

Cd36 Cas9-KO Strategy

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Project Overview

Project Name

Cd36

Project type

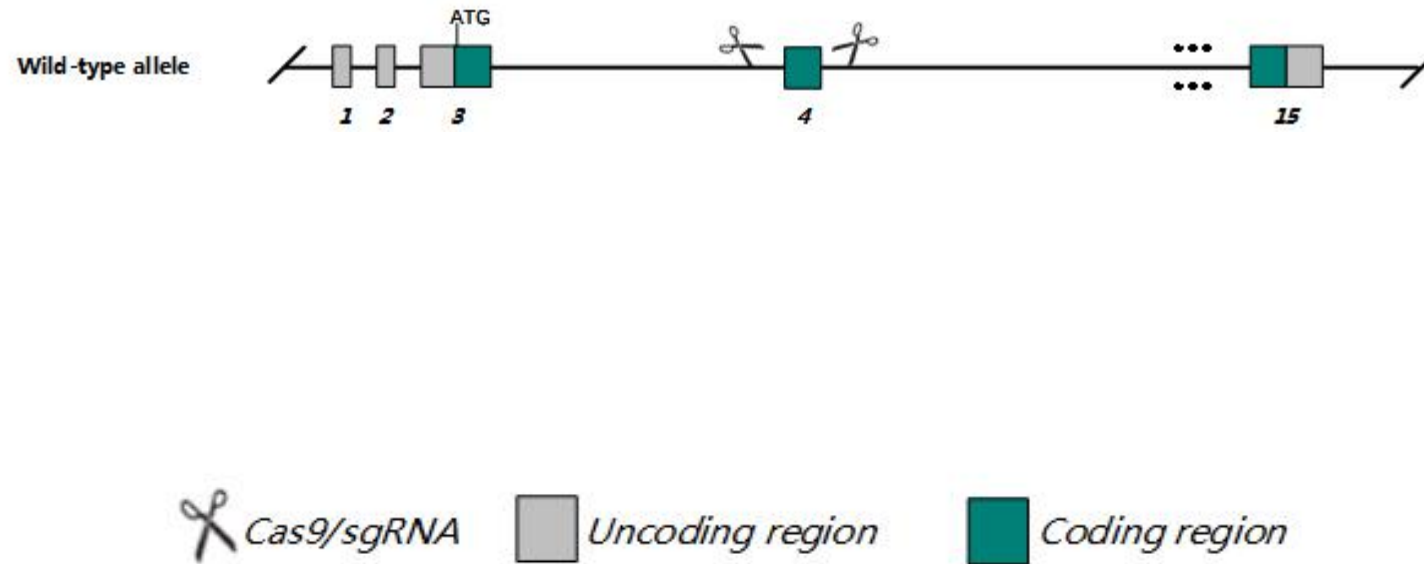
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cd36* gene. The schematic diagram is as follows:



- The *Cd36* gene has 6 transcripts. According to the structure of *Cd36* gene, exon4 of *Cd36-204* (ENSMUST00000170051.7) transcript is recommended as the knockout region. The region contains 161bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cd36* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous mutant mice exhibit an immunodeficiency phenotype, are susceptible to *S. aureus* infection and develop ocular pterygium. Mice homozygous for disruptions in this gene display abnormal lipid homeostasis which affects energy utilization in the heart.
- The *Cd36* gene is located on the Chr5. 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)

Cd36 CD36 molecule [Mus musculus (house mouse)]

Gene ID: 12491, updated on 2-Apr-2019

Summary



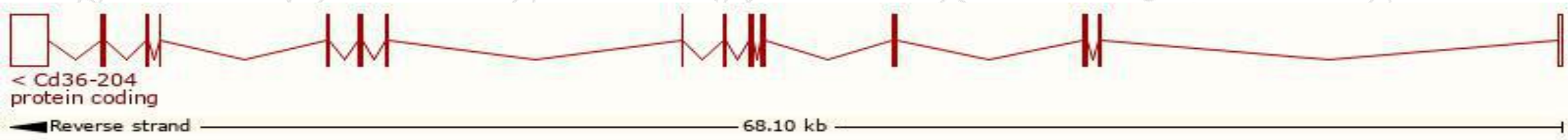
Official Symbol	Cd36 provided by MGI
Official Full Name	CD36 molecule provided by MGI
Primary source	MGI:MGI:107899
See related	Ensembl:ENSMUSG000000002944
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	FAT, GPIV, Scarb3
Expression	Biased expression in subcutaneous fat pad adult (RPKM 144.0), heart adult (RPKM 110.7) and 5 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

