

Cd200 Cas9-KO Strategy

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Project Overview

Project Name

Cd200

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cd200* gene. The schematic diagram is as follows:



- The *Cd200* gene has 11 transcripts. According to the structure of *Cd200* gene, exon2 of *Cd200-202* (ENSMUST00000163230.7) transcript is recommended as the knockout region. The region contains 82bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cd200* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for disruptions in this gene have increased levels of all macrophage lineages. Macrophage are activated and mice display an increased susceptibility to autoimmune disease.
- The non-coding transcripts 203, 205, 207, 208, 209 and 211 affect the unknown and 210 are unaffected.
- The *Cd200* gene is located on the Chr16. 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)

Cd200 CD200 antigen [Mus musculus (house mouse)]

Gene ID: 17470, updated on 31-Jan-2019

Summary



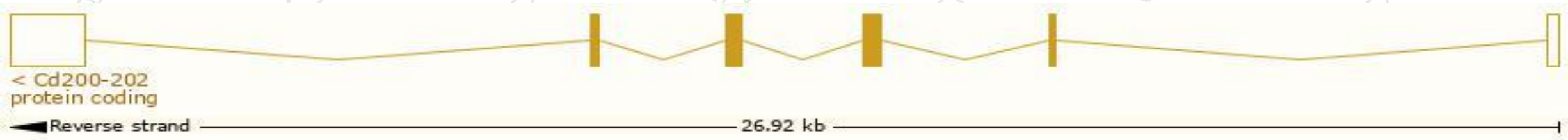
Official Symbol	Cd200 provided by MGI
Official Full Name	CD200 antigen provided by MGI
Primary source	MGI:MGI:1196990
See related	Ensembl:ENSMUSG00000022661
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Mox2, OX2
Expression	Broad expression in CNS E18 (RPKM 82.1), whole brain E14.5 (RPKM 45.1) and 16 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

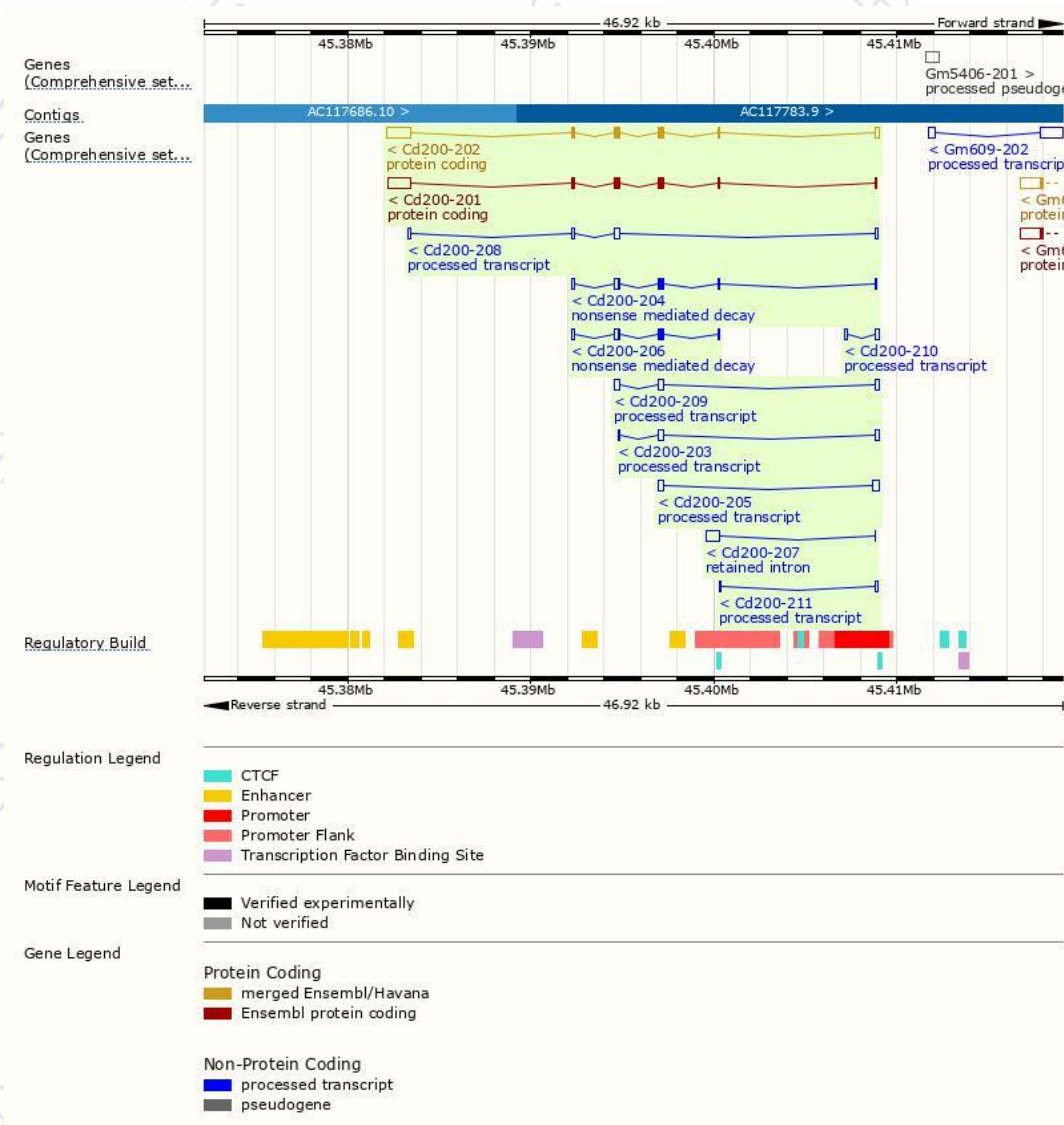
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cd200-202	ENSMUST00000163230.7	2347	278aa	Protein coding	CCDS49860	Q80VX2	TSL:1 GENCODE basic APPRIS P2
Cd200-201	ENSMUST00000023341.14	2085	269aa	Protein coding	-	E9QMY1	TSL:5 GENCODE basic APPRIS ALT2
Cd200-204	ENSMUST00000166512.1	879	150aa	Nonsense mediated decay	-	Q05D16	TSL:1
Cd200-206	ENSMUST00000167355.7	830	129aa	Nonsense mediated decay	-	E9PZI9	TSL:5
Cd200-209	ENSMUST00000171855.7	763	No protein	Processed transcript	-	-	TSL:2
Cd200-208	ENSMUST00000171328.7	708	No protein	Processed transcript	-	-	TSL:3
Cd200-205	ENSMUST00000166630.1	622	No protein	Processed transcript	-	-	TSL:3
Cd200-203	ENSMUST00000165910.7	548	No protein	Processed transcript	-	-	TSL:3
Cd200-210	ENSMUST00000172091.1	281	No protein	Processed transcript	-	-	TSL:1
Cd200-211	ENSMUST00000172297.1	235	No protein	Processed transcript	-	-	TSL:3
Cd200-207	ENSMUST00000167552.1	742	No protein	Retained intron	-	-	TSL:5

