

Klrk1 Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Klrk1

Project type

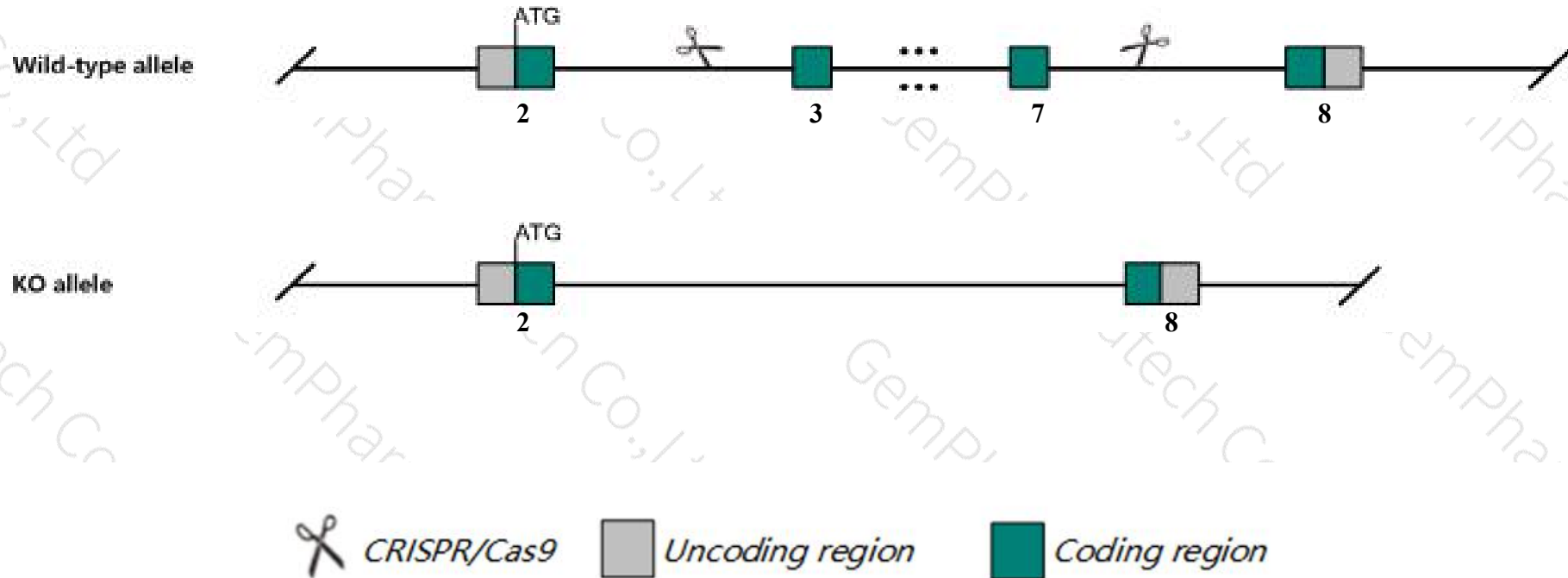
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Klrk1* gene has 6 transcripts. According to the structure of *Klrk1* gene, exon3-exon7 of *Klrk1-205* (ENSMUST00000168919.7) transcript is recommended as the knockout region. The region contains 454bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Klrk1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous null mice have defects in Natural Killer (NK) cell development, diminished NK-mediated cytolysis of tumor cells, and resistance to MCMV infection.
- The *Klrk1* gene is located on the Chr6. 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)

Klrk1 killer cell lectin-like receptor subfamily K, member 1 [*Mus musculus* (house mouse)]

Gene ID: 27007, updated on 24-Sep-2019

Summary

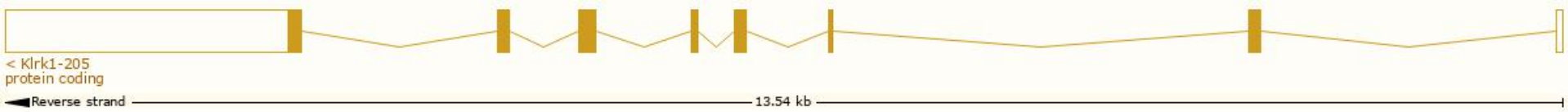
Official Symbol	Klrk1 provided by MGI
Official Full Name	killer cell lectin-like receptor subfamily K, member 1 provided by MGI
Primary source	MGI:MGI:1196250
See related	Ensembl:ENSMUSG00000030149
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Nkg2d; NKG2-D; D6H12S2489E
Expression	Low expression observed in reference dataset See more
Orthologs	human all

