H1f8 Cas9-KO Strategy

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Project Overview

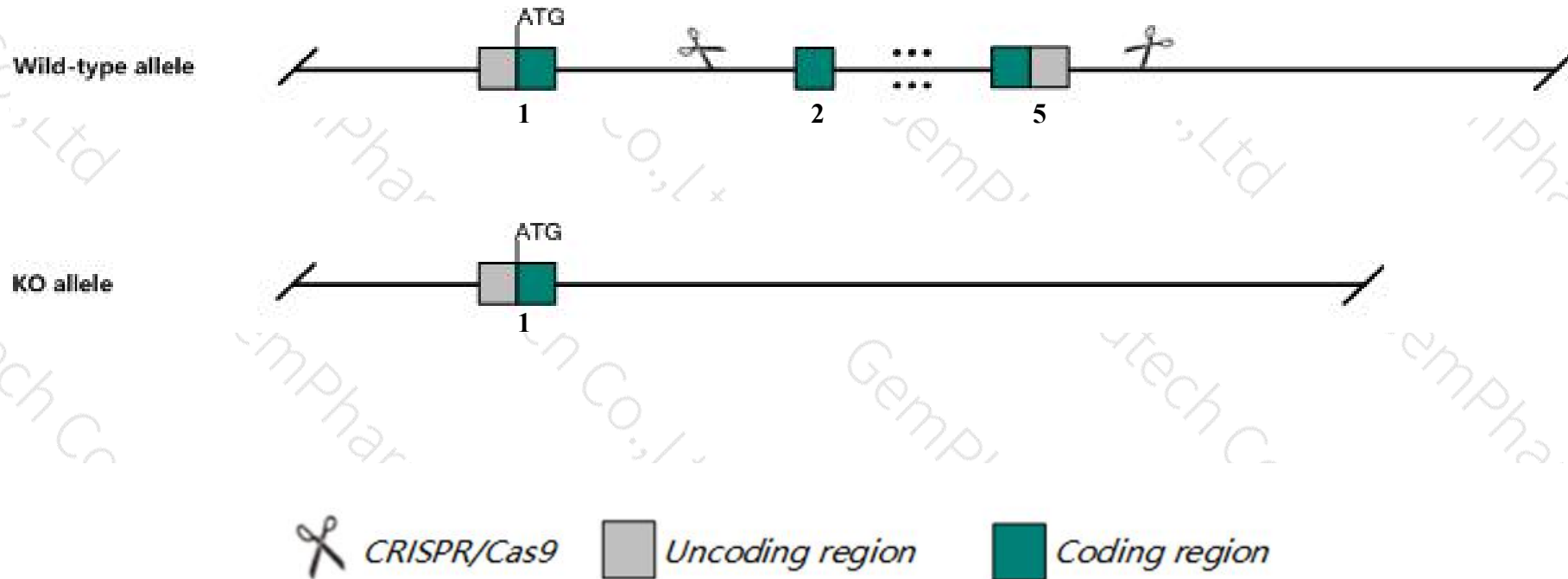|	
Project Name	*H1f8*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hlf8* gene. The schematic diagram is as follows:

➢ The *H1f8* gene has 5 transcripts. According to the structure of *H1f8* gene, exon2-exon5 of *H1f8-203* (ENSMUST00000161969.3) transcript is recommended as the knockout region.The region contains 641bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *H1f8* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

➢ According to the existing MGI data,Mice homozygous for a targeted mutation exhibit no detectable abnormalities. Oocytes develop normally and no defects in fertility or litter sizes are observed.

➢ The *H1f8* gene is located on the Chr6. 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）

H1f8 H1.8 linker histone [*Mus musculus* (house mouse)]

Gene ID: 171506, updated on 12-Aug-2019

▲ Summary

Official Symbol	H1f8 provided by MGI
Official Full Name	H1.8 linker histone provided by MGI
Primary source	MGI:MGI:2176207
See related	Ensembl:ENSMUSG00000042279
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	H1-8; H1.8; H1fo; H1oo; H1foo; C86609
Summary	Histones are basic nuclear proteins that are responsible for the nucleosome structure of the chromosomal fiber in eukaryotes. Nucleosomes consist of approximately 146 bp of DNA wrapped around a histone octamer composed of pairs of each of the four core histones (H2A, H2B, H3, and H4). The chromatin fiber is further compacted through the interaction of a linker histone, H1, with the DNA between the nucleosomes to form higher order chromatin structures. The protein encoded is a replication-independent histone that is a member of the histone H1 family. This gene contains introns, unlike most histone genes and the encoded protein is expressed only in oocytes. [provided by RefSeq, Oct 2015]
Expression	Restricted expression toward ovary adult (RPKM 8.4) See more
Orthologs	human all

