Setdb1 Cas9-KO Strategy

Designer: Shilei Zhu

Project Overview

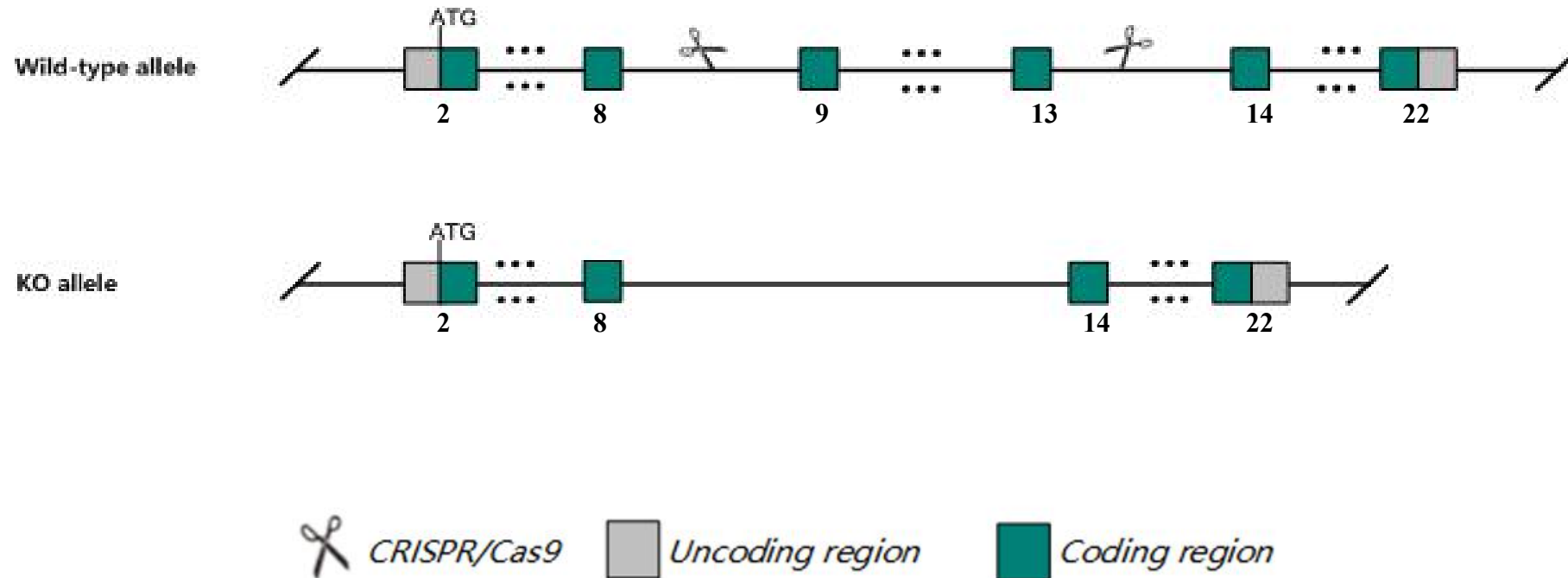|	
Project Name	***Setdb1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Setdb1* gene. The schematic diagram is as follows:

The *Setdb1* gene has 6 transcripts. According to the structure of *Setdb1* gene, exon9-exon13 of *Setdb1-201*

(ENSMUST00000015841.11) transcript is recommended as the knockout region.The region contains 1318bp coding sequenc

Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Setdb1* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

According to the existing MGI data,Homozygous inactivation of this locus results in peri-implantation lethality. Inner cell mass growth is impaired in null blastocysts.

