Inhbc Cas9-CKO Strategy

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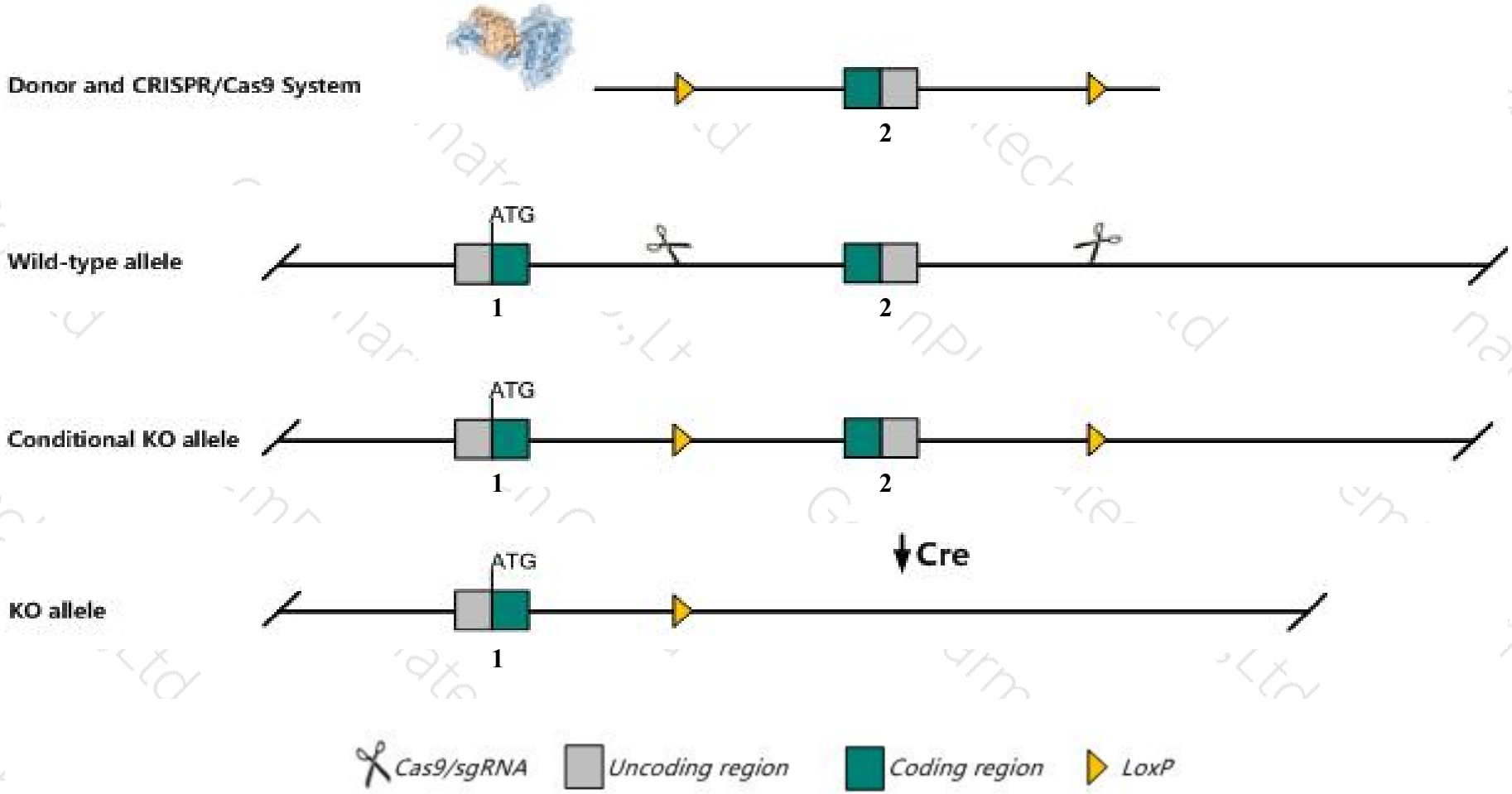
Project Overview

Project Name	***Inhbc***
Project type	**Cas9-CKO**
Strain background	**C57BL/6J**

Conditional Knockout strategy

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



Technical routes

- The *Inhbc* gene has 1 transcript. According to the structure of *Inhbc* gene, exon2 of *Inhbc-201* (ENSMUST00000026472.9) transcript is recommended as the knockout region.The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.

