

Slc6a13 Cas9-KO Strategy

Designer:

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Design Date:

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Project Overview

Project Name

Slc6a13

Project type

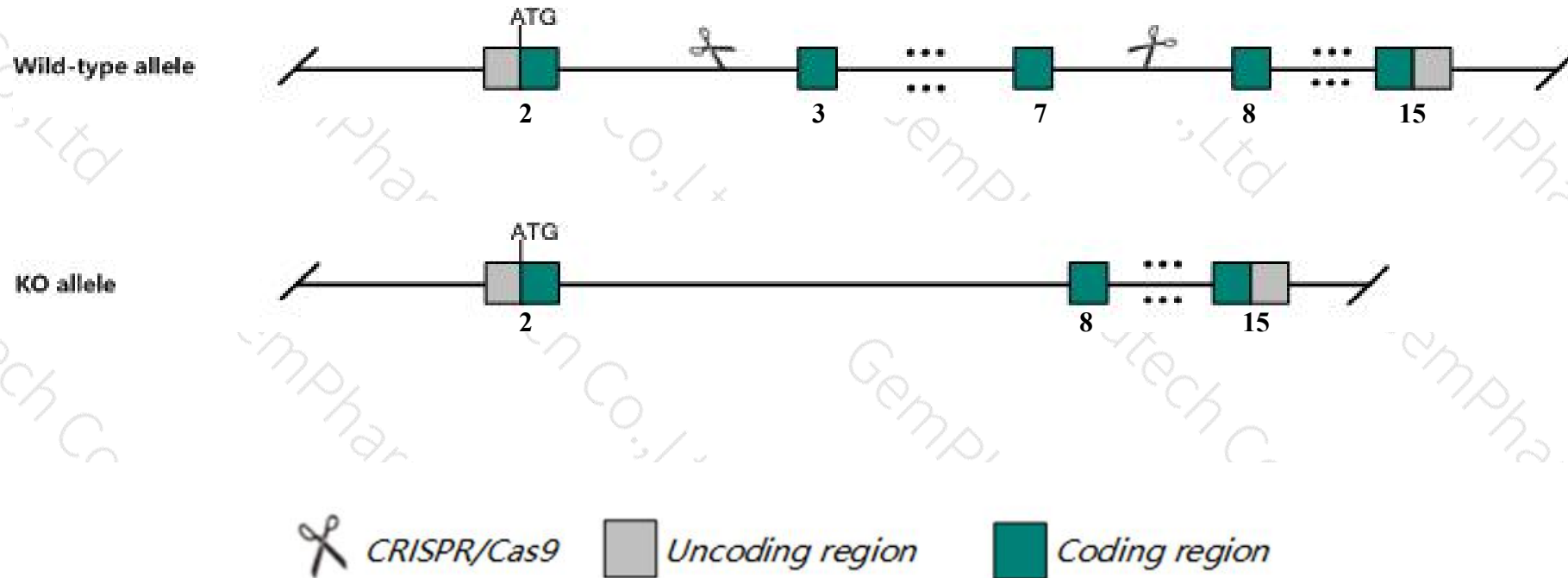
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc6a13* gene. The schematic diagram is as follows:



- The *Slc6a13* gene has 4 transcripts. According to the structure of *Slc6a13* gene, exon3-exon7 of *Slc6a13-201* (ENSMUST00000064580.13) transcript is recommended as the knockout region. The region contains 629bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc6a13* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit reduced taurine levels in the liver and increased taurine levels in the brain.
- The *Slc6a13* gene is located on the Chr6. 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)

Slc6a13 solute carrier family 6 (neurotransmitter transporter, GABA), member 13 [Mus musculus (house mouse)]

