

St18 Cas9-CKO Strategy

Designer:

Daohua Xu

Reviewer:

Huimin Su

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Project Overview

Project Name

St18

Project type

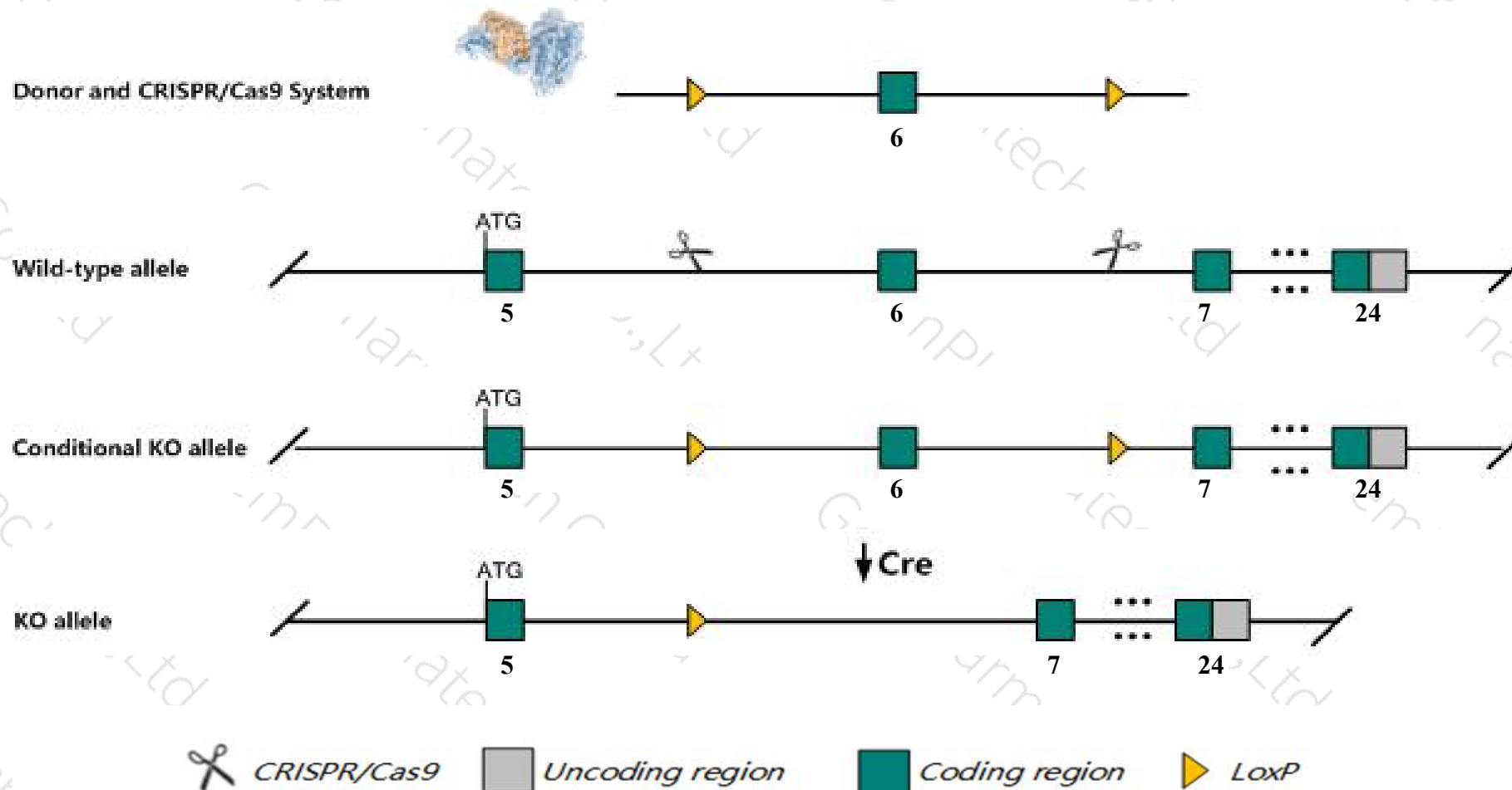
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *St18* gene. The schematic diagram is as follows:



- The *Stl8* gene has 13 transcripts. According to the structure of *Stl8* gene, exon6 of *Stl8-208* (ENSMUST00000140079.7) transcript is recommended as the knockout region. The region contains 31bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Stl8* 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

- The *St18* gene is located on the Chr1. 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)

St18 suppression of tumorigenicity 18 [Mus musculus (house mouse)]

Gene ID: 240690, updated on 3-Feb-2019

Summary



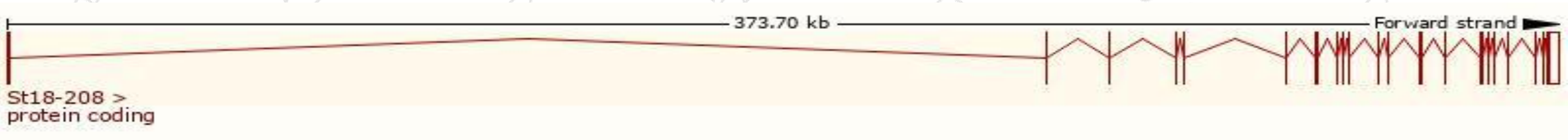
Official Symbol	St18 provided by MGI
Official Full Name	suppression of tumorigenicity 18 provided by MGI
Primary source	MGI:MGI:2446700
See related	Ensembl:ENSMUSG00000033740
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AV348974, Myt3, NZF-3, Nzf3, mKIAA0535
Expression	Biased expression in cerebellum adult (RPKM 6.1), CNS E11.5 (RPKM 3.2) and 5 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

