Slc26a5 Cas9-KO Strategy

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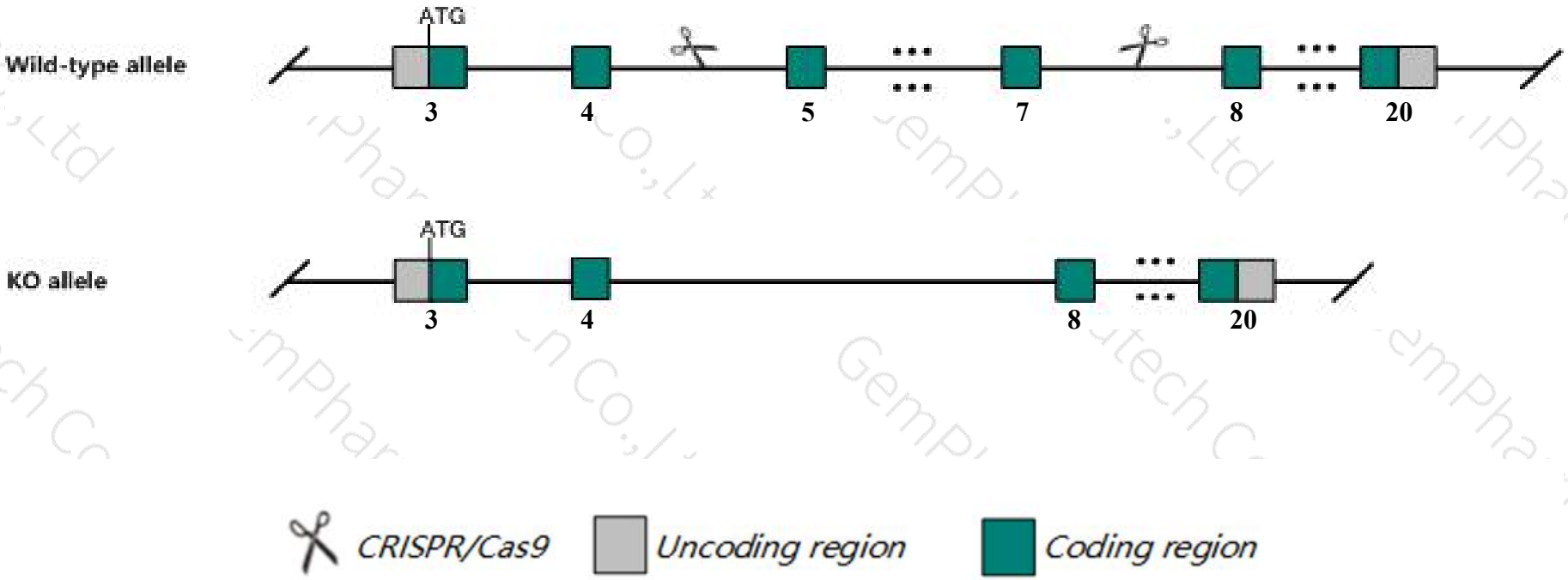
Project Overview

Project Name	***Slc26a5***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc26a5* gene. The schematic diagram is as follows:



Technical routes

➢ The *Slc26a5* gene has 5 transcripts. According to the structure of *Slc26a5* gene, exon5-exon7 of *Slc26a5-201* (ENSMUST00000030878.7) transcript is recommended as the knockout region.The region contains 443bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Slc26a5* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

➢ According to the existing MGI data,Cochlear sensitivity is decreased in mutant due to a loss of outer hair cell electromotility.

