Slc39a10 Cas9-KO Strategy

Designer:Yanhua Shen
Reviewer:Xueting Zhang
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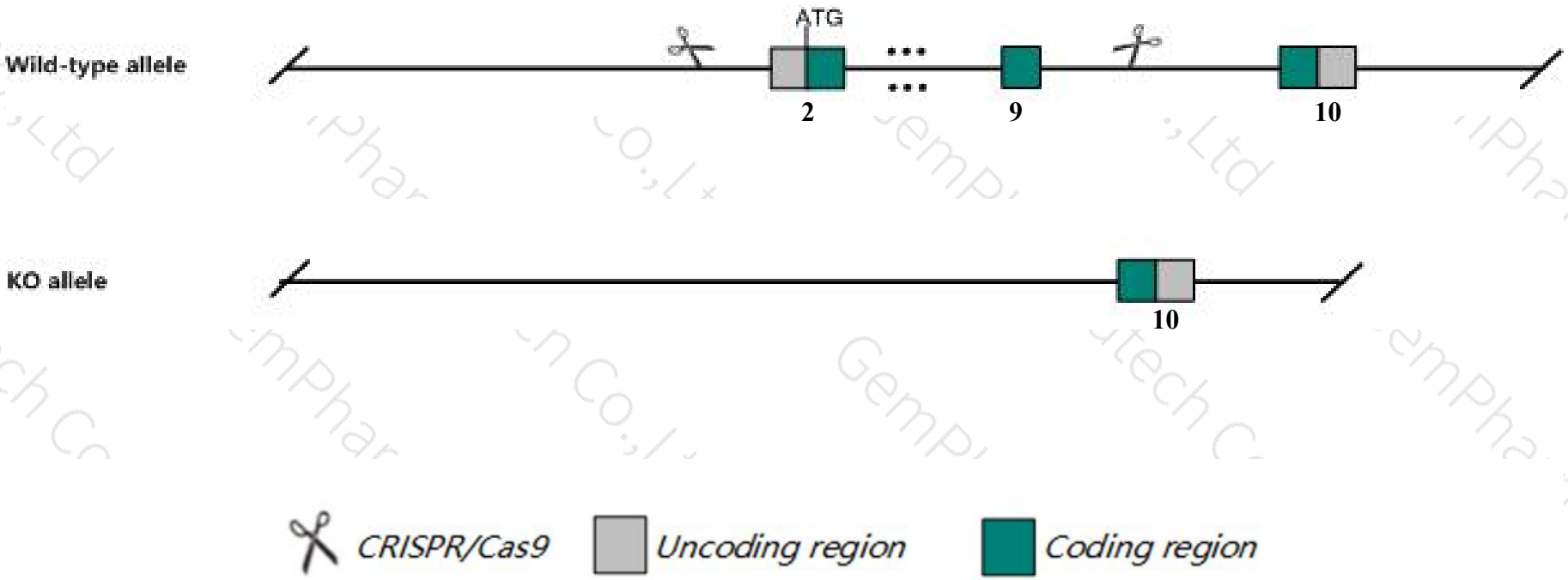
Project Overview

Project Name	***Slc39a10***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc39a10* gene. The schematic diagram is as follows:



Technical routes

➢ The *Slc39a10* gene has 4 transcripts. According to the structure of *Slc39a10* gene, exon2-exon9 of *Slc39a10-201* (ENSMUST00000027131.5) transcript is recommended as the knockout region.The region contains start codon ATG. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Slc39a10* gene. The brief process is as follows: CRISPR/Cas9 syst

Notice

➢ According to the existing MGI data,Mice with conditional loss of function display defects in cellular proliferation and differentiation.

➢The effects of transcripts 203 and 204 is unknown.

➢ The *Slc39a10* gene is located on the Chr1. 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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Slc39a10 solute carrier family 39 (zinc transporter), member 10 [*Mus musculus* (house mouse)]

Gene ID: 227059, updated on 14-Aug-2019

Summary

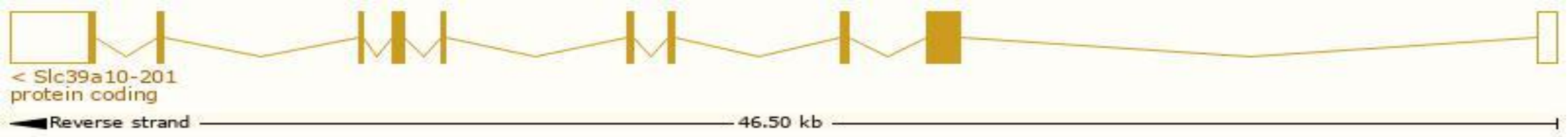
Official Symbol	Slc39a10 provided by MGI
Official Full Name	solute carrier family 39 (zinc transporter), member 10 provided by MGI
Primary source	MGI:MGI:1914515
See related	Ensembl:ENSMUSG00000025986
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Zip10; mKIAA1265; 5430433I10; 2900042E17Rik
Expression	Broad expression in cortex adult (RPKM 17.1), frontal lobe adult (RPKM 14.5) and 22 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

