

Styxl1 Cas9-KO Strategy

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Project Overview

Project Name

Styxl1

Project type

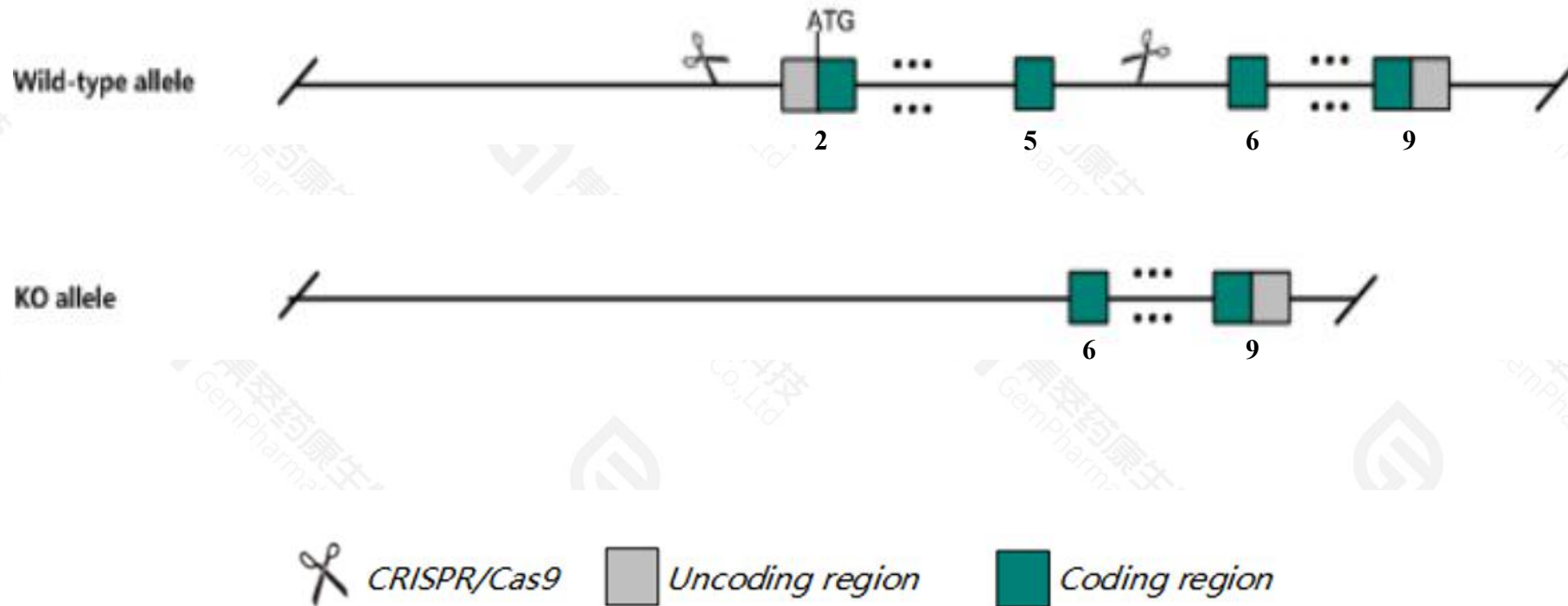
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Styx11* gene. The schematic diagram is as follows:



- The *Styx11* gene has 9 transcripts. According to the structure of *Styx11* gene, exon2-exon5 of *Styx11-201*(ENSMUST00000053906.10) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Styx11* 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.

- The *Styx11* 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.

