

Hlf Cas9-KO Strategy

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Project Overview

Project Name

Hlf

Project type

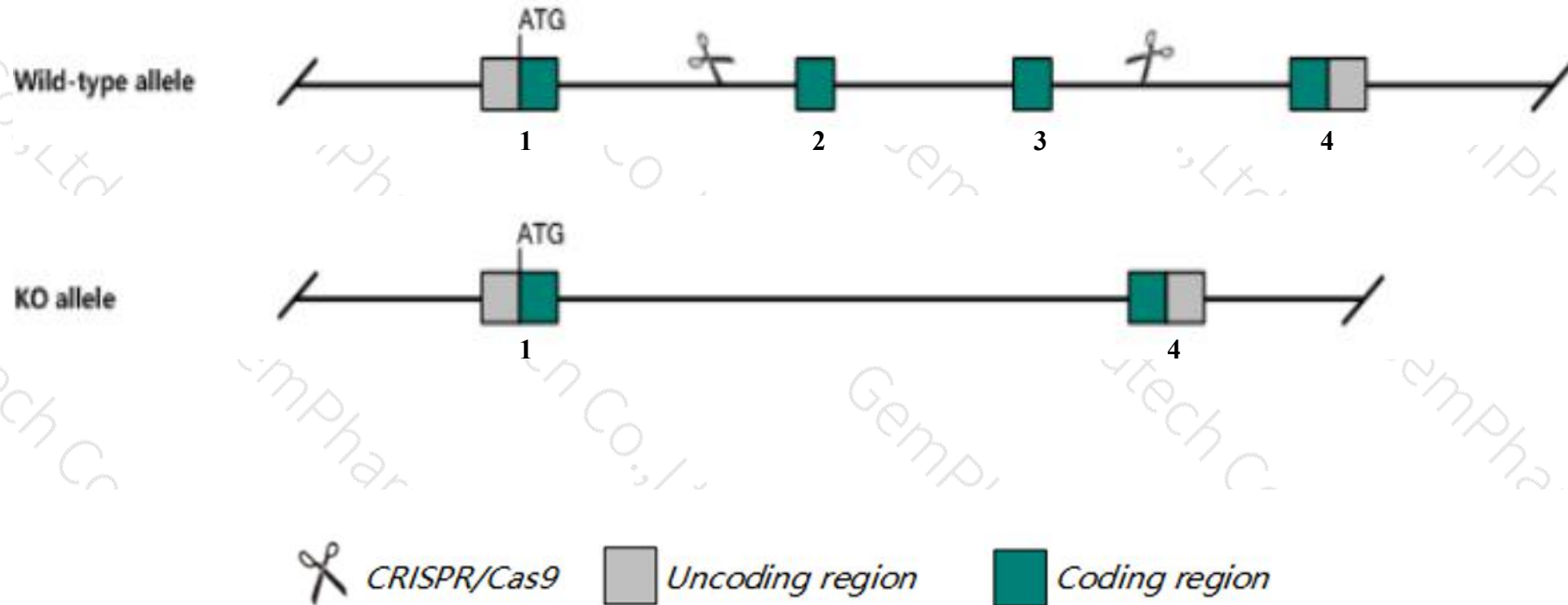
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Hlf* gene has 6 transcripts. According to the structure of *Hlf* gene, exon2-exon3 of *Hlf*-201 (ENSMUST00000004051.7) transcript is recommended as the knockout region. The region contains 557bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Hlf* gene. The brief process is as follows: CRISPR/Cas9 system we

- According to the existing MGI data, mice homozygous for a knock-out allele are viable, morphologically normal and fertile.
- The *Hlf* gene is located on the Chr11. 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)

Hlf hepatic leukemia factor [Mus musculus (house mouse)]

Gene ID: 217082, updated on 13-Mar-2020

Summary



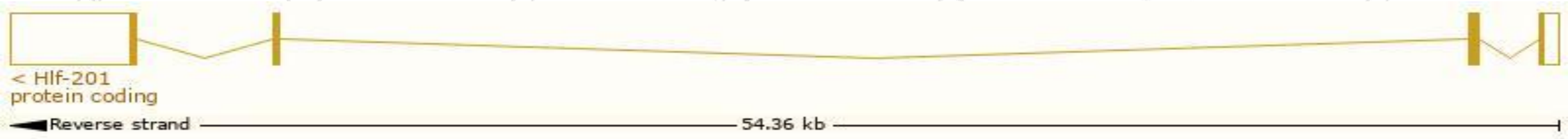
Official Symbol	Hlf provided by MGI
Official Full Name	hepatic leukemia factor provided by MGI
Primary source	MGI:MGI:96108
See related	Ensembl:ENSMUSG000000003949
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	E230015K02Rik
Expression	Broad expression in cortex adult (RPKM 20.3), frontal lobe adult (RPKM 15.0) and 16 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

