

Lnx1 Cas9-KO Strategy

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Project Overview

Project Name

Lnxl

Project type

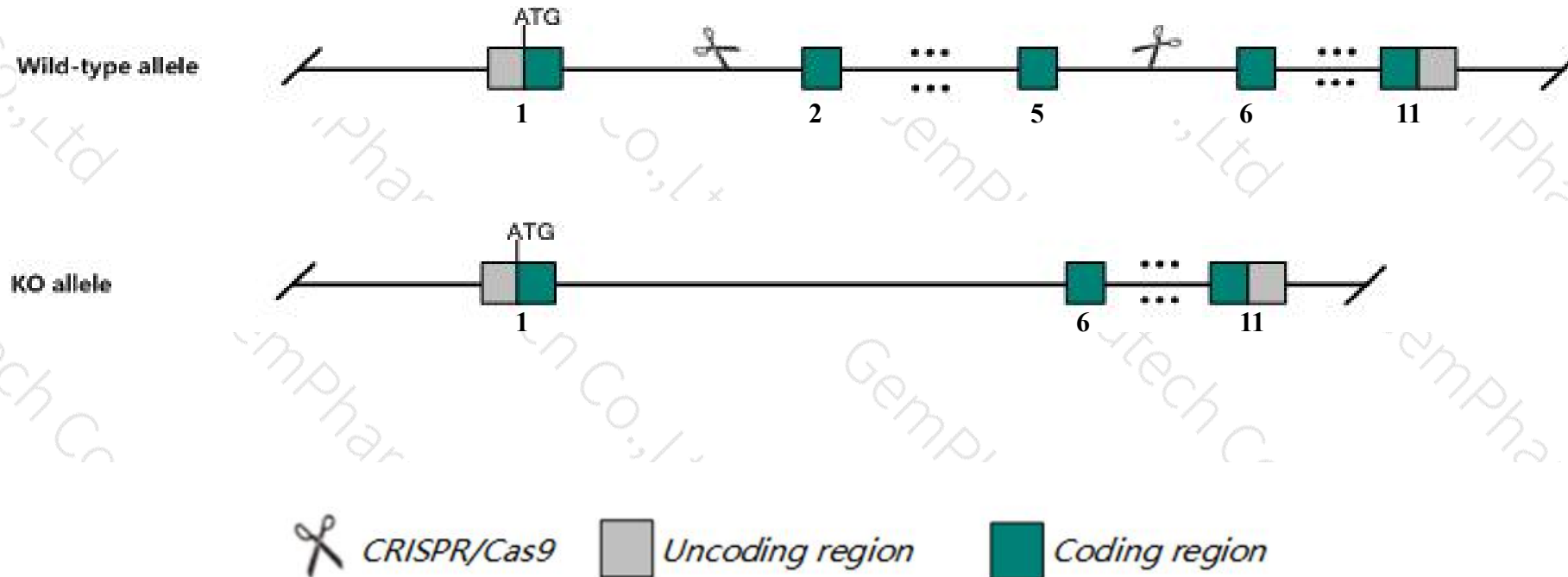
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Ln timer* gene has 9 transcripts. According to the structure of *Ln timer* gene, exon2-exon5 of *Ln timer*-202 (ENSMUST00000087161.9) transcript is recommended as the knockout region. The region contains 970bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ln timer* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Mice homozygous for a targeted mutation exhibit an increased percentage of B1-like B cells in peritoneal lavage when compared with that of controls.
- The *Lnxl* gene is located on the Chr5. 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)

Ln timer ligand of numb-protein X 1 [Mus musculus (house mouse)]

Gene ID: 16924, updated on 31-Jan-2019

Summary



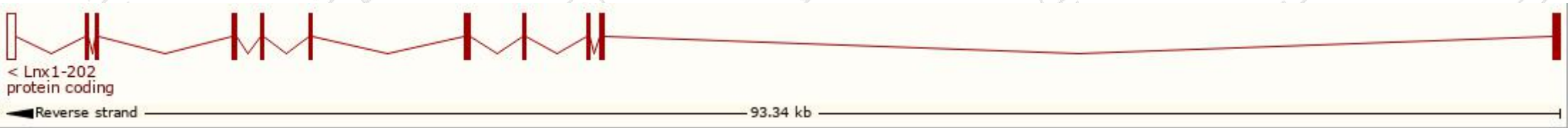
Official Symbol	Ln timer provided by MGI
Official Full Name	ligand of numb-protein X 1 provided by MGI
Primary source	MGI:MGI:1278335
See related	Ensembl:ENSMUSG000000029228
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Ln timer
Expression	Broad expression in frontal lobe adult (RPKM 6.0), cortex adult (RPKM 5.8) and 23 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

