Slc39a4 Cas9-KO Strategy

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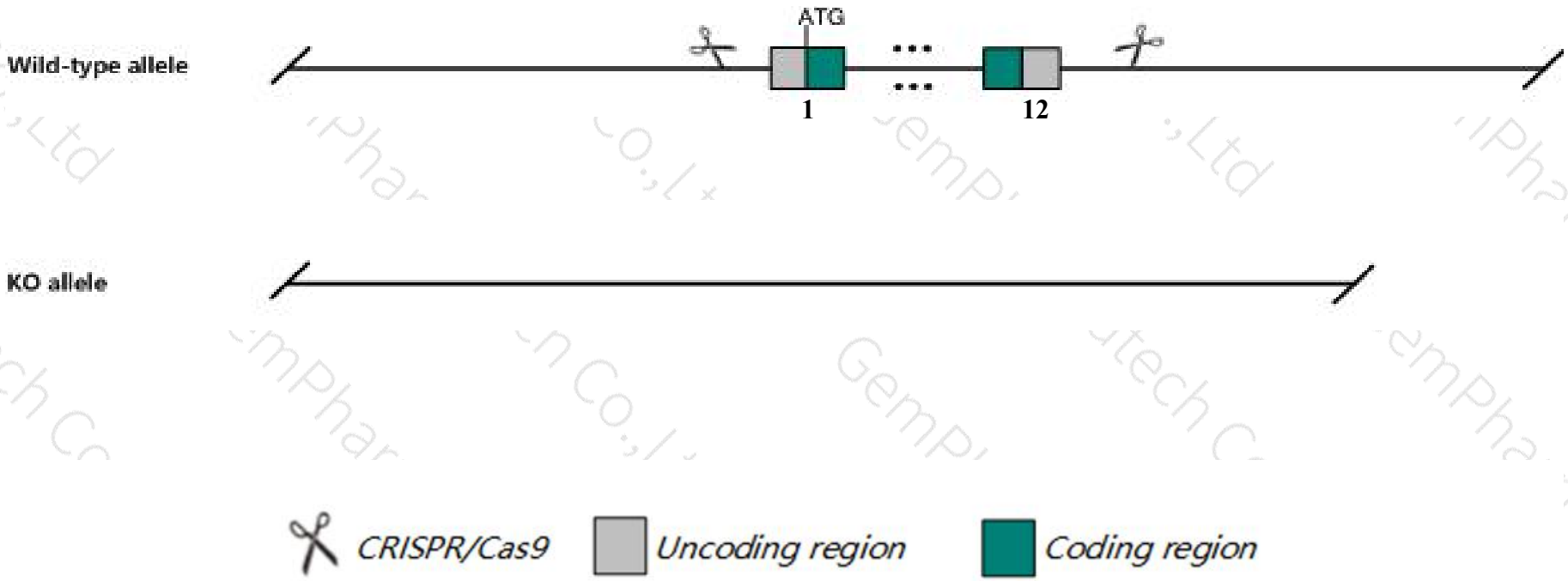
Project Overview

Project Name	***Slc39a4***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc39a4* gene. The schematic diagram is as follows:



Technical routes

➢ The *Slc39a4* gene has 4 transcripts. According to the structure of *Slc39a4* gene, exon1-exon12 of *Slc39a4-204* (ENSMUST00000230977.1) transcript is recommended as the knockout region.The region contains all of the coding sequence.Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Slc39a4* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

- According to the existing MGI data,Mice homozygous for a null allele exhibit embryonic letahlity around E10. Mice heterozygous for a null allele exhibit developmental defects similar to the teratology of zinc deficiency.
- This strategy may affect its 5-terminal regulation and 3-terminal regulation.
- This strategy may affect the 5-terminal regulation of the *Cpsf1* gene and the 3-terminal regulation of the *Vps28* gene.
- The *Slc39a4* gene is located on the Chr15. 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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Slc39a4 solute carrier family 39 (zinc transporter), member 4 [Mus musculus (house mouse)]

Gene ID: 72027, updated on 31-Jan-2019

Summary

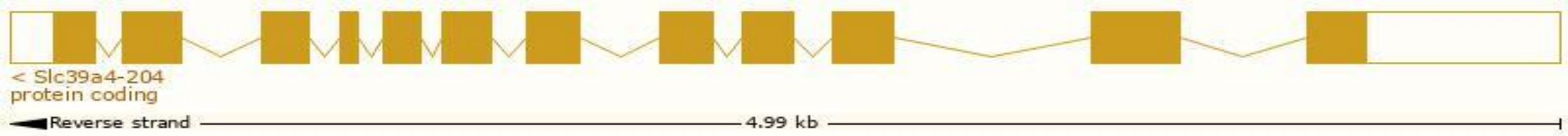
Official Symbol	Slc39a4 provided by MGI
Official Full Name	solute carrier family 39 (zinc transporter), member 4 provided by MGI
Primary source	MGI:MGI:1919277
See related	Ensembl:ENSMUSG00000063354
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1600025H15Rik, AU041686, AWMS2, ZIP4
Expression	Biased expression in duodenum adult (RPKM 110.1), small intestine adult (RPKM 81.8) and 10 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

