

Ing1 Cas9-KO Strategy

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Project Overview

Project Name

Ing1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ing1* gene. The schematic diagram is as follows:



- The *Ingl* gene has 7 transcripts. According to the structure of *Ingl* gene, exon2 of *Ingl*-201 (ENSMUST00000054399.5) 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 *Ingl* gene. The brief process is as follows: CRISPR/Cas9 system were

- According to the existing MGI data, Homozygous null mice display a slight decrease in body weight, moderately impaired maternal nurturing, increased sensitivity to gamma-irradiation, and increased incidence of B-cell derived lymphomas.
- The *Ing1* gene is located on the Chr8. 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)

Ing1 inhibitor of growth family, member 1 [*Mus musculus* (house mouse)]

Gene ID: 26356, updated on 12-Aug-2019

Summary

- Official Symbol** Ing1 provided by [MGI](#)
- Official Full Name** inhibitor of growth family, member 1 provided by [MGI](#)
- Primary source** [MGI:MGI:1349481](#)
- See related** [Ensembl:ENSMUSG00000045969](#)
- 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** mING1h; p33Ing1; AA407184; AI875420; p37Ing1b; 2610028J21Rik
- Expression** Ubiquitous expression in CNS E11.5 (RPKM 19.0), testis adult (RPKM 15.3) and 28 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 8; 8 A1.1 See Ing1 in [Genome Data Viewer](#)

Exon count: 5

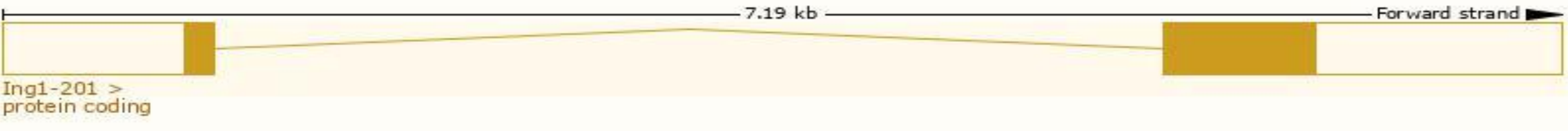
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	8	NC_000074.6 (11555762..11563251)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	8	NC_000074.5 (11556066..11563250)

Transcript information (Ensembl)

