Pif1 Cas9-KO Strategy

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Project Overview

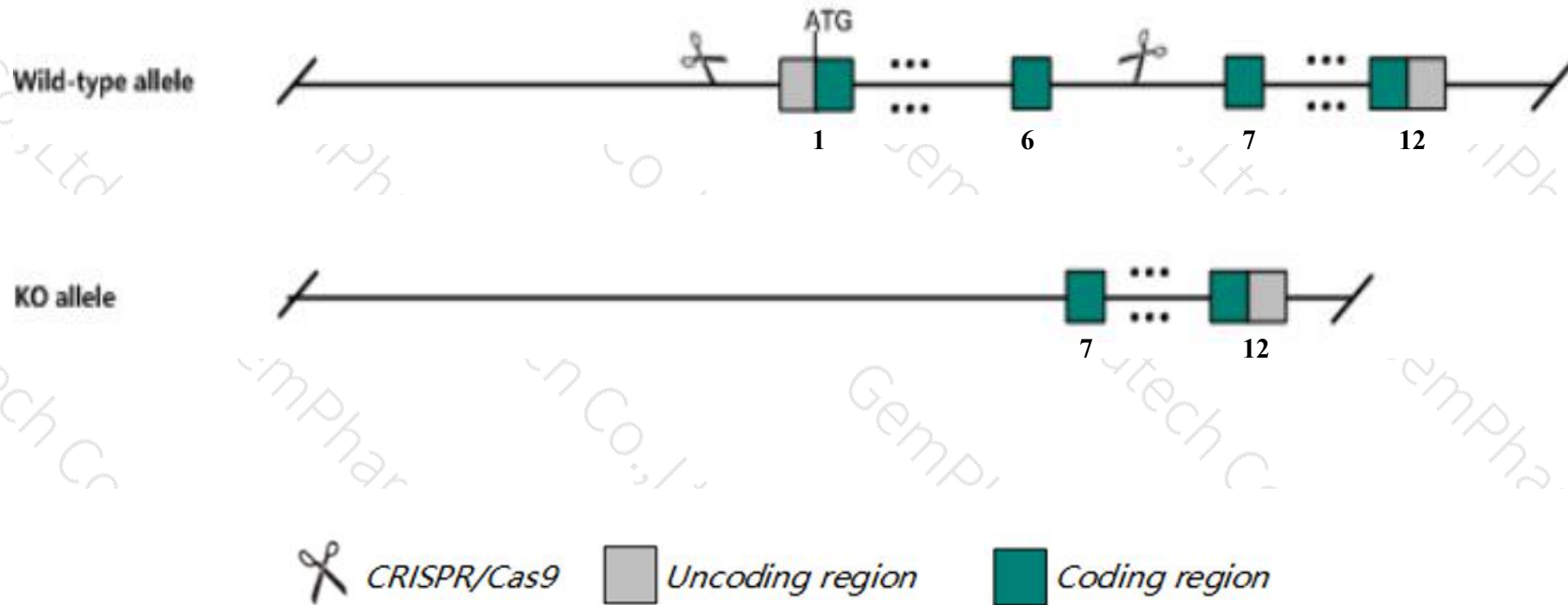|	
Project Name	*Pif1*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pif1* gene. The schematic diagram is as follows:

Technical routes

➤ The *Pif1* gene has 8 transcripts. According to the structure of *Pif1* gene, exon1-exon6 of *Pif1-201* (ENSMUST00000047099.11) transcript is recommended as the knockout region.The region contains start codon ATG. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Pif1* gene. The brief process is as follows: CRISPR/Cas9 system w

Notice

➢ According to the existing MGI data,Mice homozygous for a knock-out allele are viable and overtly normal and show no evidence of increased sensitivity to DNA damage, genetic instability, reproducible telomere length alteration or other cellular abnormalities.

