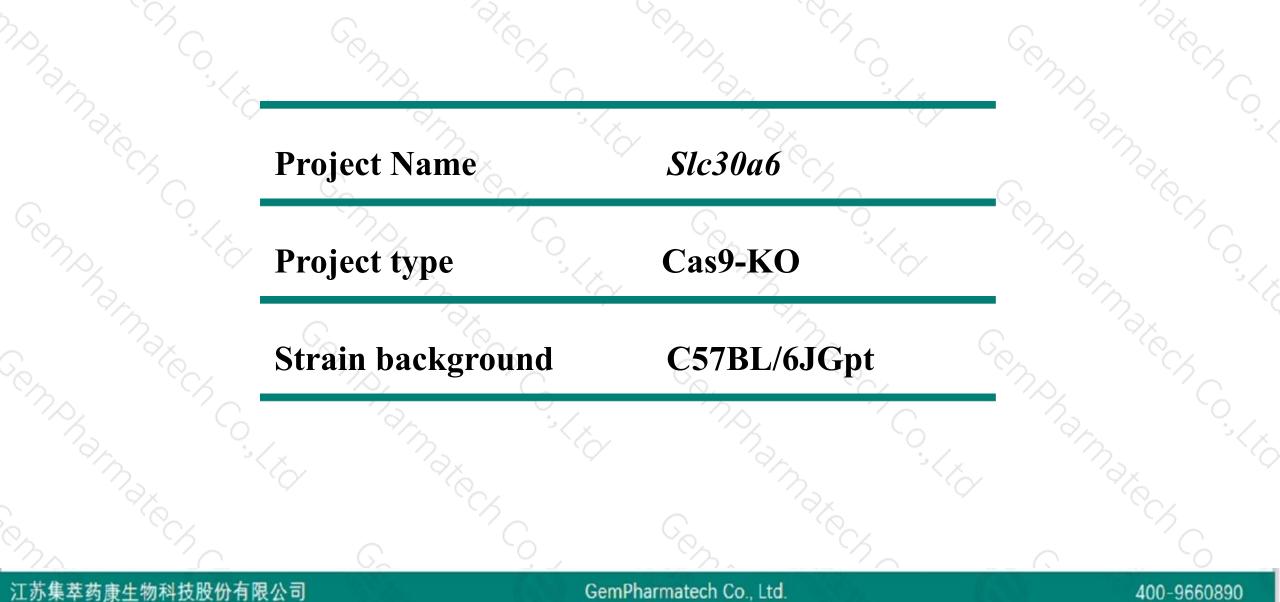


Slc30a6 Cas9-KO Strategy

Designer: Xueting Zhang Reviewer:Yanhua Shen Date:2020-03-03

Project Overview

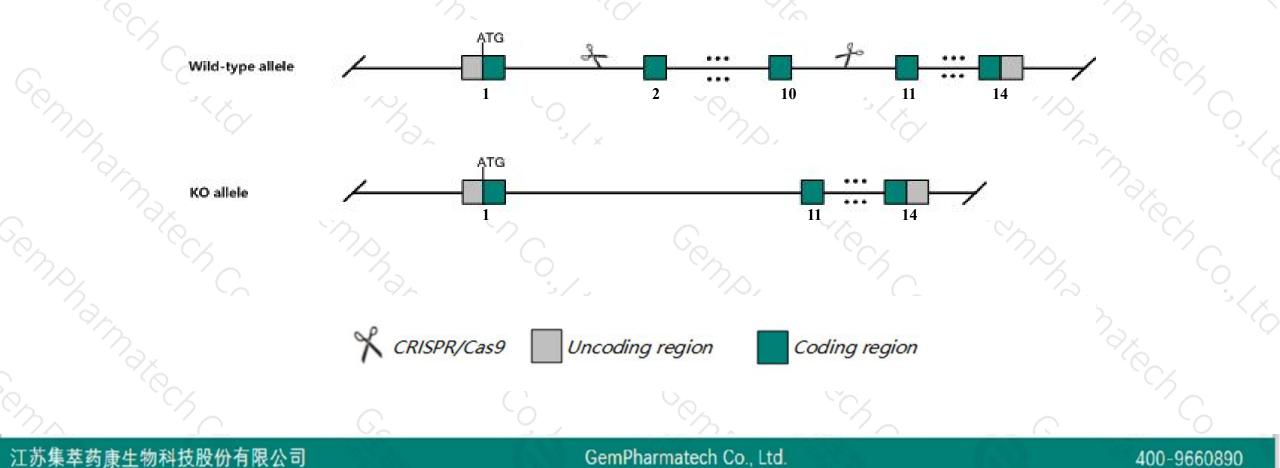




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Slc30a6 gene. The schematic diagram is as follows:





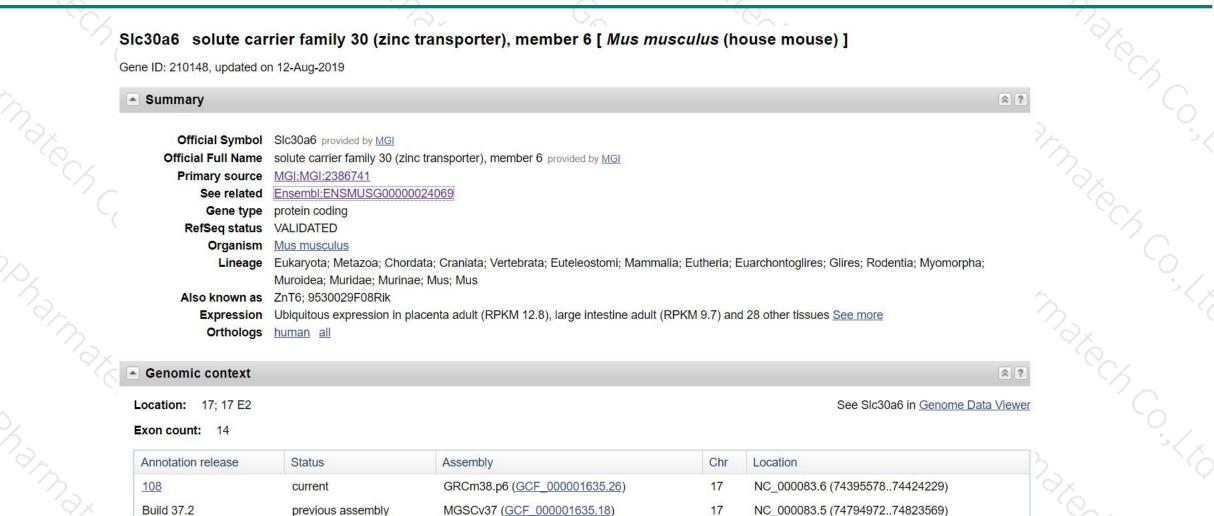
- The Slc30a6 gene has 9 transcripts. According to the structure of Slc30a6 gene, exon2-exon10 of Slc30a6-201 (ENSMUST0000024870.8) transcript is recommended as the knockout region. The region contains 662bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Slc30a6 gene. The brief process is as follows: CRISPR/Cas9 syste

- The Slc30a6 gene is located on the Chr17. 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.

Notice

Gene information (NCBI)





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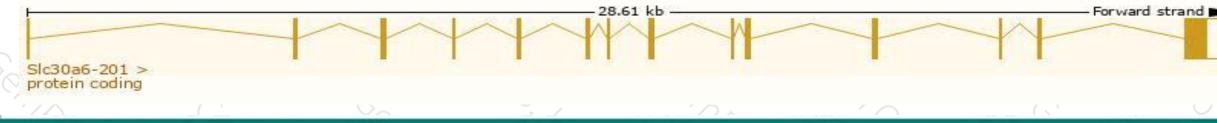
Transcript information (Ensembl)



