

Celf2 Cas9-CKO Strategy

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Project Overview

Project Name

Celf2

Project type

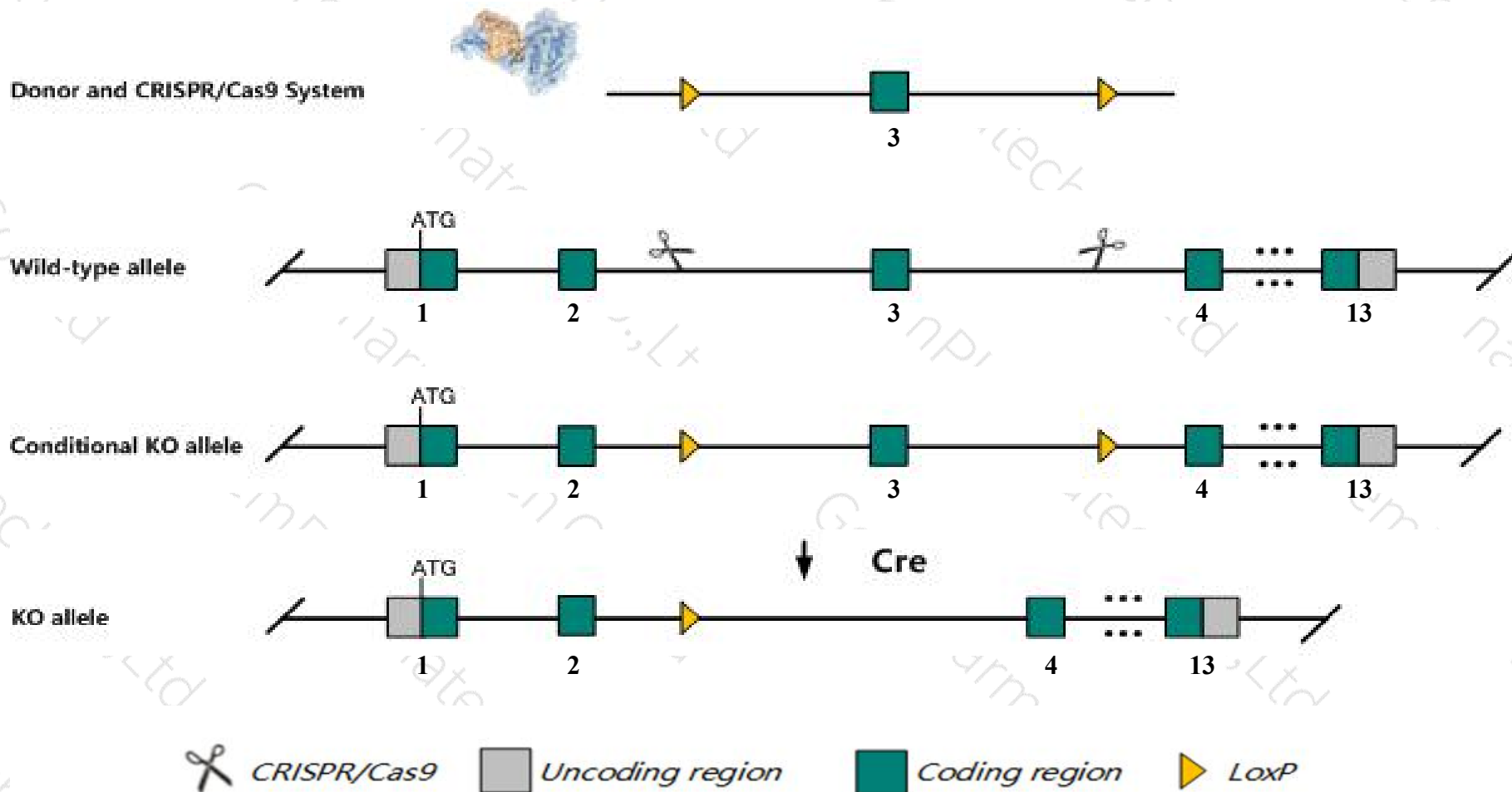
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Celf2* gene. The schematic diagram is as follows:



