

Sun1 Cas9-KO Strategy

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Project Overview

Project Name

Sun1

Project type

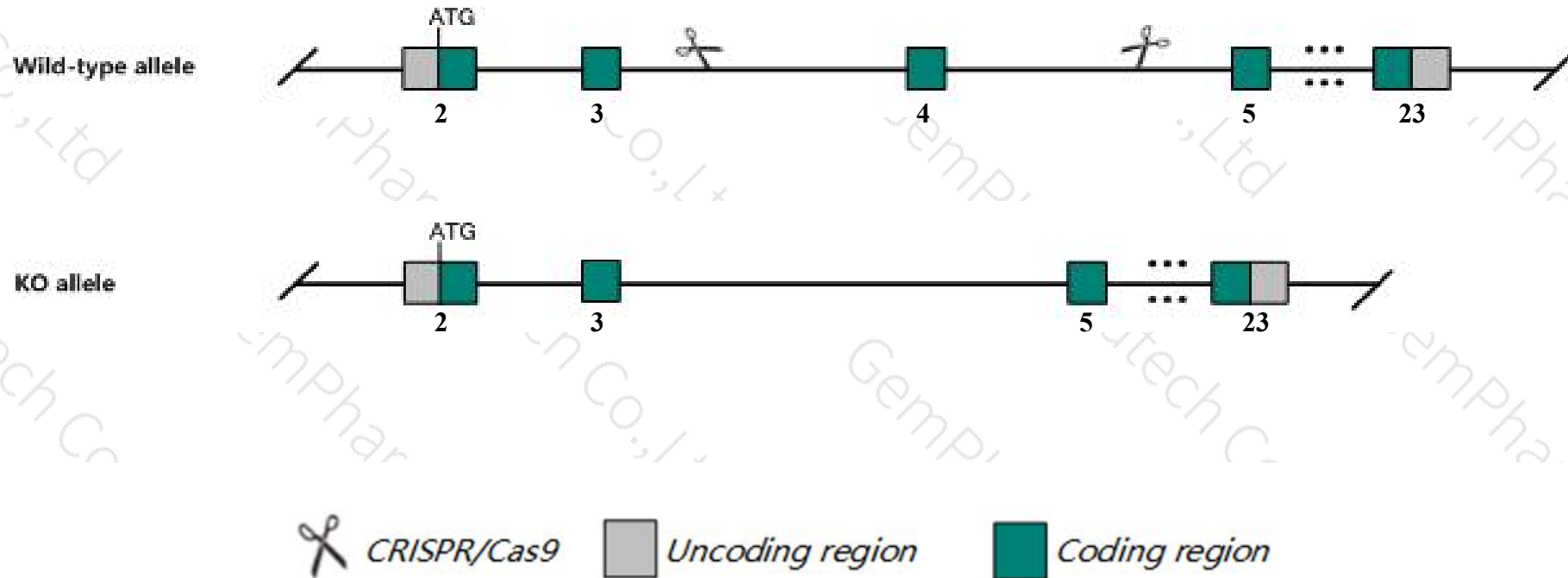
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sun1* gene. The schematic diagram is as follows:



- The *Sun1* gene has 20 transcripts. According to the structure of *Sun1* gene, exon4 of *Sun1-201* (ENSMUST00000058716.13) transcript is recommended as the knockout region. The region contains 185bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sun1* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Mice homozygous for a null allele exhibit sterility due to arrested meiosis, hearing loss associated with outer hair cell degeneration, abnormal cerebellum development, ataxia, impaired motor coordination, and abnormal Purkinje cell migration.
- Transcripts *Sun1* -209, 211, 214 may not be affected .
- The *Sun1* gene is located on the Chr5. 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)

Sun1 Sad1 and UNC84 domain containing 1 [Mus musculus (house mouse)]

