

Ncr1 Cas9-KO Strategy

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Project Overview

Project Name

Ncr1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ncr1* gene. The schematic diagram is as follows:



- The *Ncr1* gene has 2 transcripts. According to the structure of *Ncr1* gene, exon1-exon7 of *Ncr1-201* (ENSMUST00000006792.5) transcript is recommended as the knockout region. The region contains all 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 *Ncr1* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Mutations in this gene lead to alterations in susceptibility to viral infection induced morbidity/mortality, NK cell number, NK cell cytolysis, and T cell responses.
- The *Ncr1* gene is located on the Chr7. 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)

Ncr1 natural cytotoxicity triggering receptor 1 [Mus musculus (house mouse)]

Gene ID: 17086, updated on 30-Mar-2019

Summary



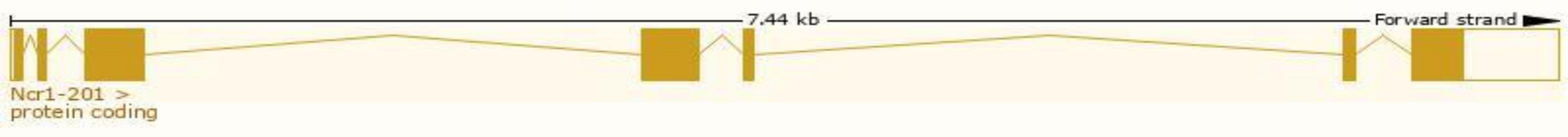
Official Symbol	Ncr1 provided by MGI
Official Full Name	natural cytotoxicity triggering receptor 1 provided by MGI
Primary source	MGI:MGI:1336212
See related	Ensembl:ENSMUSG00000062524
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Ly94, NKp46
Expression	Biased expression in spleen adult (RPKM 2.2), lung adult (RPKM 0.8) and 7 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

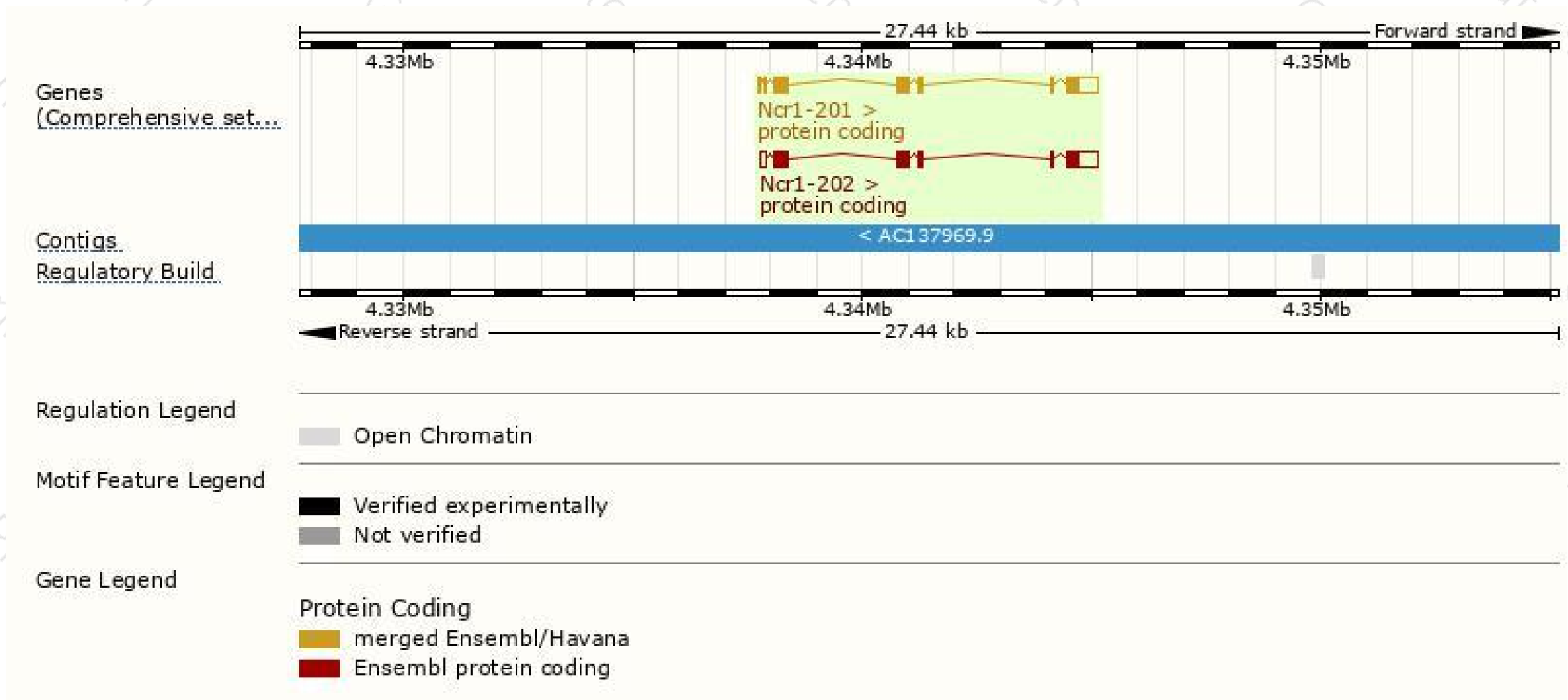
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ncr1-201	ENSMUST00000006792.5	1463	325aa	Protein coding	CCDS20734	A0A0R4IZY7	TSL:1 GENCODE basic APPRIS P2
Ncr1-202	ENSMUST00000126417.2	1495	288aa	Protein coding	-	A0A0U1RP63	TSL:1 GENCODE basic APPRIS ALT2

