

# ***Slc6a19*** Cas9-KO Strategy

Designer:Xiaojing Li  
Reviewer:JiaYu  
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# Project Overview

**Project Name**

*Slc6a19*

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc6a19* gene. The schematic diagram is as follows:



- The *Slc6a19* gene has 7 transcripts. According to the structure of *Slc6a19* gene, exon2-exon6 of *Slc6a19-201* (ENSMUST00000022048.5) transcript is recommended as the knockout region. The region contains 685bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc6a19* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit decreased body weight and impaired amino acid absorption and excretion.
- The *Slc6a19* gene is located on the Chr13. 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)

## Slc6a19 solute carrier family 6 (neurotransmitter transporter), member 19 [ *Mus musculus* (house mouse) ]

Gene ID: 74338, updated on 10-Oct-2019

### Summary

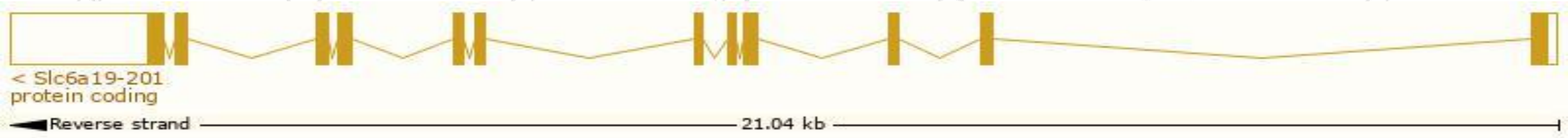
Official Symbol	Slc6a19 provided by <a href="#">MGI</a>
Official Full Name	solute carrier family 6 (neurotransmitter transporter), member 19 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:1921588</a>
See related	<a href="#">Ensembl:ENSMUSG000000021565</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	B<0>AT1; 4632401C08Rik
Expression	Biased expression in kidney adult (RPKM 169.0), large intestine adult (RPKM 126.9) and 2 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

