

Cd34 Cas9-KO Strategy

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Project Overview

Project Name

Cd34

Project type

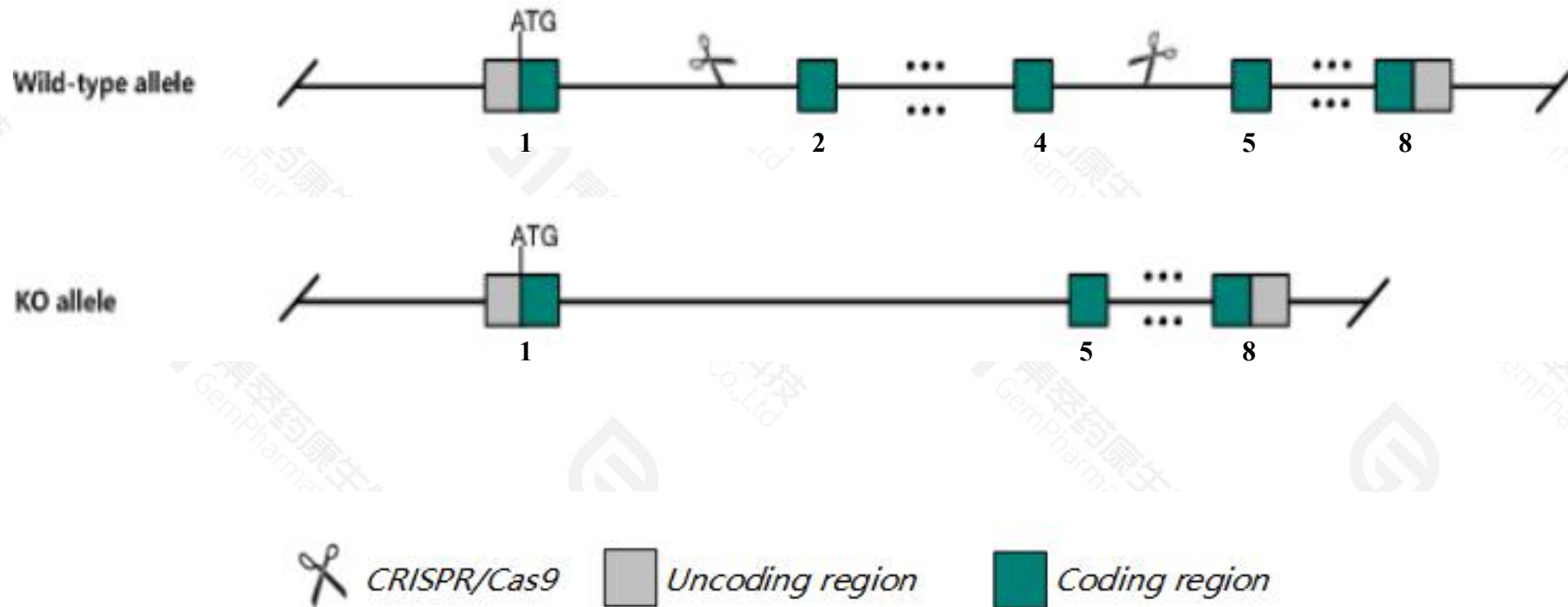
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cd34* gene. The schematic diagram is as follows:



- The *Cd34* gene has 5 transcripts. According to the structure of *Cd34* gene, exon2-exon4 of *Cd34-201*(ENSMUST00000016638.8) transcript is recommended as the knockout region. The region contains 509bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cd34* gene. The brief process is as follows: CRISPR/Cas9 system were microinjected into the fertilized eggs of C57BL/6JGpt 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 C57BL/6JGpt mice.

- According to the existing MGI data, homozygotes for a null allele show decreased splenocyte number and hematopoietic defects. Homozygotes for another null allele show reduced eosinophil accumulation after allergen exposure, impaired TPA-induced hair follicle stem cell activation and reduced incidence of chemically-induced skin tumors.
- The *Cd34* 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.

Cd34 CD34 antigen [Mus musculus (house mouse)]

Gene ID: 12490, updated on 2-Mar-2021

Summary



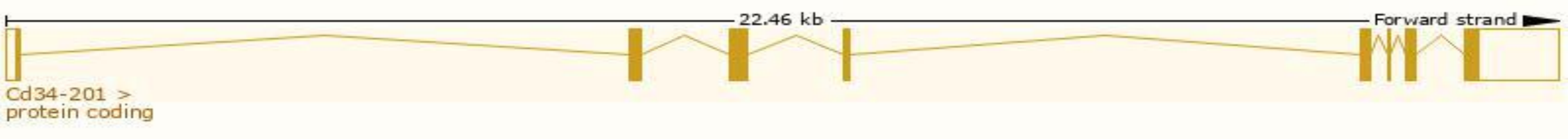
Official Symbol	Cd34 provided by MGI
Official Full Name	CD34 antigen provided by MGI
Primary source	MGI:MGI:88329
See related	Ensembl:ENSMUSG00000016494
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AU040960
Expression	Broad expression in bladder adult (RPKM 83.8), subcutaneous fat pad adult (RPKM 60.4) and 21 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

