

# Homer2 Cas9-KO Strategy

Designer:Xueting Zhang

Reviewer: Yanhua Shen

Date:2019-12-23

# **Project Overview**



**Project Name** 

Homer2

**Project type** 

Cas9-KO

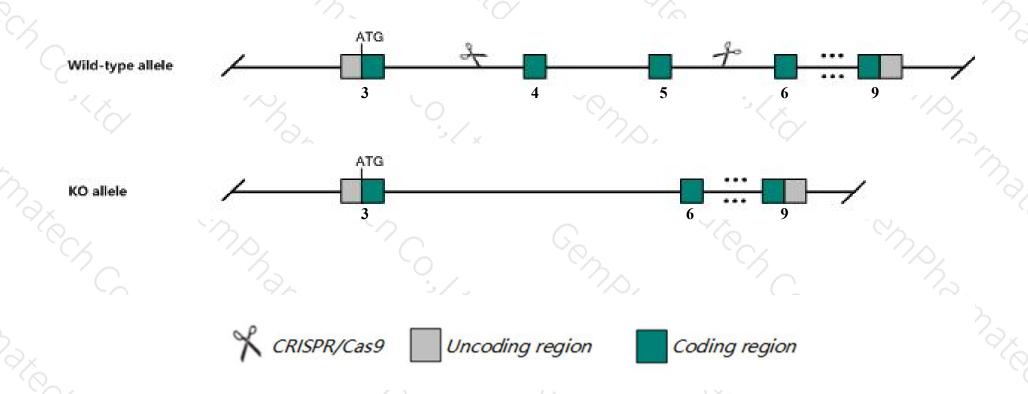
Strain background

C57BL/6JGpt

# **Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the *Homer2* gene. The schematic diagram is as follows:



### **Technical routes**



- ➤ The *Homer2* gene has 9 transcripts. According to the structure of *Homer2* gene, exon4-exon5 of *Homer2-202* (ENSMUST00000098326.2) transcript is recommended as the knockout region. The region contains 233bp coding sequence. Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Homer2* gene. The brief process is as follows: CRISPR/Cas9 syste

### **Notice**



- > According to the existing MGI data, Homozygous mutants exhibit an increase in intracellular calcium concentration and in the frequency of intracellular calcium oscillations in pancreatic acinar cells.
- > Transcript *Homer2-208* may not be affected.
- > The *Homer2* gene is located on the Chr7. 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)



#### Homer2 homer scaffolding protein 2 [ Mus musculus (house mouse) ]

Gene ID: 26557, updated on 10-Oct-2019

#### Summary

△ ?

Official Symbol Homer2 provided by MGI

Official Full Name homer scaffolding protein 2 provided by MGI

Primary source MGI:MGI:1347354

See related Ensembl: ENSMUSG00000025813

RefSeq status VALIDATED
Organism Mus musculus
Lineage Eukanyota: Mate

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as CPD; Vesl-2; AW539445; 9330120H11Rik

Expression Broad expression in frontal lobe adult (RPKM 7.6), cortex adult (RPKM 4.6) and 20 other tissues See more

Orthologs human all

#### - Genomic context

△ ?

Location: 7; 7 D3

See Homer2 in Genome Data Viewer

Exon count: 11

Annotation release	Status	Assembly	Chr	Location	
108	current	GRCm38.p6 (GCF_000001635.26)	7	NC_000073.6 (8160048181706925, complement)	
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	7	NC_000073.5 (8874536788851811, complement)	

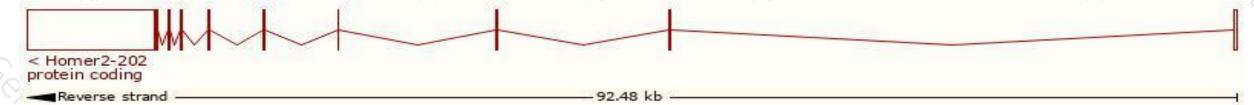
# Transcript information (Ensembl)



The gene has 9 transcripts, all transcripts are shown below:

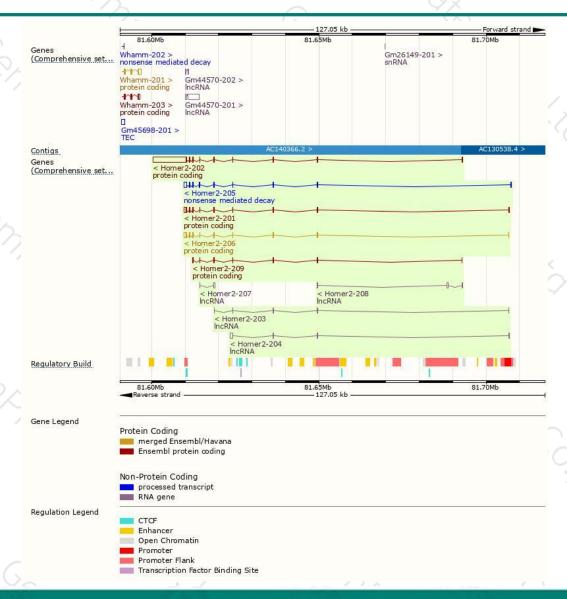
		· · · · · · · · · · · · · · · · · · ·				
Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
ENSMUST00000098326.2	10982	290aa	Protein coding	CCDS52284	E9Q4F9	TSL:5 GENCODE basic
ENSMUST00000026922.14	1736	343aa	Protein coding	CCDS85329	Q9QWW1	TSL:1 GENCODE basic APPRIS ALT1
ENSMUST00000207983.1	1634	<u>354aa</u>	Protein coding	CCDS40009	Q9QWW1	TSL:1 GENCODE basic APPRIS P3
ENSMUST00000208937.1	798	<u>179aa</u>	Protein coding	10	A0A140LHR9	CDS 3' incomplete TSL:3
ENSMUST00000207371.1	1818	252aa	Nonsense mediated decay	-	A0A140LJ06	TSL:1
ENSMUST00000207289.1	1234	No protein	IncRNA		-	TSL:1
ENSMUST00000208107.1	581	No protein	IncRNA	-	0.20	TSL:2
ENSMUST00000207991.1	478	No protein	IncRNA	20	1524	TSL:3
ENSMUST00000207039.1	457	No protein	IncRNA	8	-	TSL:2
	ENSMUST00000098326.2 ENSMUST00000026922.14 ENSMUST00000207983.1 ENSMUST00000208937.1 ENSMUST00000207371.1 ENSMUST00000207289.1 ENSMUST00000207289.1 ENSMUST00000207991.1	ENSMUST00000026922.14 1736 ENSMUST00000026922.14 1736 ENSMUST000000207983.1 1634 ENSMUST00000208937.1 798 ENSMUST00000207371.1 1818 ENSMUST00000207289.1 1234 ENSMUST00000207289.1 581 ENSMUST00000207991.1 478	ENSMUST00000098326.2         10982         290aa           ENSMUST000000026922.14         1736         343aa           ENSMUST00000207983.1         1634         354aa           ENSMUST00000208937.1         798         179aa           ENSMUST00000207371.1         1818         252aa           ENSMUST00000207289.1         1234         No protein           ENSMUST00000208107.1         581         No protein           ENSMUST00000207991.1         478         No protein	ENSMUST00000098326.2         10982         290aa         Protein coding           ENSMUST00000026922.14         1736         343aa         Protein coding           ENSMUST00000207983.1         1634         354aa         Protein coding           ENSMUST00000208937.1         798         179aa         Protein coding           ENSMUST00000207371.1         1818         252aa         Nonsense mediated decay           ENSMUST00000207289.1         1234         No protein         IncRNA           ENSMUST00000208107.1         581         No protein         IncRNA           ENSMUST00000207991.1         478         No protein         IncRNA	ENSMUST00000098326.2         10982         290aa         Protein coding         CCDS52284           ENSMUST00000026922.14         1736         343aa         Protein coding         CCDS85329           ENSMUST00000207983.1         1634         354aa         Protein coding         CCDS40009           ENSMUST00000208937.1         798         179aa         Protein coding         -           ENSMUST00000207371.1         1818         252aa         Nonsense mediated decay         -           ENSMUST00000207289.1         1234         No protein         IncRNA         -           ENSMUST00000208107.1         581         No protein         IncRNA         -           ENSMUST00000207991.1         478         No protein         IncRNA         -	ENSMUST00000098326.2         10982         290aa         Protein coding         CCDS52284         E9Q4F9           ENSMUST00000026922.14         1736         343aa         Protein coding         CCDS85329         Q9QWW1           ENSMUST00000207983.1         1634         354aa         Protein coding         CCDS40009         Q9QWW1           ENSMUST00000208937.1         798         179aa         Protein coding         -         A0A140LHR9           ENSMUST00000207371.1         1818         252aa         Nonsense mediated decay         -         A0A140LJ06           ENSMUST00000207289.1         1234         No protein         IncRNA         -         -           ENSMUST00000208107.1         581         No protein         IncRNA         -         -           ENSMUST00000207991.1         478         No protein         IncRNA         -         -

