

Fnbp1 Cas9-KO Strategy

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Project Overview

Project Name

Fnbp1

Project type

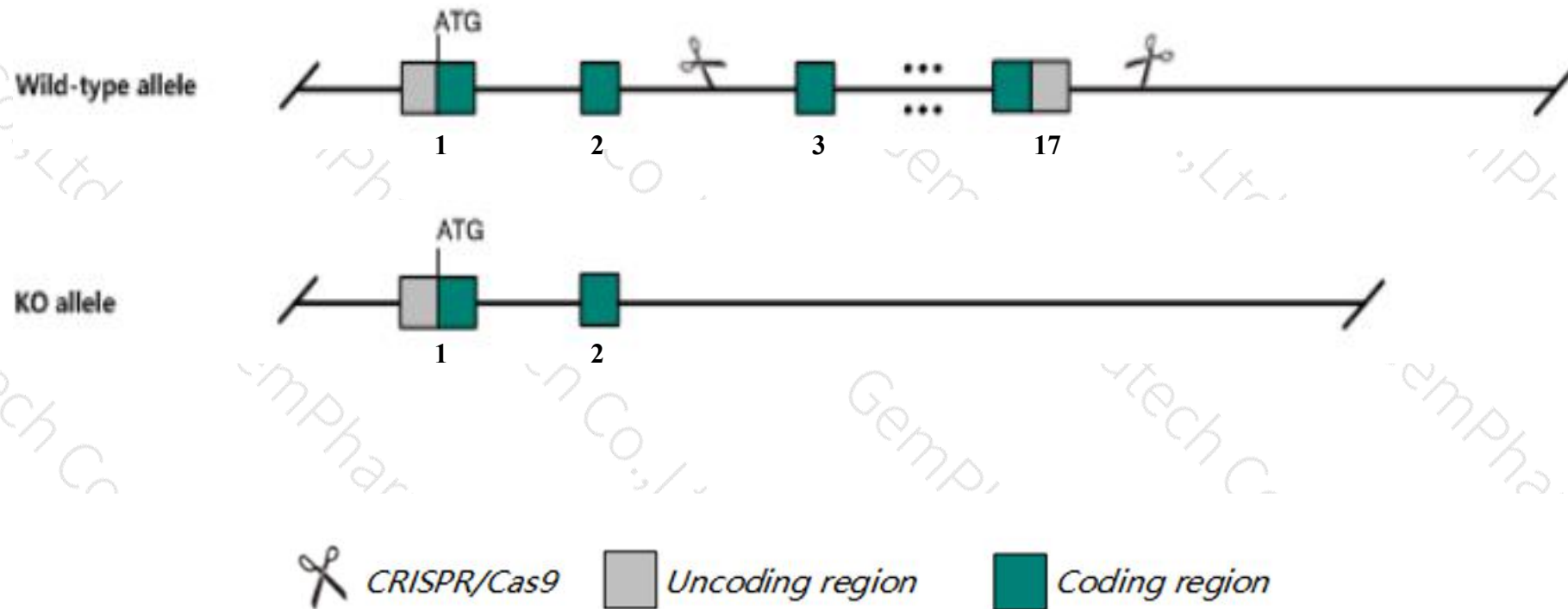
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fnbp1* gene. The schematic diagram is as follows:



- The *Fnbp1* gene has 16 transcripts. According to the structure of *Fnbp1* gene, exon3-exon17 of *Fnbp1*-208 (ENSMUST00000113560.7) transcript is recommended as the knockout region. The region contains 1711bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fnbp1* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Fnbp1* 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)

Fnbp1 formin binding protein 1 [Mus musculus (house mouse)]

Gene ID: 14269, updated on 13-Mar-2020

Summary

Official Symbol Fnbp1 provided by [MGI](#)

Official Full Name formin binding protein 1 provided by [MGI](#)

Primary source [MGI:MGI:109606](#)

See related [Ensembl:ENSMUSG00000075415](#)

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 1110057E06Rik, 2210010H06Rik, FBP1, Fbp17

Expression Ubiquitous expression in cerebellum adult (RPKM 39.4), bladder adult (RPKM 33.9) and 26 other tissues [See more](#)

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

Transcript information (Ensembl)