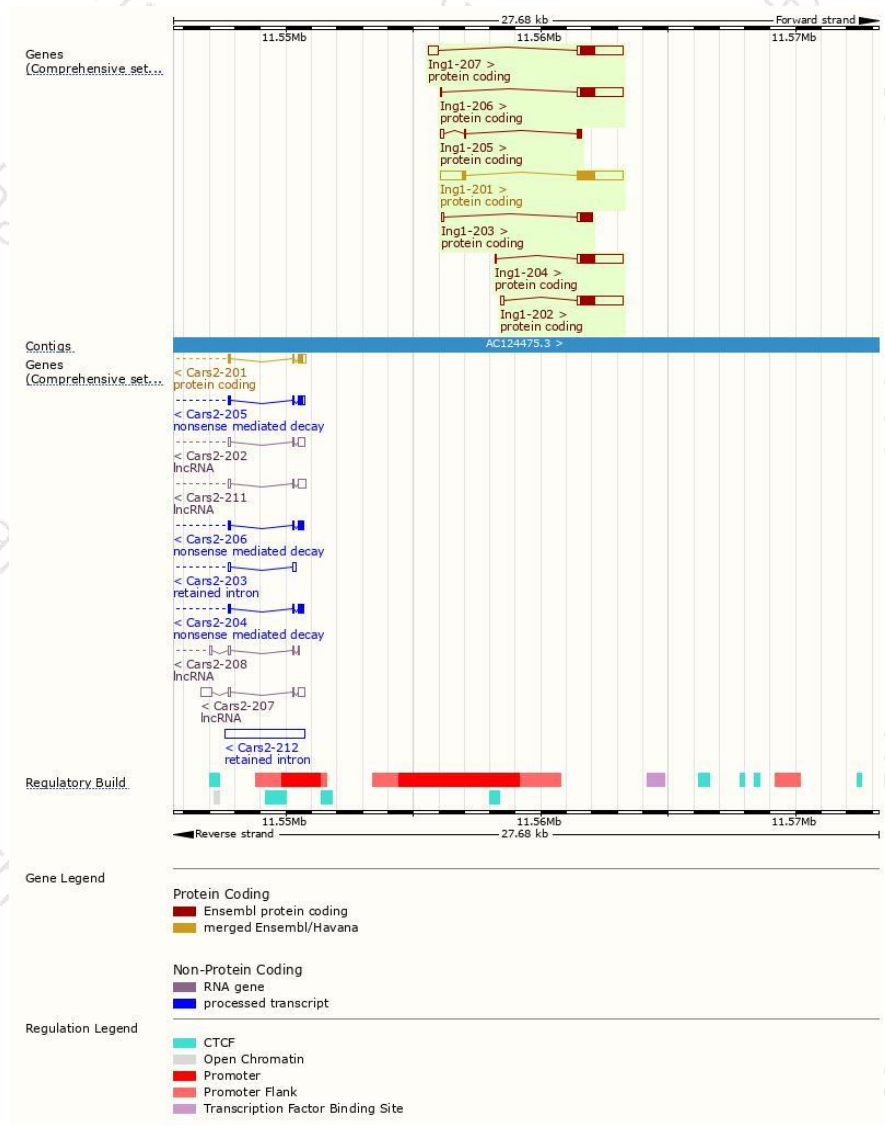
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ing1-201	ENSMUST00000054399.5	2814	279aa	Protein coding	CCDS22097	Q9QXV3	TSL:1 GENCODE basic APPRIS P1
Ing1-207	ENSMUST00000211007.1	2241	185aa	Protein coding	CCDS85499	Q3ULE3 Q9QXV3	TSL:1 GENCODE basic
Ing1-202	ENSMUST00000209565.1	1971	185aa	Protein coding	CCDS85499	Q3ULE3 Q9QXV3	TSL:1 GENCODE basic
Ing1-204	ENSMUST00000210041.1	1881	185aa	Protein coding	CCDS85499	Q3ULE3 Q9QXV3	TSL:5 GENCODE basic
Ing1-206	ENSMUST00000210740.1	1866	185aa	Protein coding	CCDS85499	Q3ULE3 Q9QXV3	TSL:1 GENCODE basic
Ing1-203	ENSMUST00000209646.1	721	161aa	Protein coding	-	A0A1B0GT89	CDS 3' incomplete TSL:3
Ing1-205	ENSMUST00000210670.1	382	77aa	Protein coding	-	A0A1B0GSP9	CDS 3' incomplete TSL:3

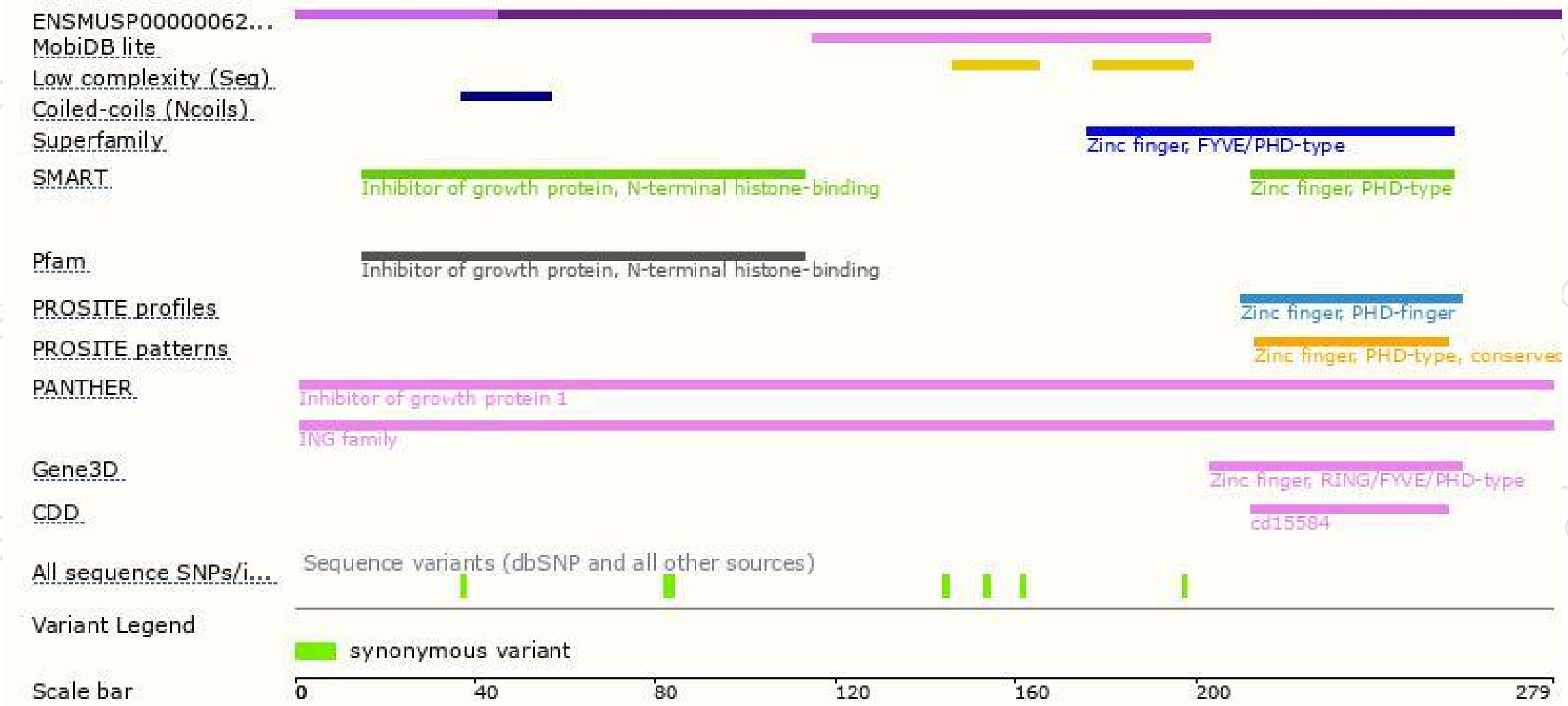
The strategy is based on the design of *Ing1-201* transcript,The transcription is shown below



