

Ly6h Cas9-KO Strategy

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Project Overview

Project Name

Ly6h

Project type

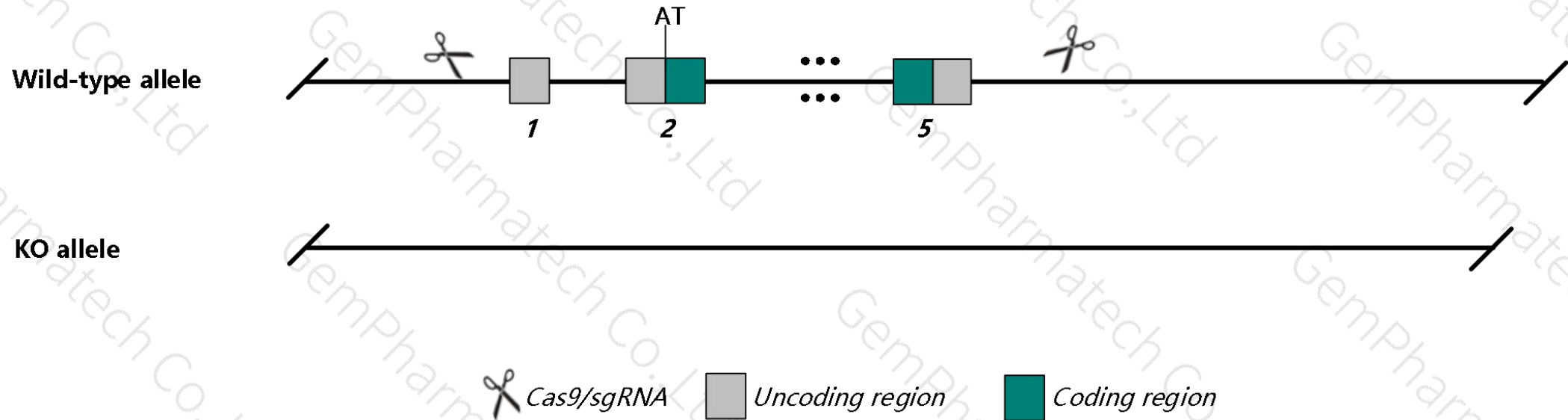
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ly6h* gene. The schematic diagram is as follows:



- The *Ly6h* gene has 8 transcripts. According to the structure of *Ly6h* gene, exon1-exon5 of *Ly6h-206* (ENSMUST00000156032.1) transcript is recommended as the knockout region. The region contains all of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ly6h* gene. The brief process is as follows: CRISPR/Cas9 system v

- The *Ly6h* gene is located on the Chr15. 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)

Ly6h lymphocyte antigen 6 complex, locus H [Mus musculus (house mouse)]

Gene ID: 23934, updated on 13-Mar-2020

Summary



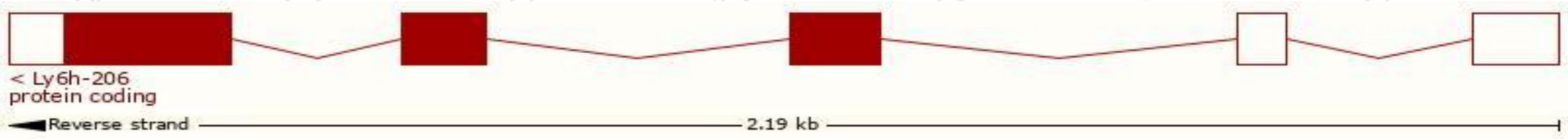
Official Symbol	Ly6h provided by MGI
Official Full Name	lymphocyte antigen 6 complex, locus H provided by MGI
Primary source	MGI:MGI:1346030
See related	Ensembl:ENSMUSG00000022577
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Expression	Biased expression in CNS E18 (RPKM 141.2), whole brain E14.5 (RPKM 99.2) and 7 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

