

Hhipl1 Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Hhipl1

Project type

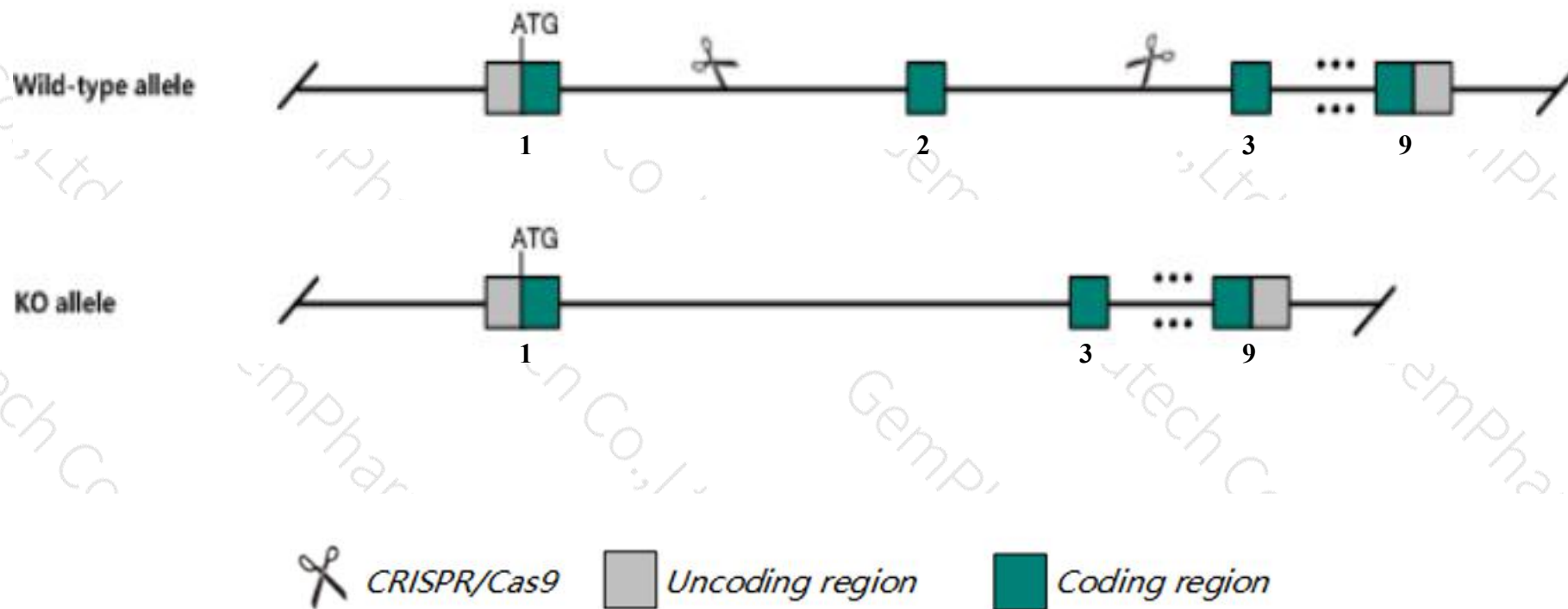
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hhip11* gene. The schematic diagram is as follows:



- The *Hhip11* gene has 2 transcripts. According to the structure of *Hhip11* gene, exon2 of *Hhip11-201* (ENSMUST00000021685.7) transcript is recommended as the knockout region. The region contains 647bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Hhip11* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Hhip11* gene is located on the Chr12. 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)

Hhip1 hedgehog interacting protein-like 1 [Mus musculus (house mouse)]

Gene ID: 214305, updated on 13-Mar-2020

Summary



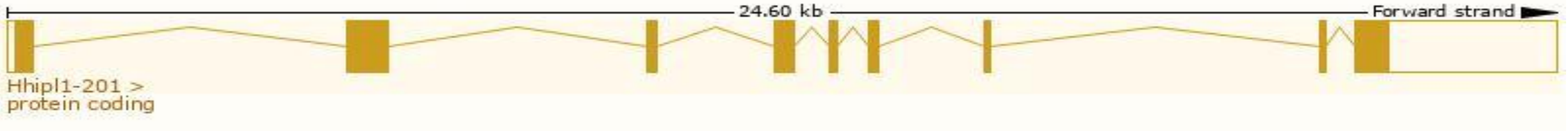
Official Symbol	Hhip1 provided by MGI
Official Full Name	hedgehog interacting protein-like 1 provided by MGI
Primary source	MGI:MGI:1919265
See related	Ensembl:ENSMUSG00000021260
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1600002O04Rik, AK129450, mKIAA1822
Expression	Ubiquitous expression in subcutaneous fat pad adult (RPKM 2.7), ovary adult (RPKM 2.3) and 24 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hhip1-201	ENSMUST00000021685.7	5174	791aa	Protein coding	CCDS36554	Q14DK5	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
Hhip1-202	ENSMUST000000223395.1	2038	No protein	Processed transcript	-	-	TSL:1

