Klrk1 Cas9-KO Strategy

Designer: Jing Jin

Reviewer: Xiaojing Li

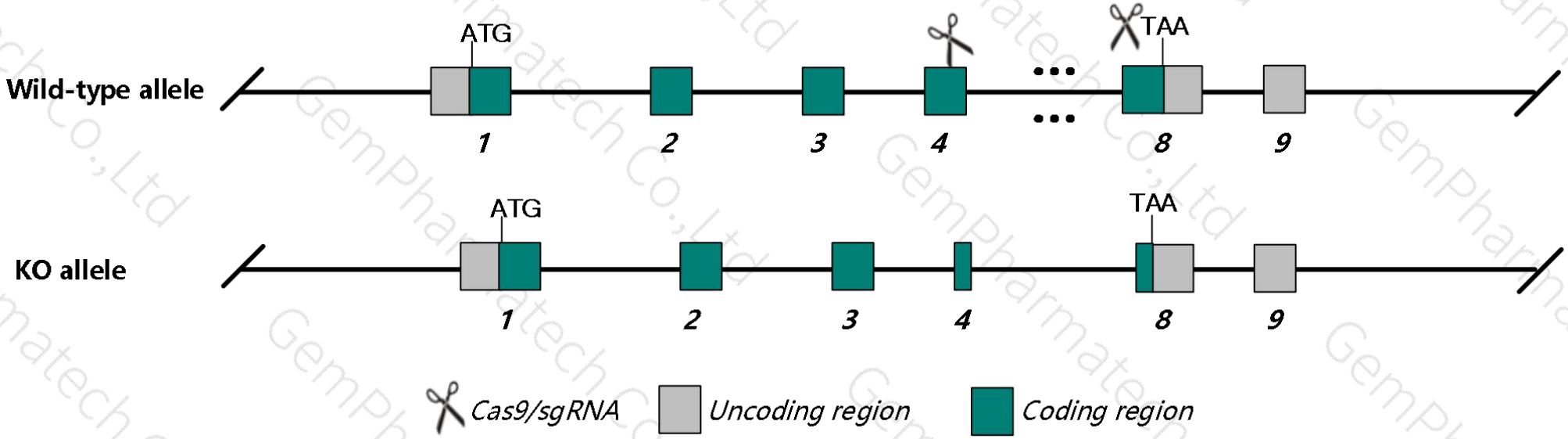
Design Date: 2020-7-8

Project Overview

Project Name	***Klrk1***
Project type	**Cas9-KO**
Strain background	**BALB/cJGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Klrk1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Klrk1* gene has 6 transcripts. According to the structure of *Klrk1* gene, exon4-exon8 of MGP_BALBcJ_T0080481.1 transcript is recommended as the knockout region. 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: sgRNA was transcribed in vitro.Cas9 and sgRNA were microinjected into the fertilized eggs of BALB/cJGpt mice.Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with BALB/cJGpt mice.

Notice

➢ 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）

集萃药康 GemPharmatech

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

Gene ID: 27007, updated on 31-Jan-2019

Summary

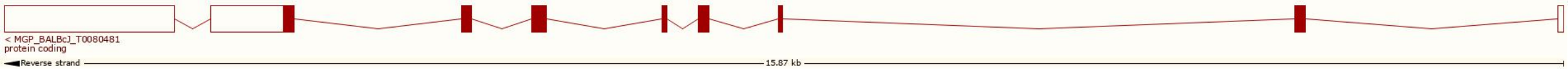
Official Symbol	Klrk1 provided by MGI
Official Full Name	killer cell lectin-like receptor subfamily K, member 1 provided by MGI
Primary source	MGI:MGI:1196250
See related	Ensembl:ENSMUSG00000030149
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata;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

Transcript information（Ensembl）

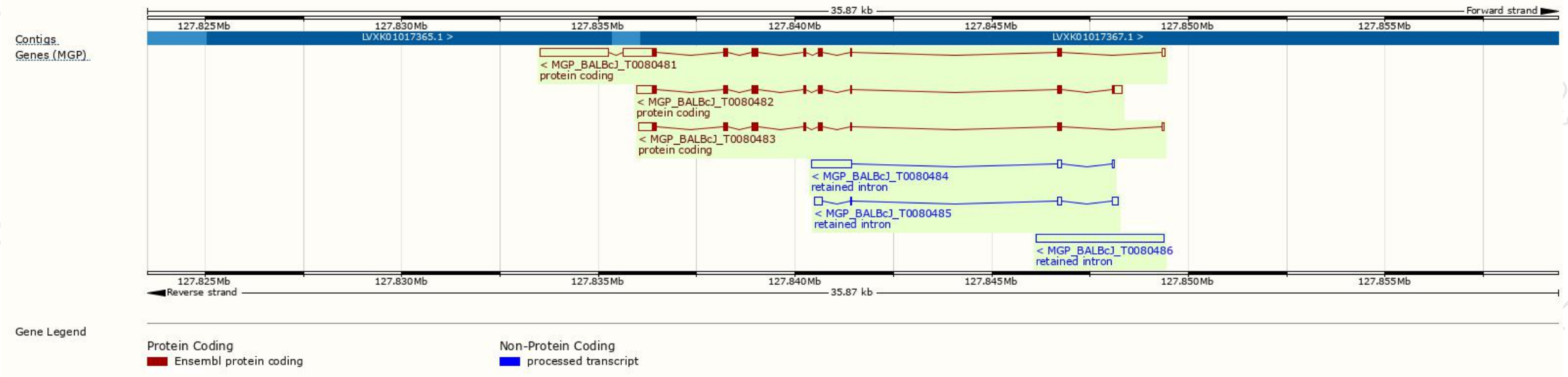
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
-	MGP_BALBcJ_T0080481.1	3205	225aa	Protein coding	CCDS39660, CCDS39661, CCDS71846	O54709 Q3TCW7 Q4FJM0	-
-	MGP_BALBcJ_T0080482.1	1281	232aa	Protein coding	-	-	-
-	MGP_BALBcJ_T0080483.1	1030	219aa	Protein coding	-	-	-
-	MGP_BALBcJ_T0080486.1	3261	No protein	Retained intron	-	-	-
-	MGP_BALBcJ_T0080484.1	1182	No protein	Retained intron	-	-	-
-	MGP_BALBcJ_T0080485.1	501	No protein	Retained intron	-	-	-

