

E2f1 Cas9-KO Strategy

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Project Overview

Project Name	<i>E2f1</i>
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Project type	Cas9-KO
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Strain background	C57BL/6JGpt
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Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *E2f1* gene. The schematic diagram is as follows:



- The *E2f1* gene has 2 transcripts. According to the structure of *E2f1* gene, exon2-exon3 of *E2f1-201* (ENSMUST00000000894.5) transcript is recommended as the knockout region. The region contains 311bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *E2f1* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Homozygous mutants show defective T lymphocyte development, impaired pancreatic growth and beta cell function, altered glucose homeostasis, testicular atrophy, salivary gland and adipose tissue defects, and increased tumor induction.
- The *E2f1* 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.
- 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)

E2f1 E2F transcription factor 1 [Mus musculus (house mouse)]

Gene ID: 13555, updated on 7-Apr-2019

Summary



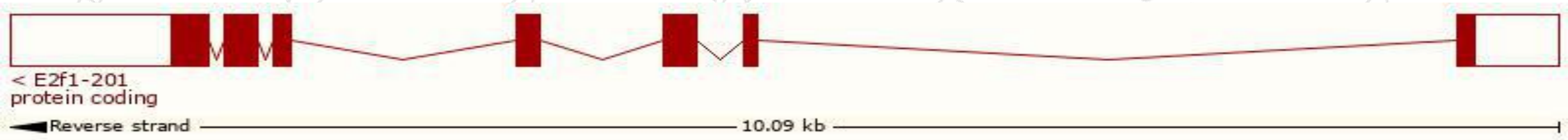
Official Symbol	E2f1 provided by MGI
Official Full Name	E2F transcription factor 1 provided by MGI
Primary source	MGI:MGI:101941
See related	Ensembl:ENSMUSG000000027490
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	E2F-1, Tg(Wnt1-cre)2Sor, mKIAA4009
Expression	Ubiquitous expression in CNS E11.5 (RPKM 15.6), liver E14.5 (RPKM 15.5) and 27 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

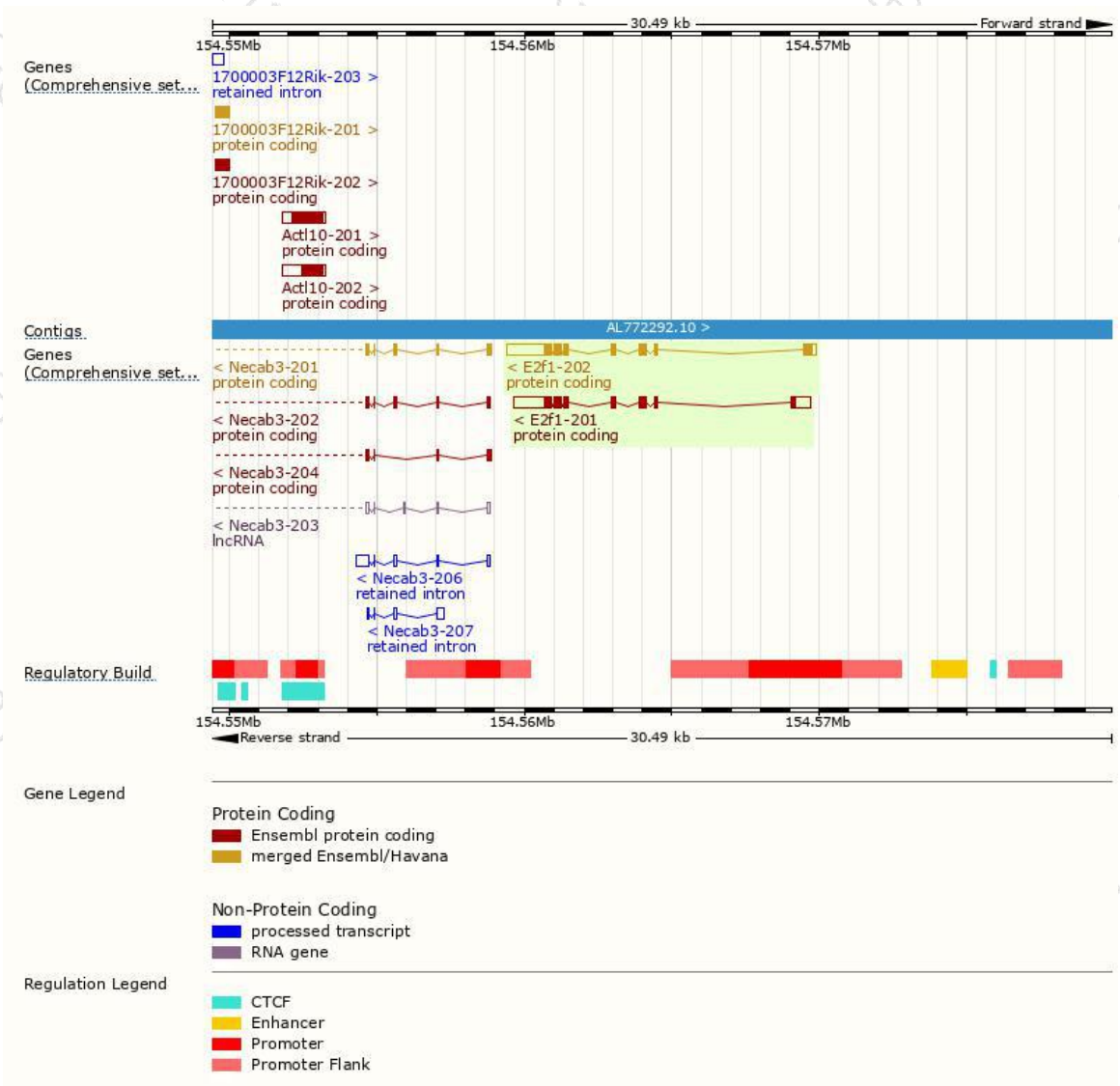
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
E2f1-201	ENSMUST00000000894.5	2755	385aa	Protein coding	CCDS71165	Q9CYB4	TSL:1 GENCODE basic APPRIS ALT2
E2f1-202	ENSMUST00000103145.10	2732	430aa	Protein coding	CCDS16935	Q547J6 Q61501	TSL:1 GENCODE basic APPRIS P3

