

Hey1 Cas9-KO Strategy

Designer:

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Design Date:

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Project Overview

Project Name

Hey1

Project type

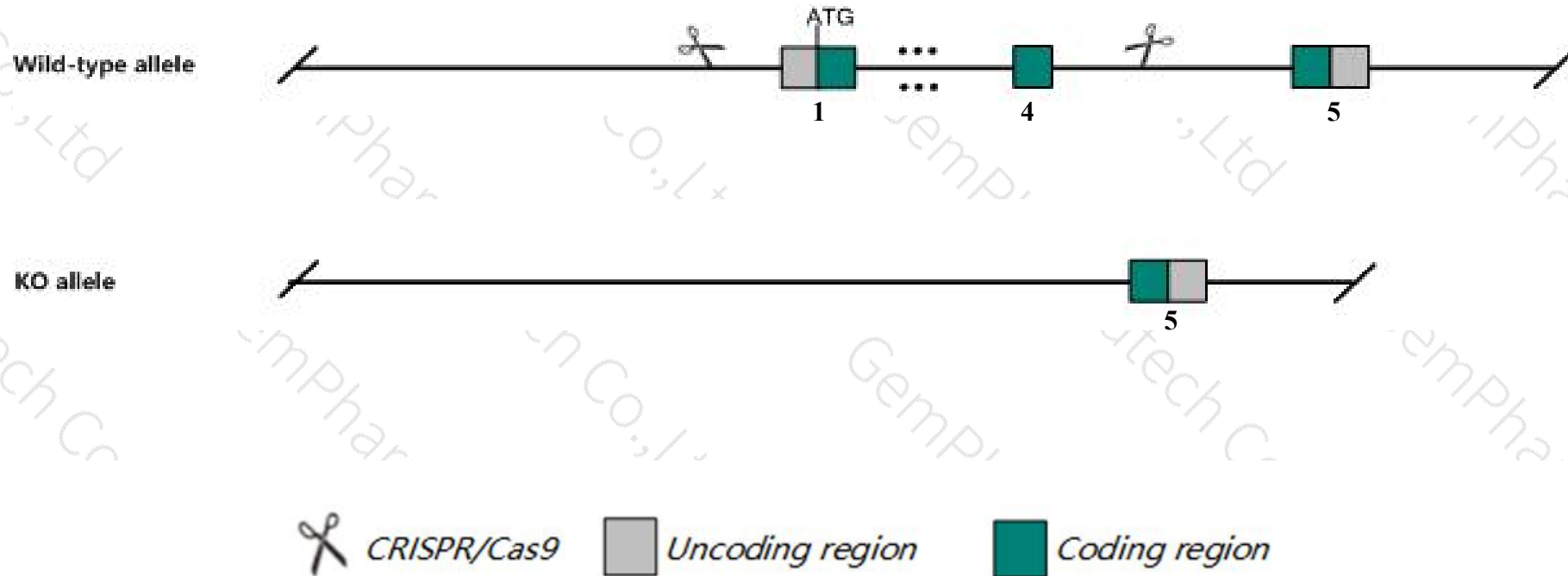
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Heyl* gene has 4 transcripts. According to the structure of *Heyl* gene, exon1-exon4 of *Heyl-201* (ENSMUST00000042412.4) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Heyl* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Homozygous null mice are healthy and fertile with no major developmental defects.
- The *Heyl* gene is located on the Chr3. 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)

Hey1 hairy/enhancer-of-split related with YRPW motif 1 [Mus musculus (house mouse)]

Gene ID: 15213, updated on 19-Mar-2019

Summary



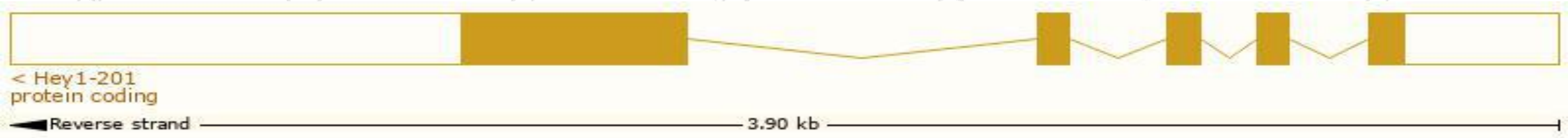
Official Symbol	Hey1 provided by MGI
Official Full Name	hairy/enhancer-of-split related with YRPW motif 1 provided by MGI
Primary source	MGI:MGI:1341800
See related	Ensembl:ENSMUSG00000040289
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI316788, AI414254, CHF2, HRT1, Herp2, Hesr1, bHLHb31, hesr-1
Expression	Broad expression in lung adult (RPKM 42.5), CNS E11.5 (RPKM 13.9) and 15 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

