

Snx27 Cas9-KO Strategy

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Project Overview

Project Name

Snx27

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Snx27* gene. The schematic diagram is as follows:



- The *Snx27* gene has 8 transcripts. According to the structure of *Snx27* gene, exon2 of *Snx27-201* (ENSMUST00000029783.15) transcript is recommended as the knockout region. The region contains 232bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Snx27* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit prenatal and postnatal lethality, decreased organ size, slow postnatal weight gain, and decreased endocytosis of Grin2c.
- The *Snx27* gene is located on the Chr3. 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)

Snx27 sorting nexin family member 27 [Mus musculus (house mouse)]

Gene ID: 76742, updated on 19-Mar-2019

Summary



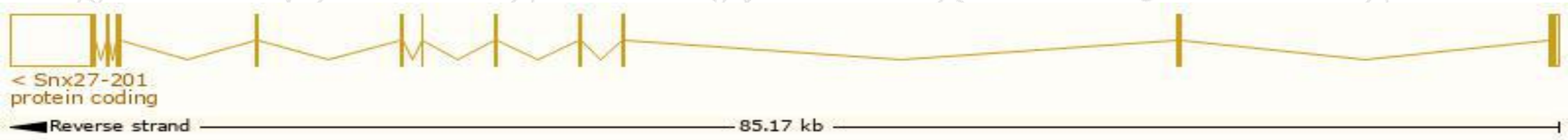
Official Symbol	Snx27 provided by MGI
Official Full Name	sorting nexin family member 27 provided by MGI
Primary source	MGI:MGI:1923992
See related	Ensembl:ENSMUSG00000028136
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	5730552M22Rik, ESTM45, ESTM47, R75405
Expression	Ubiquitous expression in CNS E18 (RPKM 6.3), cerebellum adult (RPKM 5.7) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

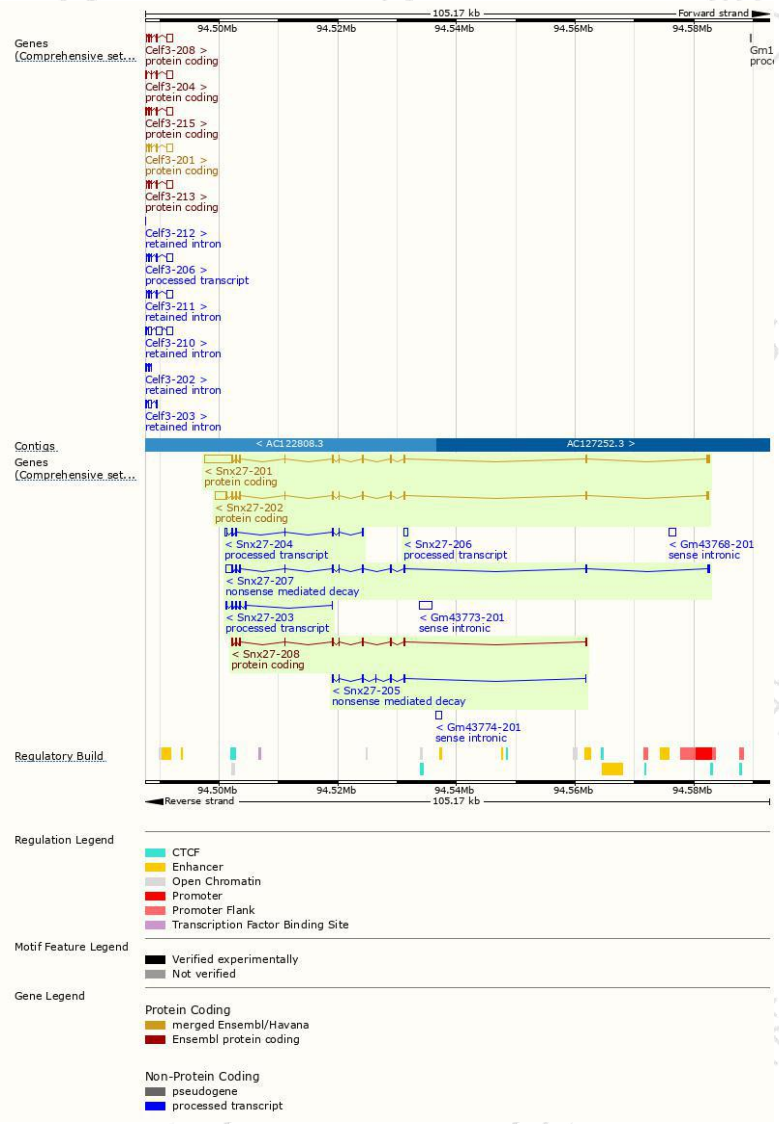
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Snx27-201	ENSMUST00000029783.15	6261	526aa	Protein coding	CCDS38538	Q3UHD6	TSL:1 GENCODE basic
Snx27-202	ENSMUST00000107283.7	3531	539aa	Protein coding	CCDS38537	Q3UHD6	TSL:1 GENCODE basic APPRIS P1
Snx27-208	ENSMUST00000200642.4	1308	435aa	Protein coding	-	A0A0G2JF85	TSL:5 GENCODE basic
Snx27-207	ENSMUST00000199462.4	2510	63aa	Nonsense mediated decay	-	A0A0G2JG07	TSL:5
Snx27-205	ENSMUST00000198426.1	599	110aa	Nonsense mediated decay	-	A0A0G2JGD5	CDS 5' incomplete TSL:3
Snx27-204	ENSMUST00000196675.4	734	No protein	Processed transcript	-	-	TSL:5
Snx27-206	ENSMUST00000198902.1	649	No protein	Processed transcript	-	-	TSL:NA
Snx27-203	ENSMUST00000196251.1	599	No protein	Processed transcript	-	-	TSL:5