Transcript information (Ensembl)

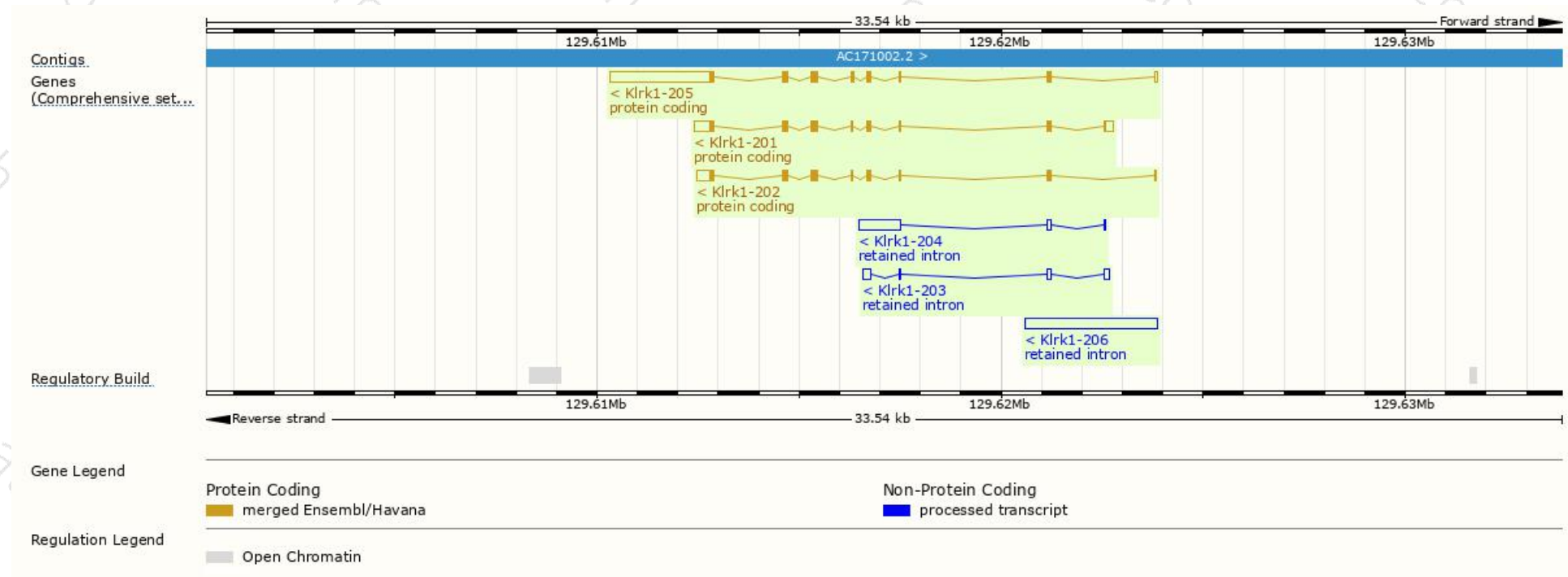
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Klrk1-205	ENSMUST00000168919.7	3197	225aa	Protein coding	CCDS71846	Q3TCW7	TSL:1 GENCODE basic APPRIS ALT2
Klrk1-201	ENSMUST00000032252.7	1270	232aa	Protein coding	CCDS39660	O54709 Q4FJM0	TSL:1 GENCODE basic APPRIS P4
Klrk1-202	ENSMUST00000095412.9	1019	219aa	Protein coding	CCDS39661	O54709	TSL:1 GENCODE basic APPRIS ALT2
Klrk1-206	ENSMUST00000204694.1	3259	No protein	Retained intron	-	-	TSL:NA
Klrk1-204	ENSMUST00000152256.7	1182	No protein	Retained intron	-	-	TSL:5
Klrk1-203	ENSMUST00000137660.1	501	No protein	Retained intron	-	-	TSL:3

