Clnk Cas9-KO Strategy

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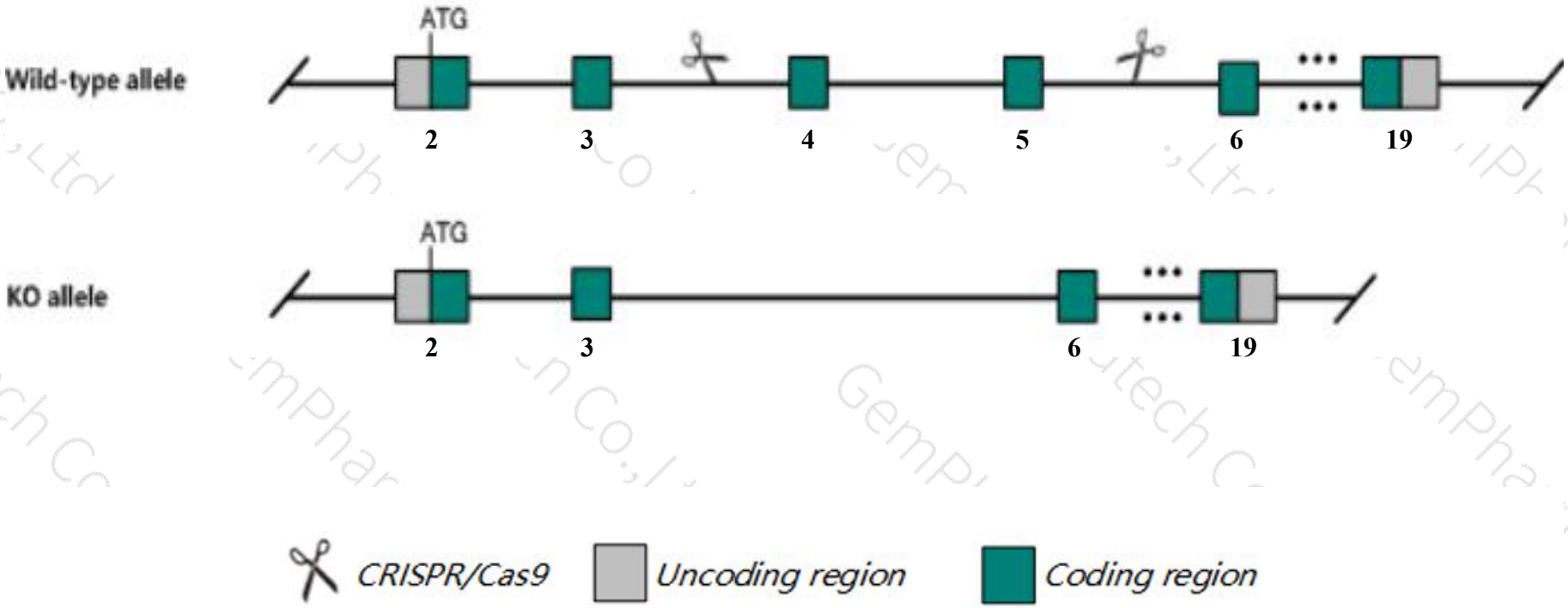
Project Overview

Project Name	***Clnk***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

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



Technical routes

➢ The *Clnk* gene has 2 transcripts. According to the structure of *Clnk* gene, exon4-exon5 of *Clnk-201* (ENSMUST00000169819.4) transcript is recommended as the knockout region.The region contains 67bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Clnk* gene. The brief process is as follows: CRISPR/Cas9 system v

Notice

- According to the existing MGI data,Mice homozygous for a reporter allele display altered natural killer (NK) T cell physiology and enhanced NK cell cytolysis. Mice homozygous for knock-out allele display abnormal mast cell physiology as well as enhanced NK cell cytolysis.

