

Pou2f1 Cas9-KO Strategy

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Project Overview

Project Name

Pou2f1

Project type

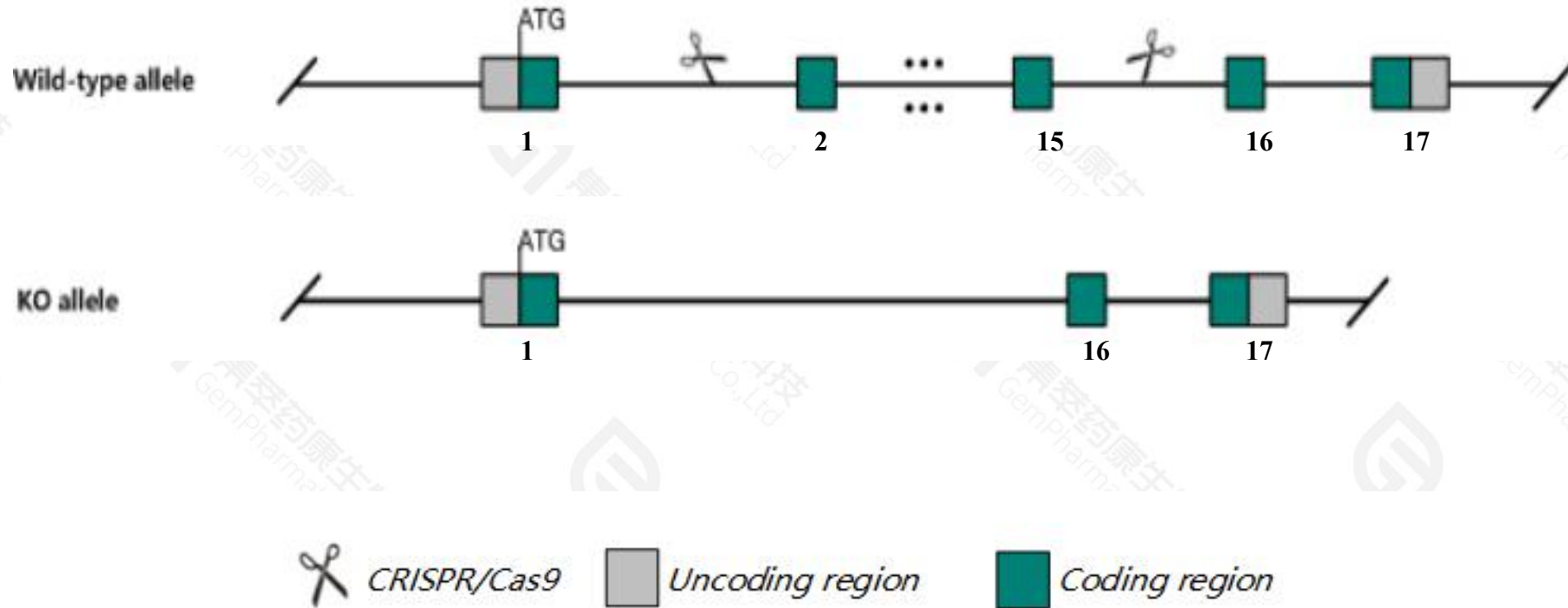
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pou2f1* gene. The schematic diagram is as follows:



- The *Pou2f1* gene has 18 transcripts. According to the structure of *Pou2f1* gene, exon2-exon15 of *Pou2f1*-208(ENSMUST00000160260.9) transcript is recommended as the knockout region. The region contains 1921bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pou2f1* gene. The brief process is as follows: CRISPR/Cas9 system 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 mutation of this gene results in prenatal lethality, with earlier lethality on either a 129/Sv or C57BL/6 background than a mixed 129/Sv and C57BL/6 background. Embryos show decreased erythropoiesis and partial penetrance of small lens size.
- The *Pou2f1* gene is located on the Chr1. 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)

Pou2f1 POU domain, class 2, transcription factor 1 [Mus musculus (house mouse)]

Gene ID: 18986, updated on 13-Mar-2020

Summary

Official Symbol Pou2f1 provided by [MGI](#)

Official Full Name POU domain, class 2, transcription factor 1 provided by [MGI](#)