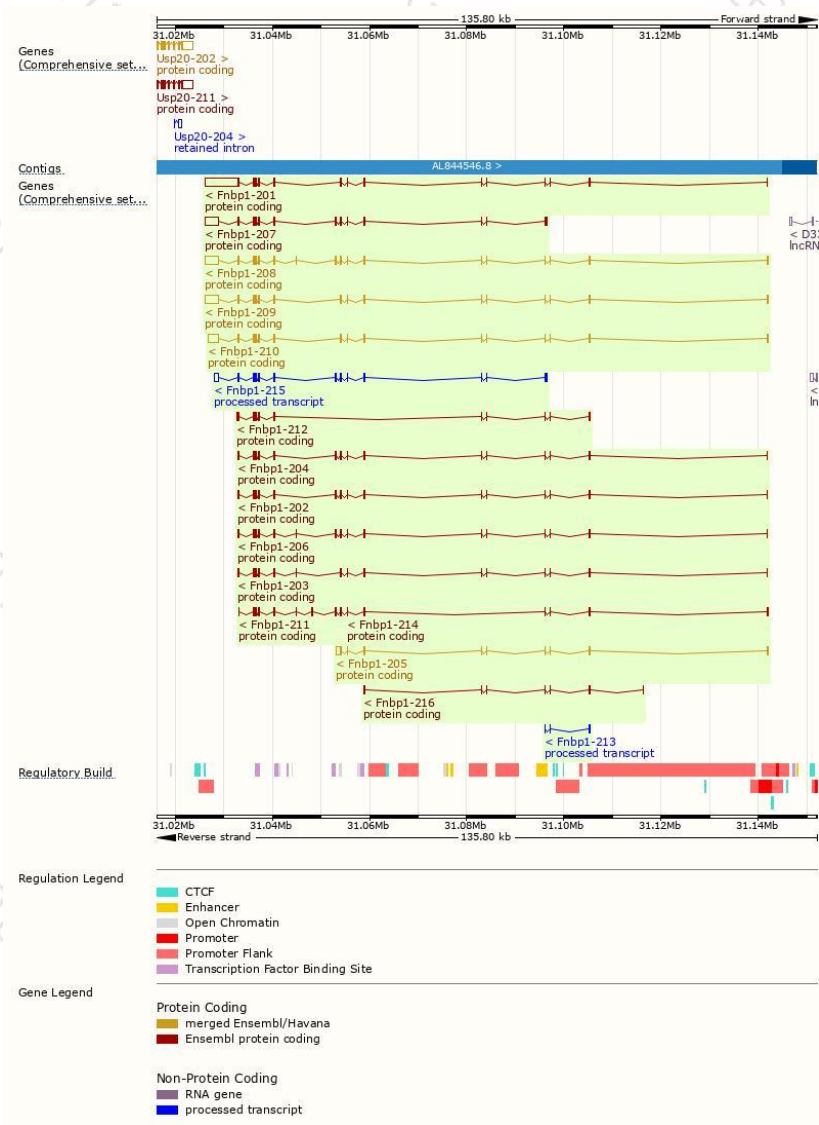
The gene has 16 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fnbp1-208	ENSMUST00000113560.7	4726	616aa	Protein coding	CCDS50561	Q80TY0	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 P1
Fnbp1-209	ENSMUST00000113562.8	4515	550aa	Protein coding	CCDS38097	Q80TY0	TSL:1 GENCODE basic
Fnbp1-207	ENSMUST00000113559.9	4378	522aa	Protein coding	CCDS50560	Q80TY0	TSL:1 GENCODE basic
Fnbp1-210	ENSMUST00000113564.8	3892	551aa	Protein coding	CCDS57165	Q80TY0	TSL:1 GENCODE basic
Fnbp1-205	ENSMUST00000113552.8	1910	338aa	Protein coding	CCDS15894	Q80TY0	TSL:1 GENCODE basic
Fnbp1-201	ENSMUST00000073879.11	8469	554aa	Protein coding	-	A2AQ43	TSL:5 GENCODE basic
Fnbp1-204	ENSMUST00000100208.8	1859	615aa	Protein coding	-	A2AQ41	TSL:5 GENCODE basic
Fnbp1-206	ENSMUST00000113555.7	1776	591aa	Protein coding	-	A2AQ45	TSL:5 GENCODE basic
Fnbp1-202	ENSMUST00000075326.10	1761	586aa	Protein coding	-	A2AQ42	TSL:5 GENCODE basic
Fnbp1-203	ENSMUST00000100207.8	1680	559aa	Protein coding	-	A2AQ44	TSL:5 GENCODE basic
Fnbp1-212	ENSMUST00000128500.7	1481	388aa	Protein coding	-	F6VFN1	CDS 5' incomplete TSL:5
Fnbp1-211	ENSMUST00000128431.2	1064	355aa	Protein coding	-	A0A0A6YWT1	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Fnbp1-216	ENSMUST00000149196.1	651	208aa	Protein coding	-	A2AQ39	CDS 3' incomplete TSL:3
Fnbp1-214	ENSMUST00000136181.7	635	160aa	Protein coding	-	A2AQ47	CDS 3' incomplete TSL:5
Fnbp1-215	ENSMUST00000138581.2	2390	No protein	Processed transcript	-	-	TSL:1
Fnbp1-213	ENSMUST00000136085.1	350	No protein	Processed transcript	-	-	TSL:2

