Clcn7 Cas9-KO Strategy

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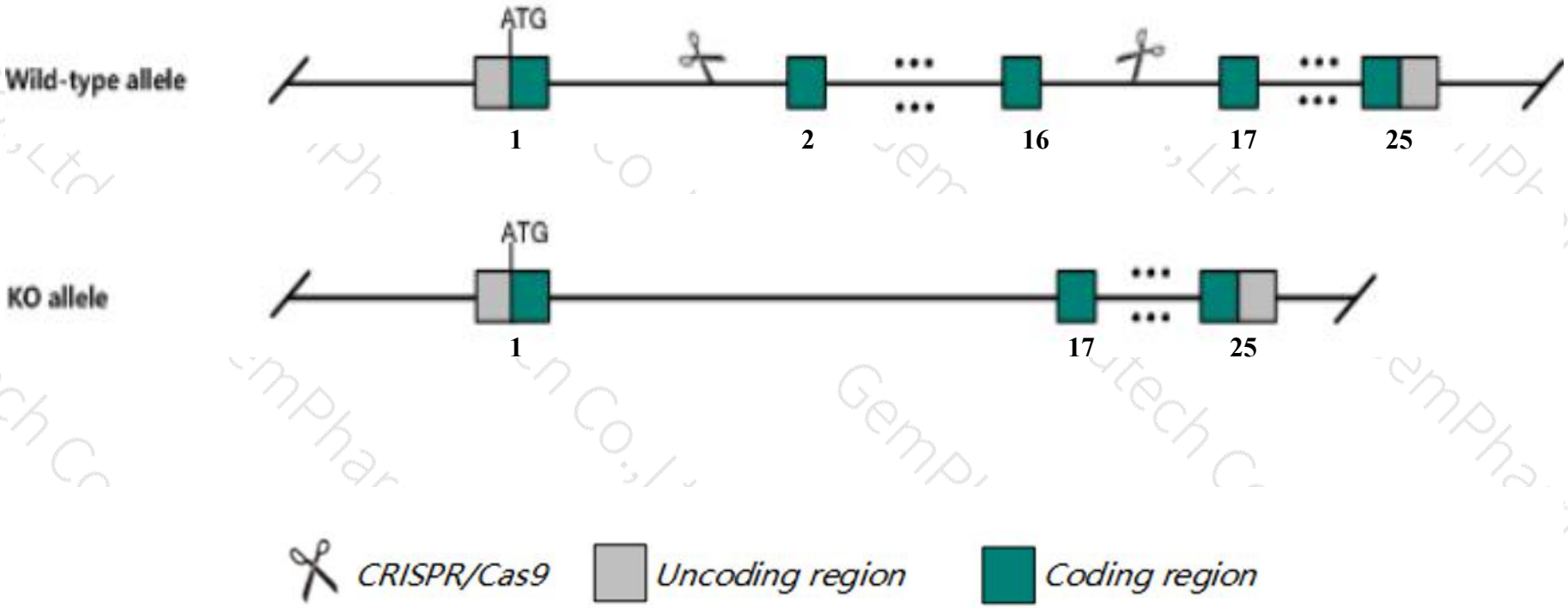
Design Date: 2020-5-7

Project Overview

Project Name	***Clcn7***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Clcn7* gene. The schematic diagram is as follows:



Technical routes

➢ The *Clcn7* gene has 7 transcripts. According to the structure of *Clcn7* gene, exon2-exon16 of *Clcn7-201* (ENSMUST00000040729.8) transcript is recommended as the knockout region.The region contains 1303bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Clcn7* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,mice homozygous for a knock-out allele exhibit postnatal lethality, abnormal bone formation, including osteopetrosis, and retinal degeneration. Mice homozygous for a conditional allele exhibit lysosomal defects with neuronal degeneration and accumulationof giant lysosomes in renal tubule cells.
- Transcript 202 may not be affected. The effect of transcript 203 is unknown.
- The *Clcn7* gene is located on the Chr17. 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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Clcn7 chloride channel, voltage-sensitive 7 [Mus musculus (house mouse)]

