

E2f2 Cas9-CKO Strategy

Designer: Xiaojing Li

Reviewer: JiaYu

Design Date: 2020-6-10

Project Overview

Project Name

E2f2

Project type

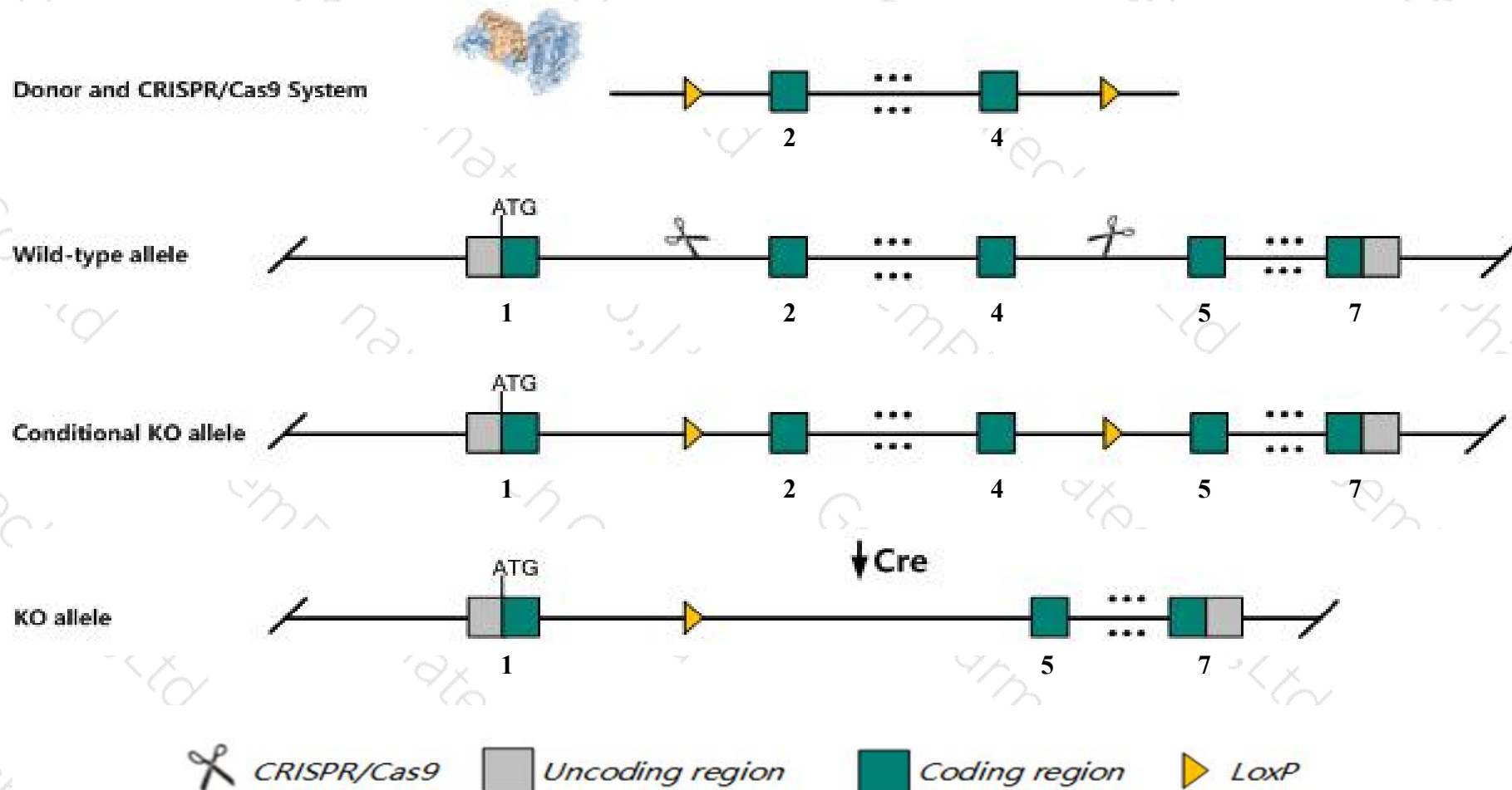
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *E2f2* gene. The schematic diagram is as follows:



Technical routes

- The *E2f2* gene has 2 transcripts. According to the structure of *E2f2* gene, exon2-exon4 of *E2f2-201* (ENSMUST00000061721.5) transcript is recommended as the knockout region. The region contains 485bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *E2f2* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, mice homozygous for a null allele exhibit premature death with signs of inflammatory and autoimmune disorders such as increased memory t cells, enlarged spleen, glomerulonephritis, inflamed liver, inflamed lung, increased double stranded dna antibodies, hair loss, and erythema.
- The *E2f2* gene is located on the Chr4. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

E2f2 E2F transcription factor 2 [Mus musculus (house mouse)]

Gene ID: 242705, updated on 13-Mar-2020

Summary



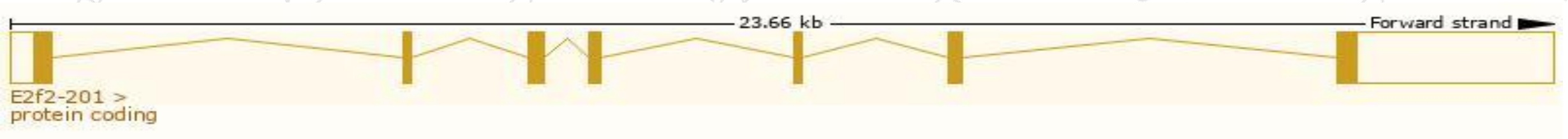
Official Symbol	E2f2 provided by MGI
Official Full Name	E2F transcription factor 2 provided by MGI
Primary source	MGI:MGI:1096341
See related	Ensembl:ENSMUSG00000018983
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	E2F-2
Expression	Biased expression in thymus adult (RPKM 60.2), liver E14.5 (RPKM 28.6) and 10 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

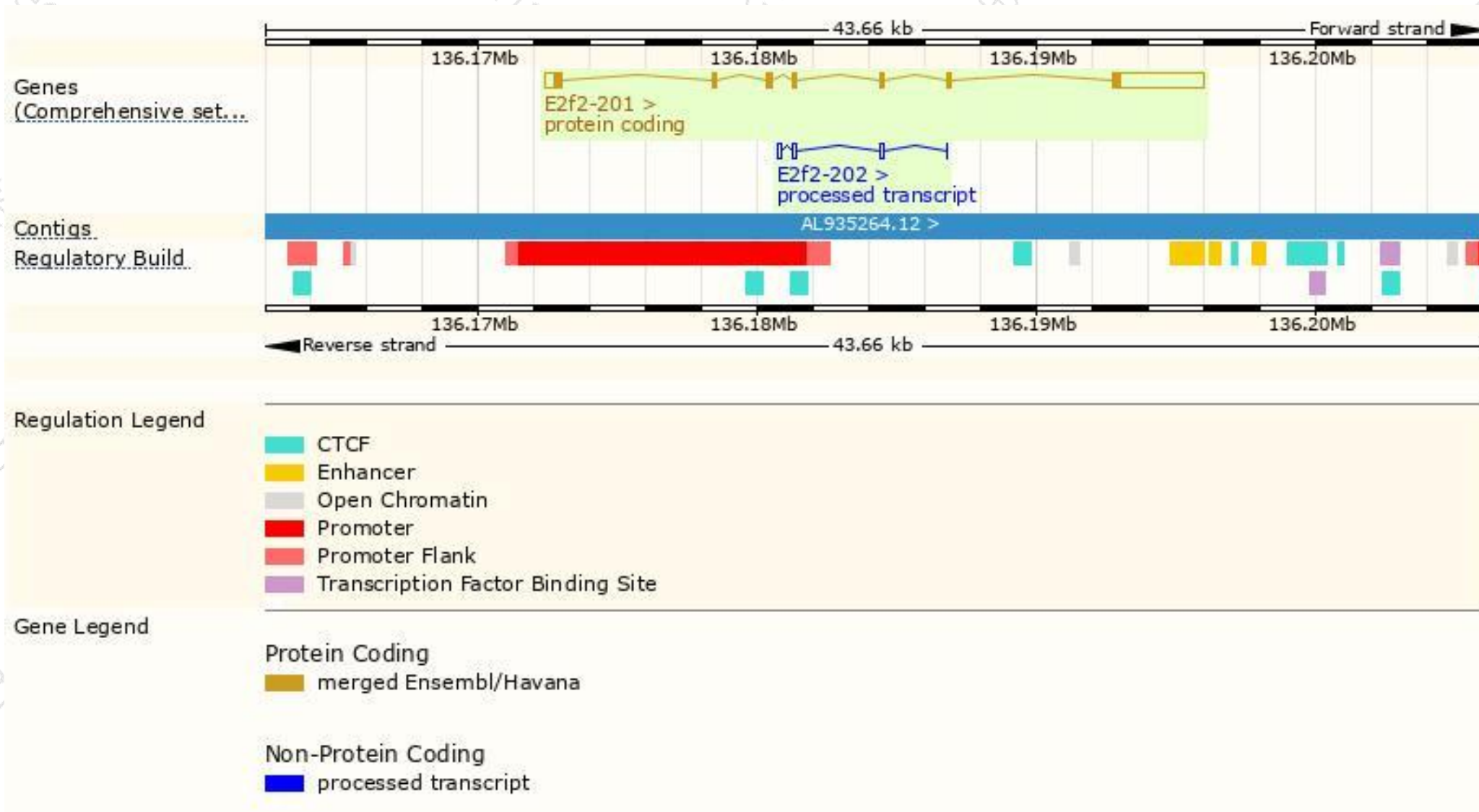
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
E2f2-201	ENSMUST00000061721.5	4739	443aa	Protein coding	CCDS18801	P56931	TSL:1 GENCODE basic APPRIS P1
E2f2-202	ENSMUST00000149750.1	426	No protein	Processed transcript	-	-	TSL:5

