

Samd4 Cas9-CKO Strategy

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Project Overview

Project Name

Samd4

Project type

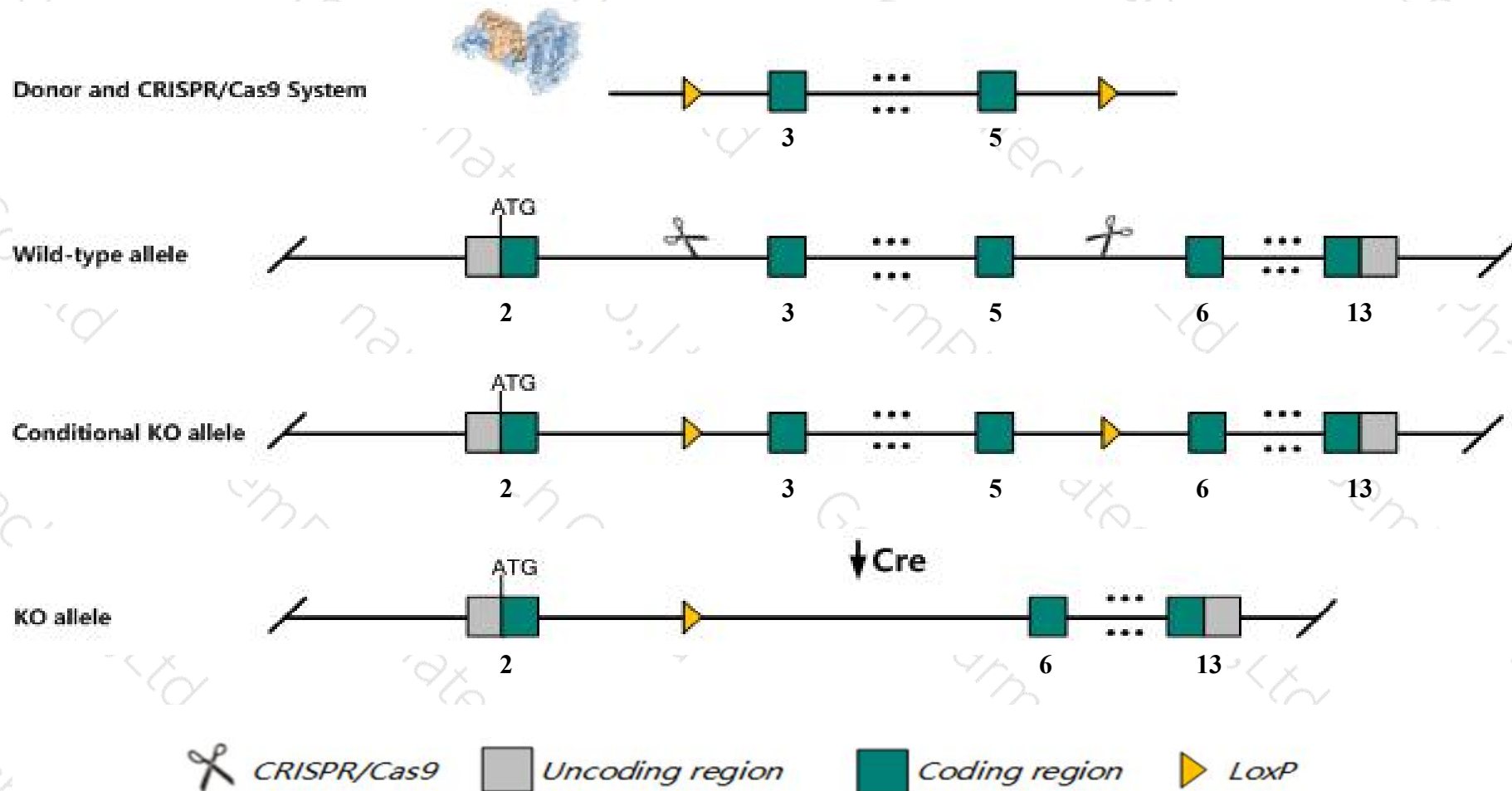
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Samd4* gene. The schematic diagram is as follows:



Technical routes

- The *Samd4* gene has 11 transcripts. According to the structure of *Samd4* gene, exon3-exon5 of *Samd4-201*(ENSMUST00000022386.14) transcript is recommended as the knockout region. The region contains 893bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Samd4* gene. The brief process is as follows: gRNA was transcribed in vitro, donor was constructed. Cas9, gRNA 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.

