

Slc20a2 Cas9-KO Strategy

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Project Overview

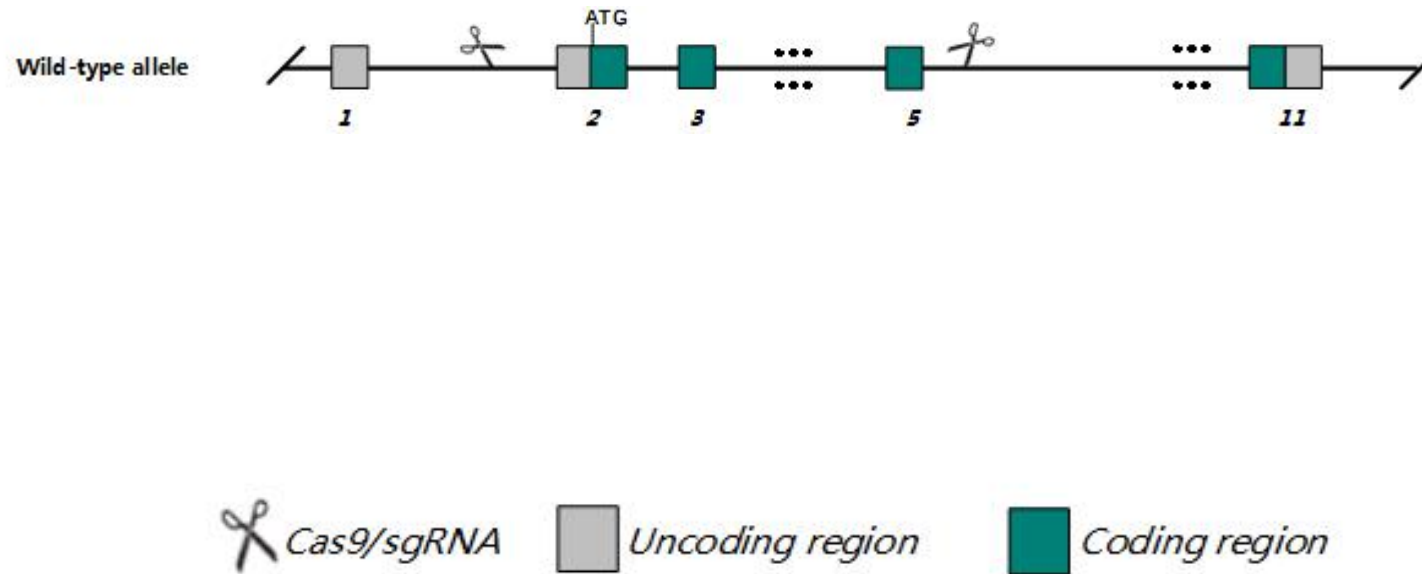
Project Name	<i>Slc20a2</i>
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Project type	Cas9-KO
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Strain background	C57BL/6JGpt
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Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc20a2* gene. The schematic diagram is as follows:



The *Slc20a2* gene has 5 transcripts. According to the structure of *Slc20a2* gene, exon2-exon5 of *Slc20a2-201* (ENSMUST00000067786.8) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Slc20a2* gene. The brief process is as follows: CRISPR/Cas9 system

According to the existing MGI data, Mice homozygous for a knock-out allele exhibit brain calcifications in the thalamus, basal ganglia and cerebral cortex, microgliosis, and a high inorganic phosphate concentration [Pi] in cerebrospinal fluid.

The *Slc20a2* gene is located on the Chr8. 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.

Slc20a2 solute carrier family 20, member 2 [Mus musculus (house mouse)]