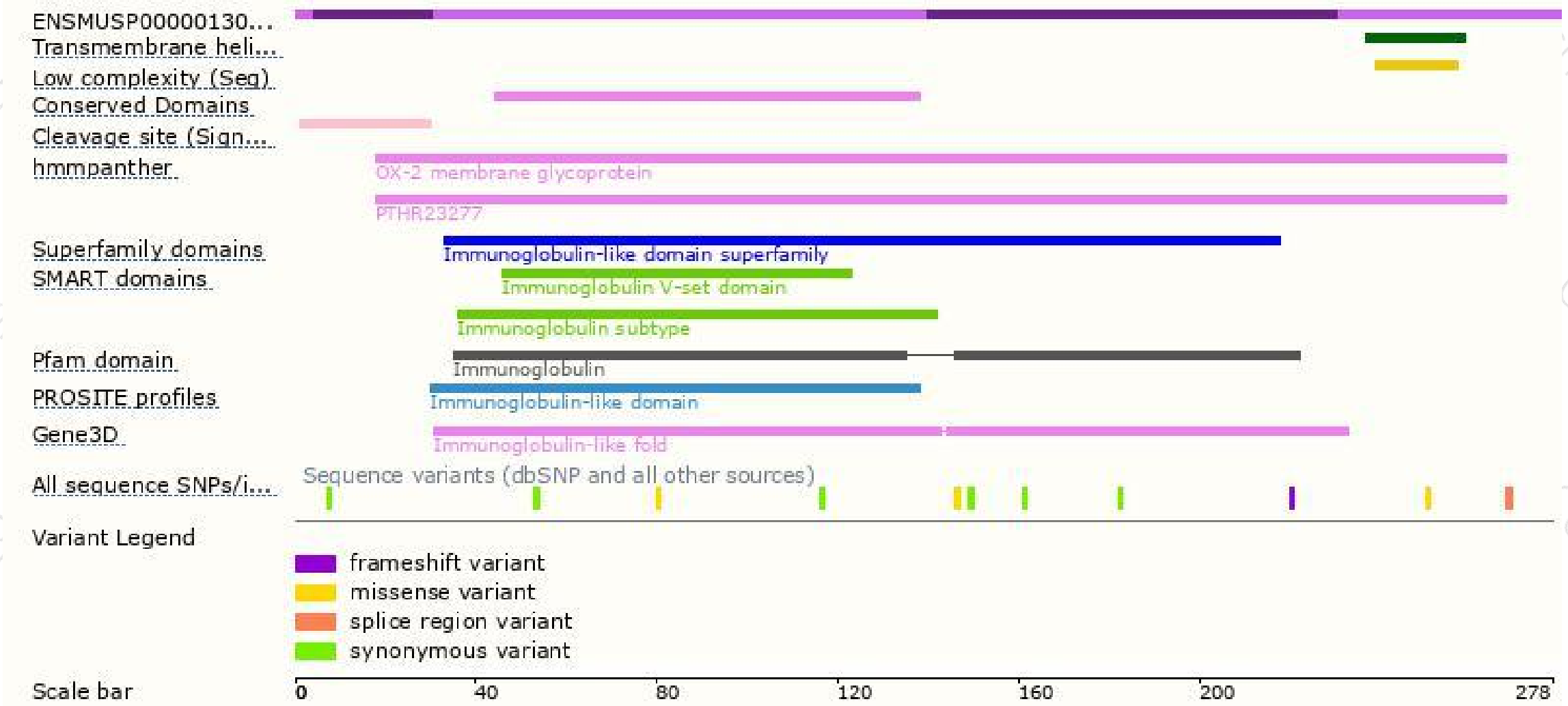
The strategy is based on the design of *Cd200-202* transcript,The transcription is shown below



