

Sik2 Cas9-KO Strategy

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Design Date:

2020-2-19

Project Overview

Project Name

Sik2

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sik2* gene. The schematic diagram is as follows:



- The *Sik2* gene has 8 transcripts. According to the structure of *Sik2* gene, exon2-exon3 of *Sik2-201* (ENSMUST00000041375.10) transcript is recommended as the knockout region. The region contains 181bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sik2* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Mice heterozygous for a knock-out allele exhibit darkened hair color in an agouti background.
- The *Sik2* 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)

Sik2 salt inducible kinase 2 [Mus musculus (house mouse)]

Gene ID: 235344, updated on 31-Jan-2019

Summary



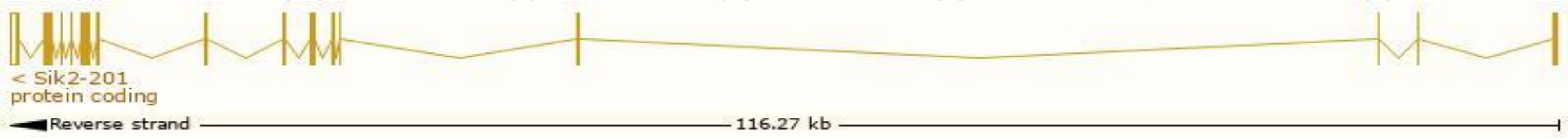
Official Symbol	Sik2 provided by MGI
Official Full Name	salt inducible kinase 2 provided by MGI
Primary source	MGI:MGI:2445031
See related	Ensembl:ENSMUSG000000037112
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	G630080D20Rik, Snf1lk2
Expression	Broad expression in subcutaneous fat pad adult (RPKM 39.2), mammary gland adult (RPKM 30.6) and 24 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

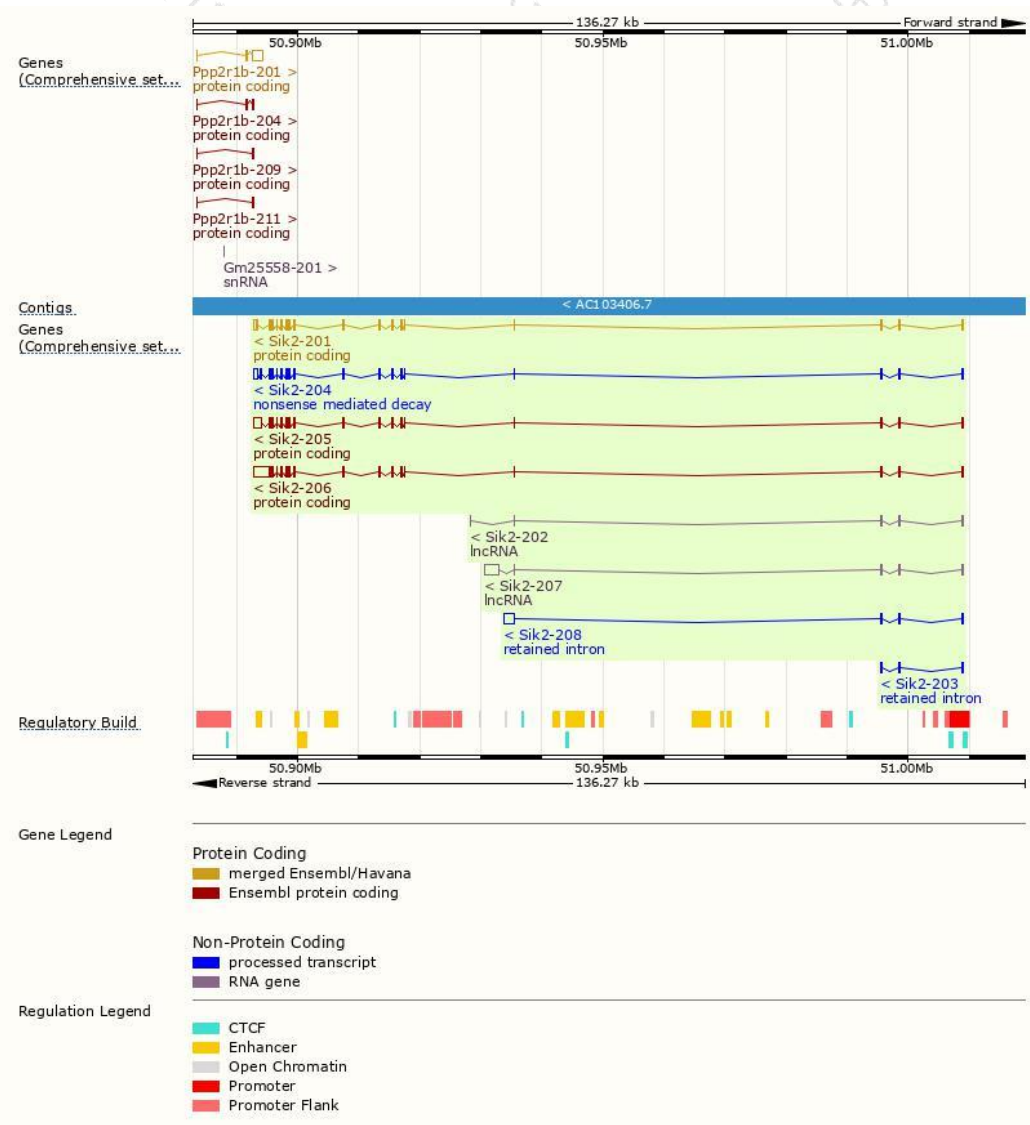
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sik2-201	ENSMUST00000041375.10	3552	931aa	Protein coding	CCDS40627	F8VPT7	TSL:1 GENCODE basic APPRIS P2
Sik2-206	ENSMUST00000176824.7	5369	927aa	Protein coding	-	H3BJC9	TSL:5 GENCODE basic APPRIS ALT2
Sik2-205	ENSMUST00000176663.7	4107	929aa	Protein coding	-	H3BKG1	TSL:5 GENCODE basic APPRIS ALT2
Sik2-204	ENSMUST00000176491.7	3576	929aa	Nonsense mediated decay	-	H3BKG1	TSL:1
Sik2-208	ENSMUST00000177346.7	2183	No protein	Retained intron	-	-	TSL:1
Sik2-203	ENSMUST00000176327.1	476	No protein	Retained intron	-	-	TSL:2
Sik2-207	ENSMUST00000177203.7	2991	No protein	lncRNA	-	-	TSL:1
Sik2-202	ENSMUST00000068484.15	654	No protein	lncRNA	-	-	TSL:5

