design Date: 2020-7-24

Project Overview

Project Name	***Foxi1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Foxi1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Foxi1* gene has 1 transcript. According to the structure of *Foxi1* gene, exon1-exon2 of *Foxi1-201*(ENSMUST00000060271.2) transcript is recommended as the knockout region.The region contains all 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 *Foxi1* gene. The brief process is as follows: gRNA was transcribed in vitro.Cas9 and gRNA 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.

Notice

➢ According to the existing MGI data,homozygotes exhibit 50% perinatal lethality and inner ear defects resulting in vestibular and cochlear dysfunction. They are deaf with signs of impaired balance, and develop renal tubular acidosis in response to a chronic acidic load. Notably, 25% of heterozygotes die at birth.

➢ The *Foxi1* gene is located on the Chr11. 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）

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Foxi1 forkhead box I1 [Mus musculus (house mouse)]

Gene ID: 14233, updated on 13-Mar-2020

Summary

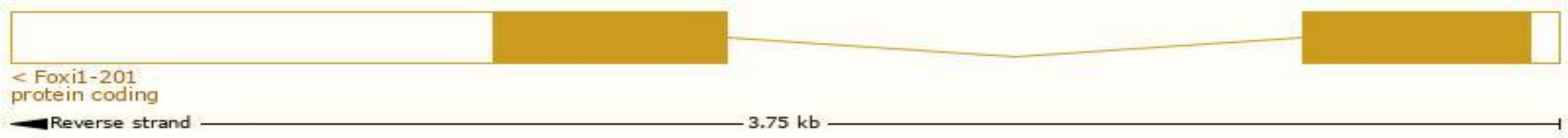
Official Symbol	Foxi1 provided by MGI
Official Full Name	forkhead box I1 provided byMGI
Primary source	MGI:MGI:1096329
See related	Ensembl:ENSMUSG00000047861
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	5830401E05Rik, FREAC6, Fkh10, HFH-3, Hfh3
Expression	Biased expression in kidney adult (RPKM 13.7), genital fat pad adult (RPKM 9.8) and 1 other tissueSee more
Orthologs	human all

Transcript information（Ensembl）

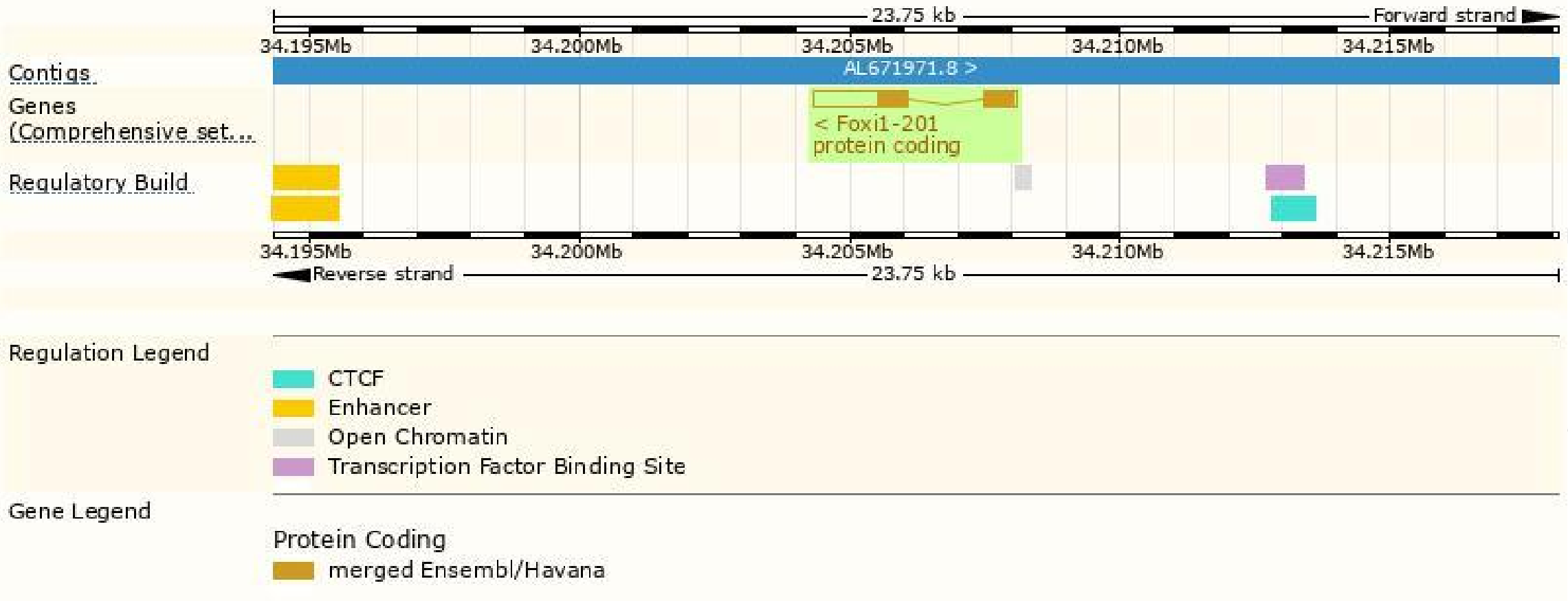
The gene has 1 transcript,and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Foxi1-201	ENSMUST00000060271.2	2357	372aa	Protein coding	CCDS24539	Q922I5	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