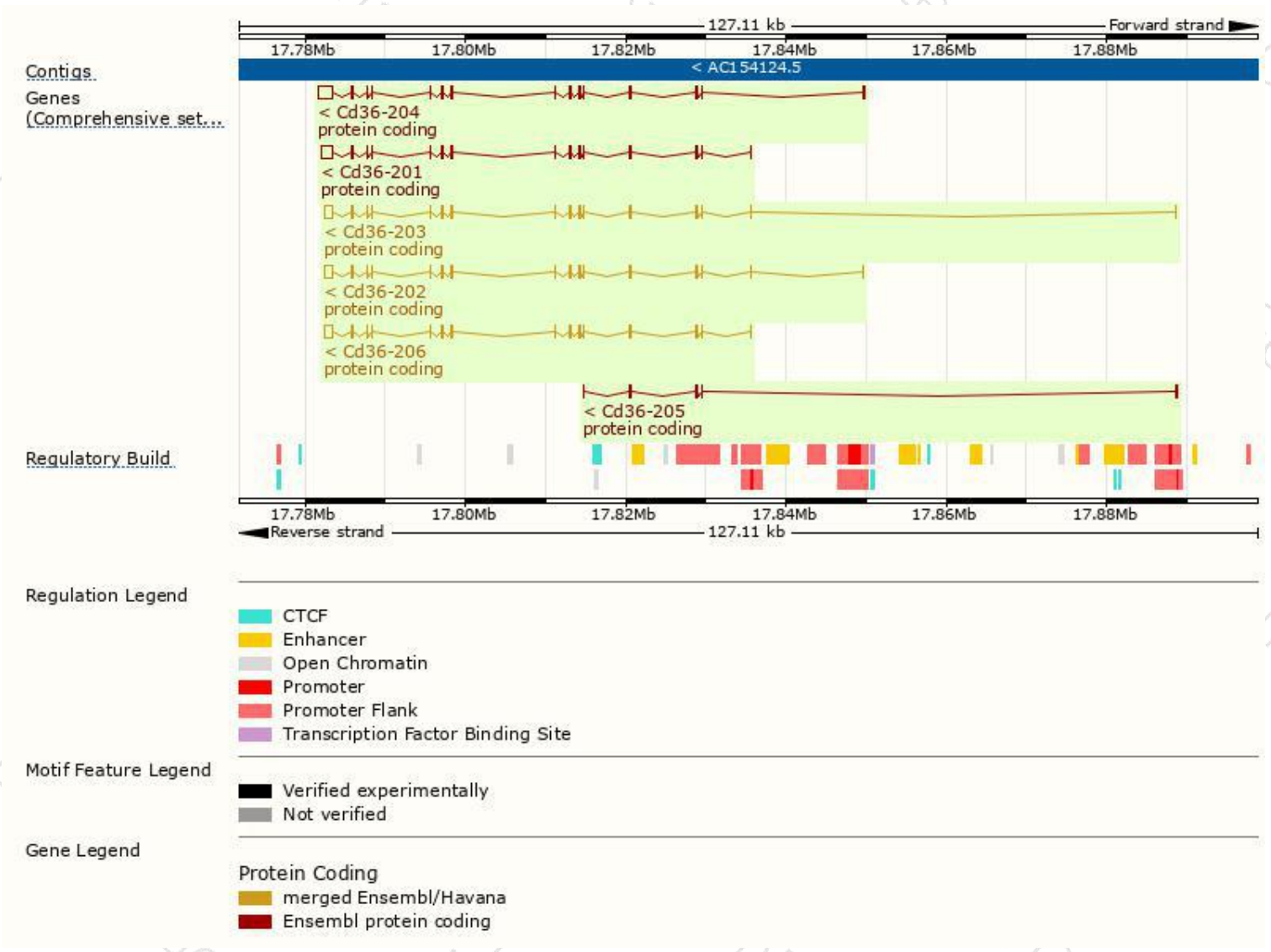
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cd36-204	ENSMUST00000170051.7	3399	472aa	Protein coding	CCDS19100	Q08857 Q3UAI3	TSL:1 GENCODE basic APPRIS P1
Cd36-201	ENSMUST00000082367.12	3016	472aa	Protein coding	CCDS19100	Q08857 Q3UAI3	TSL:1 GENCODE basic APPRIS P1
Cd36-202	ENSMUST00000165232.7	2708	472aa	Protein coding	CCDS19100	Q08857 Q3UAI3	TSL:1 GENCODE basic APPRIS P1
Cd36-203	ENSMUST00000169095.5	2677	472aa	Protein coding	CCDS19100	Q08857 Q3UAI3	TSL:1 GENCODE basic APPRIS P1
Cd36-206	ENSMUST00000197890.4	2564	472aa	Protein coding	CCDS19100	Q08857 Q3UAI3	TSL:1 GENCODE basic APPRIS P1
Cd36-205	ENSMUST00000197574.1	702	142aa	Protein coding	-	A0A0G2JFB7	CDS 3' incomplete TSL:5