The *Setdb1* gene is located on the Chr3. 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Setdb1 SET domain, bifurcated 1 [Mus musculus (house mouse)]

Gene ID: 84505, updated on 9-Apr-2019

Summary

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Official Symbol	Setdb1 provided by MGI
Official Full Name	SET domain, bifurcated 1 provided by MGI
Primary source	MGI:MGI:1934229
See related	Ensembl:ENSMUSG00000015697
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	AU022152, ESET, KMT1E, mKIAA0067
Expression	Ubiquitous expression in CNS E11.5 (RPKM 22.1), limb E14.5 (RPKM 18.8) and 28 other tissuesSee more
Orthologs	human all

Transcript information Ensembl

The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Setdb1-201	ENSMUST00000015841.11	4658	1308aa	Protein coding	CCDS17613	D3YYC3	TSL:1 GENCODE basic APPRIS P3
Setdb1-202	ENSMUST00000107170.2	4622	1308aa	Protein coding	CCDS17613	D3YYC3	TSL:1 GENCODE basic APPRIS P3
Setdb1-203	ENSMUST00000107171.9	4573	1307aa	Protein coding	CCDS50991	G5E8N3	TSL:1 GENCODE basic APPRIS ALT2
Setdb1-204	ENSMUST00000124638.7	5652	No protein	Retained intron	-	-	TSL:2
Setdb1-205	ENSMUST00000132468.1	2440	No protein	Retained intron	-	-	TSL:1
Setdb1-206	ENSMUST00000152260.1	645	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Setdb1-201* transcript,The transcription is shown below