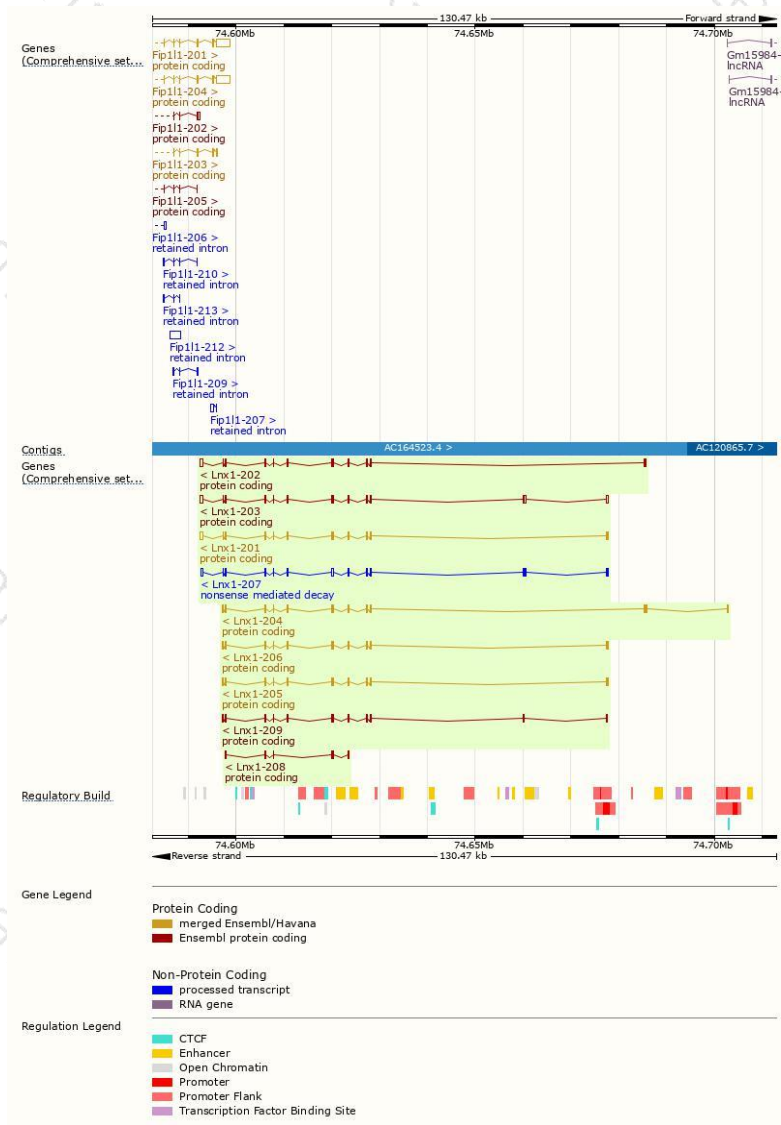
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lnx1-203	ENSMUST00000113531.8	3098	569aa	Protein coding	CCDS51522	E9Q4N3	TSL:1 GENCODE basic
Lnx1-202	ENSMUST00000087161.9	2753	728aa	Protein coding	CCDS51524	O70263	TSL:5 GENCODE basic APPRIS P1
Lnx1-201	ENSMUST00000039744.12	2727	628aa	Protein coding	CCDS19347	A4QPD4 O70263	TSL:1 GENCODE basic
Lnx1-204	ENSMUST00000117388.7	2564	728aa	Protein coding	CCDS51524	O70263	TSL:1 GENCODE basic APPRIS P1
Lnx1-206	ENSMUST00000121690.7	2302	618aa	Protein coding	CCDS51523	E9Q6Q0	TSL:1 GENCODE basic
Lnx1-205	ENSMUST00000117525.7	2259	628aa	Protein coding	CCDS19347	A4QPD4 O70263	TSL:1 GENCODE basic
Lnx1-209	ENSMUST00000153543.4	2208	569aa	Protein coding	CCDS51522	E9Q4N3	TSL:5 GENCODE basic
Lnx1-208	ENSMUST00000140084.3	966	322aa	Protein coding	-	F7AT68	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Lnx1-207	ENSMUST00000127396.7	2852	52aa	Nonsense mediated decay	-	D6RHN7	TSL:1

