Hhipl1 Cas9-CKO Strategy

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Project Overview

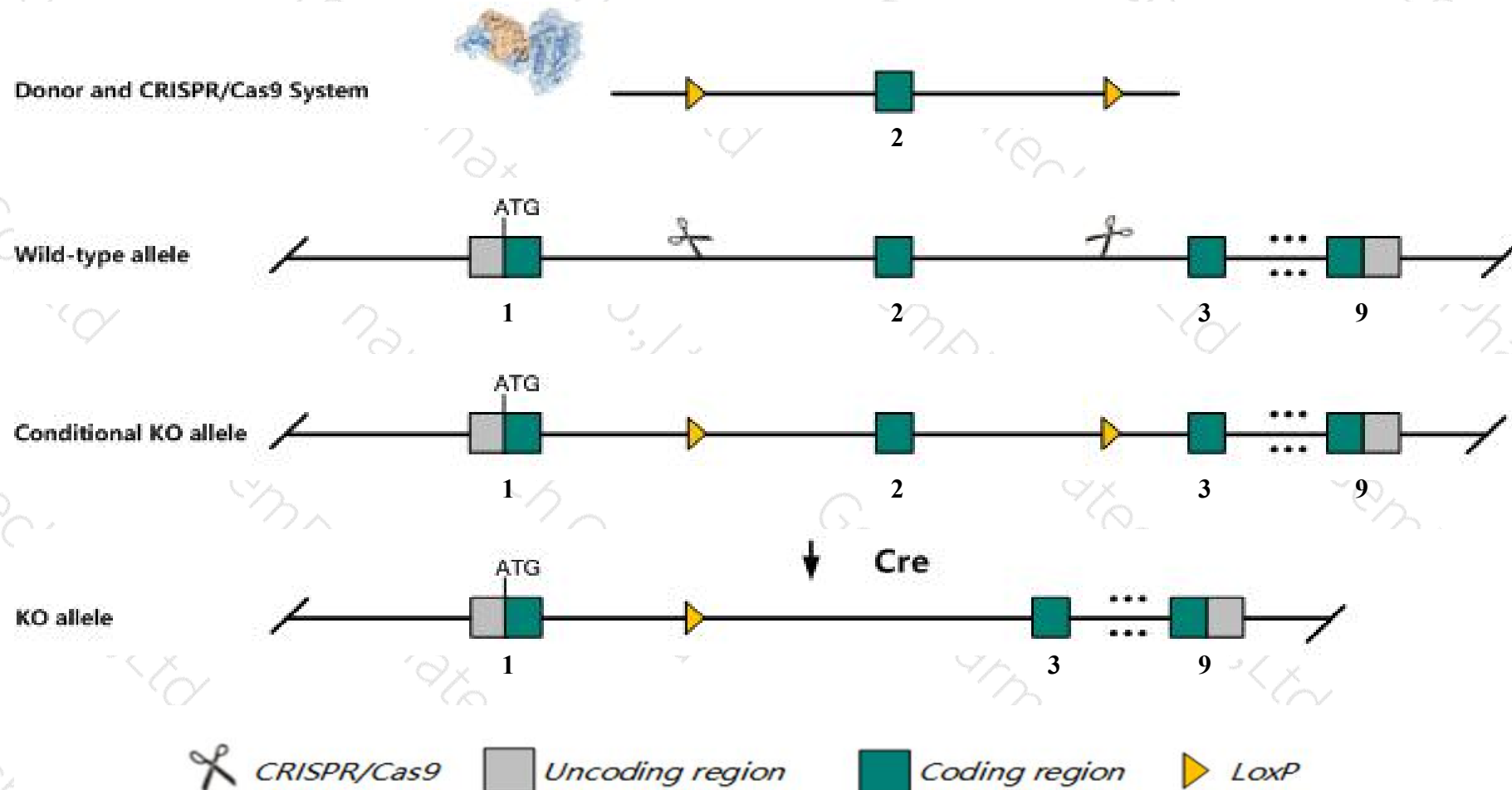|	
Project Name	*Hhipl1*
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hhipl1* gene. The schematic diagram is as follows:

Technical routes

➢ The *Hhipl1* gene has 2 transcripts. According to the structure of *Hhipl1* gene, exon2 of *Hhipl1-201* (ENSMUST00000021685.7) transcript is recommended as the knockout region.The region contains Ens 647bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Hhipl1* gene. The brief process is as follows:CRISPR/Cas9 system and Donor 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.