< Setdb1-201
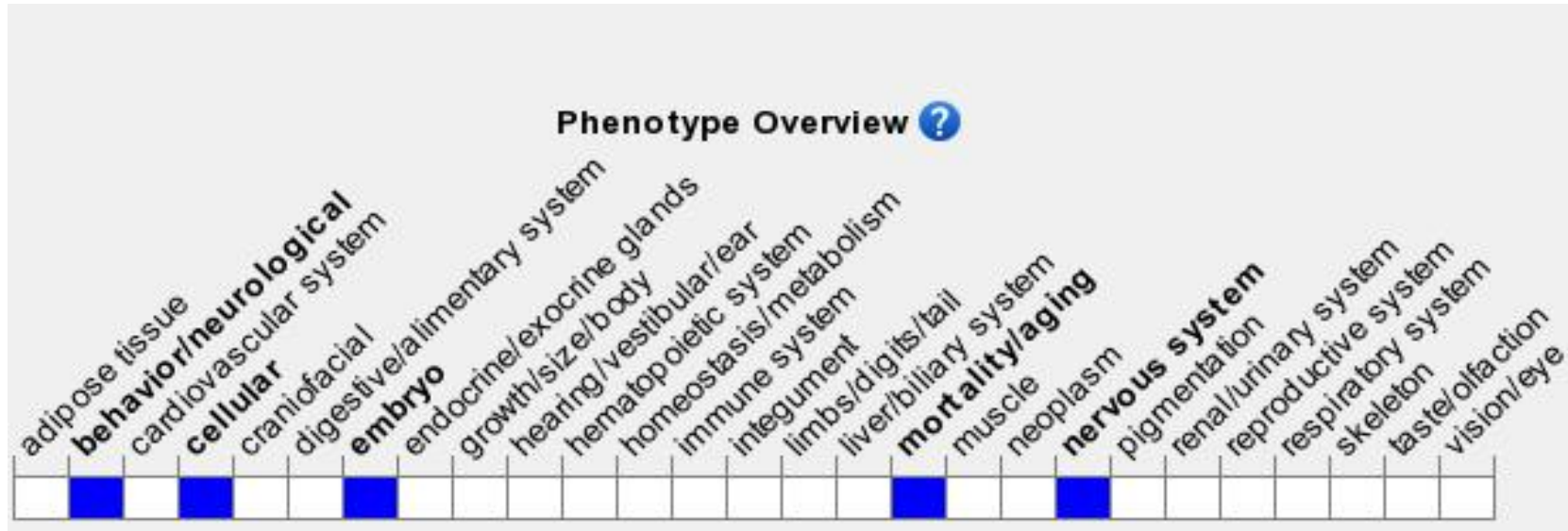protein coding

◀ Reverse strand

33.68 kb
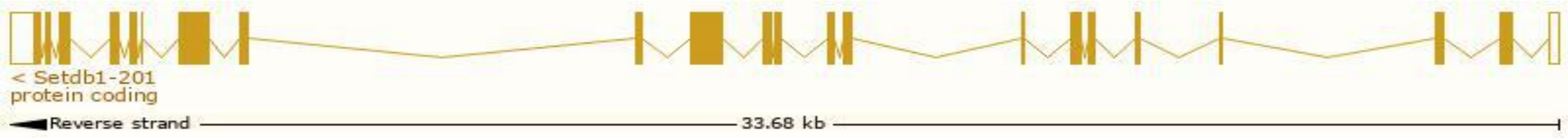
Genomic location distribution
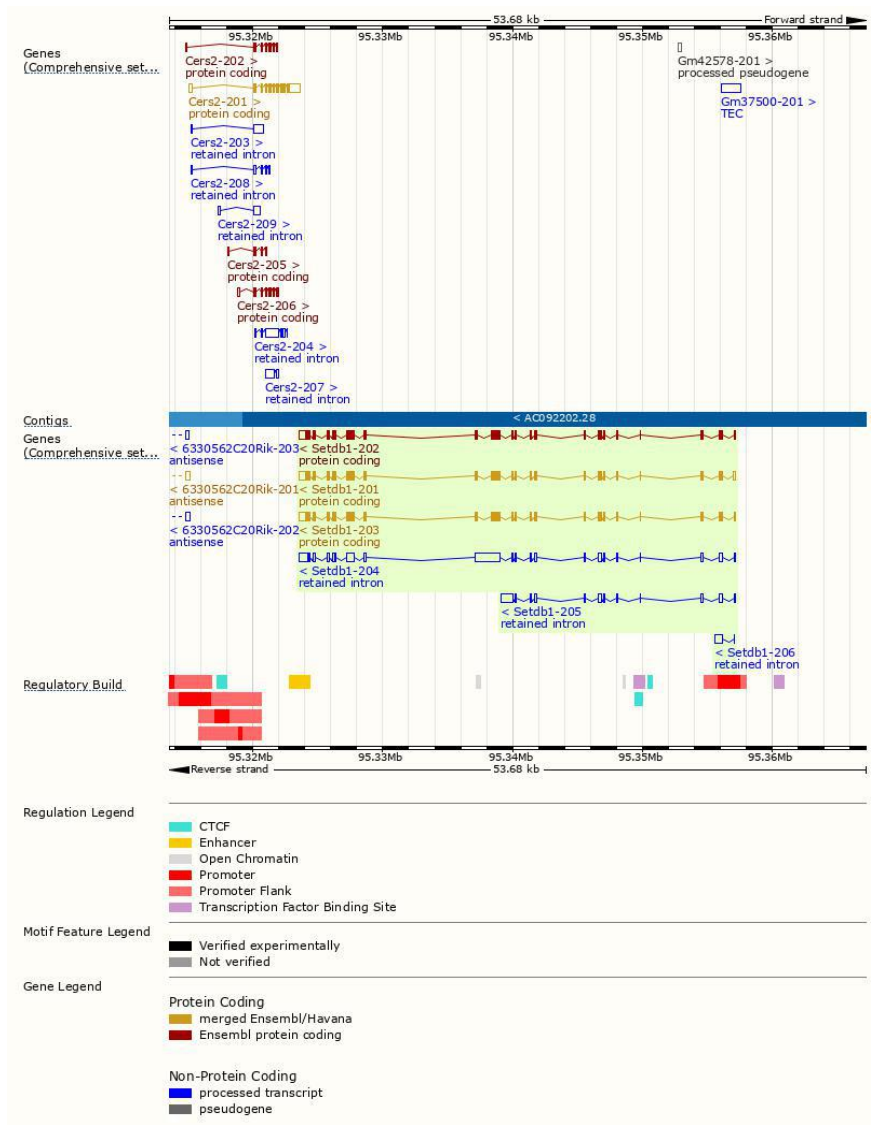
Protein domain
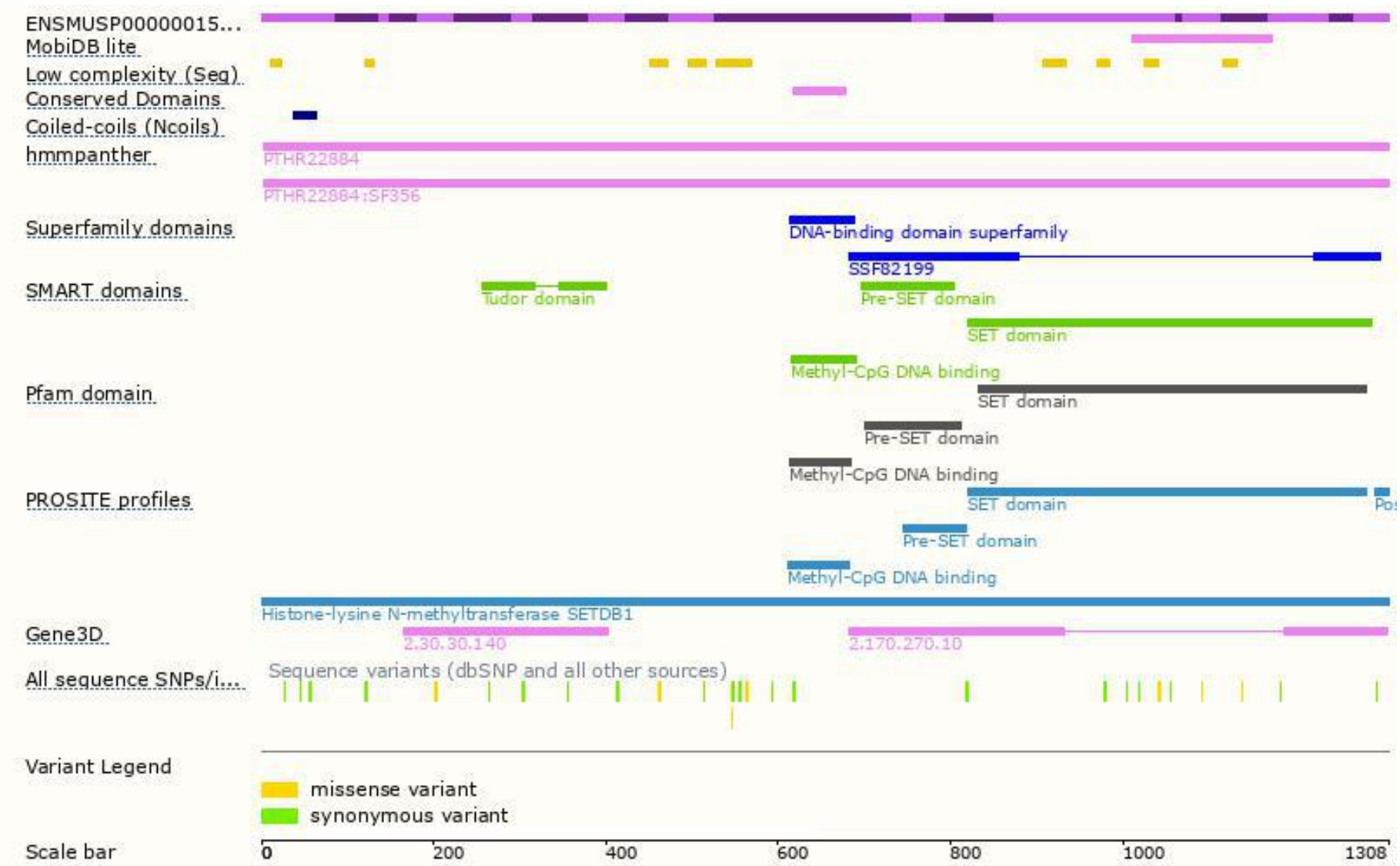
Mouse phenotype description(MGI)

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 inactivation of this locus results in peri-implantation lethality.

Inner cell mass growth is impaired in null blastocysts.

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