➢ The *Slc26a5* gene is located on the Chr5. 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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Slc26a5 solute carrier family 26, member 5 [Mus musculus (house mouse)]

Gene ID: 80979, updated on 31-Jan-2019

Summary

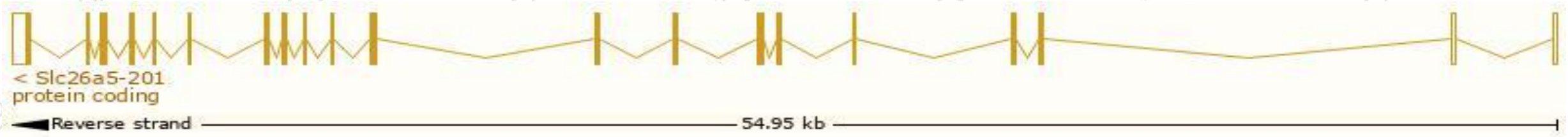
Official Symbol	Slc26a5 provided by MGI
Official Full Name	solute carrier family 26, member 5 provided by MGI
Primary source	MGI:MGI:1933154
See related	Ensembl:ENSMUSG00000029015
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Pres, prestin
Expression	Low expression observed in reference dataset See more
Orthologs	human all

Transcript information（Ensembl）

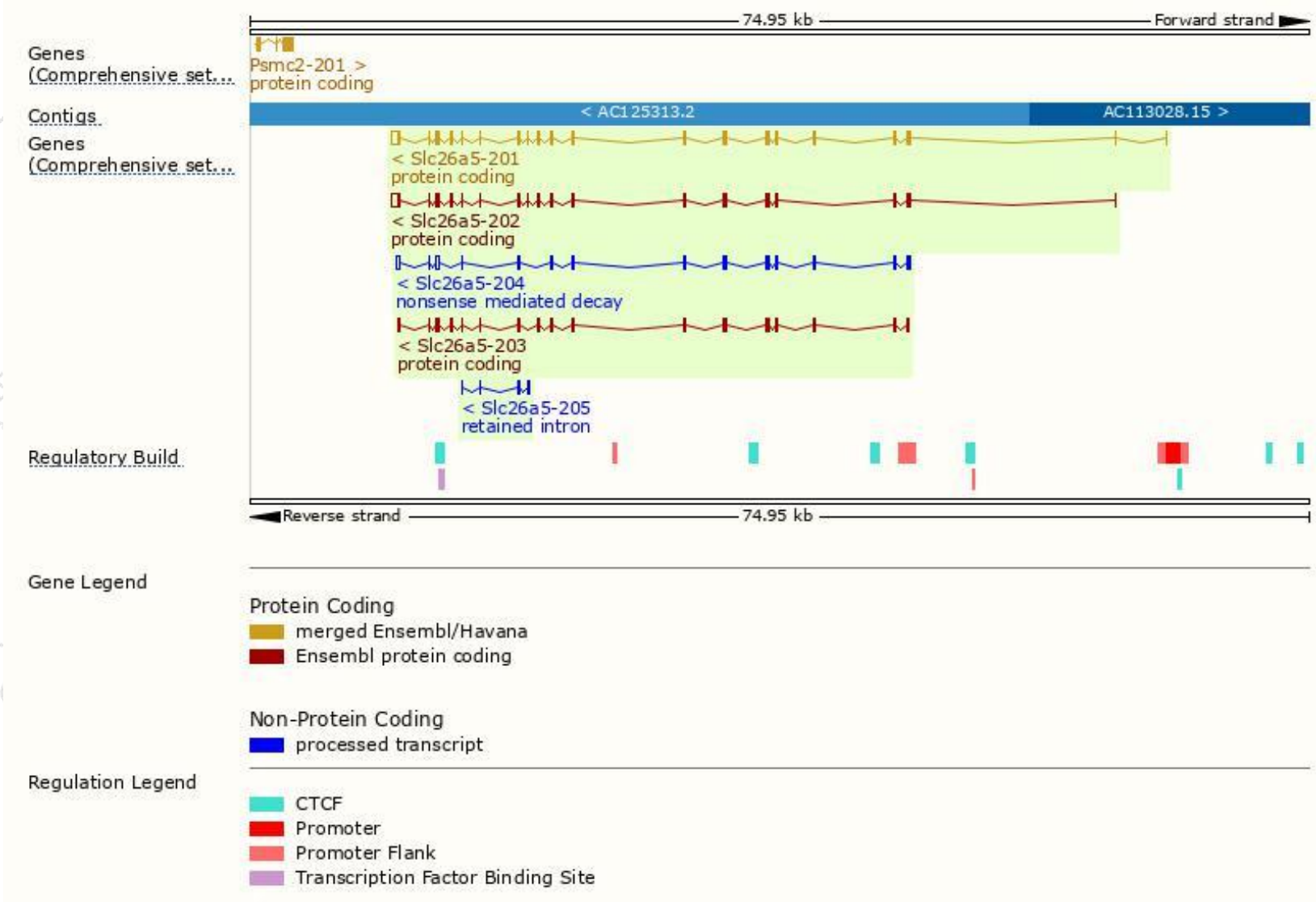
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc26a5-201	ENSMUST00000030878.7	2962	744aa	Protein coding	CCDS19109	Q99NH7	TSL:1 GENCODE basic APPRIS P1
Slc26a5-202	ENSMUST00000115176.7	2768	707aa	Protein coding	CCDS71547	Q32MT6	TSL:1 GENCODE basic
Slc26a5-203	ENSMUST00000127975.1	2141	712aa	Protein coding	-	D3Z013	CDS 3' incomplete TSL:5
Slc26a5-204	ENSMUST00000142888.7	2064	447aa	Nonsense mediated decay	-	D6RIK0	TSL:5
Slc26a5-205	ENSMUST00000150012.1	393	No protein	Retained intron	-	-	TSL:5

