Slc19a1 Cas9-CKO Strategy

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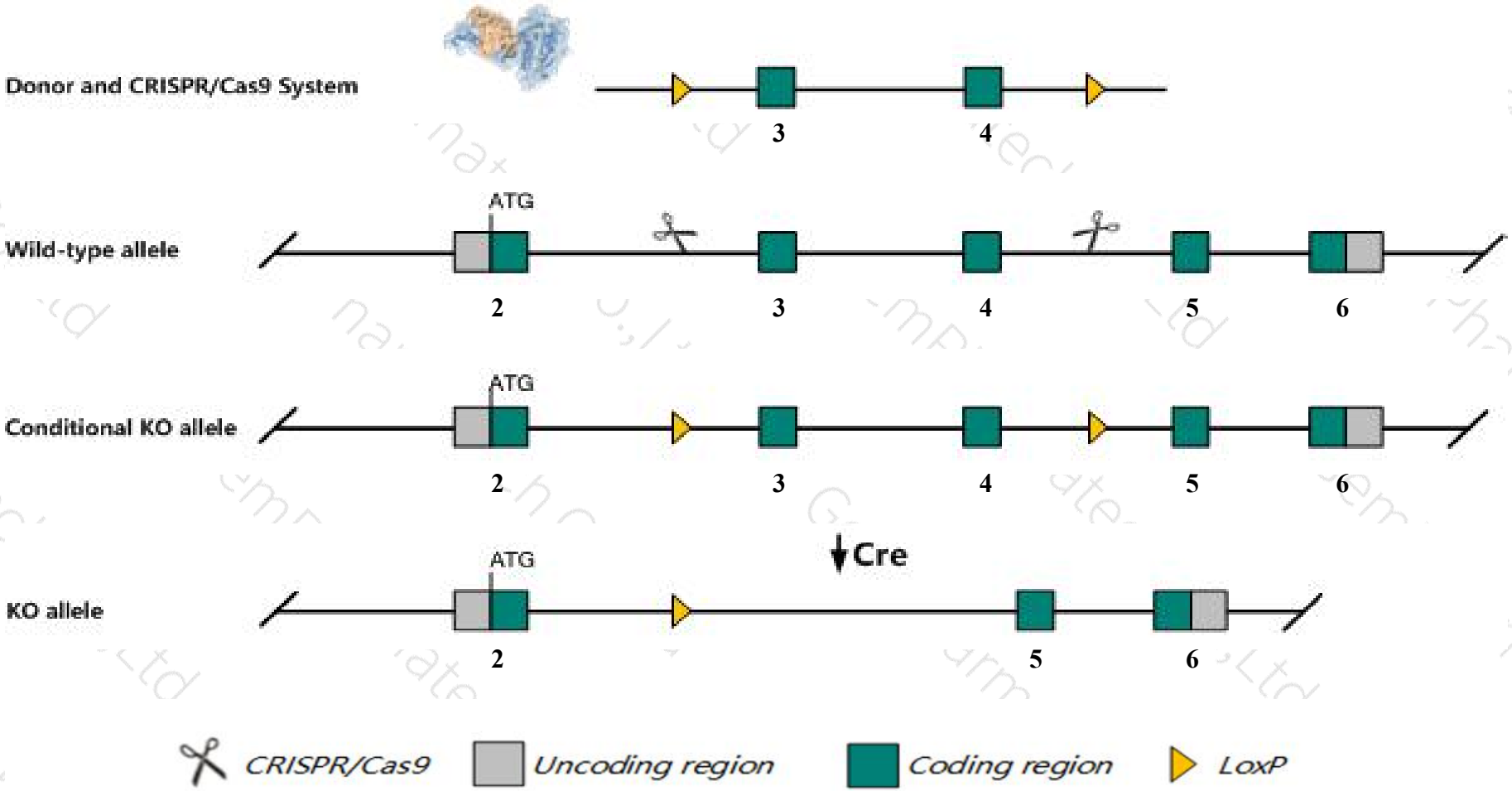
Project Overview

Project Name	***Slc19a1***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc19a1* gene. The schematic diagram is as follows:



Technical routes

- The *Slc19a1* gene has 9 transcripts. According to the structure of *Slc19a1* gene, exon3-exon4 of *Slc19a1-201* (ENSMUST00000105410.9) transcript is recommended as the knockout region.The region contains 947bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Slc19a1* 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

- According to the existing MGI data,homozygous null embryos die due to abnormalities of hematopoietic organs. mutant mice may be partially rescued with maternal folic acid supplementation, but these mice still present with hematopoietic organ defects and show impaired development of urogenital structures.