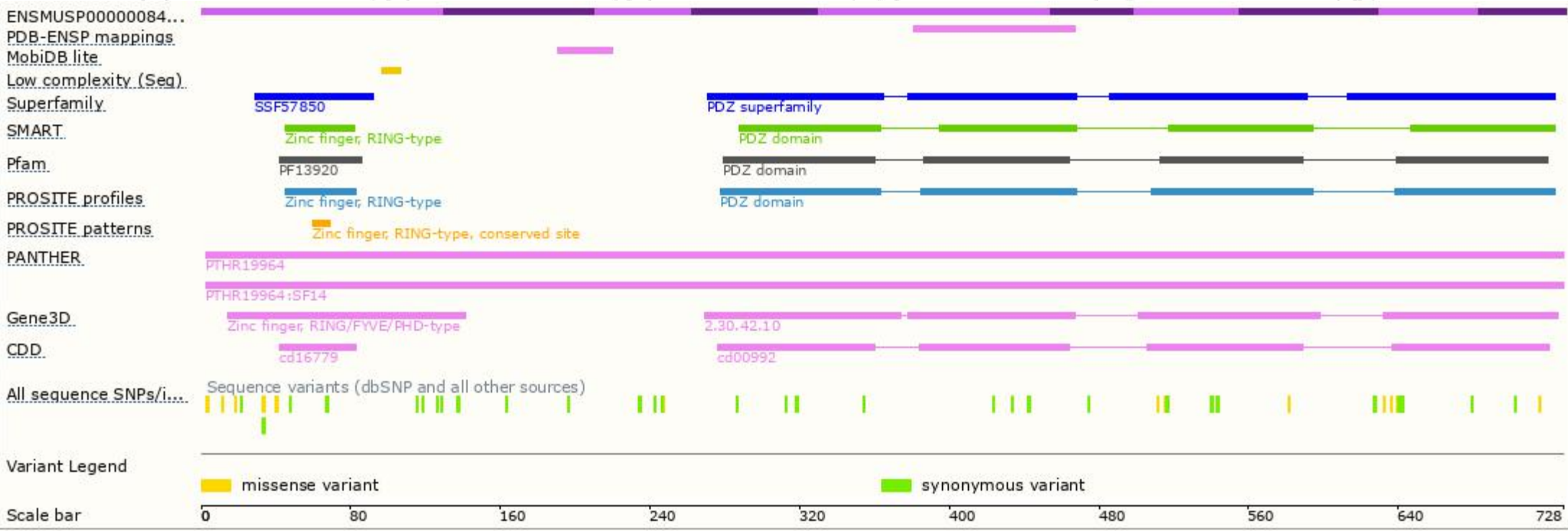
The strategy is based on the design of *Lnx1-202* transcript,The transcription is shown below



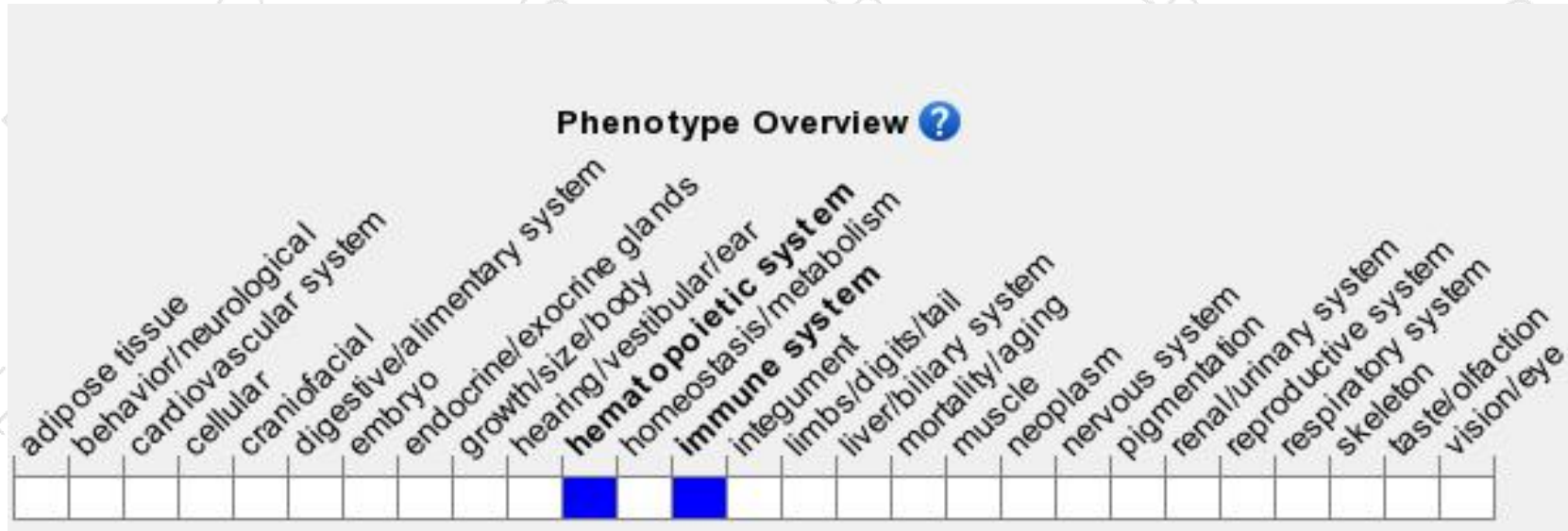
Genomic location distribution



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, Mice homozygous for a targeted mutation exhibit an increased percentage of B1-like B cells in peritoneal lavage when compared with that of controls.

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

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