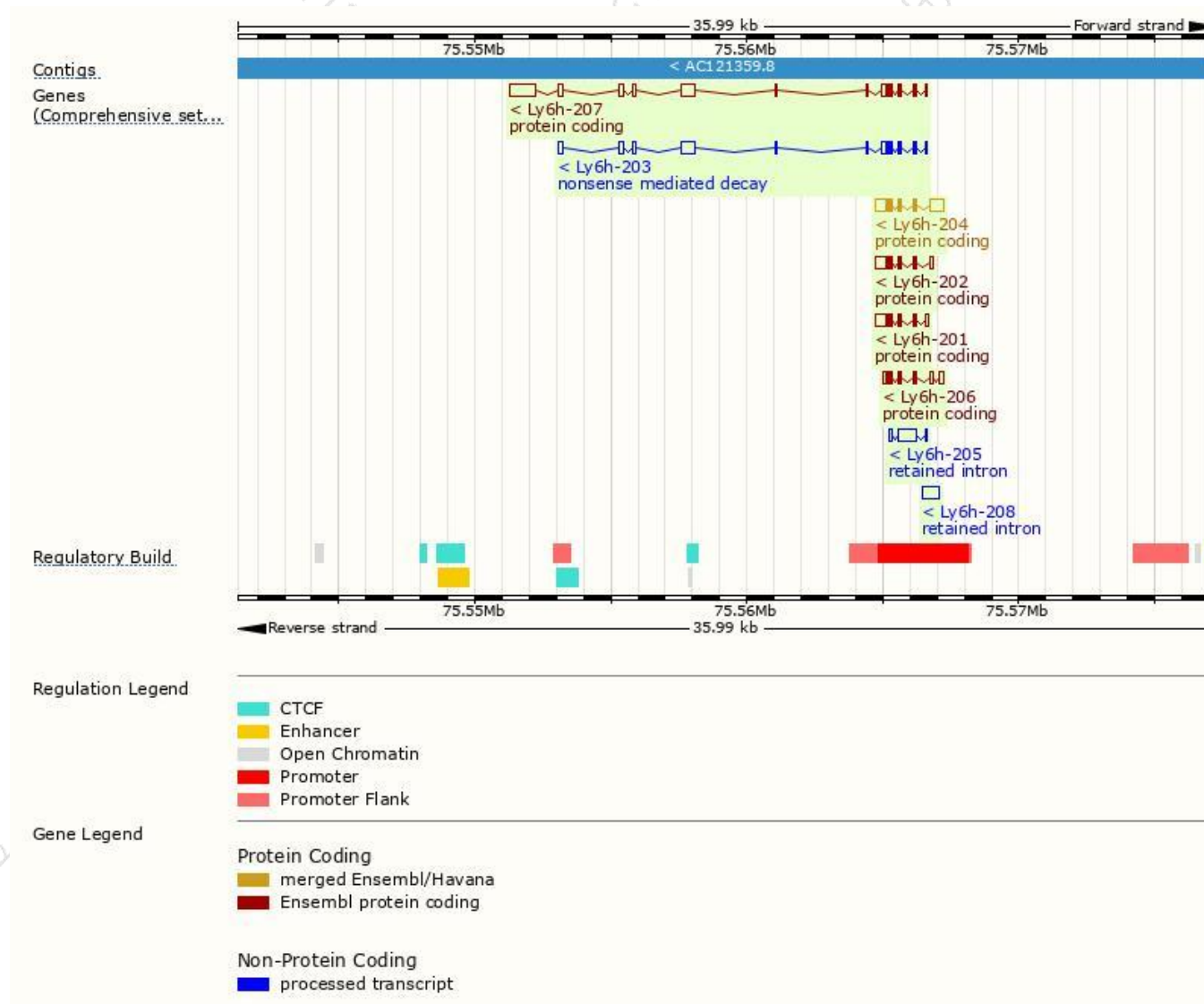
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ly6h-207	ENSMUST00000163116.7	2801	139aa	Protein coding	CCDS49640	Q544M1_Q9WUC3	TSL:2 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 ALT1
Ly6h-204	ENSMUST00000127095.7	1336	160aa	Protein coding	CCDS27544	Q8K356	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 P3
Ly6h-202	ENSMUST00000065417.14	985	139aa	Protein coding	CCDS49640	Q544M1_Q9WUC3	TSL:2 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 ALT1
Ly6h-201	ENSMUST00000023241.11	906	139aa	Protein coding	CCDS49640	Q544M1_Q9WUC3	TSL:2 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 ALT1
Ly6h-206	ENSMUST00000156032.1	752	160aa	Protein coding	CCDS27544	Q8K356	TSL:3 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 P3
Ly6h-203	ENSMUST00000126129.7	1813	139aa	Nonsense mediated decay	-	Q544M1_Q9WUC3	TSL:5
Ly6h-205	ENSMUST00000150125.1	847	No protein	Retained intron	-	-	TSL:5
Ly6h-208	ENSMUST00000228961.1	615	No protein	Retained intron	-	-	