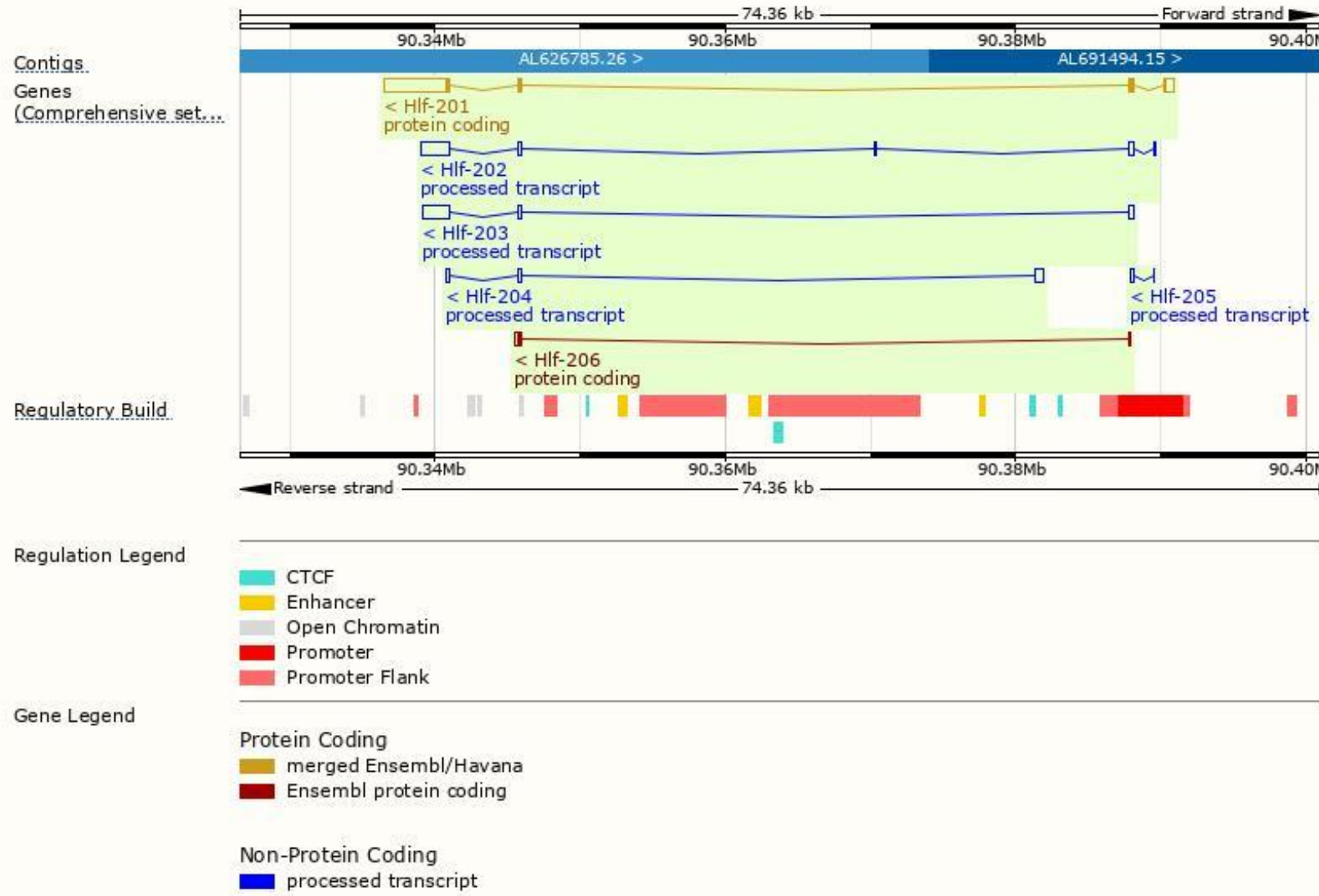
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hlf-201	ENSMUST00000004051.7	5642	295aa	Protein coding	CCDS25241	Q8BW74	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
Hlf-206	ENSMUST00000176001.1	619	142aa	Protein coding	-	H3BKN8	CDS 5' incomplete TSL:2
Hlf-202	ENSMUST00000043658.11	2712	No protein	Processed transcript	-	-	TSL:1
Hlf-203	ENSMUST00000107881.7	2476	No protein	Processed transcript	-	-	TSL:2
Hlf-204	ENSMUST00000137957.1	896	No protein	Processed transcript	-	-	TSL:3
Hlf-205	ENSMUST00000145786.1	245	No protein	Processed transcript	-	-	TSL:3

The strategy is based on the design of *Hlf-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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