

Haus1 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Haus1

Project type

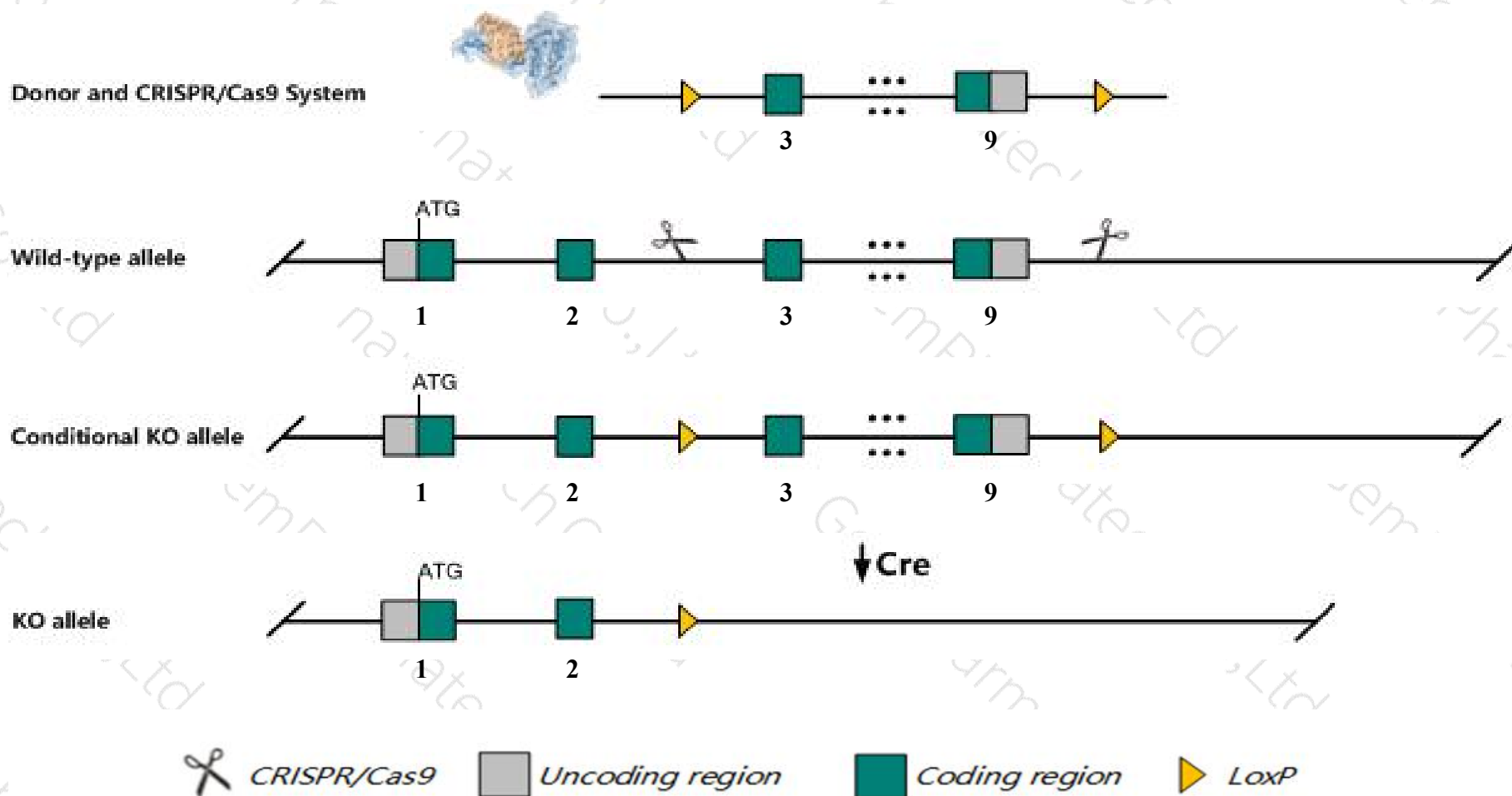
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Haus1* gene. The schematic diagram is as follows:



- The *Haus1* gene has 3 transcripts. According to the structure of *Haus1* gene, exon3-exon9 of *Haus1*-201 (ENSMUST00000048192.8) transcript is recommended as the knockout region. The region contains most of coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Haus1* 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.