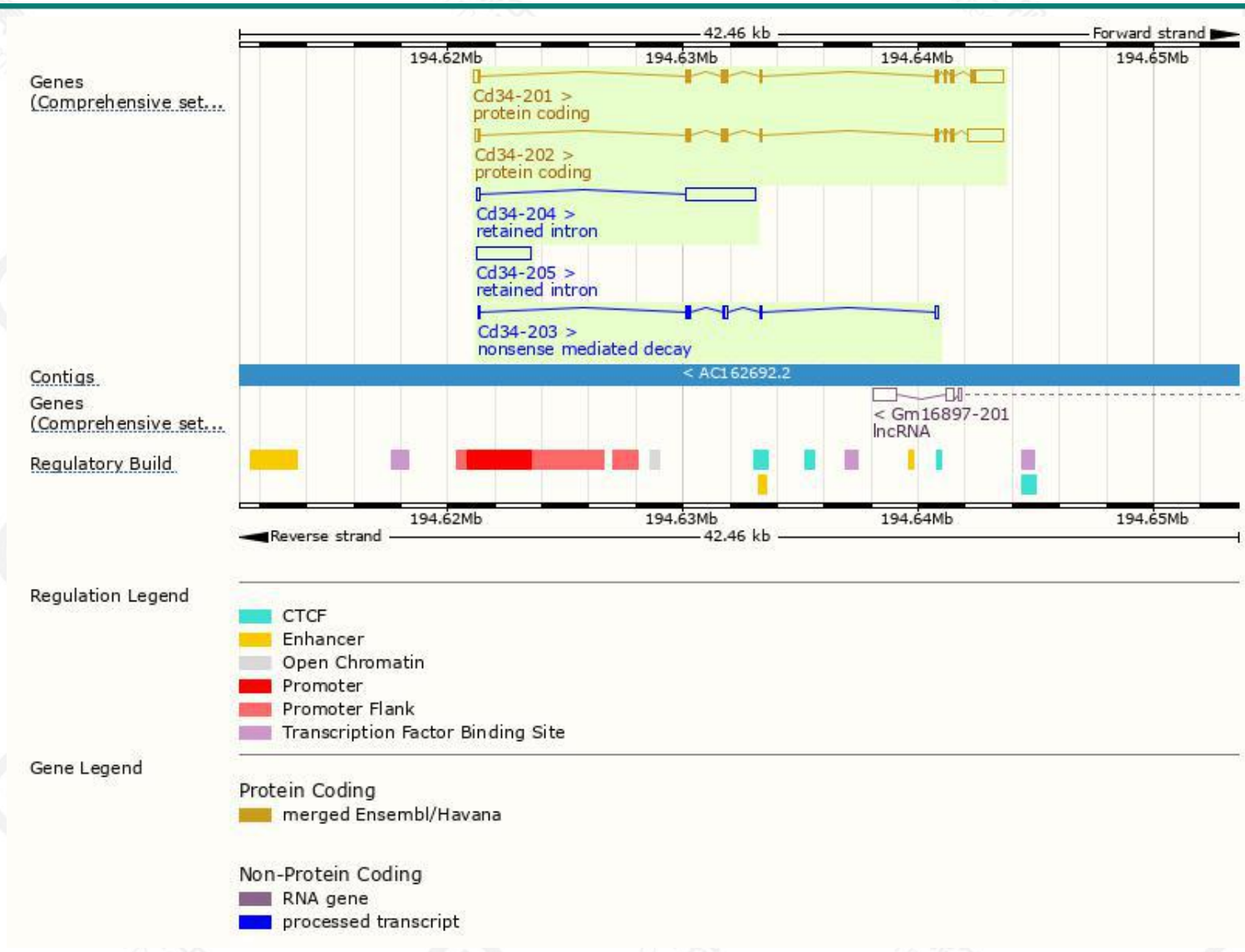
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cd34-202	ENSMUST00000110815.9	2554	325aa	Protein coding	CCDS48490		TSL:1 , GENCODE basic ,
Cd34-201	ENSMUST00000016638.8	2454	382aa	Protein coding	CCDS15640		TSL:1 , GENCODE basic , APPRIS P1 ,
Cd34-203	ENSMUST00000194036.2	616	104aa	Nonsense mediated decay	-		CDS 5' incomplete , TSL:5 ,
Cd34-204	ENSMUST00000194458.2	3063	No protein	Retained intron	-		TSL:1 ,
Cd34-205	ENSMUST00000195092.2	2279	No protein	Retained intron	-		TSL:NA ,

