

Slc25a28 Cas9-KO Strategy

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Date: 2020-02-20

Project Overview

Project Name

Slc25a28

Project type

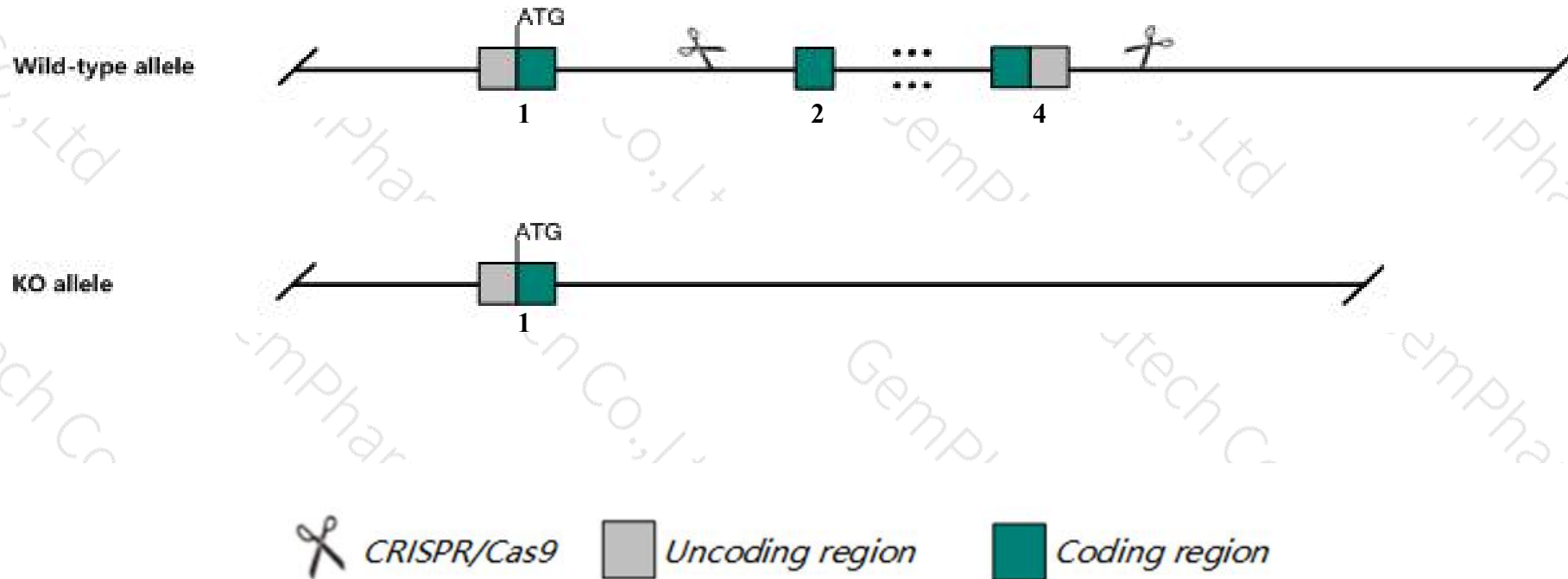
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc25a28* gene. The schematic diagram is as follows:



- The *Slc25a28* gene has 5 transcripts. According to the structure of *Slc25a28* gene, exon2-exon4 of *Slc25a28-201* (ENSMUST00000046038.8) transcript is recommended as the knockout region. The region contains most 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 *Slc25a28* gene. The brief process is as follows: CRISPR/Cas9 syst

- The knockout region is near to the N-terminal of *BC037704* gene, this strategy may influence the regulatory function of the N-terminal of *BC037704* gene.
- The *Slc25a28* gene is located on the Chr19. 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)

Slc25a28 solute carrier family 25, member 28 [*Mus musculus* (house mouse)]

Gene ID: 246696, updated on 14-Aug-2019

Summary

- Official Symbol** Slc25a28 provided by [MGI](#)
- Official Full Name** solute carrier family 25, member 28 provided by [MGI](#)
- Primary source** [MGI:MGI:2180509](#)
- See related** [Ensembl:ENSMUSG00000040414](#)
- 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** Mfrn2; Mrs3/4
- Expression** Ubiquitous expression in ovary adult (RPKM 37.3), adrenal adult (RPKM 28.9) and 28 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 19 C3; 19 36.67 cM See Slc25a28 in [Genome Data Viewer](#)

Exon count: 5

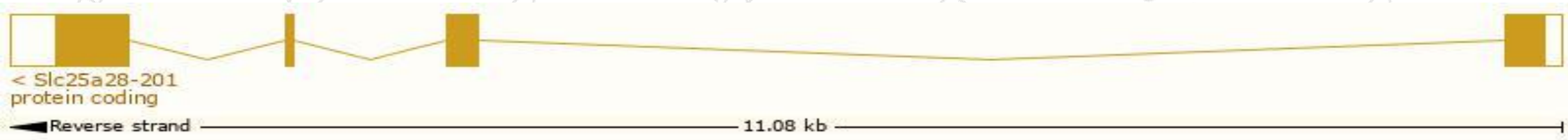
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	19	NC_000085.6 (43663801..43675006, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	19	NC_000085.5 (43738291..43749371, complement)

