

# Slc38a8 Cas9-KO Strategy

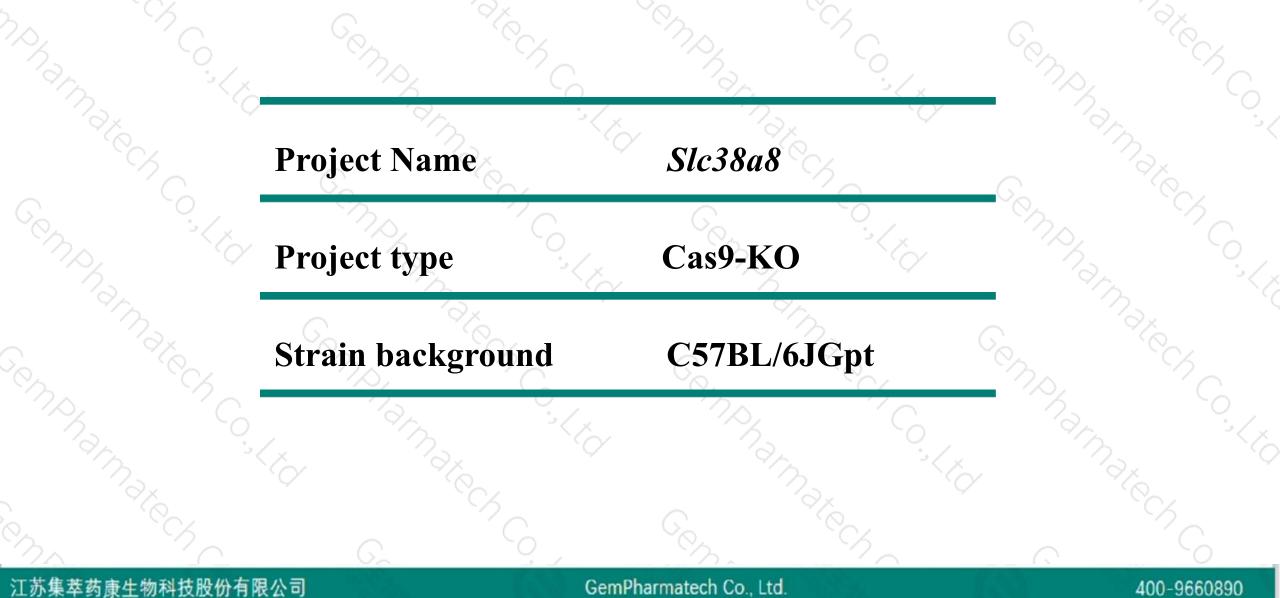
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Reviewer: Ruiuri Zhang

Design Date: 2020-4-28

### **Project Overview**

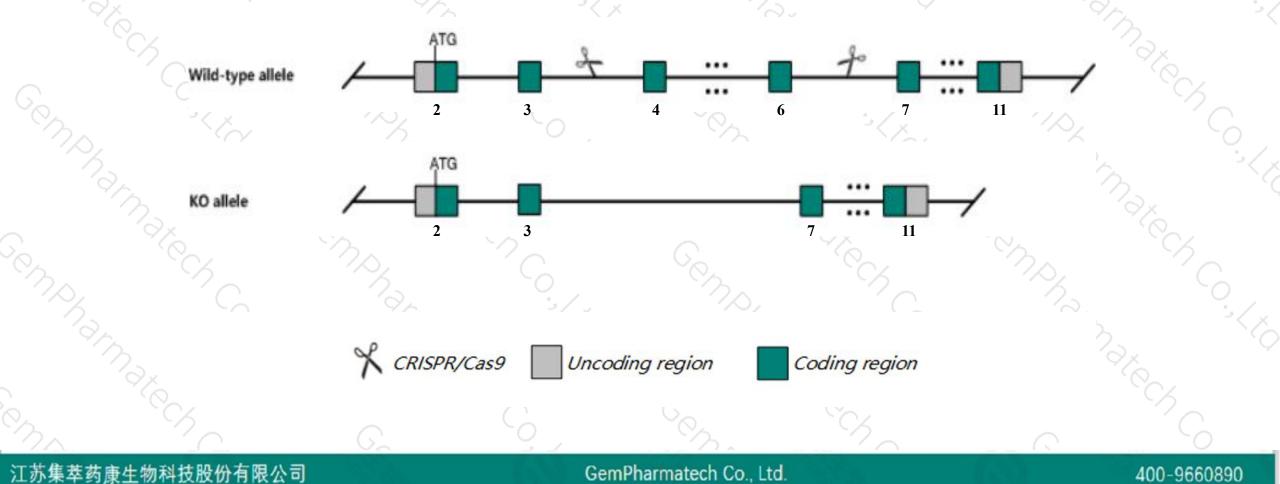




## **Knockout** strategy



This model will use CRISPR/Cas9 technology to edit the *Slc38a8* gene. The schematic diagram is as follows:





- The Slc38a8 gene has 5 transcripts. According to the structure of Slc38a8 gene, exon4-exon6 of Slc38a8-201 (ENSMUST00000036748.14) transcript is recommended as the knockout region. The region contains 293bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Slc38a8 gene. The brief process is as follows: CRISPR/Cas9 system v

## Notice



- The Slc38a8 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.

