Slc25a12 Cas9-CKO Strategy

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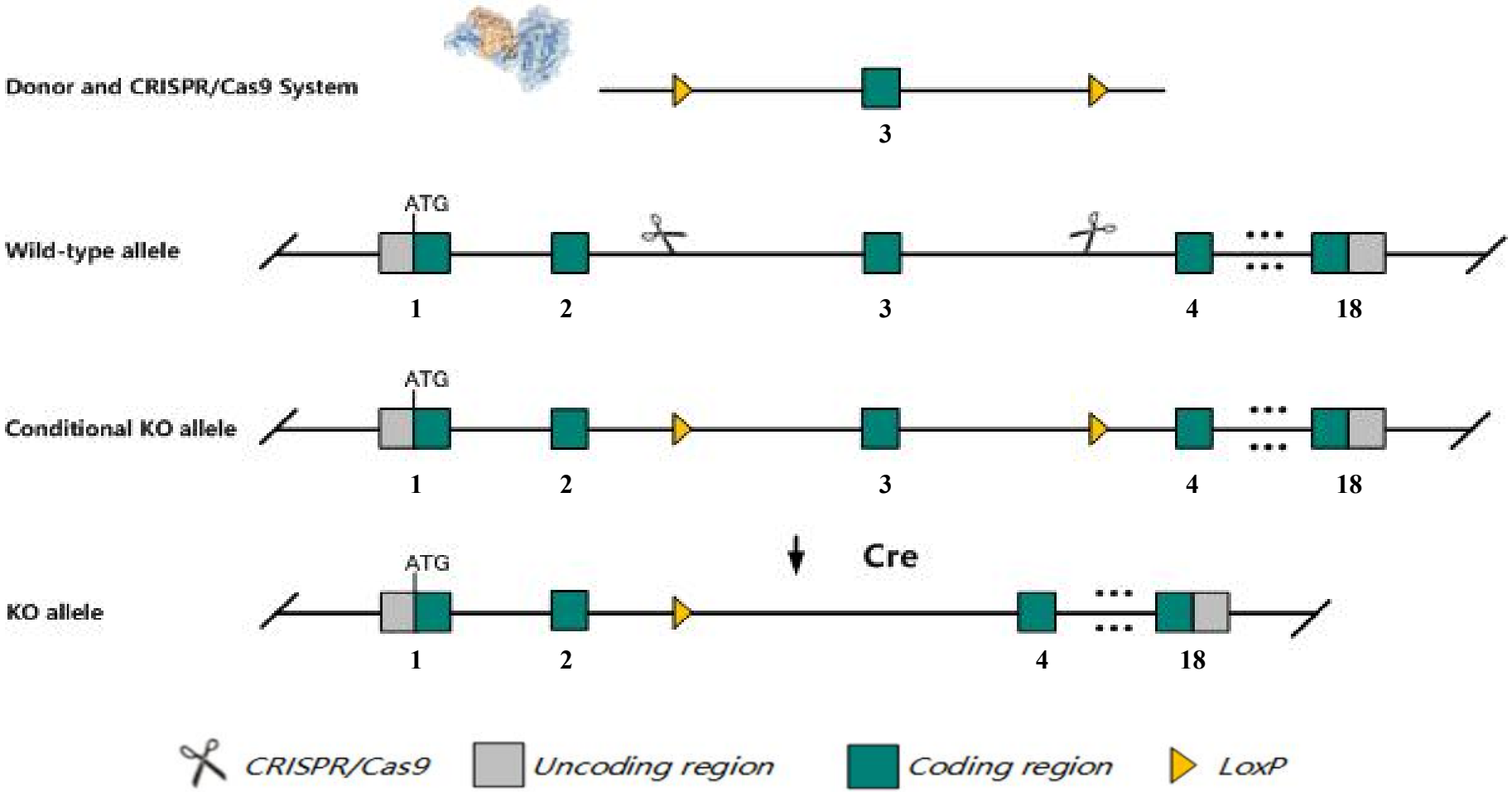
Project Overview

Project Name	***Slc25a12***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Slc25a12* gene. The schematic diagram is as follows:



Technical routes

The *Slc25a12* gene has 7 transcripts. According to the structure of *Slc25a12* gene, exon3 of *Slc25a12-206*(ENSMUST00000151937.7) transcript is recommended as the knockout region.The region contains 143bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Slc25a12* 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,mice homozygous for a null allele show severe growth defects, generalized tremors, postnatal lethality, impaired motor coordination, and CNS dysmyelination associated with decreased synthesis of myelin lipids and a striking reduction in brain aspartate and N-acetylaspartate levels.

