

Fbxl4 Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Fbxl4

Project type

Cas9-KO

Strain background

C57BL/6J

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fbxl4* gene. The schematic diagram is as follows:



- The *Fbxl4* gene has 5 transcripts. According to the structure of *Fbxl4* gene, exon4 of *Fbxl4-201* (ENSMUST00000039234.9) transcript is recommended as the knockout region. The region contains 346bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fbxl4* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

- Transcript *Fbxl4-202* may not be affected. The KO region is close to 5'UTR region of the *Gm24607* gene.
Knockout the region may affect the regulation of *Gm24607* gene.
- The *Fbxl4* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Fbxl4 F-box and leucine-rich repeat protein 4 [*Mus musculus* (house mouse)]

Gene ID: 269514, updated on 12-Aug-2019

Summary

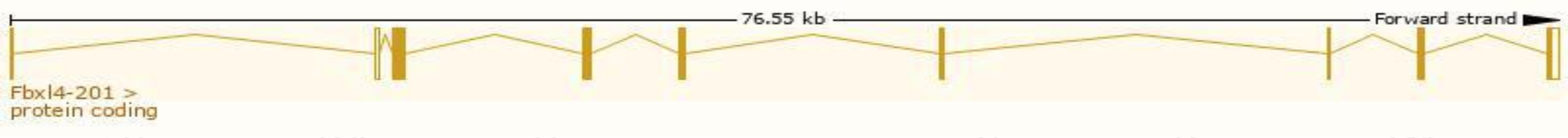
| | |
|---------------------------|---|
| Official Symbol | Fbxl4 provided by MGI |
| Official Full Name | F-box and leucine-rich repeat protein 4 provided by MGI |
| Primary source | MGI:MGI:2140367 |
| See related | Ensembl:ENSMUSG00000040410 |
| Gene type | protein coding |
| RefSeq status | VALIDATED |
| Organism | Mus musculus |
| Lineage | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| Also known as | FBL4; FBL5; AI836810 |
| Expression | Ubiquitous expression in subcutaneous fat pad adult (RPKM 7.6), genital fat pad adult (RPKM 6.8) and 28 other tissues See more |
| Orthologs | human all |

Transcript information (Ensembl)