Gene ID: 14412, updated on 19-Feb-2019

Summary



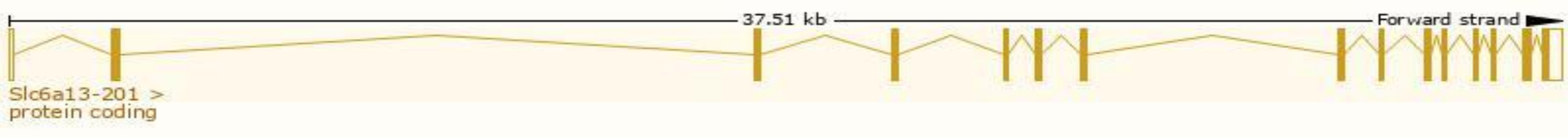
Official Symbol	Slc6a13 provided by MGI
Official Full Name	solute carrier family 6 (neurotransmitter transporter, GABA), member 13 provided by MGI
Primary source	MGI:MGI:95629
See related	Ensembl:ENSMUSG00000030108
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	GAT3, Gabt3, Gat2
Expression	Biased expression in liver adult (RPKM 100.1), kidney adult (RPKM 37.3) and 9 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

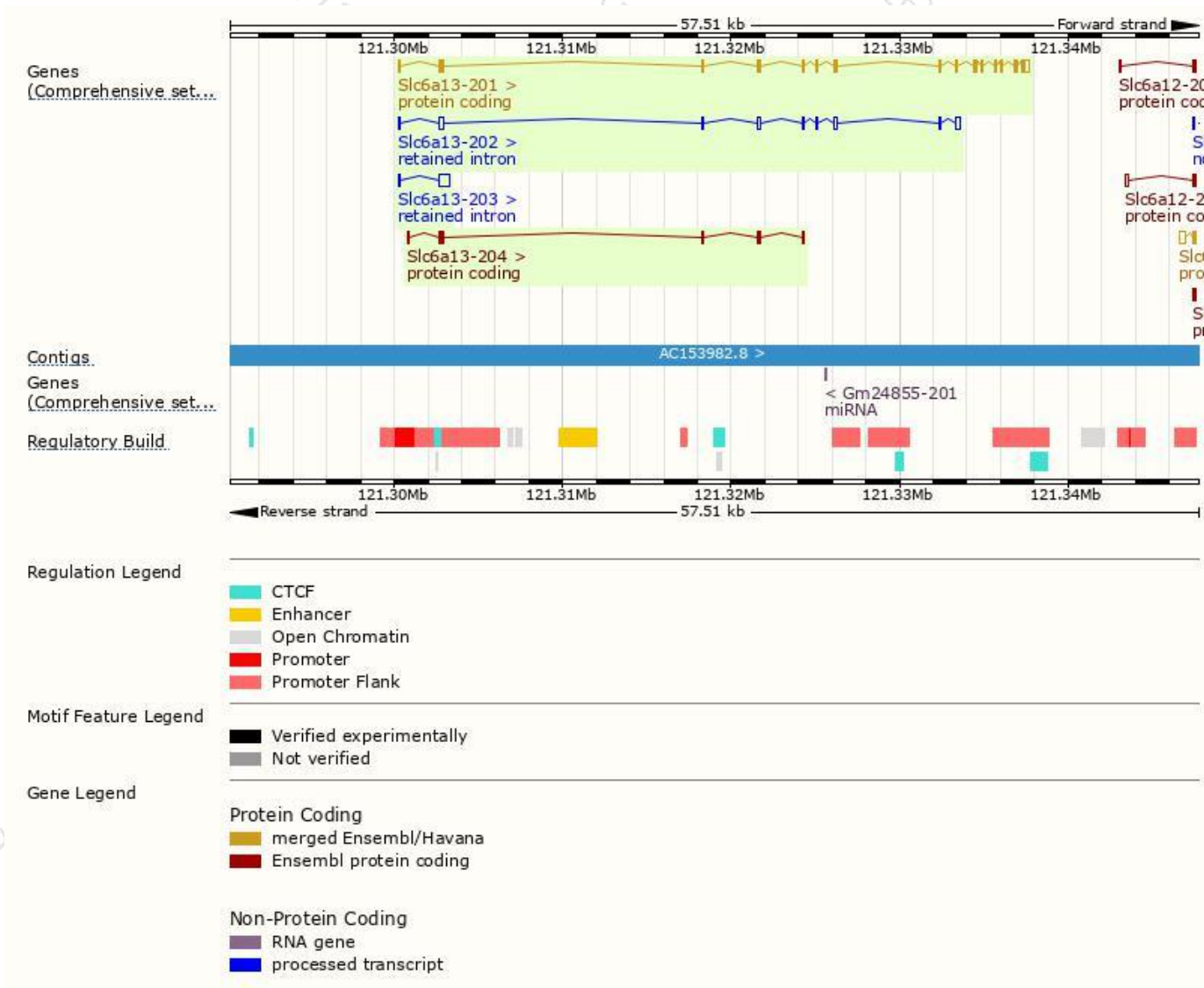
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc6a13-201	ENSMUST00000064580.13	2234	602aa	 Protein coding	CCDS20490	P31649	TSL:1 GENCODE basic APPRIS P1
Slc6a13-204	ENSMUST00000142419.1	681	192aa	 Protein coding	-	D3YWZ5	CDS 3' incomplete TSL:5
Slc6a13-202	ENSMUST00000142021.1	1254	No protein	 Retained intron	-	-	TSL:1
Slc6a13-203	ENSMUST00000142144.7	638	No protein	 Retained intron	-	-	TSL:1