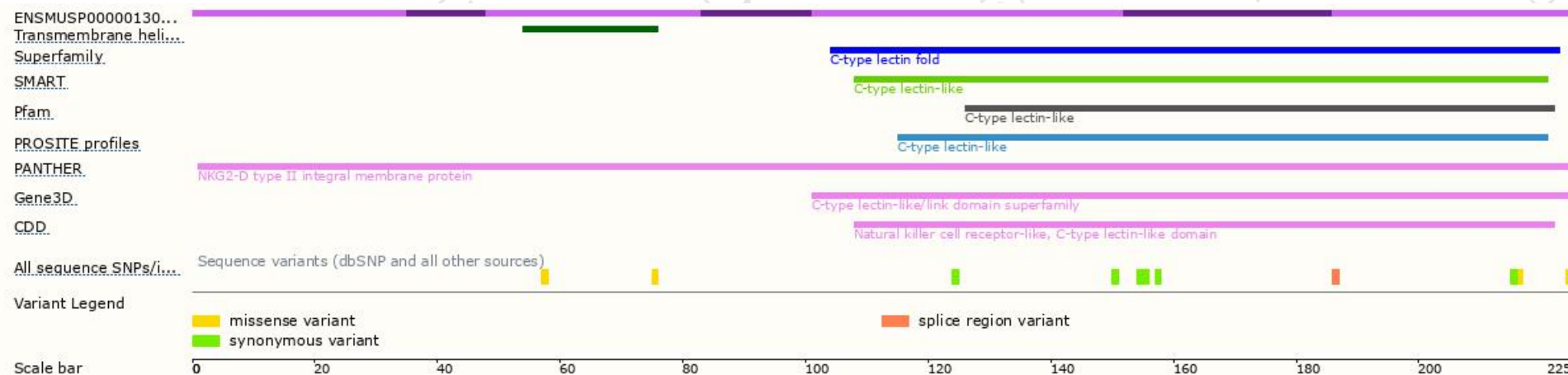
The strategy is based on the design of *Klrk1-205* transcript,The transcription is shown below



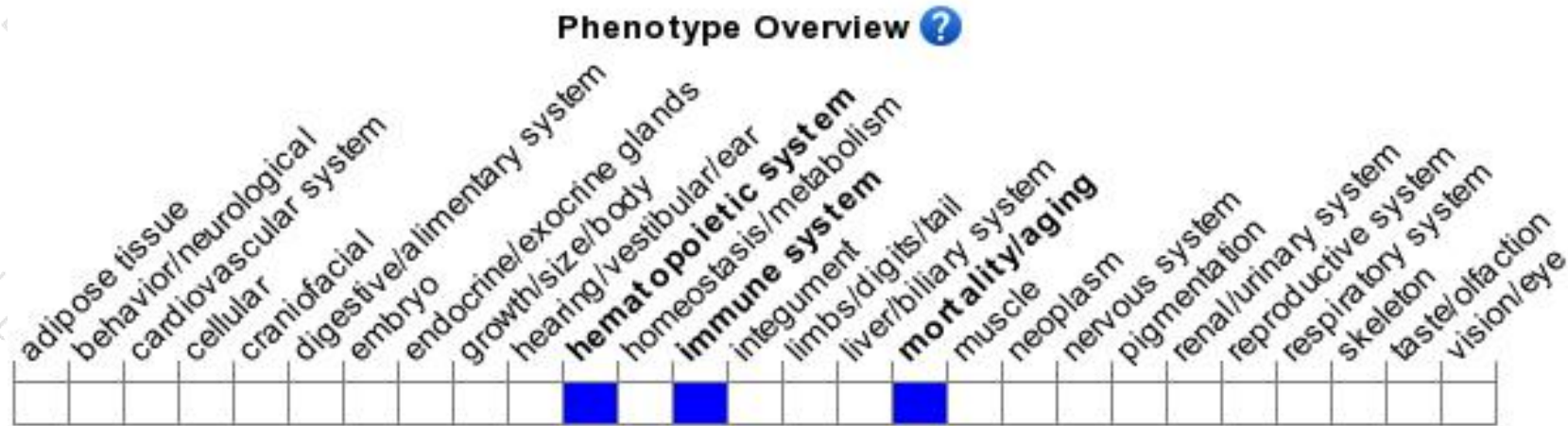
Genomic location distribution



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 have defects in Natural Killer (NK) cell development, diminished NK-mediated cytolysis of tumor cells, and resistance to MCMV infection.

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

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