Hivep2 Cas9-KO Strategy

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Reviewer: Daohua Xu

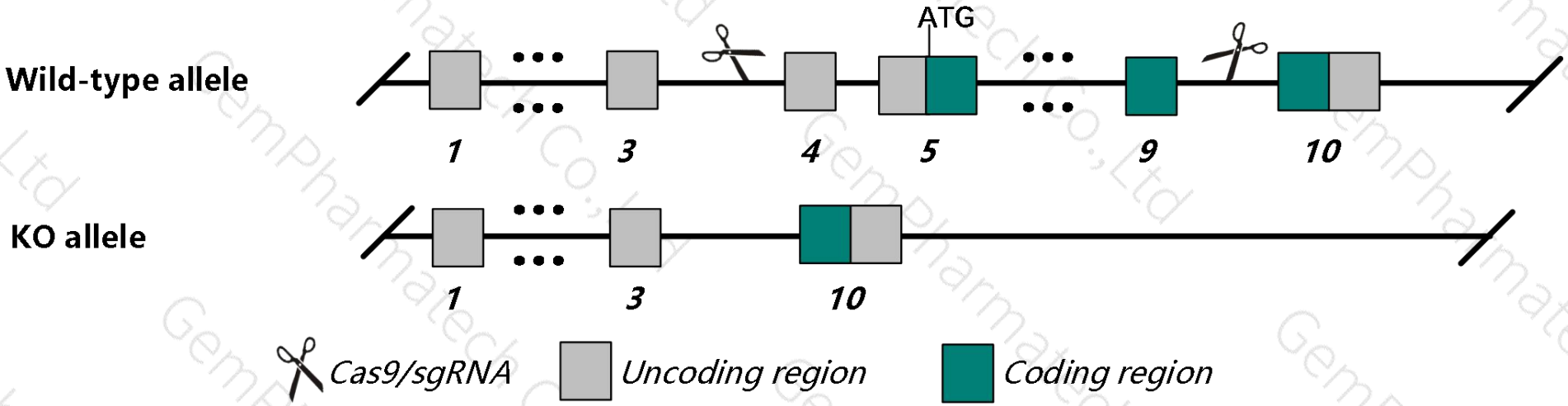
Design Date: 2020-7-21

Project Overview

Project Name	***Hivep2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hivep2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Hivep2* gene has 6 transcripts. According to the structure of *Hivep2* gene, exon4-exon9 of *Hivep2-205*(ENSMUST00000191138.6) transcript is recommended as the knockout region.The region contains most 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 *Hivep2* gene. The brief process is as follows: CRISPR/Cas9 system were microinjected into the fertilized eggs of C57BL/6JGpt mice.Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

Notice

➢ According to the existing MGI data,mice homozygous for a knock-out allele display abnormal thymus anatomy, severely defective positive selection of CD4+ and CD8+ cells, and enhanced T-helper 2 cell differentiation.

➢ Transcript *Hivep2*-202&206 may not be affected.

➢ The *Hivep2* gene is located on the Chr10. 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）

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Hivep2 human immunodeficiency virus type I enhancer binding protein 2 [Mus musculus (house mouse)]

Gene ID: 15273, updated on 13-Mar-2020

Summary

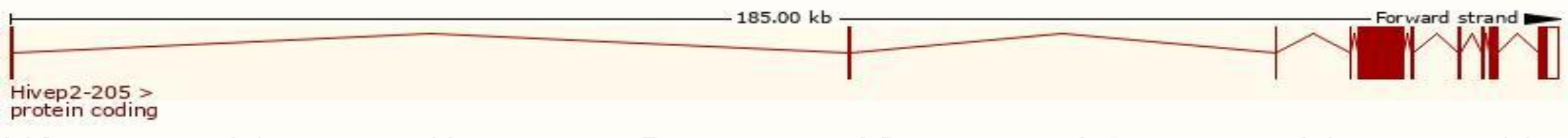
Official Symbol	Hivep2 provided by MGI
Official Full Name	human immunodeficiency virus type I enhancer binding protein 2 provided byMGI
Primary source	MGI:MGI:1338076
See related	Ensembl:ENSMUSG00000015501
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Gm20114, MIBP-1, MIBP1, Schnurri-2, Shn-2
Expression	Broad expression in cortex adult (RPKM 18.2), frontal lobe adult (RPKM 17.6) and 20 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