# Gene information (NCBI)



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SIc38a8 solute carrier family 38, member 8 [ Mus musculus (house mouse) ]

Gene ID: 234788, updated on 13-Mar-2020

#### Summary

 Official Symbol
 Slc38a8 provided by MGI

 Official Full Name
 solute carrier family 38, member 8 provided by MGI

 Primary source
 MGI:MGI:2685433

 See related
 Ensembl:ENSMUSG0000034224

 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; Muridae; Murinae; Mus; Mus

 Also known as
 Gm587

 Expression
 Low expression observed in reference dataset See more

 Orthologs
 human all

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# **Transcript information (Ensembl)**



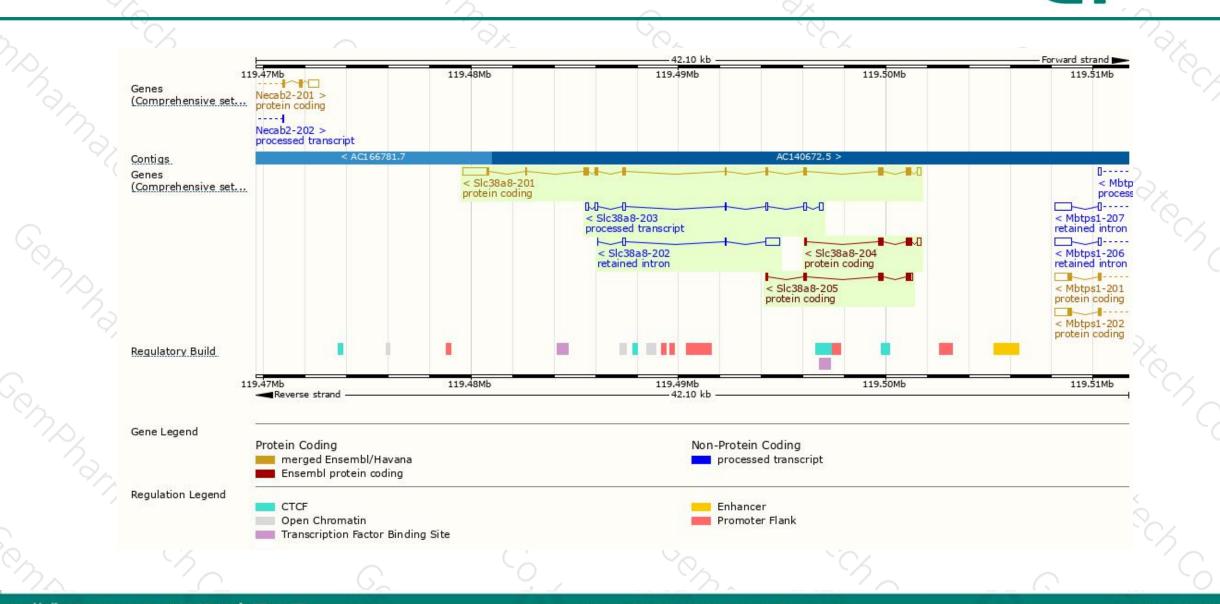
The gene has 5 transcripts, all transcripts are shown below:

Name 🖕	Transcript ID	bp 🖕	Protein 🖕	Biotype 💧	CCDS	UniProt 🖕	Flags		
SIc38a8-201	ENSMUST0000036748.14	2623	<u>432aa</u>	Protein coding	CCDS22706	<u>Q5HZH7</u> ₽	TSL:1 GENCODE basic APPRIS P1		
SIc38a8-205	ENSMUST00000138061.7	724	<u>206aa</u>	Protein coding	-	<u>D3Z7F9</u> ₽	CDS 3' incomplete TSL:3		
SIc38a8-204	ENSMUST00000133821.1	719	<u>165aa</u>	Protein coding	12	D3YUL2@	CDS 3' incomplete TSL:3		
SIc38a8-203	ENSMUST00000132838.7	869	No protein	Processed transcript	12		TSL:3		
SIc38a8-202	ENSMUST00000125594.1	899	No protein	Retained intron	1		TSL:5		

The strategy is based on the design of Slc38a8-201 transcript, the transcription is shown below



# **Genomic location distribution**



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# **Protein domain**



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	ENSMUSP00000038 Transmembrane heli Low complexity (Seg) Pfam	Amino acid tr	ansporter, transmembra	ne domain						
	PANTHER All sequence SNPs/i Variant Legend	PTHR22950;SF226 PTHR22950 Sequence variants (c	bSNP and all other so	urces)	ĩ	1 1	ī i î	0.00	1 1	) 5<
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If you have any questions, you are welcome to inquire. Tel: 400-9660890