Notice

- Some amino acids will remain at the N-terminus and some functions may be retained.
- The *Haus1* gene is located on the Chr18. 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)

Haus1 HAUS augmin-like complex, subunit 1 [Mus musculus (house mouse)]

Gene ID: 225745, updated on 13-Mar-2020

Summary



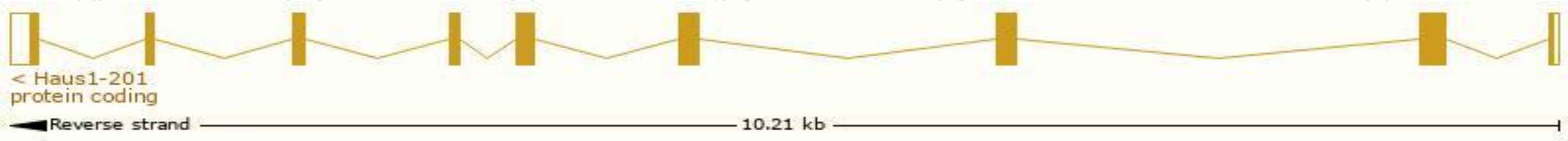
Official Symbol	Haus1 provided by MGI
Official Full Name	HAUS augmin-like complex, subunit 1 provided by MGI
Primary source	MGI:MGI:2385076
See related	Ensembl:ENSMUSG00000041840
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	BC024400, Ccdc5, HEI-C
Expression	Broad expression in CNS E11.5 (RPKM 6.2), testis adult (RPKM 5.4) and 19 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

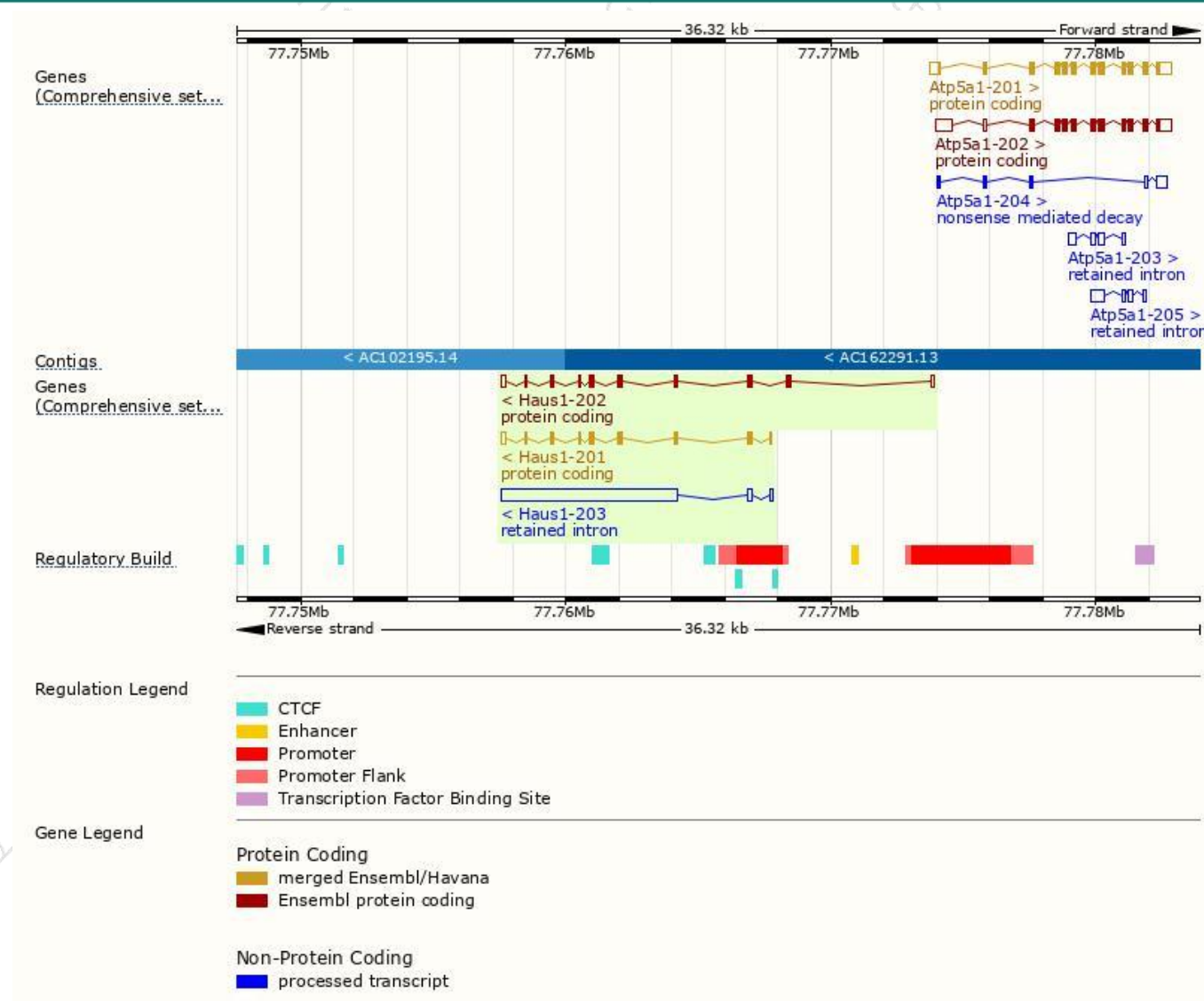
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Haus1-201	ENSMUST00000048192.8	1003	278aa	Protein coding	CCDS29357	Q8BHX1	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
Haus1-202	ENSMUST000000236234.1	1226	293aa	Protein coding	-	A0A494BB26	GENCODE basic
Haus1-203	ENSMUST000000236575.1	6882	No protein	Retained intron	-	-	

