

Styk1 Cas9-KO Strategy

Designer: Lingyan Wu

Reviewer: Rui Xiong

Design Date: 2020-4-23

Project Overview

Project Name

Styk1

Project type

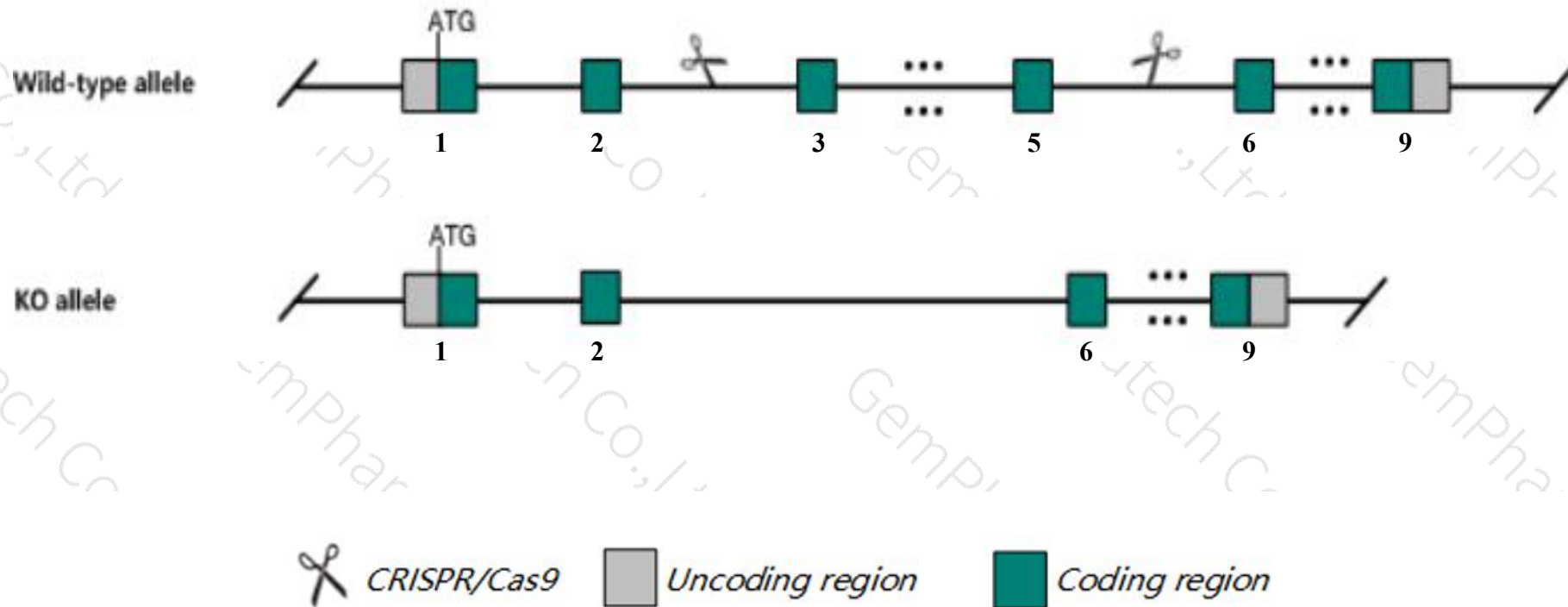
Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Styk1* gene. The schematic diagram is as follows:



- The *Styk1* gene has 5 transcripts. According to the structure of *Styk1* gene, exon3-exon5 of *Styk1-201* (ENSMUST00000049150.7) transcript is recommended as the knockout region. The region contains 533bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Styk1* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Styk1* gene is located on the Chr6. 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)

Styk1 serine/threonine/tyrosine kinase 1 [Mus musculus (house mouse)]

Gene ID: 243659, updated on 13-Mar-2020

Summary



Official Symbol	Styk1 provided by MGI
Official Full Name	serine/threonine/tyrosine kinase 1 provided by MGI
Primary source	MGI:MGI:2141396
See related	Ensembl:ENSMUSG00000032899
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	9130025L13, A1326477, Nok
Expression	Biased expression in large intestine adult (RPKM 8.7), colon adult (RPKM 6.8) and 6 other tissues See more
Orthologs	human all