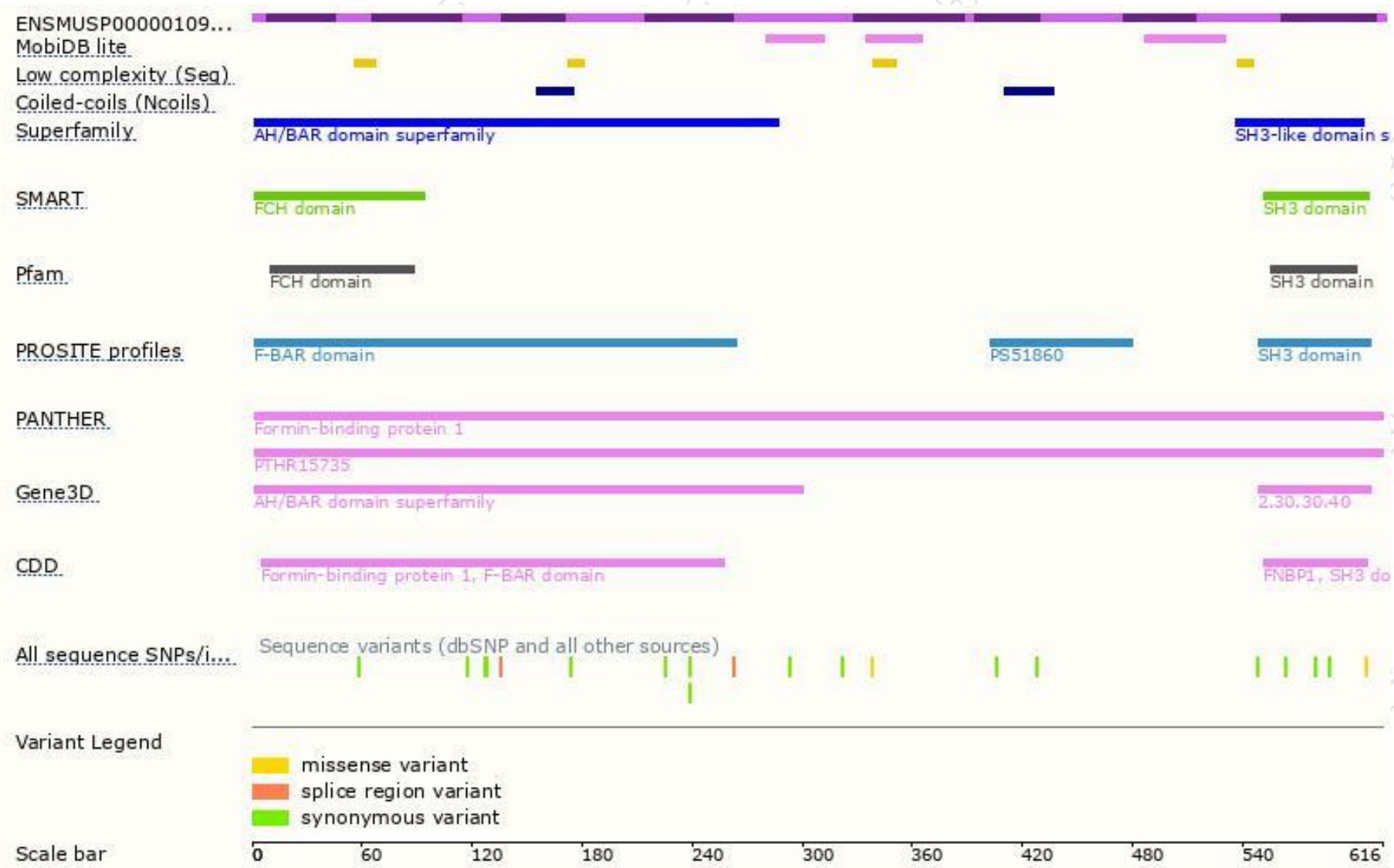
The strategy is based on the design of *Fnbp1-208* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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