

Phip Cas9-KO Strategy

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Project Overview



Project Name

Phip

Project type

Cas9-KO

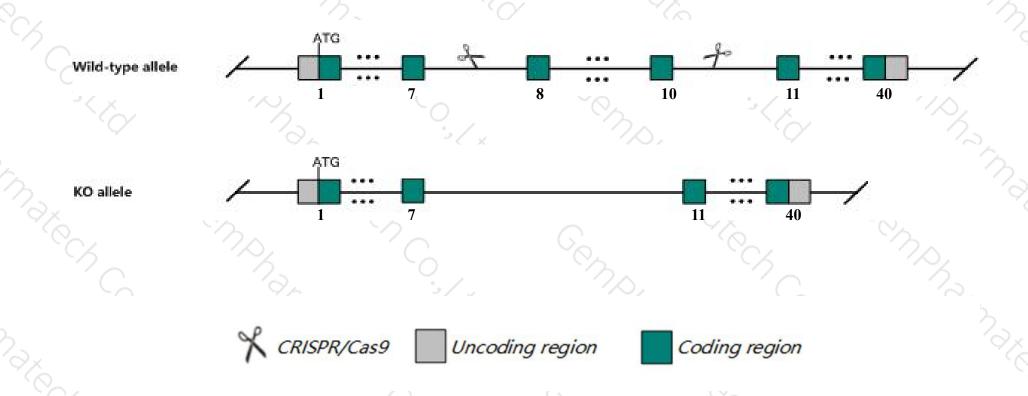
Strain background

C57BL/6JGpt

Knockout strategy



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



Technical routes



- ➤ The *Phip* gene has 16 transcripts. According to the structure of *Phip* gene, exon8-exon10 of *Phip-201*(ENSMUST00000034787.11) transcript is recommended as the knockout region. The region contains 394bp coding sequence Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Phip* gene. The brief process is as follows: CRISPR/Cas9 system v

Notice



- ➤ According to the existing MGI data, Mice homozygous for a gene trapped allele exhibit postnatal and premature lethality associated with reduced body size, small myocardial cells and hepatocytes, hypoglycemia, increased insulin sensitivity, and reduced cell growth.
- > The *Phip* 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)



Phip pleckstrin homology domain interacting protein [Mus musculus (house mouse)]

Gene ID: 83946, updated on 5-Feb-2019

Summary

☆ ?

Official Symbol Phip provided by MGI

Official Full Name pleckstrin homology domain interacting protein provided by MGI

Primary source MGI:MGI:1932404

See related Ensembl: ENSMUSG00000032253

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 2810004D21Rik, 4632404O06Rik, Ndrp, Wdr11

Expression Broad expression in CNS E11.5 (RPKM 6.9), whole brain E14.5 (RPKM 6.8) and 24 other tissuesSee more

Orthologs human all

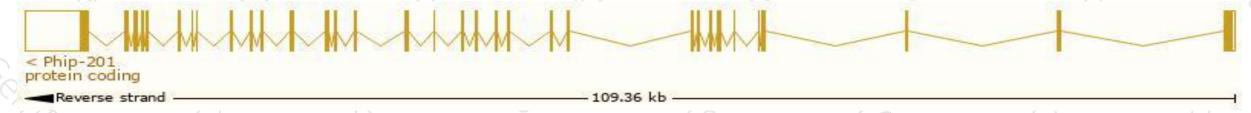
Transcript information (Ensembl)



The gene has 16 transcripts, all transcripts are shown below:

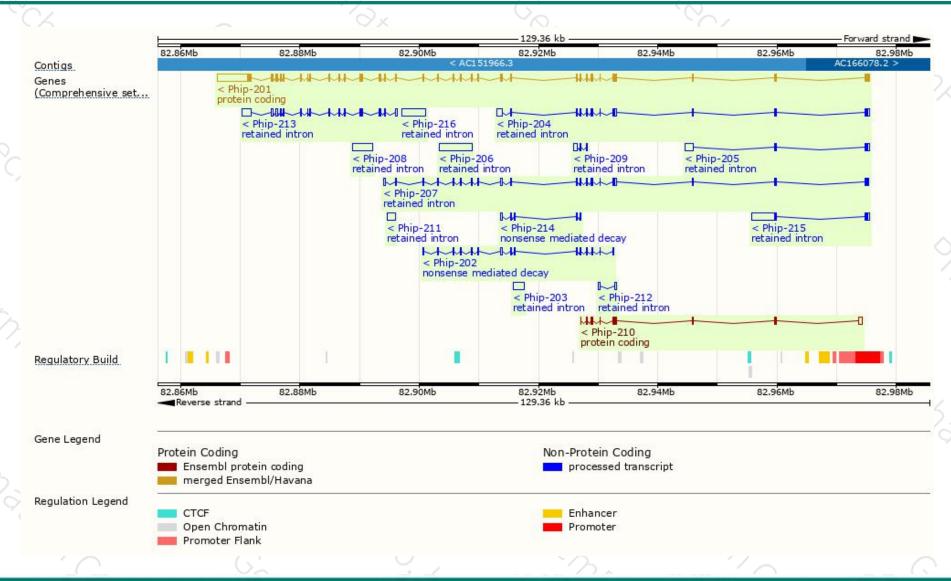
all the							
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Phip-201	ENSMUST00000034787.11	10756	1821aa	Protein coding	CCDS40706	F8VQ93	TSL:1 GENCODE basic APPRIS P
Phip-210	ENSMUST00000189985.1	1629	360aa	Protein coding		A0A087WR26	CDS 3' incomplete TSL:1
Phip-202	ENSMUST00000186089.6	1924	92aa	Nonsense mediated decay	-	A0A087WP89	CDS 5' incomplete TSL:1
Phip-214	ENSMUST00000190822.1	611	<u>84aa</u>	Nonsense mediated decay	-	A0A087WPP7	CDS 5' incomplete TSL:3
Phip-206	ENSMUST00000188850.1	5523	No protein	Retained intron		- 4	TSL:NA
Phip-215	ENSMUST00000190838.1	4274	No protein	Retained intron		-8	TSL:2
Phip-216	ENSMUST00000190936.1	3949	No protein	Retained intron	-	20	TSL:NA
Phip-213	ENSMUST00000190774.1	3830	No protein	Retained intron	-	29	TSL:1
hip-207	ENSMUST00000188868.6	3317	No protein	Retained intron			TSL:1
Phip-208	ENSMUST00000189209.1	3286	No protein	Retained intron		-81	TSL:NA
Phip-204	ENSMUST00000187021.6	2623	No protein	Retained intron		20	TSL:1
Phip-205	ENSMUST00000188828.6	1979	No protein	Retained intron	-	29	TSL:1
Phip-203	ENSMUST00000186099.1	1794	No protein	Retained intron		-	TSL:NA
Phip-211	ENSMUST00000190101.1	1481	No protein	Retained intron		-8	TSL:NA
Phip-209	ENSMUST00000189927.1	890	No protein	Retained intron	-	20	TSL:5
Phip-212	ENSMUST00000190405.1	596	No protein	Retained intron	-	20	TSL:2

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



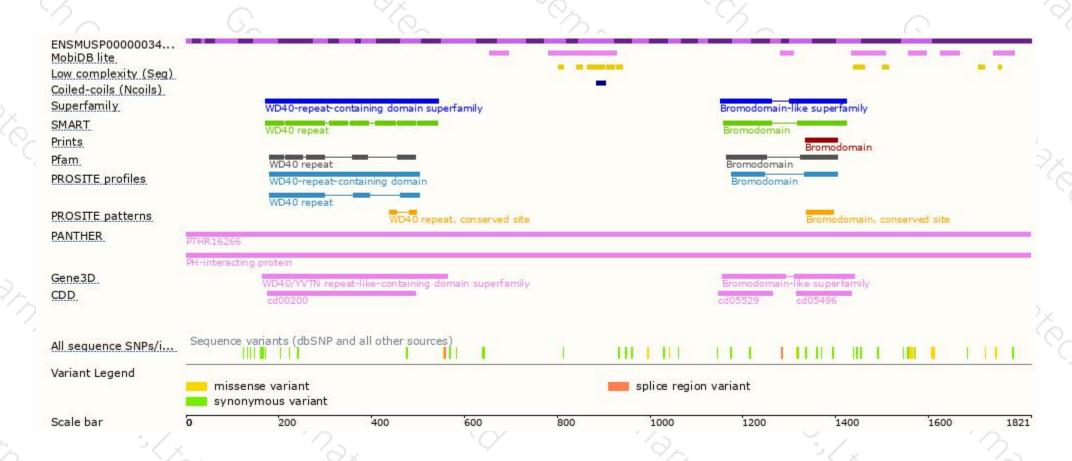
Genomic location distribution





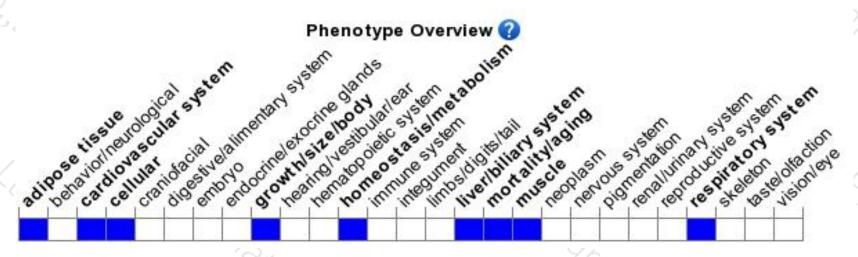
Protein domain





Mouse phenotype description(MGI)





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

According to the existing MGI data, Mice homozygous for a gene trapped allele exhibit postnatal and premature lethality associated with reduced body size, small myocardial cells and hepatocytes, hypoglycemia, increased insulin sensitivi and reduced cell growth.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