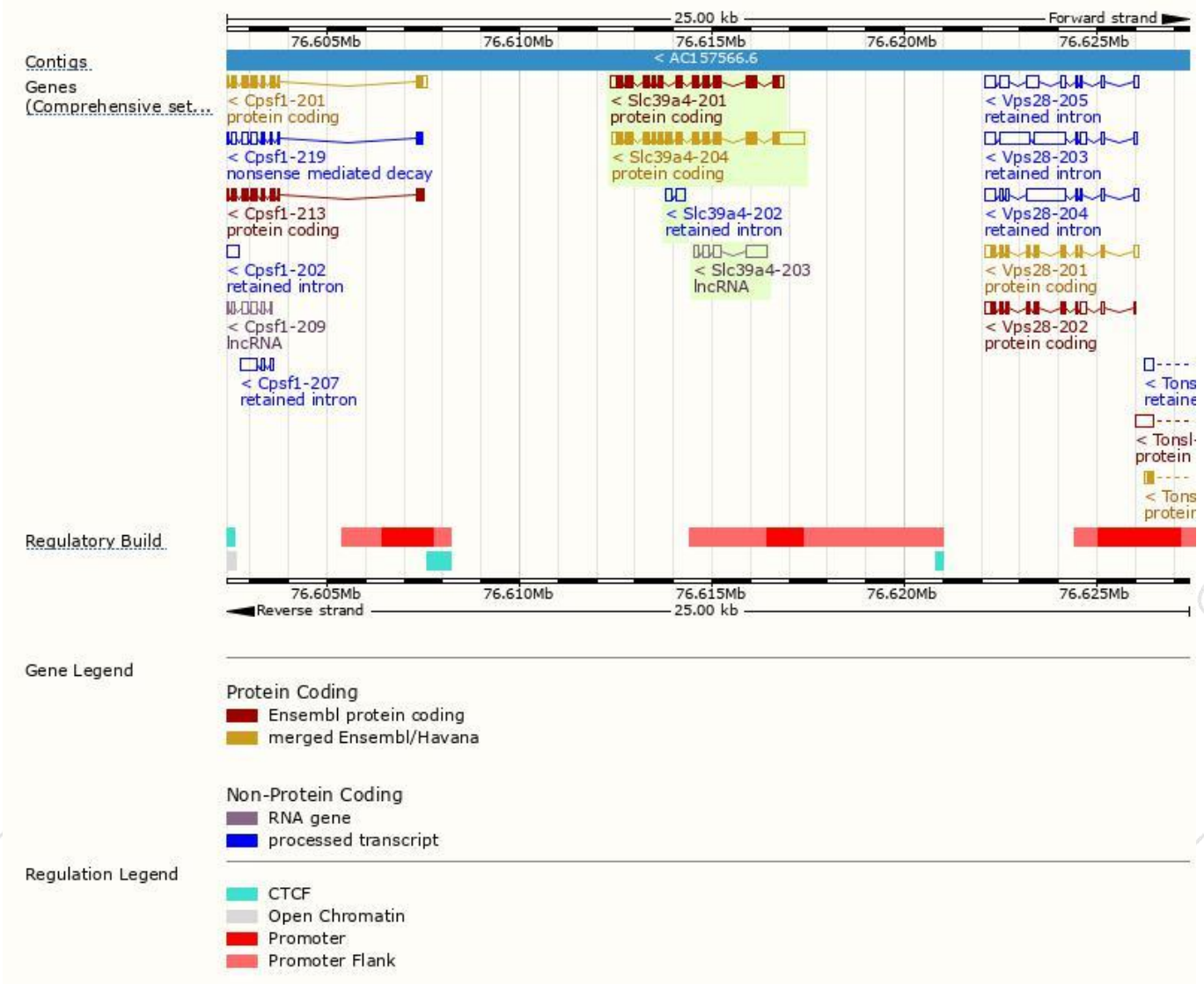
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc39a4-204	ENSMUST00000230977.1	2750	660aa	Protein coding	CCDS27578	Q78IQ7	GENCODE basic APPRIS P1
Slc39a4-201	ENSMUST00000073428.6	2063	607aa	Protein coding	-	A0A2U3TZ56	TSL:1 GENCODE basic
Slc39a4-202	ENSMUST00000229613.1	379	No protein	Retained intron	-	-	
Slc39a4-203	ENSMUST00000230317.1	1035	No protein	lncRNA	-	-	