- According to the existing MGI data, mice homozygous for an ENU-induced allele exhibit leanness, myopathy and altered glucose metabolism. Mice homozygous for a spontaneous mutation exhibit kyphosis, abnormal gait, and decreased cortical bone thickness.
- Transcript *Samd4* -204 may not be affected.
- The *Samd4* gene is located on the Chr14. 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)

Samd4 sterile alpha motif domain containing 4 [Mus musculus (house mouse)]

Gene ID: 74480, updated on 31-Jan-2019

Summary



Official Symbol	Samd4 provided by MGI
Official Full Name	sterile alpha motif domain containing 4 provided by MGI
Primary source	MGI:MGI:1921730
See related	Ensembl:ENSMUSG000000021838
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	1700024G08Rik, 1700111L17Rik, 4933436G17Rik, Samd4a, Smaug, Smaug1, sunk
Expression	Biased expression in testis adult (RPKM 72.9), bladder adult (RPKM 9.4) and 6 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

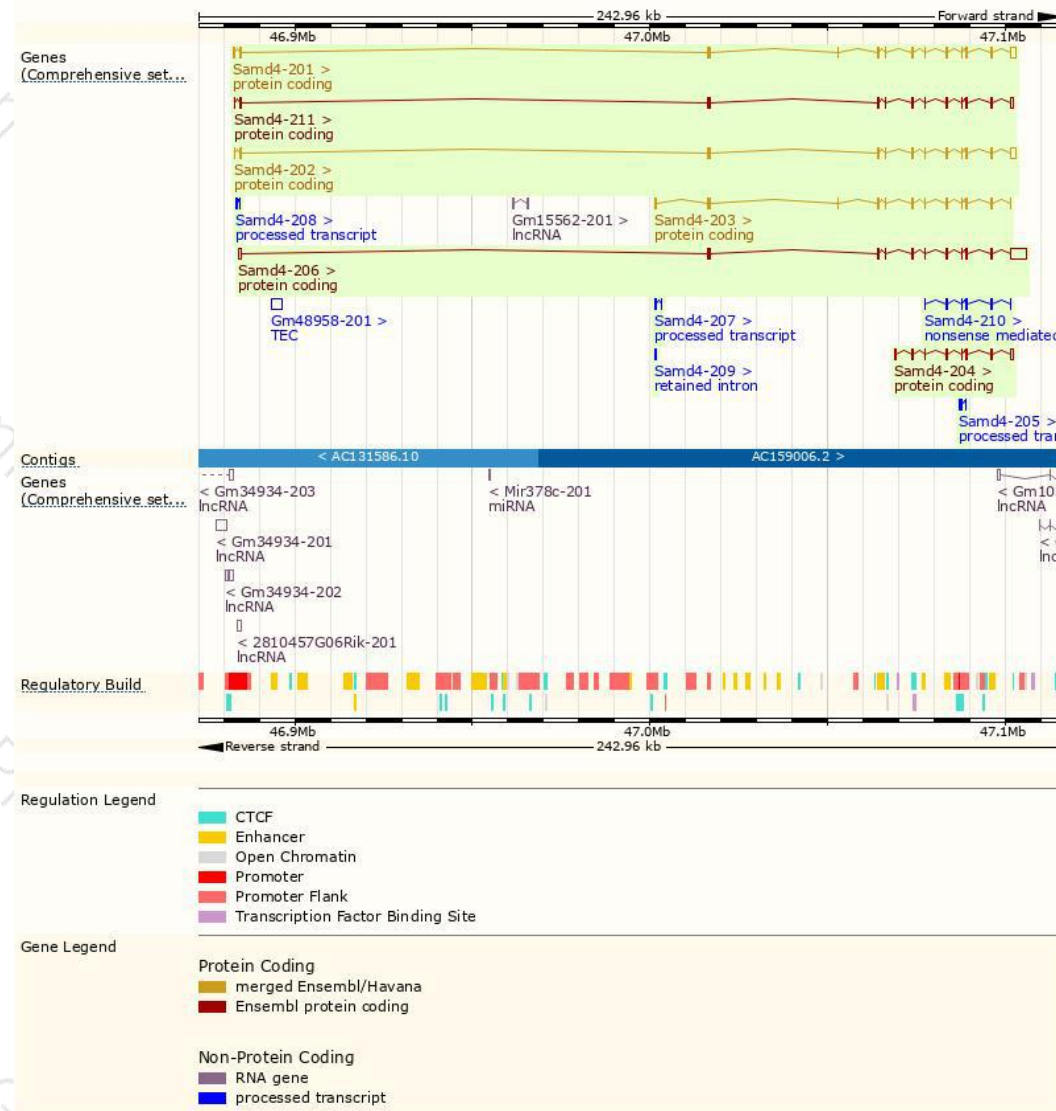
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Samd4-206	ENSMUST00000137543.8	6874	623aa	Protein coding	CCDS26983	Q8CBY1	TSL:1 GENCODE basic APPRIS ALT 2
Samd4-201	ENSMUST00000022386.14	4564	711aa	Protein coding	CCDS26982	Q8CBY1	TSL:1 GENCODE basic APPRIS P 4
Samd4-202	ENSMUST00000100672.10	4165	623aa	Protein coding	CCDS26983	Q8CBY1	TSL:1 GENCODE basic APPRIS ALT 2
Samd4-203	ENSMUST00000125113.8	2442	610aa	Protein coding	CCDS49468	A0A2D0VMX2 Q8CBY1	TSL:1 GENCODE basic APPRIS ALT 2
Samd4-204	ENSMUST00000125688.1	1773	302aa	Protein coding	CCDS79301	Q8CBY1	TSL:1 GENCODE basic
Samd4-211	ENSMUST00000228404.1	3039	522aa	Protein coding	-	A0A2I3BPM7	GENCODE basic APPRIS ALT 2
Samd4-210	ENSMUST00000227848.1	505	114aa	Nonsense mediated decay	-	A0A2I3BRV2	CDS 5' incomplete
Samd4-207	ENSMUST00000140571.1	552	No protein	Processed transcript	-	-	TSL:1
Samd4-205	ENSMUST00000130046.1	527	No protein	Processed transcript	-	-	TSL:3
Samd4-208	ENSMUST00000141767.1	385	No protein	Processed transcript	-	-	TSL:3
Samd4-209	ENSMUST00000226684.1	383	No protein	Retained intron	-	-	

