

***Sox6* Cas9-CKO Strategy**

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Project Overview

Project Name

Sox6

Project type

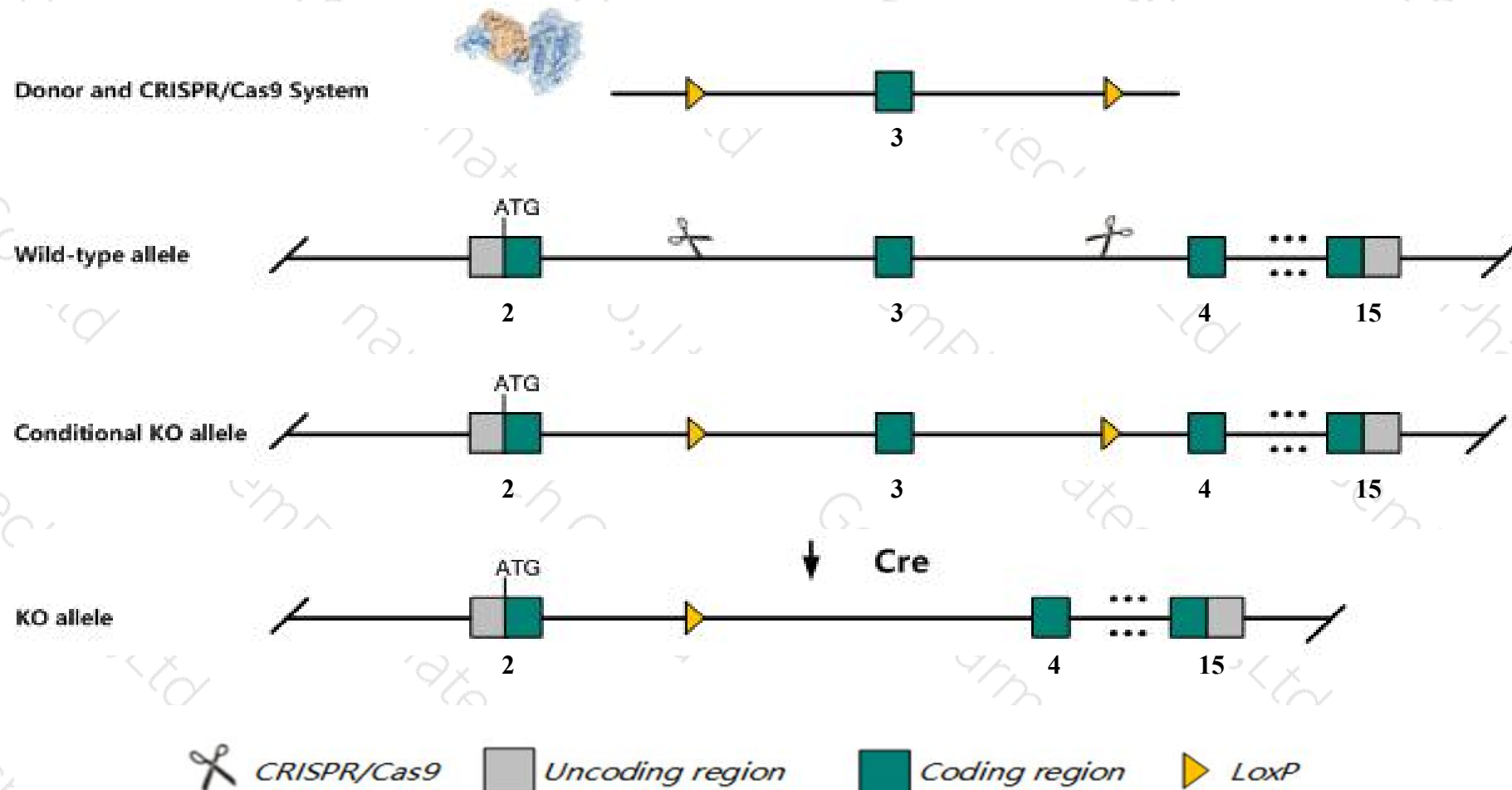
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Sox6* gene. The schematic diagram is as follows:



Technical routes

- The *Sox6* gene has 16 transcripts. According to the structure of *Sox6* gene, exon3 of *Sox6*-205(ENSMUST00000169129.7) transcript is recommended as the knockout region. The region contains 208bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Sox6* gene. The brief process is as follows: CRISPR/Cas9 system 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, homozygotes for null mutations exhibit cardioskeletal myopathy, cardiac blockage, delayed growth, and early postnatal lethality.
- *Sox6-207* may not be affected.
- The *Sox6* gene is located on the Chr7. 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)

Sox6 SRY (sex determining region Y)-box 6 [Mus musculus (house mouse)]

Gene ID: 20679, updated on 13-Mar-2020

Summary

Official Symbol Sox6 provided by [MGI](#)

Official Full Name SRY (sex determining region Y)-box 6 provided by [MGI](#)

Primary source [MGI:MGI:98368](#)

See related [Ensembl:ENSMUSG00000051910](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as AI987981, SOX-LZ

Summary This gene encodes a member of a family of transcriptional regulators containing high mobility group (HMG) DNA-binding domains. Function of the encoded protein is important for proper cardiac and skeletal development. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Mar 2013]

Expression Ubiquitous expression in testis adult (RPKM 2.9), liver E14 (RPKM 2.2) and 26 other tissues [See more](#)

Orthologs [human](#) [all](#)

Transcript information (Ensembl)

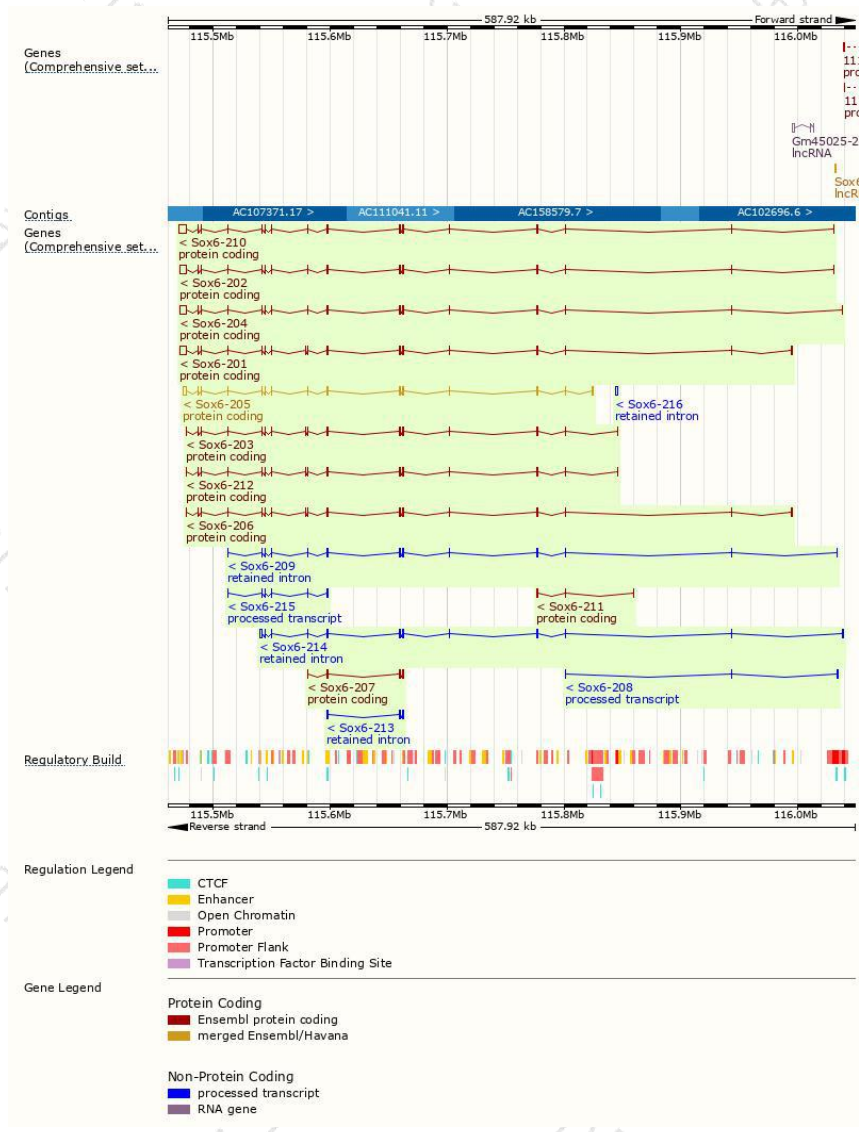
The gene has 16 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Sox6-201	ENSMUST00000072804.10	8227	827aa	Protein coding	CCDS40098	P40645_Q3V1J7	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 P4
Sox6-202	ENSMUST00000106612.7	8193	785aa	Protein coding	CCDS40097	Q8BSS6	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 ALT2
Sox6-204	ENSMUST00000166877.7	8079	787aa	Protein coding	CCDS52369	E9PUW0	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 ALT2
Sox6-205	ENSMUST00000169129.7	5122	787aa	Protein coding	CCDS52369	E9PUW0	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 ALT2
Sox6-203	ENSMUST00000166207.2	2825	827aa	Protein coding	CCDS40098	P40645_Q3V1J7	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 P4
Sox6-210	ENSMUST00000206034.1	8668	786aa	Protein coding	-	A0A0U1RPC1	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 ALT2
Sox6-206	ENSMUST00000205405.1	2903	828aa	Protein coding	-	A0A0U1RNW8	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 ALT2
Sox6-212	ENSMUST00000206369.1	2863	828aa	Protein coding	-	A0A0U1RNW8	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 ALT2
Sox6-211	ENSMUST00000206123.1	448	125aa	Protein coding	-	A0A0U1RNI3	CDS 3' incomplete TSL:2
Sox6-207	ENSMUST00000205479.1	331	111aa	Protein coding	-	A0A0U1RNH0	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Sox6-215	ENSMUST00000206775.1	828	No protein	Processed transcript	-	-	TSL:5
Sox6-208	ENSMUST00000205818.1	479	No protein	Processed transcript	-	-	TSL:5
Sox6-214	ENSMUST00000206573.1	3855	No protein	Retained intron	-	-	TSL:2
Sox6-209	ENSMUST00000205980.1	2258	No protein	Retained intron	-	-	TSL:5
Sox6-216	ENSMUST00000206912.1	1980	No protein	Retained intron	-	-	TSL:NA
Sox6-213	ENSMUST00000206427.1	553	No protein	Retained intron	-	-	TSL:5

