

Zfpn1 Cas9-KO Strategy

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Project Overview

Project Name

Zfpm1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Zfpm1* gene has 5 transcripts. According to the structure of *Zfpm1* gene, exon4 of *Zfpm1-201* (ENSMUST00000054052.14) transcript is recommended as the knockout region. The region contains 134bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Zfpm1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous mutants have poorly vascularized yolk sacs and small, pale livers. Mutants die between embryonic days 10.5 and 12.5 with severe anemia associated with a block in megakaryocyte development.
- The knockout region is located in the intron of the Gm20388 and its effect is unknown after knockout.
- The *Zfpml* gene is located on the Chr8. 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)

Zfpm1 zinc finger protein, multitype 1 [Mus musculus (house mouse)]

Gene ID: 22761, updated on 2-Apr-2019

Summary



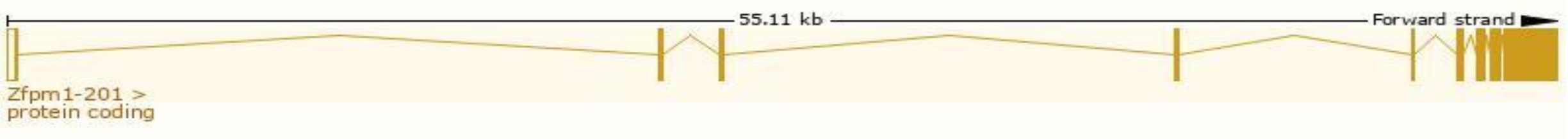
| | |
|---------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Official Symbol | Zfpm1 provided by MGI |
| Official Full Name | zinc finger protein, multitype 1 provided by MGI |
| Primary source | MGI:MGI:1095400 |
| See related | Ensembl:ENSMUSG00000049577 |
| 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 | FOG, Fog1 |
| Expression | Broad expression in duodenum adult (RPKM 90.0), small intestine adult (RPKM 68.4) and 20 other tissues See more |
| Orthologs | human all |

Transcript information (Ensembl)

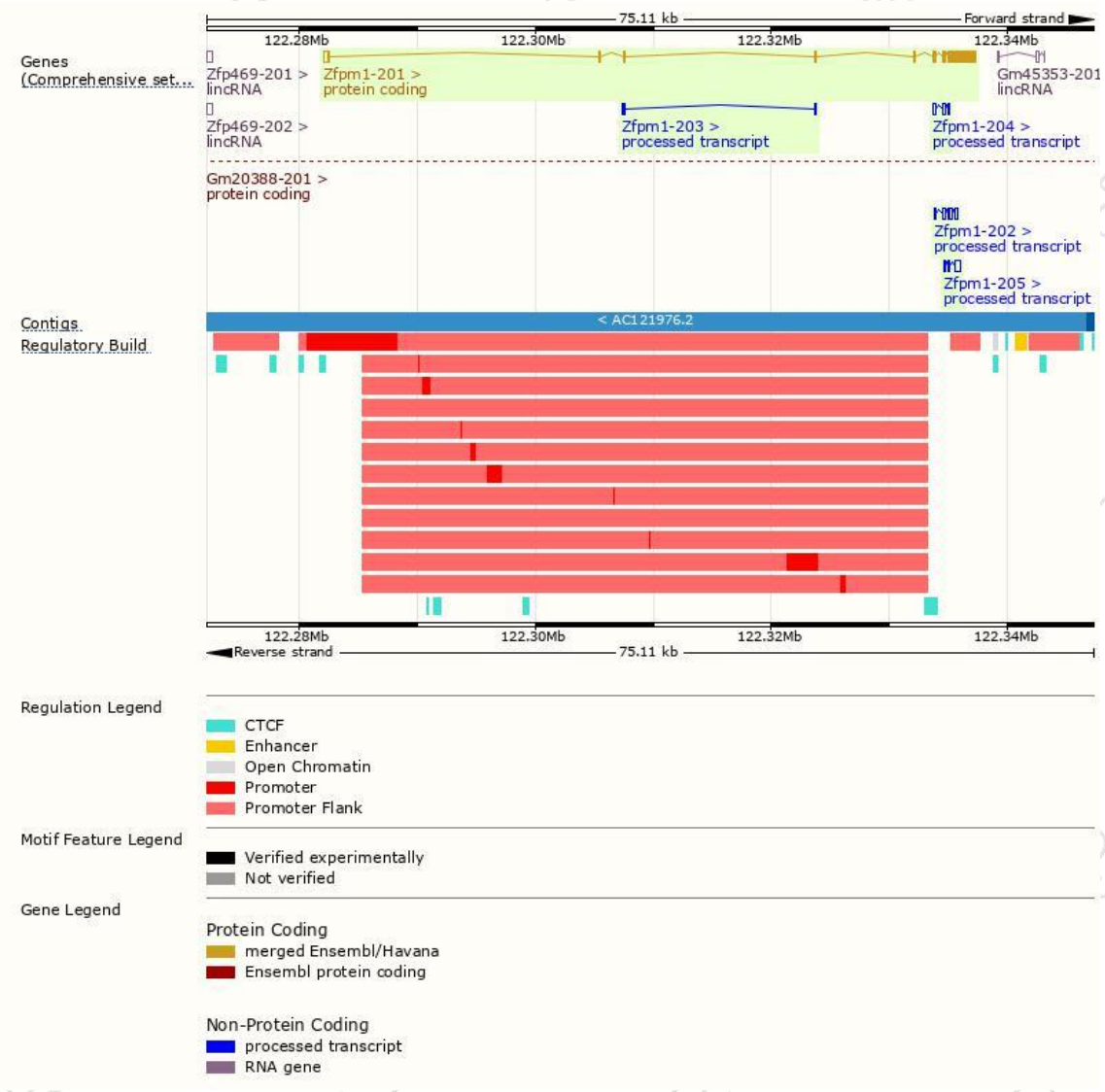
The gene has 5 transcripts,all transcripts are shown below:

| Name ▲ | Transcript ID ▲ | bp ▲ | Protein ▲ | Biotype ▲ | CCDS ▲ | UniProt ▲ | Flags ▲ |
|-----------|---------------------------------------|------|-----------------------|----------------|---------------------------|------------------------|-------------------------------|
| Zfpm1-201 | ENSMUST00000054052.14 | 3390 | 995aa | Protein coding | CCDS22733 | O35615 | TSL:1 Gencode basic APPRIS P1 |
| Zfpm1-202 | ENSMUST00000176690.1 | 865 | No protein | lncRNA | - | - | TSL:3 |
| Zfpm1-203 | ENSMUST00000176883.1 | 314 | No protein | lncRNA | - | - | TSL:3 |
| Zfpm1-204 | ENSMUST00000177356.1 | 559 | No protein | lncRNA | - | - | TSL:2 |
| Zfpm1-205 | ENSMUST00000212315.1 | 704 | No protein | lncRNA | - | - | TSL:5 |

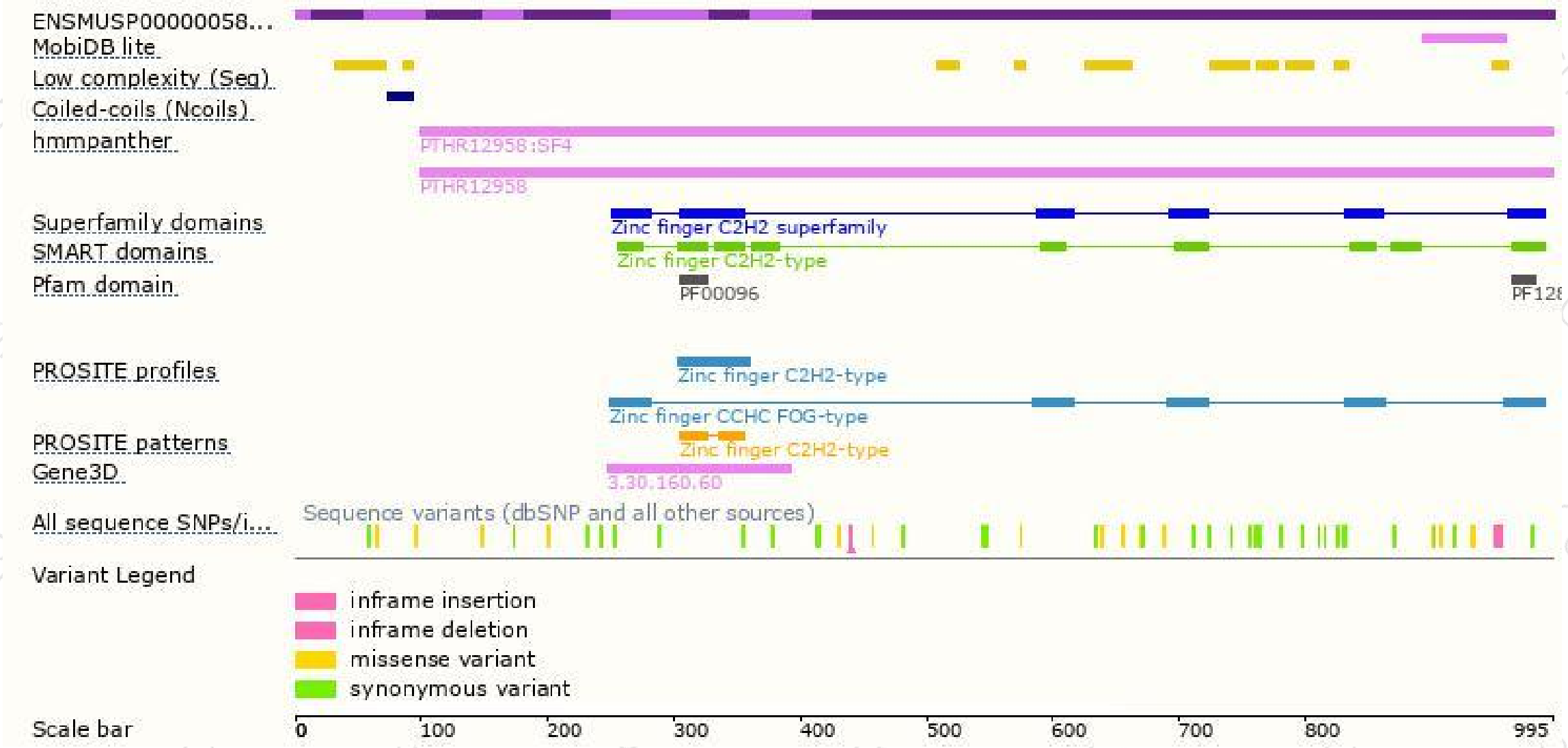
The strategy is based on the design of *Zfpm1-201* transcript,The transcription is shown below



Genomic location distribution

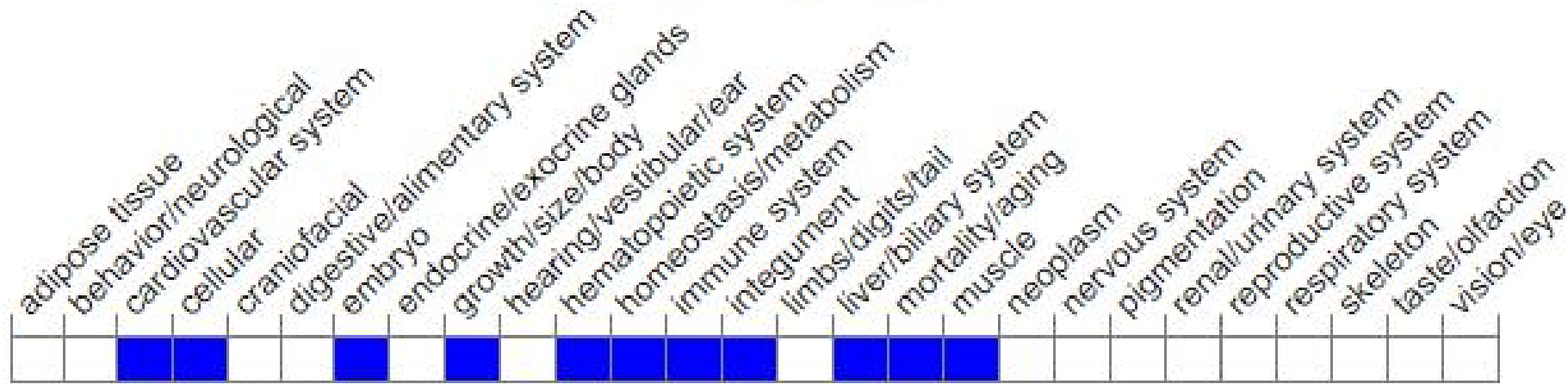


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview ?



Click cells to view annotations.

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 have poorly vascularized yolk sacs and small, pale livers.

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

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