The gene has 9 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags		
SIc30a6-201	ENSMUST00000024870.8	2148	<u>460aa</u>	Protein coding	CCDS37691	Q8BJM5	TSL:1 GENCODE basic APPRIS P		
SIc30a6-202	ENSMUST00000179074.8	1938	<u>465aa</u>	Protein coding	CCDS57109	J3QMX8	TSL:1 GENCODE basic		
SIc30a6-207	ENSMUST00000233799.1	600	<u>187aa</u>	Protein coding	2	A0A3B2WCC9	CDS 3' incomplete		
SIc30a6-204	ENSMUST00000233042.1	545	<u>104aa</u>	Protein coding	-	A0A3B2WCW5	GENCODE basic		
SIc30a6-208	ENSMUST00000234515.1	1589	<u>147aa</u>	Nonsense mediated decay	ā	ā			
SIc30a6-209	ENSMUST00000235003.1	1507	<u>181aa</u>	Nonsense mediated decay	-	-			
SIc30a6-203	ENSMUST00000232866.1	813	<u>140aa</u>	Nonsense mediated decay		A0A3B2WCJ8	CDS 5' incomplete		
SIc30a6-205	ENSMUST00000233157.1	816	No protein	Retained intron	-	-			
SIc30a6-206	ENSMUST00000233180.1	770	No protein	Retained intron					

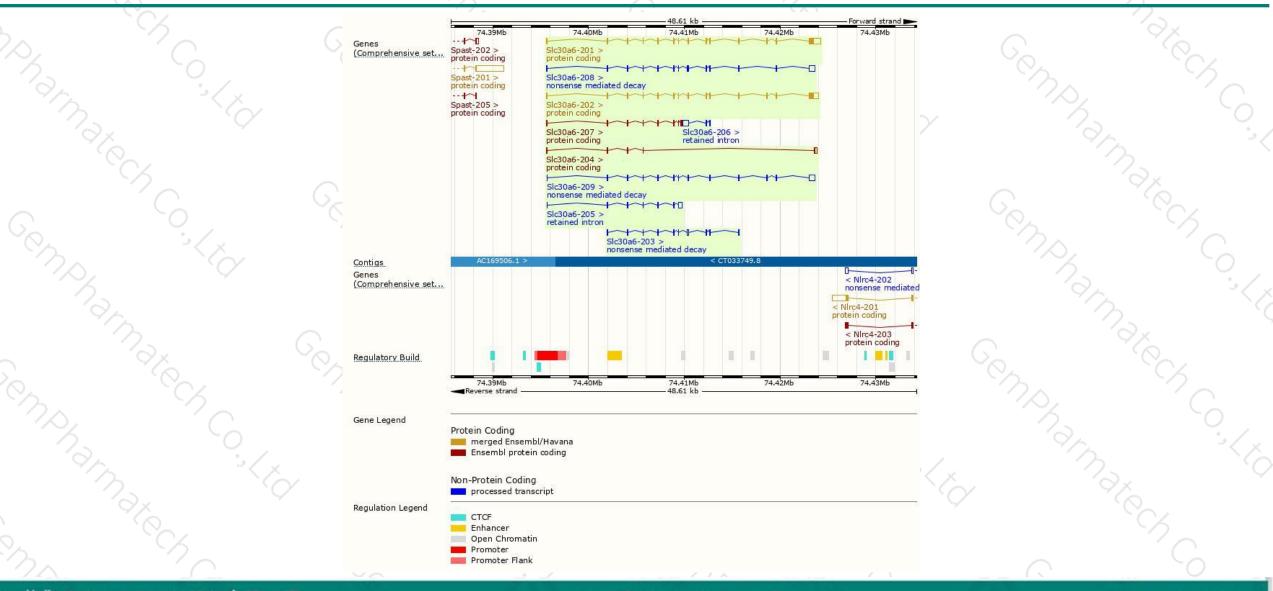
The strategy is based on the design of *Slc30a6-201* transcript, The transcription is shown below



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Genomic location distribution



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Protein domain



		nign					\sim						°C/
2	Scale bar	nr s	nissense v	ariant In variant	120	160	200	240	280	320	360	400	460
	All sequence SNPs/i Variant Legend	10	ameshift		and all oth	ner sources		1.1	11	<u>u</u>	6/0	11	<u> </u>
	PANTHER Gene3D	PTHR46	Cation eff			nain superfa							
	Pfam	_	141166434121413	flux protein				-					(
	Superfamily		Cation effl	ux transmer	nbrane dom	ain superfar	nily						
	Low complexity (Seg) TIGRFAM		Cation ef	flux protein	_					-	, E		
4	ENSMUSP00000024 Transmembrane heli			-	-	70			10				- 17



If you have any questions, you are welcome to inquire. Tel: 400-9660890



