Hes3 Cas9-KO Strategy

Designer:Xueting Zhang
Reviewer:Yanhua Shen
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Project Overview

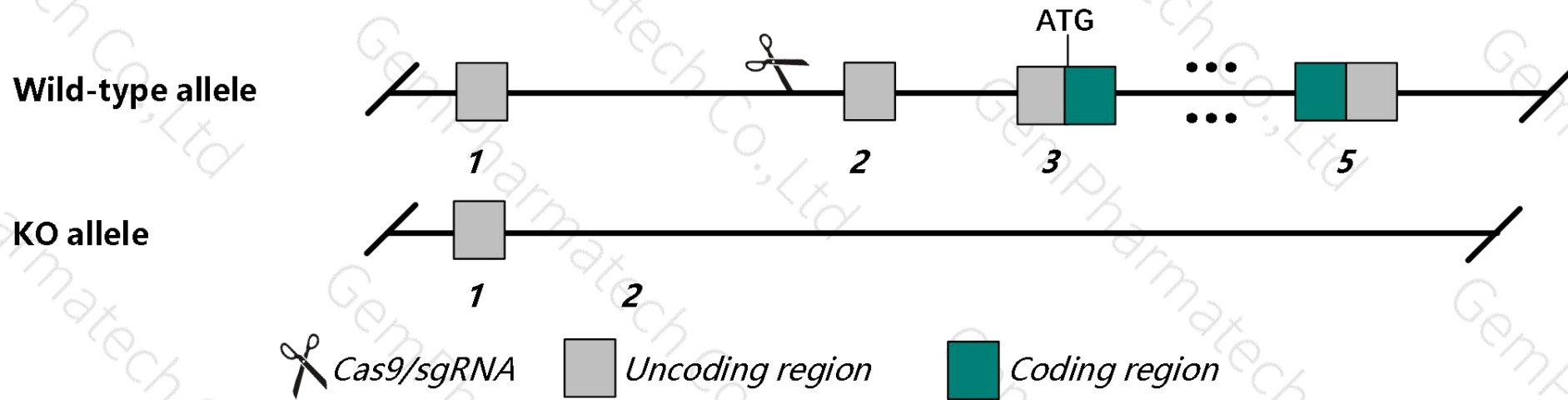|	
Project Name	*Hes3*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hes3* gene. The schematic diagram is as follows:

Technical routes

➢ The *Hes3* gene has 2 transcripts. According to the structure of *Hes3* gene, exon2-exon5 of *Hes3-201* (ENSMUST00000094438.1) 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 *Hes3* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ According to the existing MGI data,Homozygous null mice are fertile and display no obvious abnormalities.

➢ The knockout region is near to the N-terminal of *Icmt* gene and the C-terminal of *Gpr153* gene,this strategy may influence the regulatory function of the N-terminal of *Icmt* gene and the C-terminal of *Gpr153* gene.

➢ The *Hes3* gene is located on the Chr4. 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）

Hes3 hes family bHLH transcription factor 3 [*Mus musculus* (house mouse)]

Gene ID: 15207, updated on 3-Sep-2019

▲ Summary

Official Symbol	Hes3 provided by MGI
Official Full Name	hes family bHLH transcription factor 3 provided by MGI
Primary source	MGI:MGI:104877
See related	Ensembl:ENSMUSG00000028946
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	Hes-3; bHLHb43
Expression	Biased expression in cerebellum adult (RPKM 9.7) and CNS E11.5 (RPKM 0.6) See more
Orthologs	human all