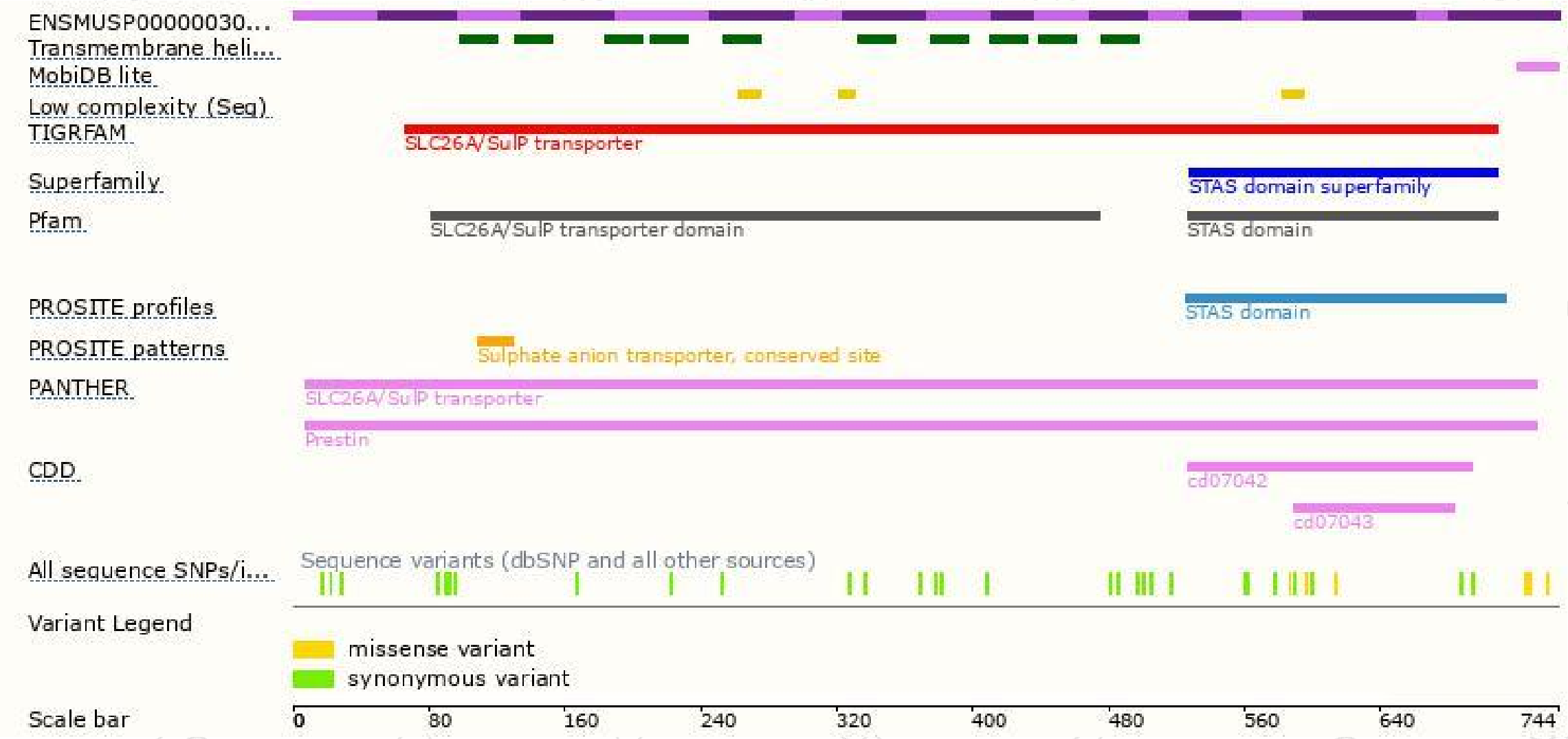
The strategy is based on the design of *Slc26a5-201* transcript,The transcription is shown below