The strategy is based on the design of *Ncr1-201* transcript,The transcription is shown below



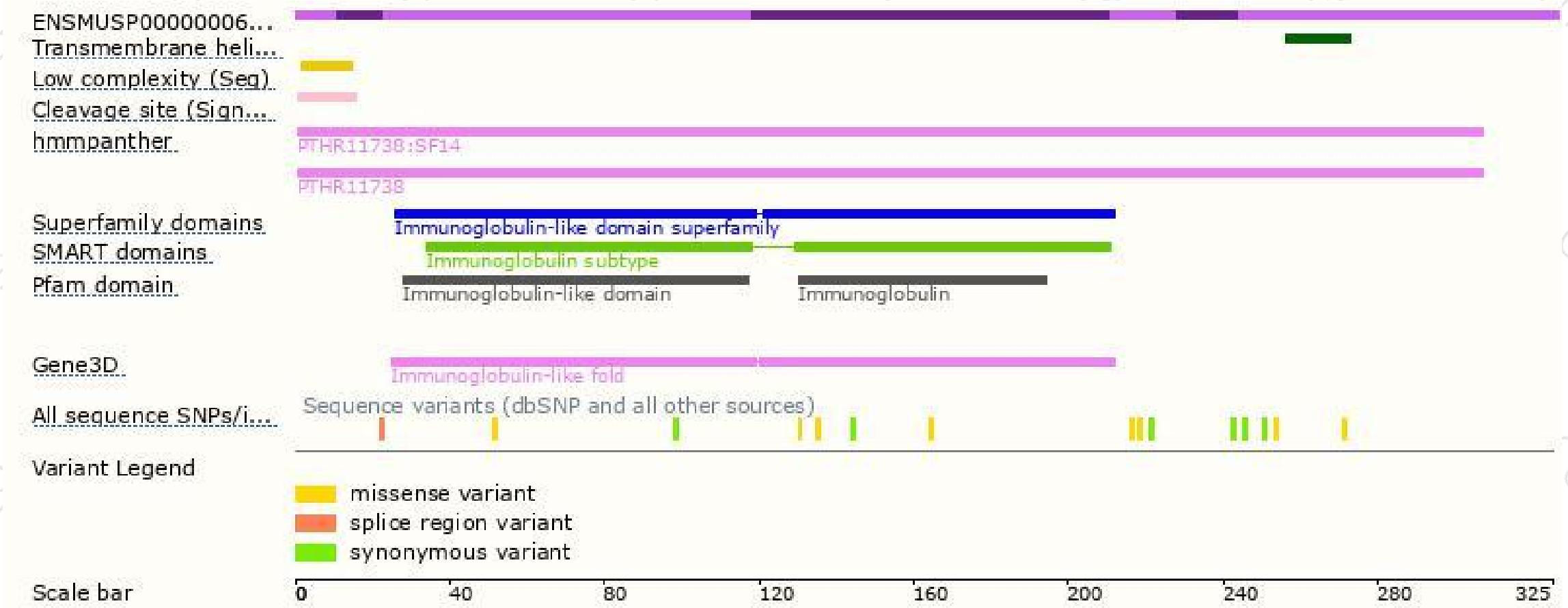
Genomic location distribution



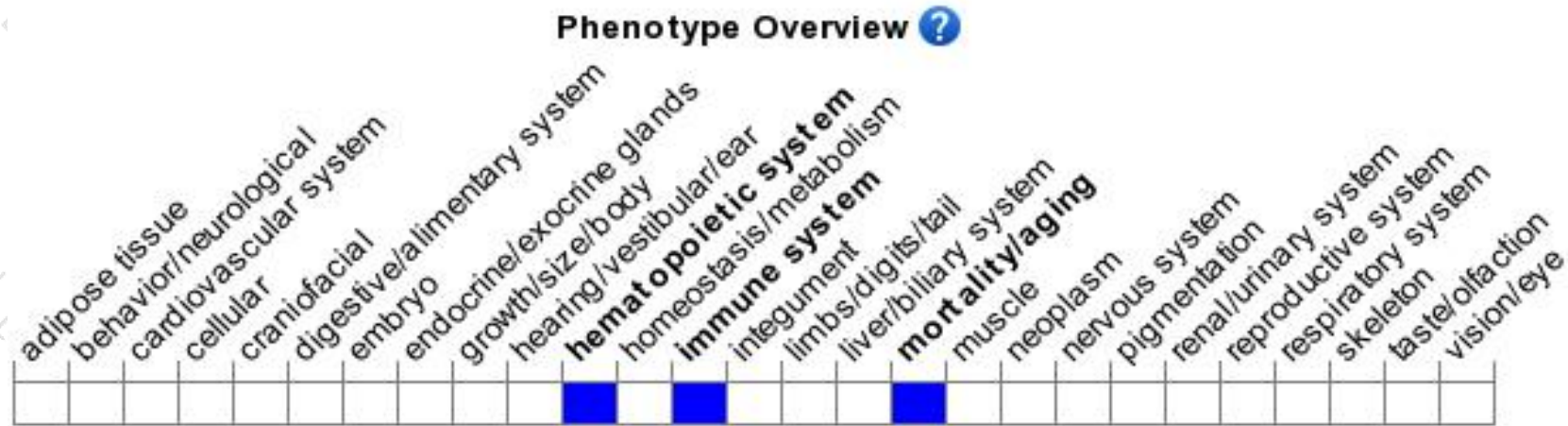
Protein domain



集萃药康
GemPharmatech



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, Mutations in this gene lead to alterations in susceptibility to viral infection induced morbidity/mortality, NK cell number, NK cell cytolysis, and T cell responses.

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

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