Ackr1 Cas9-KO Strategy

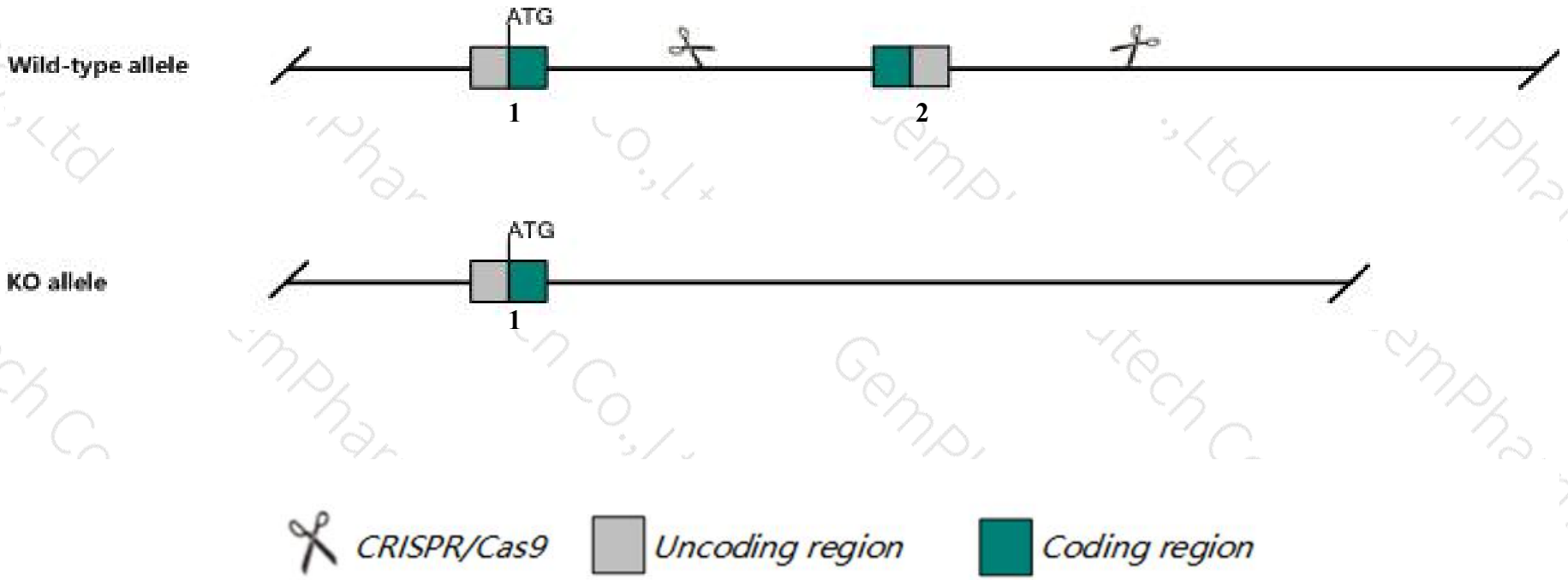
Designer: JiaYu

Project Overview

Project Name	***Ackr1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ackr1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Ackr1* gene has 3 transcript. According to the structure of *Ackr1* gene, exon2 of *Ackr1-201* (ENSMUST00000038227.5) transcript is recommended as the knockout region.The region contains 1040bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Ackr1* gene. The brief process is as follows: CRISPR/Cas9 system we

Notice

➢ According to the existing MGI data, Homozygous null mutants are healthy, but erythrocytes lack CXC and CC chemokine-binding activity, such that when challenged with LPS result in increased inflammatory infiltrates in lung and liver.

➢ The *Ackr1* gene is located on the Chr1. 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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Ackr1 atypical chemokine receptor 1 (Duffy blood group) [*Mus musculus* (house mouse)]

Gene ID: 13349, updated on 4-Jun-2019

Summary

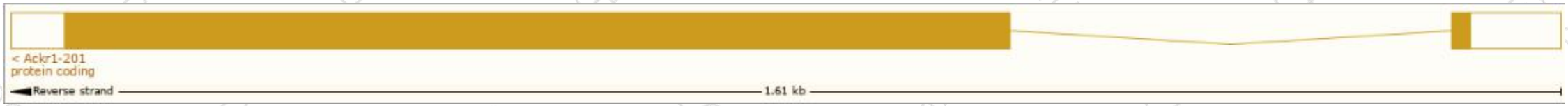
Official Symbol	Ackr1 provided by MGI
Official Full Name	atypical chemokine receptor 1 (Duffy blood group) provided by MGI
Primary source	MGI:MGI:1097689
See related	Ensembl:ENSMUSG00000037872
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	FY; Dfy; GPD; Darc; CCBP1; CD234; ESTM35; AA162249
Expression	Broad expression in cerebellum adult (RPKM 65.4), liver E14.5 (RPKM 38.7) and 18 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

