

Celf3 Cas9-KO Strategy

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Project Overview

Project Name

Celf3

Project type

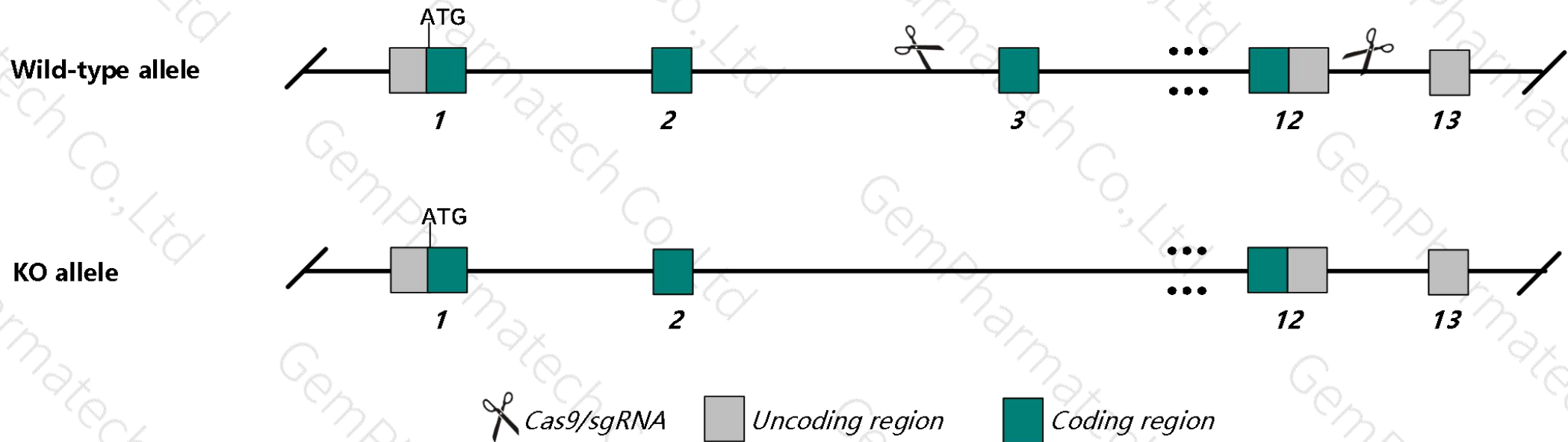
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Celf3* gene. The schematic diagram is as follows:



- The *Celf3* gene has 15 transcripts. According to the structure of *Celf3* gene, exon3-exon12 of *Celf3*-215 (ENSMUST00000200342.4) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Celf3* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, male mice homozygous for a null mutation display reduced sperm counts and motility but are fertile.
- Transcript 210 gene may be destroyed.
- The *Celf3* gene is located on the Chr3. 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)

Celf3 CUGBP, Elav-like family member 3 [Mus musculus (house mouse)]

Gene ID: 78784, updated on 20-Mar-2020

Summary



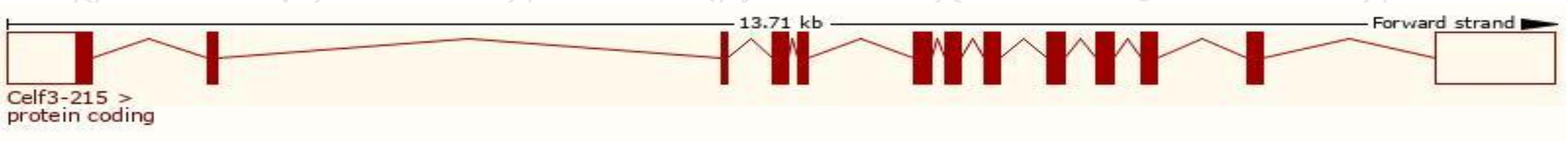
Official Symbol	Celf3 provided by MGI
Official Full Name	CUGBP, Elav-like family member 3 provided by MGI
Primary source	MGI:MGI:1926034
See related	Ensembl:ENSMUSG00000028137
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4930415M08Rik, BRUNOL1, CAGH4, ERDA4, ETR-1, Tnrc4
Expression	Biased expression in whole brain E14.5 (RPKM 85.2), CNS E14 (RPKM 68.5) and 8 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