Primary source [MGI:MGI:101898](#)

See related [Ensembl:ENSMUSG00000026565](#)

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 2810482H01Rik, NF-A1, Oct-1, Oct1, Otf-1, Otf1

Expression Ubiquitous expression in thymus adult (RPKM 4.4), whole brain E14.5 (RPKM 3.7) and 28 other tissues [See more](#)

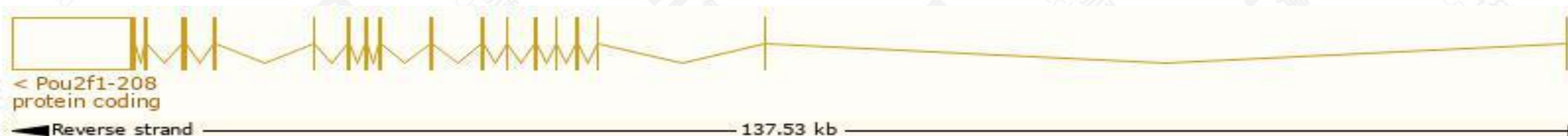
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

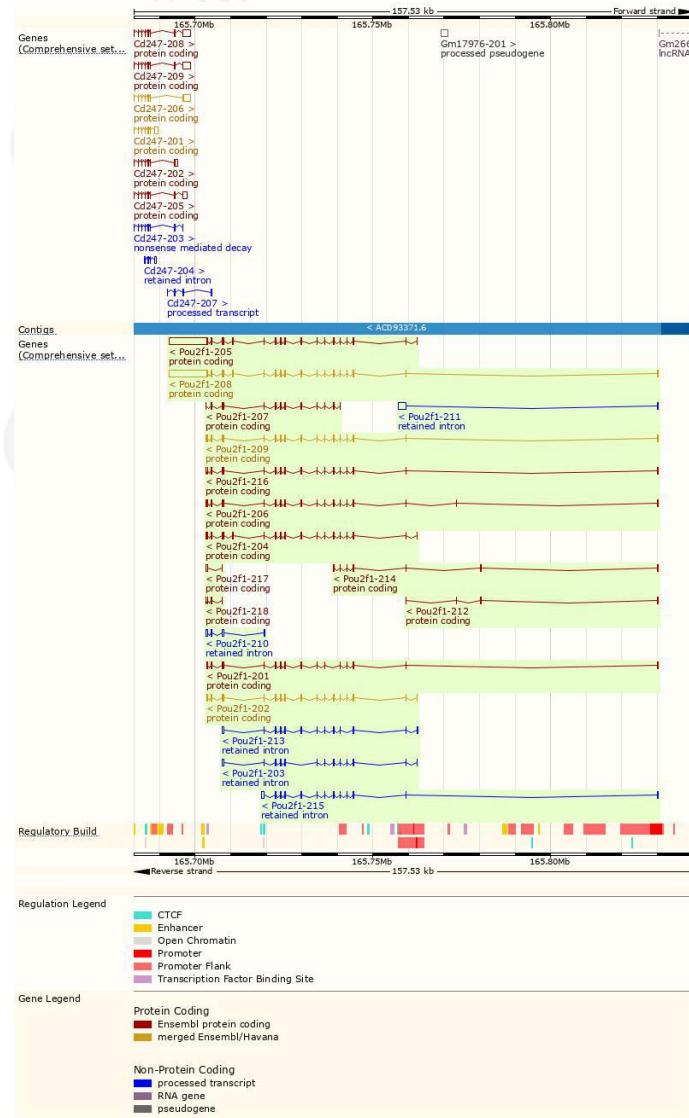
The gene has 18 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pou2f1-205	ENSMUST00000111427.8	13050	782aa	Protein coding	CCDS35761	F8VQL7	TSL:2 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
Pou2f1-208	ENSMUST00000160260.8	13022	793aa	Protein coding	CCDS35760	A0A0R4J1Z4	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 ALT2
Pou2f1-209	ENSMUST00000160908.7	2591	769aa	Protein coding	CCDS48430	E9Q6Z8	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 ALT2
Pou2f1-202	ENSMUST00000069609.11	2402	758aa	Protein coding	CCDS15444	P25425	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 P3
Pou2f1-206	ENSMUST00000111429.10	2679	746aa	Protein coding	-	P25425	TSL:5 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
Pou2f1-204	ENSMUST00000111426.10	2671	758aa	Protein coding	-	A0A0A0MQE0	TSL:5 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
Pou2f1-201	ENSMUST00000027850.14	2258	706aa	Protein coding	-	I1E4X2	TSL:5 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
Pou2f1-216	ENSMUST00000184643.7	2201	701aa	Protein coding	-	P25425	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 ALT2
Pou2f1-207	ENSMUST00000159212.8	1745	580aa	Protein coding	-	A0A0A0MQM6	CDS 5' incomplete TSL:5
Pou2f1-214	ENSMUST00000177358.7	626	163aa	Protein coding	-	H3BKX3	CDS 3' incomplete TSL:3
Pou2f1-217	ENSMUST00000184799.1	592	14aa	Protein coding	-	V9GXQ7	CDS 5' incomplete TSL:1
Pou2f1-212	ENSMUST00000176800.1	254	7aa	Protein coding	-	A0A1Y7VFH6	CDS 3' incomplete TSL:1
Pou2f1-218	ENSMUST00000194366.5	223	74aa	Protein coding	-	A0A0A6YWN1	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:1
Pou2f1-215	ENSMUST00000177472.1	2335	No protein	Retained intron	-	-	TSL:1
Pou2f1-213	ENSMUST00000176942.7	2206	No protein	Retained intron	-	-	TSL:1
Pou2f1-211	ENSMUST00000176101.1	2139	No protein	Retained intron	-	-	TSL:1
Pou2f1-203	ENSMUST00000082225.12	1859	No protein	Retained intron	-	-	TSL:1
Pou2f1-210	ENSMUST00000176004.1	1210	No protein	Retained intron	-	-	TSL:1

