GemPharmatech™

Shroom4 Cas9-KO Strategy

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Design Date: 2023-03-07

Overview

Target Gene Name

- Shroom4

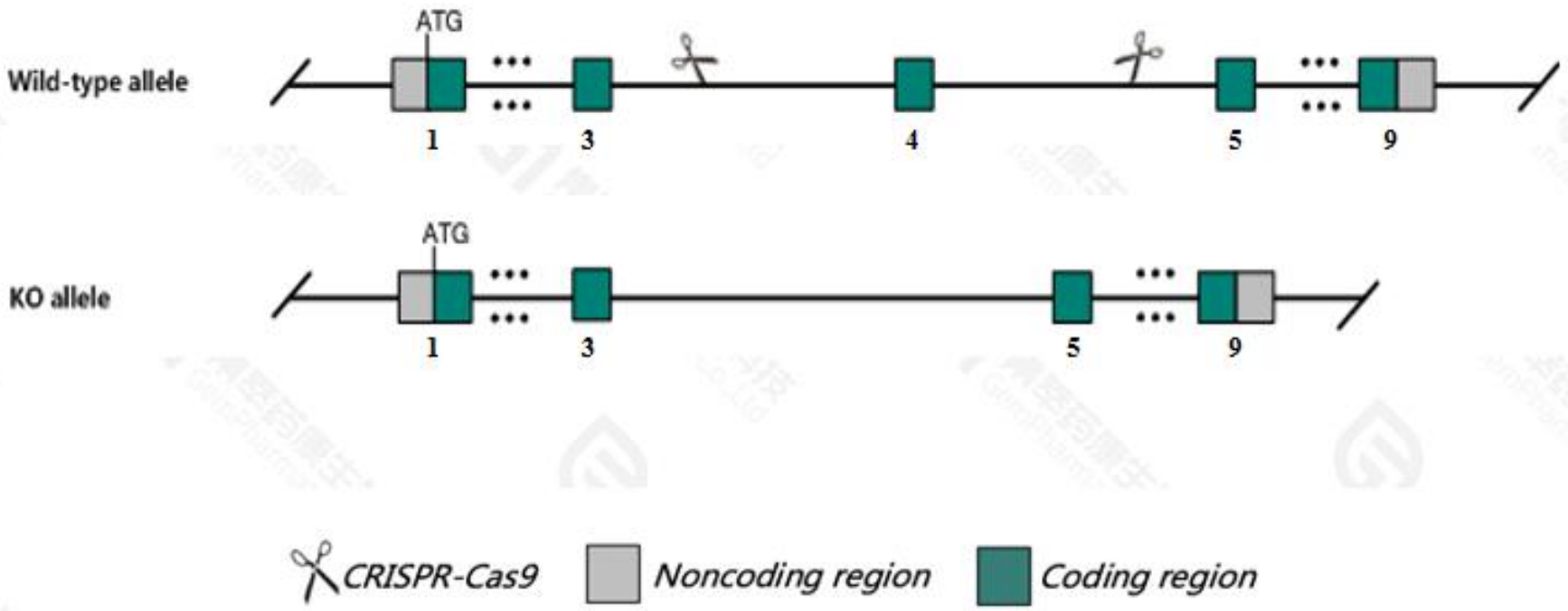
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy

