

Slc16a3 Cas9-CKO Strategy

Designer:

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Design Date:

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Project Overview

Project Name

Slc16a3

Project type

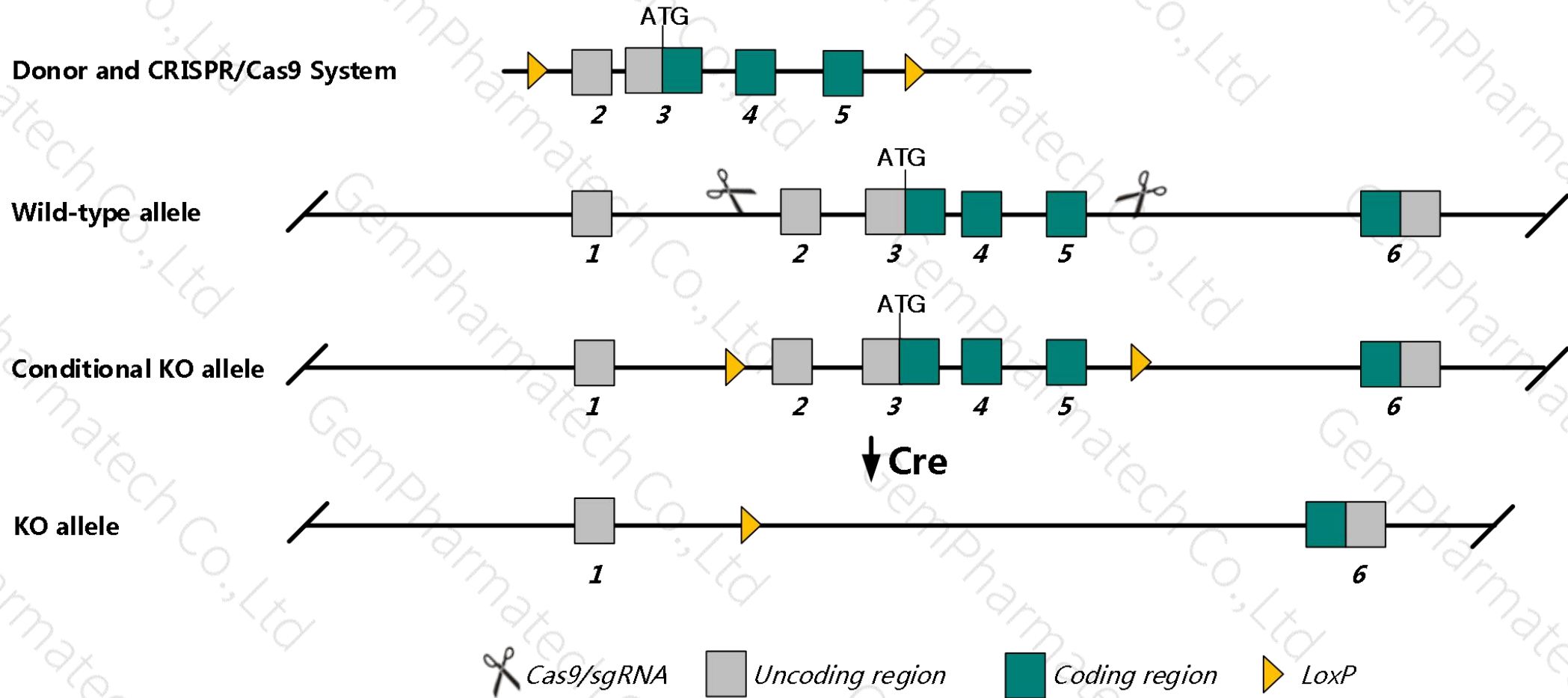
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc16a3* gene. The schematic diagram is as follows:



- The *Slc16a3* gene has 8 transcripts. According to the structure of *Slc16a3* gene, exon2-exon5 of *Slc16a3-201* (ENSMUST00000070653.12) transcript is recommended as the knockout region. The region contains the initiation codon ATG coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Slc16a3* gene. The brief process is as follows: CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice

- The *Slc16a3* gene is located on the Chr11. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Slc16a3 solute carrier family 16 (monocarboxylic acid transporters), member 3 [Mus musculus (house mouse)]

Gene ID: 80879, updated on 3-Feb-2019

Summary



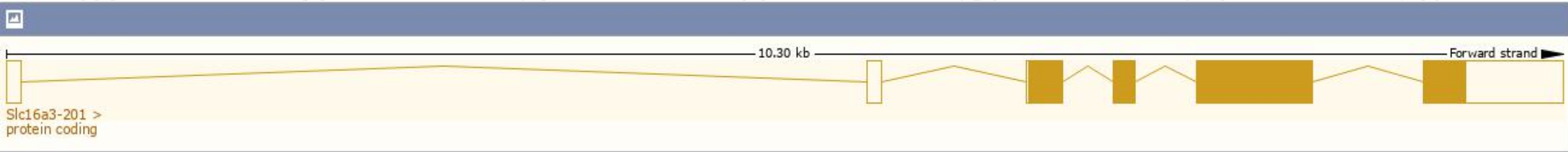
Official Symbol	Slc16a3 provided by MGI
Official Full Name	solute carrier family 16 (monocarboxylic acid transporters), member 3 provided by MGI
Primary source	MGI:MGI:1933438
See related	Ensembl:ENSMUSG000000025161
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Mct3, Mct4
Expression	Broad expression in placenta adult (RPKM 14.2), duodenum adult (RPKM 13.7) and 22 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