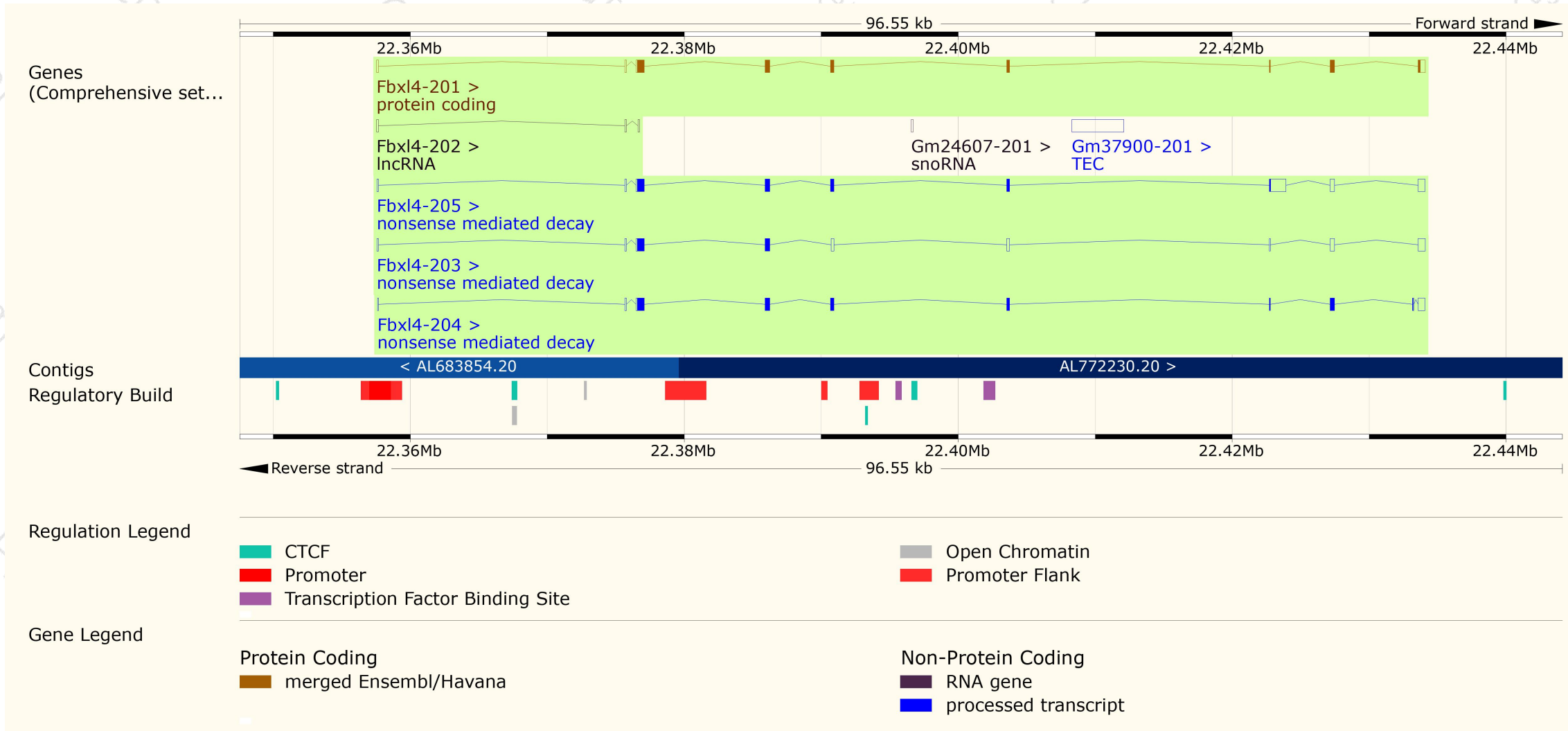
The gene has 5 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-----------|--------------------------------------|------|-----------------------|-------------------------|---------------------------|------------------------|-------------------------------|
| Fbxl4-201 | ENSMUST00000039234.9 | 2546 | 621aa | Protein coding | CCDS18004 | Q8BH70 | TSL:1 GENCODE basic APPRIS P1 |
| Fbxl4-205 | ENSMUST00000185029.7 | 3641 | 466aa | Nonsense mediated decay | - | V9GWT8 | TSL:1 |
| Fbxl4-204 | ENSMUST00000184582.1 | 2570 | 582aa | Nonsense mediated decay | - | V9GXH8 | TSL:1 |
| Fbxl4-203 | ENSMUST00000184455.7 | 2478 | 290aa | Nonsense mediated decay | - | V9GWU9 | TSL:1 |
| Fbxl4-202 | ENSMUST00000131972.7 | 342 | No protein | Processed transcript | - | - | TSL:2 |

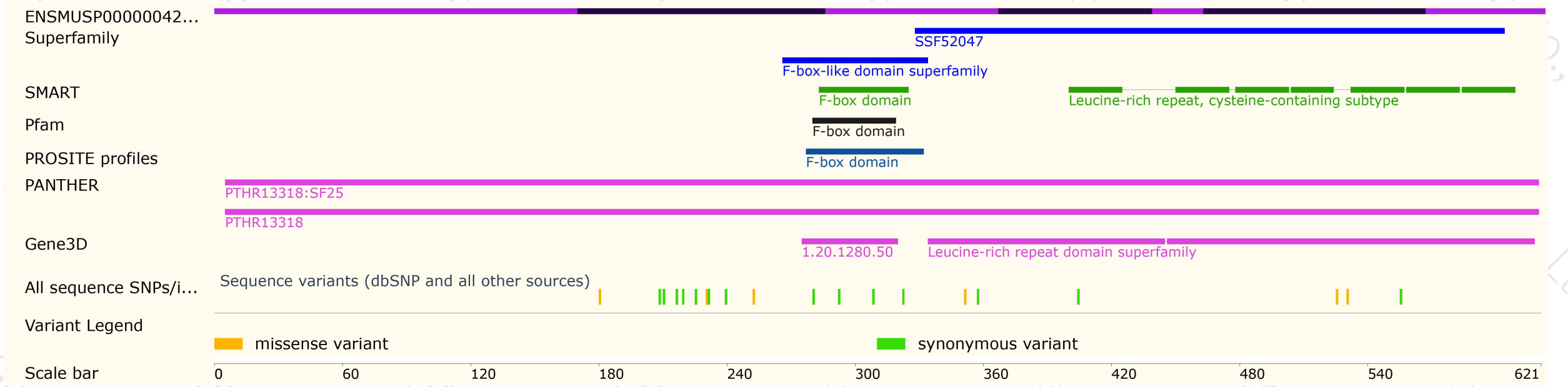
The strategy is based on the design of *Fbxl4-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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