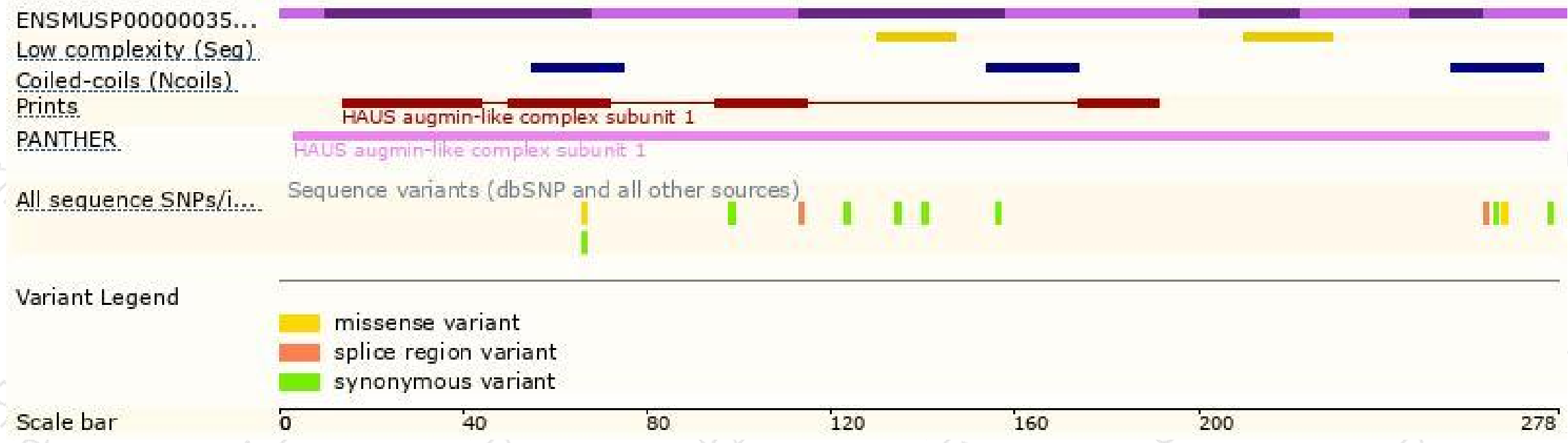
The strategy is based on the design of *Haus1-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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