

Inhbe Cas9-CKO Strategy

Designer: Xueting Zhang

Reviewer: Zihe Cui

Design Date: 2022-08-26

Overview

Target Gene Name

• Inhbe

Project Type

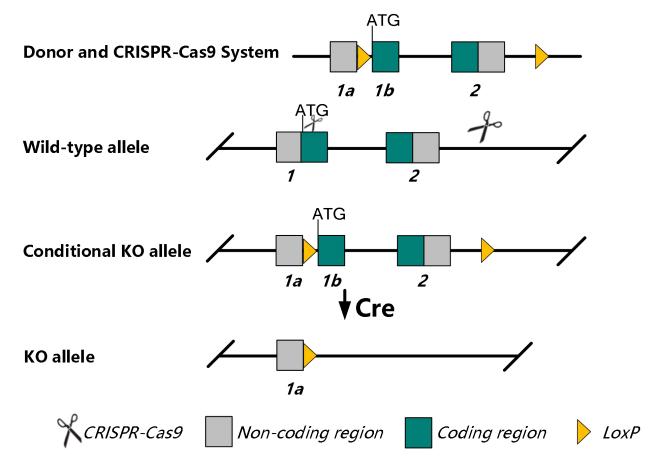
• Cas9-CKO

Genetic Background

• C57BL/6JGpt



Strain Strategy

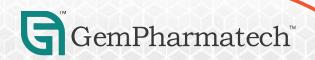


Schematic representation of CRISPR-Cas9 engineering used to edit the Inhbe gene.



Technical Information

- The *Inhbe* gene has 1 transcripts. According to the structure of *Inhbe* gene, exon1-2 of *Inhbe*-201 (ENSMUST0000059718.6) transcript is recommended as the knockout region. The region contains all the coding sequences. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Inhbe* 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- 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.



Gene Information

Inhbe inhibin beta-E [Mus musculus (house mouse)]

Try the new Transcript table

Gene ID: 16326, updated on 5-Aug-2022



Summary △ ? Official Symbol Inhbe provided by MGI Official Full Name inhibin beta-E provided by MGI Primary source MGI:MGI:109269 See related Ensembl:ENSMUSG00000047492 AllianceGenome:MGI:109269 Gene type protein coding RefSeg status REVIEWED Organism Mus musculus Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Summary This gene encodes a member of the TGF-beta (transforming growth factor-beta) superfamily of proteins. The encoded preproprotein is proteolytically processed to generate an inhibin beta subunit. Inhibins have been implicated in regulating numerous cellular processes including cell proliferation, apoptosis, immune response and hormone secretion. This gene may be upregulated under conditions of endoplasmic reticulum stress, and this protein may inhibit cellular proliferation and growth in pancreas and liver. [provided by RefSeq, Sep 2016] Expression Biased expression in liver E18 (RPKM 23.1) and liver adult (RPKM 22.2) See more Orthologs human all Try the new Gene table

Genomic context

Location: 10 D3; 10 74.5 cM

See Inhbe in Genome Data Viewer

Exon count: 2

Annotation release	Status	Assembly	Chr	Location
109	current	GRCm39 (GCF_000001635.27)	10	NC_000076.7 (127185271127187717, complement)
108.20200622	previous assembly	GRCm38.p6 (GCF_000001635.26)	10	NC_000076.6 (127349402127351848, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	10	NC_000076.5 (126786458126788828, complement)

Source: https://www.ncbi.nlm.nih.gov/

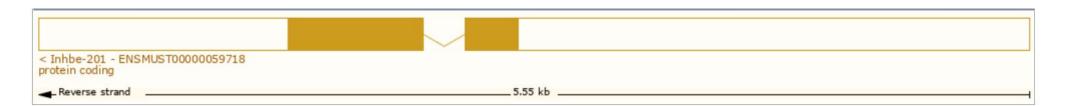


Transcript Information

The gene has 1 transcript, the transcript is shown below:



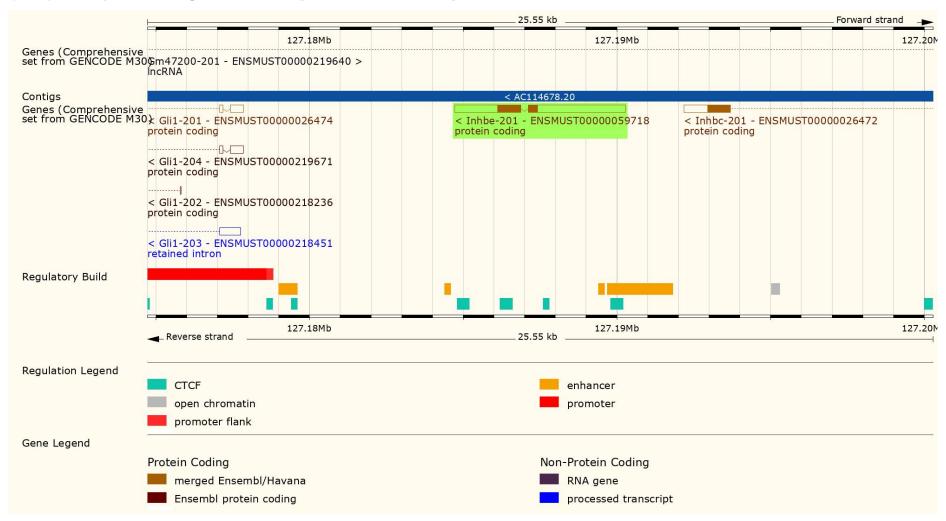
The strategy is based on the design of *Inhbe*-201 transcript, the transcription is shown below:



Source: https://www.ensembl.org



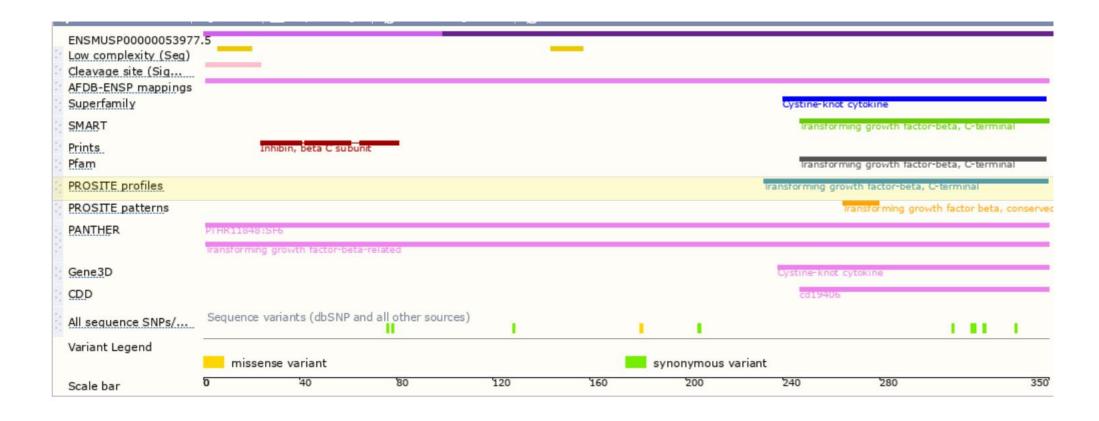
Genomic Information





Source: : https://www.ensembl.org

Protein Information





Source: : https://www.ensembl.org

Mouse Phenotype Information (MGI)

• Mice homozygous for a null mutation are fertile with normal liver and reproductive morphology and physiology.



Important Information

- The insertion of loxp is close to the 5' side of the transcript Gli1 gene. The expression of Gli1 gene may be affected.
- The insertion of loxp is overlapped with the predictd gene Gm47200. The expression of Gm47200 gene may be affected.
- The function of the 5' side of *Inhbe* gene may be affected before Cre recombinase.
- *Inhbe* is located on Chr10. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 the existing technology level.