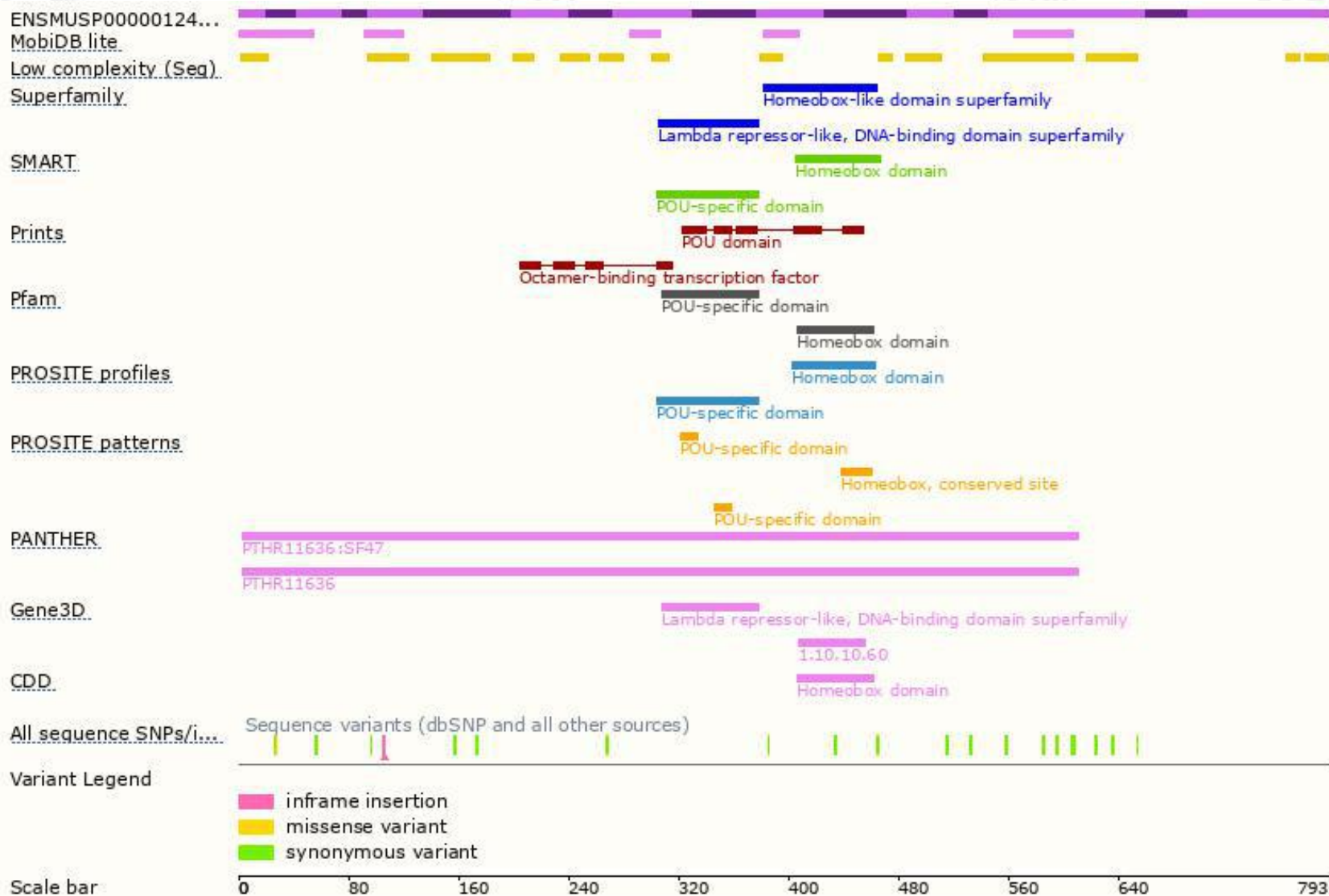
The strategy is based on the design of *Pou2f1-208* transcript, the transcription is shown below:



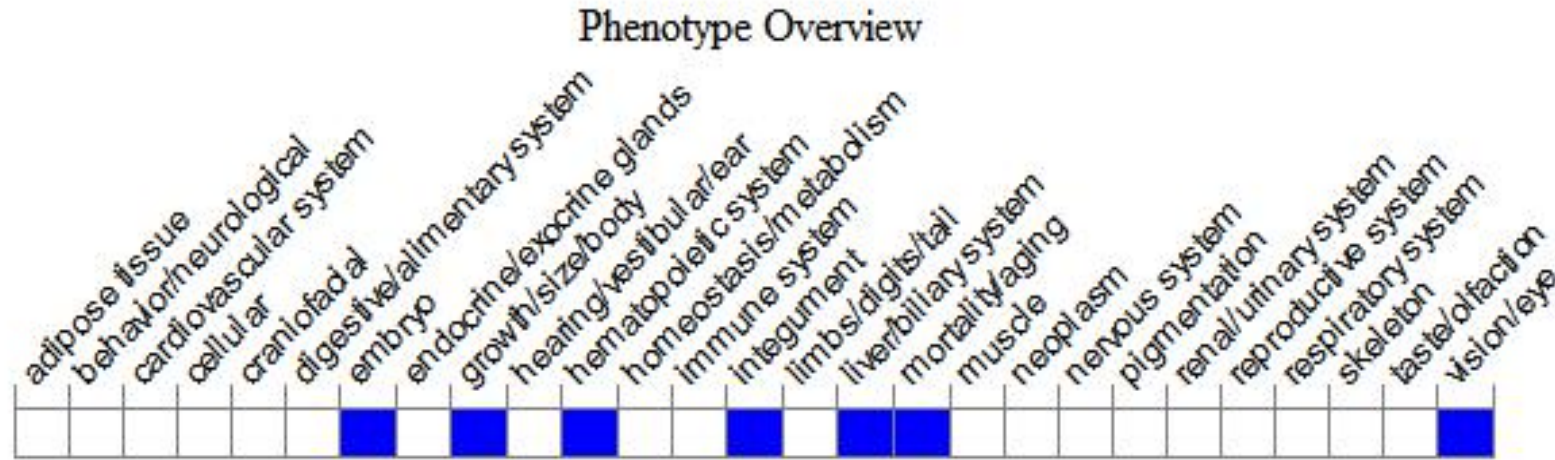
Genomic location distribution



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 mutation of this gene results in prenatal lethality, with earlier lethality on either a 129/Sv or C57BL/6 background than a mixed 129/Sv and C57BL/6 background. Embryos show decreased erythropoiesis and partial penetrance of small lens size.

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

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