

Mc **Cas9-KO Strategy**

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Project Overview

Project Name

Mcam

Project type

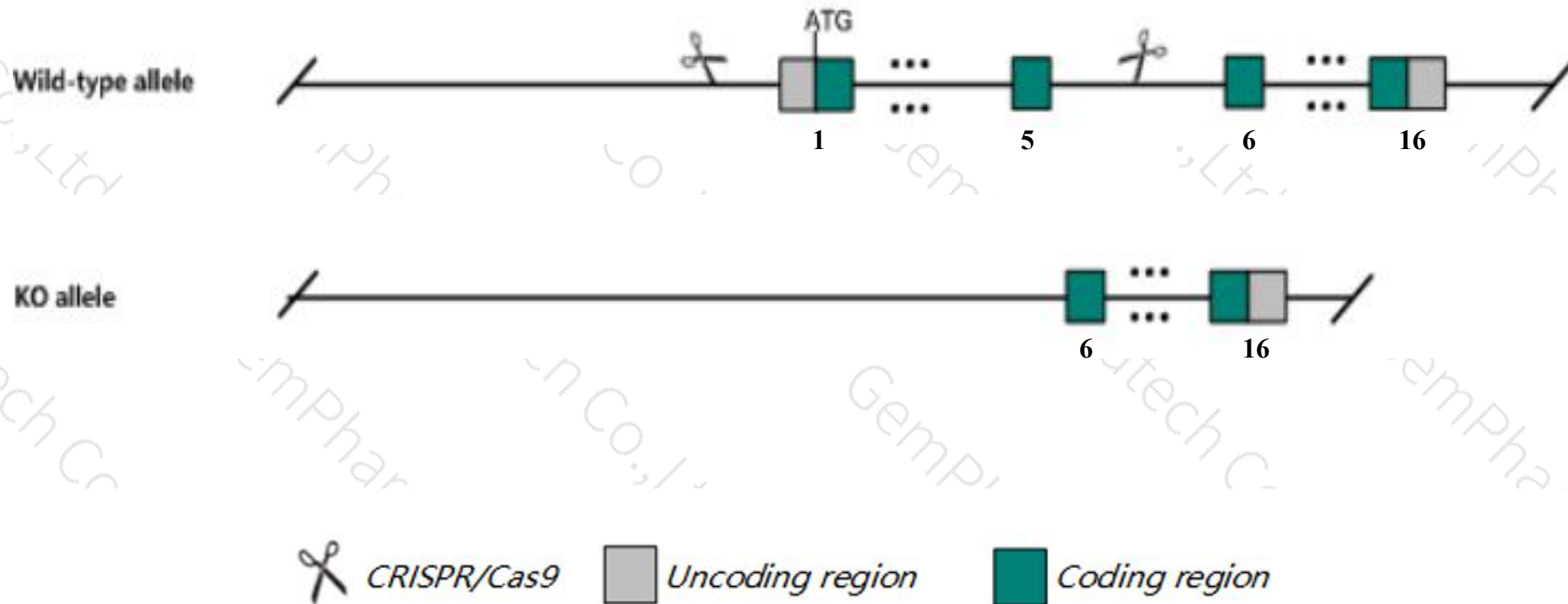
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Mcam* gene has 6 transcripts. According to the structure of *Mcam* gene, exon1-exon5 of *Mcam-201* (ENSMUST00000034650.14) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mcam* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a conditional allele activated in endothelial cells exhibit impaired VEGF-induced angiogenesis in Matrigel.
- The KO region contains functional region of the *Gm10687* gene. Knockout the region may affect the function of *Gm10687* gene.
- The *Mcam* gene is located on the Chr9. 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)

Mcam melanoma cell adhesion molecule [Mus musculus (house mouse)]

