

Haus5 Cas9-KO Strategy

Designer:

Yanhua Shen

Reviewer:

Xueting Zhang

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Project Overview

Project Name

Haus5

Project type

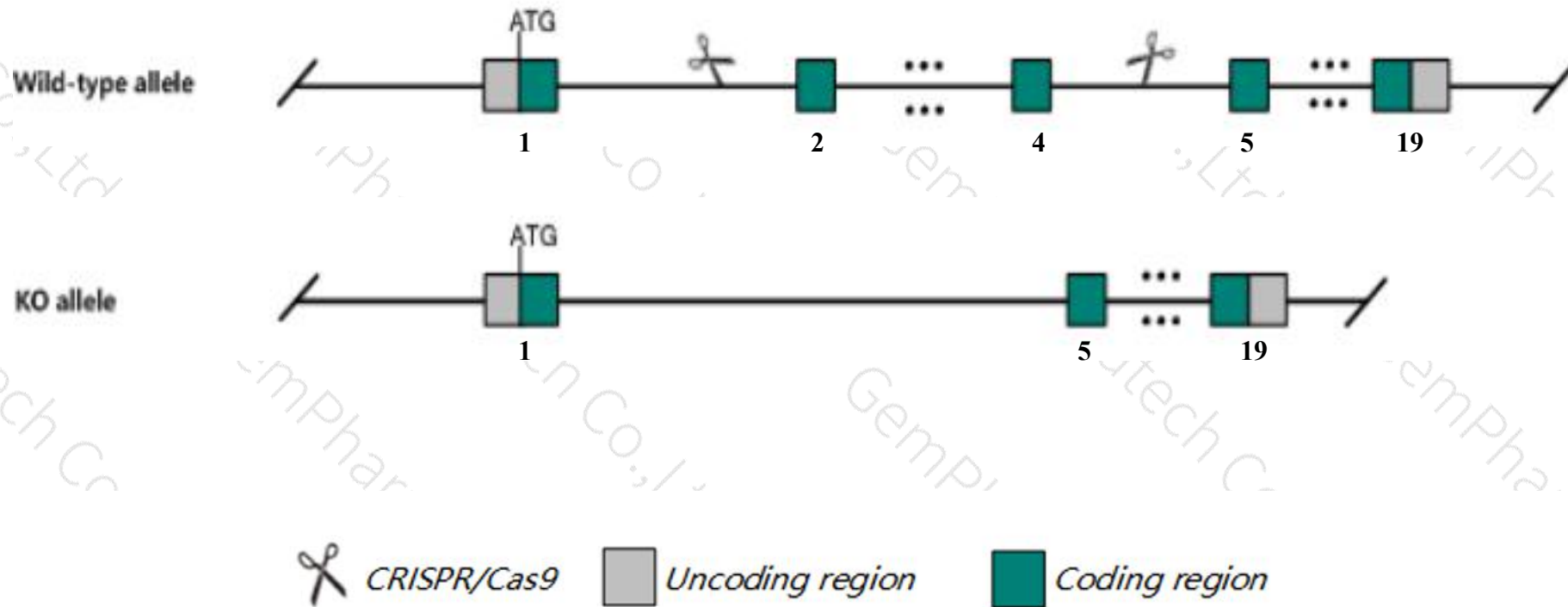
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Haus5* gene. The schematic diagram is as follows:



- The *Haus5* gene has 6 transcripts. According to the structure of *Haus5* gene, exon2-exon4 of *Haus5-201* (ENSMUST00000019697.8) transcript is recommended as the knockout region. The region contains 121bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Haus5* gene. The brief process is as follows: CRISPR/Cas9 system

- Transcripts 204,205, 206 may not be affected.
- *Gm21982-201* gene may be destroyed.
- The *Haus5* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Haus5 HAUS augmin-like complex, subunit 5 [Mus musculus (house mouse)]

