

# *Phf8* Cas9-KO Strategy

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# Project Overview

**Project Name**

*Phf8*

**Project type**

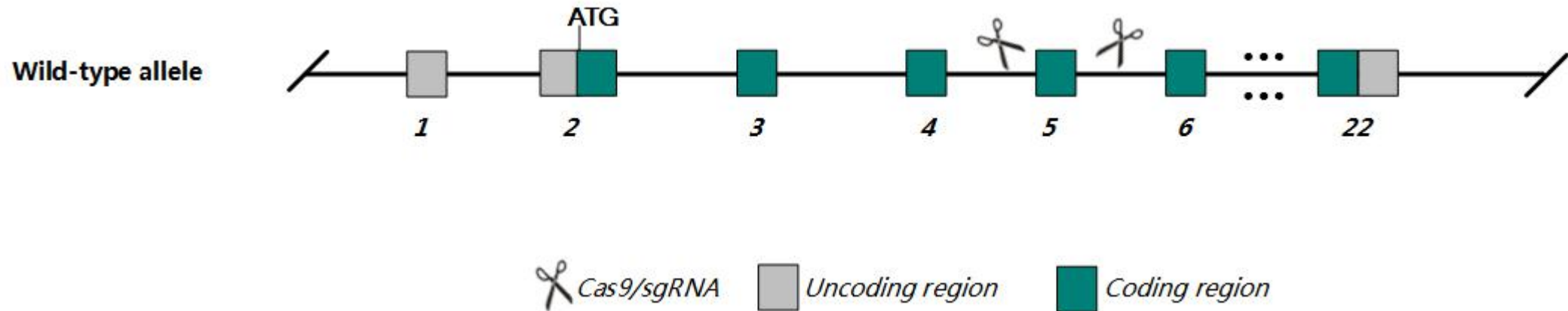
**Cas9-KO**

**Strain background**

**C57BL/6N**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Phf8* gene. The schematic diagram is as follows:



- In this project we use CRISPR/Cas9 technology to modify *Phf8* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6N 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/6N mice.

- The *Phf8* gene is located on the ChrX, 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)