- The *Slc19a1* gene is located on the Chr10. 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）

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Slc19a1 solute carrier family 19 (folate transporter), member 1 [Mus musculus (house mouse)]

Gene ID: 20509, updated on 13-Mar-2020

Summary

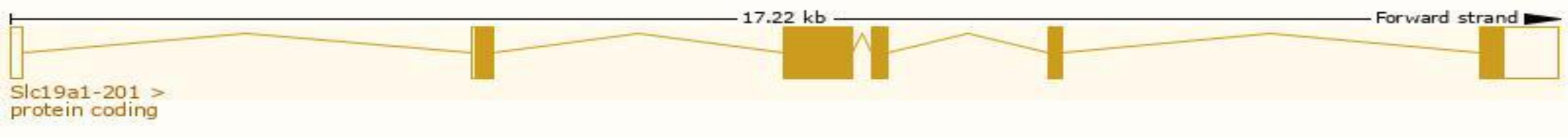
Official Symbol	Slc19a1 provided by MGI
Official Full Name	solute carrier family 19 (folate transporter), member 1 provided by MGI
Primary source	MGI:MGI:103182
See related	Ensembl:ENSMUSG00000001436
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI323572, RFC, RFC-1, RFC1
Expression	Ubiquitous expression in kidney adult (RPKM 62.7), ovary adult (RPKM 25.1) and 26 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

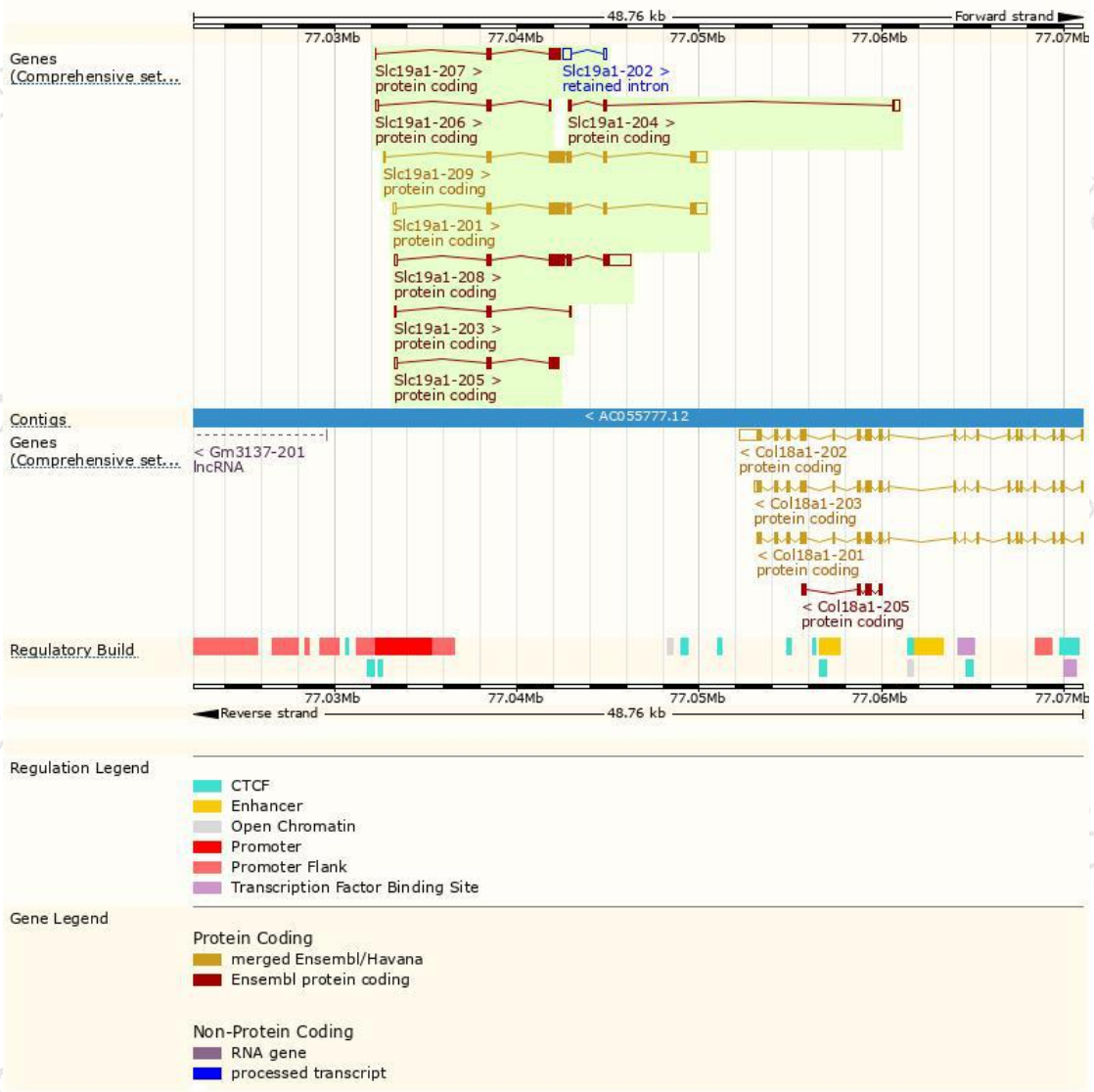
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc19a1-201	ENSMUST00000105410.9	2347	512aa	Protein coding	CCDS35947	P41438 Q542F3	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P2
Slc19a1-209	ENSMUST00000144234.7	2309	512aa	Protein coding	CCDS35947	P41438 Q542F3	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P2
Slc19a1-208	ENSMUST00000136925.7	2863	476aa	Protein coding	-	E9Q8X6	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
Slc19a1-205	ENSMUST00000132984.1	877	232aa	Protein coding	-	D3Z4F3	CDS 3' incomplete TSL:2
Slc19a1-207	ENSMUST00000136150.7	826	243aa	Protein coding	-	D3YU74	CDS 3' incomplete TSL:3
Slc19a1-204	ENSMUST00000131031.1	685	116aa	Protein coding	-	F6YWA3	CDS 5' incomplete TSL:3
Slc19a1-206	ENSMUST00000133059.7	391	71aa	Protein coding	-	D3Z0I6	CDS 3' incomplete TSL:3
Slc19a1-203	ENSMUST00000130703.7	356	80aa	Protein coding	-	D3YZE1	CDS 3' incomplete TSL:3
Slc19a1-202	ENSMUST00000127249.1	613	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Slc19a1-201* transcript,the transcription is shown below:

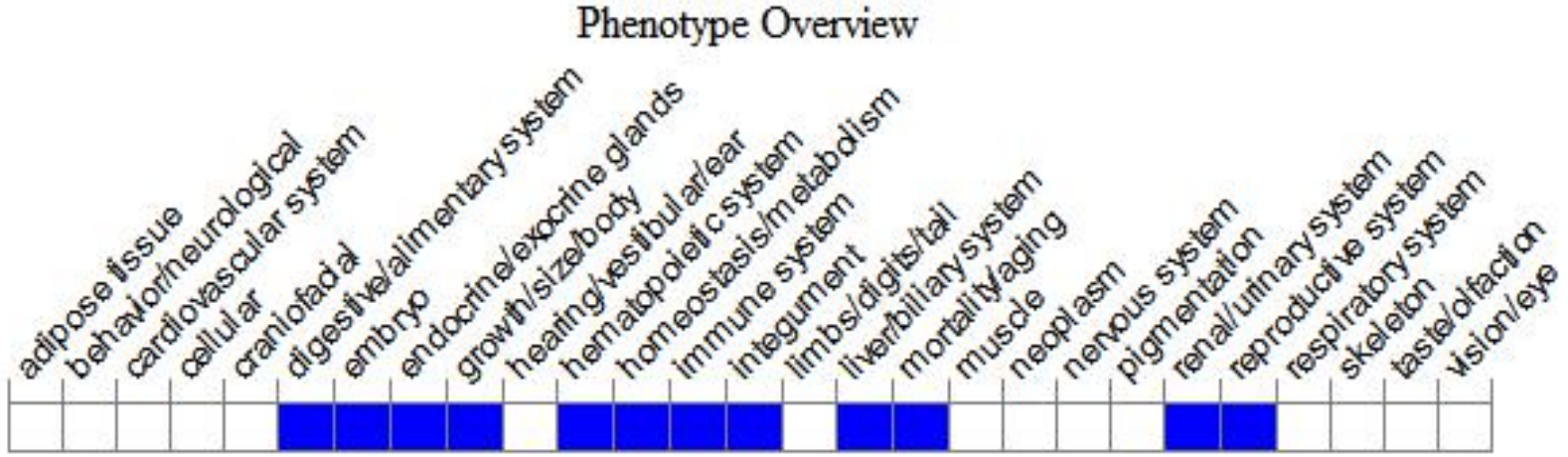


Genomic location distribution



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,homozygous null embryos die due to abnormalities of hematopoietic organs. Mutant mice may be partially rescued with maternal folic acid supplementation, but these mice still present with hematopoietic organ defects and show impaired development of urogenital structures.

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

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