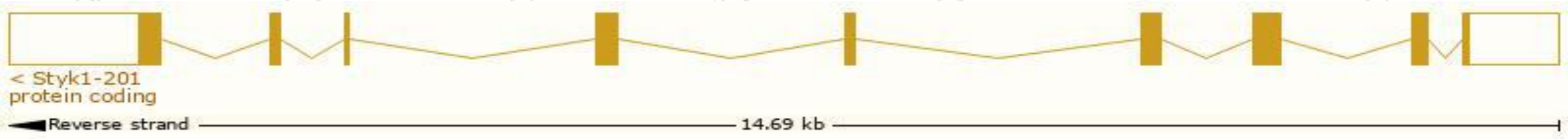
Transcript information（Ensembl）



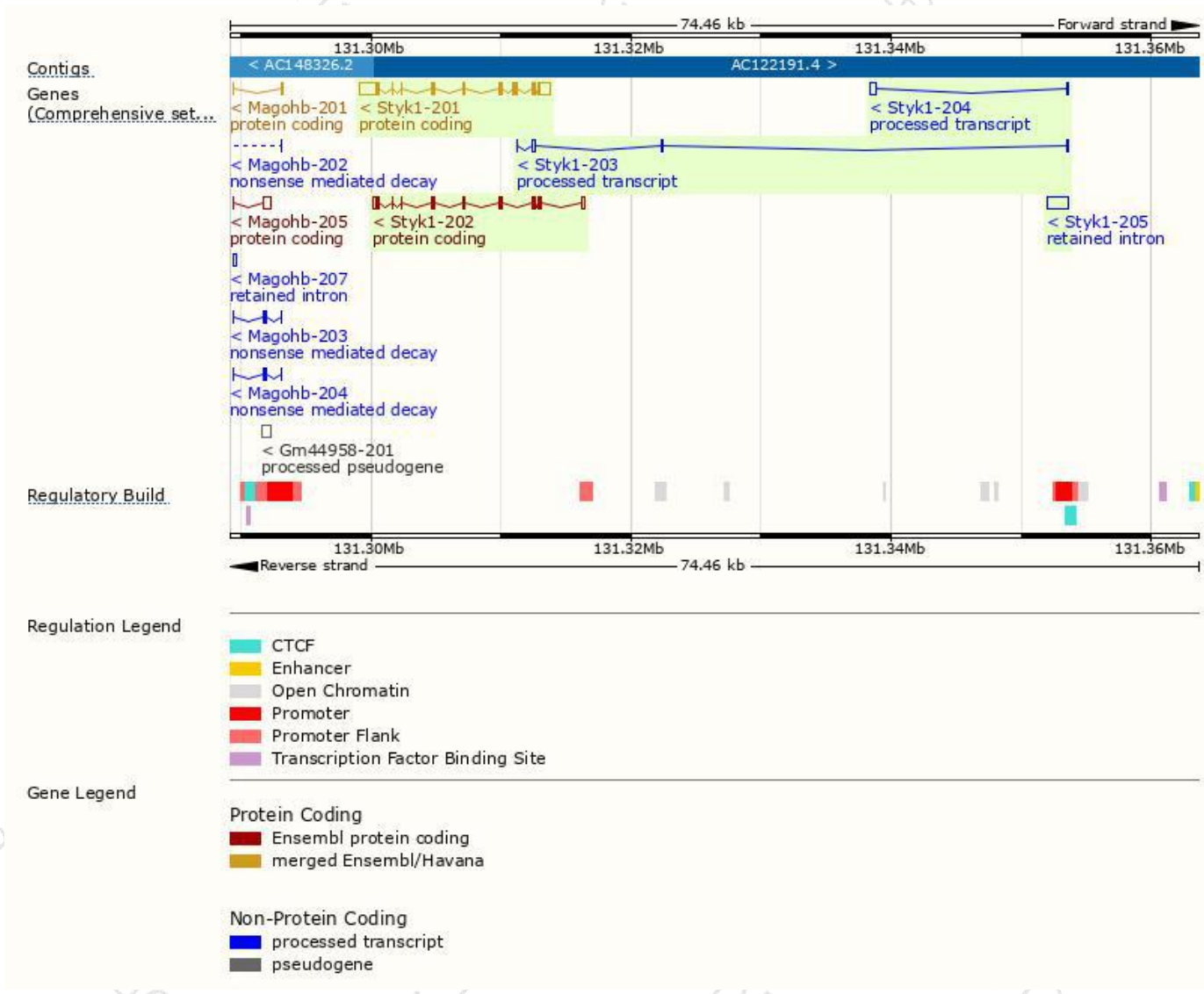
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Styk1-201	ENSMUST00000049150.7	3380	429aa	Protein coding	CCDS20604	Q6J9G1	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 P2
Styk1-202	ENSMUST00000121078.1	1549	340aa	Protein coding	-	Q6J9G1	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
Styk1-204	ENSMUST00000145390.1	628	No protein	Processed transcript	-	-	TSL:3
Styk1-203	ENSMUST00000135859.1	422	No protein	Processed transcript	-	-	TSL:5
Styk1-205	ENSMUST00000204371.1	1621	No protein	Retained intron	-	-	TSL:NA

The strategy is based on the design of *Styk1-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

Tel: 400-9660890