Technical routes

- The *Celf2* gene has 28 transcripts. According to the structure of *Celf2* gene, exon3 of *Celf2*-204 (ENSMUST00000114924.9) transcript is recommended as the knockout region. The region contains 83bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Celf2* gene. The brief process is as follows: gRNA was transcribed in vitro, donor was constructed. Cas9, gRNA and Donor 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.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- The *Celf2* gene is located on the Chr2. 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.
- Transcript *Celf2*-216&220&222 may not be affected.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risk of loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Celf2 CUGBP, Elav-like family member 2 [Mus musculus (house mouse)]

Gene ID: 14007, updated on 31-Jan-2019

Summary



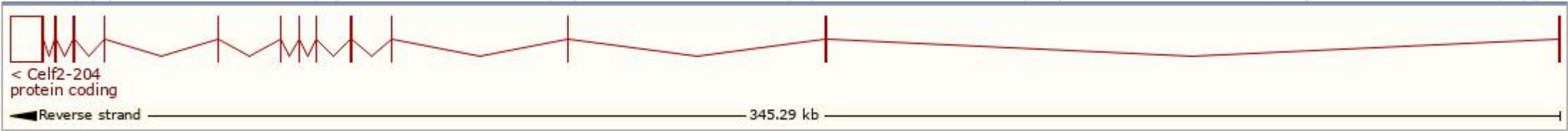
Official Symbol	Celf2 provided by MGI
Official Full Name	CUGBP, Elav-like family member 2 provided by MGI
Primary source	MGI:MGI:1338822
See related	Ensembl:ENSMUSG00000002107
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	B230218O03, B230345P09Rik, C88023, CELF-2, CUG-BP2, Cugbp2, D230046B21Rik, Etr-3, Napor, Napor-2, mETR-3
Expression	Broad expression in CNS E18 (RPKM 23.9), frontal lobe adult (RPKM 20.6) and 15 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

