Sin3a Cas9-KO Strategy

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Reviewer: Yumeng Wang

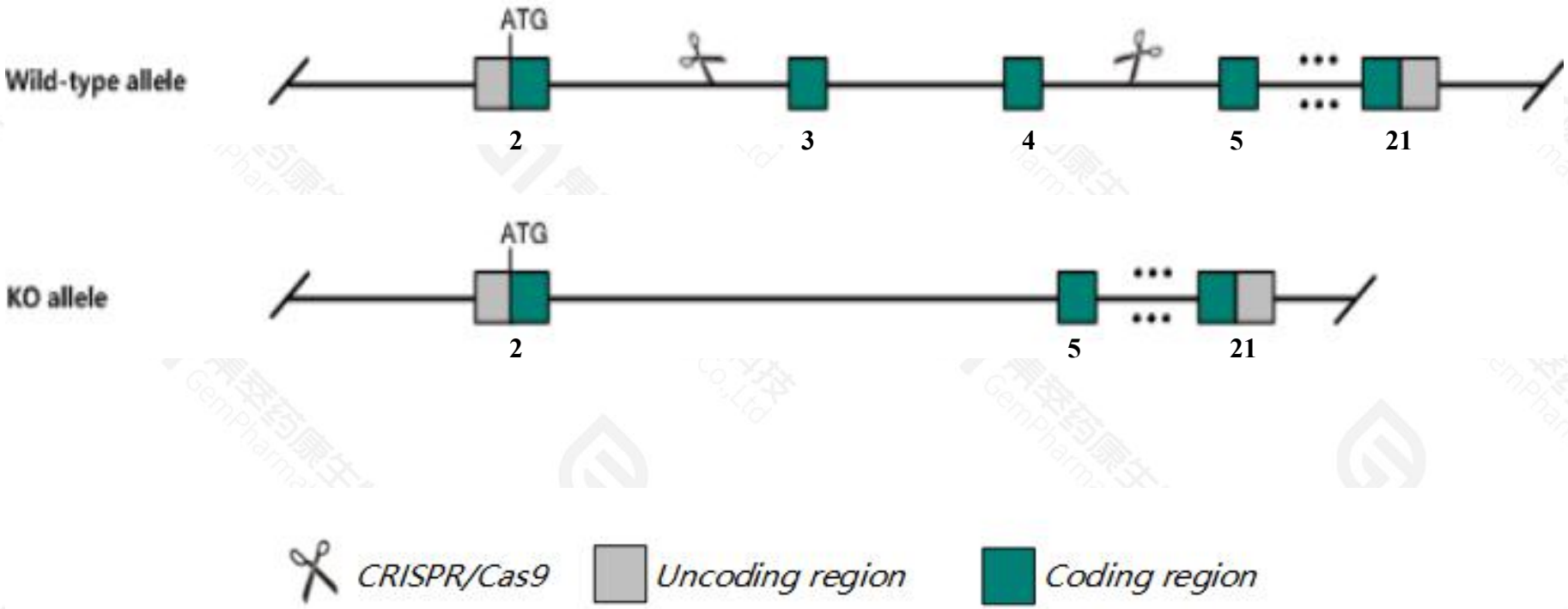
Design Date: 2021-9-27

Project Overview

Project Name	***Sin3a***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sin3a* gene. The schematic diagram is as follows:



Technical routes

➢ The *Sin3a* gene has 9 transcripts. According to the structure of *Sin3a* gene, exon3-exon4 of *Sin3a-206*(ENSMUST00000168177.8) transcript is recommended as the knockout region.The region contains 284bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Sin3a* gene. The brief process is as follows: CRISPR/Cas9 system 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.

Notice

➢ According to the existing MGI data,targeted disruption of this gene results in early embryonic lethality. Homozygous null MEFs display poor cell proliferation, reduced S-phase and increased G2/M fractions, a block in DNA replication, and enhanced apoptosis; however, no increase in chromosomal instability is observed.

➢ The *Sin3a* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information （NCBI）

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Sin3a transcriptional regulator, SIN3A (yeast) [Mus musculus (house mouse)]

Gene ID: 20466, updated on 13-Mar-2020

Summary

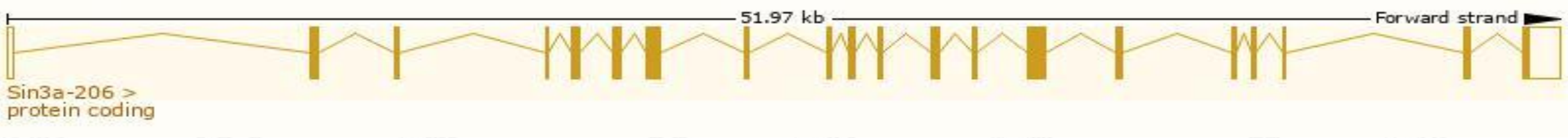
Official Symbol	Sin3a provided by MGI
Official Full Name	transcriptional regulator, SIN3A (yeast) provided by MGI
Primary source	MGI:MGI:107157
See related	Ensembl:ENSMUSG00000042557
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AW553200, Sin3, mKIAA4126, mSin3A
Expression	Ubiquitous expression in CNS E11.5 (RPKM 17.1), thymus adult (RPKM 15.7) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