➢ The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice

➢ The *Hhipl1* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

Hhipl1 hedgehog interacting protein-like 1 [Mus musculus (house mouse)]

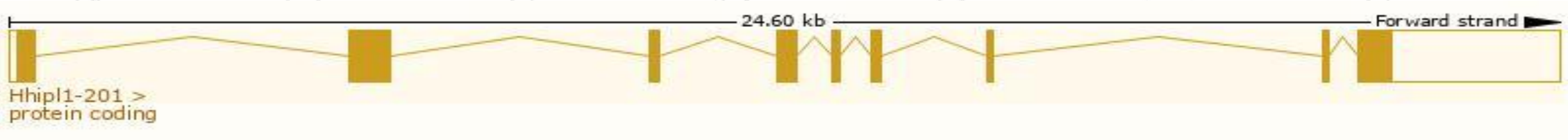Gene ID: 214305, updated on 13-Mar-2020

Summary

Official Symbol	Hhipl1 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 tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

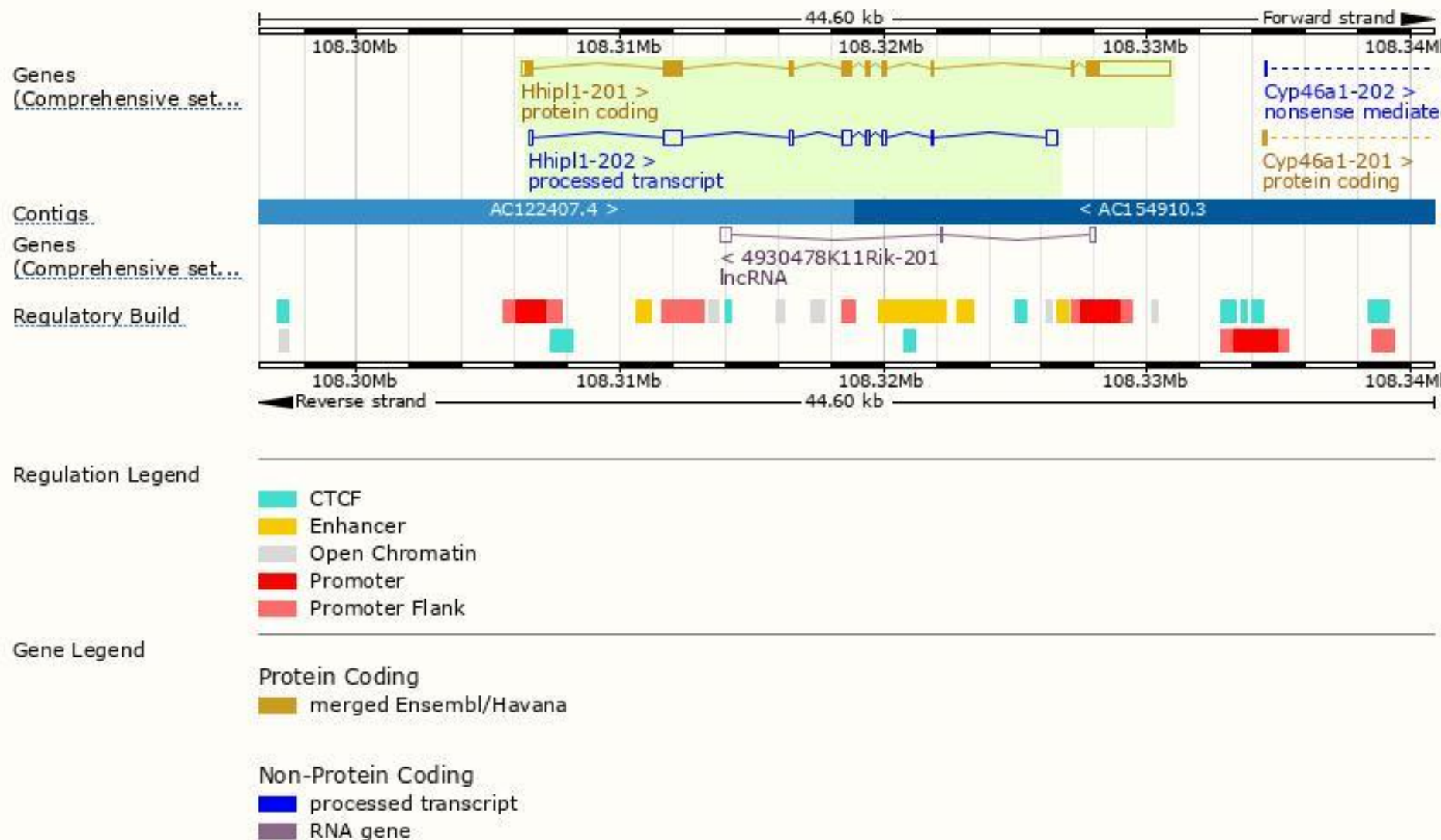The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hhipl1-201	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
Hhipl1-202	ENSMUST00000223395.1	2038	No protein	Processed transcript	-	-	TSL:1