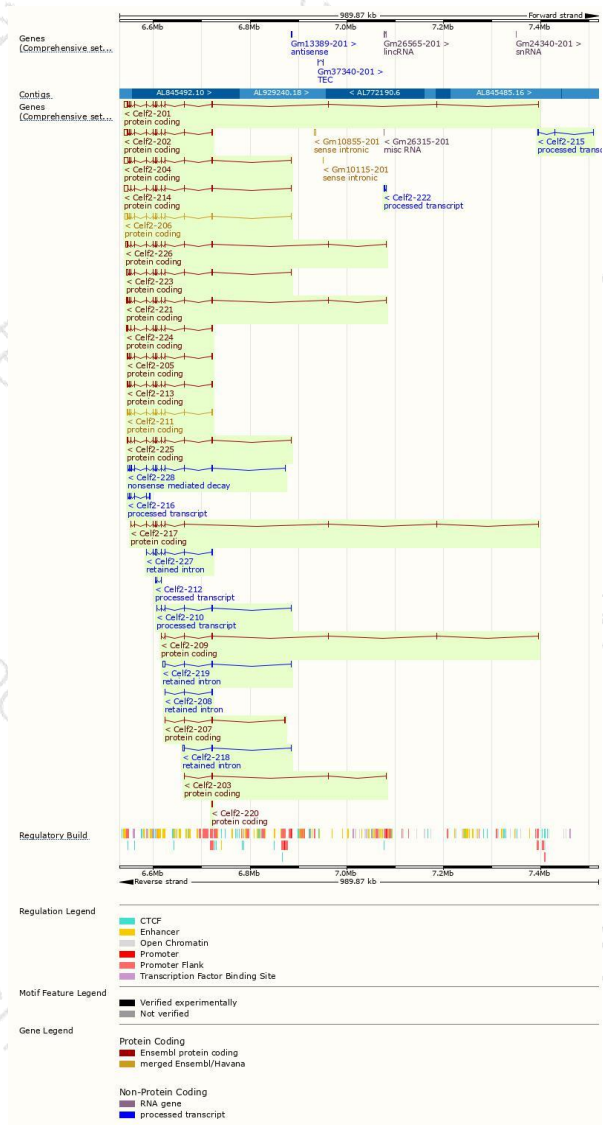
The gene has 28 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Celf2-214	ENSMUST00000170438.7	8856	478aa	Protein coding	CCDS50493	E9QA47	TSL:5 GENCODE basic
Celf2-204	ENSMUST00000114924.9	8798	525aa	Protein coding	CCDS50494	Q9Z0H4	TSL:1 GENCODE basic
Celf2-201	ENSMUST00000002176.12	7718	484aa	Protein coding	CCDS50491	Q9Z0H4	TSL:1 GENCODE basic APPRIS ALT1
Celf2-202	ENSMUST00000100429.10	7491	484aa	Protein coding	CCDS50491	Q9Z0H4	TSL:5 GENCODE basic APPRIS ALT1
Celf2-206	ENSMUST00000114934.10	5470	525aa	Protein coding	CCDS50494	Q9Z0H4	TSL:1 GENCODE basic
Celf2-226	ENSMUST00000183209.7	3852	472aa	Protein coding	CCDS59632	S4R1S7	TSL:1 GENCODE basic
Celf2-221	ENSMUST00000182706.7	2525	520aa	Protein coding	CCDS59633	Q9Z0H4	TSL:1 GENCODE basic
Celf2-211	ENSMUST00000142941.7	2338	490aa	Protein coding	CCDS50492	Q9Z0H4	TSL:5 GENCODE basic APPRIS P4
Celf2-213	ENSMUST00000150624.8	2332	488aa	Protein coding	CCDS84468	Q9Z0H4	TSL:1 GENCODE basic APPRIS ALT1
Celf2-224	ENSMUST00000182879.7	2223	440aa	Protein coding	CCDS79729	A0A0R4J2B0	TSL:1 GENCODE basic
Celf2-205	ENSMUST00000114927.8	1721	488aa	Protein coding	CCDS84468	Q9Z0H4	TSL:5 GENCODE basic APPRIS ALT1
Celf2-223	ENSMUST00000182851.7	3587	508aa	Protein coding	-	Q9Z0H4	TSL:1 GENCODE basic APPRIS ALT2
Celf2-225	ENSMUST00000183091.7	2177	460aa	Protein coding	-	S4R2U7	TSL:5 GENCODE basic
Celf2-217	ENSMUST00000182404.7	1024	276aa	Protein coding	-	S4R2S7	CDS 3' incomplete TSL:5
Celf2-209	ENSMUST00000137733.8	630	134aa	Protein coding	-	S4R2L5	CDS 3' incomplete TSL:3
Celf2-203	ENSMUST00000114923.2	529	159aa	Protein coding	-	A3KGT0	TSL:3 GENCODE basic
Celf2-207	ENSMUST00000123142.2	402	92aa	Protein coding	-	S4R2J2	CDS 3' incomplete TSL:5
Celf2-220	ENSMUST00000182657.1	331	45aa	Protein coding	-	S4R2U1	CDS 3' incomplete TSL:1
Celf2-228	ENSMUST00000183984.7	1996	443aa	Nonsense mediated decay	-	V9GX43	CDS 5' incomplete TSL:5
Celf2-222	ENSMUST00000182749.1	1967	No protein	Processed transcript	-	-	TSL:5
Celf2-216	ENSMUST00000182355.1	1240	No protein	Processed transcript	-	-	TSL:1
Celf2-210	ENSMUST00000138347.8	923	No protein	Processed transcript	-	-	TSL:5
Celf2-215	ENSMUST00000182037.1	769	No protein	Processed transcript	-	-	TSL:3
Celf2-212	ENSMUST00000148321.8	405	No protein	Processed transcript	-	-	TSL:5
Celf2-219	ENSMUST00000182560.7	4802	No protein	Retained intron	-	-	TSL:2
Celf2-227	ENSMUST00000183269.7	4798	No protein	Retained intron	-	-	TSL:2
Celf2-218	ENSMUST00000182523.1	4143	No protein	Retained intron	-	-	TSL:2
Celf2-208	ENSMUST00000126742.1	2075	No protein	Retained intron	-	-	TSL:2

