

E2f7 Cas9-KO Strategy

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Project Overview

Project Name

E2f7

Project type

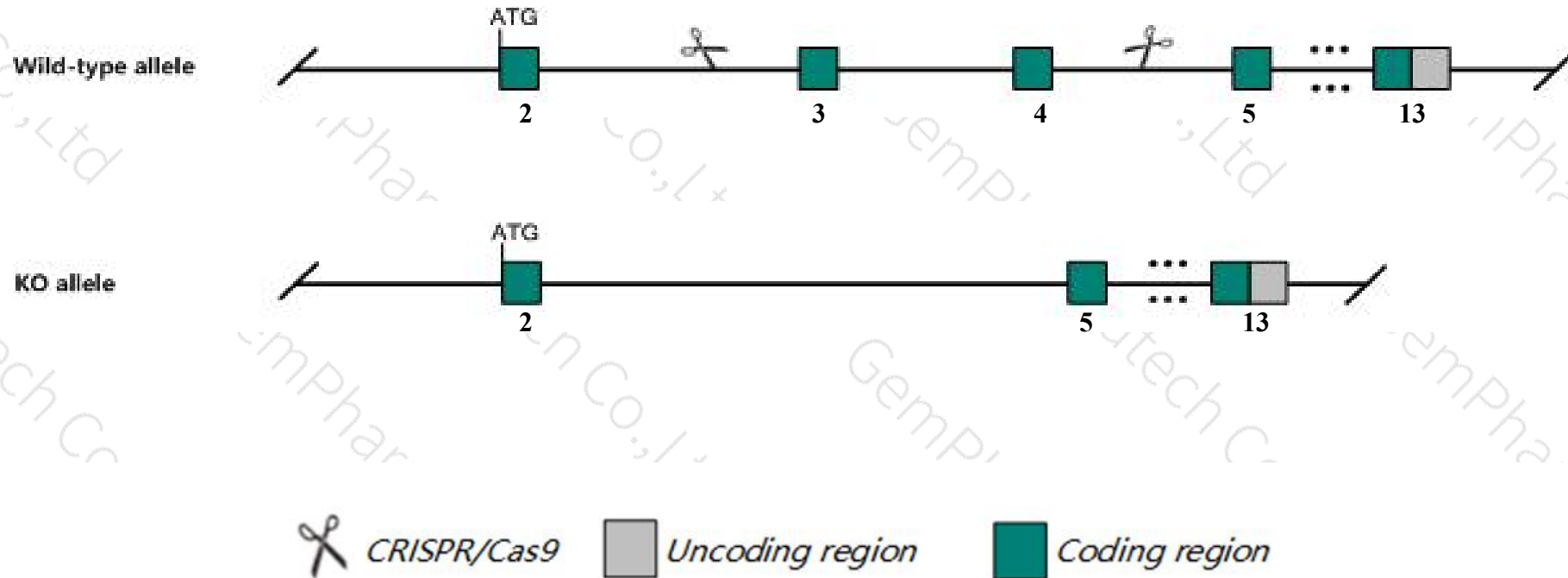
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *E2f7* gene. The schematic diagram is as follows:



- The *E2f7* gene has 9 transcripts. According to the structure of *E2f7* gene, exon3-exon4 of *E2f7-201* (ENSMUST00000073781.11) transcript is recommended as the knockout region. The region contains 448bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *E2f7* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Mice homozygous for a knock-out allele develop normally through puberty and survive to old age.
- The *E2f7* gene is located on the Chr10. 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)

E2f7 E2F transcription factor 7 [*Mus musculus* (house mouse)]

Gene ID: 52679, updated on 24-Oct-2019

Summary

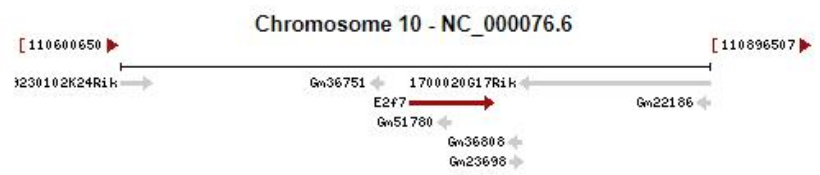
- Official Symbol** E2f7 provided by [MGI](#)
- Official Full Name** E2F transcription factor 7 provided by [MGI](#)
- Primary source** [MGI:MGI:1289147](#)
- See related** [Ensembl:ENSMUSG00000020185](#)
- Gene type** protein coding
- RefSeq status** VALIDATED
- Organism** [Mus musculus](#)
- Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
- Also known as** E2F-7; D10Erd739e; A630014C11Rik
- Expression** Biased expression in CNS E11.5 (RPKM 3.1), limb E14.5 (RPKM 2.4) and 14 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 10 D1; 10 57.74 cM [See E2f7 in Genome Data Viewer](#)