▲ Genomic context

Location: 4 E2; 4 83.01 cM

See Hes3 in Genome Data Viewer

Exon count: 8

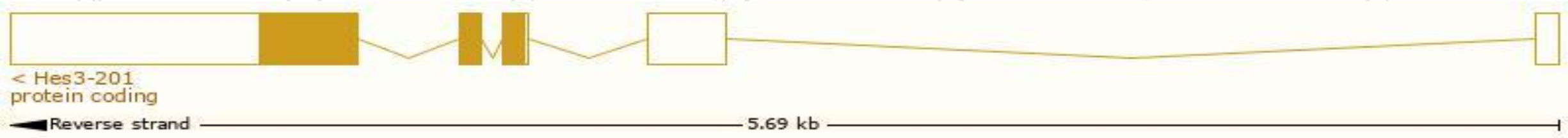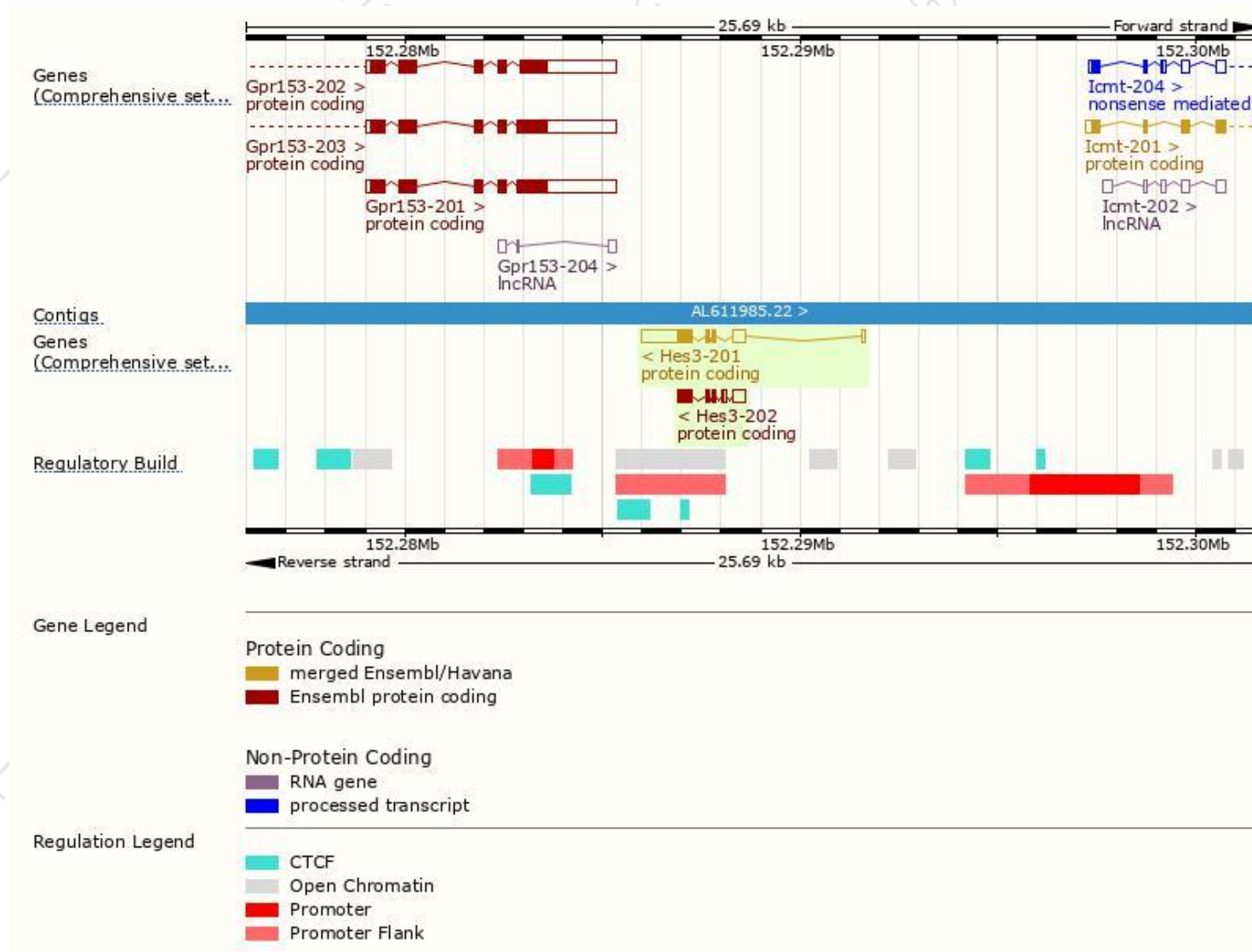| Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	4	NC_000070.6 (152285250..152291911, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	4	NC_000070.5 (151660081..151665771, complement)

Transcript information（Ensembl）

The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hes3-201	ENSMUST00000094438.1	1829	175aa	Protein coding	CCDS18997	Q61657	TSL:1 GENCODE basic APPRIS P2
Hes3-202	ENSMUST00000218045.1	962	200aa	Protein coding	-	A0A1W2P7Y8	TSL:5 GENCODE basic APPRIS ALT2

