

# *E4f1* Cas9-KO Strategy

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**Reviewer: Jia Yu**

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# Project Overview

**Project Name**

*E4f1*

**Project type**

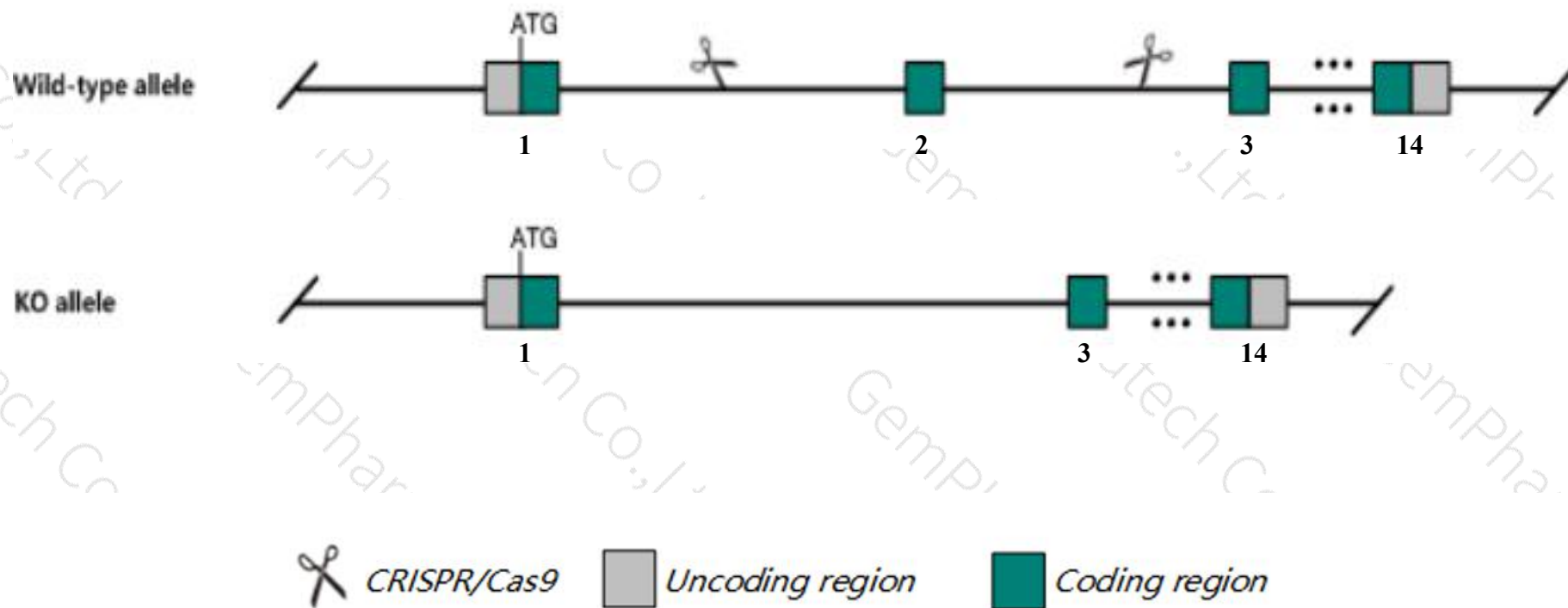
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *E4f1* gene. The schematic diagram is as follows:



➤ The *E4f1* gene has 8 transcripts. According to the structure of *E4f1* gene, exon2 of *E4f1-201*(ENSMUST00000056032.8) transcript is recommended as the knockout region. The region contains 152bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *E4f1* gene. The brief process is as follows: gRNA was transcribed in vitro. Cas9 and gRNA 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.

