Fmn2 Cas9-CKO Strategy

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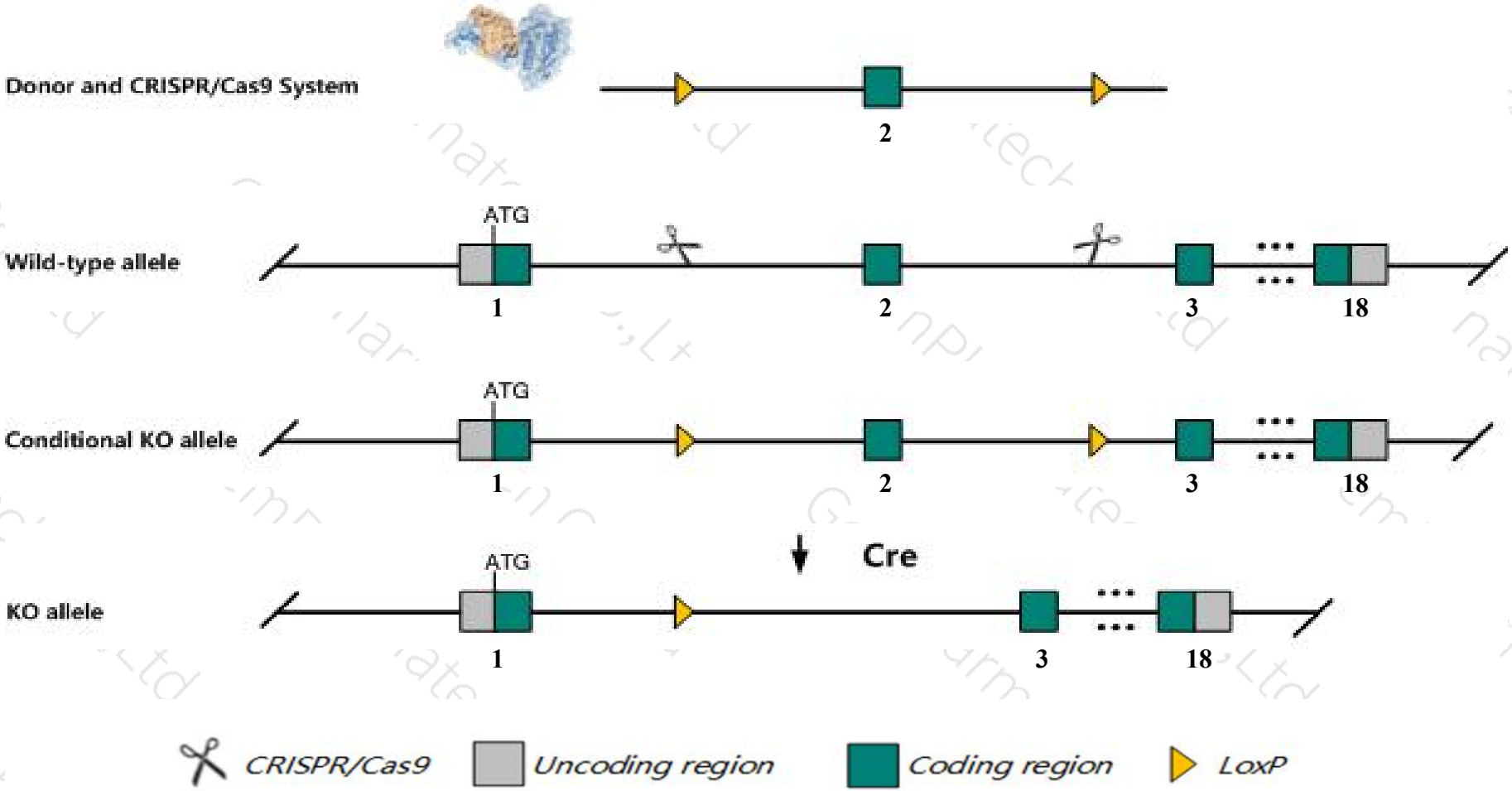
Project Overview

Project Name	***Fmn2***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fmn2* gene. The schematic diagram is as follows:



Technical routes

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- The *Fmn2* gene has 6 transcripts. According to the structure of *Fmn2* gene, exon2 of *Fmn2-201* (ENSMUST00000030039.12) transcript is recommended as the knockout region.The region contains 167bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Fmn2* gene. The brief process is as follows:CRISPR/Cas9 system and Donor 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.

- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice

- According to the existing MGI data,Female mice homozygous for a knock-out allele display polyploid embryo formation, recurrent pregnancy loss, hypofertility, and inadequate nursing behavior.
- Transcript *Fmn2*-203&204&205 may not be affected.
- The effect on transcript *Fmn2*-206 is unknown.
- The N-terminal of *Fmn2* gene will remain 516aa,it may remain the partial function of *Fmn2* gene.
- The *Fmn2* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Fmn2 formin 2 [*Mus musculus* (house mouse)]

Gene ID: 54418, updated on 10-Oct-2019

Summary

Official Symbol	Fmn2 provided by MGI
Official Full Name	formin 2 provided by MGI
Primary source	MGI:MGI:1859252
See related	Ensembl:ENSMUSG00000028354
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	AU024104
Expression	Biased expression in frontal lobe adult (RPKM 7.4), cortex adult (RPKM 7.0) and 6 other tissues See more
Orthologs	human all

Genomic context

Location: 1 H3; 1 81.04 cM

See Fmn2 in Genome Data Viewer

Exon count: 18

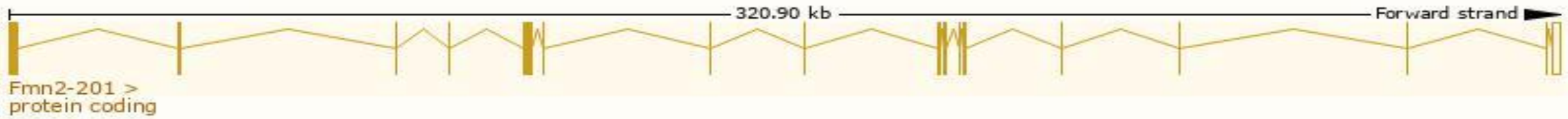
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	1	NC_000067.6 (174501752..174822729)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	1	NC_000067.5 (176431956..176752860)

Transcript information（Ensembl）

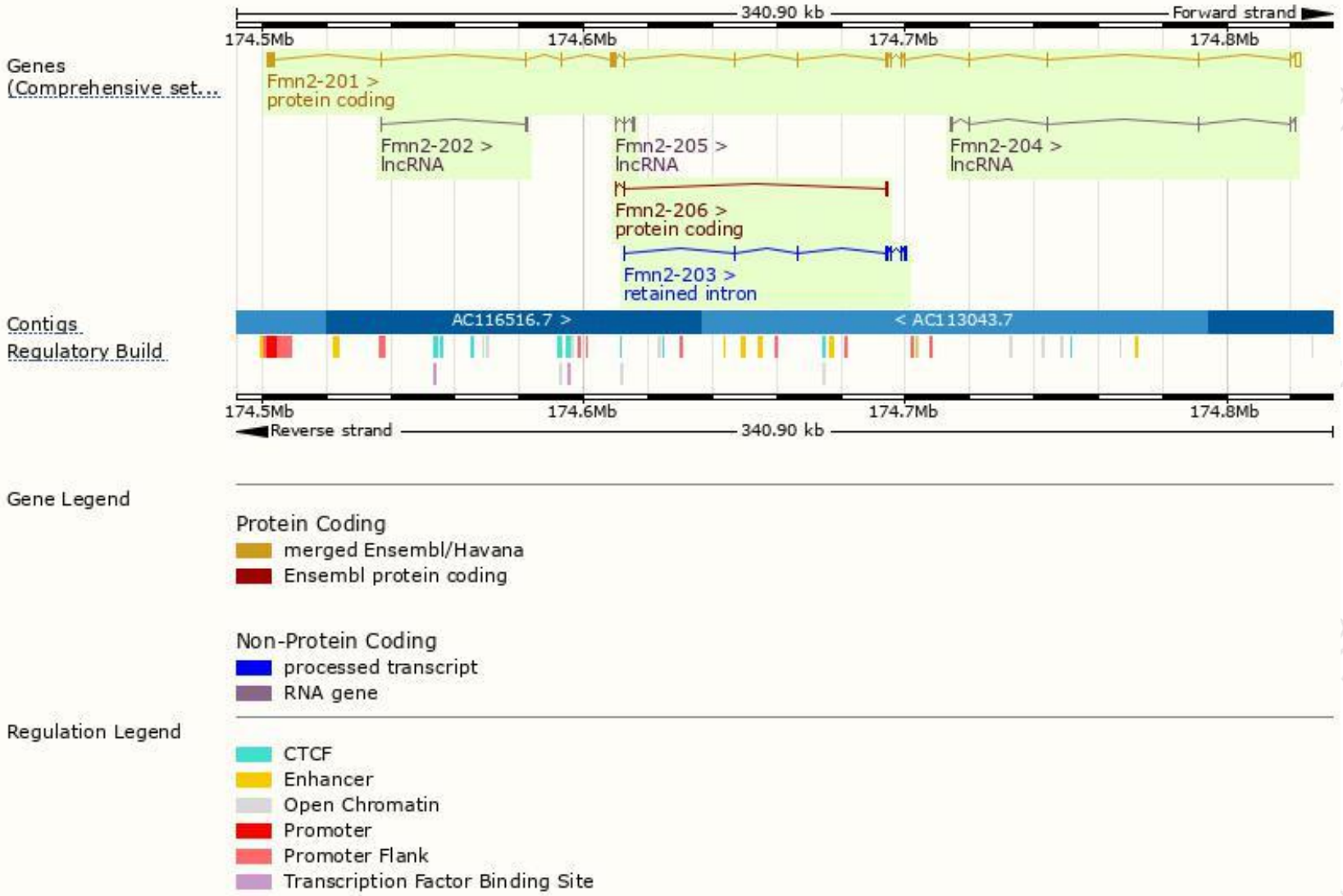
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fmn2-201	ENSMUST00000030039.12	6442	1578aa	Protein coding	CCDS48459	Q9JL04	TSL:1 GENCODE basic APPRIS P1
Fmn2-206	ENSMUST00000195621.1	433	145aa	Protein coding	-	A0A0A6YY57	CDS 5' and 3' incomplete TSL:3
Fmn2-203	ENSMUST00000191971.1	1535	No protein	Retained intron	-	-	TSL:1
Fmn2-202	ENSMUST00000191821.1	724	No protein	lncRNA	-	-	TSL:3
Fmn2-204	ENSMUST00000193905.1	600	No protein	lncRNA	-	-	TSL:5
Fmn2-205	ENSMUST00000195300.1	497	No protein	lncRNA	-	-	TSL:5