Exon count: 14

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	10	NC_000076.6 (110745439..110787384)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	10	NC_000076.5 (110182521..110224440)

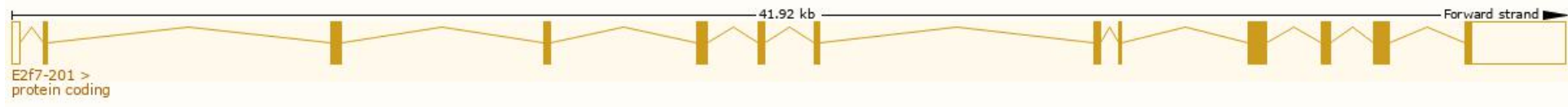


Transcript information (Ensembl)

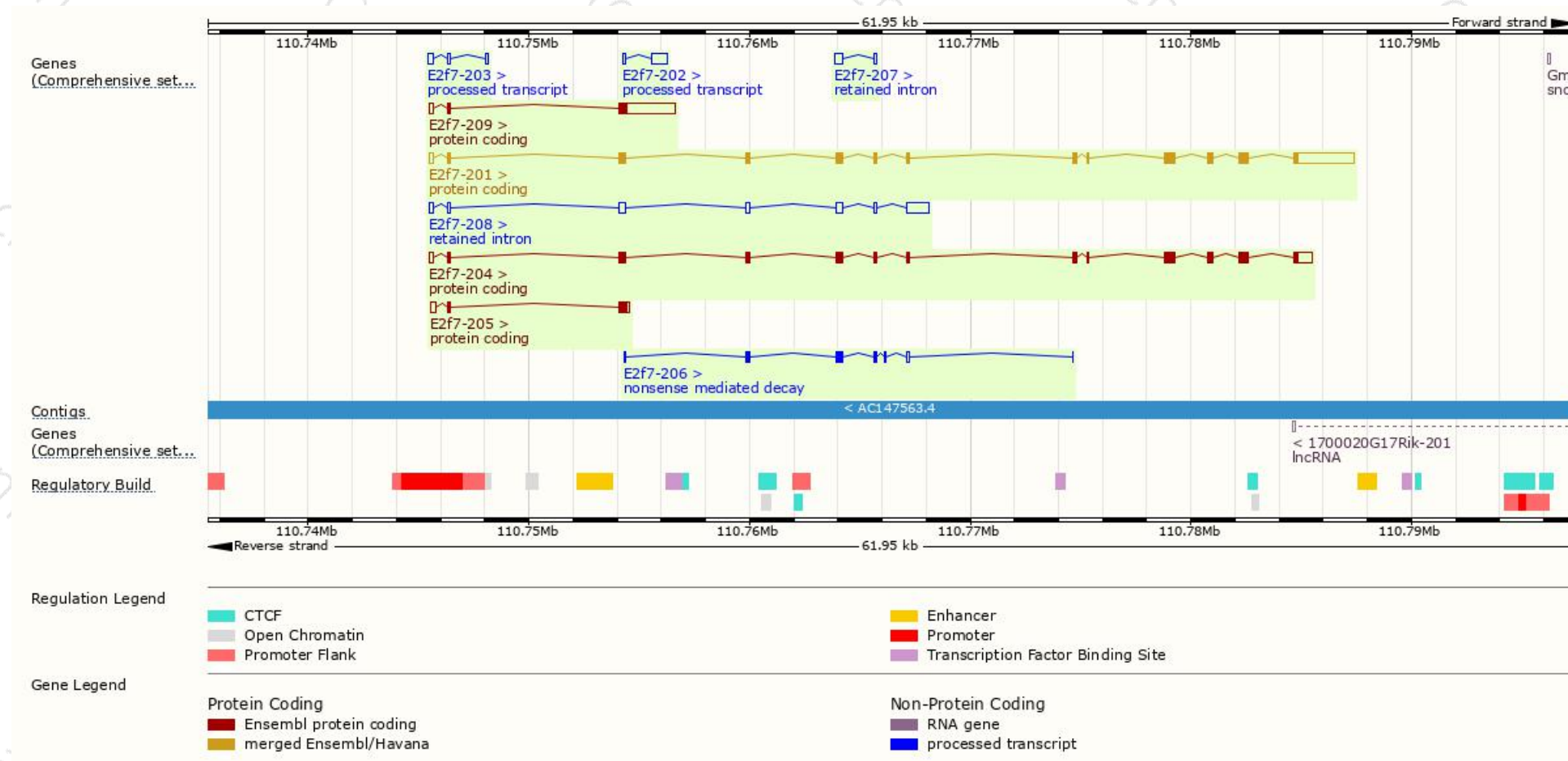
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
E2f7-201	ENSMUST00000073781.11	5473	904aa	Protein coding	CCDS36055	Q6S7F2	TSL:1 GENCODE basic APPRIS P1
E2f7-204	ENSMUST00000173471.7	3567	904aa	Protein coding	CCDS36055	Q6S7F2	TSL:1 GENCODE basic APPRIS P1
E2f7-209	ENSMUST00000174857.7	2865	140aa	Protein coding	-	Q8BQ55	TSL:1 GENCODE basic
E2f7-205	ENSMUST00000173634.1	827	140aa	Protein coding	-	Q8BQ55	TSL:2 GENCODE basic
E2f7-206	ENSMUST00000173948.1	817	219aa	Nonsense mediated decay	-	G3UYD4	CDS 5' incomplete TSL:5
E2f7-202	ENSMUST00000172574.1	811	No protein	Processed transcript	-	-	TSL:3
E2f7-203	ENSMUST00000173294.7	438	No protein	Processed transcript	-	-	TSL:3
E2f7-208	ENSMUST00000174810.7	2226	No protein	Retained intron	-	-	TSL:1
E2f7-207	ENSMUST00000174593.1	501	No protein	Retained intron	-	-	TSL:3