- According to the existing MGI data, homozygous null mice display early embryonic lethality with mitotic progression failure and increased apoptosis.
- The *E4f1* gene is located on the Chr17. 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)

## E4f1 E4F transcription factor 1 [Mus musculus (house mouse)]

Gene ID: 13560, updated on 13-Mar-2020

### Summary

**Official Symbol** E4f1 provided by MGI

**Official Full Name** E4F transcription factor 1 provided by MGI

**Primary source** MGI:MGI:109530

**See related** [Ensembl:ENSMUSG00000024137](#)

**Gene type** protein coding

**RefSeq status** REVIEWED

**Organism** [Mus musculus](#)

**Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

**Also known as** p120E4F, phi-AP3

**Summary** This gene encodes a member of the GLI-Kruppel zinc finger family. The encoded protein is likely to be multi-functional, with both adenovirus E1A-regulated transcription factor and ubiquitin E3 ligase activities, including roles in cell cycle regulation and the ubiquitination of p53. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Sep 2014]

**Expression** Ubiquitous expression in ovary adult (RPKM 25.6), thymus adult (RPKM 24.6) and 28 other tissues [See more](#)

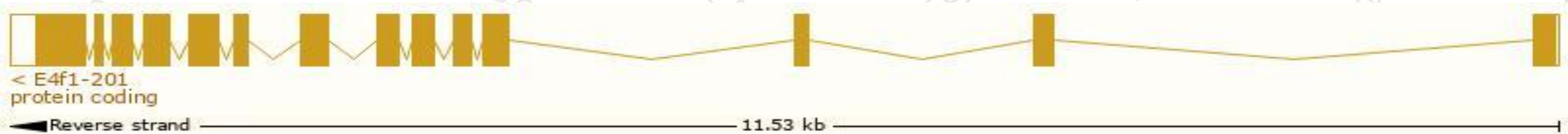