The strategy is based on the design of *Homer2-202* transcript, The transcription is shown below



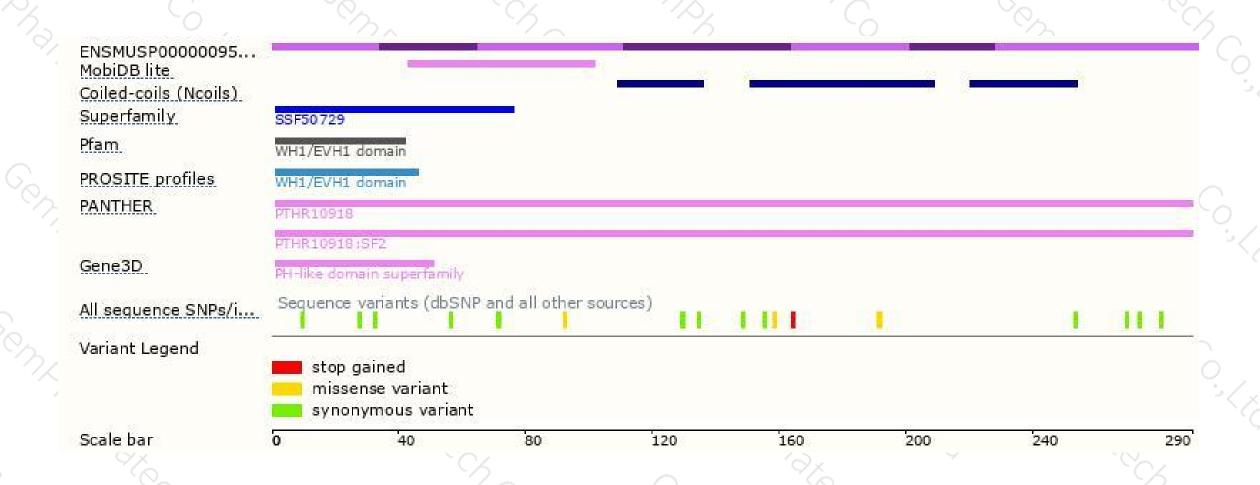
### Genomic location distribution





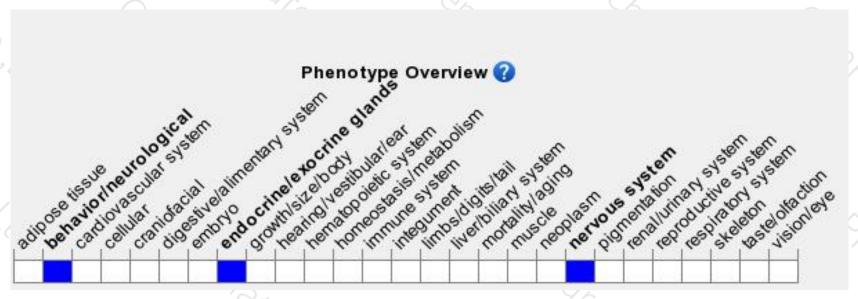
### Protein domain





# 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, Homozygous mutants exhibit an increase in intracellular calcium concentration and in the frequency of intracellular calcium oscillations in pancreatic acinar cells.



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