- The *Clnk* 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）

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Clnk cytokine-dependent hematopoietic cell linker [Mus musculus (house mouse)]

Gene ID: 27278, updated on 31-Jan-2019

Summary

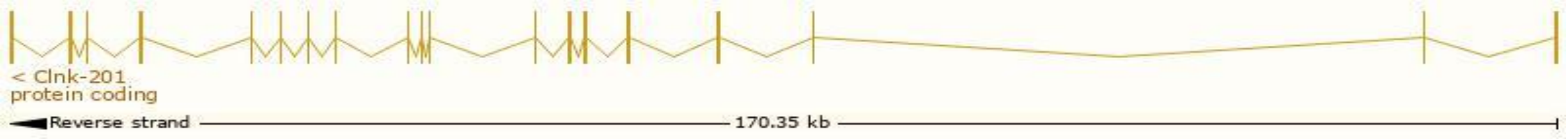
Official Symbol	Clnk provided by MGI
Official Full Name	cytokine-dependent hematopoietic cell linker provided by MGI
Primary source	MGI:MGI:1351468
See related	Ensembl:ENSMUSG00000039315
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	MIST
Expression	Low expression observed in reference dataset See more
Orthologs	human all

Transcript information（Ensembl）

The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Clnk-201	ENSMUST00000169819.4	1700	435aa	Protein coding	CCDS51486	Q9QZE2	TSL:1 GENCODE basic APPRIS P2
Clnk-202	ENSMUST00000171633.4	1700	435aa	Protein coding	-	E9PXZ8	TSL:5 GENCODE basic APPRIS ALT2

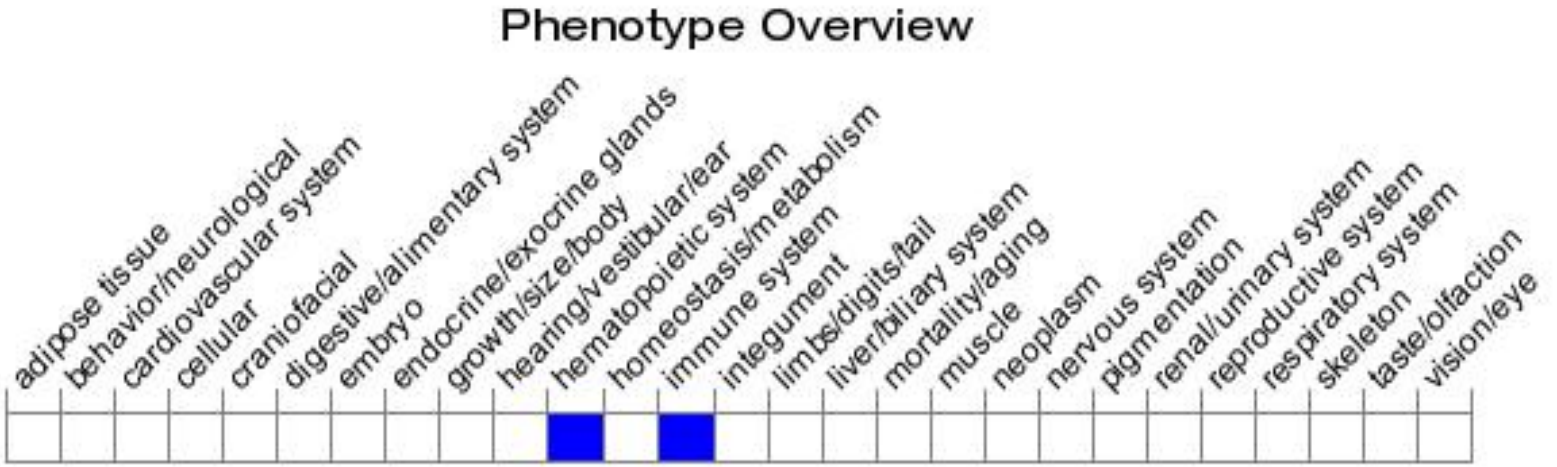
The strategy is based on the design of *Clnk-201* transcript,The transcription is shown below



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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