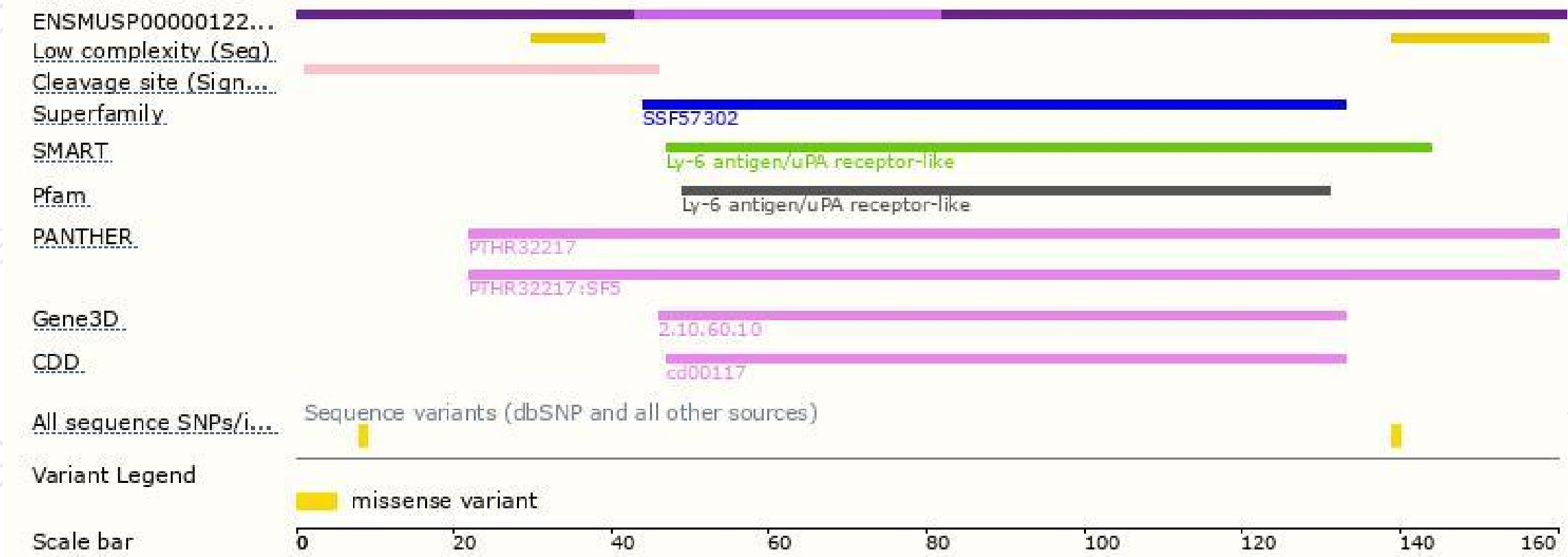
The strategy is based on the design of *Ly6h-206* transcript,the transcription is shown below:



Genomic location distribution



Protein domain



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

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