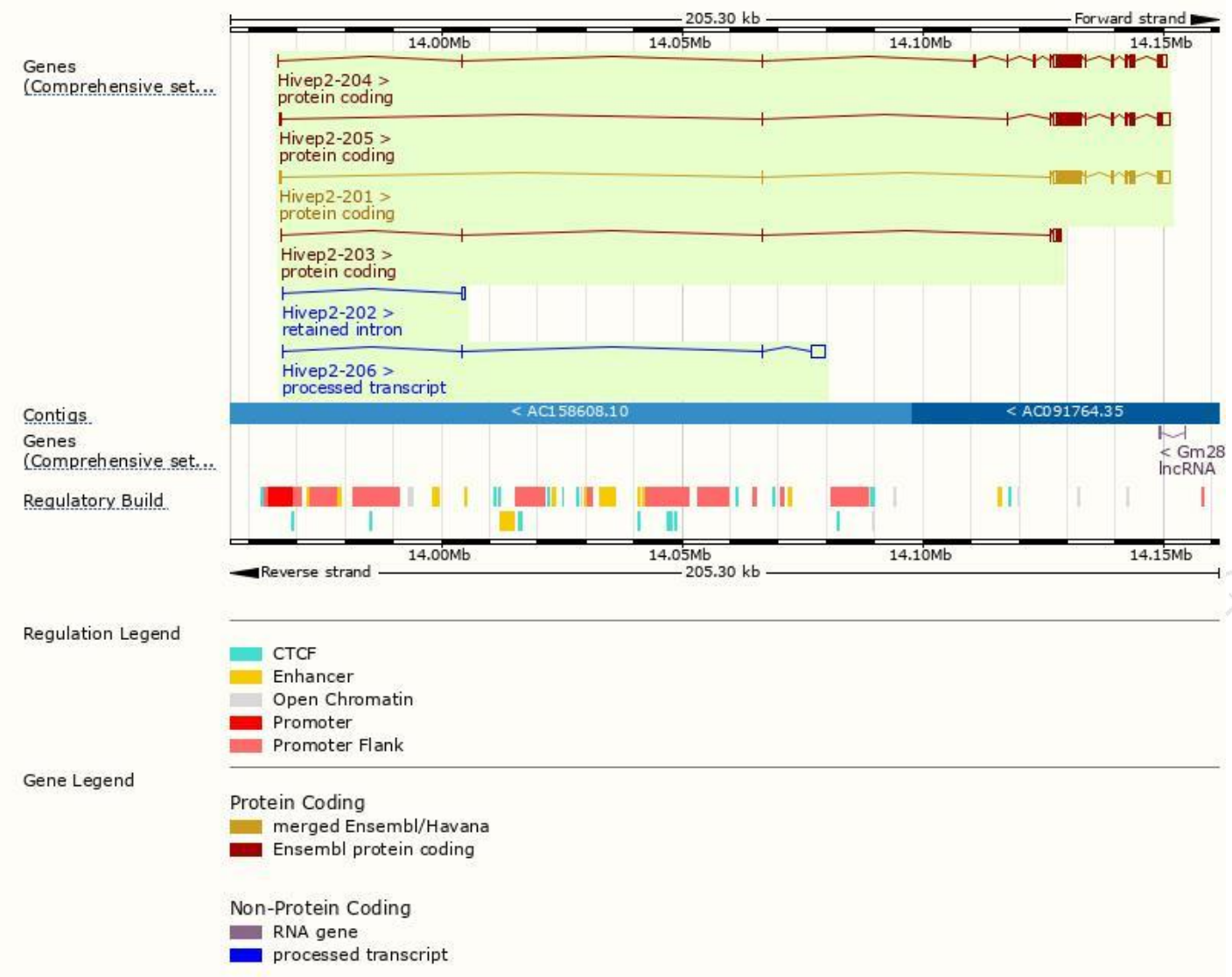
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hivep2-205	ENSMUST00000191138.6	9846	2430aa	Protein coding	CCDS23704	Q3UHF7	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
Hivep2-201	ENSMUST00000015645.10	9763	2430aa	Protein coding	CCDS23704	Q3UHF7	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
Hivep2-204	ENSMUST00000187083.6	9268	2430aa	Protein coding	CCDS23704	Q3UHF7	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
Hivep2-203	ENSMUST00000186989.6	1762	373aa	Protein coding	-	A0A087WQF9	CDS 3' incomplete TSL:1
Hivep2-206	ENSMUST00000191464.1	2899	No protein	Processed transcript	-	-	TSL:1
Hivep2-202	ENSMUST00000185392.1	758	No protein	Retained intron	-	-	TSL:5