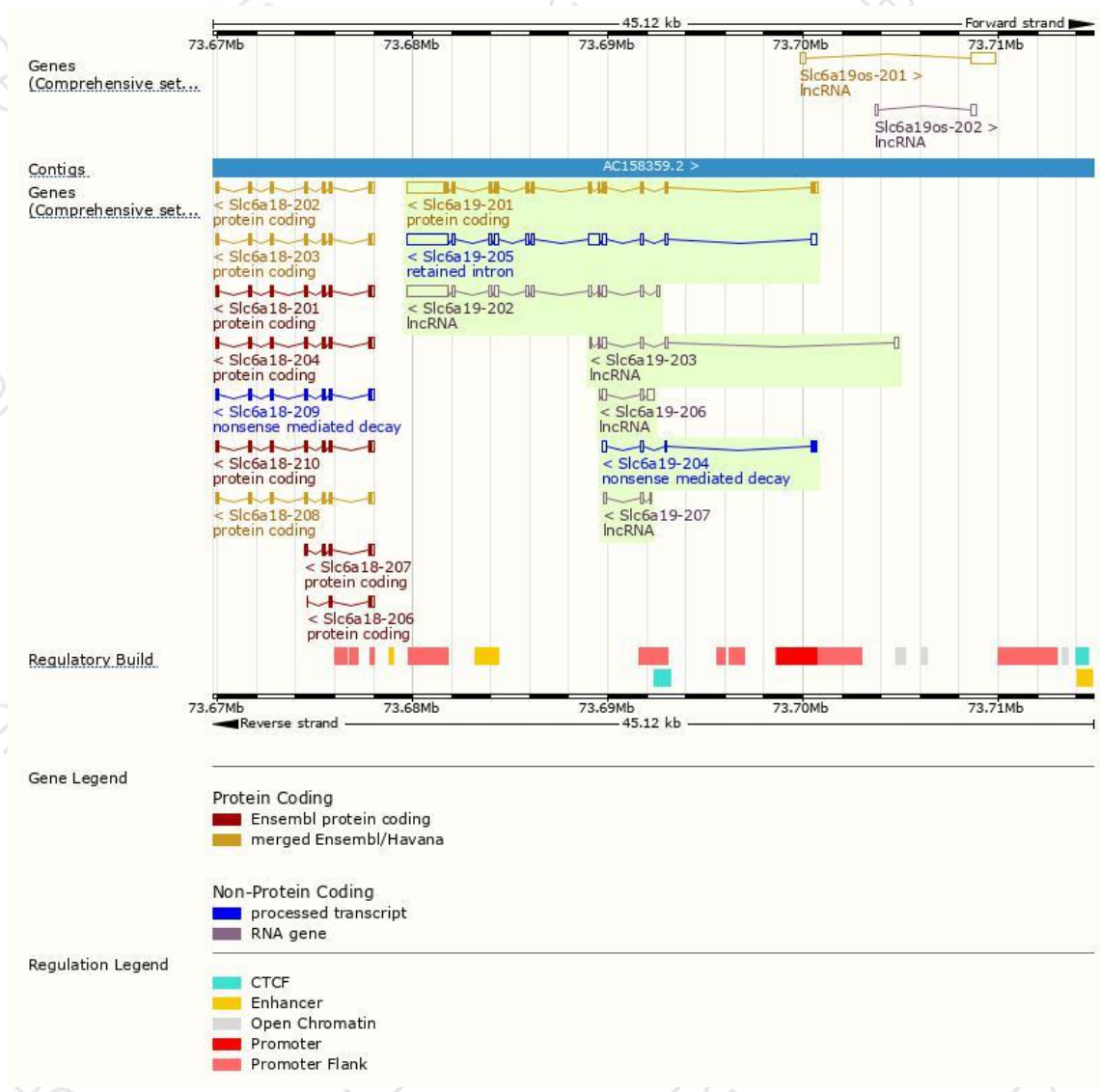
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc6a19-201	<a href="#">ENSMUST00000022048.5</a>	3936	<a href="#">634aa</a>	Protein coding	<a href="#">CCDS26634</a>	<a href="#">Q3KN89 Q9D687</a>	TSL:1 GENCODE basic APPRIS P1
Slc6a19-204	<a href="#">ENSMUST00000124406.7</a>	607	<a href="#">83aa</a>	Nonsense mediated decay	-	<a href="#">D6RJ80</a>	TSL:3
Slc6a19-205	<a href="#">ENSMUST00000132085.7</a>	4192	No protein	Retained intron	-	-	TSL:1
Slc6a19-202	<a href="#">ENSMUST00000120322.7</a>	3592	No protein	lncRNA	-	-	TSL:1
Slc6a19-203	<a href="#">ENSMUST00000123997.7</a>	839	No protein	lncRNA	-	-	TSL:5
Slc6a19-206	<a href="#">ENSMUST00000139087.7</a>	745	No protein	lncRNA	-	-	TSL:3
Slc6a19-207	<a href="#">ENSMUST00000140878.1</a>	360	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Slc6a19-201* transcript,The transcription is shown below

