

Cfb Cas9-KO Strategy

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Project Overview

Project Name

Cfb

Project type

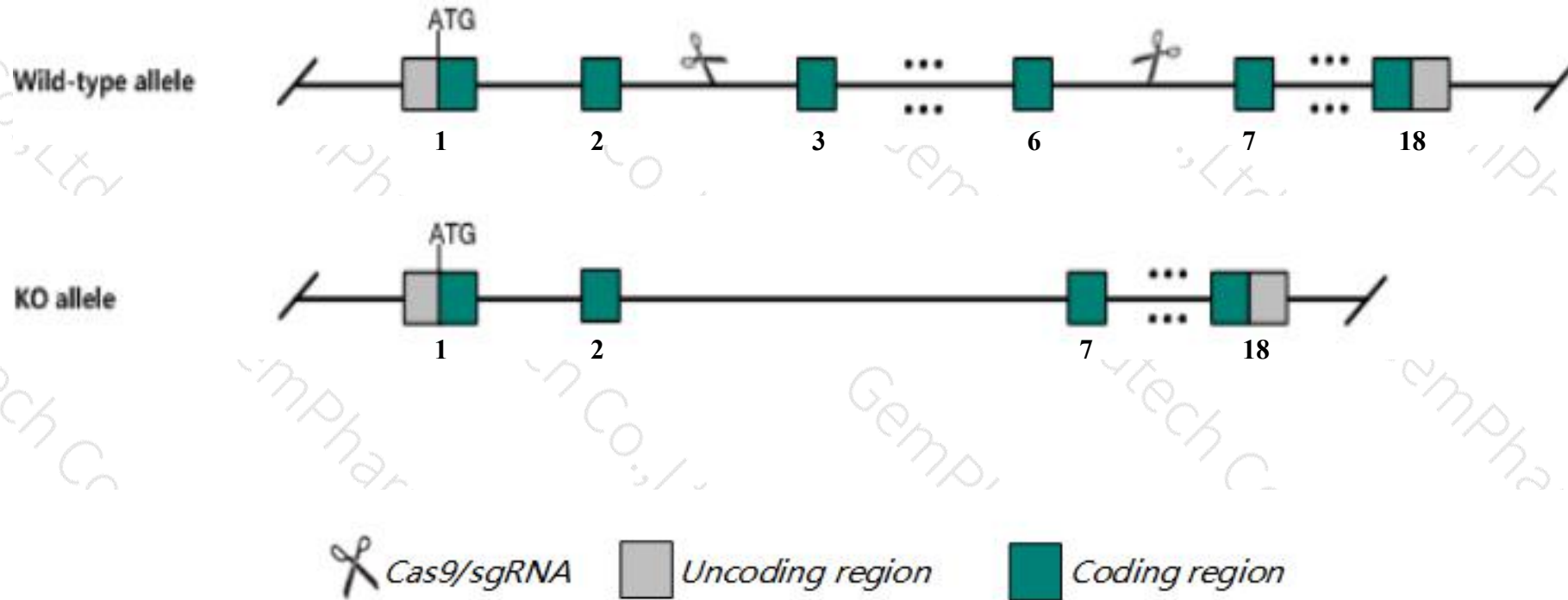
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Cfb* gene has 8 transcripts. According to the structure of *Cfb* gene, exon3-exon6 of *Cfb*-201(ENSMUST00000025229.10) transcript is recommended as the knockout region. The region contains 599bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cfb* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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 targeted null mutations lack the alternative complement pathway, and have reduced overall complement activity.
- The KO region contains functional region of the *Gm20547* gene. Knockout the region may affect the function of *Gm20547* gene.
- Transcript *Cfb-204*, *Cfb-205* and *Cfb-208* may not be affected.
- The *Cfb* gene is located on the Chr17. 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)

Cfb complement factor B [Mus musculus (house mouse)]