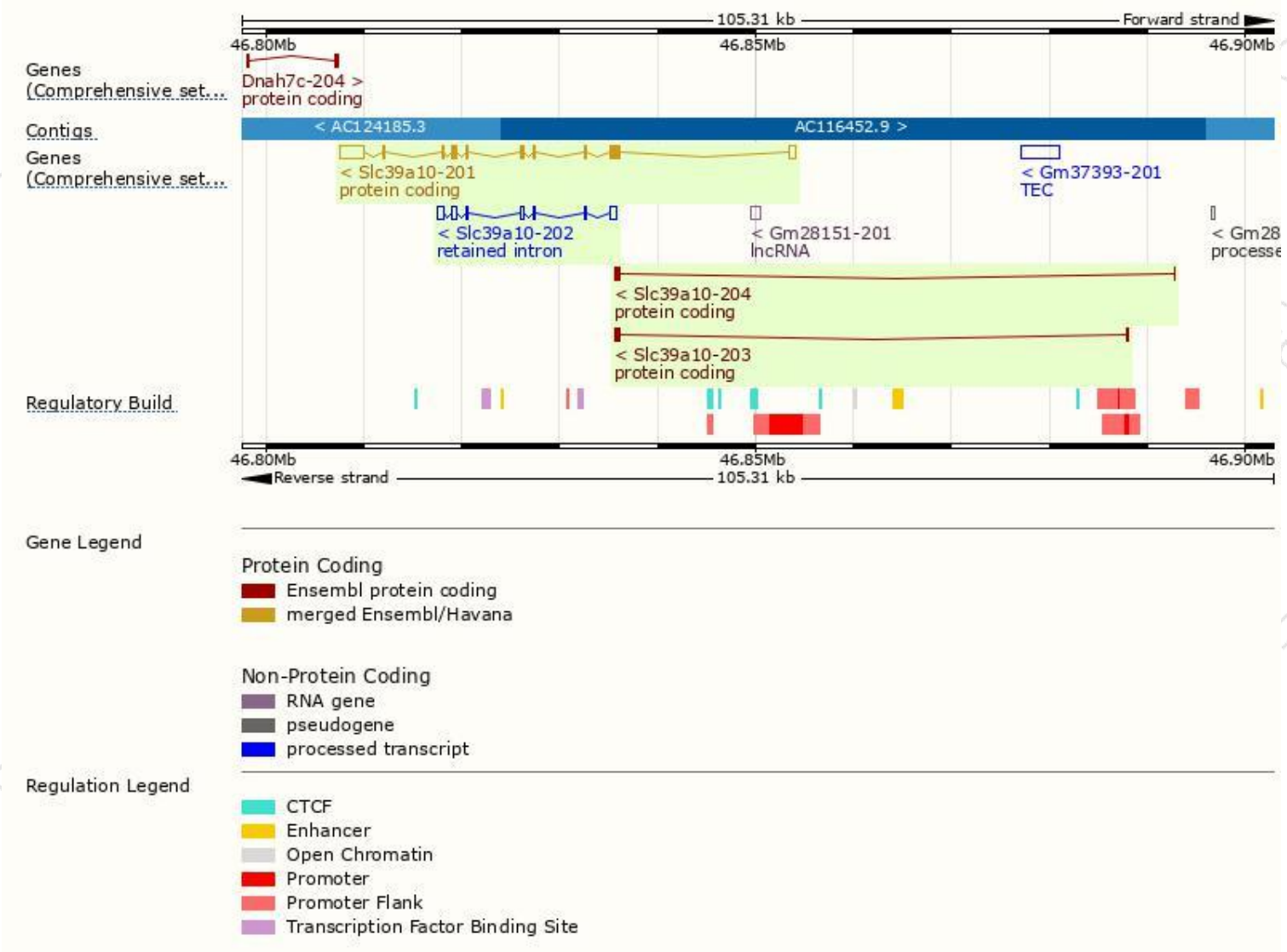
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc39a10-201	ENSMUST00000027131.5	5498	833aa	Protein coding	CCDS14936	Q6P5F6	TSL:1 GENCODE basic APPRIS P1
Slc39a10-204	ENSMUST00000186852.1	565	167aa	Protein coding	-	A0A087WQF7	CDS 3' incomplete TSL:3
Slc39a10-203	ENSMUST00000185520.1	497	144aa	Protein coding	-	A0A087WRC8	CDS 3' incomplete TSL:3
Slc39a10-202	ENSMUST00000141226.2	2372	No protein	Retained intron	-	-	TSL:1