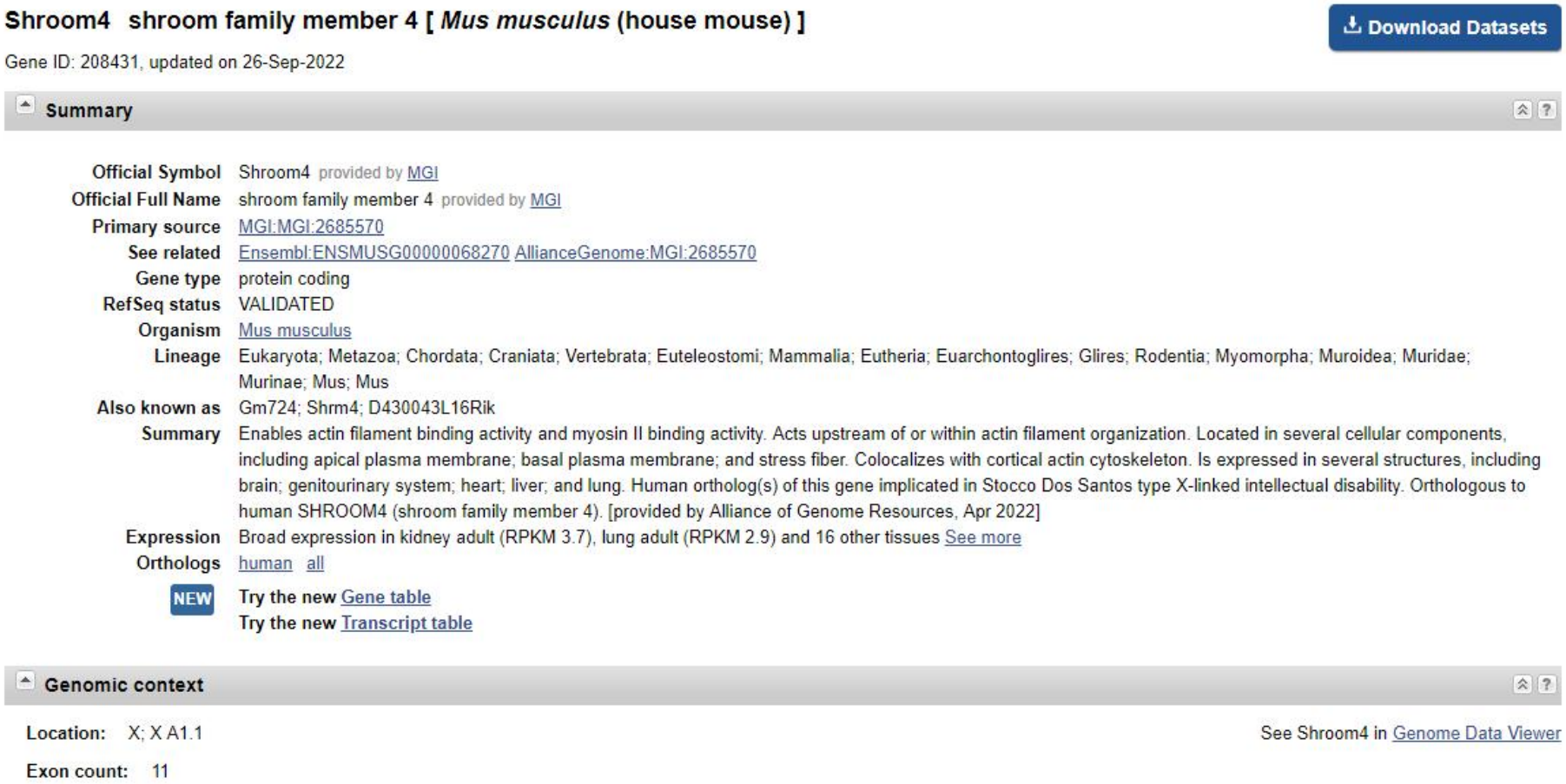


Schematic representation of CRISPR-Cas9 engineering used to edit the *Shroom4* gene.

Technical Information

- The *Shroom4* gene has 3 transcripts. According to the structure of *Shroom4* gene, exon4 of *Shroom4-202*(ENSMUST00000103005.10) transcript is recommended as the knockout region. The region contains 2464bp of coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Shroom4* gene. The brief process is as follows: gRNAs were transcribed in vitro. Cas9 and gRNAs 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.

Gene Information



Shroom4 shroom family member 4 [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 208431, updated on 26-Sep-2022

Summary

Official Symbol	Shroom4 provided by MGI
Official Full Name	shroom family member 4 provided by MGI
Primary source	MGI:MGI:2685570
See related	Ensembl:ENSMUSG00000068270 AllianceGenome:MGI:2685570
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	Gm724; Shrm4; D430043L16Rik
Summary	Enables actin filament binding activity and myosin II binding activity. Acts upstream of or within actin filament organization. Located in several cellular components, including apical plasma membrane; basal plasma membrane; and stress fiber. Colocalizes with cortical actin cytoskeleton. Is expressed in several structures, including brain; genitourinary system; heart; liver; and lung. Human ortholog(s) of this gene implicated in Stocco Dos Santos type X-linked intellectual disability. Orthologous to human SHROOM4 (shroom family member 4). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Broad expression in kidney adult (RPKM 3.7), lung adult (RPKM 2.9) and 16 other tissues See more
Orthologs	human all

