

# *Slc6a12* Cas9-KO Strategy

**Designer:**

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**Design Date:**

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# Project Overview

**Project Name**

*Slc6a12*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc6a12* gene. The schematic diagram is as follows:



- The *Slc6a12* gene has 10 transcripts. According to the structure of *Slc6a12* gene, exon3-exon6 of *Slc6a12-201* (ENSMUST00000032200.15) transcript is recommended as the knockout region. The region contains 497bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc6a12* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a targeted allele exhibit normal seizure threshold.
- The *Slc6a12* 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)

## Slc6a12 solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12 [Mus musculus (house mouse)]

Gene ID: 14411, updated on 31-Jan-2019

### Summary



**Official Symbol** Slc6a12 provided by [MGI](#)

**Official Full Name** solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12 provided by [MGI](#)

**Primary source** [MGI:MGI:95628](#)

**See related** [Ensembl:ENSMUSG00000030109](#)

**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** BGT1, GAT-2, GAT2, Gabt2

**Expression** Biased expression in liver adult (RPKM 40.1), placenta adult (RPKM 10.5) and 1 other tissue [See more](#)

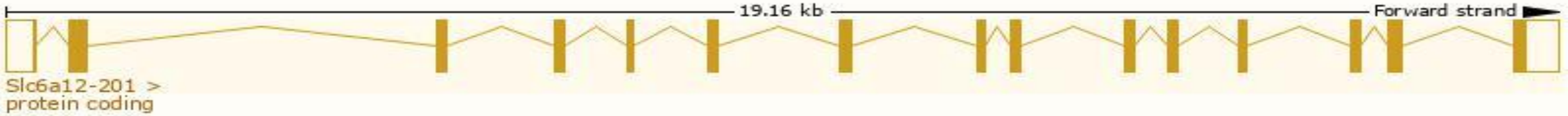
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