Gene ID: 14962, updated on 13-Mar-2020

Summary



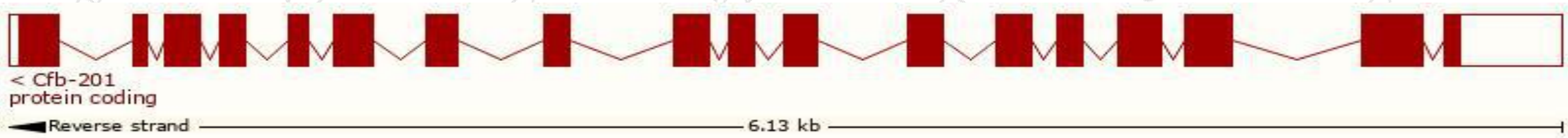
Official Symbol	Cfb provided by MGI
Official Full Name	complement factor B provided by MGI
Primary source	MGI:MGI:105975
See related	Ensembl:ENSMUSG00000090231
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI195813, AI255840, B, Bf, C2, Fb, H2-Bf
Expression	Biased expression in liver E18 (RPKM 279.0), liver adult (RPKM 221.3) and 9 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

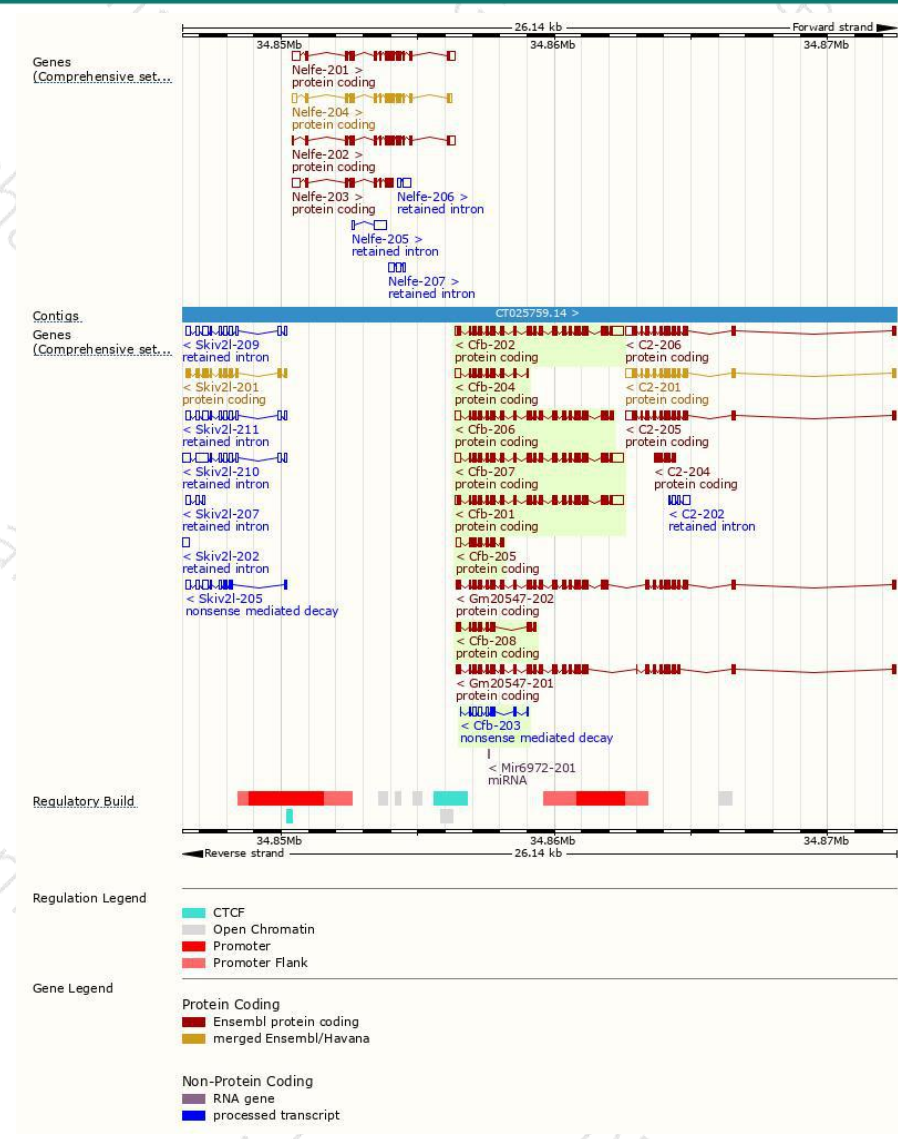
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cfb-201	ENSMUST00000025229.10	2737	763aa	Protein coding	CCDS28663	B8JJM5	TSL:1 GENCODE basic APPRIS P2
Cfb-207	ENSMUST00000176203.8	2733	713aa	Protein coding	CCDS50079	B8JJM6	TSL:1 GENCODE basic
Cfb-202	ENSMUST00000128767.7	2751	761aa	Protein coding	-	P04186 Q3UEG8	TSL:1 GENCODE basic APPRIS ALT2
Cfb-206	ENSMUST00000154526.7	2397	711aa	Protein coding	-	F6XQ00	TSL:1 GENCODE basic
Cfb-204	ENSMUST00000141295.7	973	259aa	Protein coding	-	F6W2T4	CDS 5' incomplete TSL:5
Cfb-208	ENSMUST00000176332.1	905	296aa	Protein coding	-	H3BK95	CDS 5' incomplete TSL:5
Cfb-205	ENSMUST00000153400.7	887	234aa	Protein coding	-	B8JJM3	CDS 5' incomplete TSL:5
Cfb-203	ENSMUST00000133127.1	655	81aa	Nonsense mediated decay	-	F6WZA2	CDS 5' incomplete TSL:5