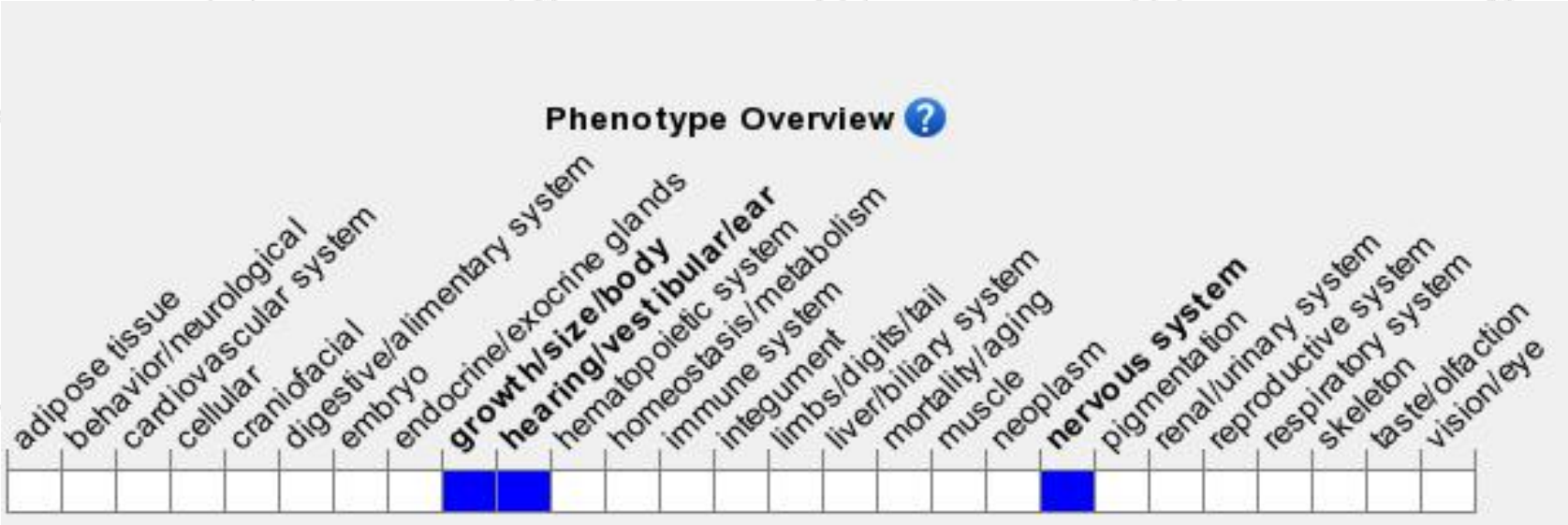
Genomic location distribution



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,Cochlear sensitivity is decreased in mutant due to a loss of outer hair cell electromotility.

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

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