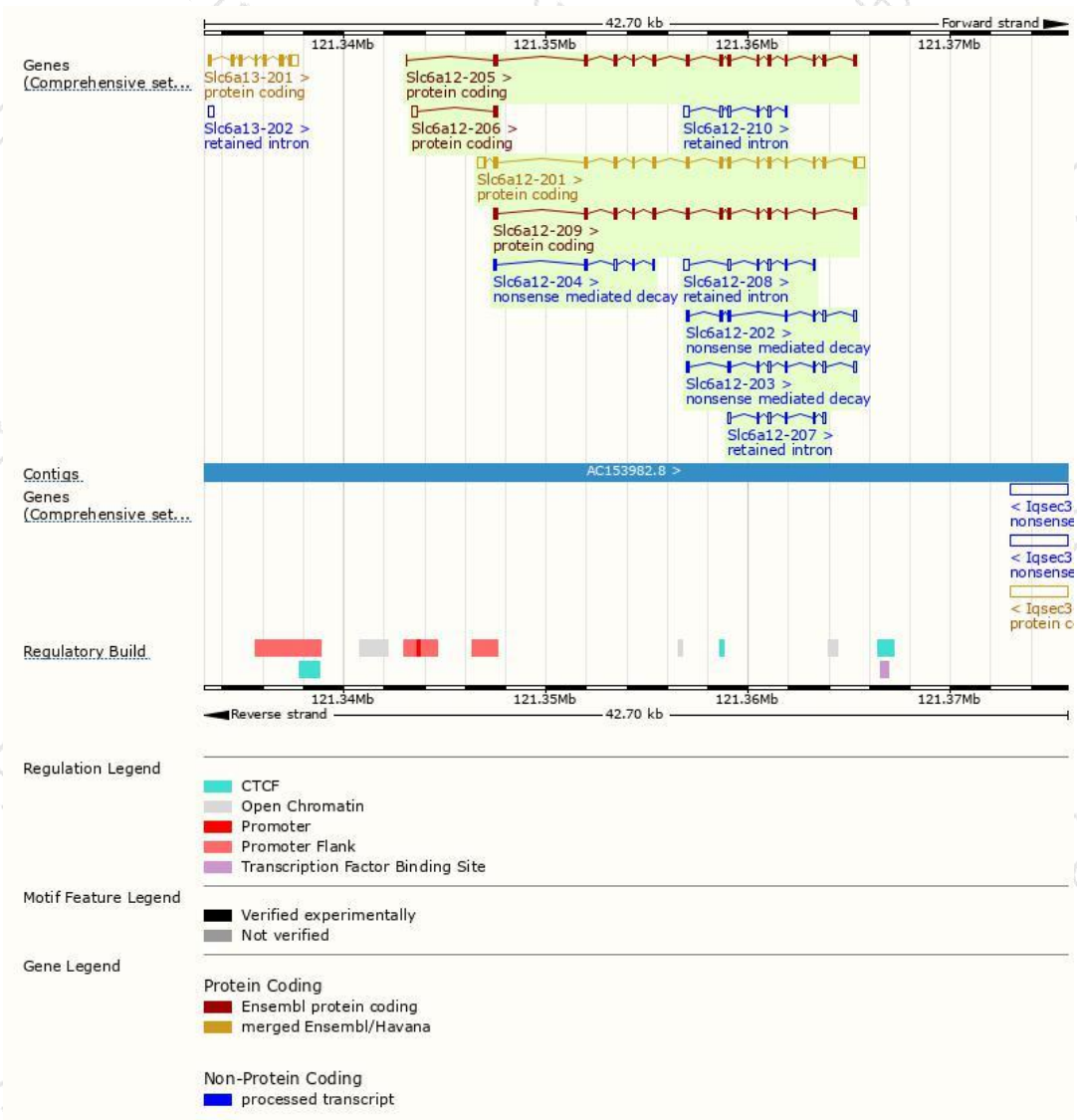
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc6a12-201	<a href="#">ENSMUST00000032200.15</a>	2644	<a href="#">628aa</a>	Protein coding	<a href="#">CCDS39616</a>	<a href="#">Q8VCS9</a>	TSL:1 GENCODE basic APPRIS P2
Slc6a12-205	<a href="#">ENSMUST00000166457.7</a>	1891	<a href="#">614aa</a>	Protein coding	-	<a href="#">G5E8Z4</a>	TSL:1 GENCODE basic APPRIS ALT2
Slc6a12-209	<a href="#">ENSMUST00000171008.7</a>	1674	<a href="#">557aa</a>	Protein coding	-	<a href="#">E9PXG1</a>	TSL:5 GENCODE basic APPRIS ALT2
Slc6a12-206	<a href="#">ENSMUST00000168295.1</a>	428	<a href="#">63aa</a>	Protein coding	-	<a href="#">E9PW98</a>	CDS 3' incomplete TSL:5
Slc6a12-203	<a href="#">ENSMUST00000165456.7</a>	1030	<a href="#">81aa</a>	Nonsense mediated decay	-	<a href="#">F7AYZ6</a>	CDS 5' incomplete TSL:5
Slc6a12-202	<a href="#">ENSMUST00000163771.7</a>	883	<a href="#">130aa</a>	Nonsense mediated decay	-	<a href="#">F6SJH4</a>	CDS 5' incomplete TSL:5
Slc6a12-204	<a href="#">ENSMUST00000166390.1</a>	500	<a href="#">65aa</a>	Nonsense mediated decay	-	<a href="#">E9Q5U8</a>	TSL:5
Slc6a12-207	<a href="#">ENSMUST00000170339.1</a>	808	No protein	Retained intron	-	-	TSL:5
Slc6a12-208	<a href="#">ENSMUST00000170582.7</a>	797	No protein	Retained intron	-	-	TSL:5
Slc6a12-210	<a href="#">ENSMUST00000171874.7</a>	790	No protein	Retained intron	-	-	TSL:5