Gene ID: 77053, updated on 19-Mar-2019

Summary



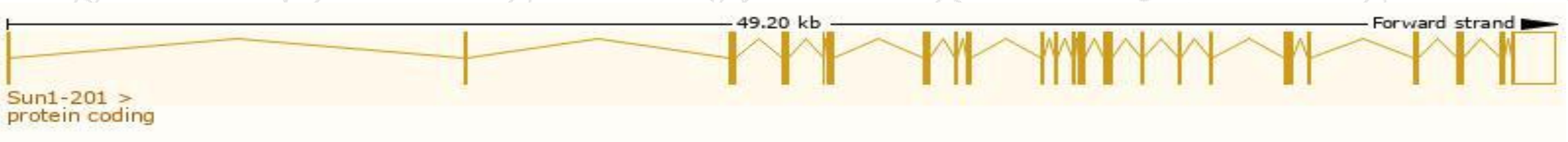
Official Symbol	Sun1 provided by MGI
Official Full Name	Sad1 and UNC84 domain containing 1 provided by MGI
Primary source	MGI:MGI:1924303
See related	Ensembl:ENSMUSG00000036817
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4632417G13Rik, 5730434D03Rik, Unc84a, mKIAA0810
Expression	Ubiquitous expression in testis adult (RPKM 24.4), bladder adult (RPKM 22.9) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

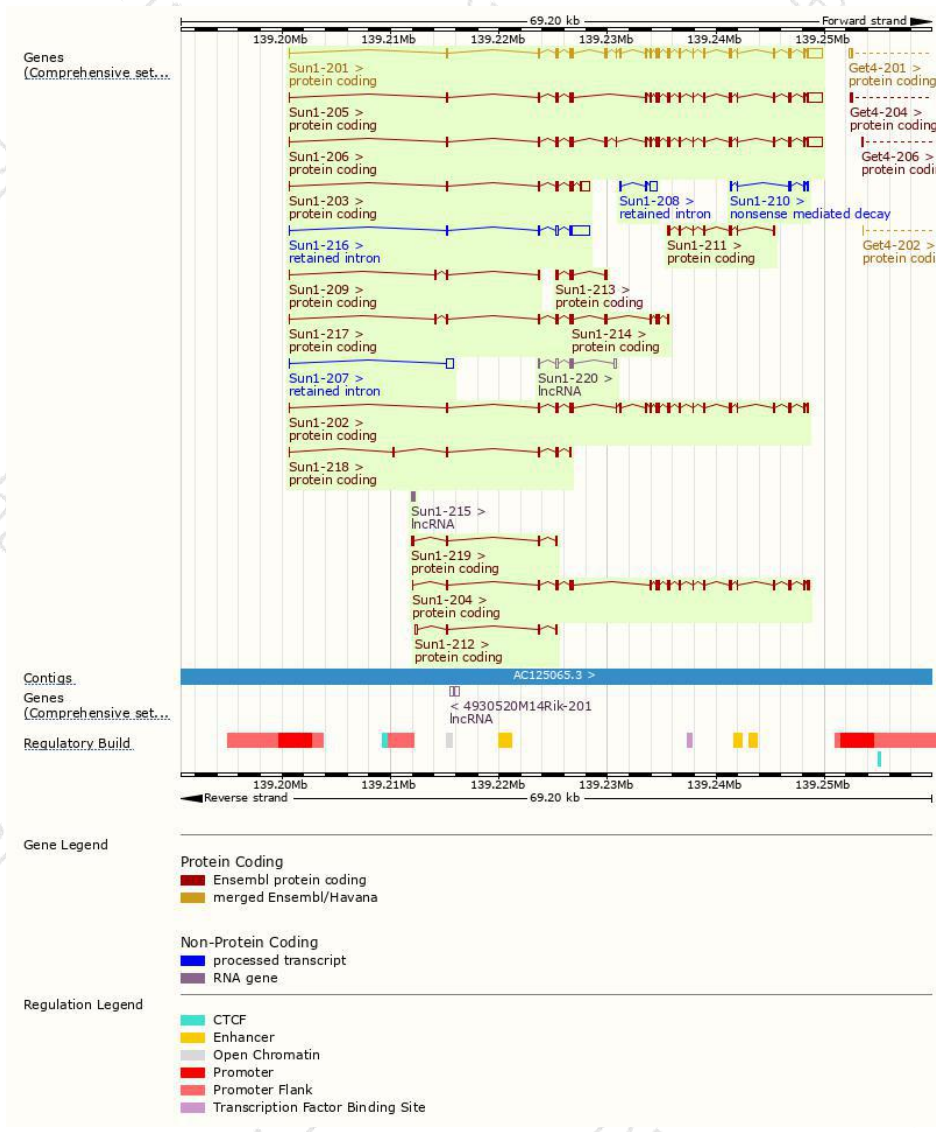
The gene has 20 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sun1-201	ENSMUST00000058716.13	4134	913aa	Protein coding	CCDS19804	Q9D666	TSL:1 GENCODE basic APPRIS P3
Sun1-206	ENSMUST00000110884.8	3955	876aa	Protein coding	CCDS57395	Q9D666	TSL:1 GENCODE basic APPRIS ALT2
Sun1-205	ENSMUST00000110883.8	3714	790aa	Protein coding	CCDS57397	Q9D666	TSL:1 GENCODE basic APPRIS ALT2
Sun1-202	ENSMUST00000078690.12	2608	849aa	Protein coding	CCDS57396	Q9D666	TSL:5 GENCODE basic APPRIS ALT2
Sun1-204	ENSMUST00000110882.7	2454	757aa	Protein coding	CCDS57398	Q9D666	TSL:5 GENCODE basic APPRIS ALT2
Sun1-203	ENSMUST00000100517.9	1522	239aa	Protein coding	-	Q3TSM1	TSL:1 GENCODE basic
Sun1-211	ENSMUST00000128817.7	774	258aa	Protein coding	-	F6RMJ1	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Sun1-214	ENSMUST00000135926.1	768	256aa	Protein coding	-	F6XYA0	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Sun1-218	ENSMUST00000146715.7	650	160aa	Protein coding	-	D3Z3N5	CDS 3' incomplete TSL:5
Sun1-219	ENSMUST00000148772.7	641	175aa	Protein coding	-	D3YUW9	CDS 3' incomplete TSL:3
Sun1-217	ENSMUST00000143562.7	621	158aa	Protein coding	-	D3Z5Q2	CDS 3' incomplete TSL:5
Sun1-213	ENSMUST00000135720.2	593	197aa	Protein coding	-	F7BX07	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:2
Sun1-212	ENSMUST00000129079.1	566	131aa	Protein coding	-	D3Z1X3	CDS 3' incomplete TSL:3
Sun1-209	ENSMUST00000127045.7	387	53aa	Protein coding	-	D3Z0L7	CDS 3' incomplete TSL:3
Sun1-210	ENSMUST00000127310.1	569	117aa	Nonsense mediated decay	-	F7AJ01	CDS 5' incomplete TSL:3
Sun1-216	ENSMUST00000142473.7	2168	No protein	Retained intron	-	-	TSL:2
Sun1-208	ENSMUST00000126108.1	876	No protein	Retained intron	-	-	TSL:5
Sun1-207	ENSMUST00000123414.1	643	No protein	Retained intron	-	-	TSL:2
Sun1-220	ENSMUST00000153469.3	725	No protein	lncRNA	-	-	TSL:3
Sun1-215	ENSMUST00000136311.1	233	No protein	lncRNA	-	-	TSL:5