Gene ID: 84004, updated on 12-Mar-2019

Summary



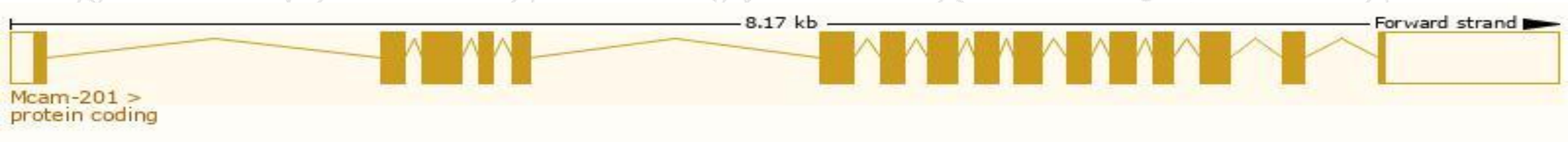
Official Symbol	Mcam provided by MGI
Official Full Name	melanoma cell adhesion molecule provided by MGI
Primary source	MGI:MGI:1933966
See related	Ensembl:ENSMUSG000000032135
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1-gicerin, AV025631, CD146, CD149, Muc18, s-endo, s-gicerin
Expression	Broad expression in subcutaneous fat pad adult (RPKM 97.6), lung adult (RPKM 73.6) and 21 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

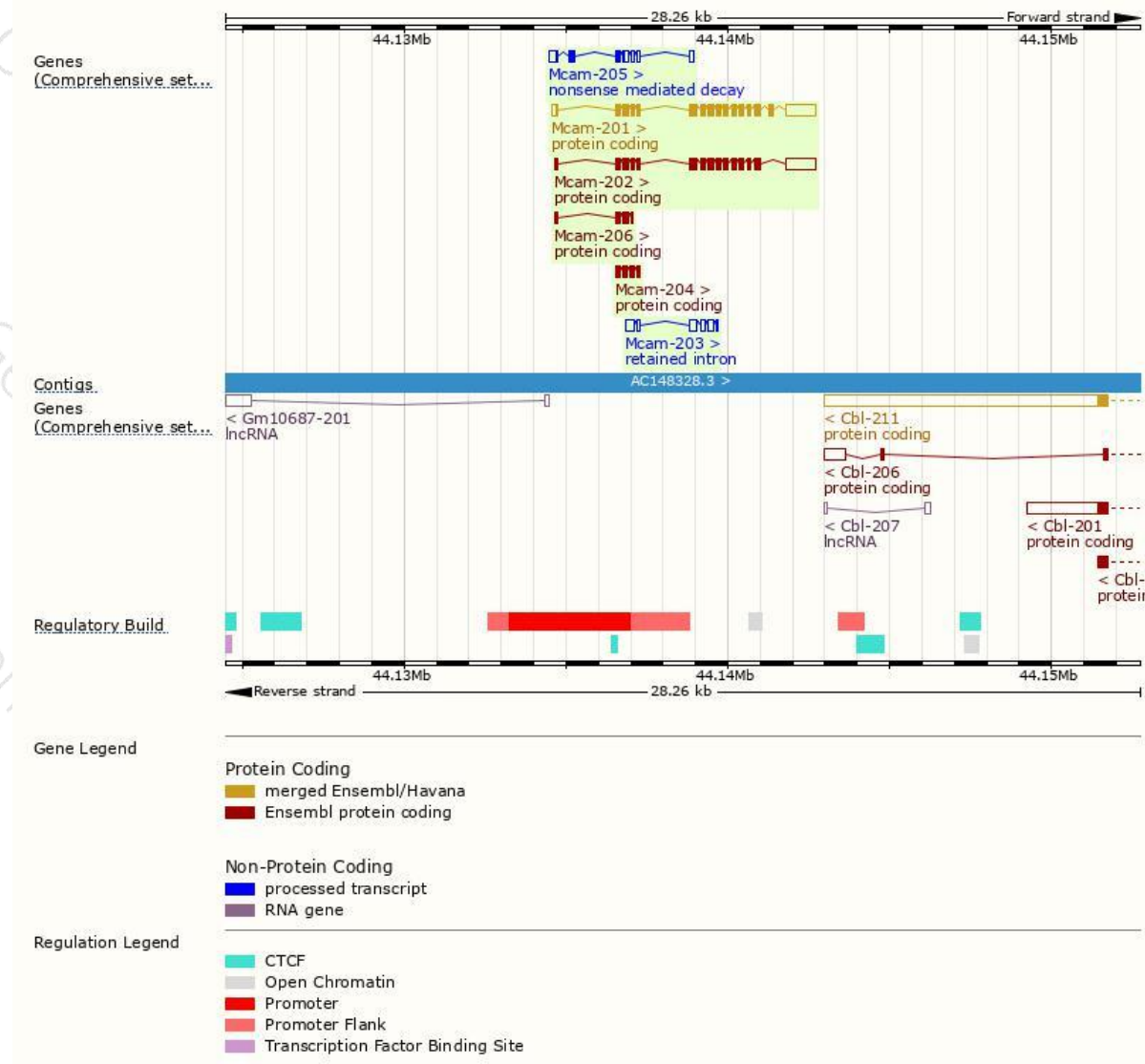
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mcam-201	ENSMUST00000034650.14	2989	648aa	Protein coding	CCDS23097	Q8R2Y2	TSL:1 GENCODE basic APPRIS P2
Mcam-202	ENSMUST00000098852.2	2772	606aa	Protein coding	-	Q8R2Y2	TSL:1 GENCODE basic APPRIS ALT 2
Mcam-206	ENSMUST00000216002.1	457	142aa	Protein coding	-	A0A1L1SQC5	CDS 3' incomplete TSL:2
Mcam-204	ENSMUST00000147836.1	449	149aa	Protein coding	-	F7ATH5	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:2
Mcam-205	ENSMUST00000149241.7	1061	146aa	Nonsense mediated decay	-	D6RFP0	TSL:5
Mcam-203	ENSMUST00000132490.1	832	No protein	Retained intron	-	-	TSL:5