Transcript information（Ensembl）

The gene has 5 transcripts,all transcripts are shown below:

| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags		
H1f8-203	ENSMUST00000161969.3	1122	246aa	▌Protein coding	CCDS85133 ⌐	Q8VIK3 ⌐	TSL:1	GENCODE basic	APPRIS ALT2
H1f8-201	ENSMUST00000037831.13	1113	304aa	▌Protein coding	CCDS20447 ⌐	Q8VIK3 ⌐	TSL:1	GENCODE basic	APPRIS P3
H1f8-202	ENSMUST00000161617.6	785	251aa	▌Protein coding	-	E0CZ52 ⌐	CDS 3' incomplete	TSL:3	
H1f8-205	ENSMUST00000205177.1	520	64aa	▌Protein coding	-	A0A0N4SV54 ⌐	CDS 5' incomplete	TSL:3	
H1f8-204	ENSMUST00000162084.7	1192	46aa	▌Nonsense mediated decay	-	E0CYL2 ⌐	TSL:1		

The strategy is based on the design of *H1f8-203* transcript,The transcription is shown below
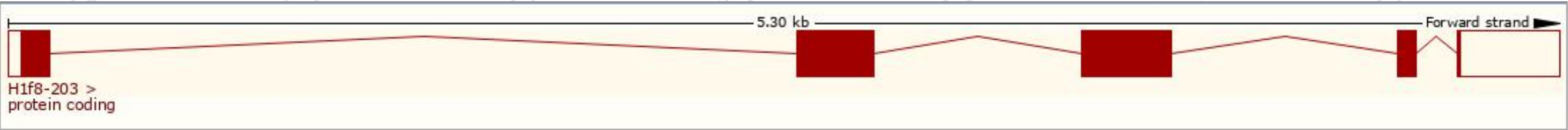
Genomic location distribution
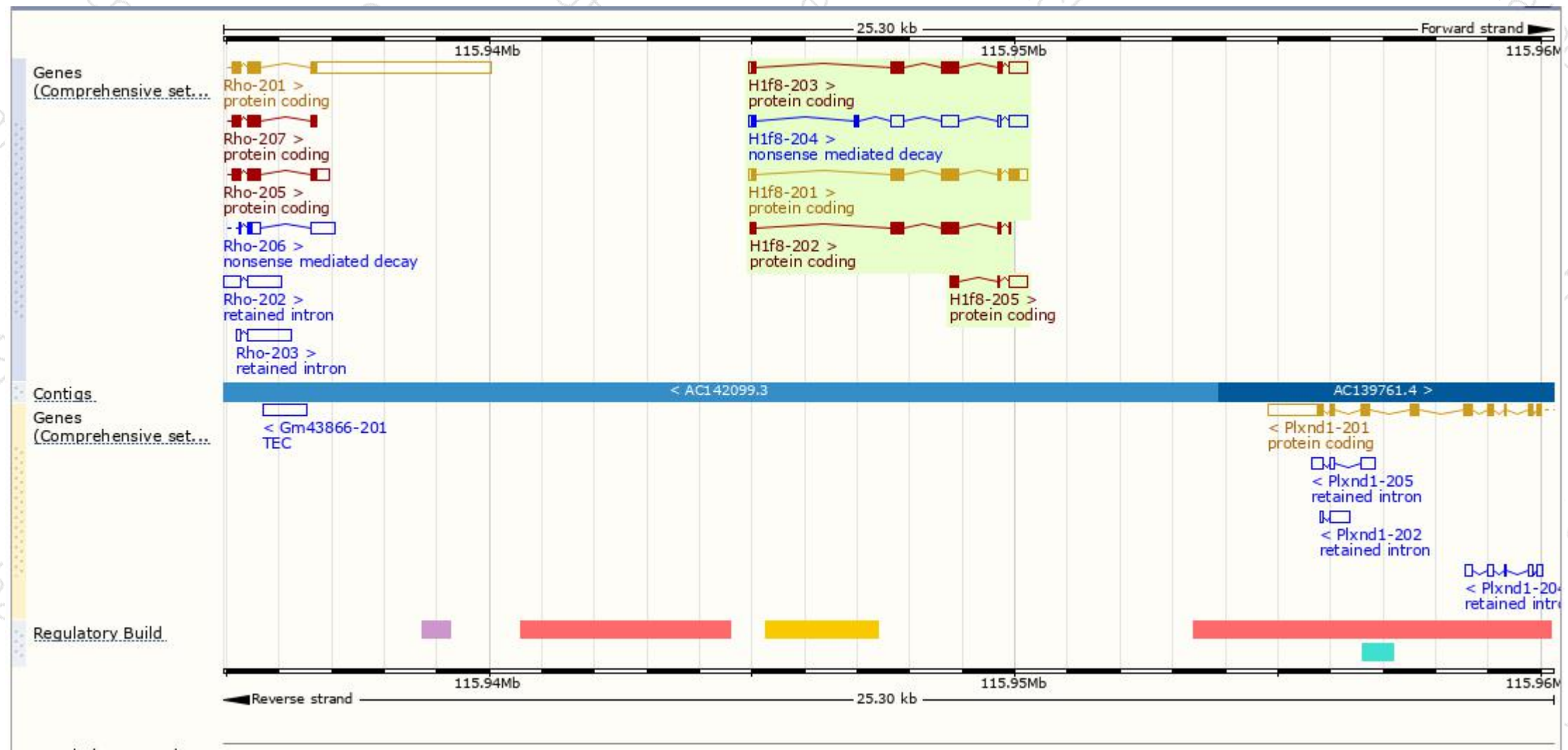
Protein domain
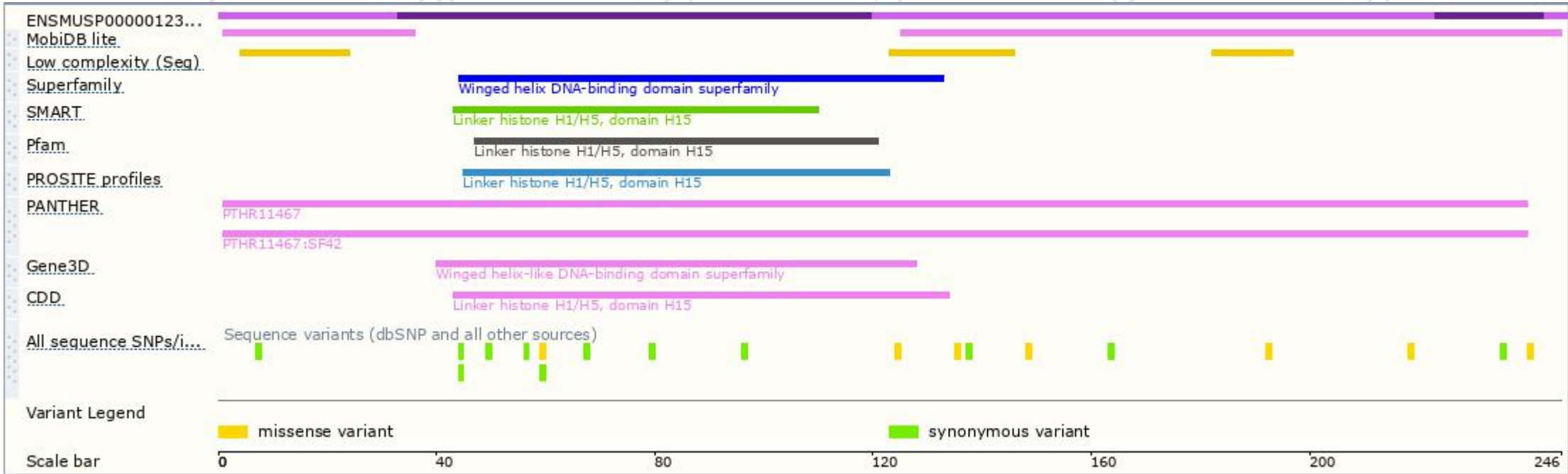
Mouse phenotype description(MGI)

Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

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