

# Setd2 Cas9-CKO Strategy

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Reviewer: Shilei Zhu

**Design Date:** 2018/9/27

# **Project Overview**



**Project Name** 

Setd2

**Project type** 

Cas9-CKO

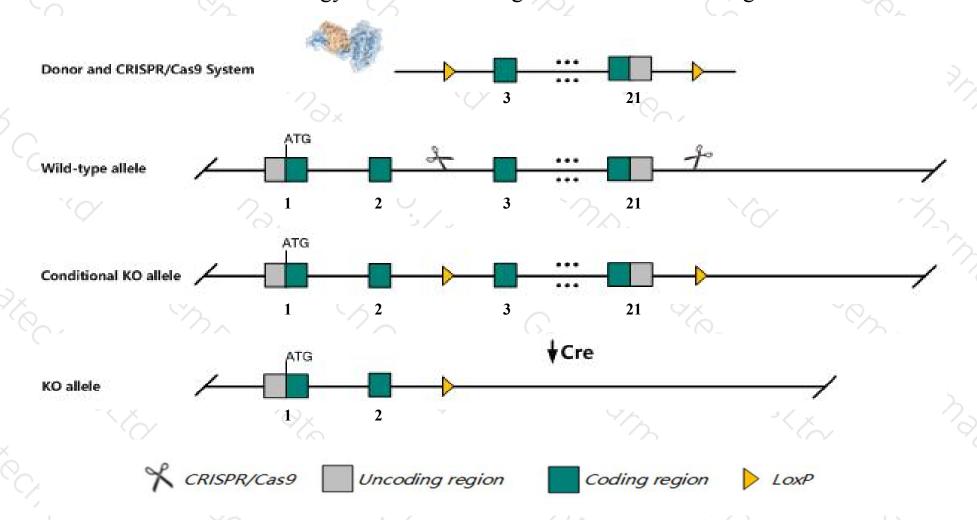
Strain background

C57BL/6JGpt

## Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Setd2 gene. The schematic diagram is as follows:



### Technical routes



- The Setd2 gene has 10 transcripts. According to the structure of Setd2 gene, exon3-exon21 of Setd2-201 (ENSMUST00000153838.7) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Setd2* 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 knock-out allele exhibit impaired embryonic vascular remodeling in the embryo proper, yolk sac, and placenta that leads to death around E10.5.
- The *Setd2* gene is located on the Chr9. 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)



#### Setd2 SET domain containing 2 [Mus musculus (house mouse)]

Gene ID: 235626, updated on 24-Feb-2019

#### Summary

☆ ?

Official Symbol Setd2 provided by MGI

Official Full Name SET domain containing 2 provided by MGI

Primary source MGI:MGI:1918177

See related Ensembl: ENSMUSG00000044791

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 4921524K10Rik, BC031601, KMT3A

Expression Ubiquitous expression in CNS E11.5 (RPKM 11.9), CNS E14 (RPKM 11.1) and 28 other tissuesSee more

Orthologs <u>human</u> all

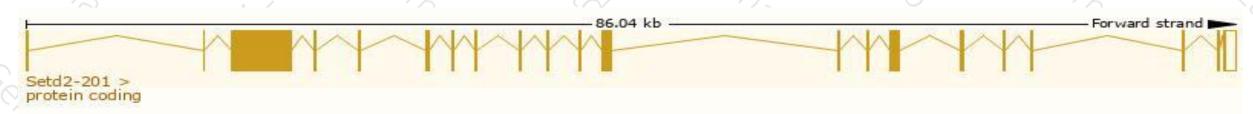
# Transcript information (Ensembl)



The gene has 10 transcripts, all transcripts are shown below:

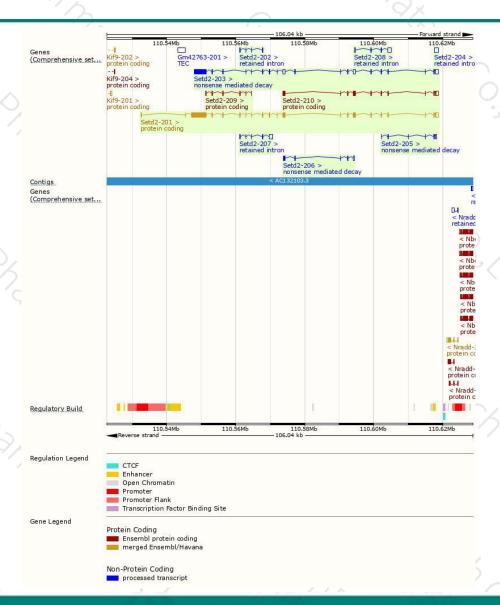
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Setd2-201	ENSMUST00000153838.7	835	0 <u>2537aa</u>	Protein coding	CCDS40781	E9Q5F9	TSL:5 GENCODE basic APPRIS P1
Setd2-210	ENSMUST00000200460.4	291	0 <u>760aa</u>	Protein coding	100	A0A0G2JEZ4	CDS 5' incomplete TSL:1
Setd2-209	ENSMUST00000198823.1	<u>3.1</u> 713	238aa	Protein coding	127	A0A0G2JDY1	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TS
Setd2-203	ENSMUST00000196814.4	744	2 <u>1263aa</u>	Nonsense mediated decay	626	A0A0G2JH06	CDS 5' incomplete TSL:5
Setd2-206	ENSMUST00000197655.1	<u>.1</u> 117	3 <u>169aa</u>	Nonsense mediated decay		A0A0G2JEW8	CDS 5' incomplete TSL:5
Setd2-205	ENSMUST00000197399.1	0.1 76	<u>72aa</u>	Nonsense mediated decay	100	A0A0G2JDZ6	CDS 5' incomplete TSL:5
Setd2-208	ENSMUST00000198697.1	173	5 No protein	Retained intron	(4)	-	TSL:2
Setd2-207	ENSMUST00000198587.1	<u>.1</u> 139	B No protein	Retained intron	16 <u>2</u> 8	10	TSL:1
Setd2-204	ENSMUST00000197260.1	100	7 No protein	Retained intron		-	TSL:NA
Setd2-202	ENSMUST00000195911.4	.4 52	No protein	Retained intron	-	8-	TSL:2
Setd2-204	ENSMUST00000197260.1	100	7 No protein	Retained intron	(31)		TSL:NA

The strategy is based on the design of Setd2-201 transcript, The transcription is shown below



### Genomic location distribution





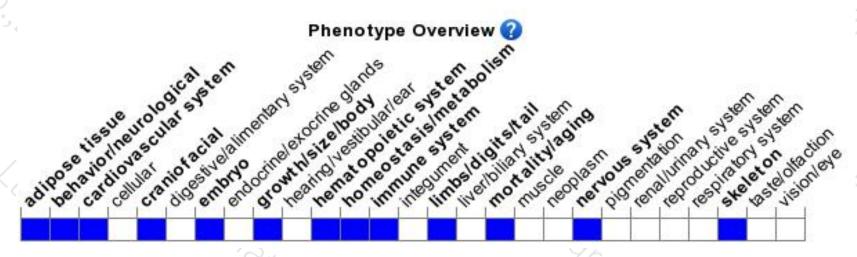
### Protein domain





# 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, Mice homozygous for a knock-out allele exhibit impaired embryonic vascular remodeling in the embryo proper, yolk sac, and placenta that leads to death around E10.5.



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