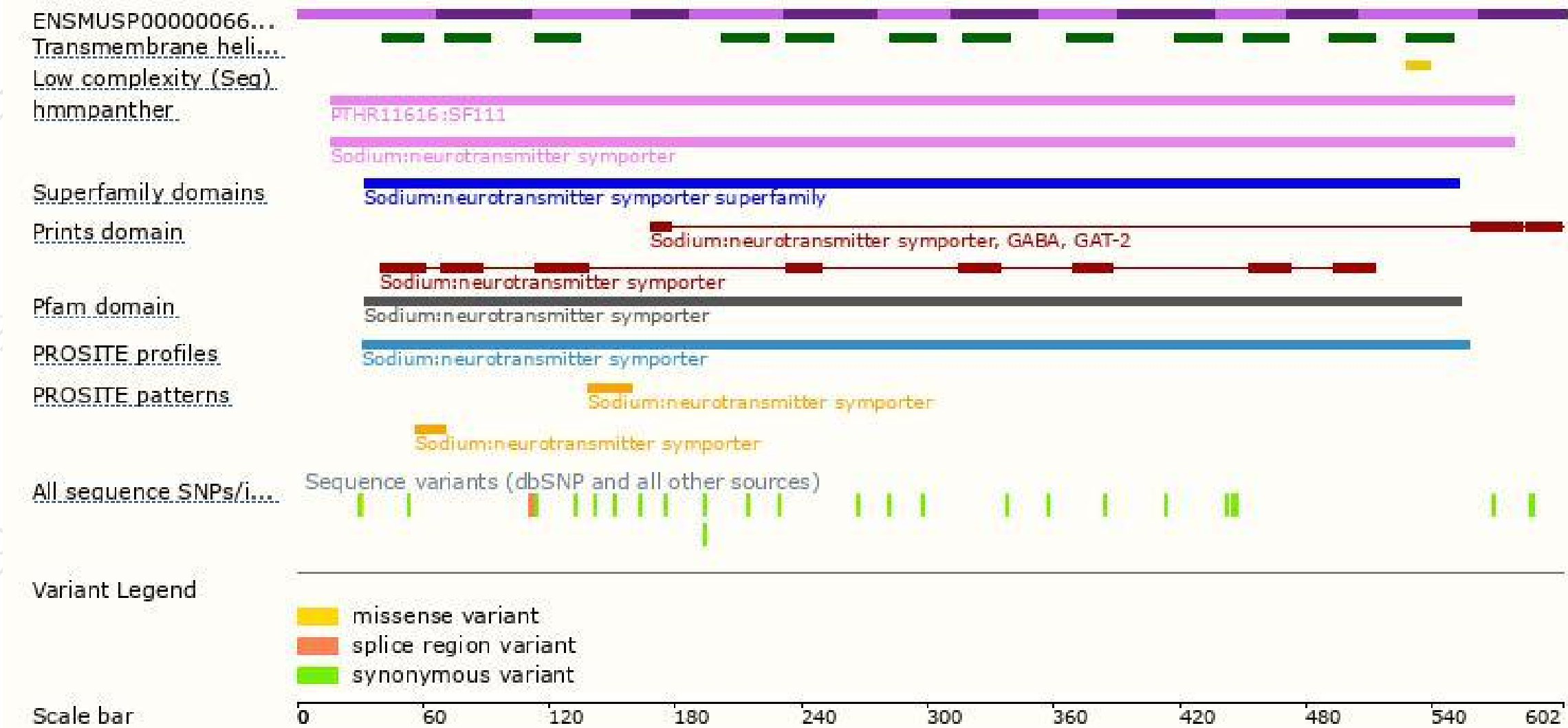
The strategy is based on the design of *Slc6a13-201* transcript,The transcription is shown below



