

Ino80 Cas9-KO Strategy

Designer:

Huan Fan

Reviewer:

Huan Wang

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Project Overview

Project Name

Ino80

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ino80* gene. The schematic diagram is as follows:



- The *Ino80* gene has 3 transcripts. According to the structure of *Ino80* gene, exon5-exon6 of *Ino80-201* (ENSMUST00000049920.13) transcript is recommended as the knockout region. The region contains 283bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ino80* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Embryos homozygous for a knock-out allele die around E7.5 and show absence of anterior and distal visceral endoderm. Another null allele results in embryonic lethality by E13.5-E14.5 with severe growth retardation and developmental defects. Heterozygotes show defects in hindlimb extension reflex.
- The *Ino80* gene is located on the Chr2. 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)

Ino80 INO80 complex subunit [Mus musculus (house mouse)]

Gene ID: 68142, updated on 31-Jan-2019

Summary



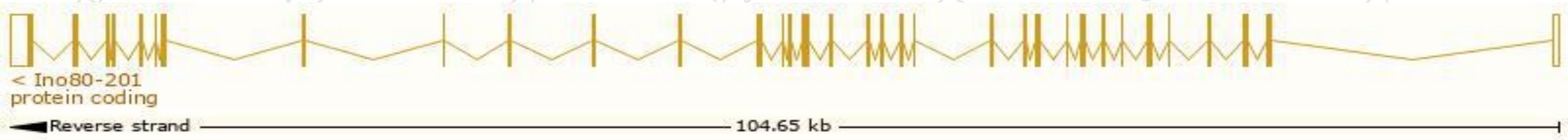
Official Symbol	Ino80 provided by MGI
Official Full Name	INO80 complex subunit provided by MGI
Primary source	MGI:MGI:1915392
See related	Ensembl:ENSMUSG000000034154
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2310079N15Rik, 4632409L19Rik, Inoc1
Expression	Ubiquitous expression in thymus adult (RPKM 5.8), limb E14.5 (RPKM 5.7) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

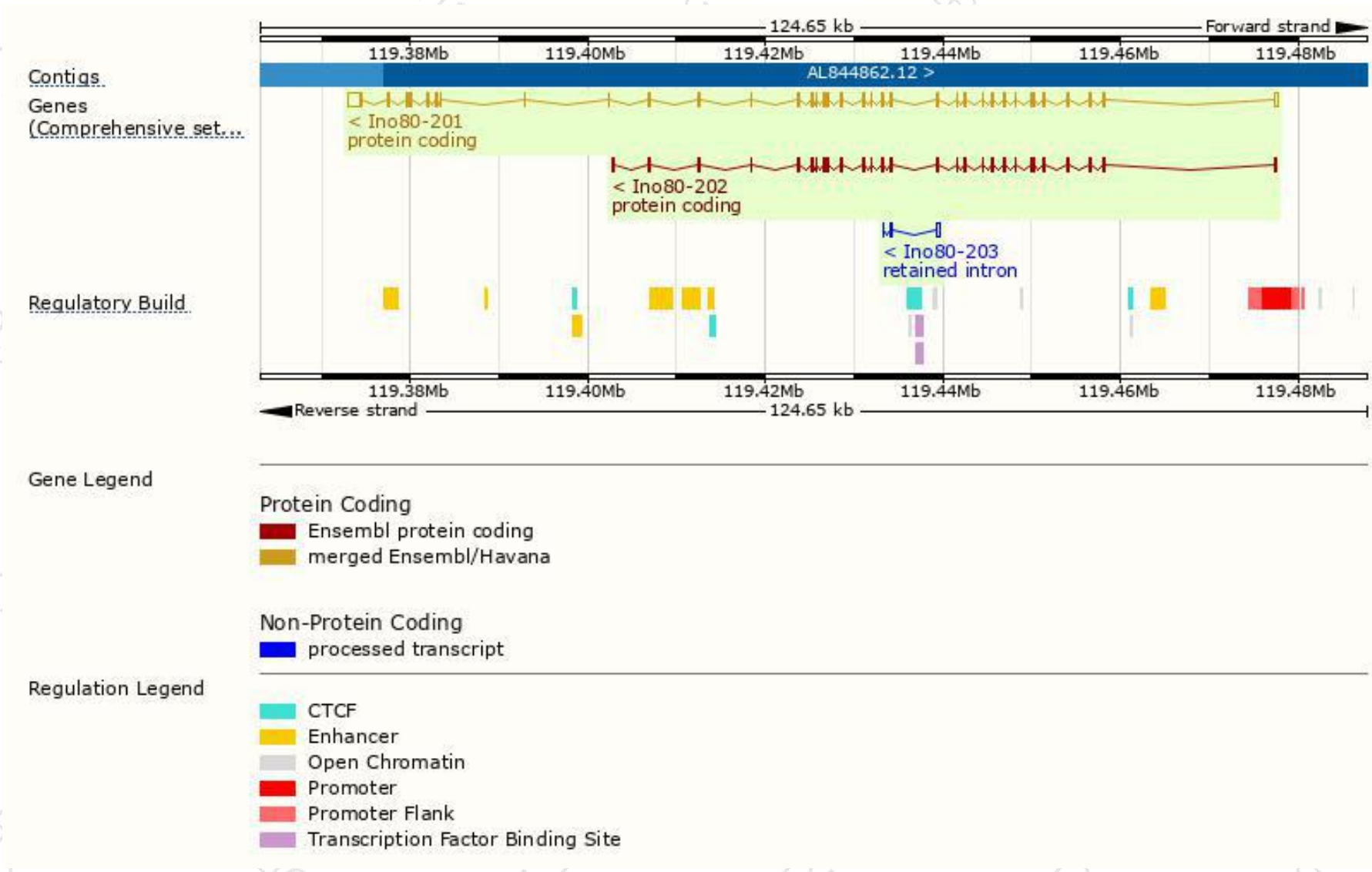
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ino80-201	ENSMUST00000049920.13	6354	1559aa	Protein coding	CCDS16602	Q6ZPV2	TSL:5 GENCODE basic APPRIS P1
Ino80-202	ENSMUST00000110808.1	3928	1141aa	Protein coding	-	Z4YL66	TSL:1 GENCODE basic
Ino80-203	ENSMUST00000138707.1	406	No protein	Retained intron	-	-	TSL:3