Gene ID: 26373, updated on 13-Mar-2020

Summary

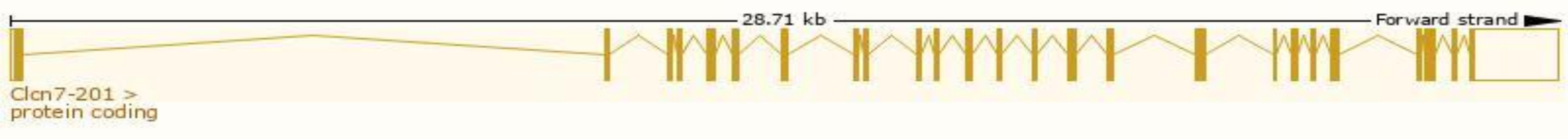
Official Symbol	Clcn7 provided by MGI
Official Full Name	chloride channel, voltage-sensitive 7 provided by MGI
Primary source	MGI:MGI:1347048
See related	Ensembl:ENSMUSG00000036636
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	ClC-7, D17Wsu51e
Expression	Ubiquitous expression in genital fat pad adult (RPKM 32.4), kidney adult (RPKM 17.7) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

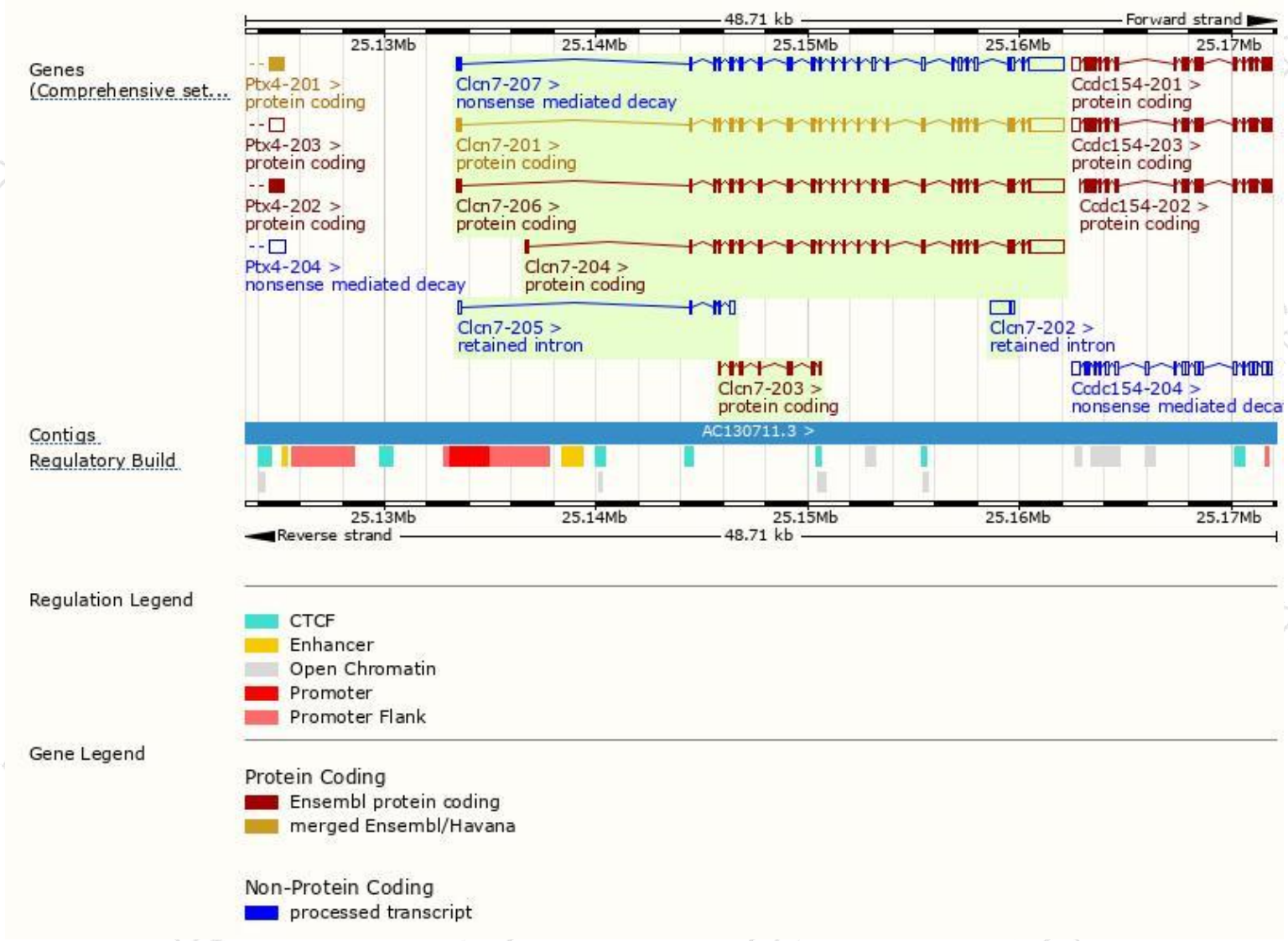
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Clcn7-201	ENSMUST00000040729.8	4071	803aa	Protein coding	CCDS28509	O70496 Q6RUT9	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 P3
Clcn7-204	ENSMUST00000160961.7	3983	783aa	Protein coding	CCDS84282	E9PYL4	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 ALT2
Clcn7-206	ENSMUST00000162862.2	4237	860aa	Protein coding	-	F6SUM2	TSL:5 GENCODE basic
Clcn7-203	ENSMUST00000159773.1	605	202aa	Protein coding	-	F7BK14	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Clcn7-207	ENSMUST00000233633.1	4067	391aa	Nonsense mediated decay	-	A0A3B2W4I8	
Clcn7-202	ENSMUST00000159426.1	1006	No protein	Retained intron	-	-	TSL:5
Clcn7-205	ENSMUST00000162722.1	584	No protein	Retained intron	-	-	TSL:2