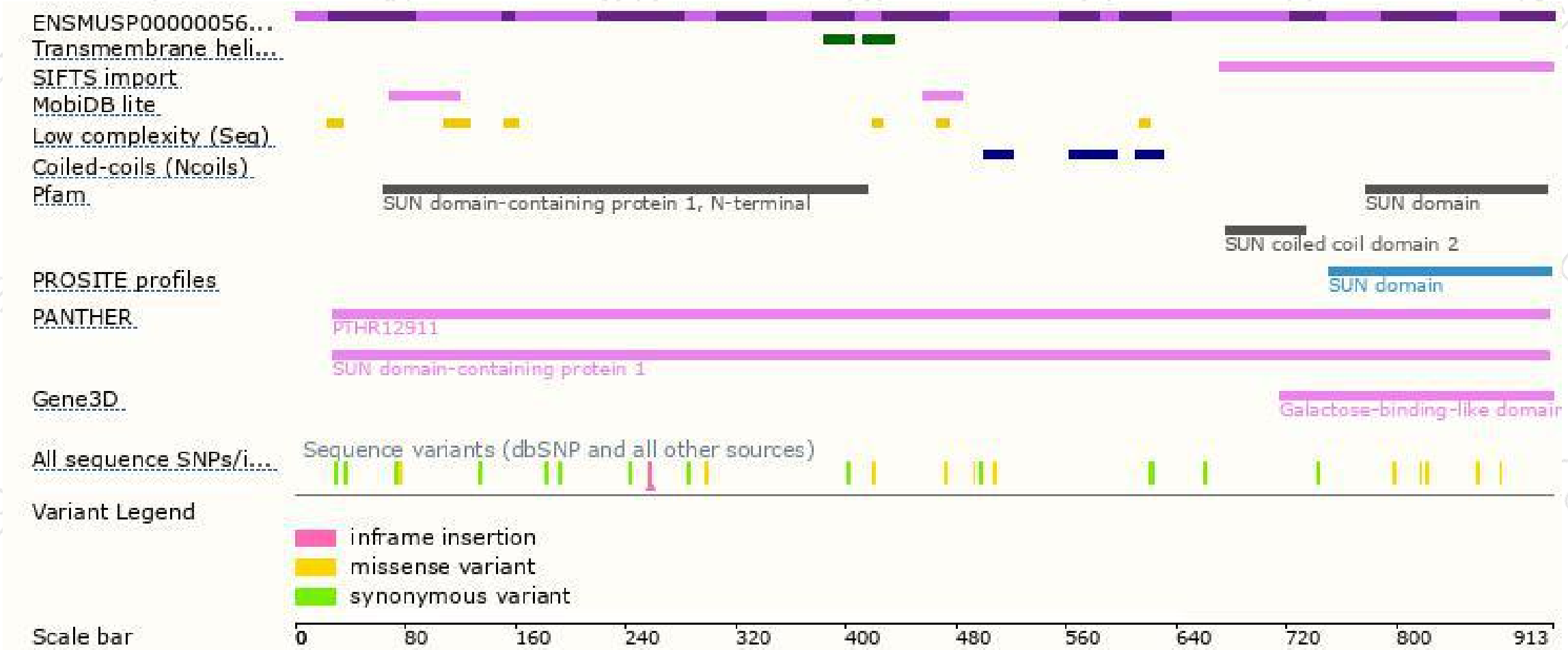
The strategy is based on the design of *Sun1-201* transcript,The transcription is shown below