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



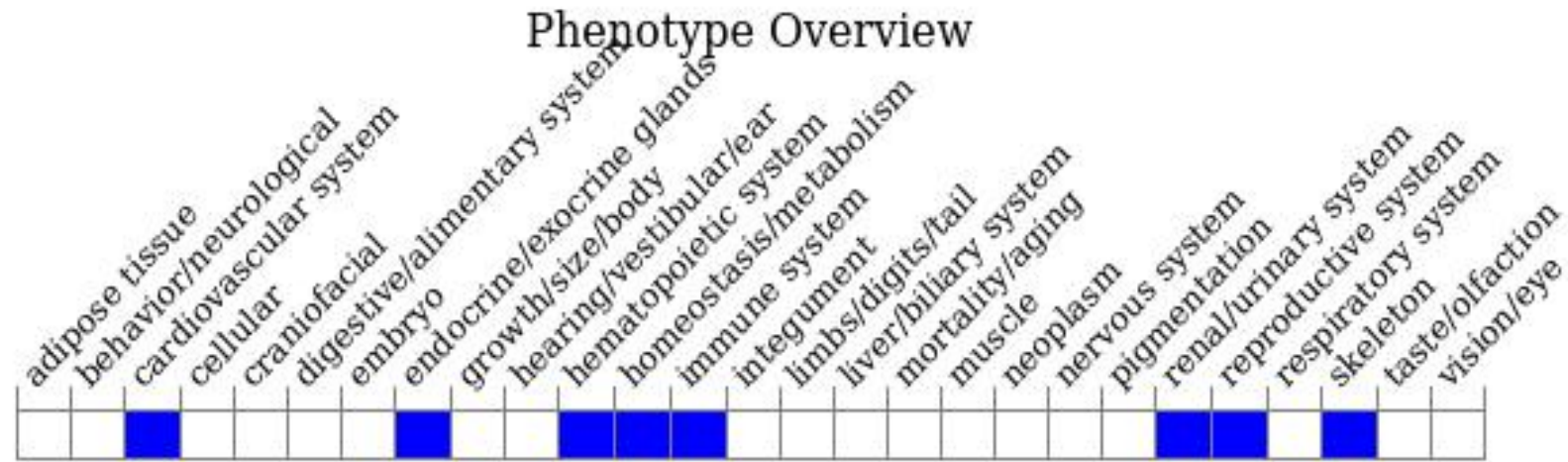
Genomic location distribution



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 targeted null mutations lack the alternative complement pathway, and have reduced overall complement activity.

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

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