

Slc11a2 Cas9-CKO Strategy

Designer:

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Design Date:

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Project Overview



Project Name

Slc11a2

Project type

Cas9-CKO

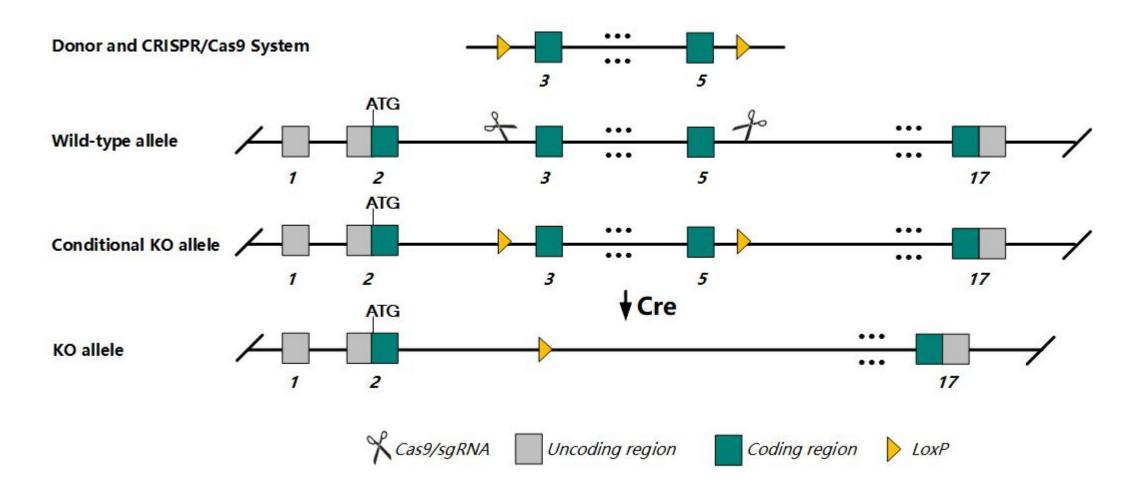
Strain background

C57BL/6JGpt

Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Slc11a2* gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Slc11a2* gene has 8 transcripts. According to the structure of *Slc11a2* gene, exon3-exon5 of *Slc11a2-201* (ENSMUST00000023774.11)transcript is recommended as the knockout region. The region contains 395bp coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Slc11a2* gene. The brief process is as follows:gRNA was transcribed in vitro, donor was constructed.Cas9, gRNA 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



- ➤ According to the existing MGI data, Homozygotes for a spontaneous mutation exhibit microcytic, hypochromic anemia associated with impaired intestinal iron absorption and erythroblast iron uptake. Mutants have reduced viability and fertility.
- The *Slc11a2* gene is located on the Chr15. 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)



SIc11a2 solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 [Mus musculus (house mouse)]

Gene ID: 18174, updated on 2-Apr-2019

Summary



Official Symbol Slc11a2 provided by MGI

Official Full Name solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2 provided by MGI

Primary source MGI:MGI:1345279

See related Ensembl:ENSMUSG00000023030

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 DCT1, DMT1, Nramp2, mk, van

Expression Ubiquitous expression in duodenum adult (RPKM 20.4), kidney adult (RPKM 16.6) and 28 other tissuesSee more

Orthologs <u>human</u> all

Transcript information (Ensembl)



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

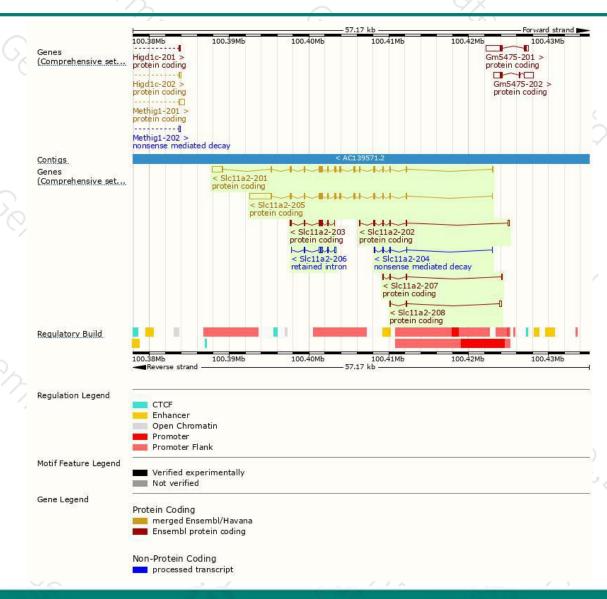
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
SIc11a2-205	ENSMUST00000138843.7	4415	<u>561aa</u>	Protein coding	CCDS49733	P49282	TSL:1 GENCODE basic APPRIS ALT2
SIc11a2-201	ENSMUST00000023774.11	3025	<u>568aa</u>	Protein coding	CCDS37211	P49282	TSL:1 GENCODE basic APPRIS P3
SIc11a2-203	ENSMUST00000124324.1	718	220aa	Protein coding	-	F6ZM31	CDS 5' incomplete TSL:2
SIc11a2-202	ENSMUST00000123461.7	709	<u>170aa</u>	Protein coding	29	D3Z314	CDS 3' incomplete TSL:3
SIc11a2-207	ENSMUST00000154331.1	389	<u>110aa</u>	Protein coding	-	D3Z0R6	CDS 3' incomplete TSL:1
SIc11a2-208	ENSMUST00000154676.1	387	<u>50aa</u>	Protein coding	*	D3YXP3	CDS 3' incomplete TSL:5
SIc11a2-204	ENSMUST00000136168.1	393	<u>68aa</u>	Nonsense mediated decay	ų.	D6RGP0	TSL:3
SIc11a2-206	ENSMUST00000140535.1	709	No protein	Retained intron		- 12	TSL:2

The strategy is based on the design of Slc11a2-201 transcript, The transcription is shown below



Genomic location distribution





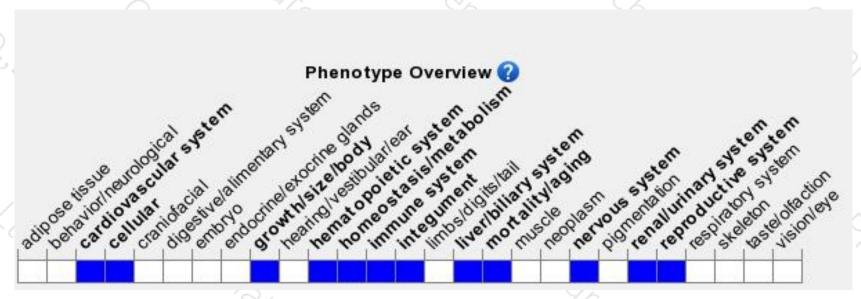
Protein domain





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, Homozygotes for a spontaneous mutation exhibit microcytic, hypochromic anemia associated with impaired intestinal iron absorption and erythroblast iron uptake. Mutants have reduced viability and fertility.



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