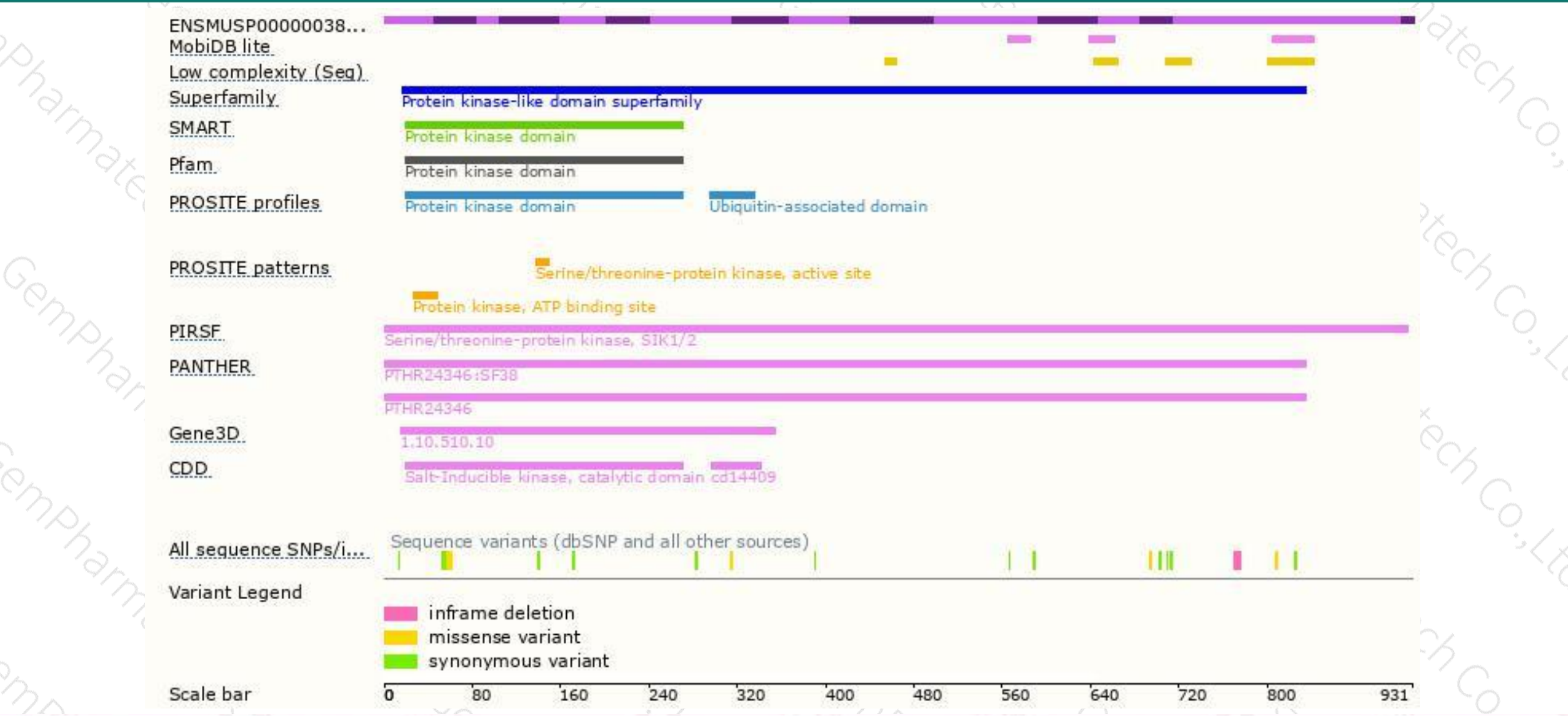
The strategy is based on the design of *Sik2-201* transcript,The transcription is shown below