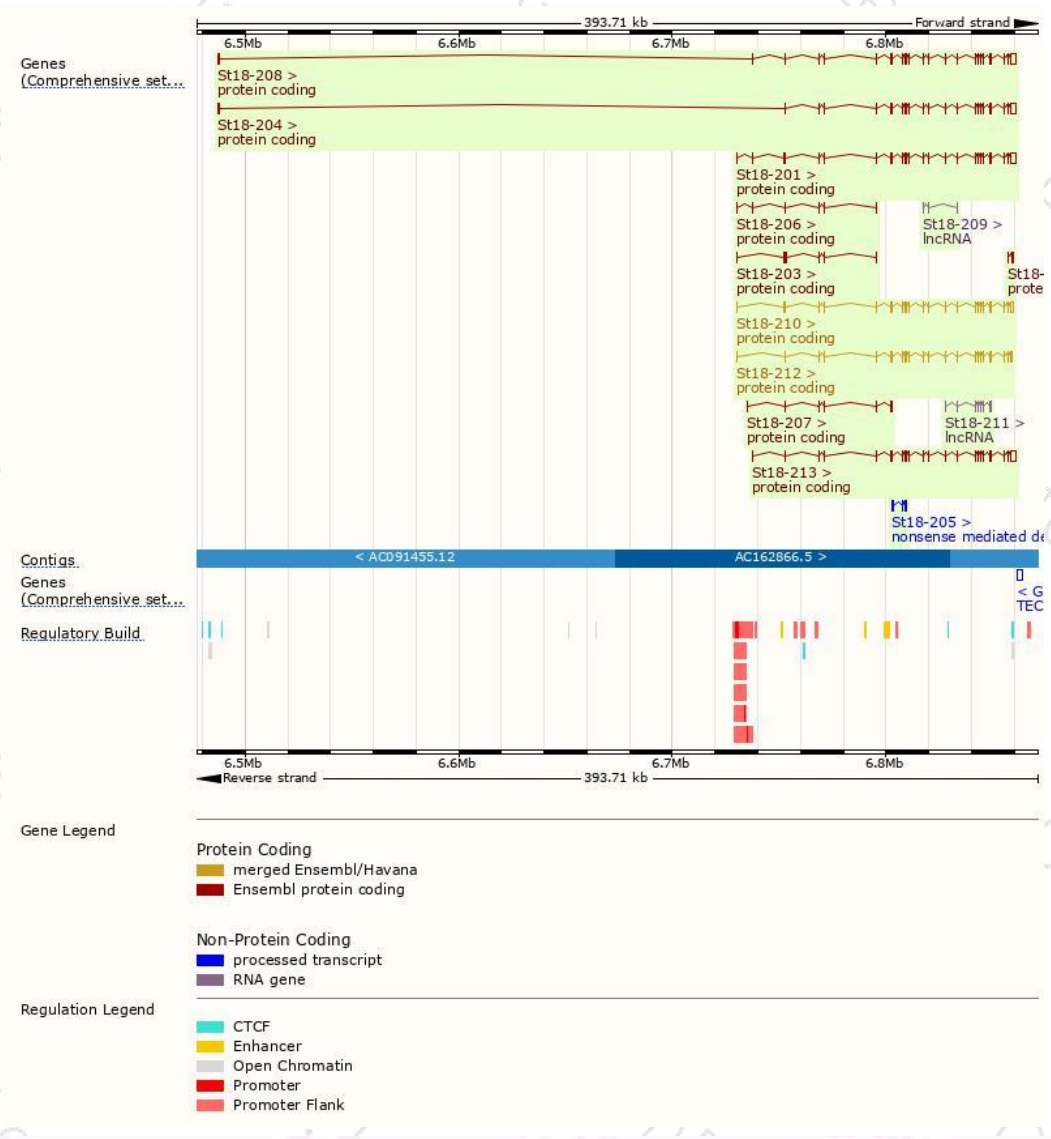
The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
St18-208	ENSMUST00000140079.7	5892	1045aa	Protein coding	CCDS14810	Q148A0 Q80TY4	TSL:1 GENCODE basic APPRIS P1
St18-201	ENSMUST00000043578.12	5862	1045aa	Protein coding	CCDS14810	Q148A0 Q80TY4	TSL:1 GENCODE basic APPRIS P1
St18-204	ENSMUST00000131494.7	5720	1045aa	Protein coding	CCDS14810	Q148A0 Q80TY4	TSL:1 GENCODE basic APPRIS P1
St18-213	ENSMUST00000163727.3	5604	1045aa	Protein coding	CCDS14810	Q148A0 Q80TY4	TSL:5 GENCODE basic APPRIS P1
St18-210	ENSMUST00000150761.7	4264	1045aa	Protein coding	CCDS14810	Q148A0 Q80TY4	TSL:1 GENCODE basic APPRIS P1
St18-212	ENSMUST00000151281.7	3533	1045aa	Protein coding	CCDS14810	Q148A0 Q80TY4	TSL:1 GENCODE basic APPRIS P1
St18-207	ENSMUST00000139838.7	792	215aa	Protein coding	-	D3YZ65	CDS 3' incomplete TSL:3
St18-202	ENSMUST00000130338.1	720	95aa	Protein coding	-	A0A0A6YVU2	CDS 5' incomplete TSL:3
St18-203	ENSMUST00000131467.7	585	83aa	Protein coding	-	D3YUH3	CDS 3' incomplete TSL:3
St18-206	ENSMUST00000139756.7	435	42aa	Protein coding	-	A0A0A6YXN3	CDS 3' incomplete TSL:3
St18-205	ENSMUST00000132207.1	684	108aa	Nonsense mediated decay	-	A0A0A6YY81	CDS 5' incomplete TSL:3
St18-211	ENSMUST00000151015.1	817	No protein	Processed transcript	-	-	TSL:5
St18-209	ENSMUST00000142304.1	445	No protein	Processed transcript	-	-	TSL:3