Gene ID: 71909, updated on 13-Mar-2020

Summary



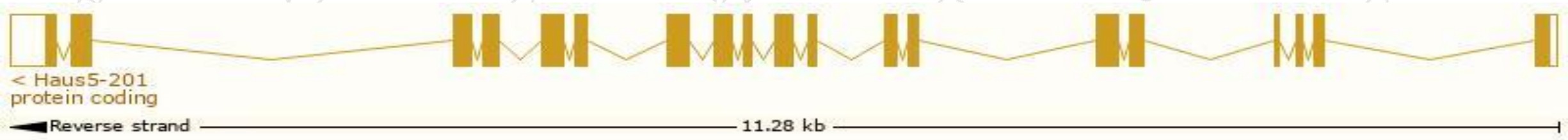
Official Symbol	Haus5 provided by MGI
Official Full Name	HAUS augmin-like complex, subunit 5 provided by MGI
Primary source	MGI:MGI:1919159
See related	Ensembl:ENSMUSG00000078762
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2310022K01Rik
Expression	Ubiquitous expression in CNS E11.5 (RPKM 14.0), liver E14.5 (RPKM 13.5) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

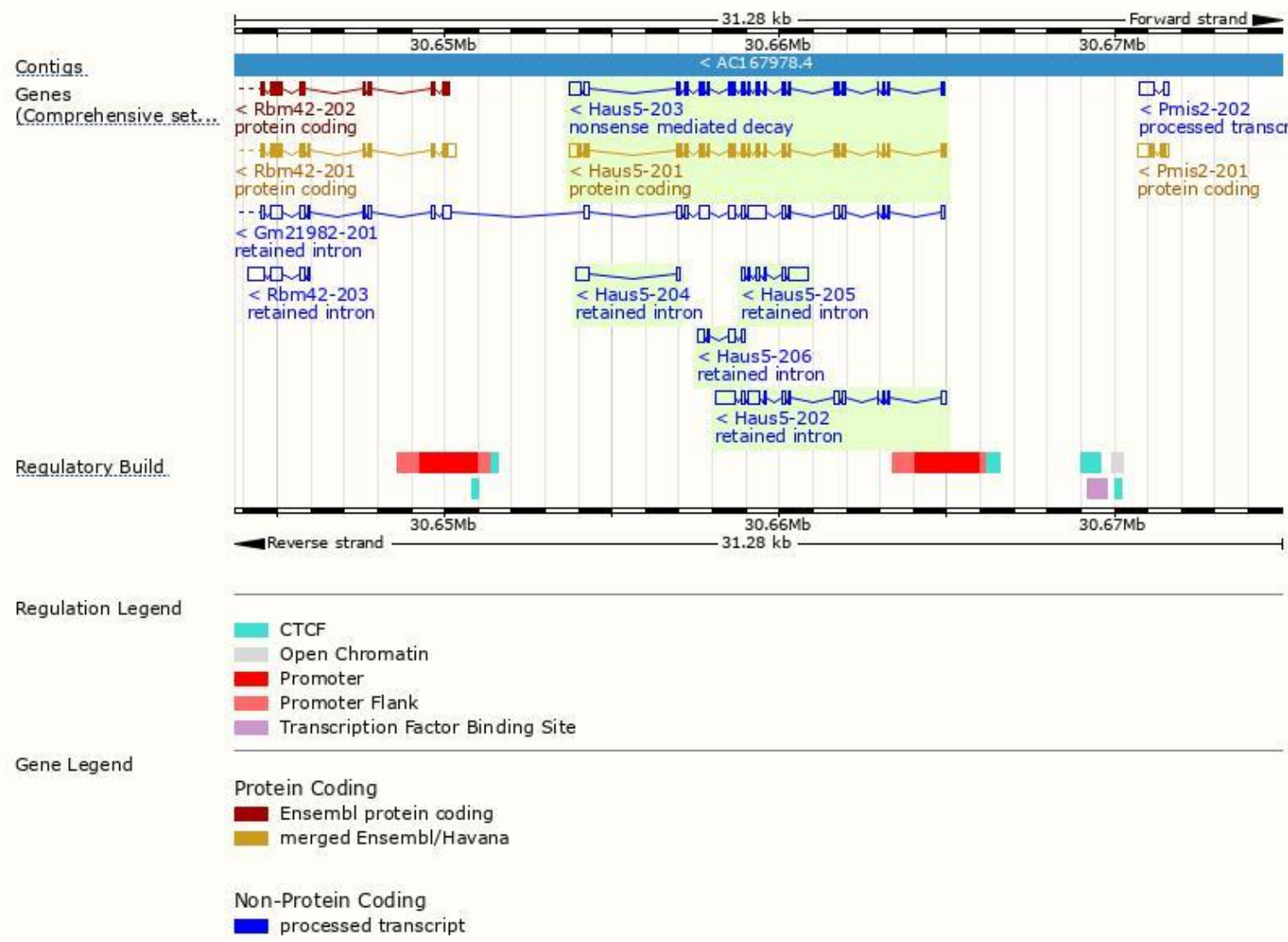
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Haus5-201	ENSMUST00000019697.8	2187	619aa	Protein coding	CCDS52180	Q9D786	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 P1
Haus5-203	ENSMUST00000132862.7	2070	517aa	Nonsense mediated decay	-	Q9D786	TSL:1
Haus5-202	ENSMUST00000126511.7	1788	No protein	Retained intron	-	-	TSL:2
Haus5-205	ENSMUST00000142741.1	1064	No protein	Retained intron	-	-	TSL:2
Haus5-206	ENSMUST00000142823.1	539	No protein	Retained intron	-	-	TSL:2
Haus5-204	ENSMUST00000132982.1	420	No protein	Retained intron	-	-	TSL:3