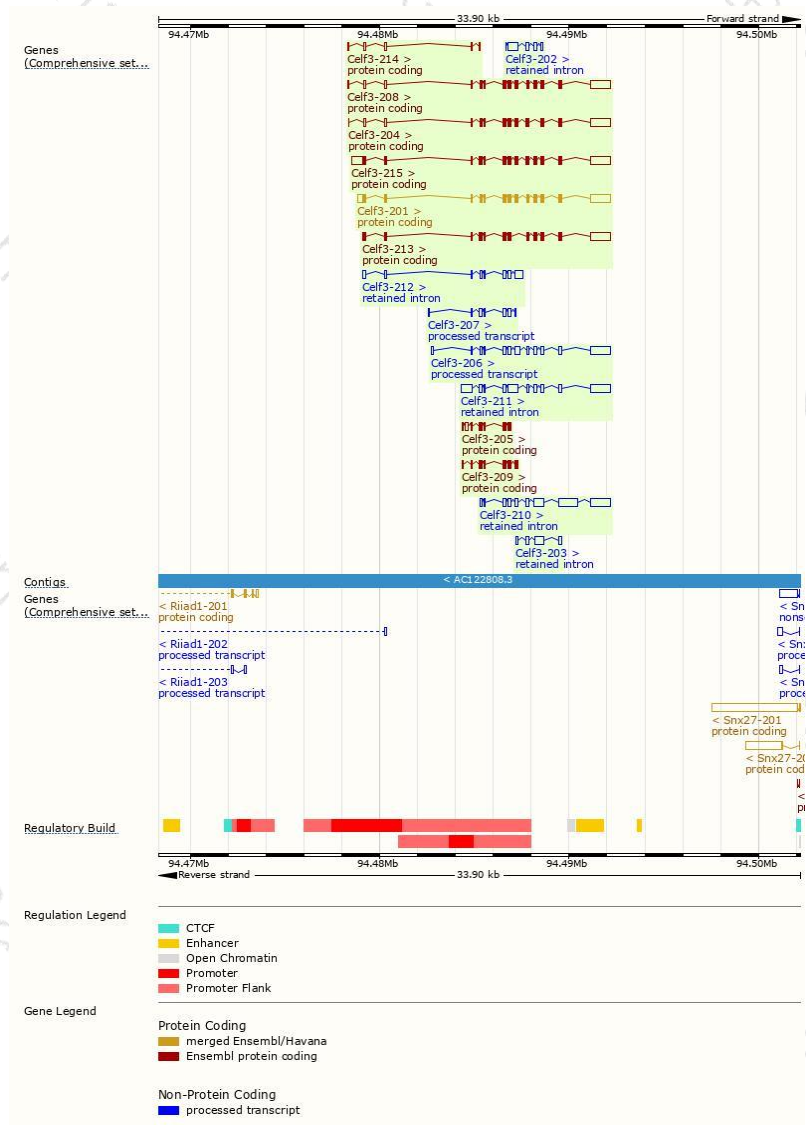
The gene has 15 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Celf3-215	ENSMUST00000200342.4	3173	494aa	Protein coding	CCDS79972	Q8CIN6	TSL:1 GENCODE basic
Celf3-201	ENSMUST0000029784.9	2744	465aa	Protein coding	CCDS38536	Q8CIN6	TSL:1 GENCODE basic APPRIS P1
Celf3-208	ENSMUST00000198316.4	2505	389aa	Protein coding	CCDS79974	A0A0G2JDL2	TSL:1 GENCODE basic
Celf3-204	ENSMUST00000197558.4	2414	370aa	Protein coding	CCDS79973	A0A0G2JGX2	TSL:1 GENCODE basic
Celf3-213	ENSMUST00000199775.4	2351	416aa	Protein coding	-	A0A0G2JGE2	TSL:5 GENCODE basic
Celf3-205	ENSMUST00000197677.4	779	182aa	Protein coding	-	A0A0G2JFA4	CDS 3' incomplete TSL:3
Celf3-209	ENSMUST00000198384.2	726	231aa	Protein coding	-	A0A0G2JDX3	CDS 3' incomplete TSL:5
Celf3-214	ENSMUST00000199884.4	366	31aa	Protein coding	-	A0A0G2JF00	CDS 3' incomplete TSL:2
Celf3-206	ENSMUST00000197699.4	2441	No protein	Processed transcript	-	-	TSL:1
Celf3-207	ENSMUST00000198067.4	669	No protein	Processed transcript	-	-	TSL:5
Celf3-210	ENSMUST00000198796.4	3363	No protein	Retained intron	-	-	TSL:1
Celf3-211	ENSMUST00000199148.4	2932	No protein	Retained intron	-	-	TSL:1
Celf3-212	ENSMUST00000199159.4	1193	No protein	Retained intron	-	-	TSL:1
Celf3-202	ENSMUST00000196985.4	889	No protein	Retained intron	-	-	TSL:5
Celf3-203	ENSMUST00000197033.1	855	No protein	Retained intron	-	-	TSL:5