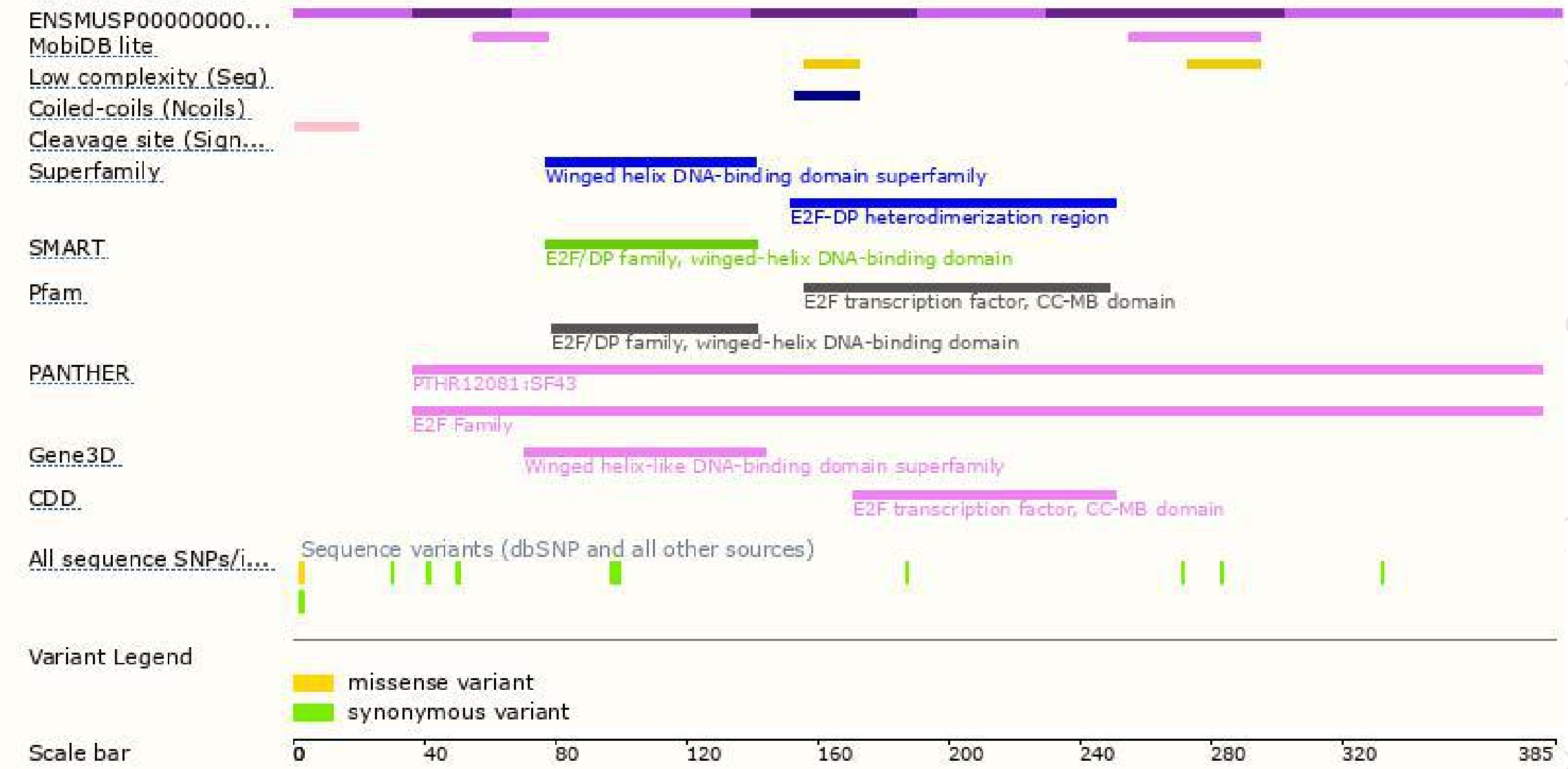
The strategy is based on the design of *E2f1-201* transcript,The transcription is shown below