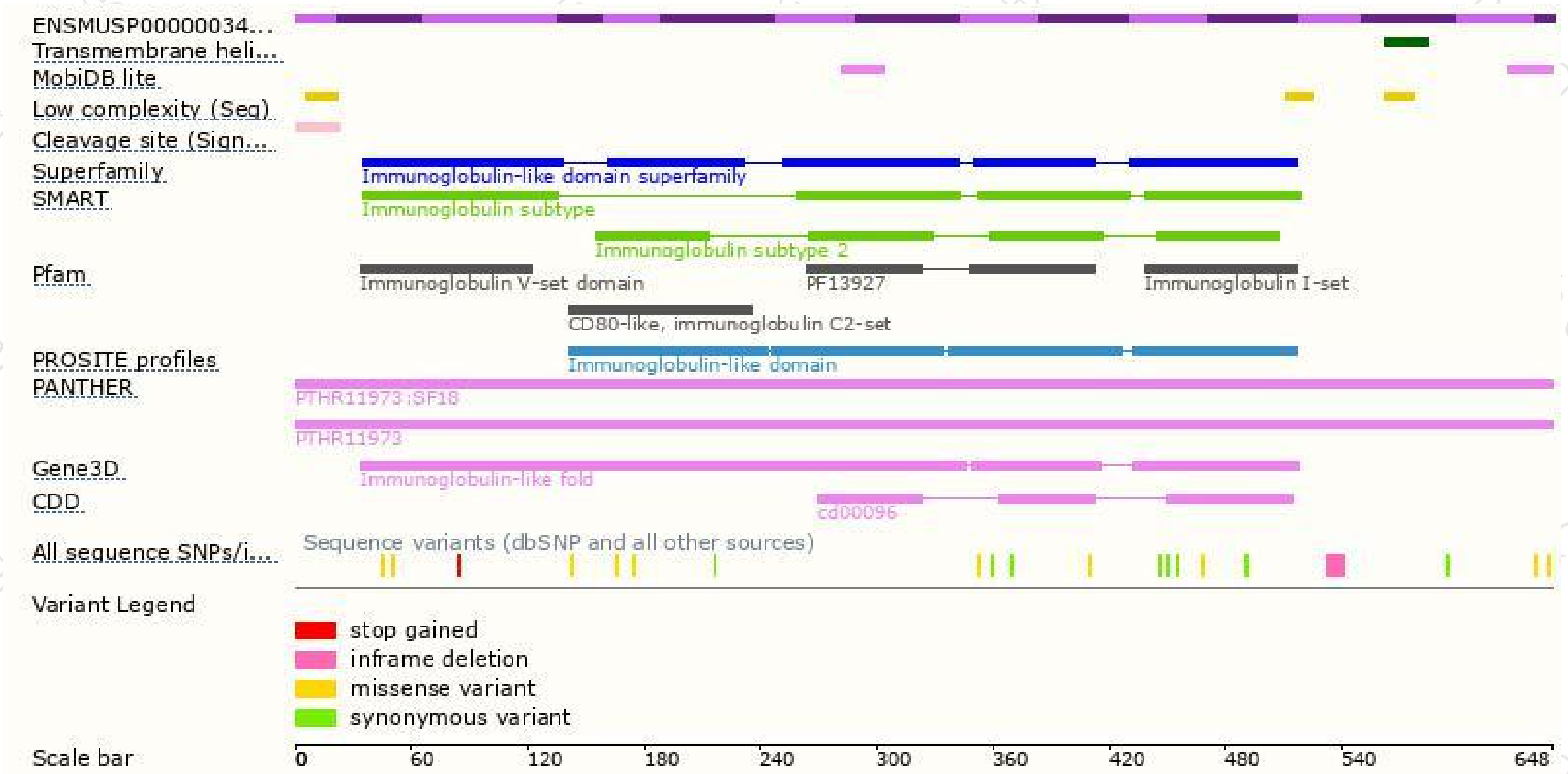
The strategy is based on the design of *Mcam-201* transcript,The transcription is shown below