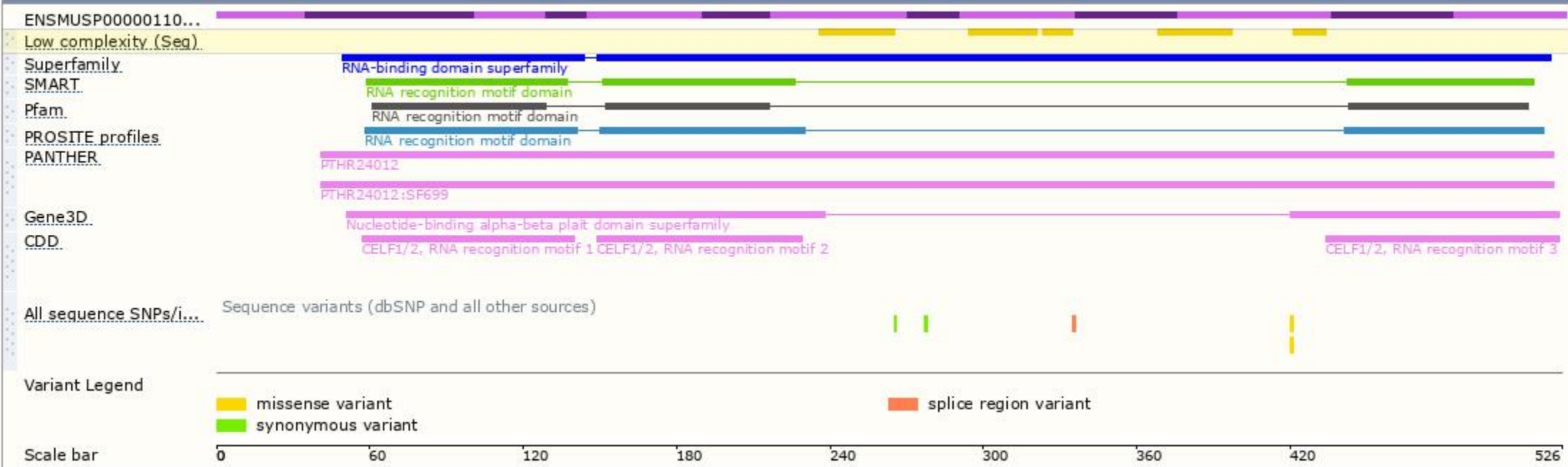
The strategy is based on the design of *Celf2-204* transcript,The transcription is shown below



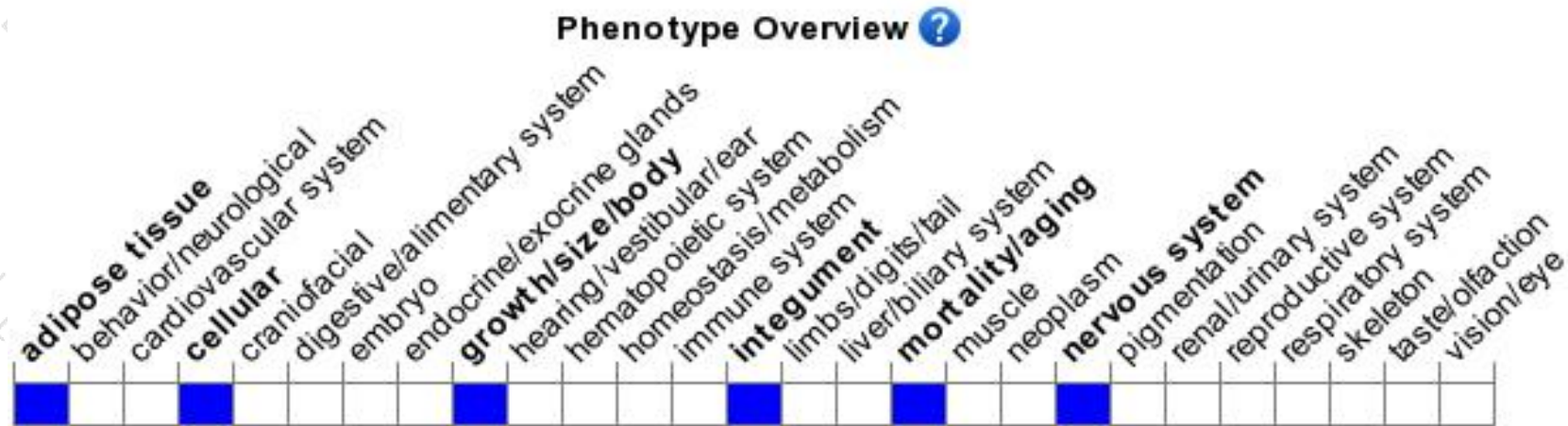
Genomic location distribution



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/>).

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

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