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

- The flox mice was 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.

Notice

- According to the existing MGI data,Mice homozygous for a null mutation display decreased serum albumin in females but are fertile with normal liver and reproductive morphology and physiology.
- The floxed region is near to the N-terminal of *Inhbe* gene,this strategy may influence the regulatory function of the N-terminal of *Inhbe* gene.
- The partial sequence of intron of *Gm47200* gene will be deleted together in this strategy.
- The *Inhbc* gene is located on the Chr10. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Inhbc inhibin beta-C [*Mus musculus* (house mouse)]

Gene ID: 16325, updated on 12-Aug-2019

Summary

Official Symbol Inhbc provided by MGI
Official Full Name inhibin beta-C provided by MGI
Primary source MGI:MGI:105932
See related Ensembl:ENSMUSG00000025405
Gene type protein coding
RefSeq status REVIEWED
Organism Mus musculus
Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
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 a subunit of homodimeric and heterodimeric activin complexes. The heterodimeric complex may function in the inhibition of activin A signaling. Transgenic mice overexpressing this gene exhibit defects in testis, liver and prostate. [provided by RefSeq, Aug 2016]
Expression Biased expression in liver adult (RPKM 24.9), liver E18 (RPKM 4.1) and 2 other tissues See more
Orthologs human all

Genomic context

Location: 10 D3; 10 74.5 cM

See Inhbc in Genome Data Viewer

Exon count: 2

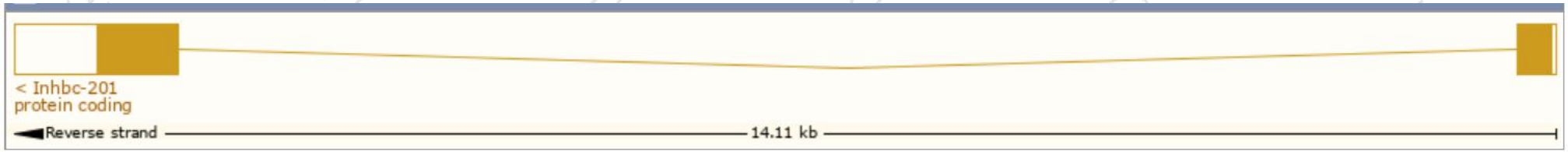
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	10	NC_000076.6 (127356322..127370548, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	10	NC_000076.5 (126793381..126807600, complement)