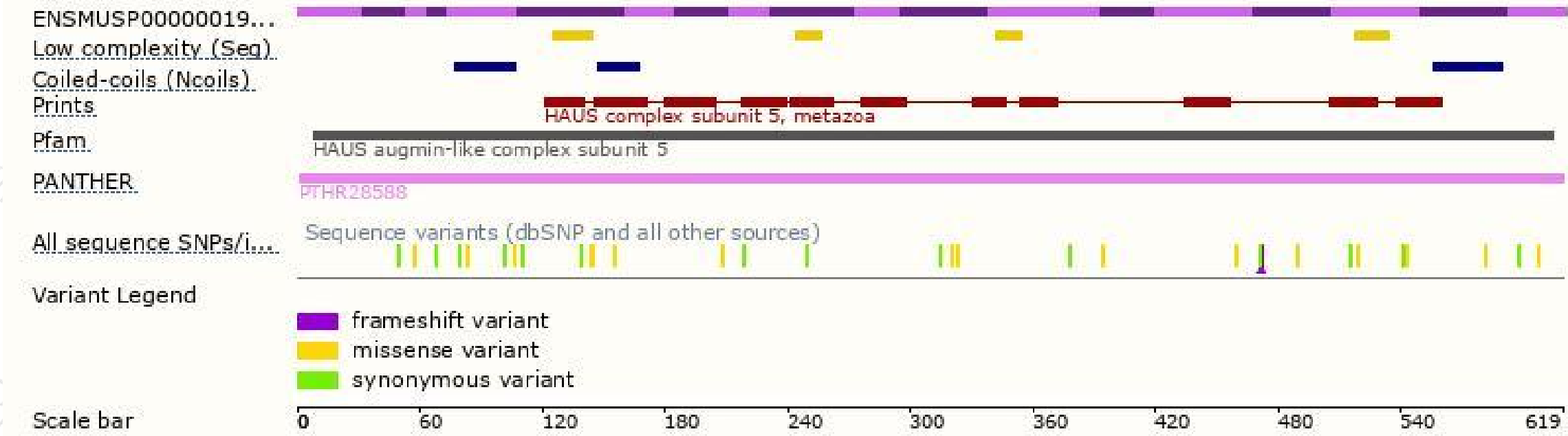
The strategy is based on the design of *Haus5-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

Tel: 400-9660890