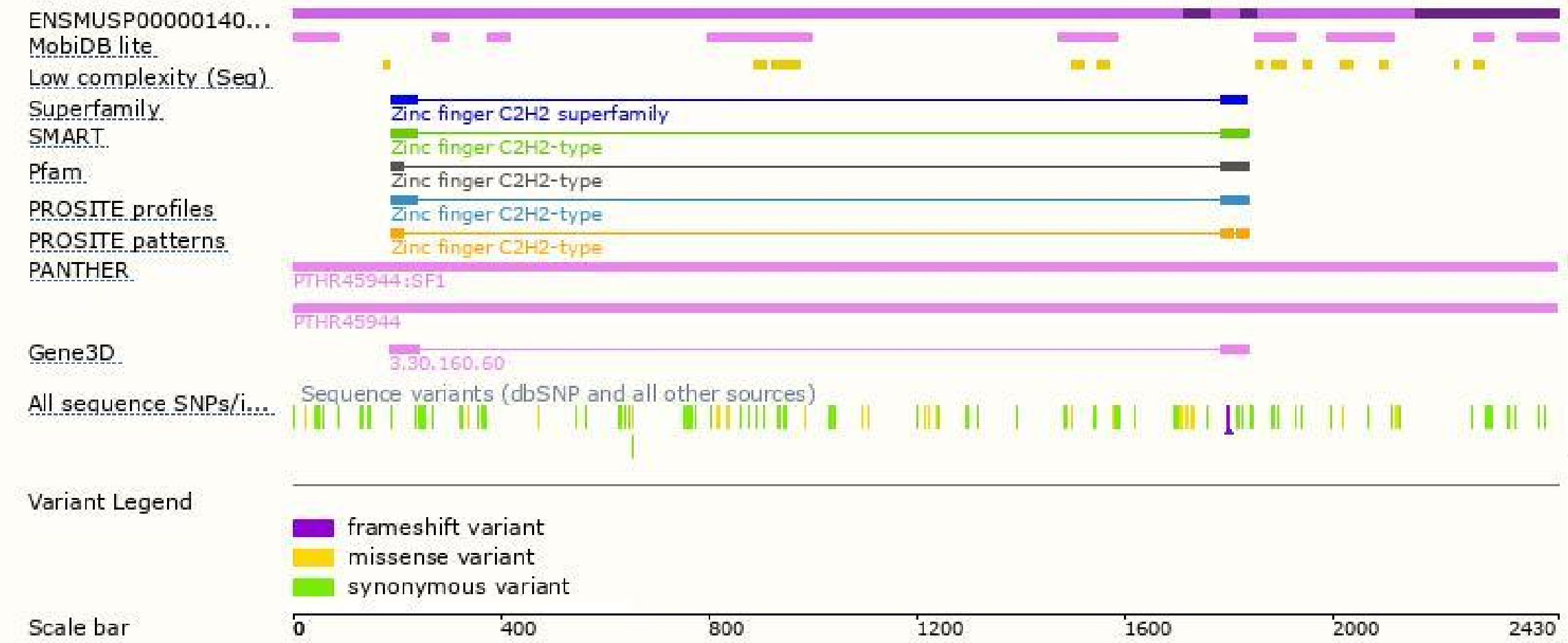
The strategy is based on the design of *Hivep2-205* transcript,the transcription is shown below:



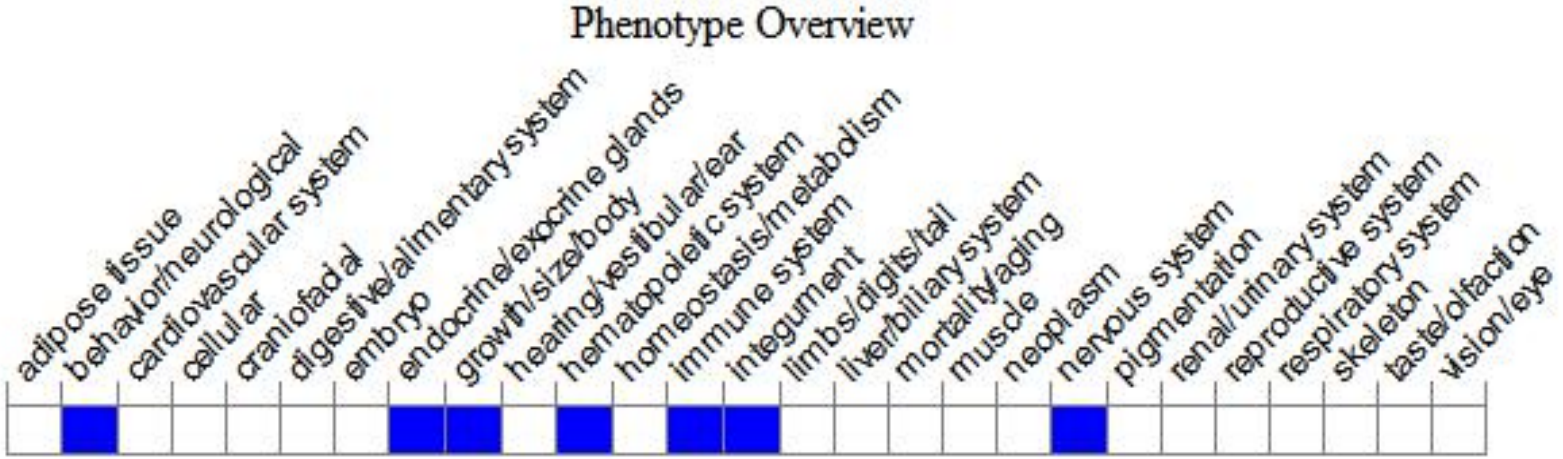
Genomic location distribution



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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