Transcript information（Ensembl）

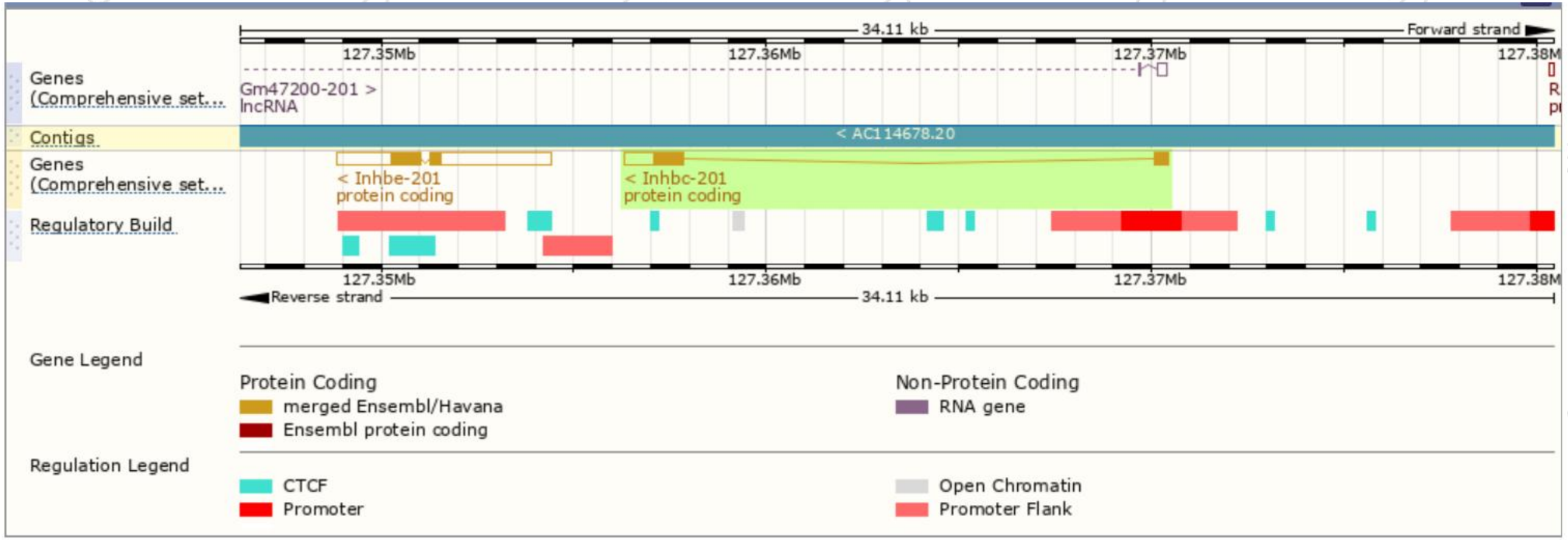
The gene has 1 transcript,the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Inhbc-201	ENSMUST00000026472.9	1859	352aa	Protein coding	CCDS24240	P55104	TSL:1 GENCODE basic APPRIS P1

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

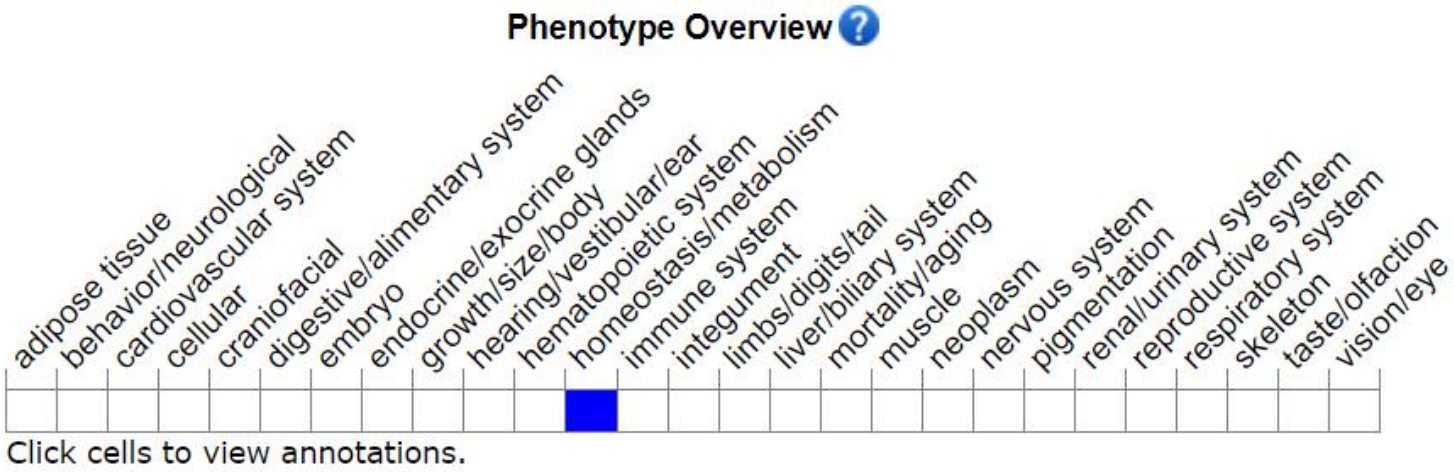


Genomic location distribution



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/).

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

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