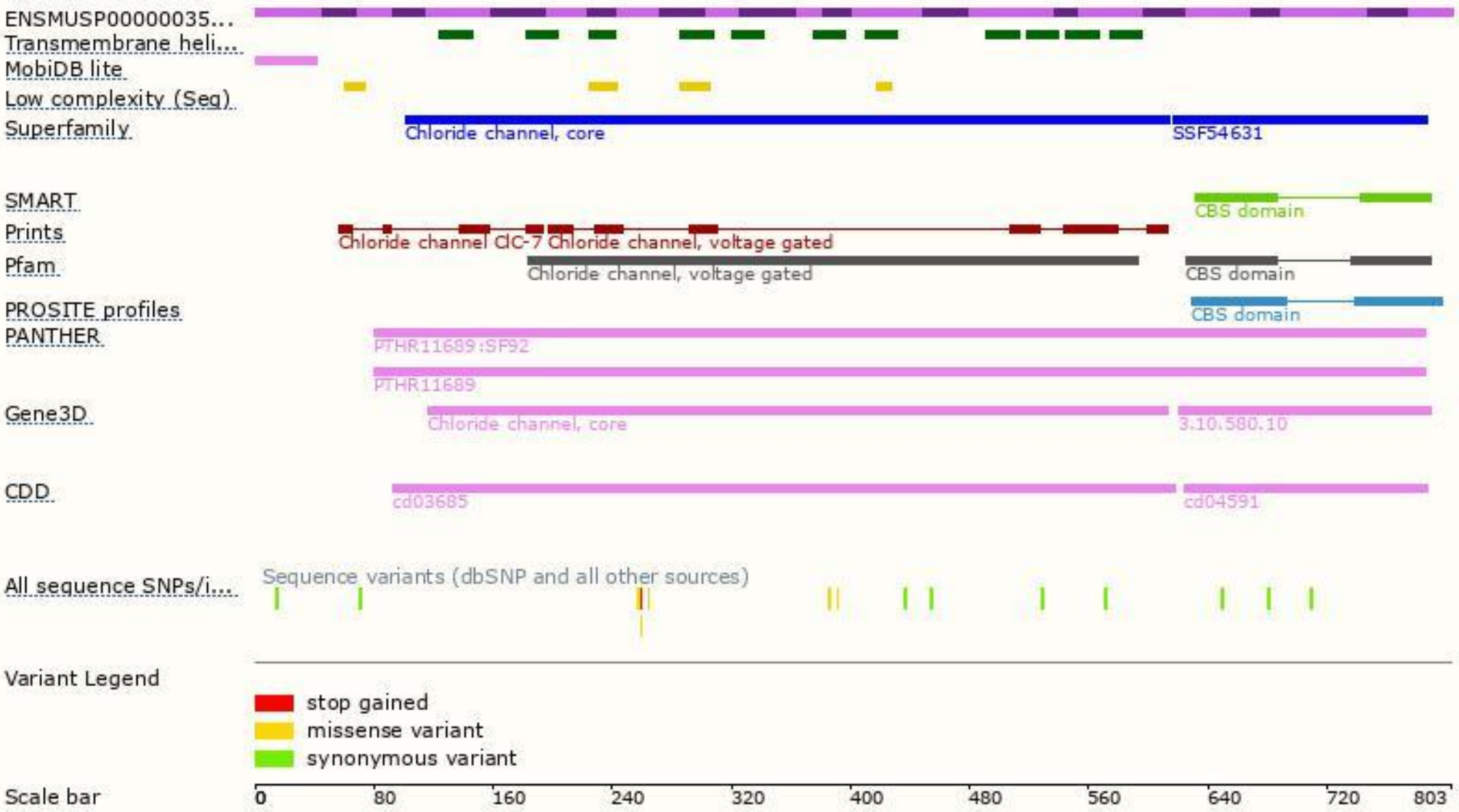
The strategy is based on the design of *Clcn7-201* transcript,the transcription is shown below:



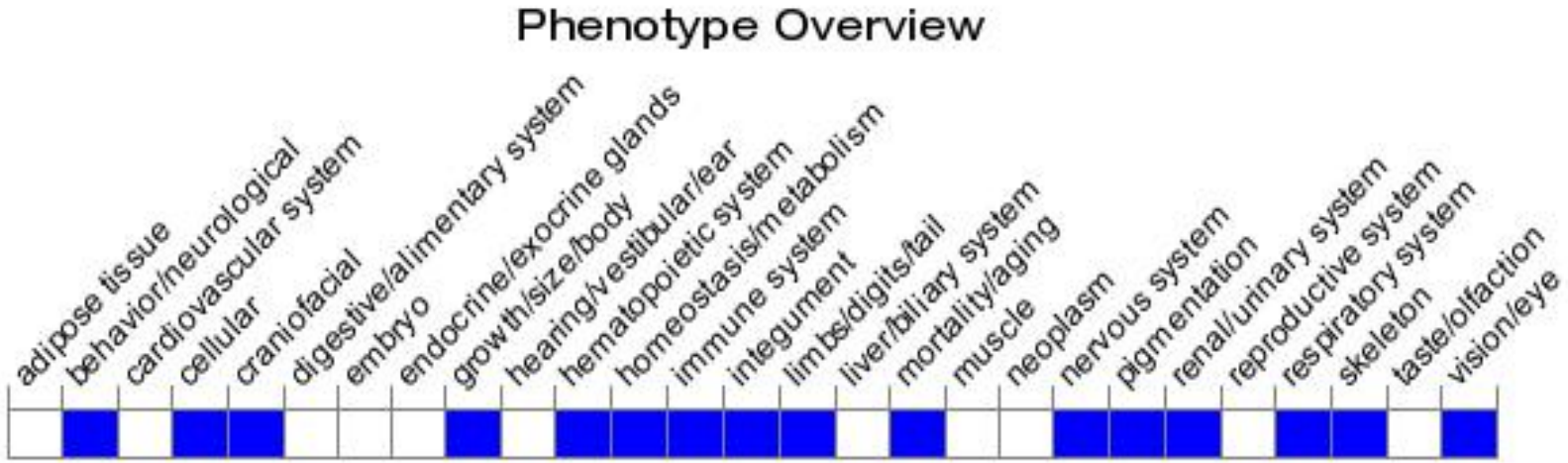
Genomic location distribution



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 knock-out allele exhibit postnatal lethality, abnormal bone formation, including osteopetrosis, and retinal degeneration. Mice homozygous for a conditional allele exhibit lysosomal defects with neuronal degeneration and accumulationof giant lysosomes in renal tubule cells.

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

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