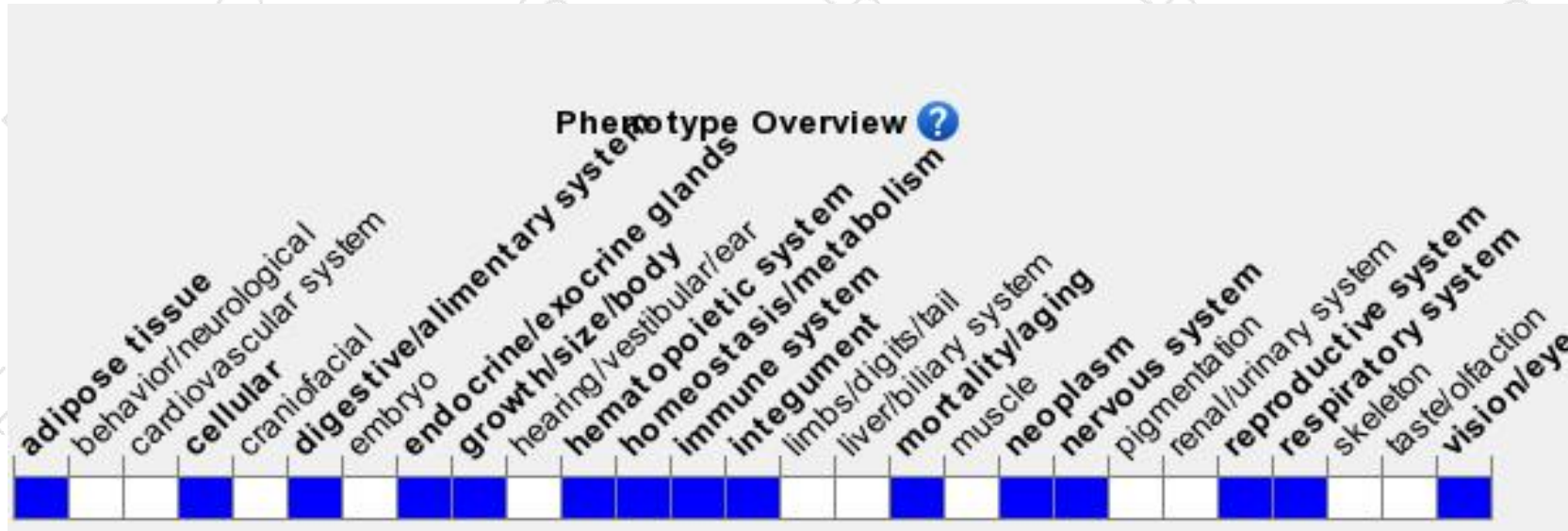
Genomic location distribution



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, Homozygous mutants show defective T lymphocyte development, impaired pancreatic growth and beta cell function, altered glucose homeostasis, testicular atrophy, salivary gland and adipose tissue defects, and increased tumor induction.

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

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