The strategy is based on the design of *Samd4-201* transcript,the transcription is shown below:



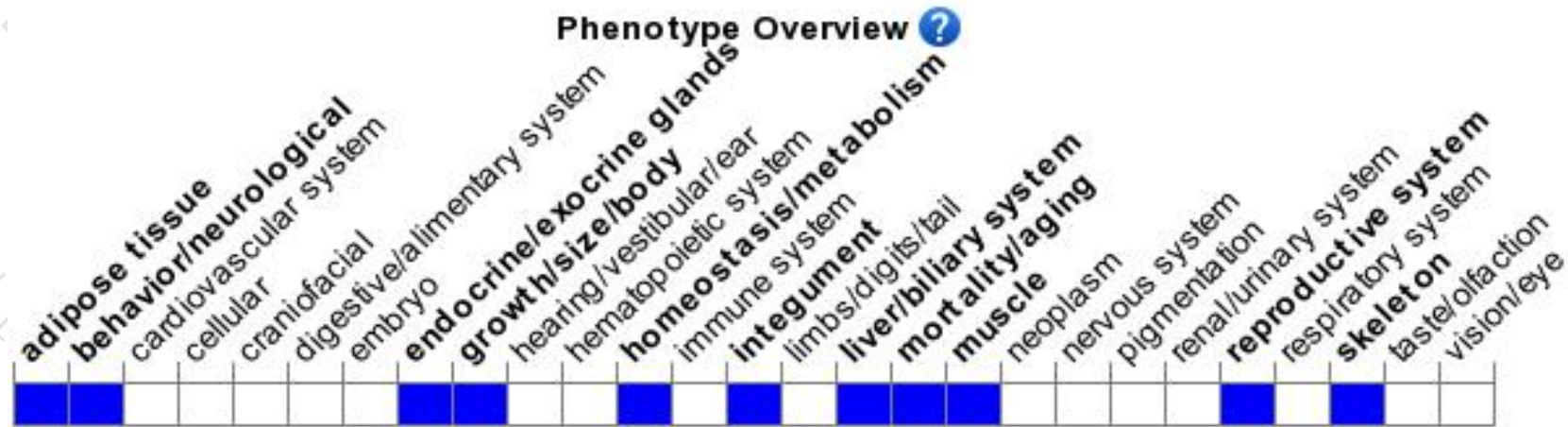
Genomic location distribution



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 an ENU-induced allele exhibit leanness, myopathy and altered glucose metabolism. Mice homozygous for a spontaneous mutation exhibit kyphosis, abnormal gait, and decreased cortical bone thickness.

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

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