Inhba Cas9-KO Strategy

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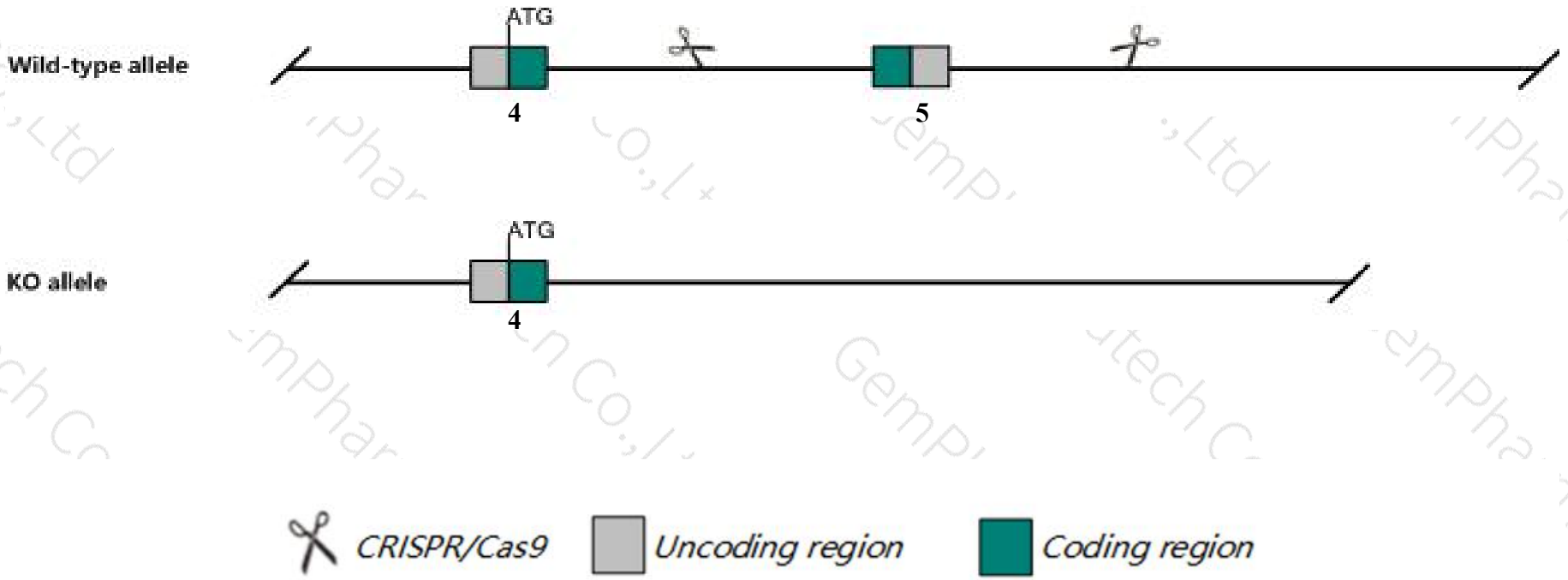
Project Overview

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

Knockout strategy

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



Technical routes

➢ The *Inhba* gene has 2 transcripts. According to the structure of *Inhba* gene, exon5 of *Inhba-201* (ENSMUST00000042603.13) transcript is recommended as the knockout region.The region contains 887bp coding sequence. Knock out the region will result in disruption of protein function.

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

Notice

➢ According to the existing MGI data,Homozygotes for a targeted null mutation lack vibrissae and lower incisors, have defects in their secondary palates, and die shortly after birth.

➢ The KO region contains functional region of the *B230303A05Rik and Gm48444* gene.Knockout the region may affect the function of *B230303A05Rik and Gm48444* gene.