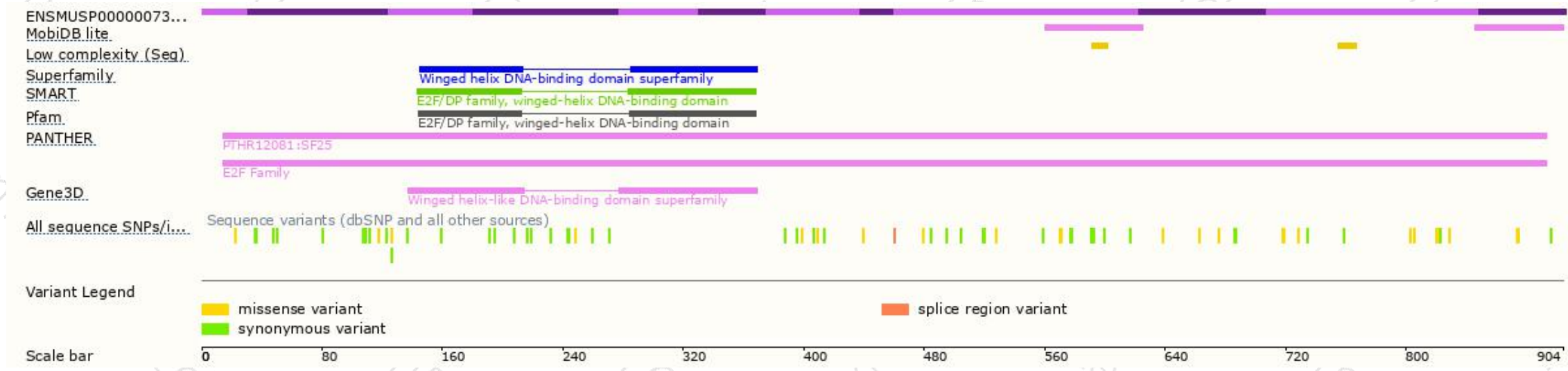
The strategy is based on the design of *E2f7-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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