The strategy is based on the design of *Hhipl1-201* transcript,The transcription is shown below
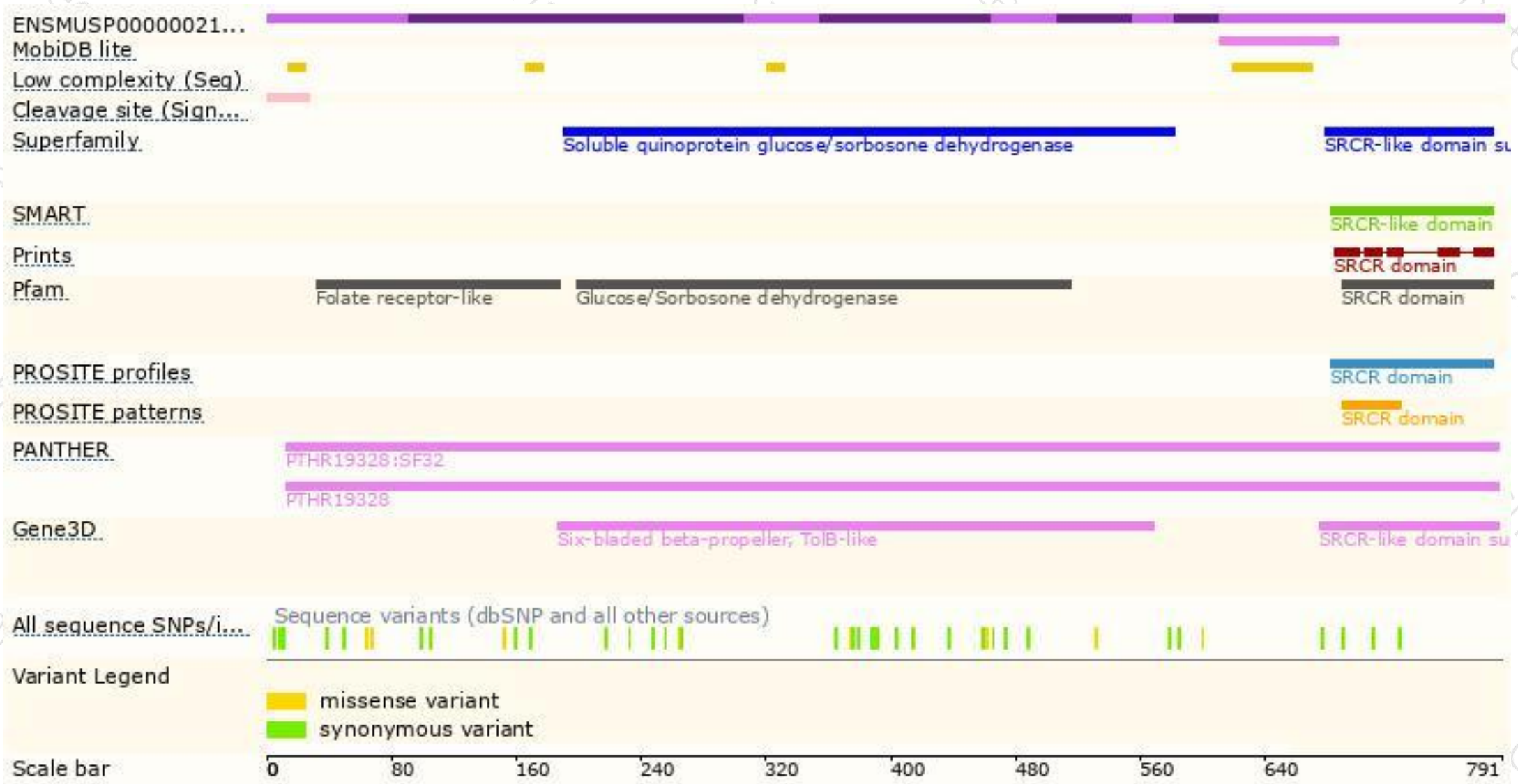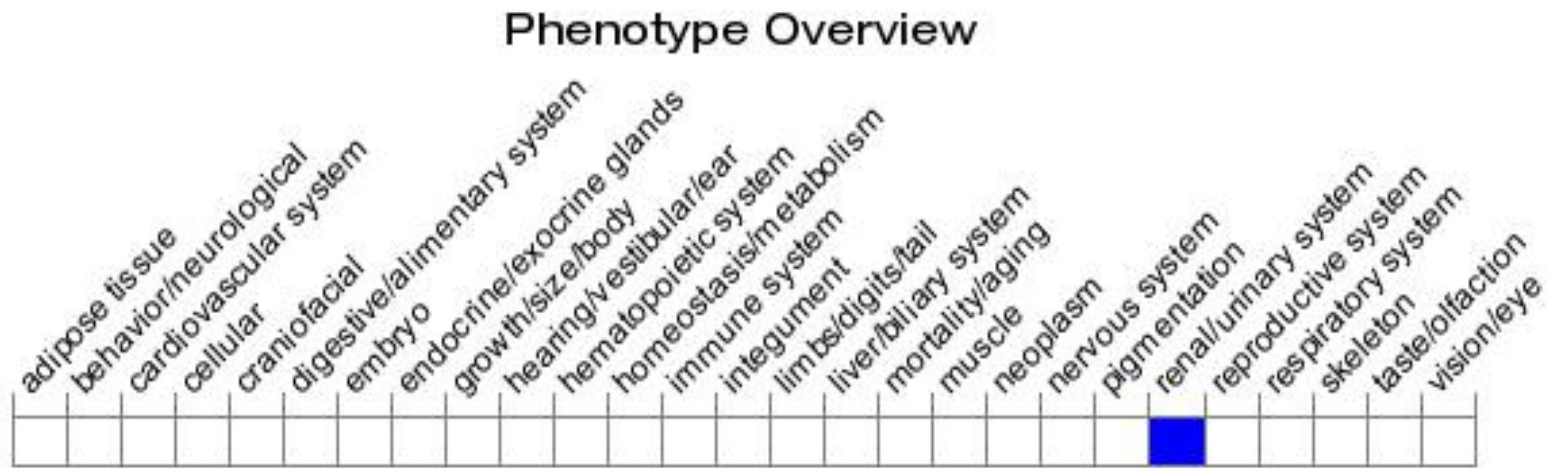

24.60 kb — Forward strand

Hhipl1-201 >
protein coding

Genomic location distribution

Protein domain

ENSMUSP00000021...		
MobiDB lite		
Low complexity (Seg)		
Cleavage site (Sign...		
Superfamily	Soluble quinoprotein glucose/sorbosone dehydrogenase	SRCR-like domain su
SMART		SRCR-like domain
Prints		SRCR domain
Pfam	Folate receptor-like	Glucose/Sorbosone dehydrogenase	SRCR domain
PROSITE profiles		SRCR domain
PROSITE patterns		SRCR domain
PANTHER	PTHR19328:SF32	
	PTHR19328	
Gene3D	Six-bladed beta-propeller, TolB-like	SRCR-like domain su
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)	

Variant Legend

🟨 missense variant
🟩 synonymous variant

Scale bar   0   80   160   240   320   400   480   560   640   791

Mouse phenotype description(MGI)

Phenotype Overview

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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