Slc20a1 Cas9-KO Strategy

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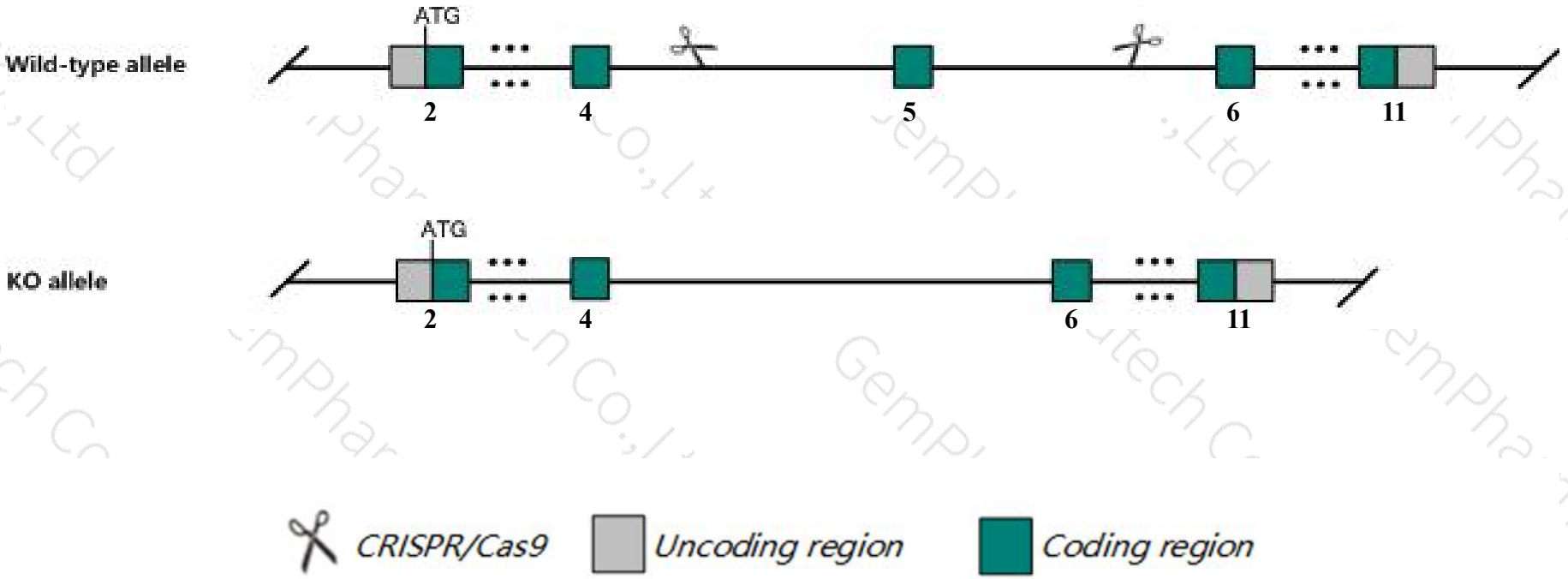
Project Overview

Project Name	***Slc20a1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc20a1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Slc20a1* gene has 8 transcripts. According to the structure of *Slc20a1* gene, exon5 of *Slc20a1-201* (ENSMUST00000028880.9) transcript is recommended as the knockout region.The region contains 97bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Slc20a1* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

- According to the existing MGI data,Mice homozygous for a knock-out allele exhibit mid-gestation lethality associated with abnormal vitelline vasculature, growth retardation, and anemia.

- The *Slc20a1* gene is located on the Chr2. 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）

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Slc20a1 solute carrier family 20, member 1 [Mus musculus (house mouse)]

Gene ID: 20515, updated on 31-Jan-2019

Summary

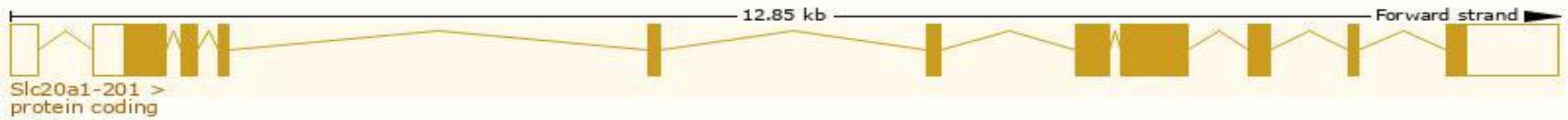
Official Symbol	Slc20a1 provided by MGI
Official Full Name	solute carrier family 20, member 1 provided byMGI
Primary source	MGI:MGI:108392
See related	Ensembl:ENSMUSG00000027397
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI607883, Glvr-1, Glvr1
Expression	Ubiquitous expression in colon adult (RPKM 22.0), frontal lobe adult (RPKM 18.6) and 27 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