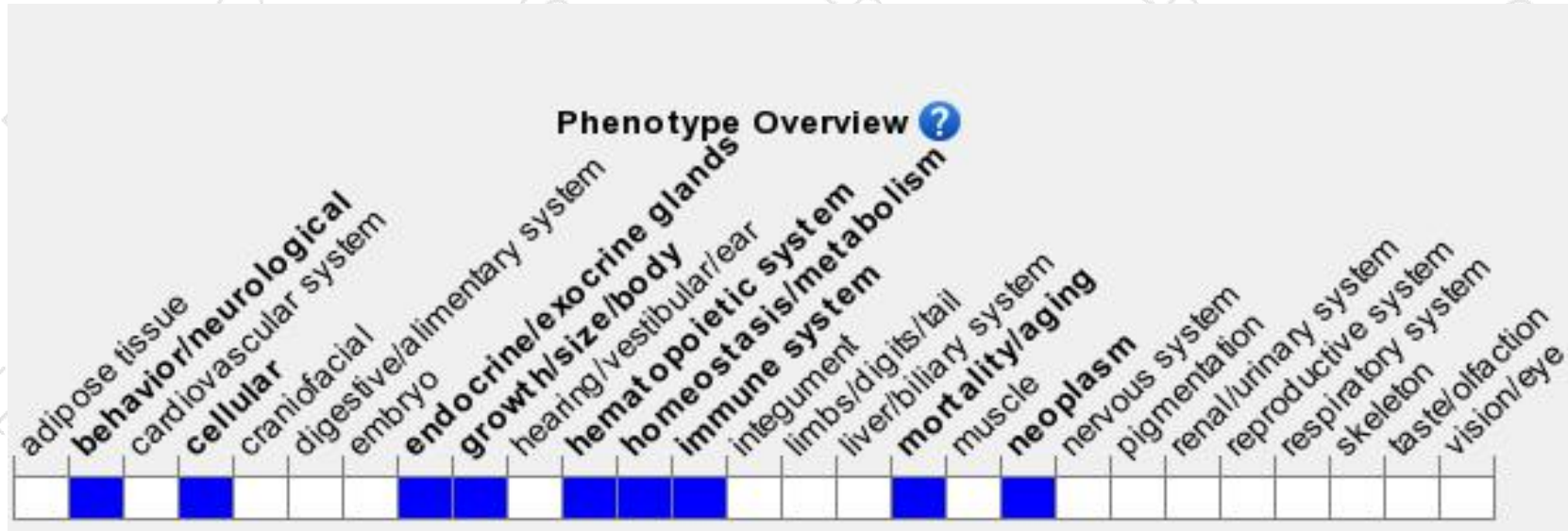
Genomic location distribution



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, Homozygous null mice display a slight decrease in body weight, moderately impaired maternal nurturing, increased sensitivity to gamma-irradiation, and increased incidence of B-cell derived lymphomas.

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

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