➢ The *Inhba* gene is located on the Chr13. 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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Inhba inhibin beta-A [Mus musculus (house mouse)]

Gene ID: 16323, updated on 31-Jan-2019

Summary

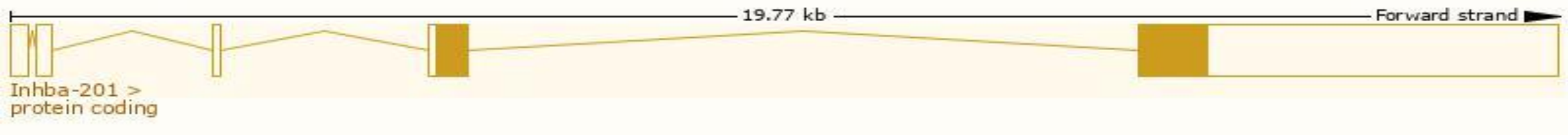
Official Symbol	Inhba provided by MGI
Official Full Name	inhibin beta-A provided byMGI
Primary source	MGI:MGI:96570
See related	Ensembl:ENSMUSG00000041324
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Summary	This gene encodes a member of the TGF-beta (transforming growth factor-beta) superfamily of proteins. The encoded preproprotein is proteolytically processed to generate a subunit of the dimeric activin and inhibin protein complexes. These complexes activate and inhibit, respectively, follicle stimulating hormone secretion from the pituitary gland. The encoded protein also plays a role in eye, tooth and testis development. Homozygous knockout mice for this gene lack whiskers and exhibit tooth and palate defects, leading to neonatal lethality. [provided by RefSeq, Aug 2016]
Expression	Biased expression in ovary adult (RPKM 8.8), liver E18 (RPKM 1.2) and 5 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

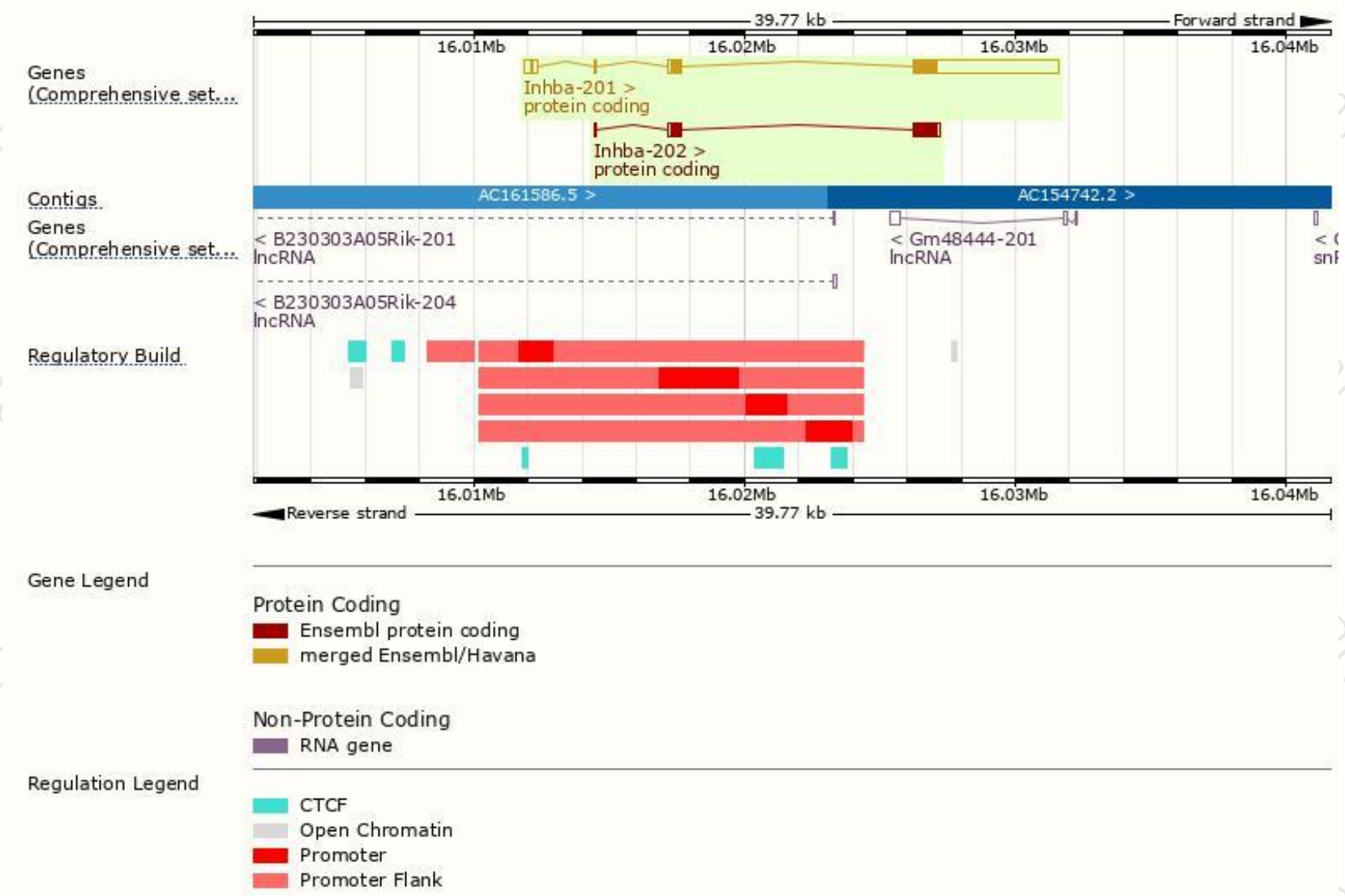
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Inhba-201	ENSMUST00000042603.13	6390	424aa	Protein coding	CCDS26251	Q04998 Q3UY39	TSL:1 GENCODE basic APPRIS P1
Inhba-202	ENSMUST00000164993.1	1529	424aa	Protein coding	CCDS26251	Q04998 Q3UY39	TSL:1 GENCODE basic APPRIS P1