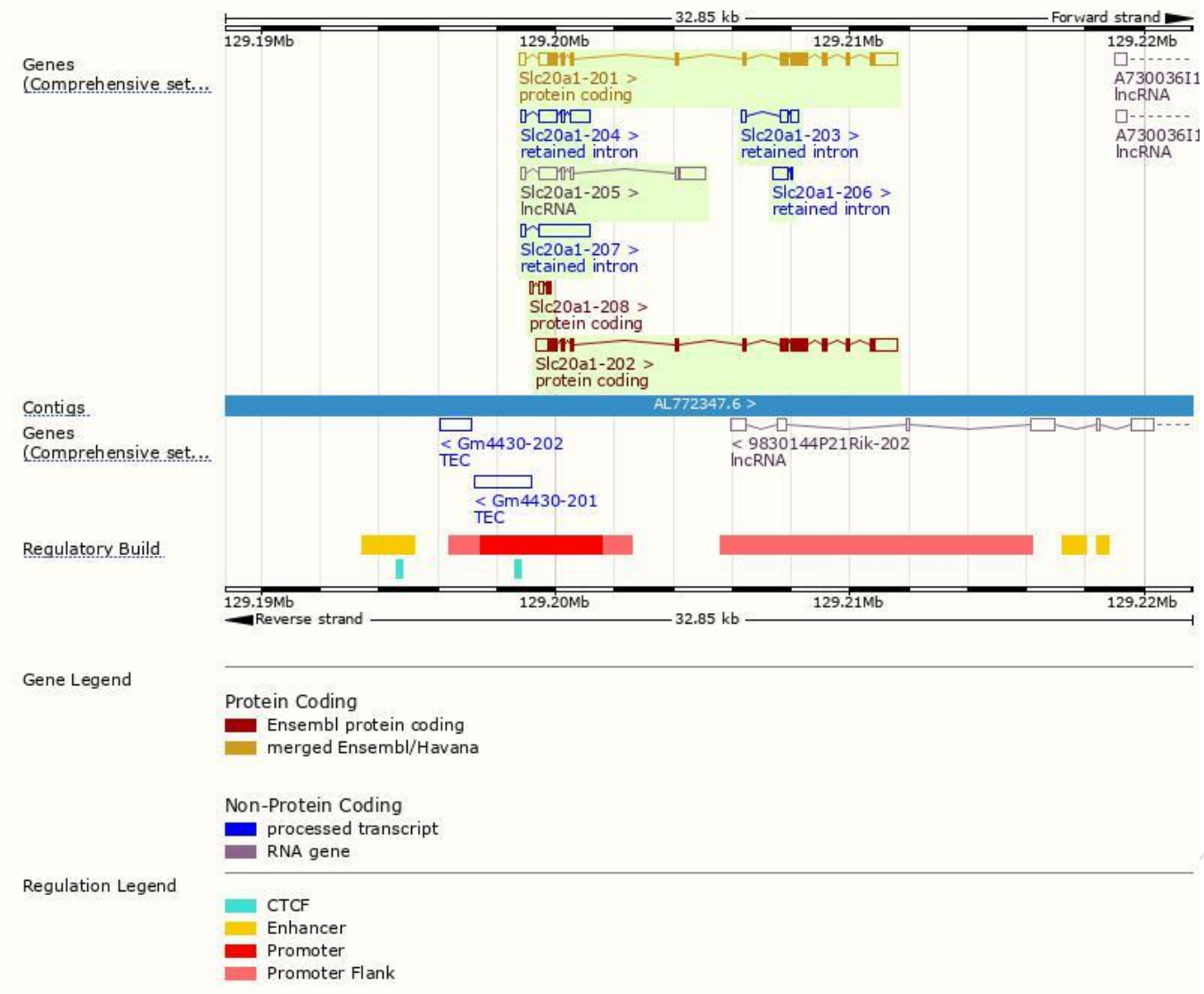
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc20a1-201	ENSMUST00000028880.9	3316	681aa	Protein coding	CCDS16722	Q61609	TSL:1 GENCODE basic APPRIS P1
Slc20a1-202	ENSMUST00000110315.1	3219	681aa	Protein coding	CCDS16722	Q61609	TSL:1 GENCODE basic APPRIS P1
Slc20a1-208	ENSMUST00000148988.1	347	32aa	Protein coding	-	B0R035	CDS 3' incomplete TSL:3
Slc20a1-207	ENSMUST00000144744.7	1918	No protein	Retained intron	-	-	TSL:1
Slc20a1-204	ENSMUST00000140907.7	1628	No protein	Retained intron	-	-	TSL:1
Slc20a1-203	ENSMUST00000125714.1	712	No protein	Retained intron	-	-	TSL:2
Slc20a1-206	ENSMUST00000144025.1	552	No protein	Retained intron	-	-	TSL:3
Slc20a1-205	ENSMUST00000141285.1	1989	No protein	lncRNA	-	-	TSL:1