Styxl1 serine/threonine/tyrosine interacting-like 1 [Mus musculus (house mouse)]

Gene ID: 76571, updated on 13-Mar-2020

Summary



Official Symbol Styxl1 provided by [MGI](#)

Official Full Name serine/threonine/tyrosine interacting-like 1 provided by [MGI](#)

Primary source [MGI:MGI:1923821](#)

See related [Ensembl:ENSMUSG00000019178](#)

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 1700011C14Rik, Dusp24, Mkstyx

Expression Biased expression in testis adult (RPKM 12.2), ovary adult (RPKM 0.7) and 1 other tissue [See more](#)

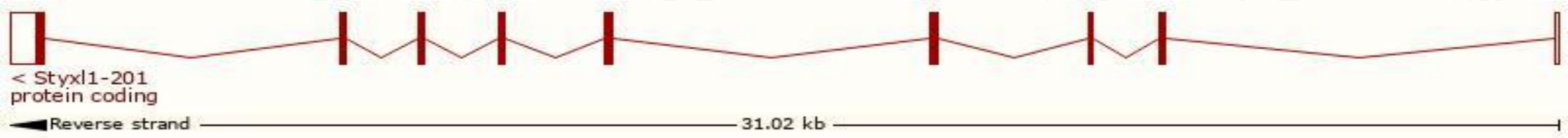
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

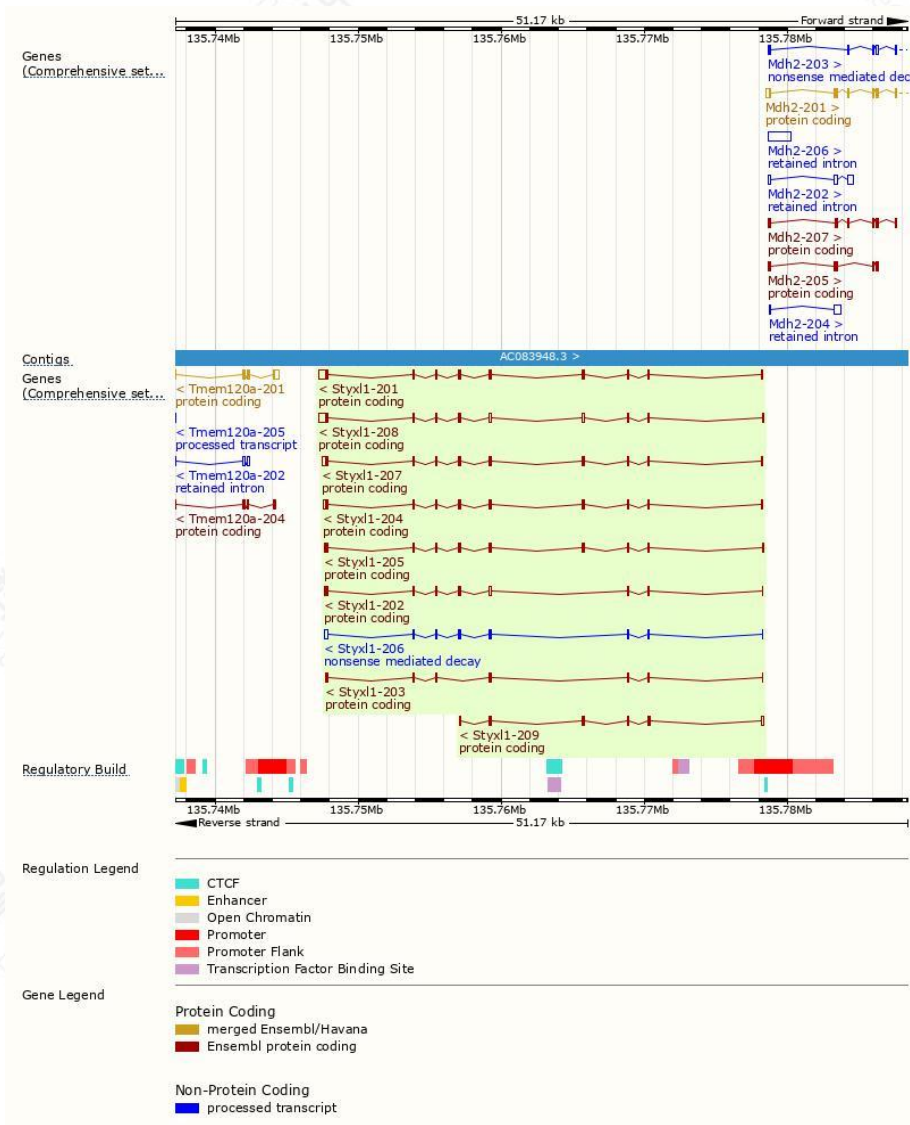
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Styxl1-208	ENSMUST00000178515.7	1651	177aa	Protein coding	CCDS71679	Q9DAG7	TSL:1 GENCODE basic
Styxl1-201	ENSMUST00000053906.10	1582	321aa	Protein coding	CCDS19745	Q9DAR2	TSL:1 GENCODE basic APPRIS P1
Styxl1-204	ENSMUST00000111163.8	1276	321aa	Protein coding	CCDS19745	Q9DAR2	TSL:1 GENCODE basic APPRIS P1
Styxl1-205	ENSMUST00000111164.8	1243	321aa	Protein coding	CCDS19745	Q9DAR2	TSL:1 GENCODE basic APPRIS P1
Styxl1-207	ENSMUST00000177559.7	1236	321aa	Protein coding	CCDS19745	Q9DAR2	TSL:5 GENCODE basic APPRIS P1
Styxl1-202	ENSMUST00000111161.8	963	177aa	Protein coding	CCDS71679	Q9DAG7	TSL:1 GENCODE basic
Styxl1-203	ENSMUST00000111162.7	726	217aa	Protein coding	CCDS71680	D3YZ02	TSL:5 GENCODE basic
Styxl1-209	ENSMUST00000178796.1	680	174aa	Protein coding	-	J3QK74	CDS 3' incomplete TSL:5
Styxl1-206	ENSMUST00000142343.7	963	137aa	Nonsense mediated decay	-	J3QNW1	TSL:1