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

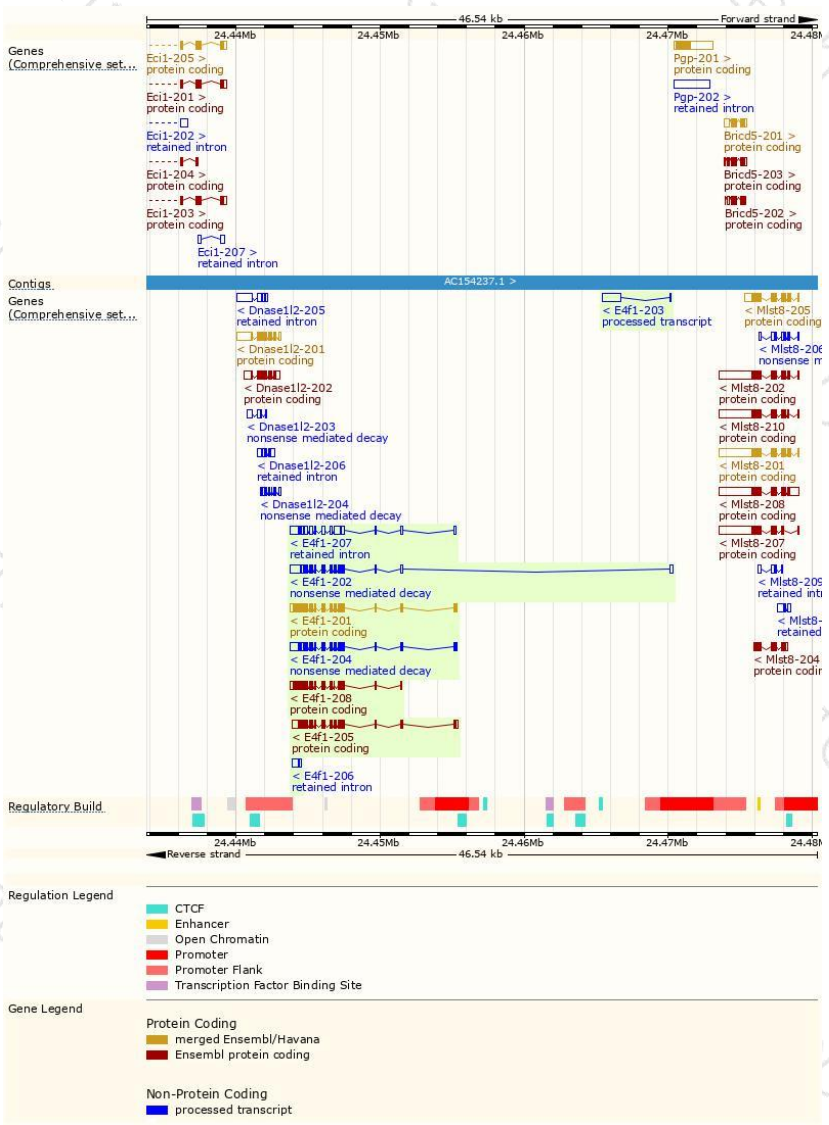
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
E4f1-201	<a href="#">ENSMUST0000056032.8</a>	2574	<a href="#">782aa</a>	Protein coding	<a href="#">CCDS28481</a>	<a href="#">Q8CCE9</a>	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P2
E4f1-205	<a href="#">ENSMUST00000226941.1</a>	2642	<a href="#">684aa</a>	Protein coding	-	<a href="#">Q8CCE9</a>	GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
E4f1-208	<a href="#">ENSMUST00000228882.1</a>	2226	<a href="#">675aa</a>	Protein coding	-	<a href="#">A0A2I3BR50</a>	CDS 5' incomplete
E4f1-202	<a href="#">ENSMUST00000226654.1</a>	2674	<a href="#">427aa</a>	Nonsense mediated decay	-	<a href="#">A0A2I3BRE9</a>	
E4f1-204	<a href="#">ENSMUST00000226754.1</a>	2552	<a href="#">586aa</a>	Nonsense mediated decay	-	<a href="#">A0A2I3BPE3</a>	
E4f1-203	<a href="#">ENSMUST00000226743.1</a>	1377	No protein	Processed transcript	-	-	
E4f1-207	<a href="#">ENSMUST00000227293.1</a>	2708	No protein	Retained intron	-	-	
E4f1-206	<a href="#">ENSMUST00000227241.1</a>	556	No protein	Retained intron	-	-	