Gene ID: 20516, updated on 31-Jan-2019

Summary



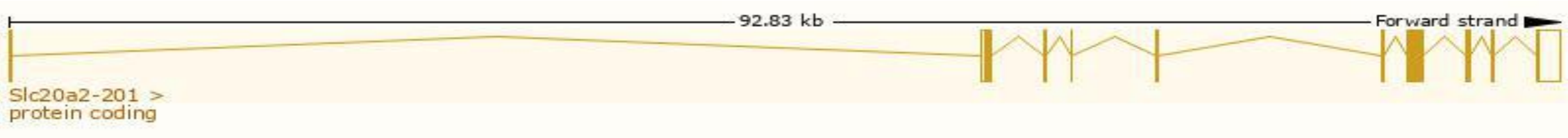
Official Symbol	Slc20a2 provided by MGI
Official Full Name	solute carrier family 20, member 2 provided by MGI
Primary source	MGI:MGI:97851
See related	Ensembl:ENSMUSG00000037656
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	MolPit2, Pit-2, Pit2, Ram-1, Ram1
Expression	Ubiquitous expression in heart adult (RPKM 44.7), cerebellum adult (RPKM 21.7) and 28 other tissues See more
Orthologs	human all

Transcript information Ensembl

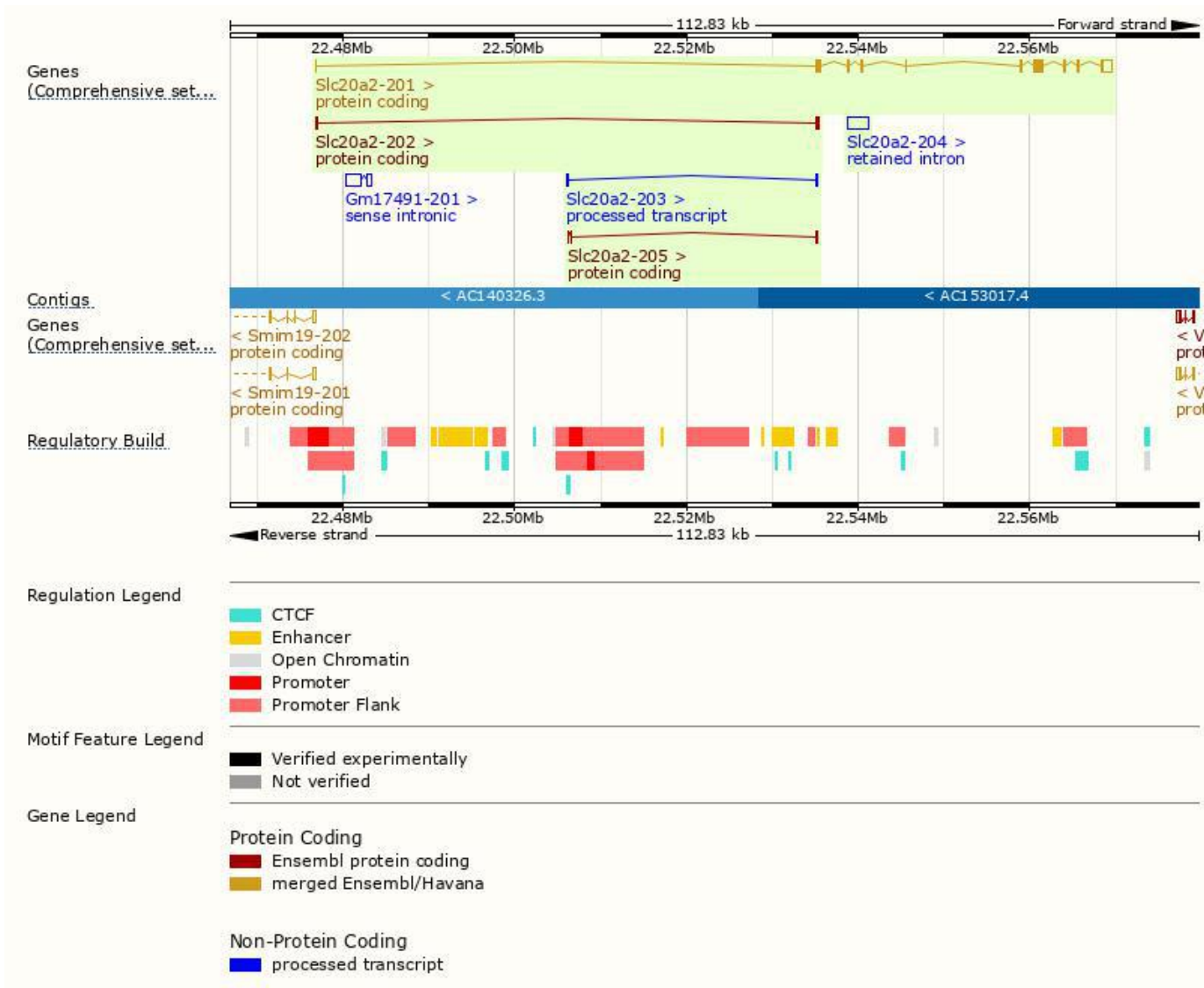
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc20a2-201	ENSMUST00000067786.8	3566	656aa	Protein coding	CCDS22178	Q80UP8	TSL:1 GENCODE basic APPRIS P1
Slc20a2-202	ENSMUST00000209305.1	490	28aa	Protein coding	-	A0A1B0GR62	CDS 3' incomplete TSL:2
Slc20a2-205	ENSMUST00000210854.1	436	10aa	Protein coding	-	A0A1B0GRL3	CDS 3' incomplete TSL:2
Slc20a2-203	ENSMUST00000209347.1	371	No protein	Processed transcript	-	-	TSL:3
Slc20a2-204	ENSMUST00000210388.1	2522	No protein	Retained intron	-	-	TSL:NA