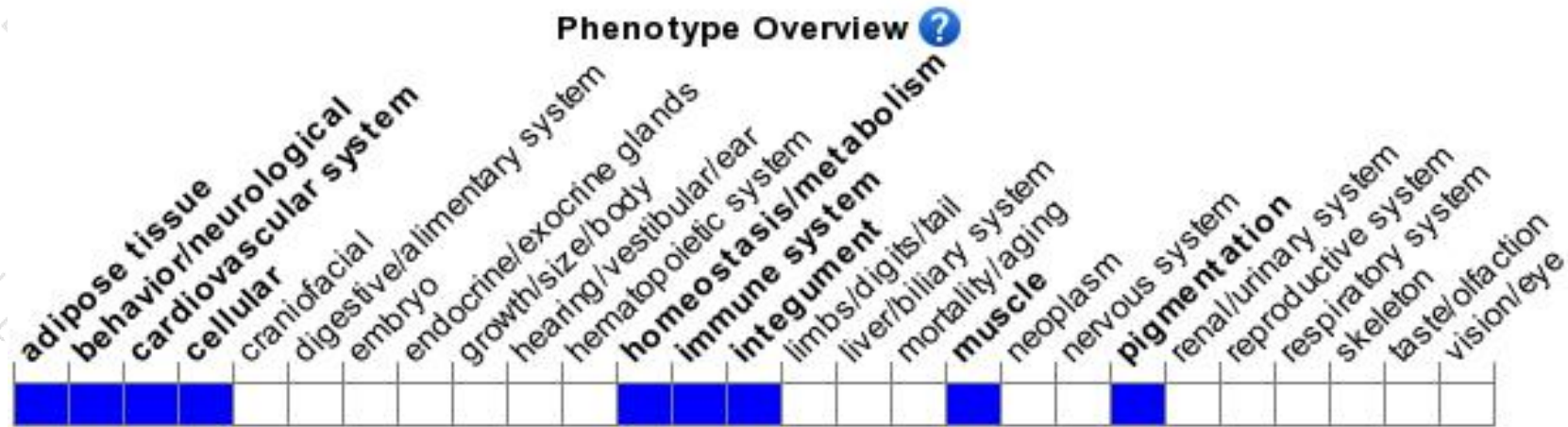
Genomic location distribution



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 heterozygous for a knock-out allele exhibit darkened hair color in an agouti background.

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

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