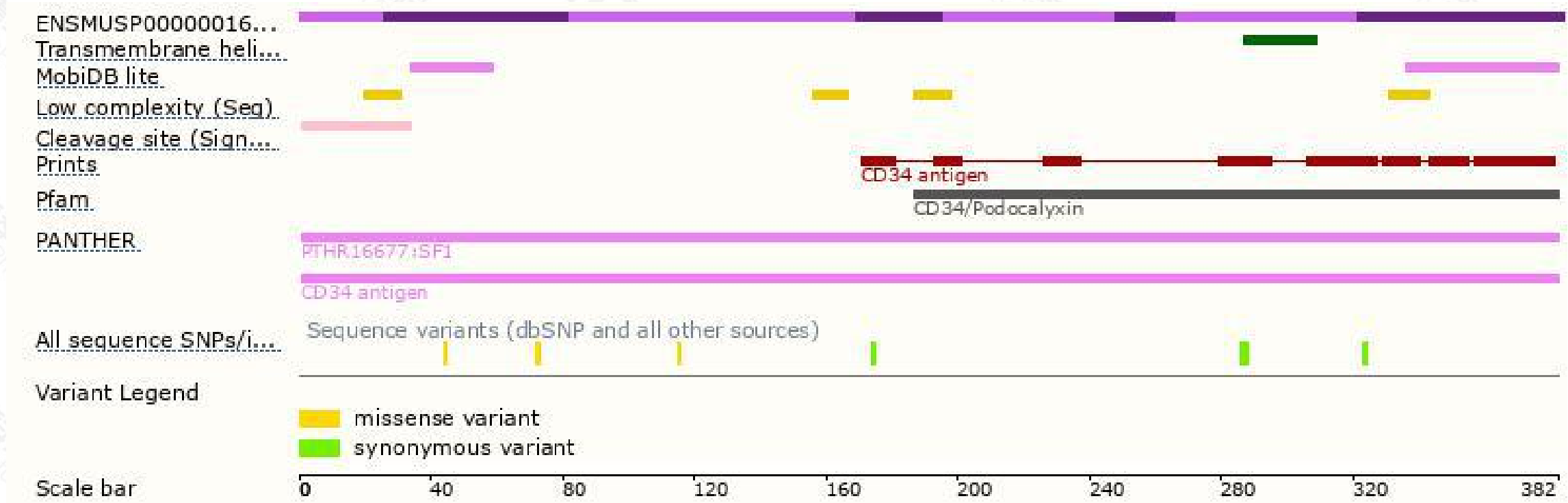
The strategy is based on the design of *Cd34-201* transcript,the transcription is shown below:



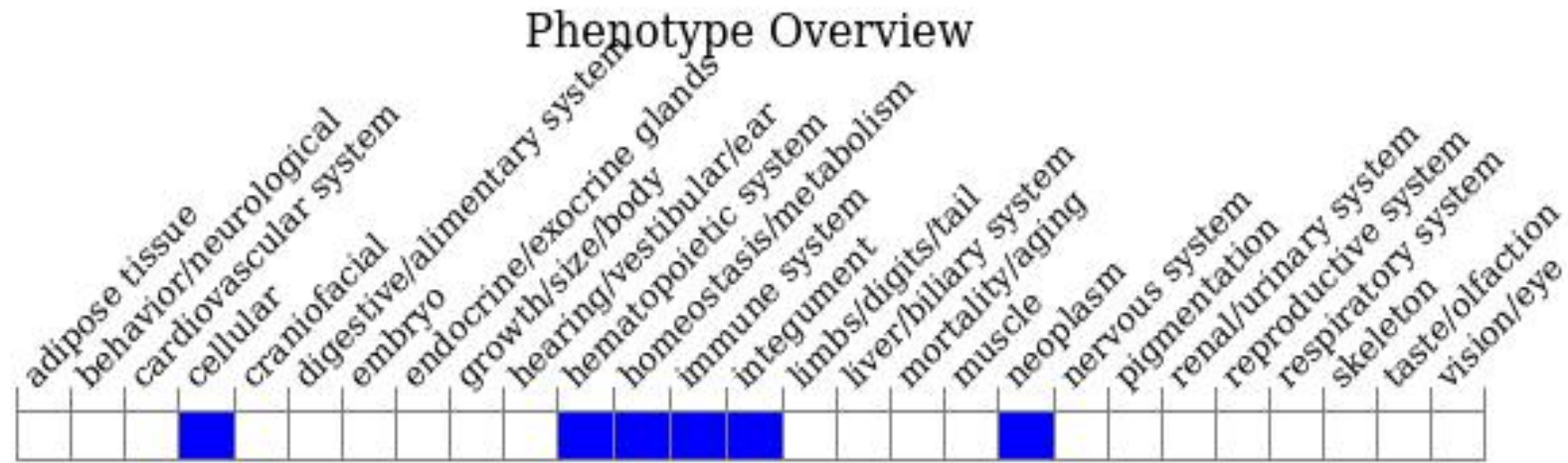
Genomic location distribution



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, homozygotes for a null allele show decreased splenocyte number and hematopoietic defects. Homozygotes for another null allele show reduced eosinophil accumulation after allergen exposure, impaired TPA-induced hair follicle stem cell activation and reduced incidence of chemically-induced skin tumors.

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