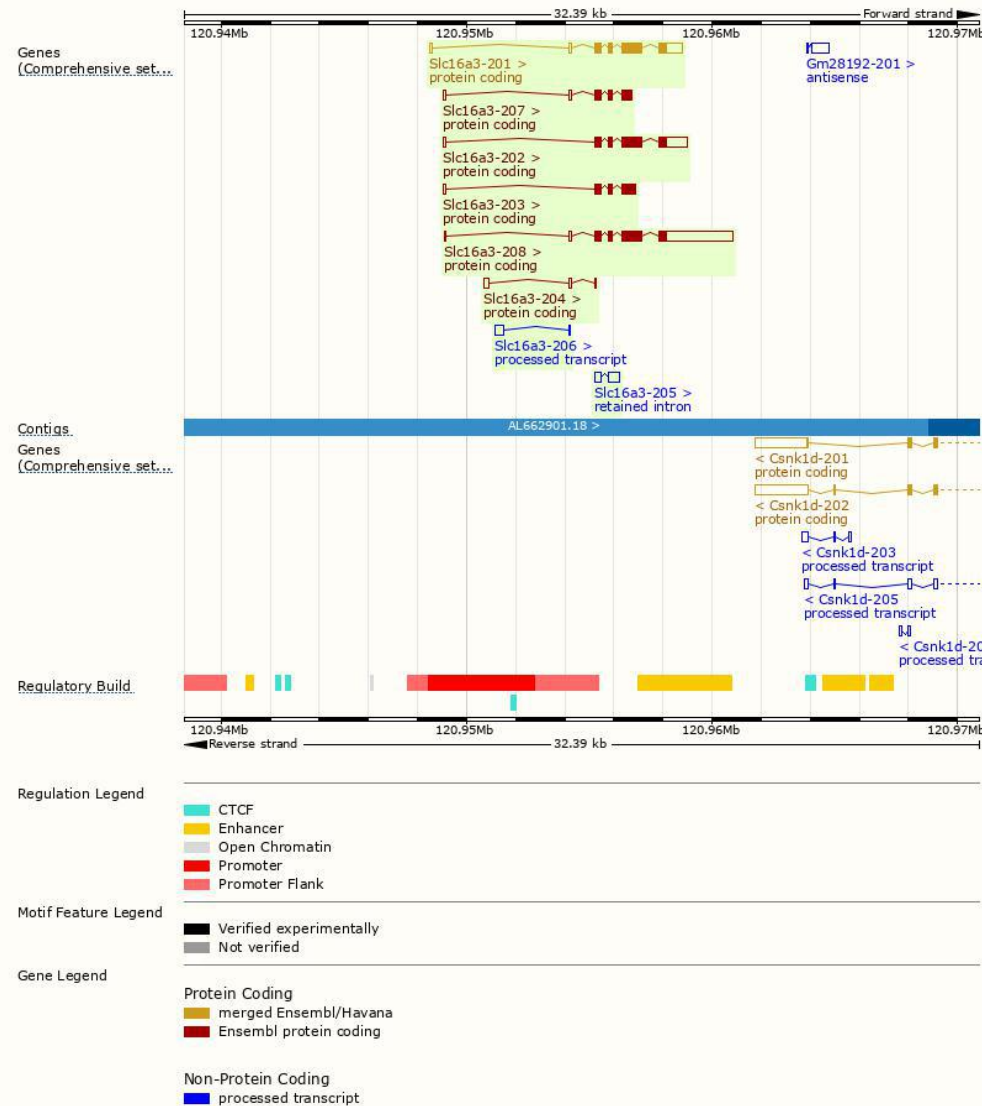
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc16a3-208	ENSMUST00000168579.7	4335	470aa	Protein coding	CCDS25761	P57787 Q3UDP9	TSL:1 GENCODE basic APPRIS P1
Slc16a3-202	ENSMUST00000100130.9	2386	470aa	Protein coding	CCDS25761	P57787 Q3UDP9	TSL:1 GENCODE basic APPRIS P1
Slc16a3-201	ENSMUST00000070653.12	2272	470aa	Protein coding	CCDS25761	P57787 Q3UDP9	TSL:1 GENCODE basic APPRIS P1
Slc16a3-203	ENSMUST00000129473.7	975	291aa	Protein coding	-	B1ATM2	CDS 3' incomplete TSL:3
Slc16a3-207	ENSMUST00000154187.7	974	253aa	Protein coding	-	B1ATM1	CDS 3' incomplete TSL:2
Slc16a3-204	ENSMUST00000133029.1	353	9aa	Protein coding	-	A0A0G2JD98	CDS 3' incomplete TSL:3
Slc16a3-206	ENSMUST00000140467.1	395	No protein	Processed transcript	-	-	TSL:3
Slc16a3-205	ENSMUST00000134540.1	677	No protein	Retained intron	-	-	TSL:2