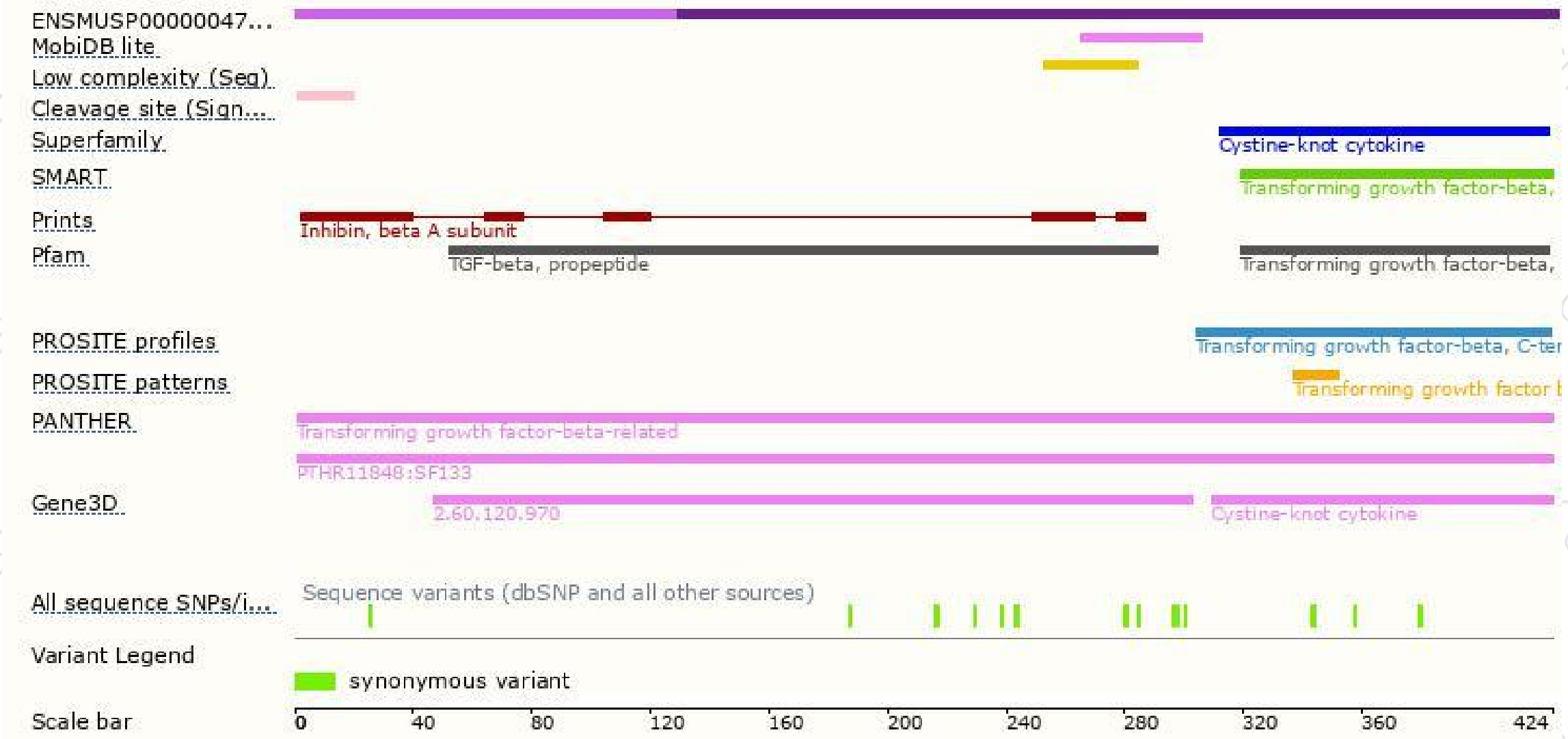
The strategy is based on the design of *Inhba-201* transcript,The transcription is shown below