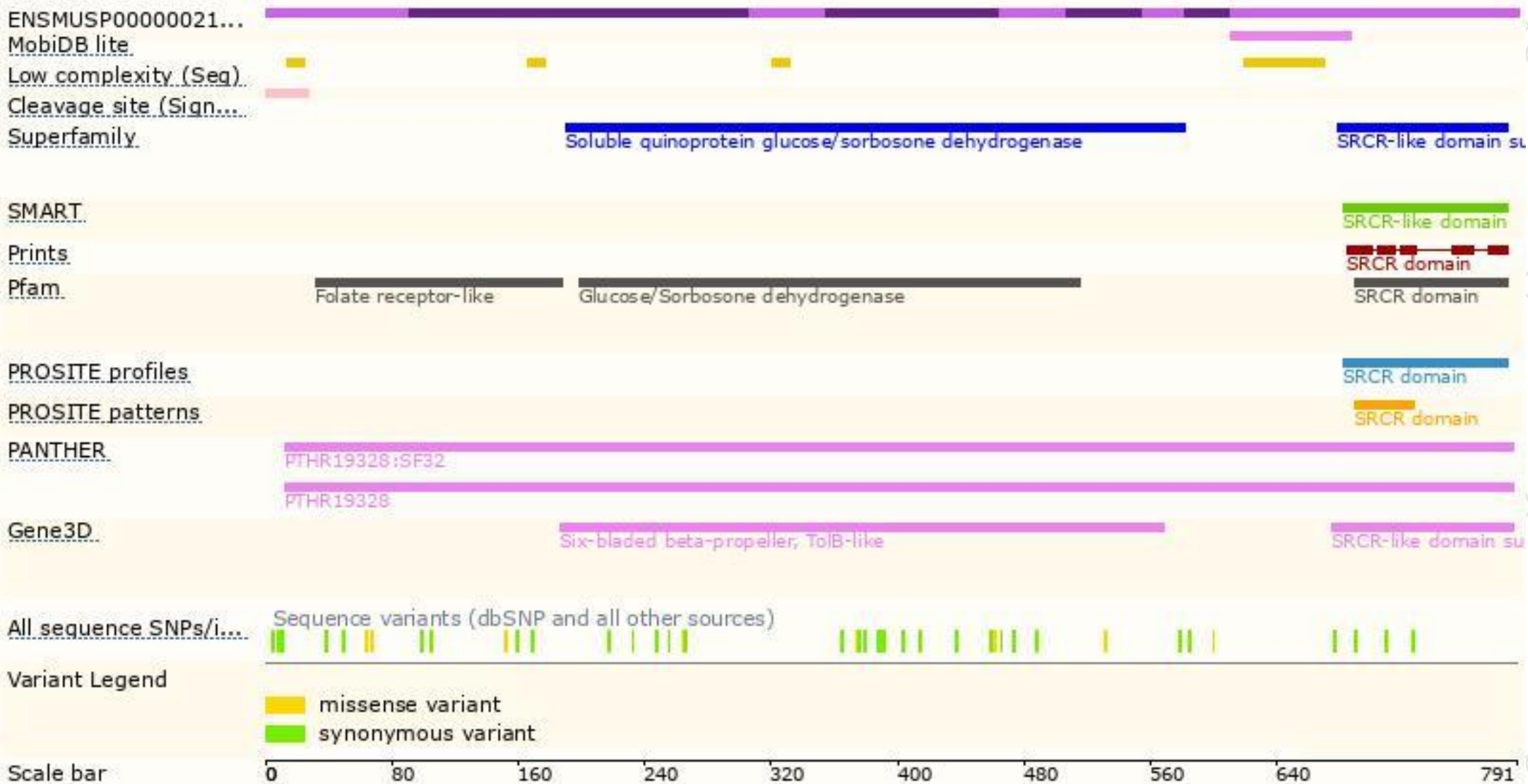
The strategy is based on the design of *Hhip1-201* transcript,The transcription is shown below



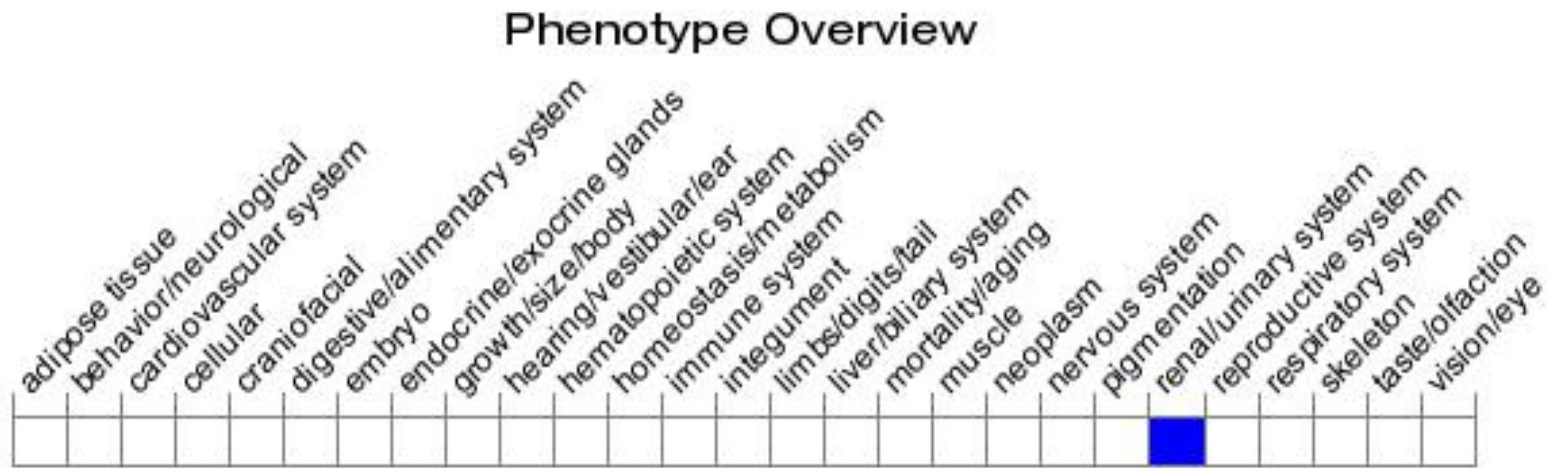
Genomic location distribution



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/>).

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

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