➢ The *Pif1* gene is located on the Chr9. 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）

Pif1 PIF1 5'-to-3' DNA helicase [Mus musculus (house mouse)]

Gene ID: 208084, updated on 13-Mar-2020

▲ Summary

|	
Official Symbol	Pif1 provided by MGI
Official Full Name	PIF1 5'-to-3' DNA helicase provided by MGI
Primary source	MGI:MGI:2143057
See related	Ensembl:ENSMUSG00000041064
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	4631410M14, AI449441
Expression	Broad expression in CNS E11.5 (RPKM 6.1), thymus adult (RPKM 5.9) and 15 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 8 transcripts,all transcripts are shown below:

| Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pif1-201	ENSMUST00000047099.11	3685	650aa	Protein coding	CCDS23295	Q80SX8	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
Pif1-203	ENSMUST00000134538.7	3395	650aa	Protein coding	CCDS23295	Q80SX8	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
Pif1-202	ENSMUST00000131483.1	3309	650aa	Protein coding	CCDS23295	Q80SX8	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
Pif1-205	ENSMUST00000141046.1	742	157aa	Protein coding	-	D3YZ87	CDS 3' incomplete TSL:2
Pif1-204	ENSMUST00000136205.1	371	9aa	Protein coding	-	A0A1C7ZMZ4	CDS 3' incomplete TSL:3
Pif1-208	ENSMUST00000154970.7	3725	411aa	Nonsense mediated decay	-	D6RFC6	TSL:1
Pif1-206	ENSMUST00000152529.1	3897	No protein	Retained intron	-	-	TSL:2
Pif1-207	ENSMUST00000152885.7	2450	No protein	Retained intron	-	-	TSL:2