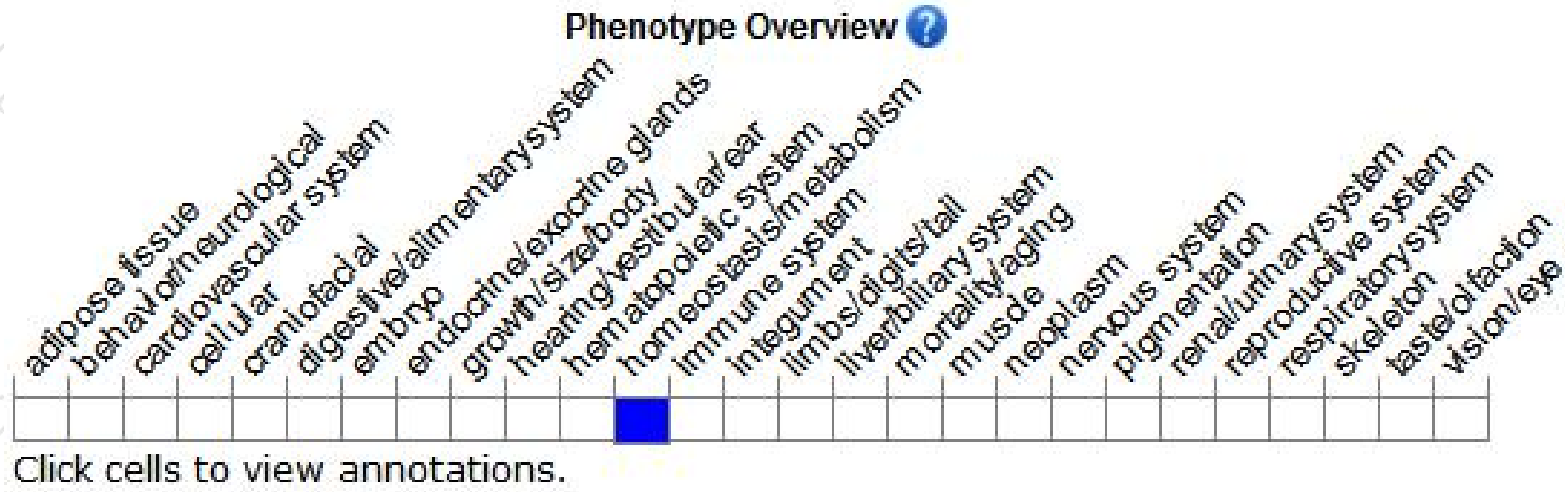
Genomic location distribution



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, Mice homozygous for a knock-out allele exhibit reduced taurine levels in the liver and increased taurine levels in the brain.

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

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