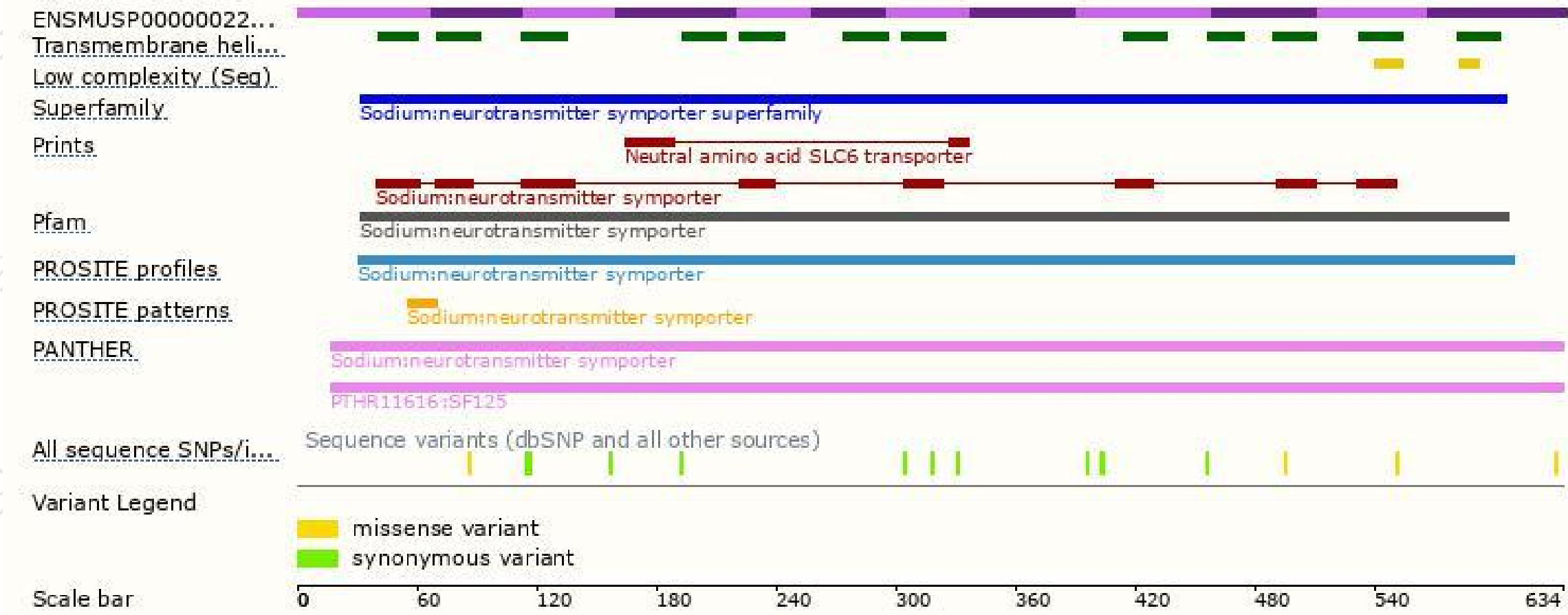


# Genomic location distribution

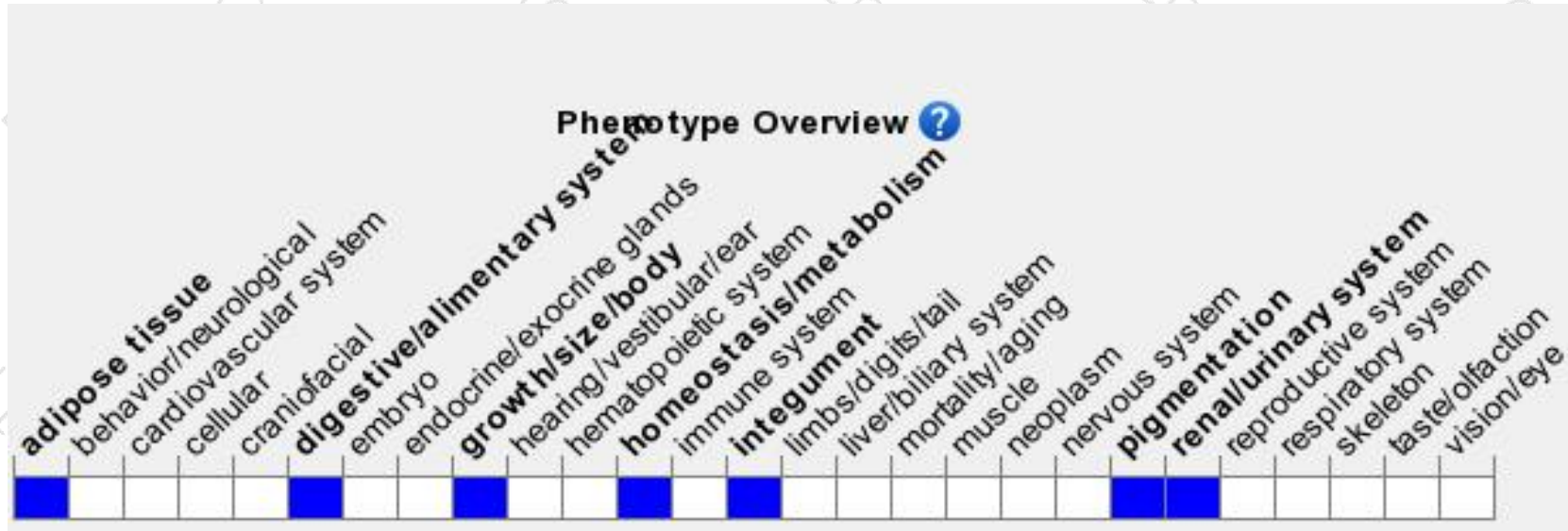




# Protein domain



# 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 decreased body weight and impaired amino acid absorption and excretion.

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

Tel: 400-9660890