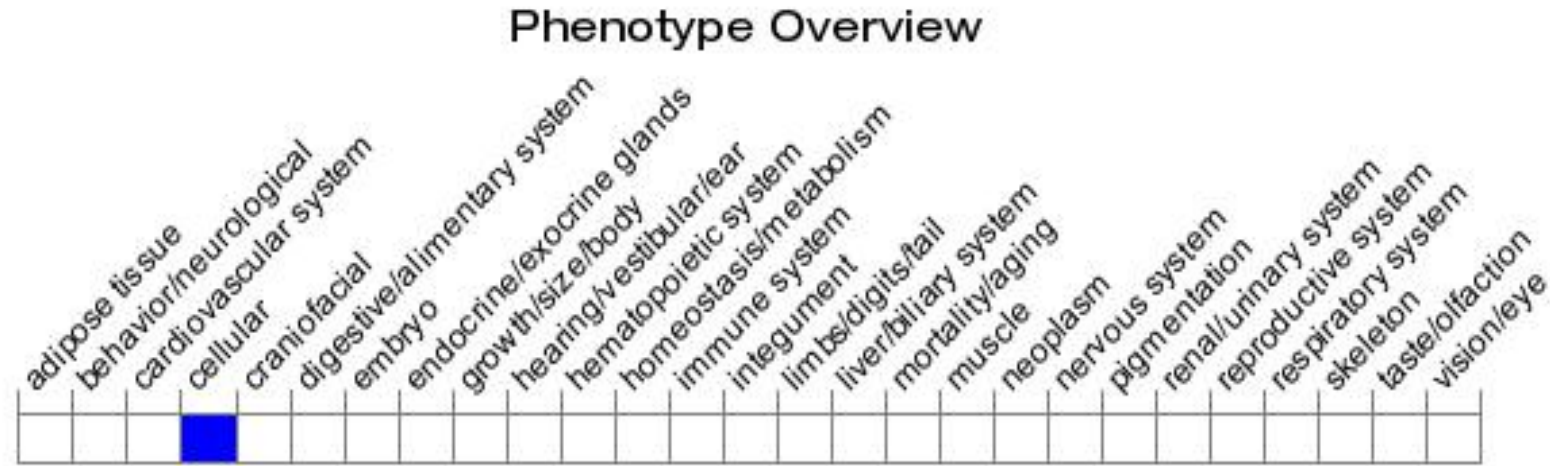The strategy is based on the design of *Pif1-201* transcript,The transcription is shown below
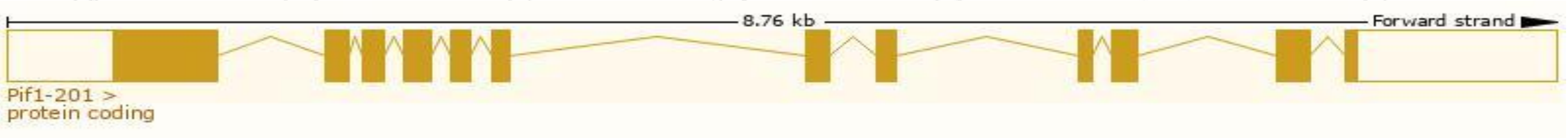
Genomic location distribution
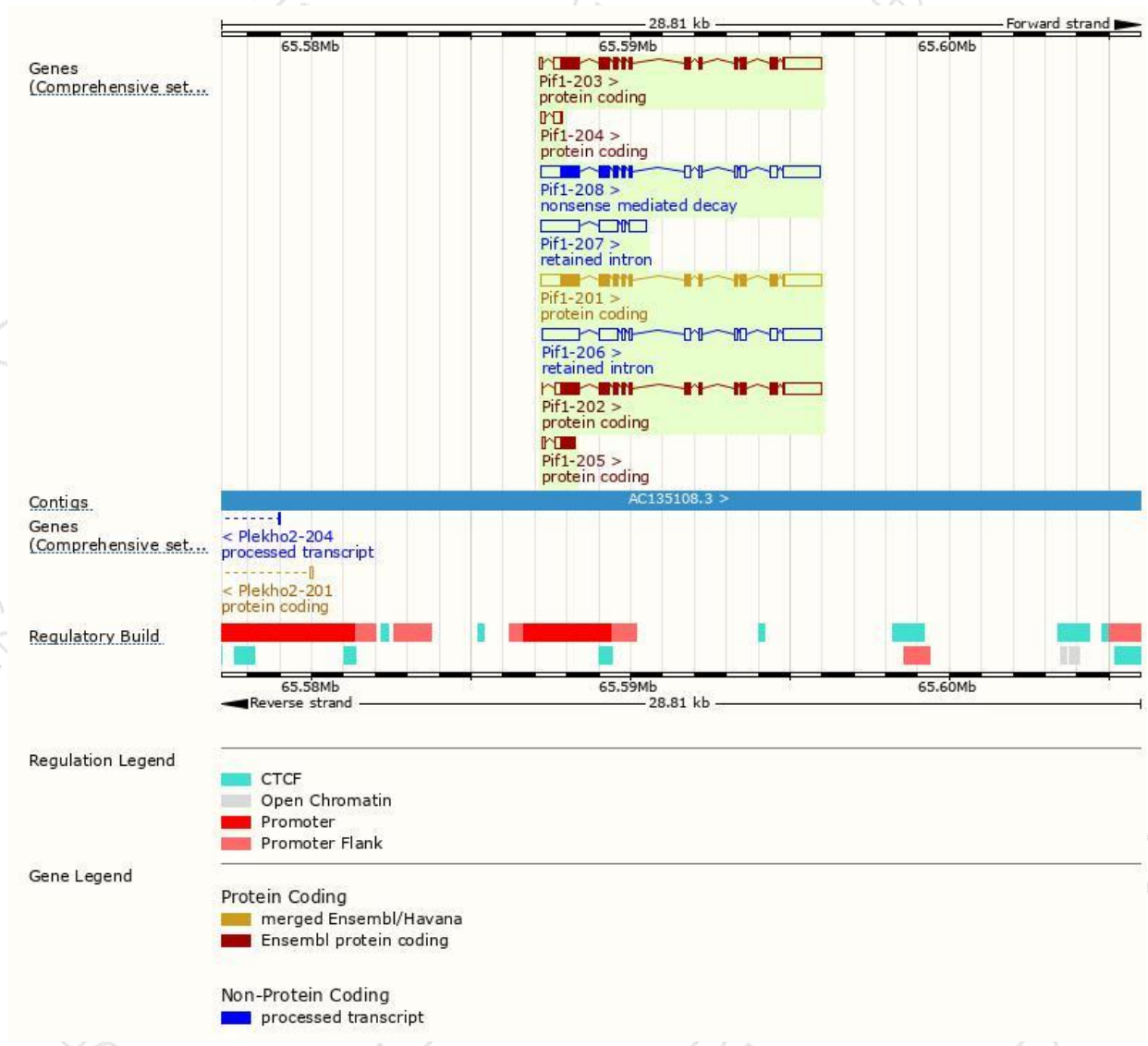
Protein domain
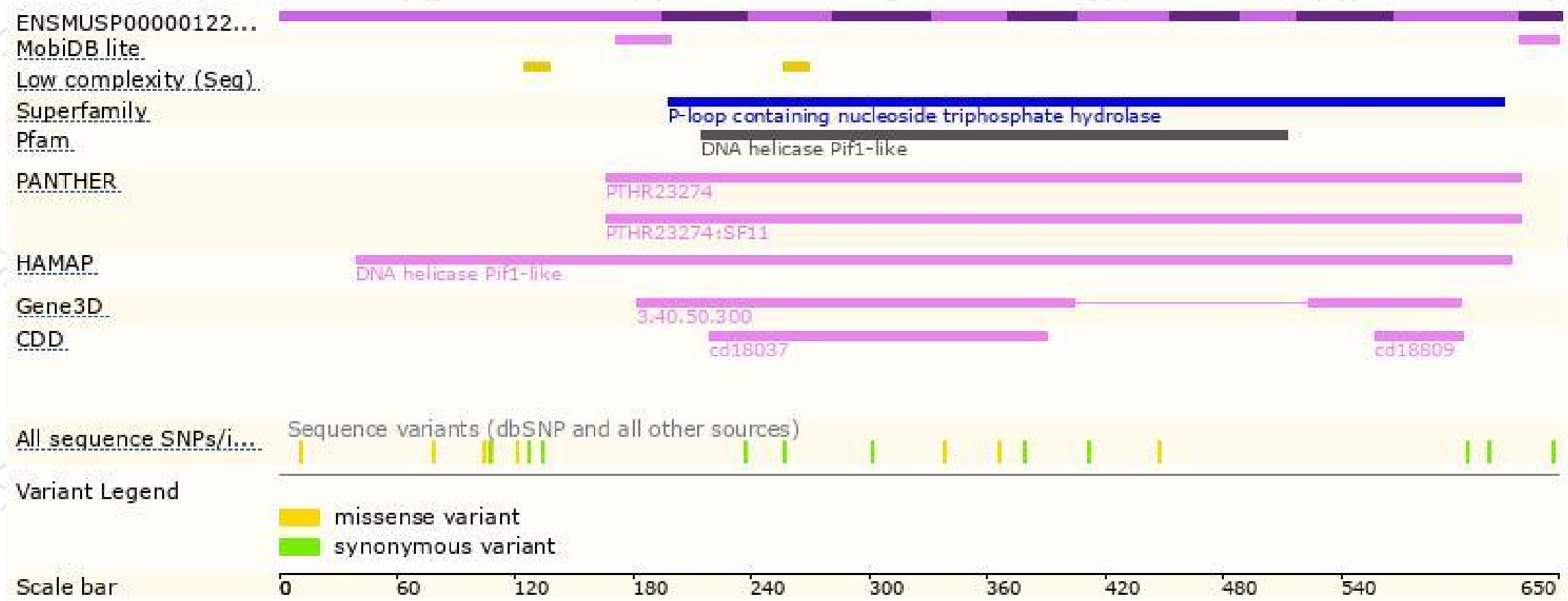
Mouse phenotype description(MGI)

Phenotype Overview

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

According to the existing MGI data,Mice homozygous for a knock-out allele are viable and overtly normal and show no evidence of increased sensitivity to DNA damage, genetic instability, reproducible telomere length alteration or other cellular abnormalities.

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