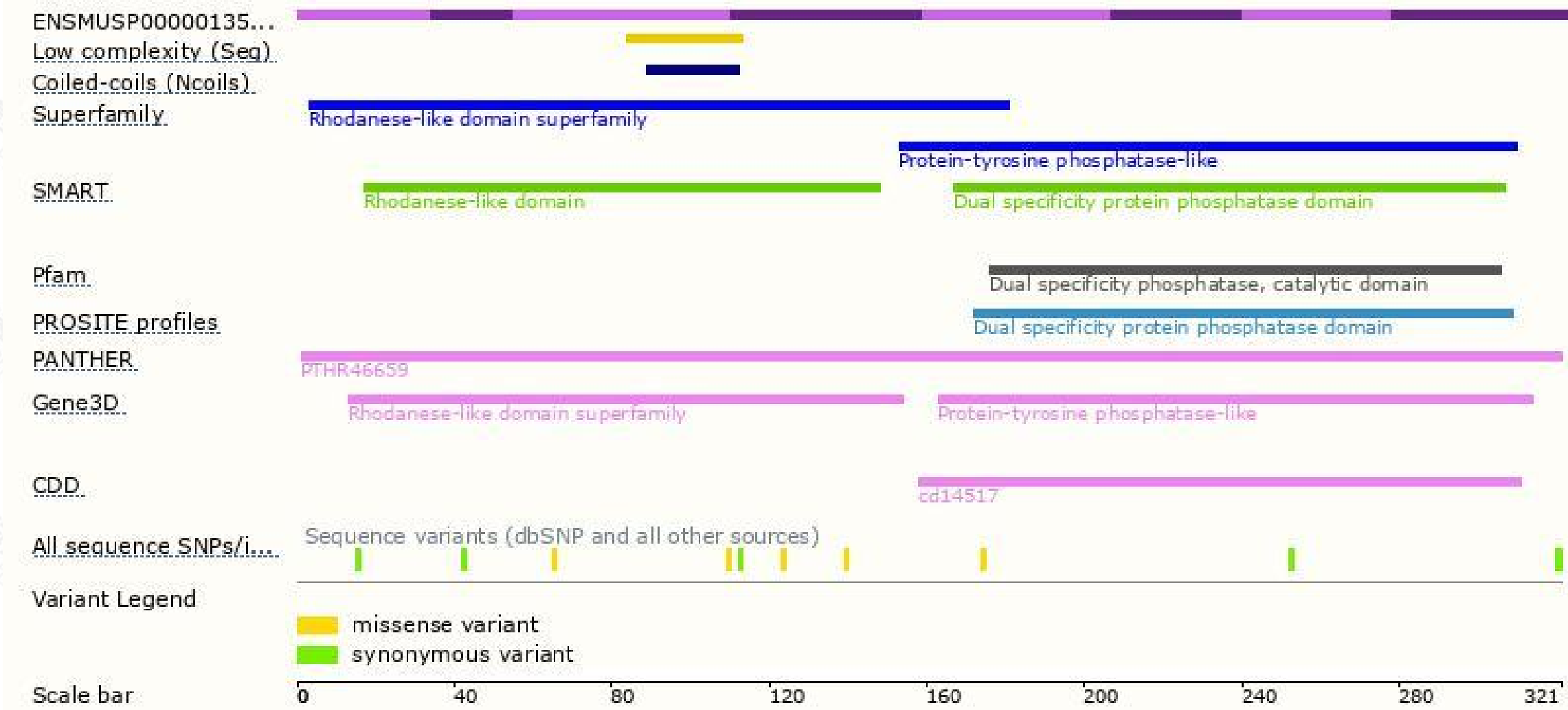
The strategy is based on the design of *Styxl1-201* transcript,the transcription is shown below:



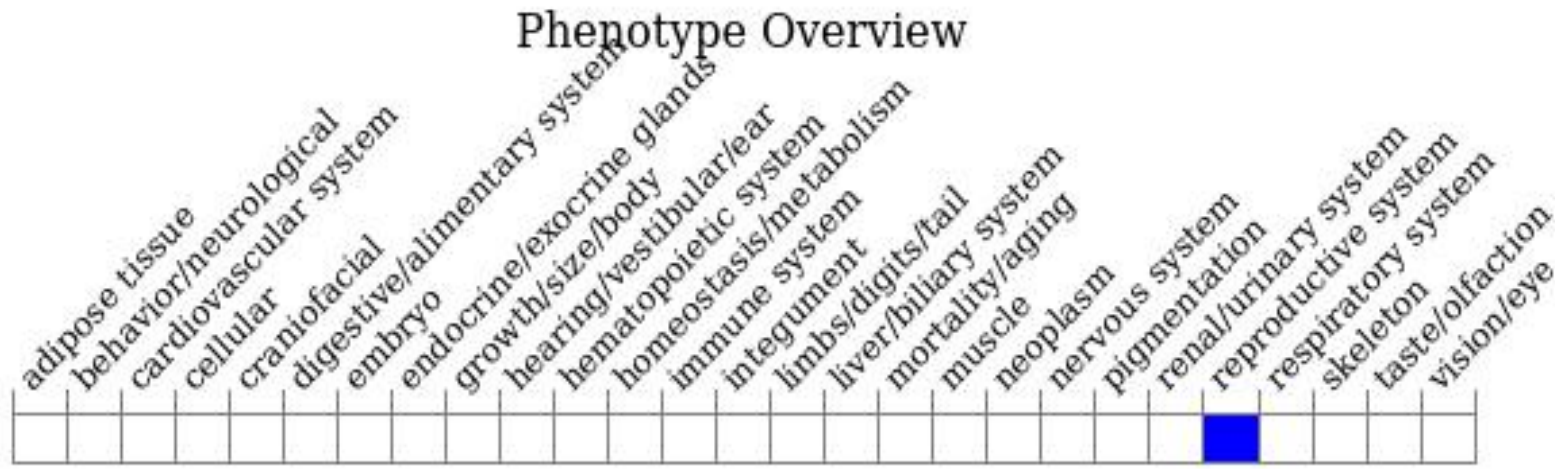
Genomic location distribution



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/>).

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

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