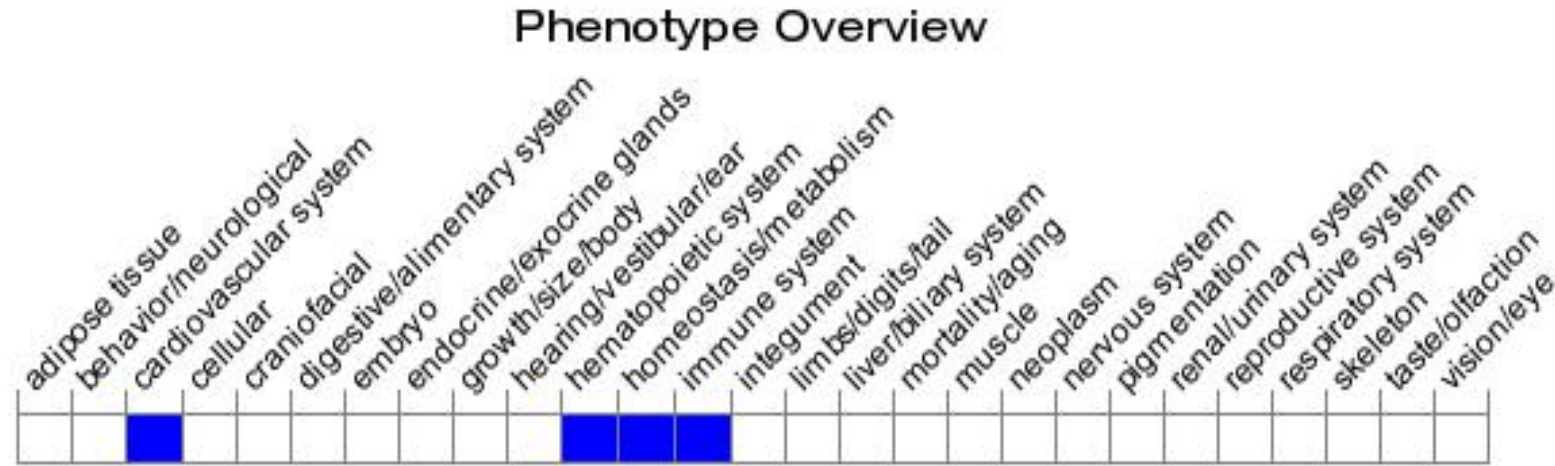
Genomic location distribution



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, Mice homozygous for a conditional allele activated in endothelial cells exhibit impaired VEGF-induced angiogenesis in Matrigel.

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

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