Transcript information (Ensembl)

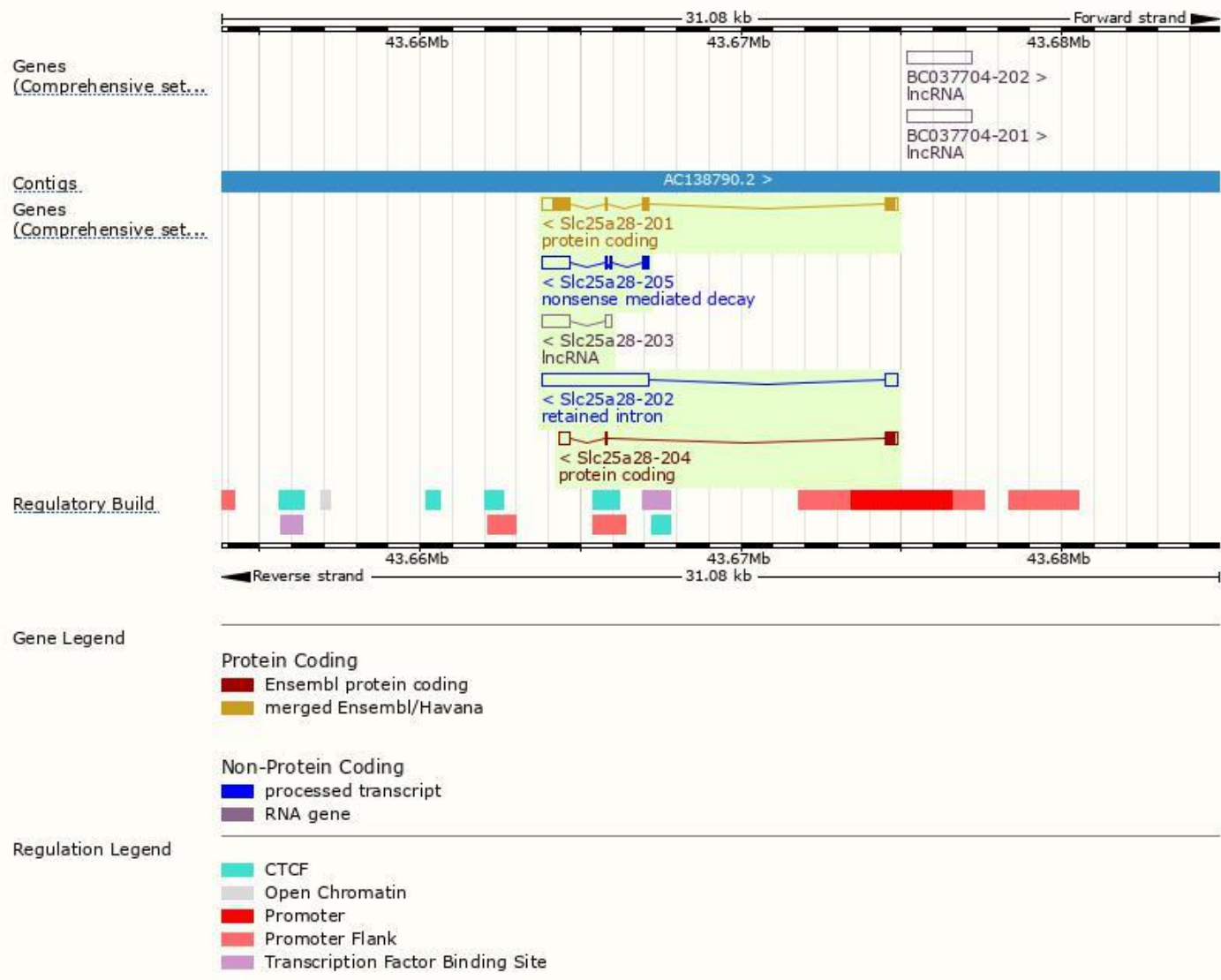
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc25a28-201	ENSMUST00000046038.8	1535	364aa	Protein coding	CCDS29834	Q8R0Z5	TSL:1 GENCODE basic APPRIS P1
Slc25a28-204	ENSMUST00000236433.1	767	111aa	Protein coding	-	-	GENCODE basic
Slc25a28-205	ENSMUST00000237364.1	1194	83aa	Nonsense mediated decay	-	-	CDS 5' incomplete
Slc25a28-202	ENSMUST00000235953.1	3724	No protein	Retained intron	-	-	
Slc25a28-203	ENSMUST00000236286.1	1046	No protein	lncRNA	-	-	

