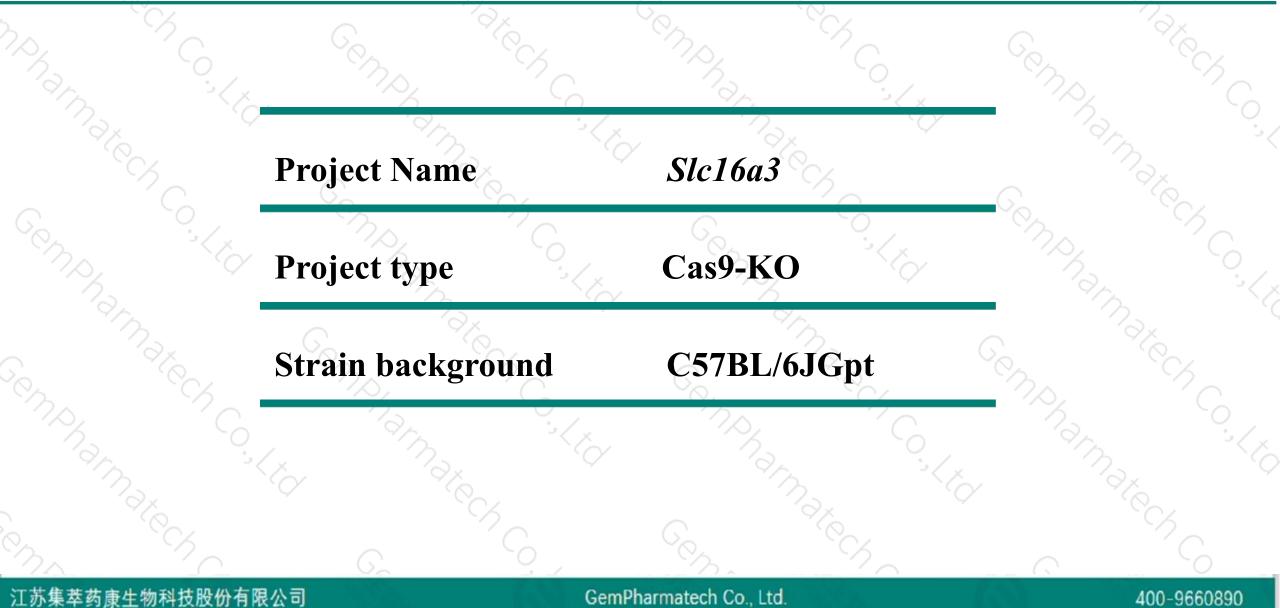


Slc16a3 Cas9-KO Strategy

Designer: Design Date: Yupeng Yang 2019-7-26

Project Overview

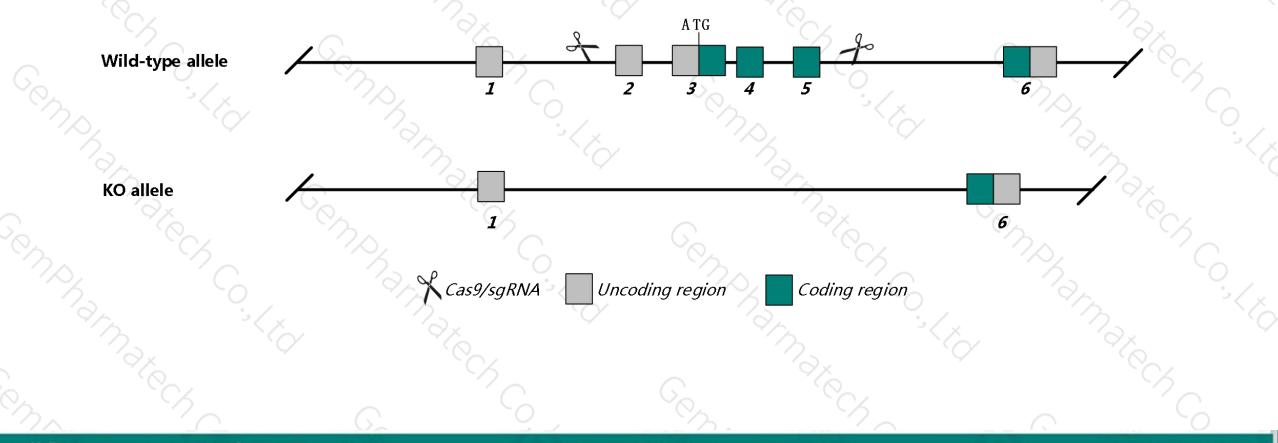




Knockout strategy



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



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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 t



- 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 knockout on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)



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SIc16a3 solute carrier family 16 (monocarboxylic acid transporters), member 3 [Mus musculus (house mouse)]

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

Summary

Official Symbol	SIc16a3 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:ENSMUSG0000025161
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

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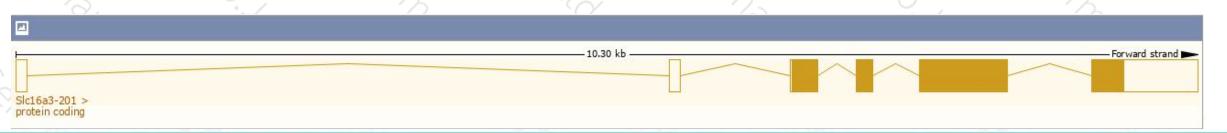
Transcript information (Ensembl)