## Phf8 PHD finger protein 8 [ *Mus musculus* (house mouse) ]

Gene ID: 320595, updated on 12-Aug-2019

### Summary

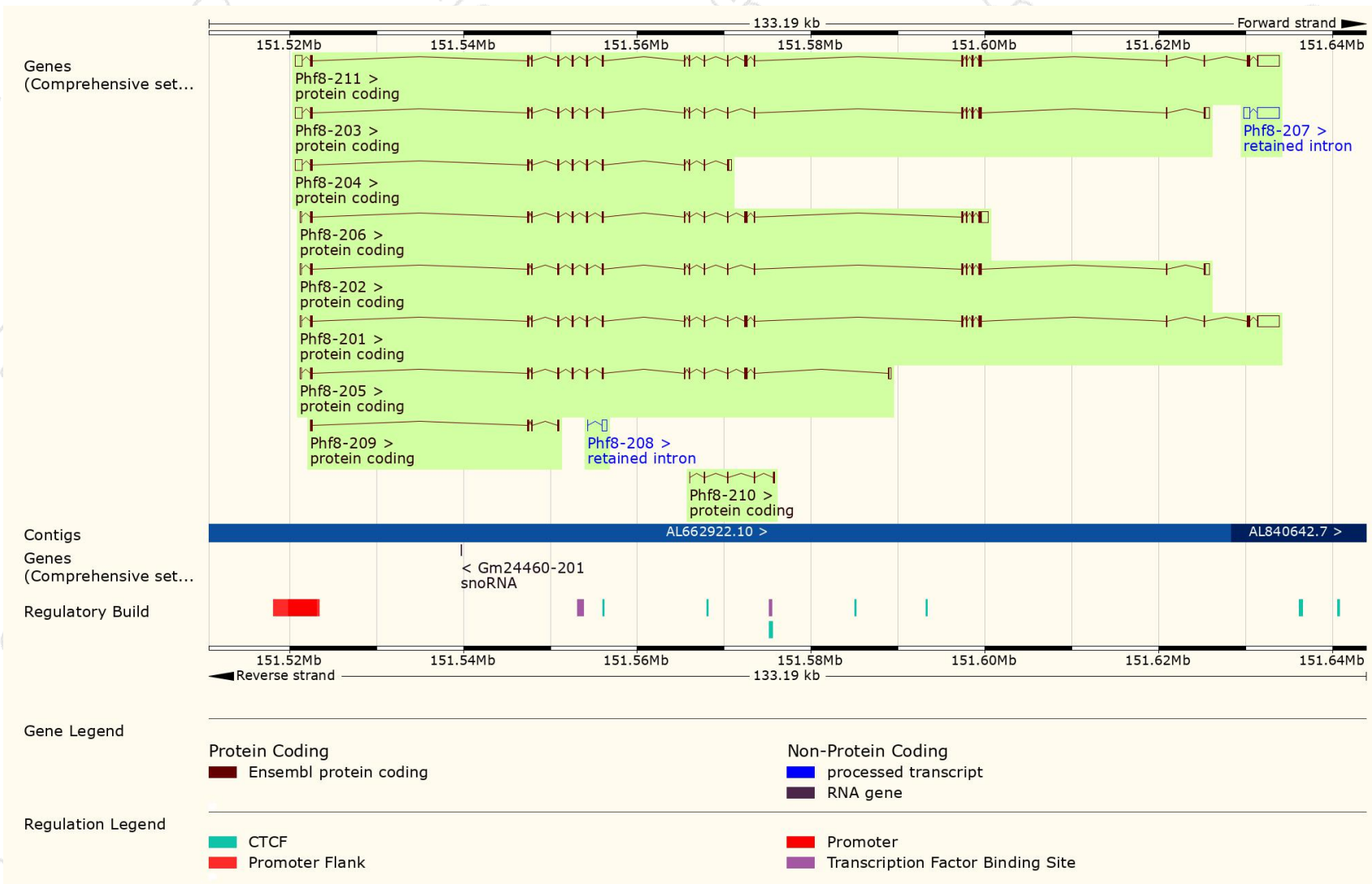
Official Symbol	Phf8 provided by <a href="#">MGI</a>
Official Full Name	PHD finger protein 8 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:2444341</a>
See related	<a href="#">Ensembl:ENSMUSG000000041229</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	mKIAA1111; 9830141C09Rik
Expression	Ubiquitous expression in genital fat pad adult (RPKM 7.8), thymus adult (RPKM 4.9) and 28 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

The gene has 11 transcripts,all transcripts are shown below:

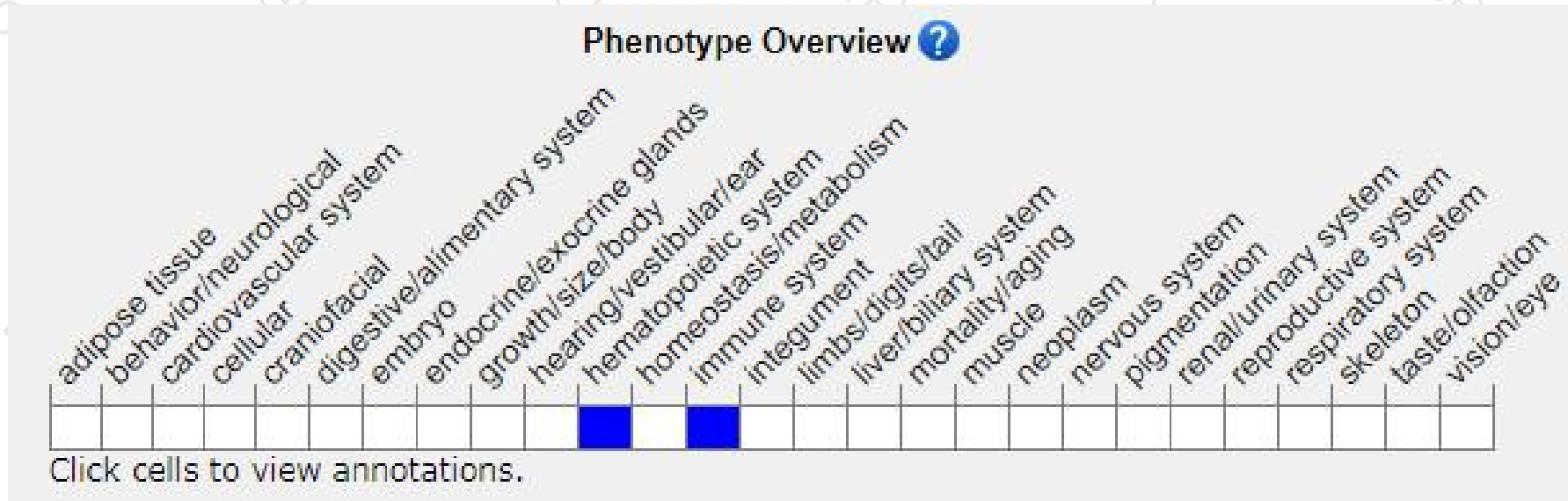
Name ▲	Transcript ID ▲	bp ▲	Protein ▲	Biotype ▲	CCDS ▲	UniProt ▲	Flags ▲
Phf8-201	<a href="#">ENSMUST00000046950.12</a>	5728	<a href="#">1023aa</a>	Protein coding	<a href="#">CCDS53223</a>	<a href="#">Q80TJ7</a>	TSL:5 Gencode basic APPRIS ALT2
Phf8-202	<a href="#">ENSMUST00000046962.10</a>	3105	<a href="#">795aa</a>	Protein coding	<a href="#">CCDS30470</a>	<a href="#">A2ABV3</a> <a href="#">Q80TJ7</a>	TSL:1 Gencode basic APPRIS P3
Phf8-203	<a href="#">ENSMUST00000112662.8</a>	3732	<a href="#">795aa</a>	Protein coding	<a href="#">CCDS30470</a>	<a href="#">A2ABV3</a> <a href="#">Q80TJ7</a>	TSL:5 Gencode basic APPRIS P3
Phf8-204	<a href="#">ENSMUST00000112666.7</a>	2556	<a href="#">464aa</a>	Protein coding	-	<a href="#">Q80TJ7</a>	TSL:1 Gencode basic APPRIS ALT2
Phf8-205	<a href="#">ENSMUST00000112668.8</a>	2291	<a href="#">602aa</a>	Protein coding	-	<a href="#">A2ABV1</a>	TSL:1 Gencode basic APPRIS ALT2
Phf8-206	<a href="#">ENSMUST00000112670.7</a>	3484	<a href="#">820aa</a>	Protein coding	-	<a href="#">Z4YL84</a>	TSL:1 Gencode basic APPRIS ALT2
Phf8-207	<a href="#">ENSMUST00000138318.1</a>	3191	No protein	Retained intron	-	-	TSL:1
Phf8-208	<a href="#">ENSMUST00000141715.1</a>	572	No protein	Retained intron	-	-	TSL:3
Phf8-209	<a href="#">ENSMUST00000148622.2</a>	573	<a href="#">151aa</a>	Protein coding	-	<a href="#">A2ABU9</a>	CDS 3' incomplete TSL:3
Phf8-210	<a href="#">ENSMUST00000151941.1</a>	516	<a href="#">124aa</a>	Protein coding	-	<a href="#">F7BTQ5</a>	CDS 5' incomplete TSL:3
Phf8-211	<a href="#">ENSMUST00000168501.7</a>	6359	<a href="#">1023aa</a>	Protein coding	<a href="#">CCDS53223</a>	<a href="#">Q80TJ7</a>	TSL:5 Gencode basic APPRIS ALT2

# Genomic location distribution





# 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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