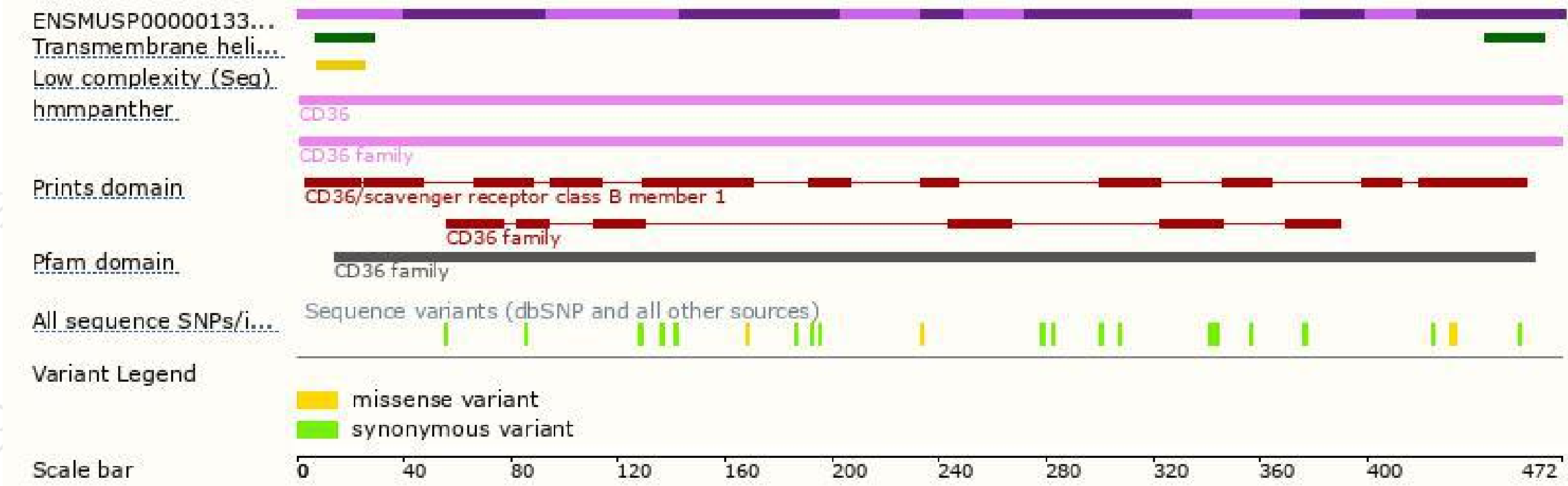
The strategy is based on the design of *Cd36-204* transcript,The transcription is shown below



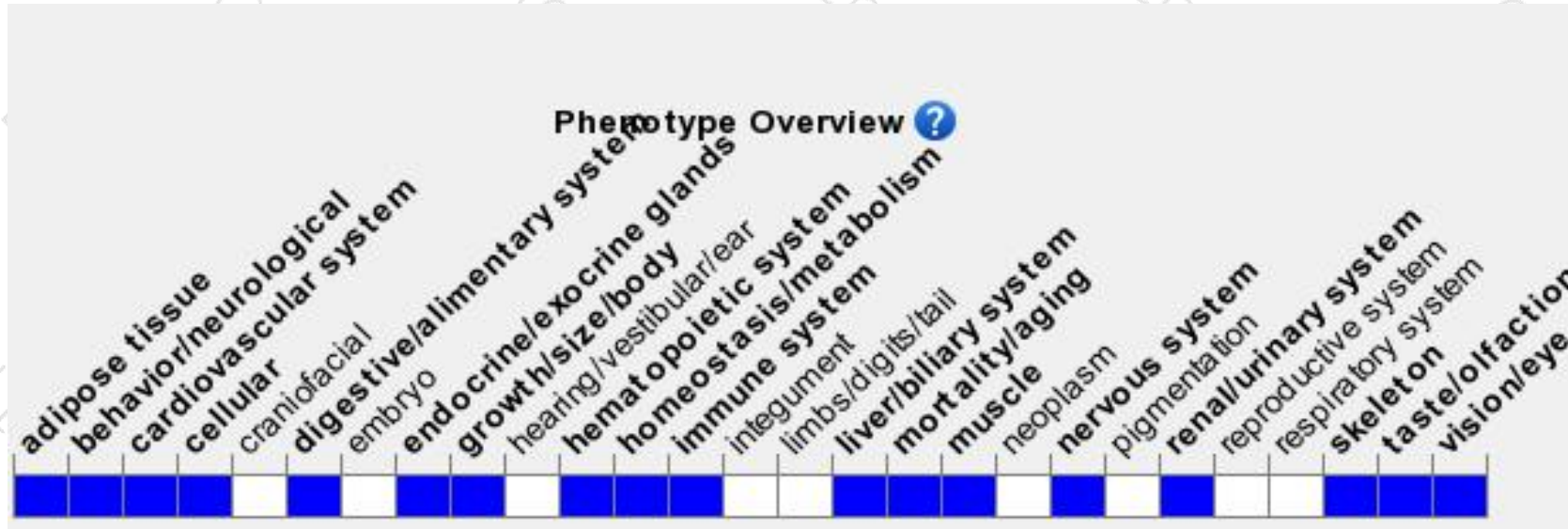
Genomic location distribution



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/>).

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

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