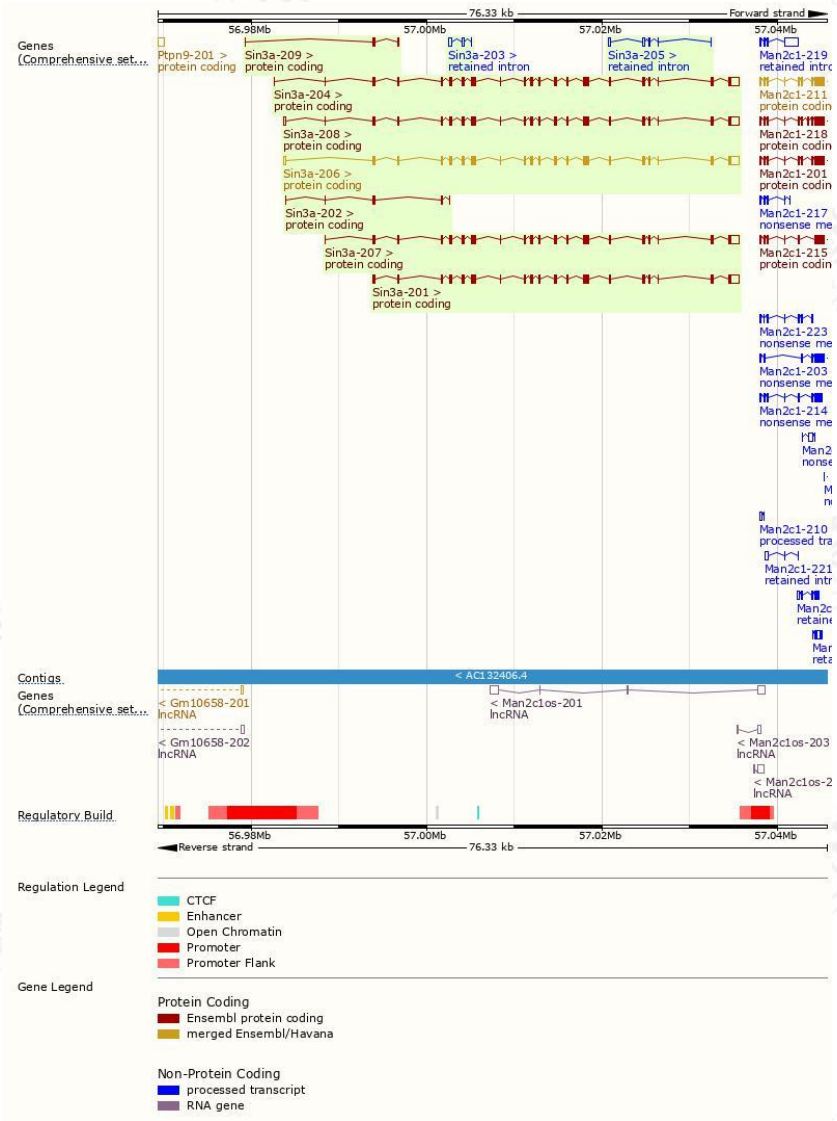
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sin3a-208	ENSMUST00000168678.7	5206	1274aa	Protein coding	CCDS23216	Q60520	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 P3
Sin3a-206	ENSMUST00000168177.7	5086	1277aa	Protein coding	CCDS52805	Q60520	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 ALT1
Sin3a-204	ENSMUST00000167715.7	4961	1274aa	Protein coding	CCDS23216	Q60520	TSL:5 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 P3
Sin3a-207	ENSMUST00000168502.7	4899	1277aa	Protein coding	CCDS52805	Q60520	TSL:5 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 ALT1
Sin3a-201	ENSMUST00000049169.5	4845	1274aa	Protein coding	CCDS23216	Q60520	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 P3
Sin3a-202	ENSMUST00000163400.7	544	133aa	Protein coding	-	E9PXF9	CDS 3' incomplete TSL:5
Sin3a-209	ENSMUST00000169879.7	364	102aa	Protein coding	-	E9Q2L1	CDS 3' incomplete TSL:5
Sin3a-203	ENSMUST00000165927.1	641	No protein	Retained intron	-	-	TSL:2
Sin3a-205	ENSMUST00000167963.1	640	No protein	Retained intron	-	-	TSL:2