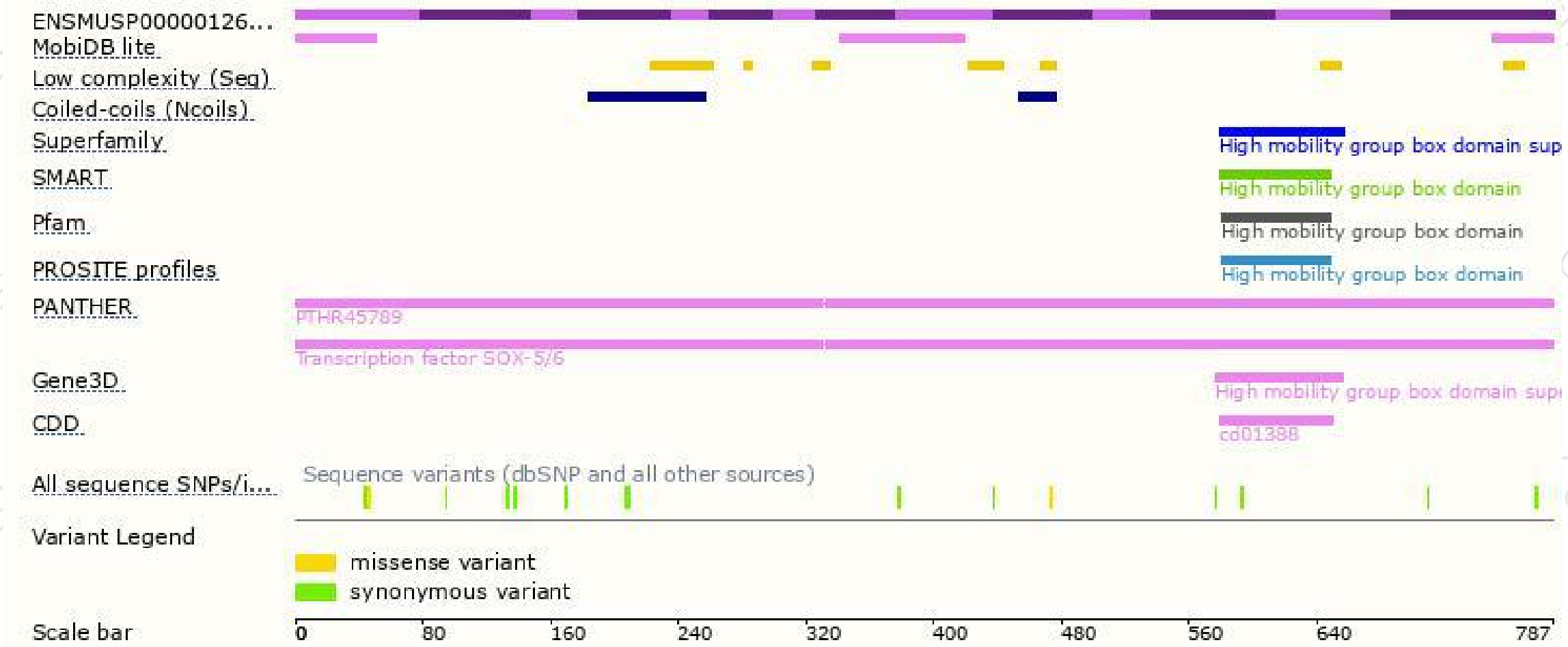
The strategy is based on the design of Sox6-205 transcript,the transcription is shown below:



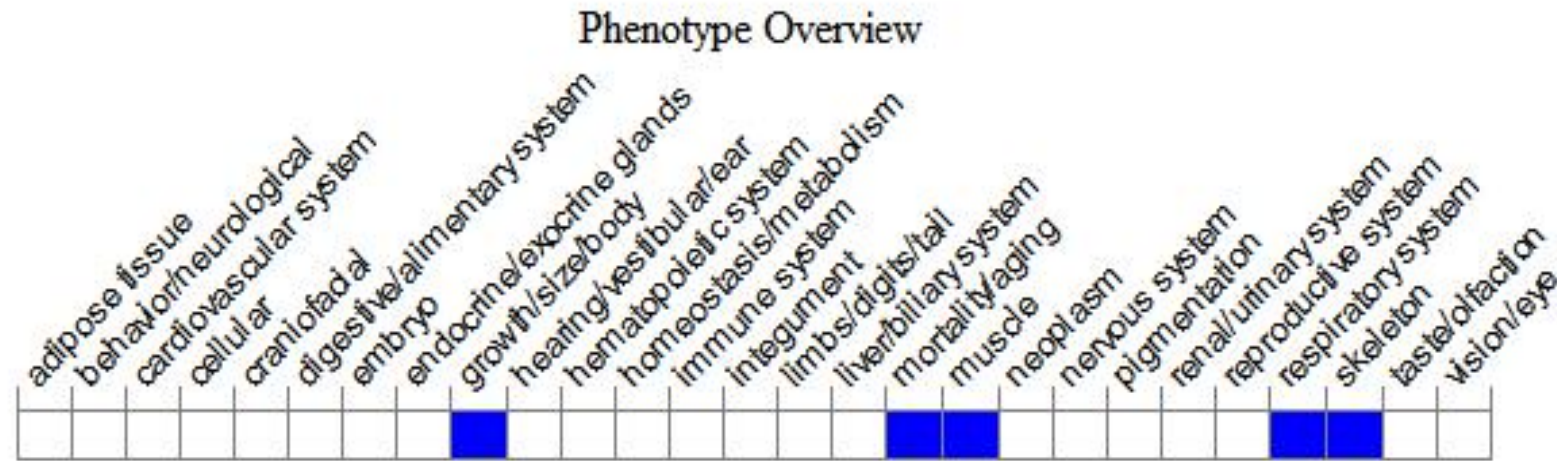
Genomic location distribution



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, homozygotes for null mutations exhibit cardioskeletal myopathy, cardiac blockage, delayed growth, and early postnatal lethality.

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

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