The strategy is based on the design of *Slc6a12-201* transcript,The transcription is shown below

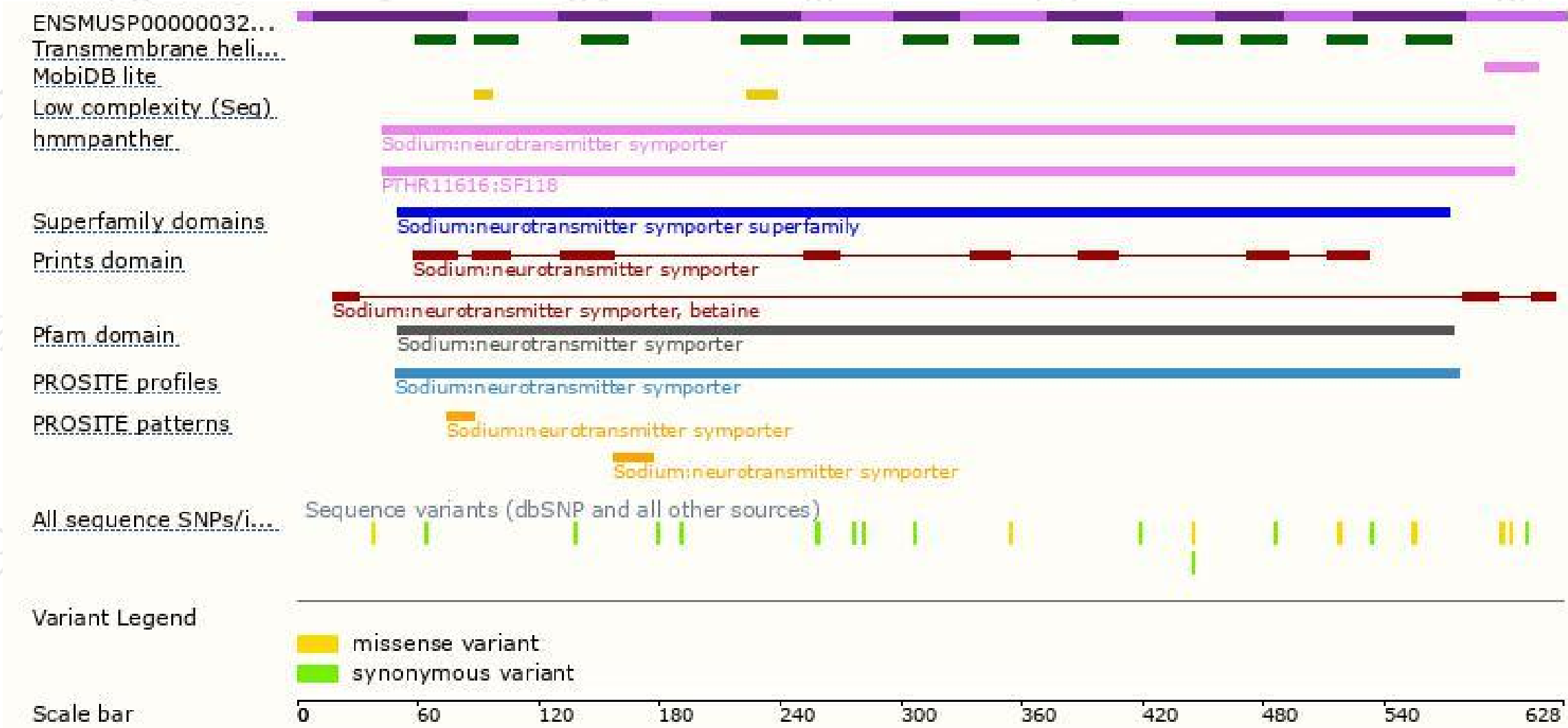


# Genomic location distribution





# Protein domain



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

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