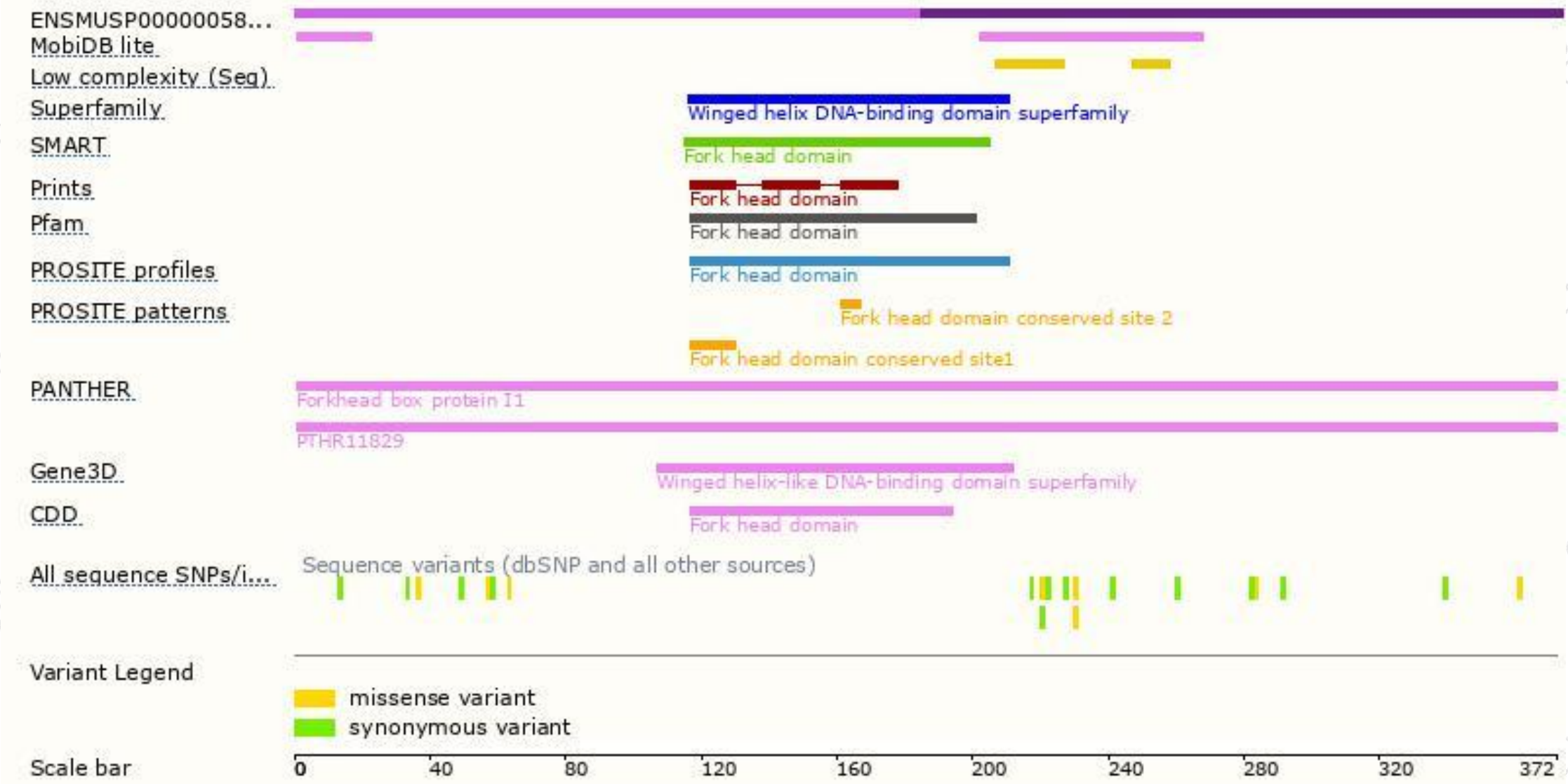
The strategy is based on the design of *Foxi1-201* transcript,the transcription is shown below:



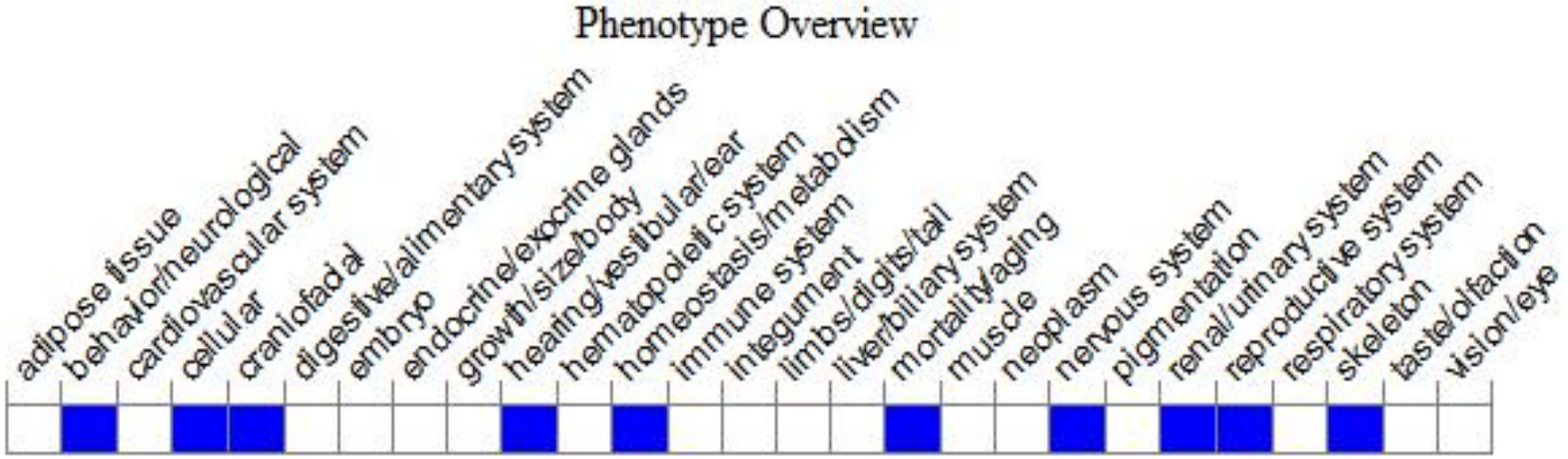
Genomic location distribution



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,homozygotes exhibit 50% perinatal lethality and inner ear defects resulting in vestibular and cochlear dysfunction. They are deaf with signs of impaired balance, and develop renal tubular acidosis in response to a chronic acidic load. Notably, 25% of heterozygotes die at birth.

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

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