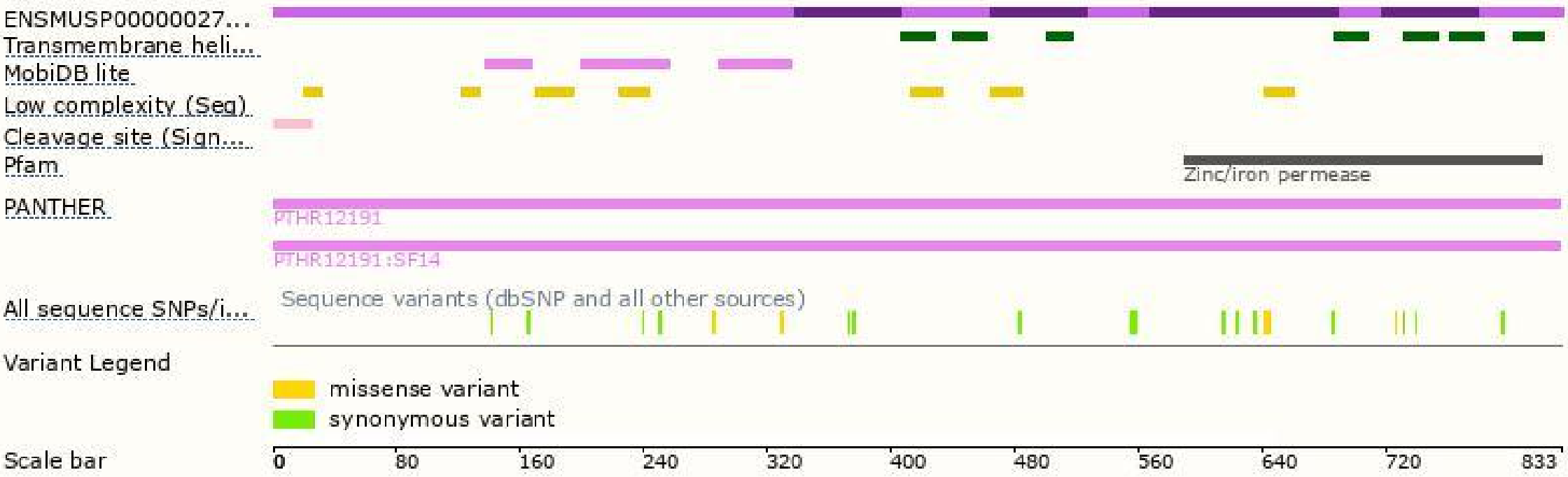
The strategy is based on the design of *Slc39a10-201* transcript,The transcription is shown below



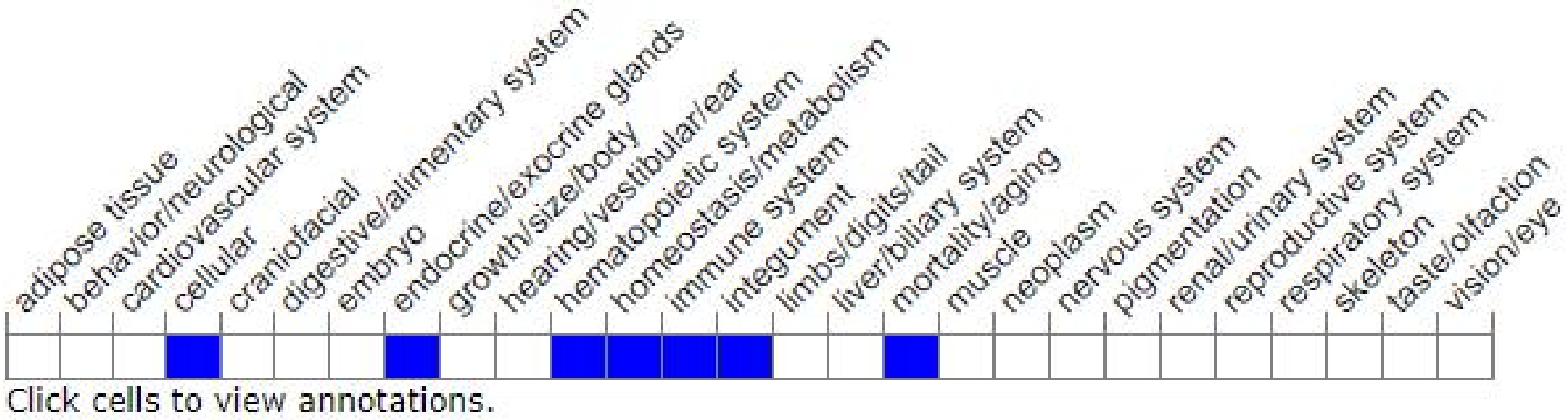
Genomic location distribution



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/).

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

Tel: 400-9660890

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GemPharmatech Co.,Ltd