The strategy is based on the design of *Snx27-201* transcript,The transcription is shown below



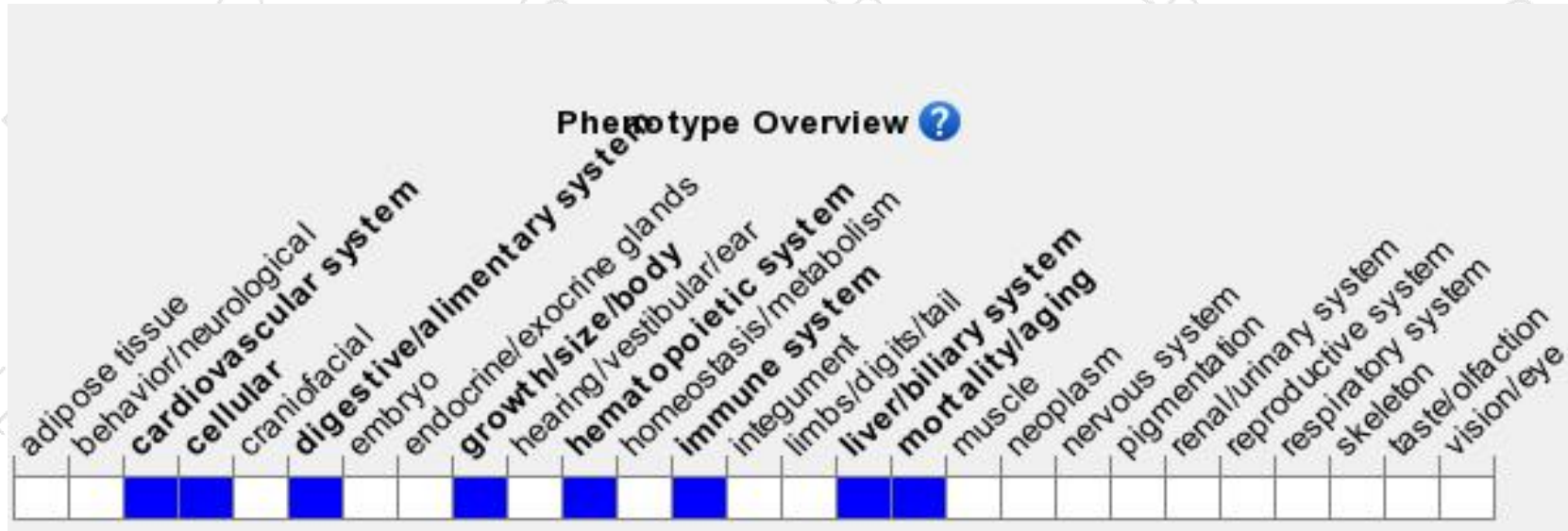
Genomic location distribution



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 prenatal and postnatal lethality, decreased organ size, slow postnatal weight gain, and decreased endocytosis of Grin2c.

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

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