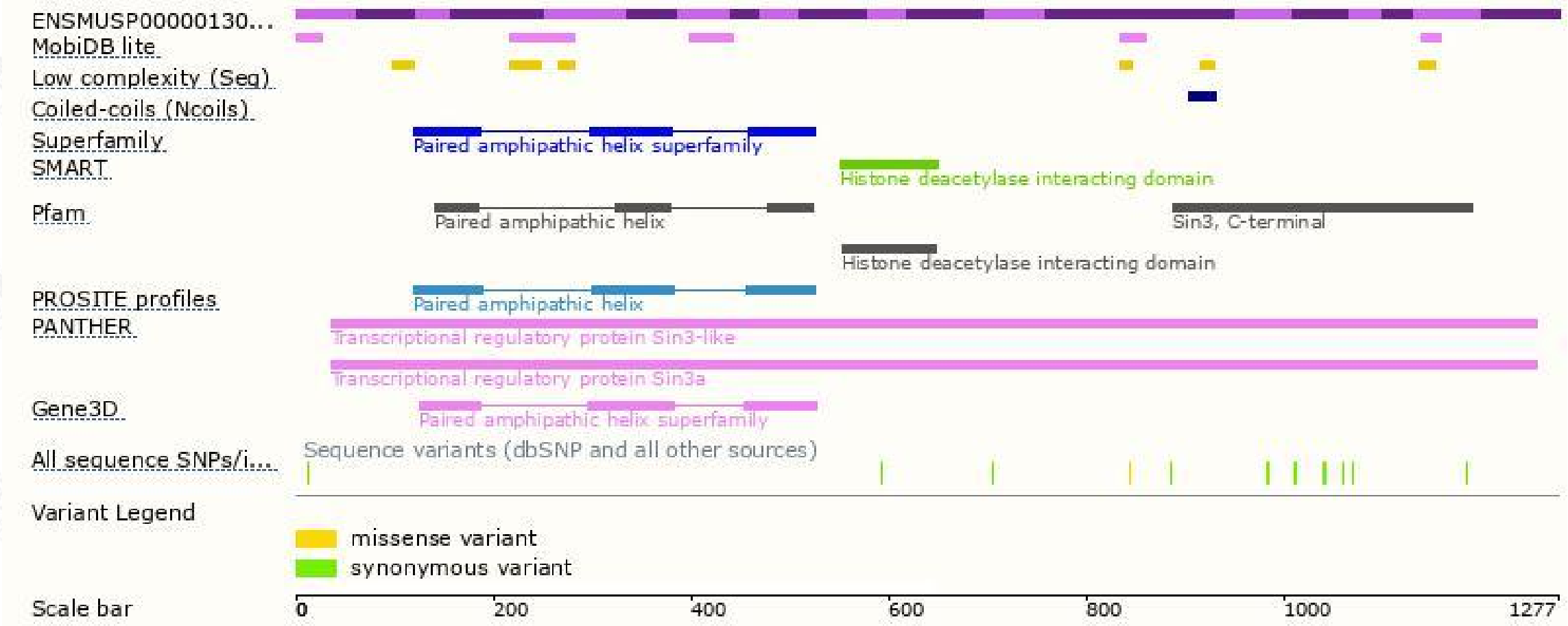
The strategy is based on the design of *Sin3a-206* transcript,the transcription is shown below:



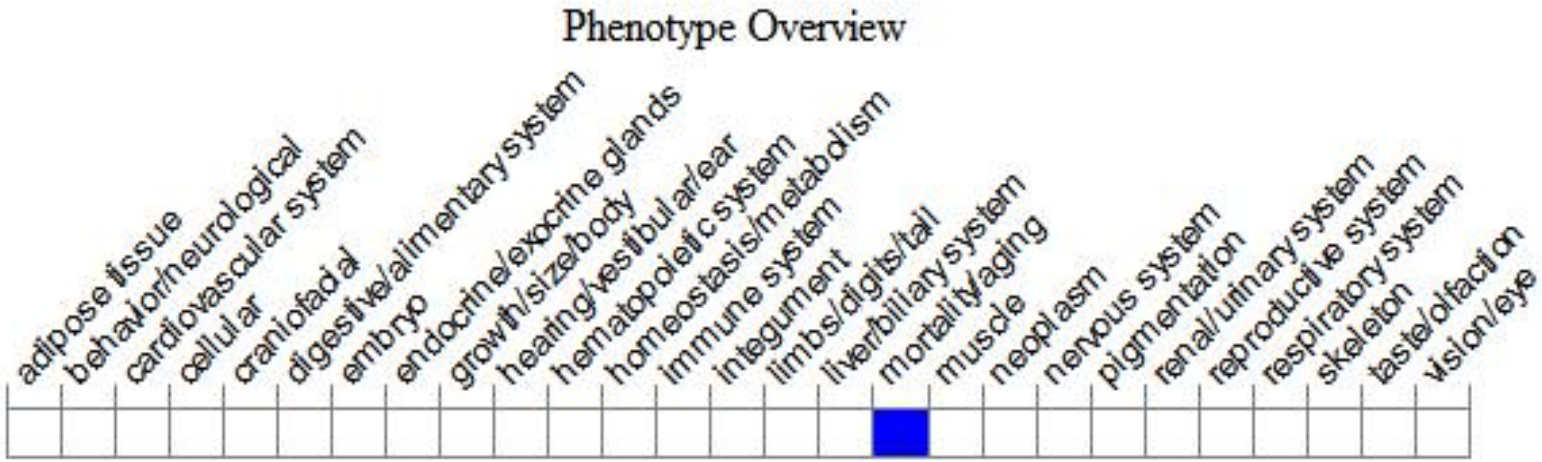
Genomic location distribution



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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