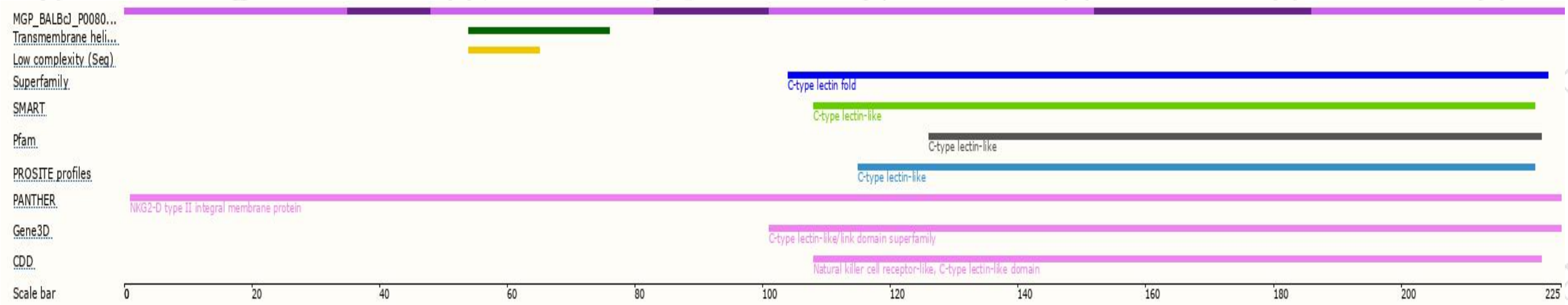
The strategy is based on the design of *MGP_BALBcJ_T0080481.1* transcript,the transcription is shown below:



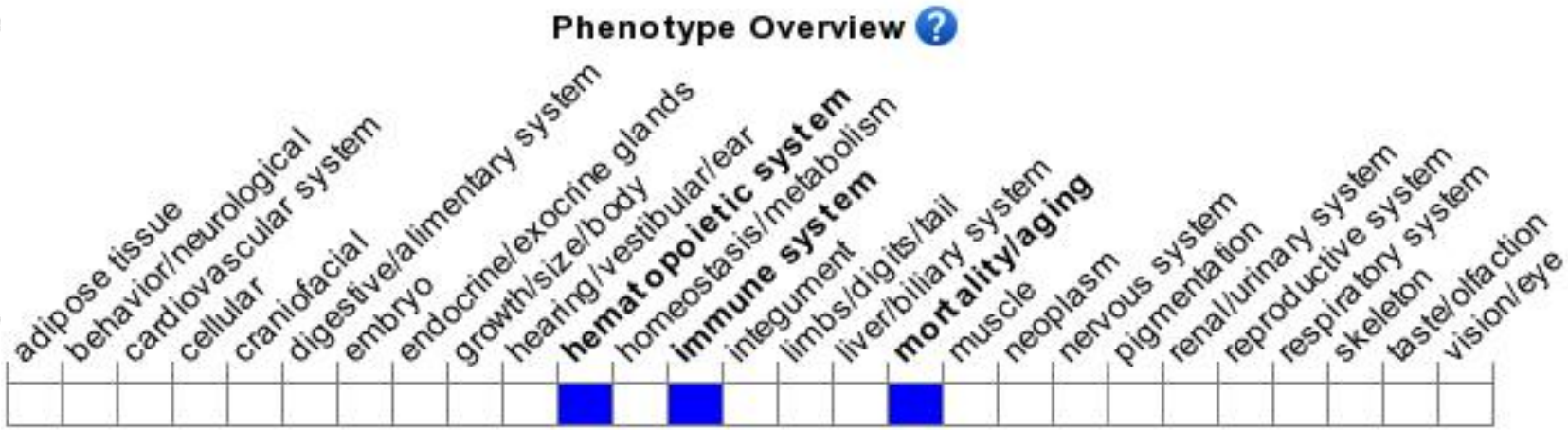
Genomic location distribution



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.

集萃药康
GemPharmatech

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

Tel: 025-5864 1534

集萃药康生物科技
GemPharmatech Co.,Ltd