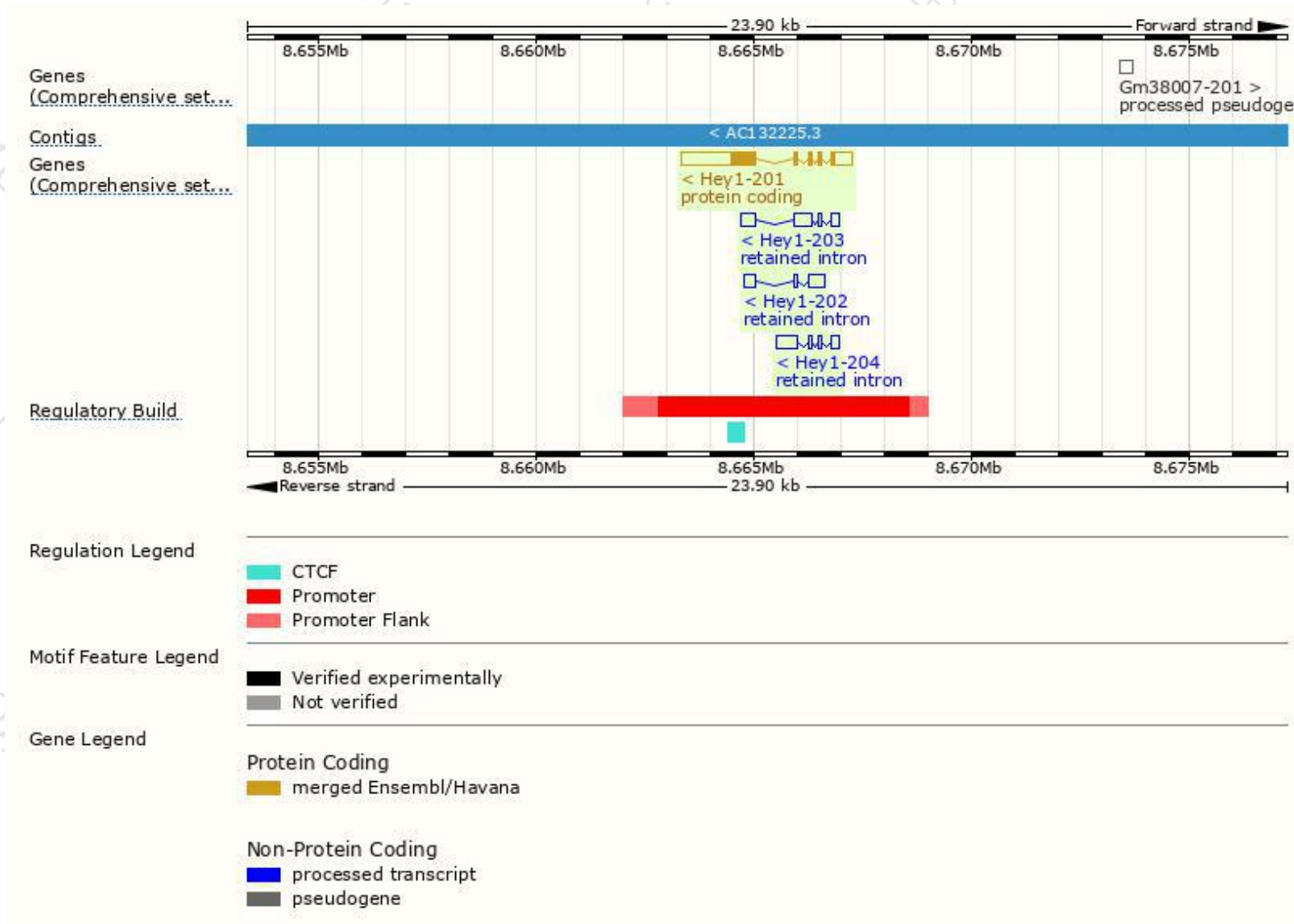
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hey1-201	ENSMUST00000042412.4	2423	299aa	Protein coding	CCDS17232	Q9QUM5	TSL:1 GENCODE basic APPRIS P1
Hey1-203	ENSMUST00000192550.5	1056	No protein	Retained intron	-	-	TSL:5
Hey1-204	ENSMUST00000194299.1	828	No protein	Retained intron	-	-	TSL:2
Hey1-202	ENSMUST00000192102.1	705	No protein	Retained intron	-	-	TSL:2