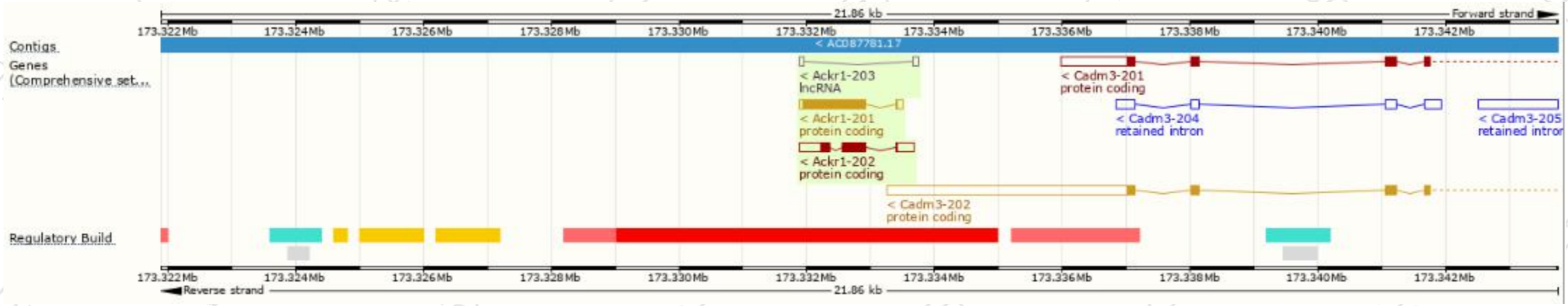
The gene has 3 transcript,and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ackr1-201	ENSMUST00000038227.5	1153	334aa	Protein coding	CCDS35789	A0A0R4J0J4	TSL:1 GENCODE basic APPRIS P1
Ackr1-202	ENSMUST00000194046.1	1122	174aa	Protein coding	-	A0A0A6YWZ3	TSL:1 GENCODE basic
Ackr1-203	ENSMUST00000194298.1	167	No protein	lncRNA	-	-	TSL:3

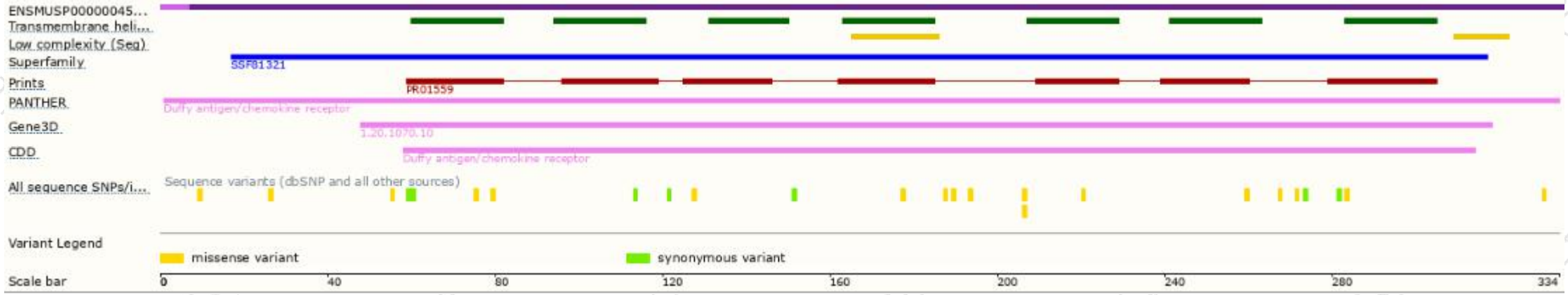
The strategy is based on the design of *Ackr1-201* transcript,The transcription is shown below



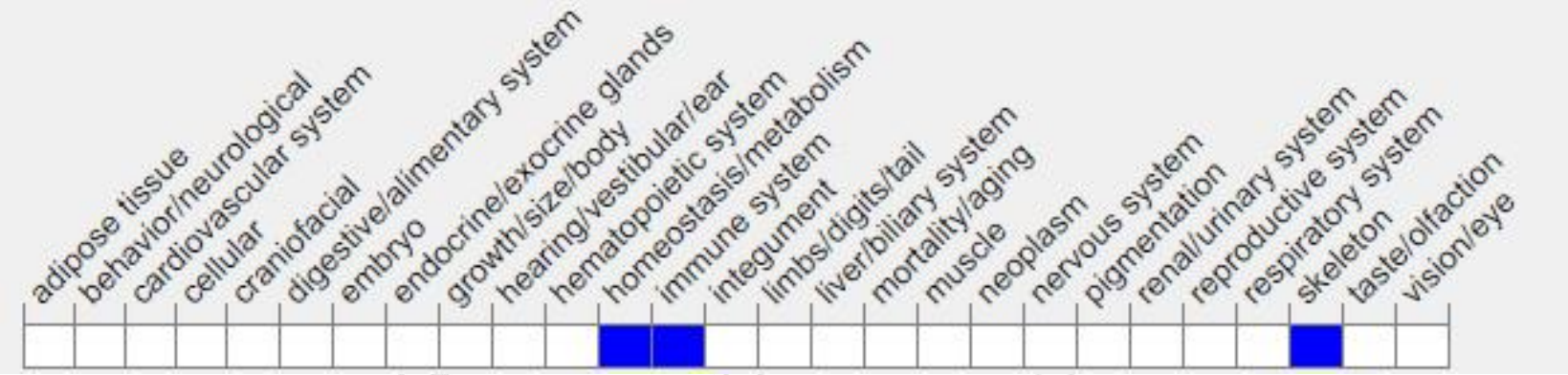
Genomic location distribution



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/).

According to the existing MGI data, Homozygous null mutants are healthy, but erythrocytes lack CXC and CC chemokine-binding activity, such that when challenged with LPS result in increased inflammatory infiltrates in lung and liver.

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

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