NEW Try the new Gene table
Try the new Transcript table

Genomic context

Location: X; X A1.1 — See Shroom4 in Genome Data Viewer

Exon count: 11

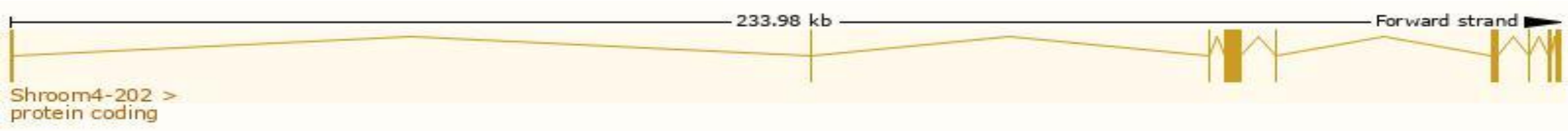
Source: https://www.ncbi.nlm.nih.gov/

Transcript Information

The gene has 3 transcripts, all transcripts are shown below:

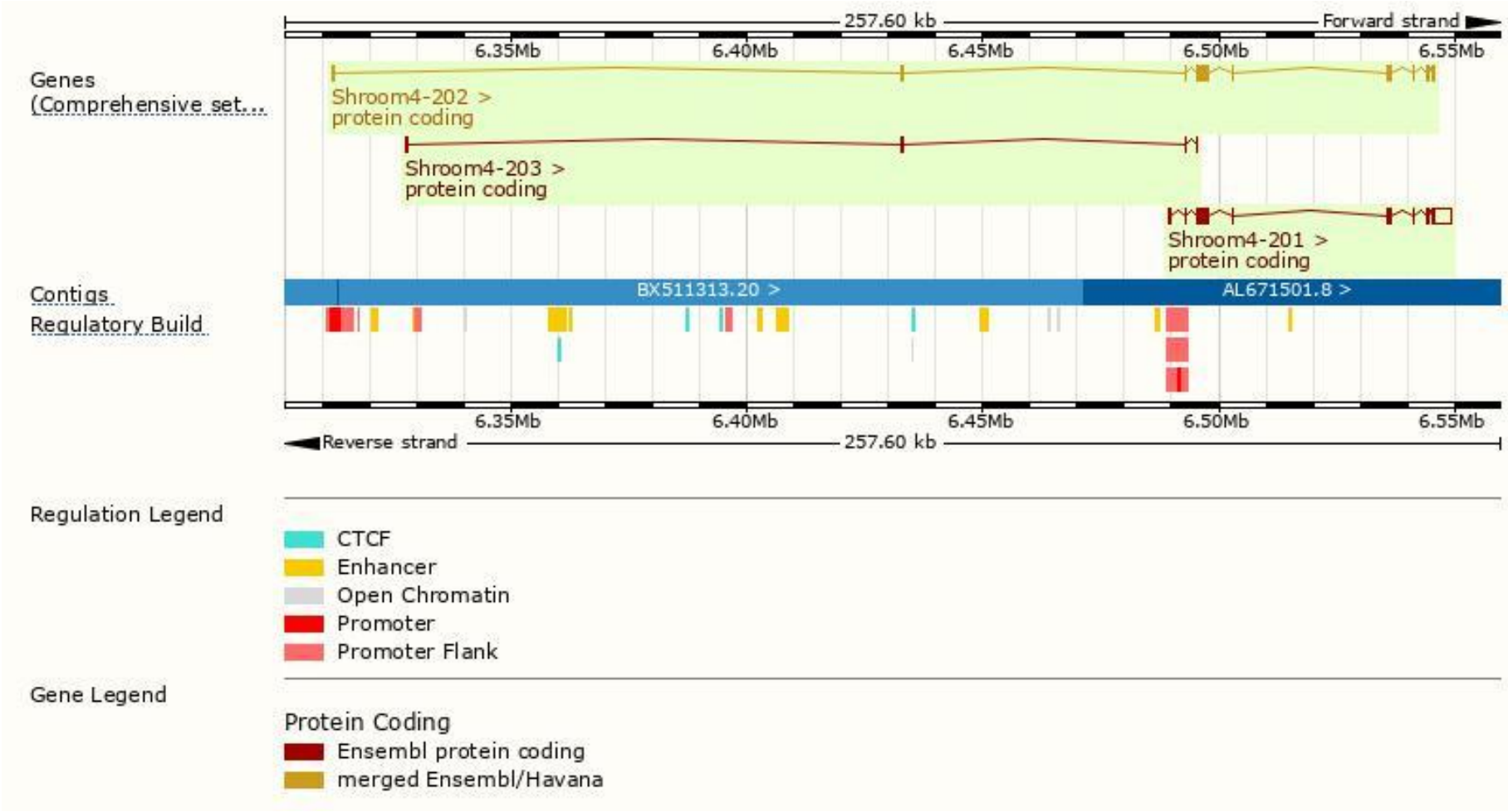
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000103005.10	Shroom4-202	4839	1475aa	Protein coding	CCDS29959	Q1W617-1	Ensembl Canonical, GENCODE basic, APPRIS P1, TSL:1
ENSMUST00000089520.3	Shroom4-201	8201	1359aa	Protein coding	CCDS85744	Q1W617-2	GENCODE basic, TSL:1
ENSMUST00000143641.4	Shroom4-203	755	200aa	Protein coding		E9PUX3	TSL:3, CDS 3' incomplete