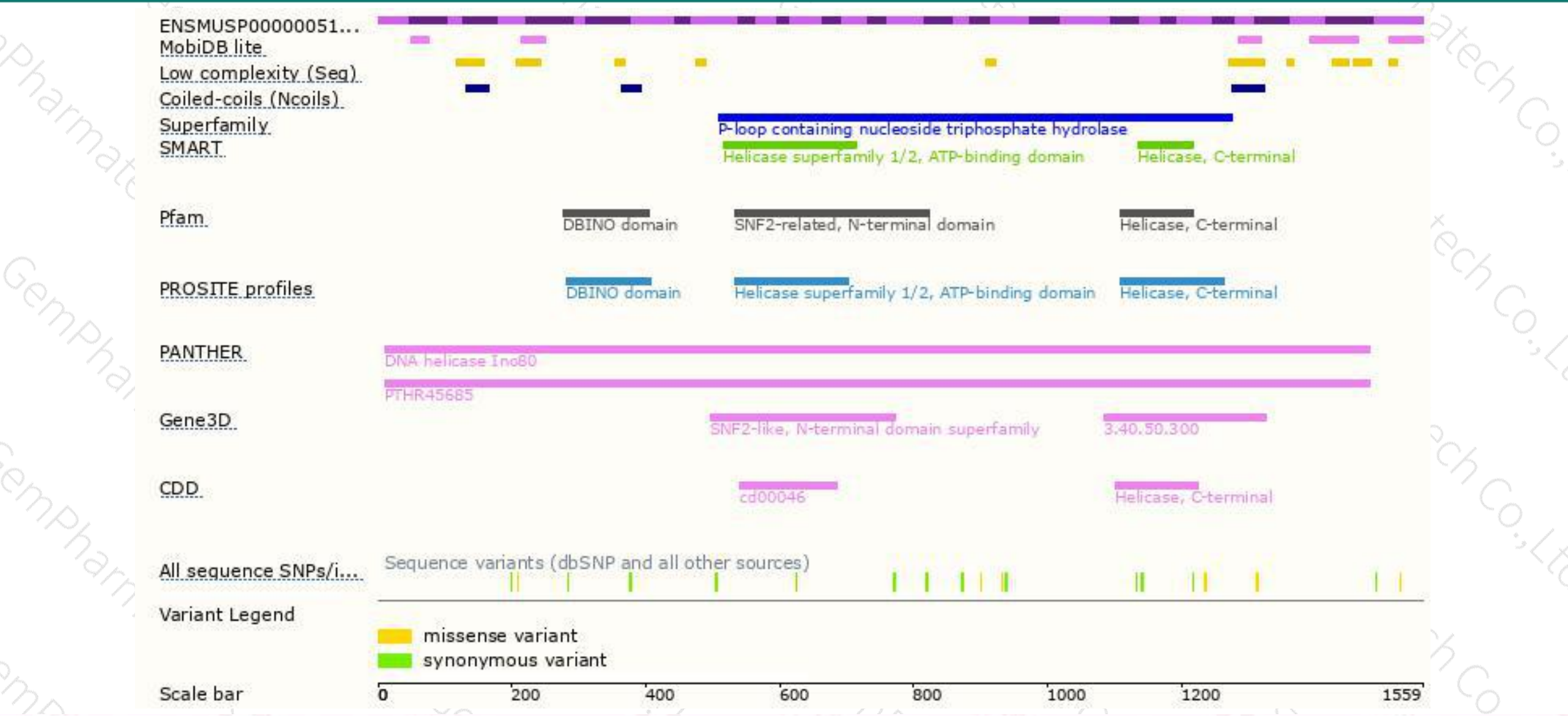
The strategy is based on the design of *Ino80-201* transcript,The transcription is shown below