The *Slc25a12* gene is located on the Chr2. 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.

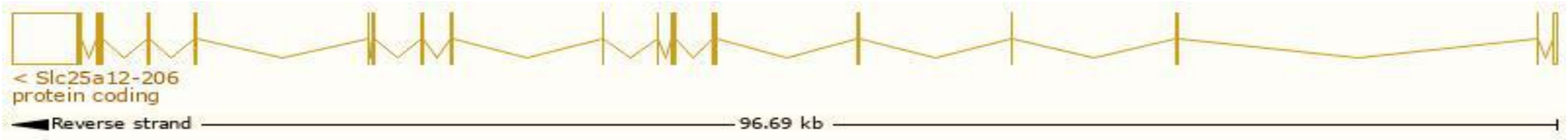
Gene information NCBI

Transcript information Ensembl

The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Slc25a12-206	ENSMUST00000151937.7	6351	677aa	Protein coding	CCDS16113	Q8BH59	TSL:1 GENCODE basic APPRIS P1
Slc25a12-207	ENSMUST00000184169.7	2392	87aa	Nonsense mediated decay	-	V9GXX9	TSL:5
Slc25a12-205	ENSMUST00000147553.1	994	No protein	Processed transcript	-	-	TSL:3
Slc25a12-203	ENSMUST00000137916.1	790	No protein	Processed transcript	-	-	TSL:2
Slc25a12-201	ENSMUST00000126493.7	550	No protein	Processed transcript	-	-	TSL:5
Slc25a12-204	ENSMUST00000146653.1	204	No protein	Processed transcript	-	-	TSL:5
Slc25a12-202	ENSMUST00000130715.1	414	No protein	Retained intron	-	-	TSL:1

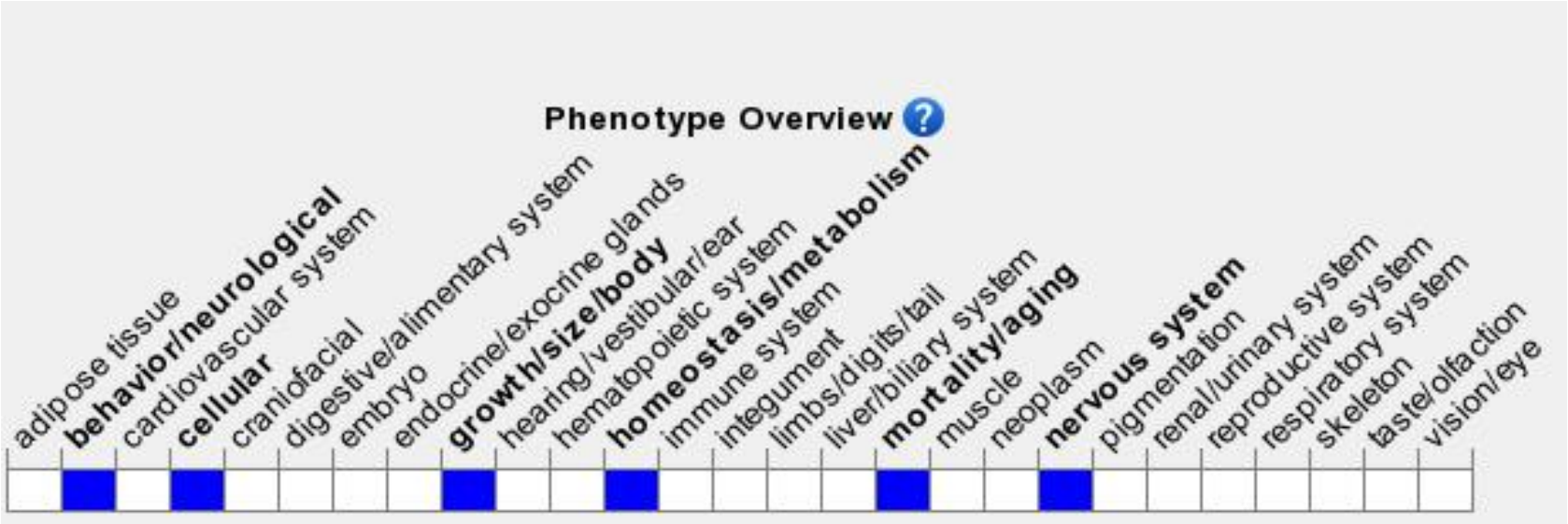
The strategy is based on the design of *Slc25a12-206* transcript,the transcription is shown below:



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/).

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