The strategy is based on the design of *Shroom4-202* transcript, the transcription is shown below:



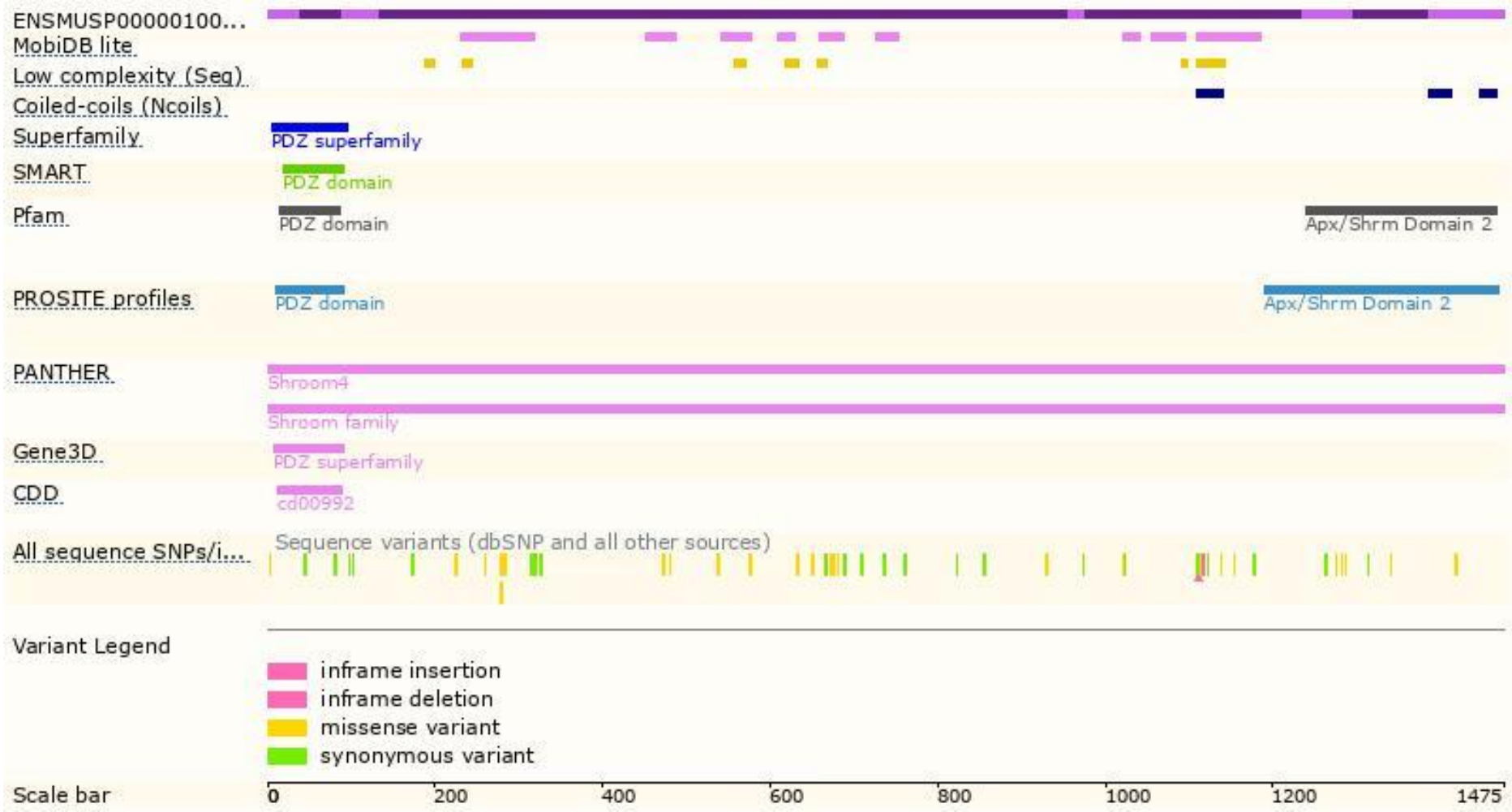
Source: https://www.ensembl.org

Genomic Information



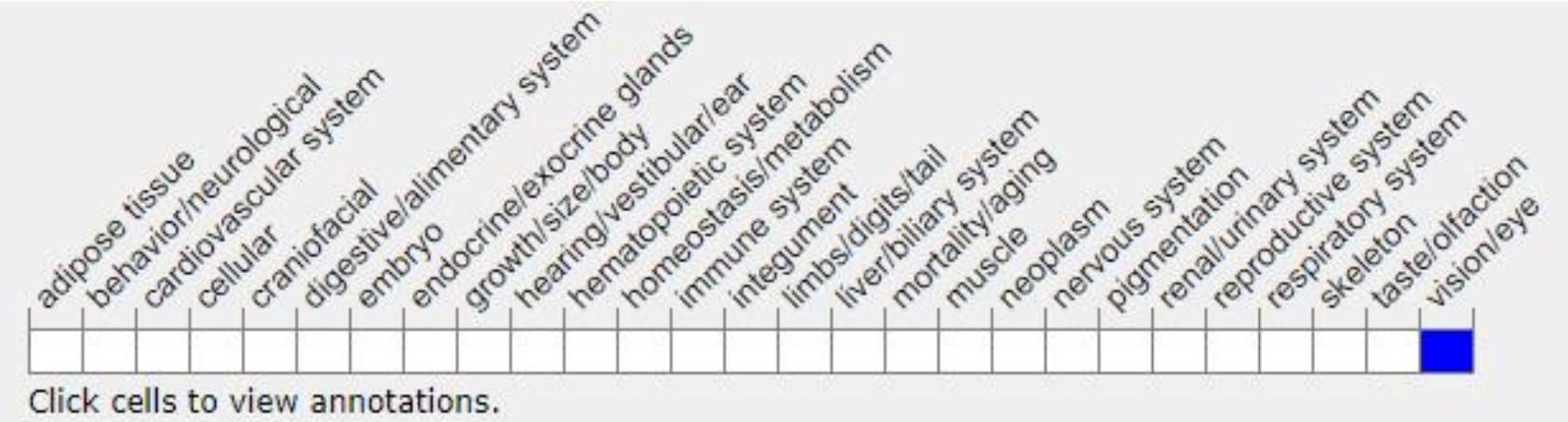
Source: : https://www.ensembl.org

Protein Information



Source: : https://www.ensembl.org

Mouse Phenotype Information (MGI)



- Phenotypes affected by the mutations of *Shroom4* gene are marked in blue. Data quoted from MGI database(http://www.informatics.jax.org/).

Source: https://www.informatics.jax.org

Important Information

- The *Shroom4* gene is located on the ChrX. 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.