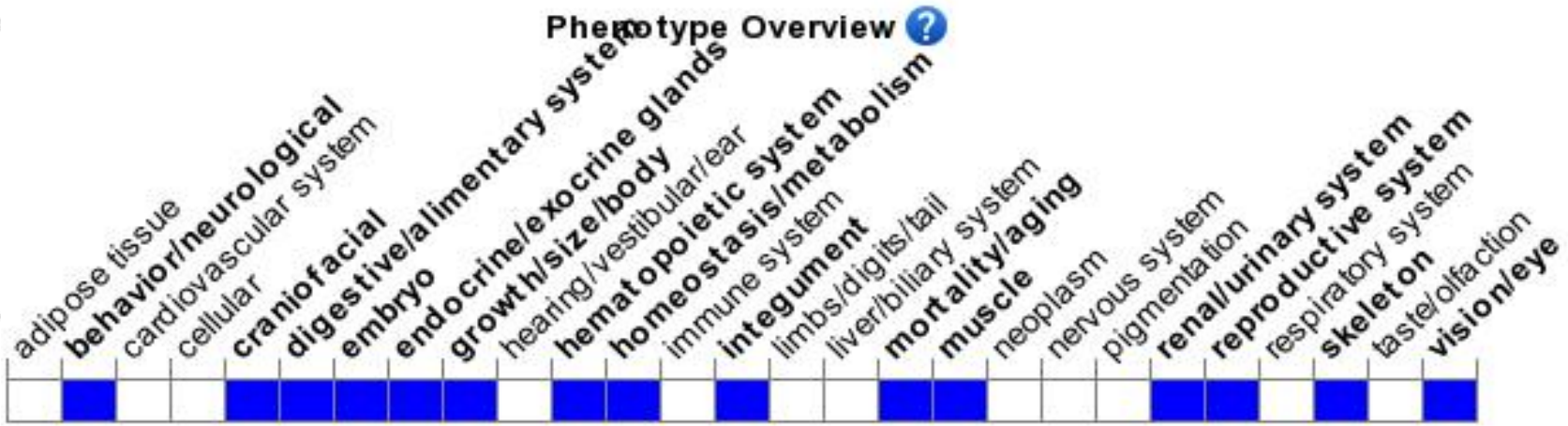
Genomic location distribution



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 for a targeted null mutation lack vibrissae and lower incisors, have defects in their secondary palates, and die shortly after birth.

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

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