The strategy is based on the design of *E4f1-201* transcript,the transcription is shown below:

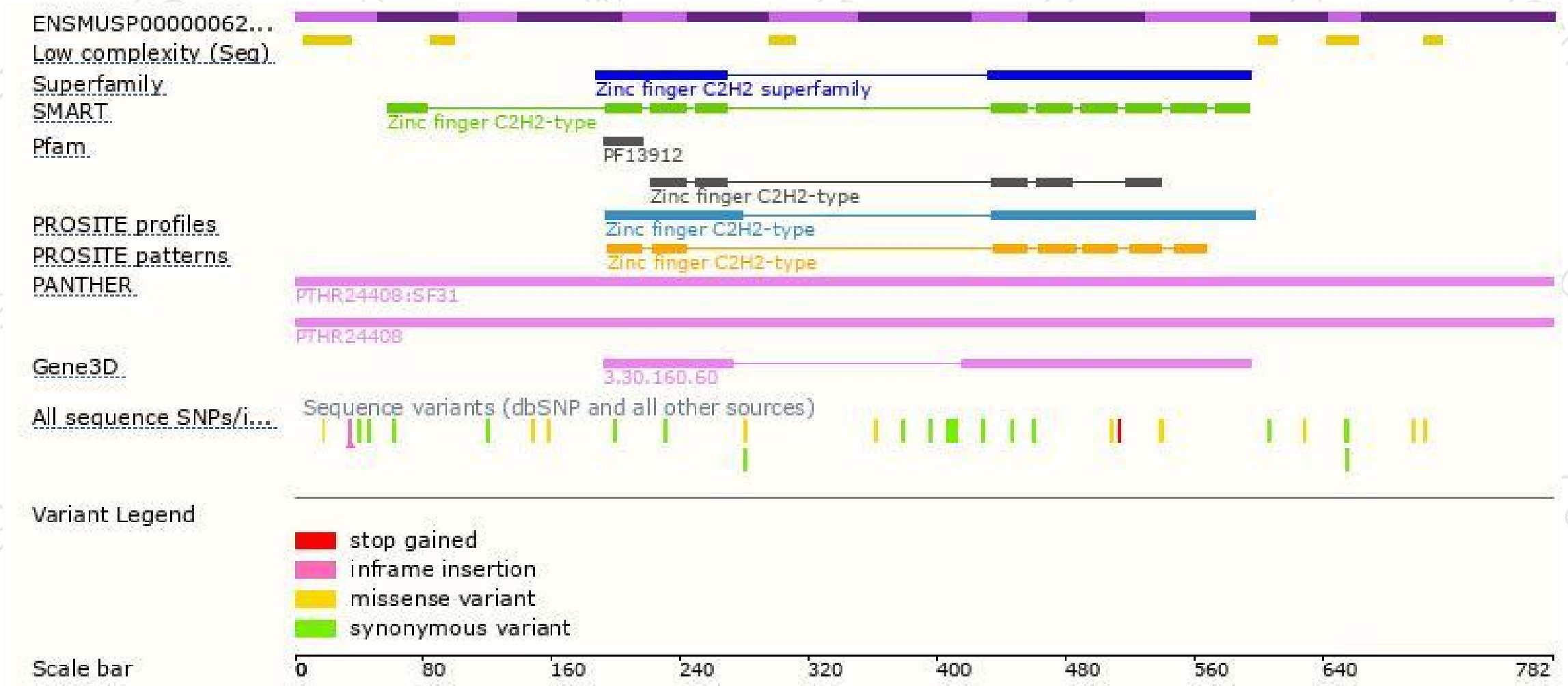


# Genomic location distribution

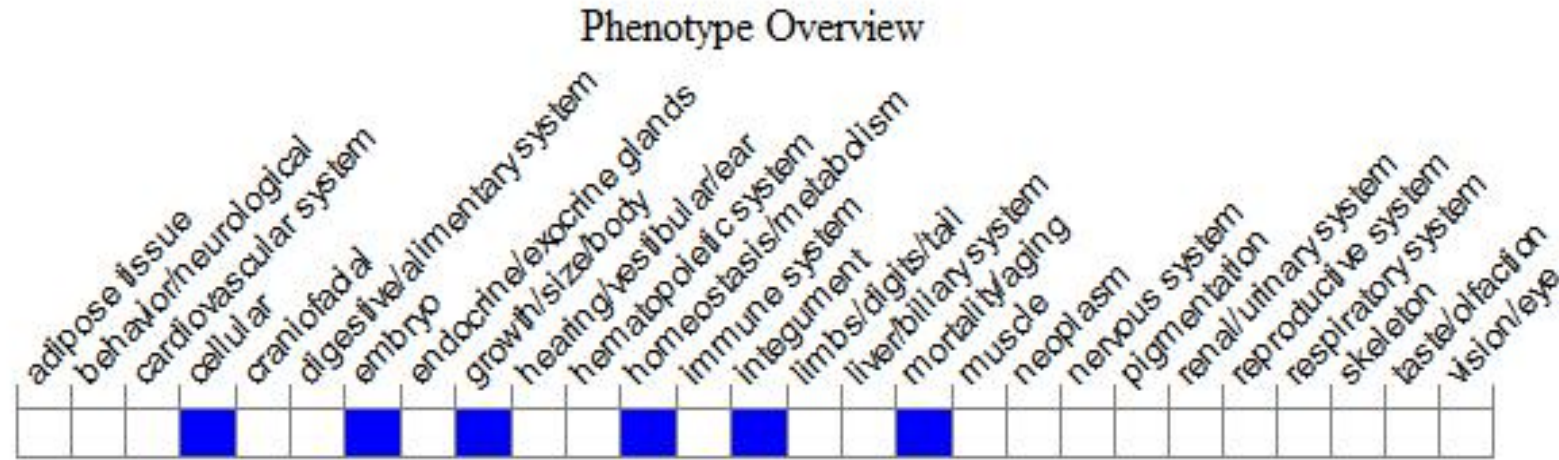




# Protein domain



# 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 null mice display early embryonic lethality with mitotic progression failure and increased apoptosis.

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

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