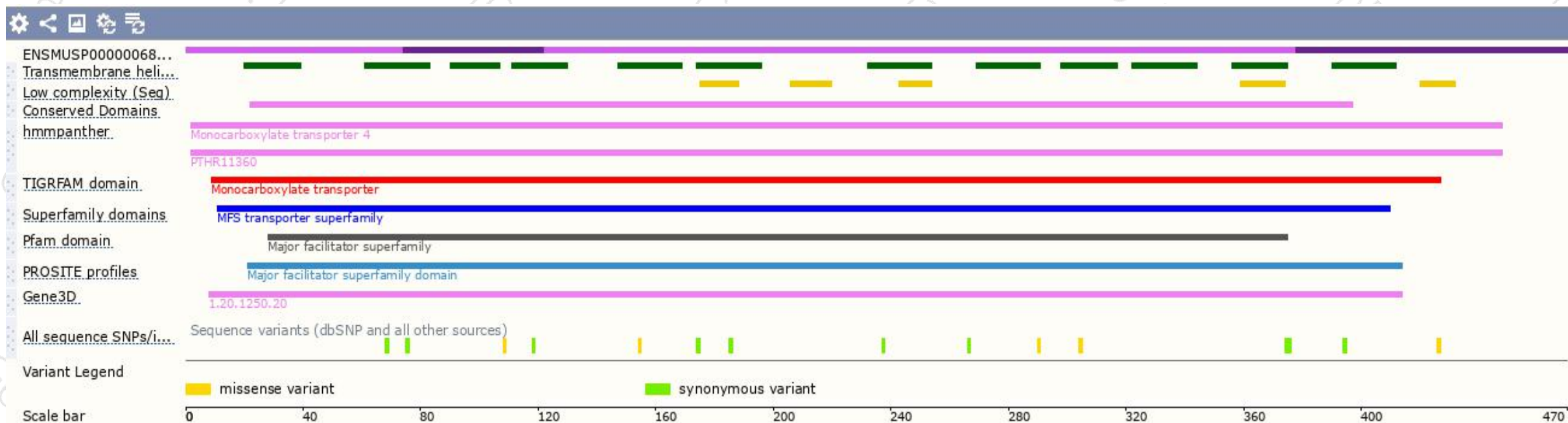
The strategy is based on the design of *Slc16a3-201* transcript,The transcription is shown below



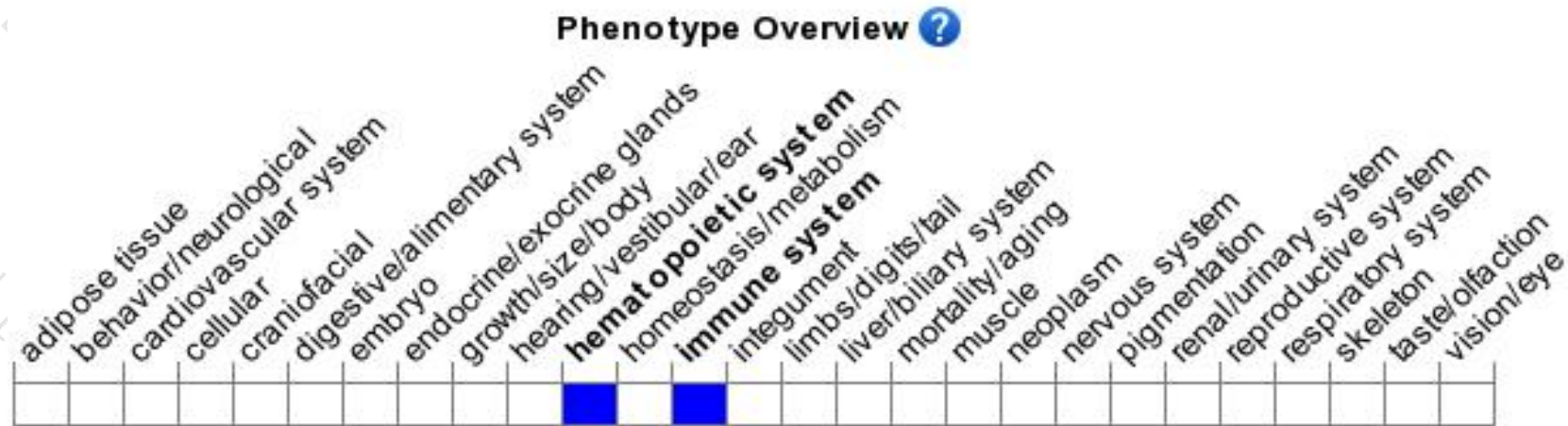
Genomic location distribution



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/>).

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

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