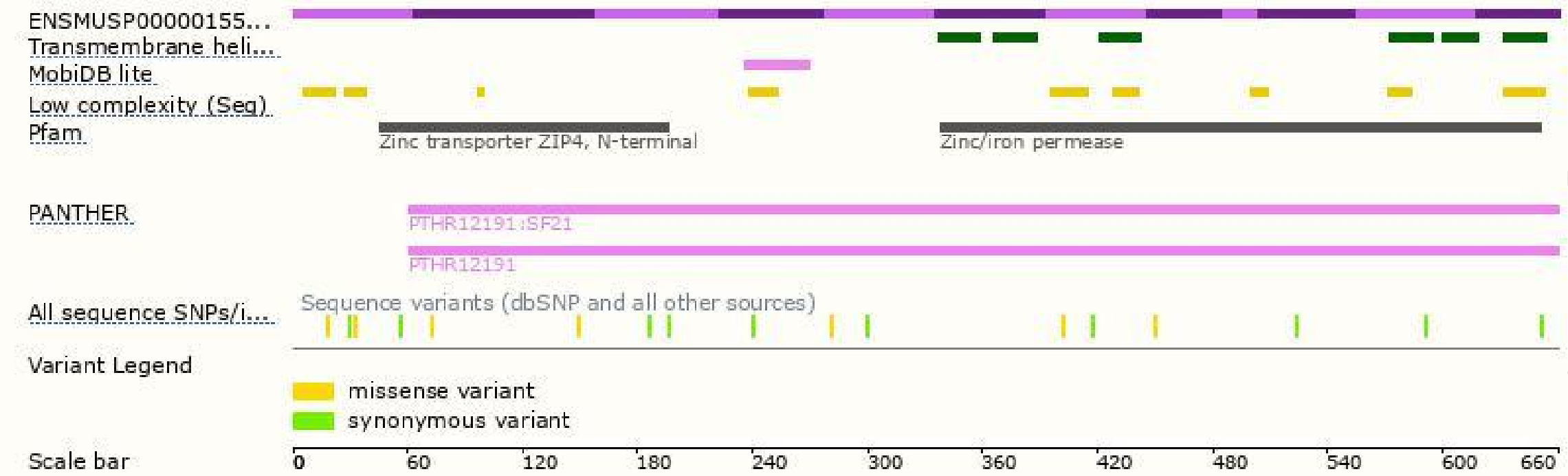
The strategy is based on the design of *Slc39a4-204* transcript,The transcription is shown below



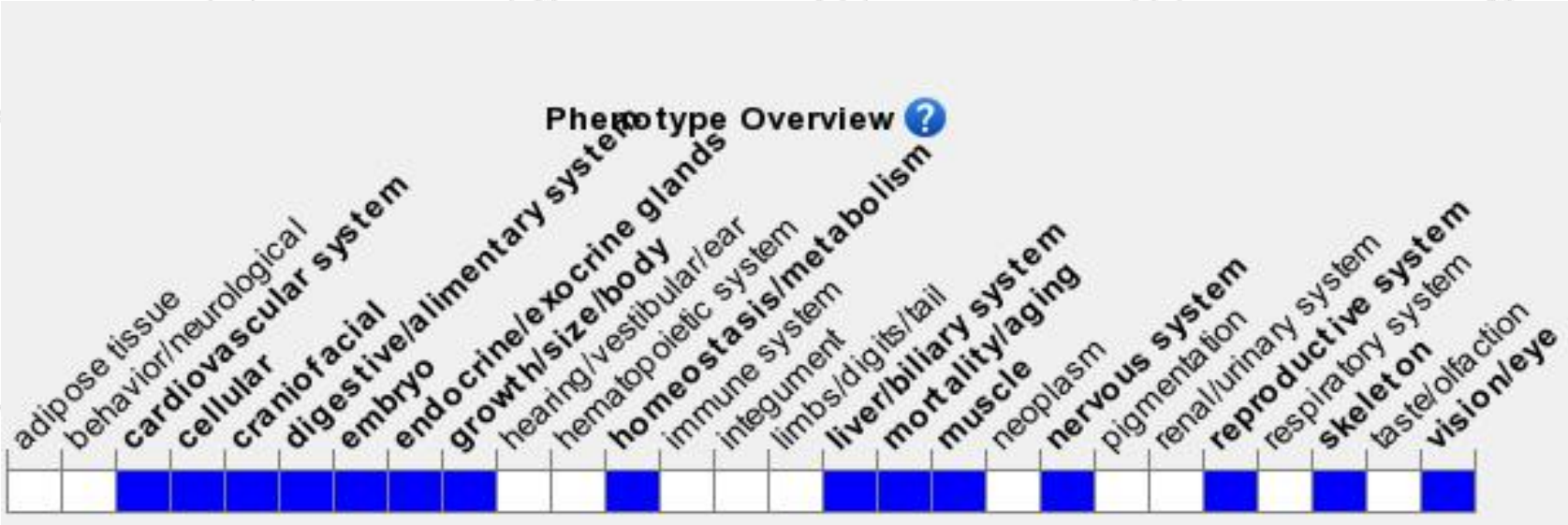
Genomic location distribution



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 null allele exhibit embryonic letahlity around E10. Mice heterozygous for a null allele exhibit developmental defects similar to the teratology of zinc deficiency.

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

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