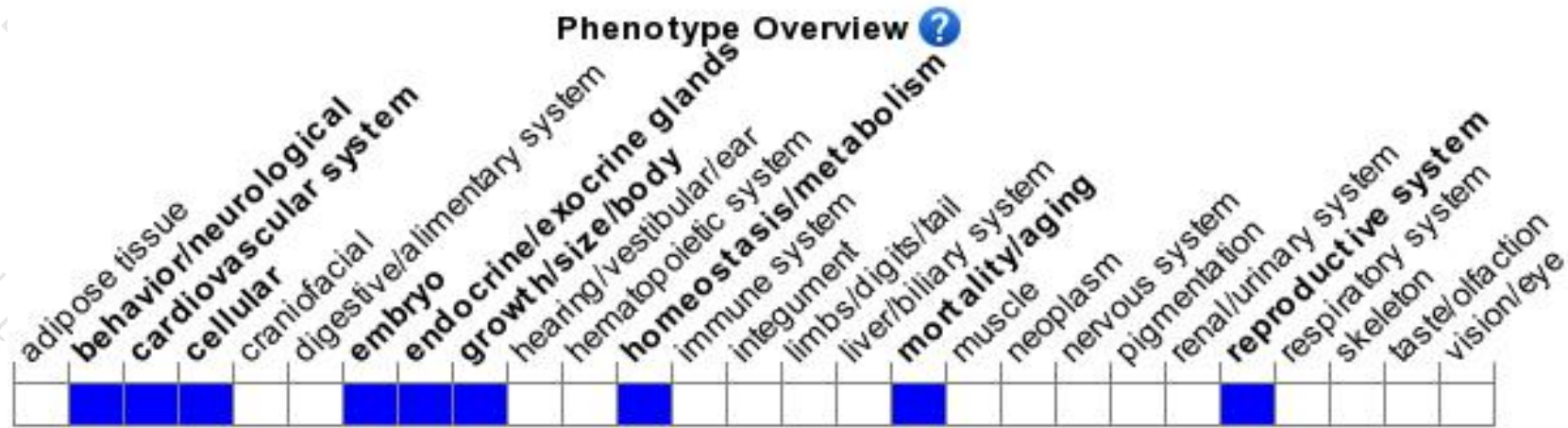
Genomic location distribution



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, Embryos homozygous for a knock-out allele die around E7.5 and show absence of anterior and distal visceral endoderm. Another null allele results in embryonic lethality by E13.5-E14.5 with severe growth retardation and developmental defects. Heterozygotes show defects in hindlimb extension reflex.

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

Tel: 400-9660890