The strategy is based on the design of *Hes3-201* transcript,The transcription is shown below
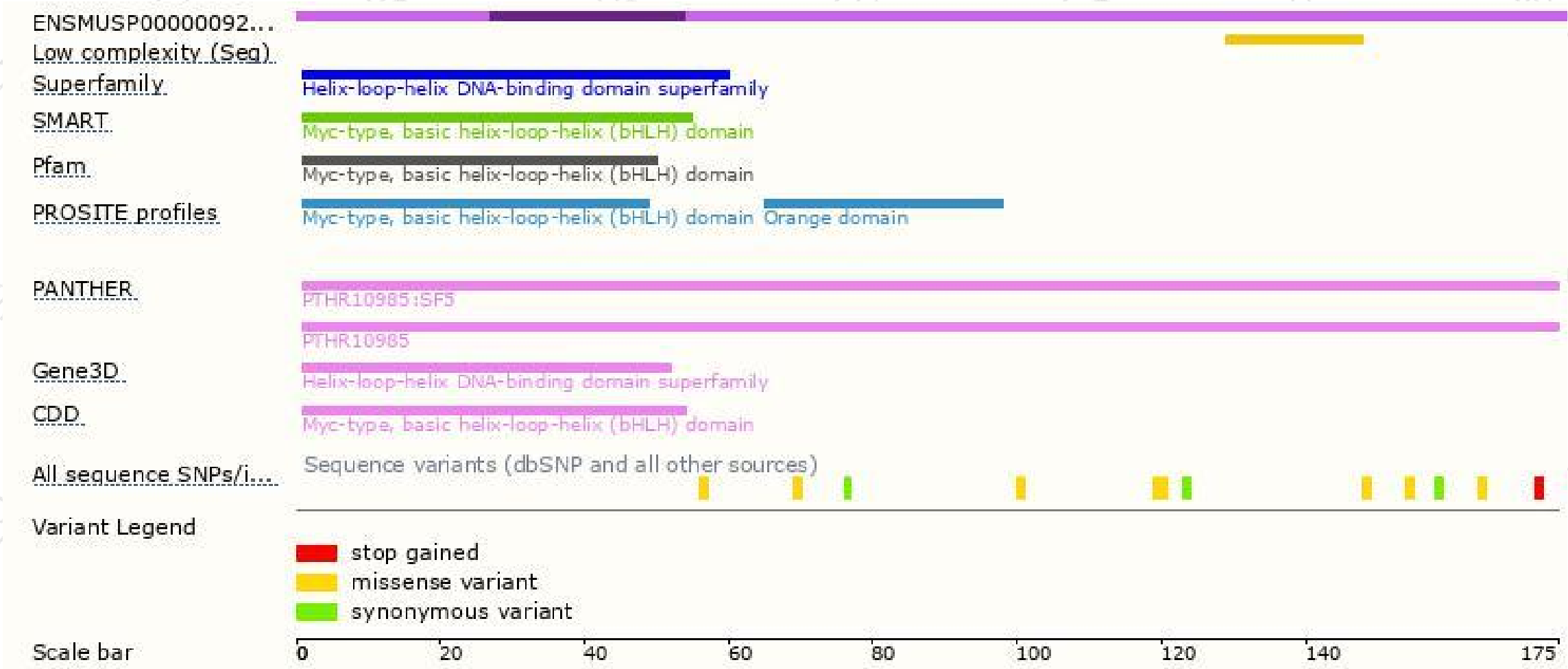

< Hes3-201
protein coding

◄ Reverse strand

5.69 kb

Genomic location distribution

Protein domain

ENSMUSP00000092...
Low complexity (Seg)
Superfamily — Helix-loop-helix DNA-binding domain superfamily
SMART — Myc-type, basic helix-loop-helix (bHLH) domain
Pfam — Myc-type, basic helix-loop-helix (bHLH) domain
PROSITE profiles — Myc-type, basic helix-loop-helix (bHLH) domain Orange domain

PANTHER — PTHR10985:SF5
PTHR10985
Gene3D — Helix-loop-helix DNA-binding domain superfamily
CDD — Myc-type, basic helix-loop-helix (bHLH) domain

All sequence SNPs/i... — Sequence variants (dbSNP and all other sources)

Variant Legend
  ▮ stop gained
  ▮ missense variant
  ▮ synonymous variant

Scale bar   0   20   40   60   80   100   120   140   175

If you have any questions, you are welcome to inquire.
Tel: 400-9660890

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