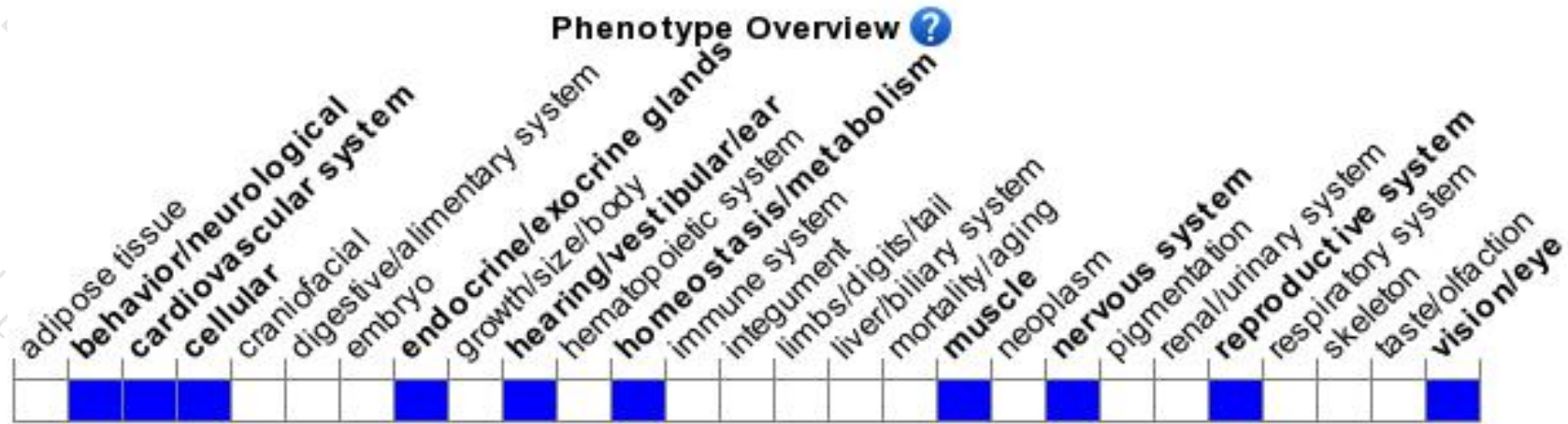
Genomic location distribution



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 null allele exhibit sterility due to arrested meiosis, hearing loss associated with outer hair cell degeneration, abnormal cerebellum development, ataxia, impaired motor coordination, and abnormal Purkinje cell migration.

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

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