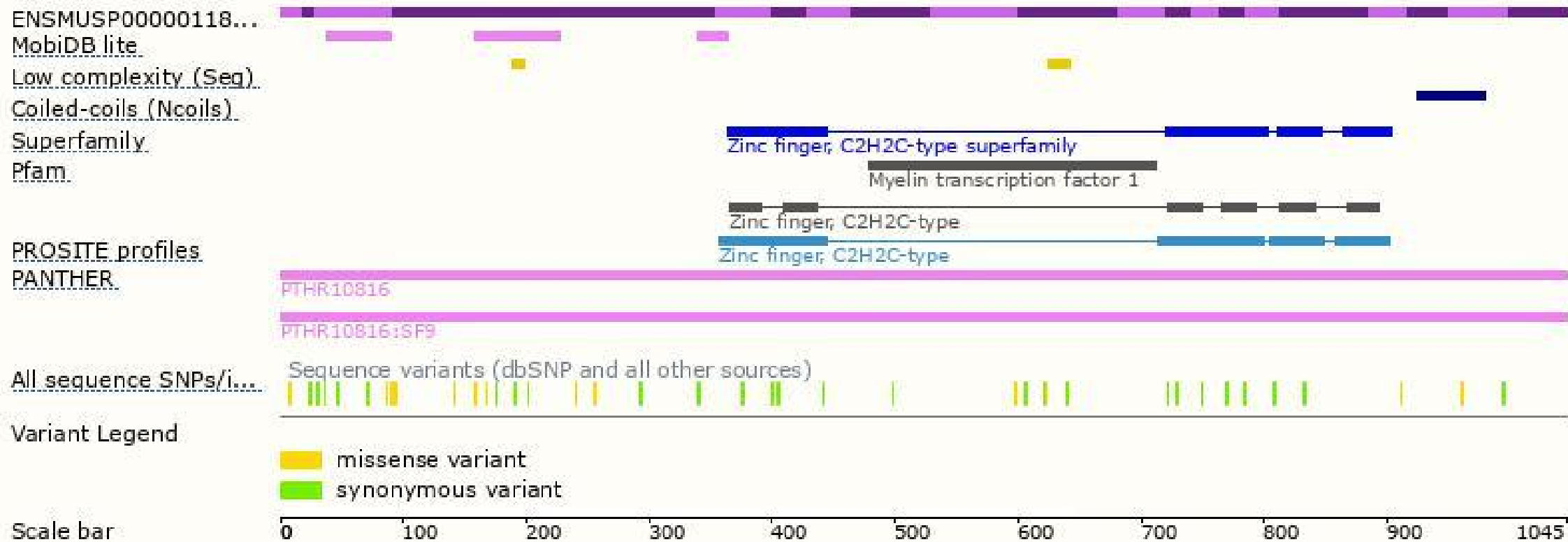
The strategy is based on the design of *St18-208* transcript,The transcription is shown below



Genomic location distribution

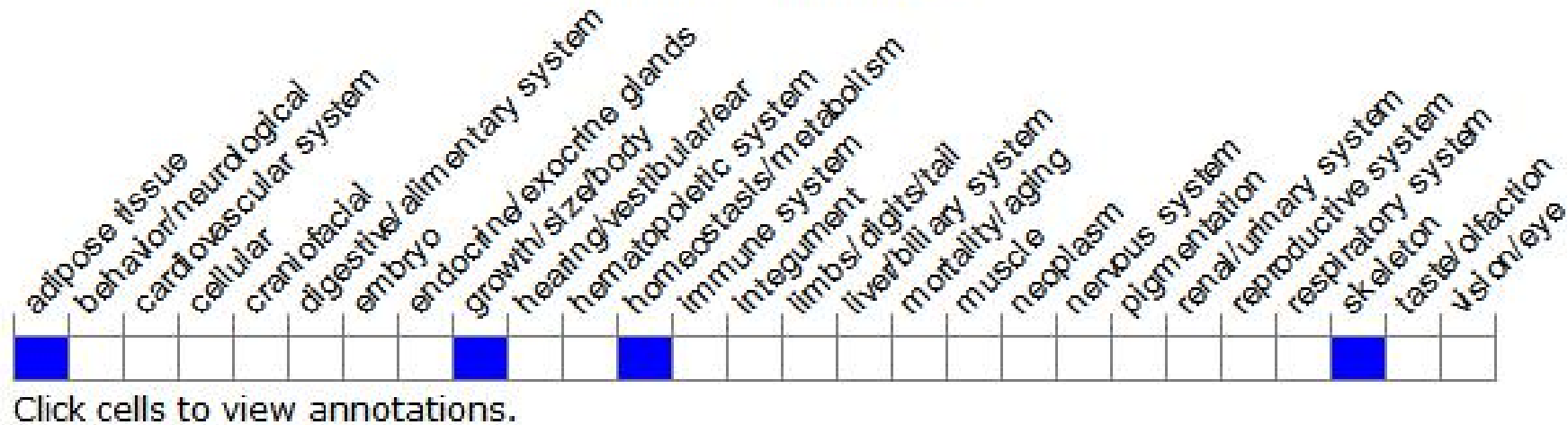


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview ?



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).

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

Tel: 400-9660890