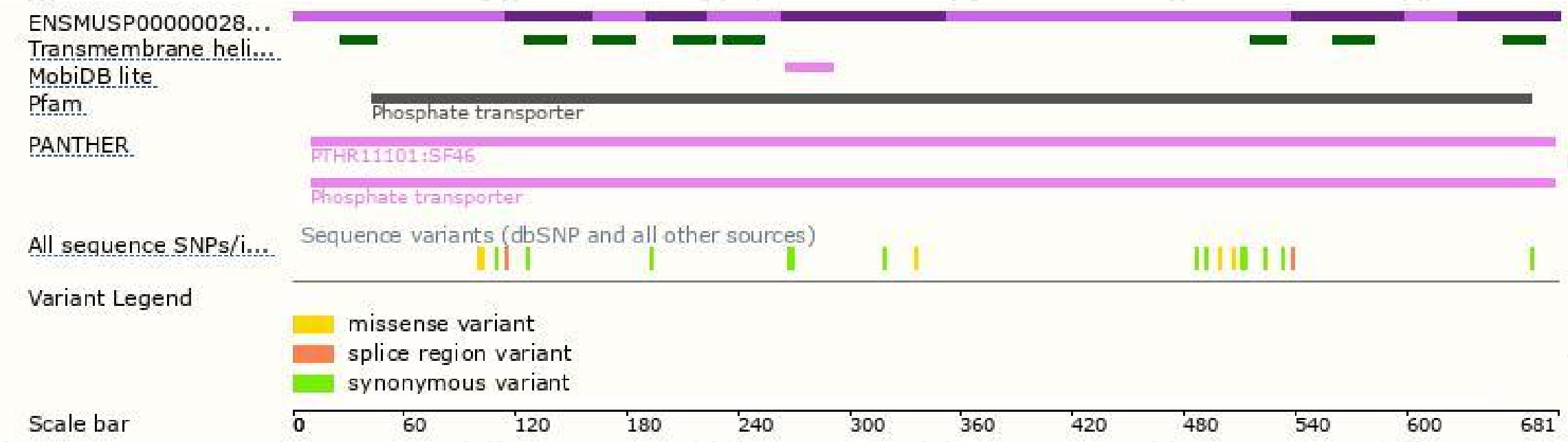
The strategy is based on the design of *Slc20a1-201* transcript,The transcription is shown below



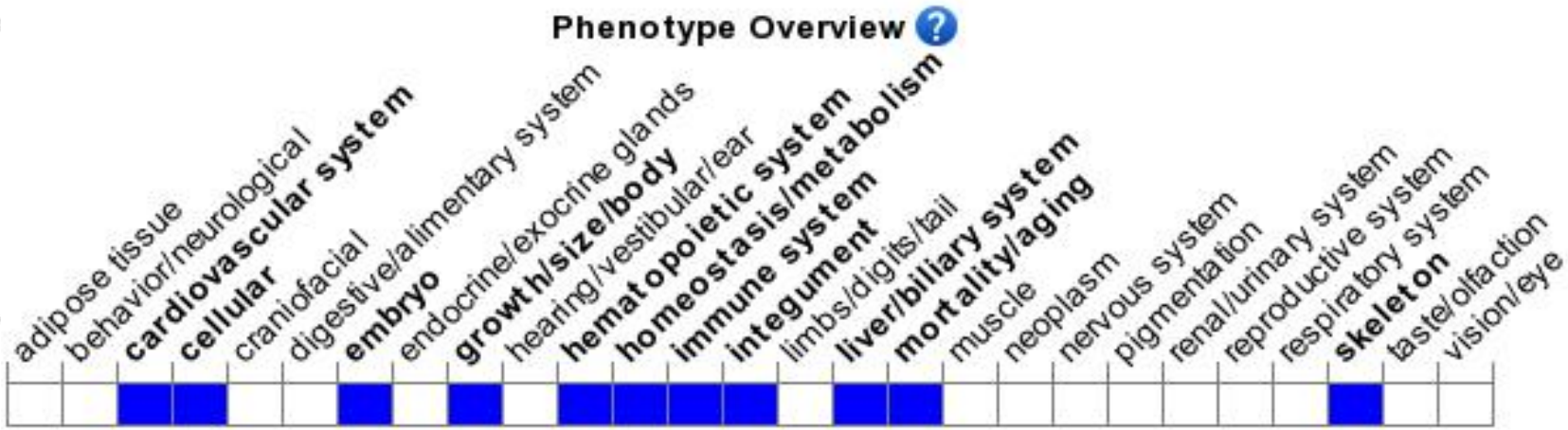
Genomic location distribution



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 mid-gestation lethality associated with abnormal vitelline vasculature, growth retardation, and anemia.

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

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