The strategy is based on the design of *E2f2-201* transcript,the transcription is shown below:



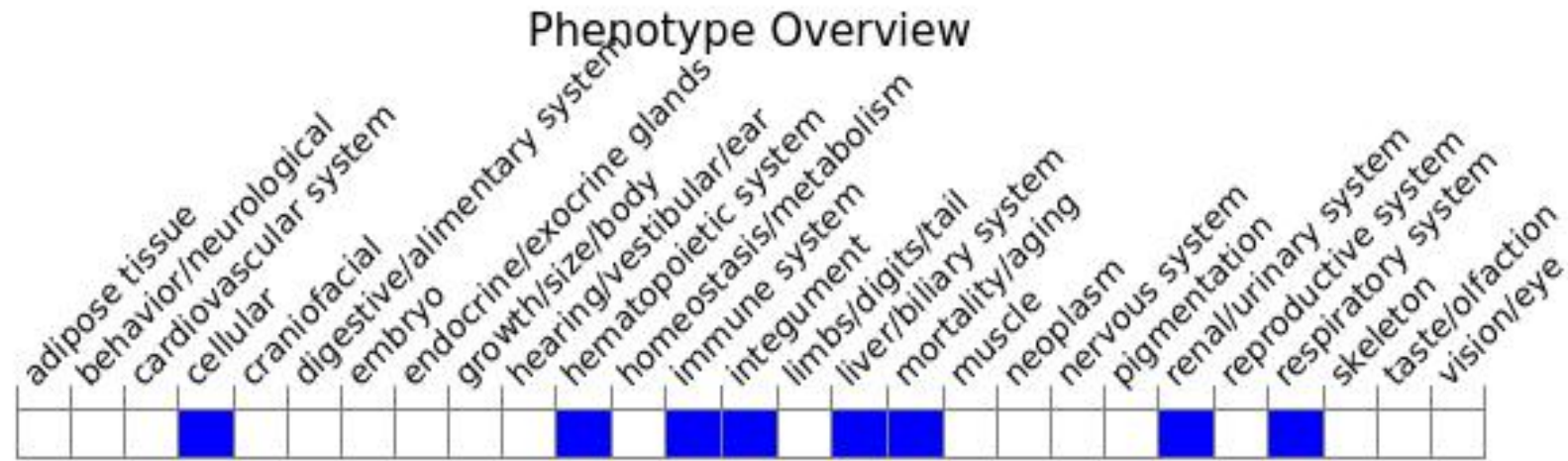
Genomic location distribution



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 null allele exhibit premature death with signs of inflammatory and autoimmune disorders such as increased memory T cells, enlarged spleen, glomerulonephritis, inflamed liver, inflamed lung, increased double stranded DNA antibodies, hair loss, and erythema.

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

Tel: 400-9660890