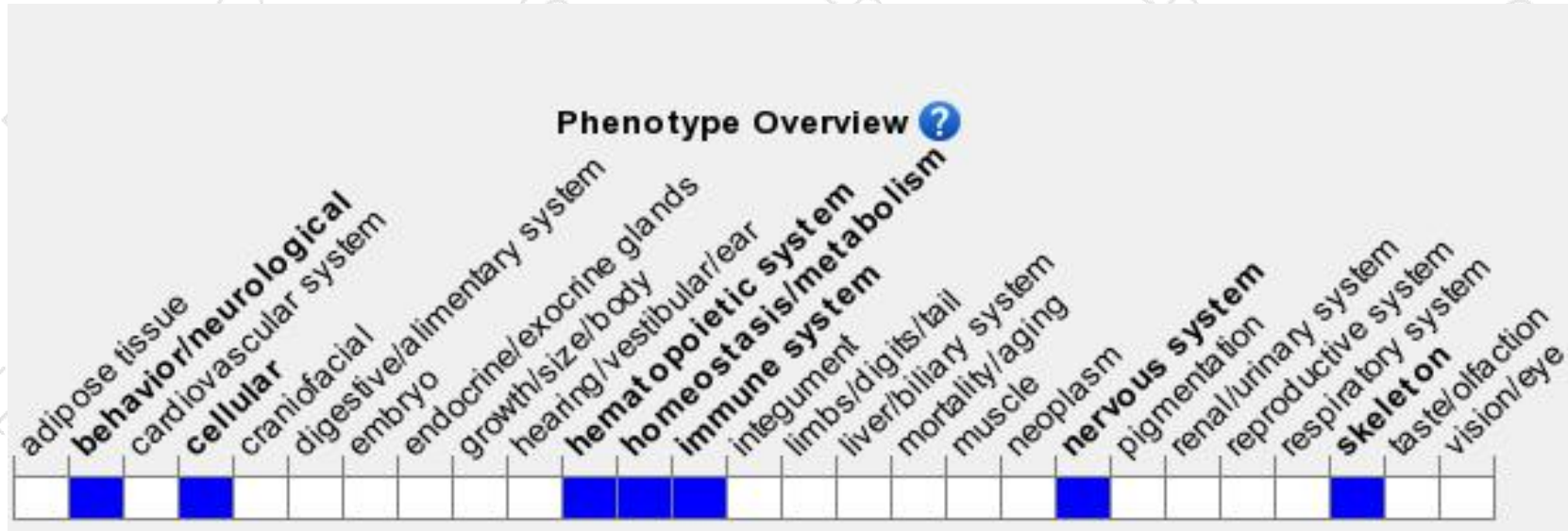
Genomic location distribution



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, Mice homozygous for disruptions in this gene have increased levels of all macrophage lineages. Macrophage are activated and mice display an increased susceptibility to autoimmune disease.

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

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