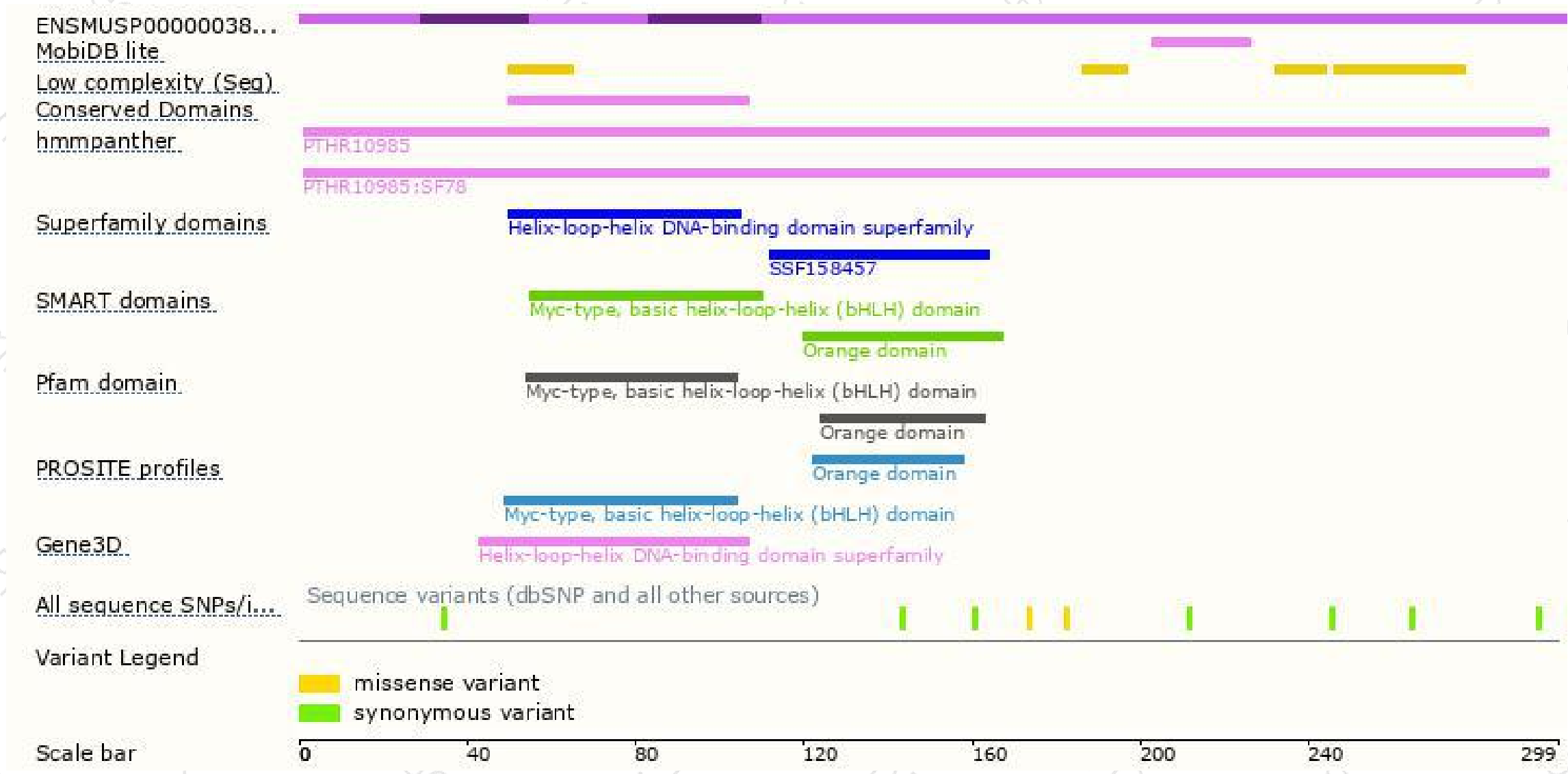
The strategy is based on the design of *Hey1-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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