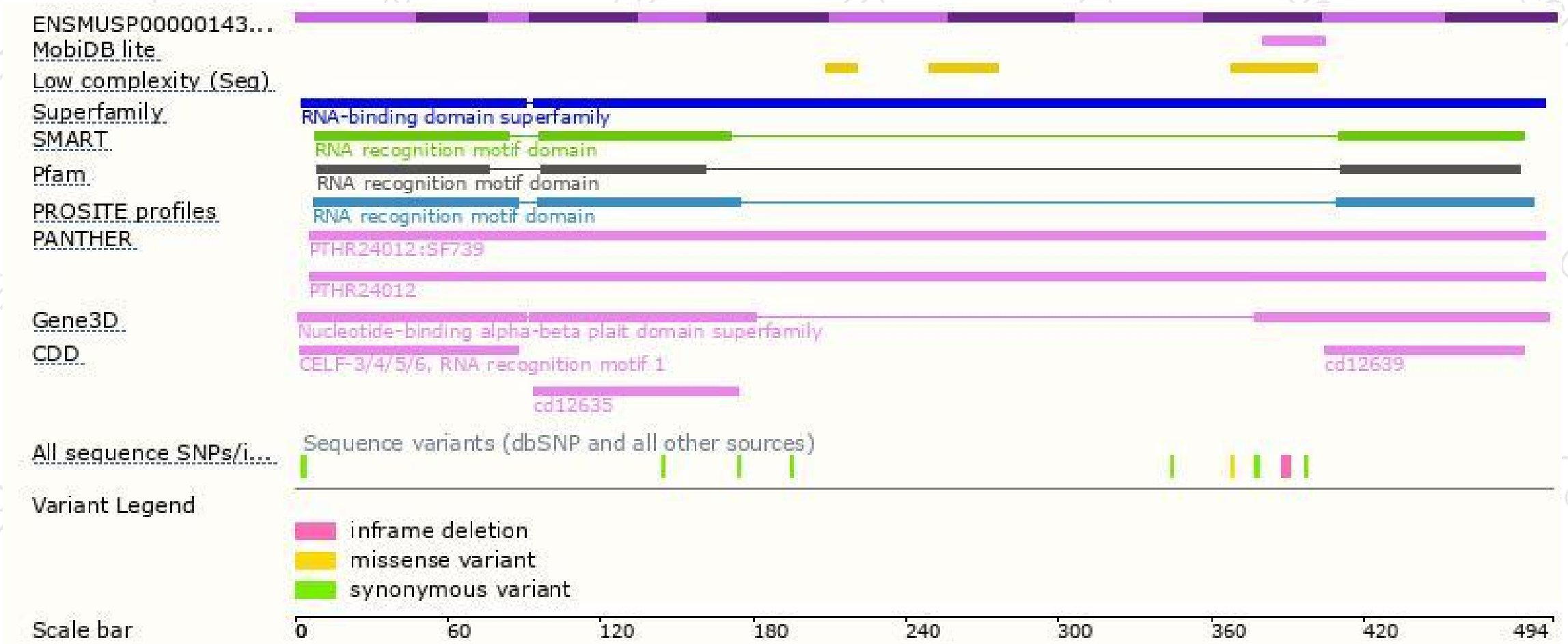
The strategy is based on the design of *Celf3-215* transcript,the transcription is shown below:



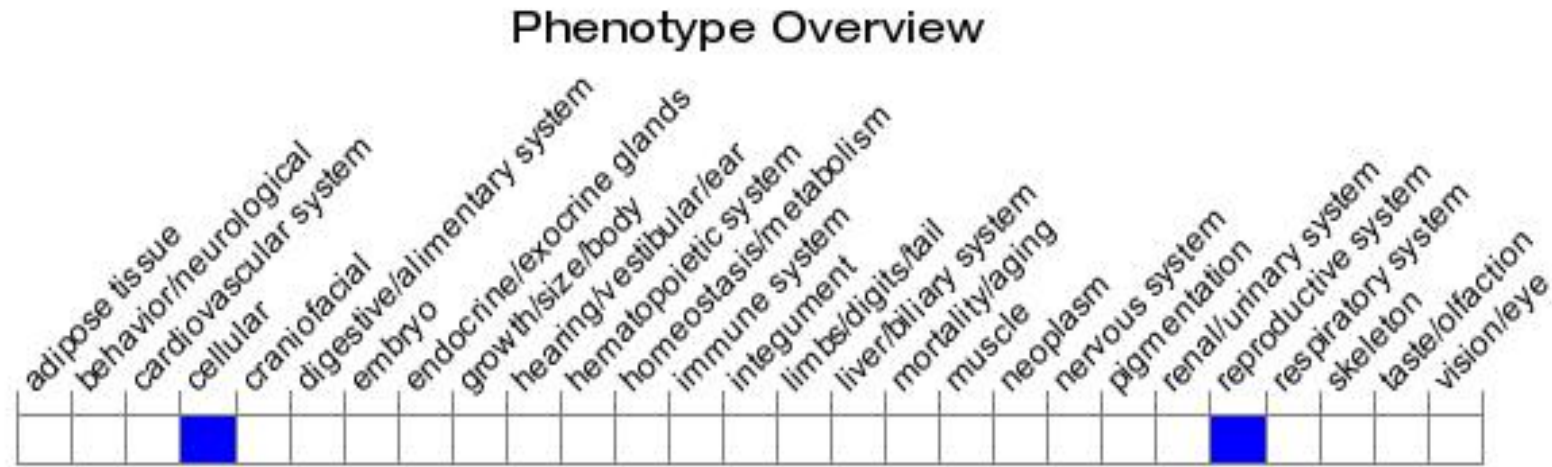
Genomic location distribution



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, male mice homozygous for a null mutation display reduced sperm counts and motility but are fertile.

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

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