The strategy is based on the design of *Slc20a2-201* transcript,The transcription is shown below



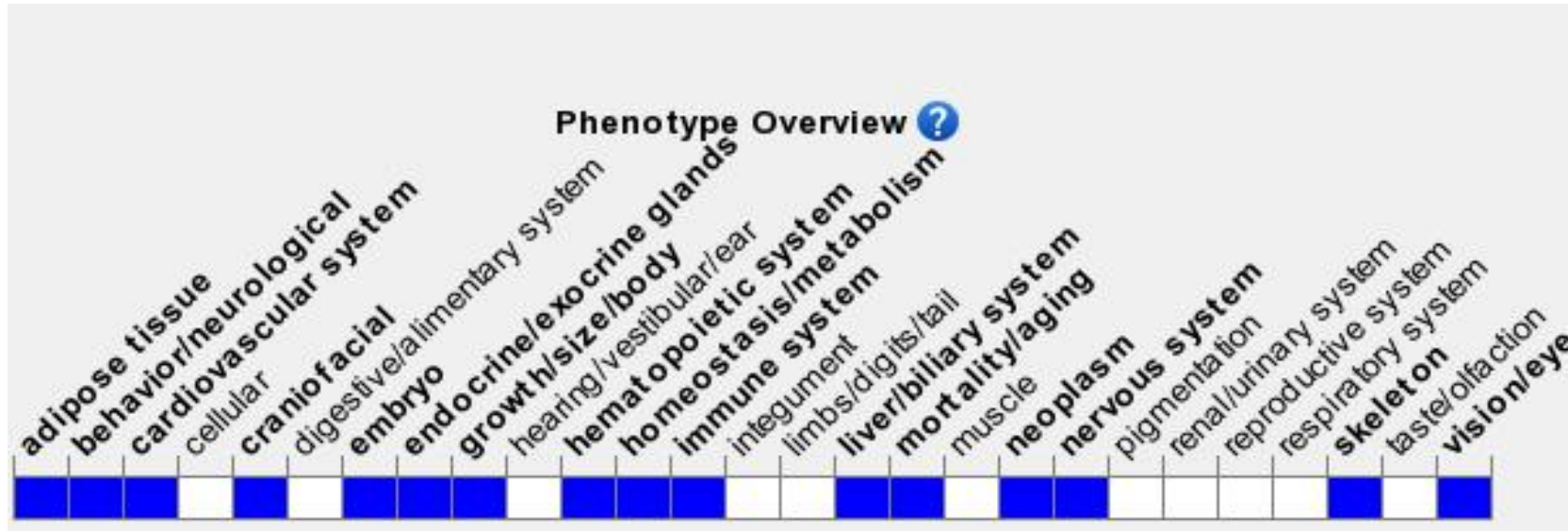
Genomic location distribution



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 brain calcifications in the thalamus, basal ganglia and cerebral cortex, microgliosis, and a high inorganic phosphate concentration [Pi] in cerebrospinal fluid.

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