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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags		
SIc16a3-208	ENSMUST00000168579.7	4335	<u>470aa</u>	Protein coding	CCDS25761	P57787 Q3UDP9	TSL:1 GENCODE basic APPRIS P1		
SIc16a3-202	ENSMUST00000100130.9	2386	<u>470aa</u>	Protein coding	CCDS25761	P57787 Q3UDP9	9 TSL:1 GENCODE basic APPRIS P1		
SIc16a3-201	ENSMUST00000070653.12	2272	<u>470aa</u>	Protein coding	CCDS25761	P57787 Q3UDP9	TSL:1 GENCODE basic APPRIS P1		
SIc16a3-203	ENSMUST00000129473.7	975	<u>291aa</u>	Protein coding	121	B1ATM2	CDS 3' incomplete TSL:3		
SIc16a3-207	ENSMUST00000154187.7	974	<u>253aa</u>	Protein coding	(75)	B1ATM1	CDS 3' incomplete TSL:2		
SIc16a3-204	ENSMUST00000133029.1	353	<u>9aa</u>	Protein coding	(1 1)	A0A0G2JD98	CDS 3' incomplete TSL:3		
SIc16a3-206	ENSMUST00000140467.1	395	No protein	Processed transcript	120	34	TSL:3		
Sic16a3-205	ENSMUST00000134540.1	677	No protein	Retained intron	121	62	TSL:2		

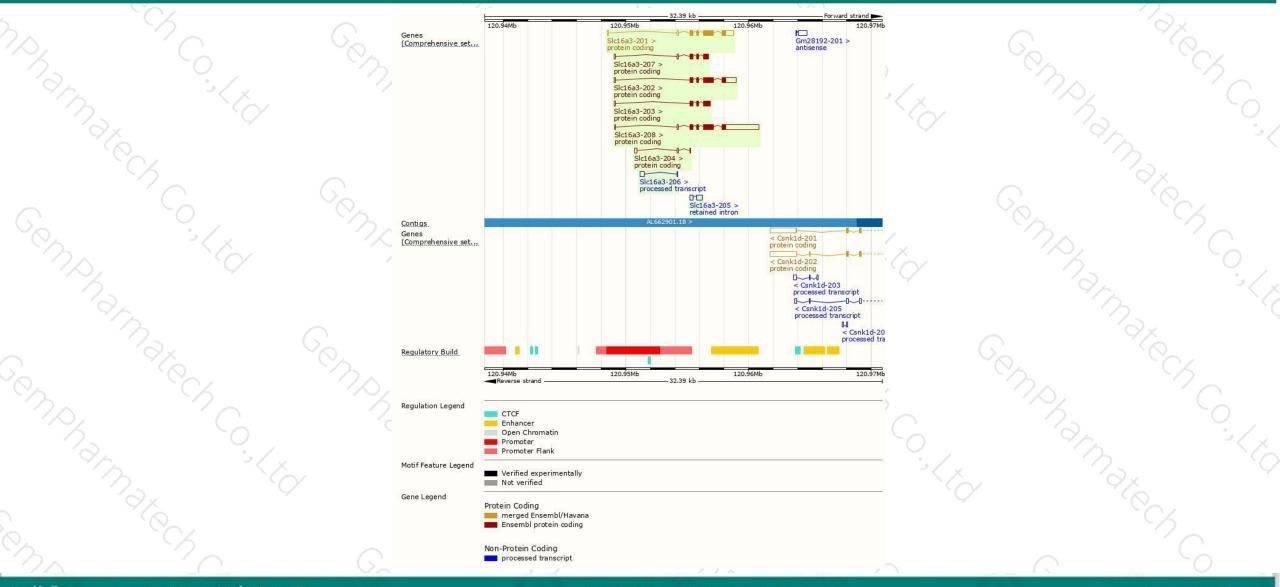
The strategy is based on the design of Slc16a3-201 transcript, The transcription is shown below



Genomic location distribution



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Protein domain



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	PTHR11360						
TIGRFAM domain	Monocarboxylate transporter					<i></i>	N N
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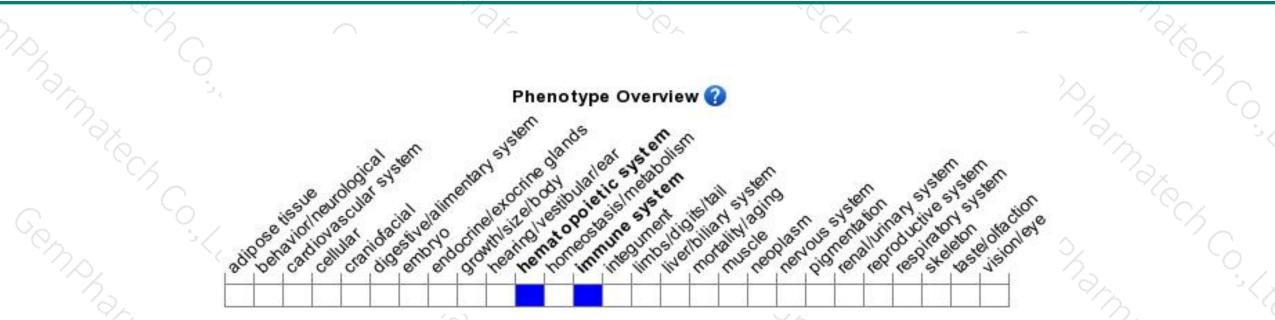
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# Mouse phenotype description(MGI)





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. Tel: 400-9660890