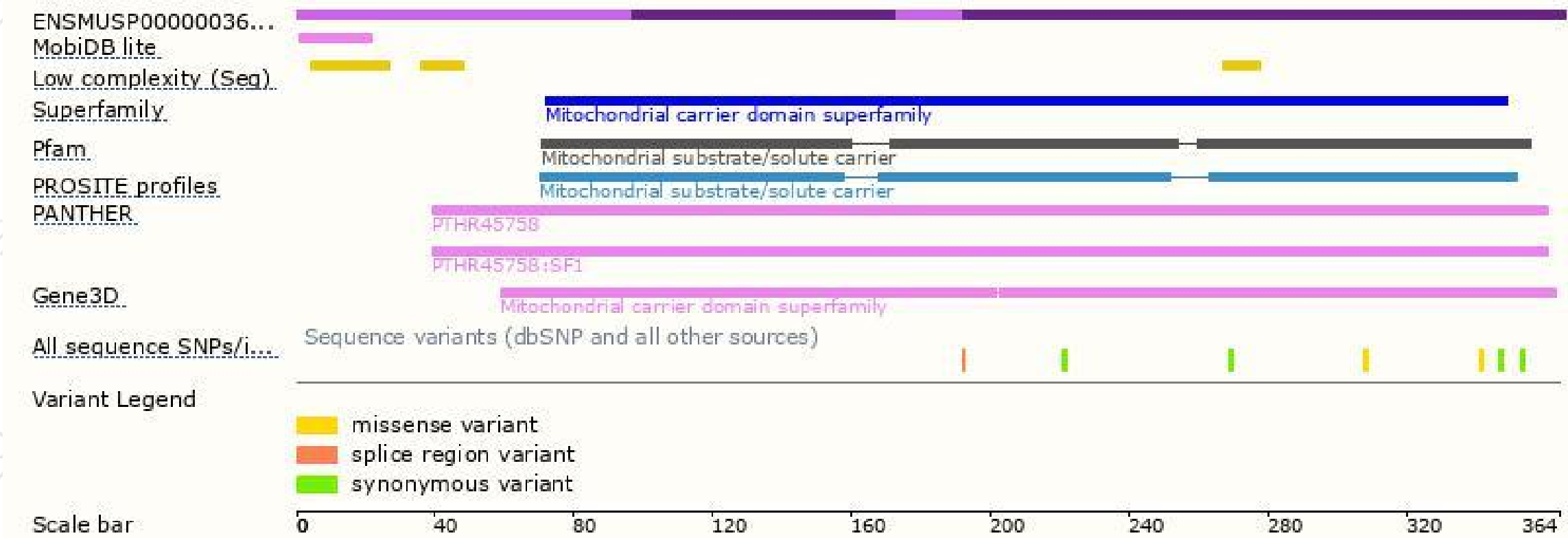
The strategy is based on the design of *Slc25a28-201* transcript,The transcription is shown below



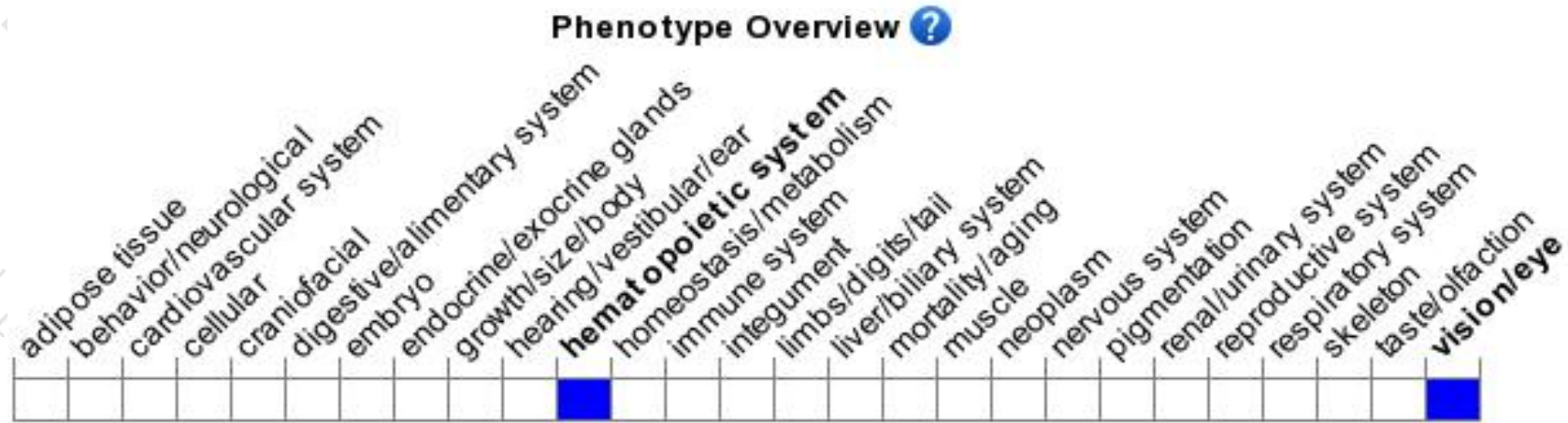
Genomic location distribution



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/>).

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

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