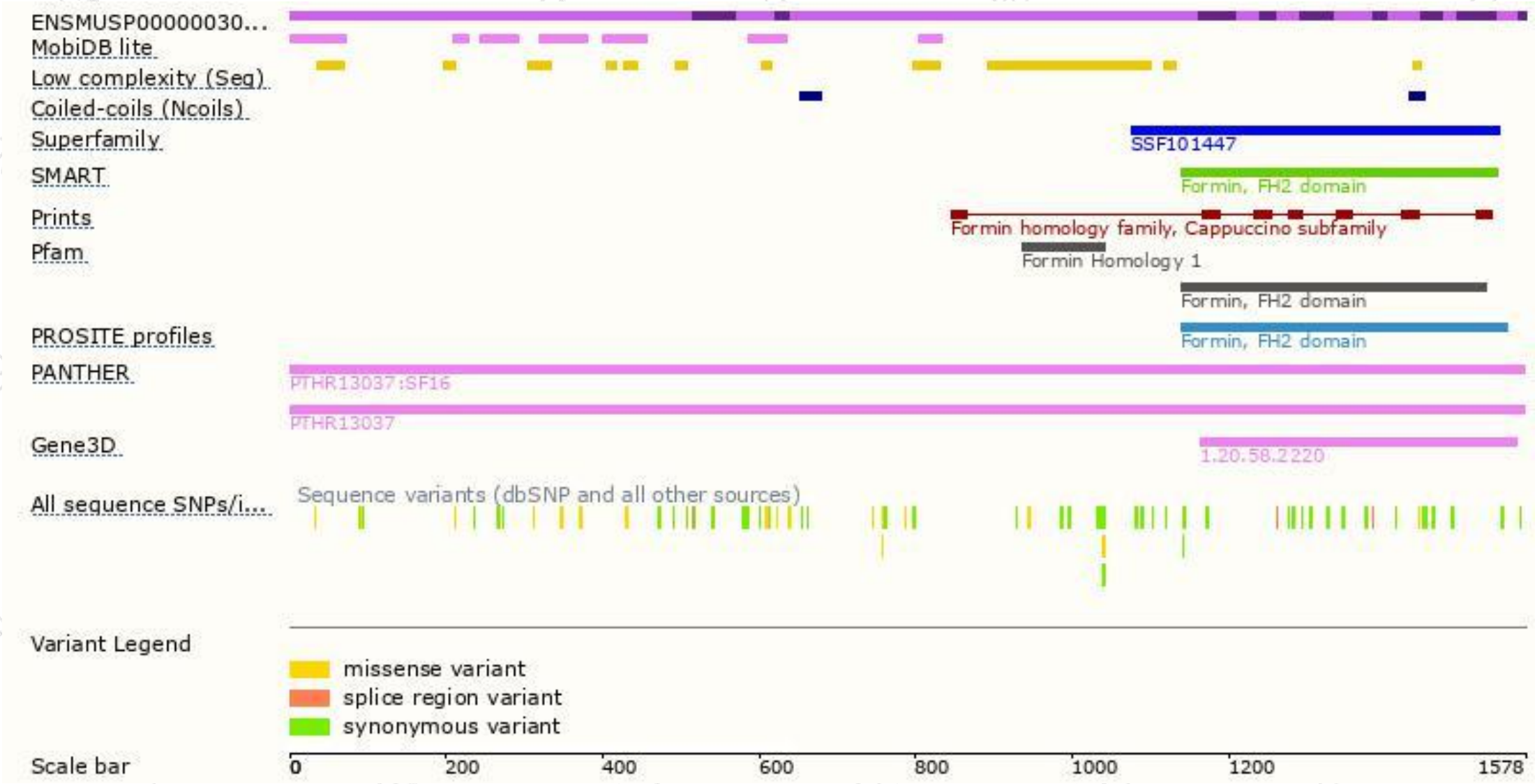
The strategy is based on the design of *Fmn2-201* transcript,The transcription is shown below



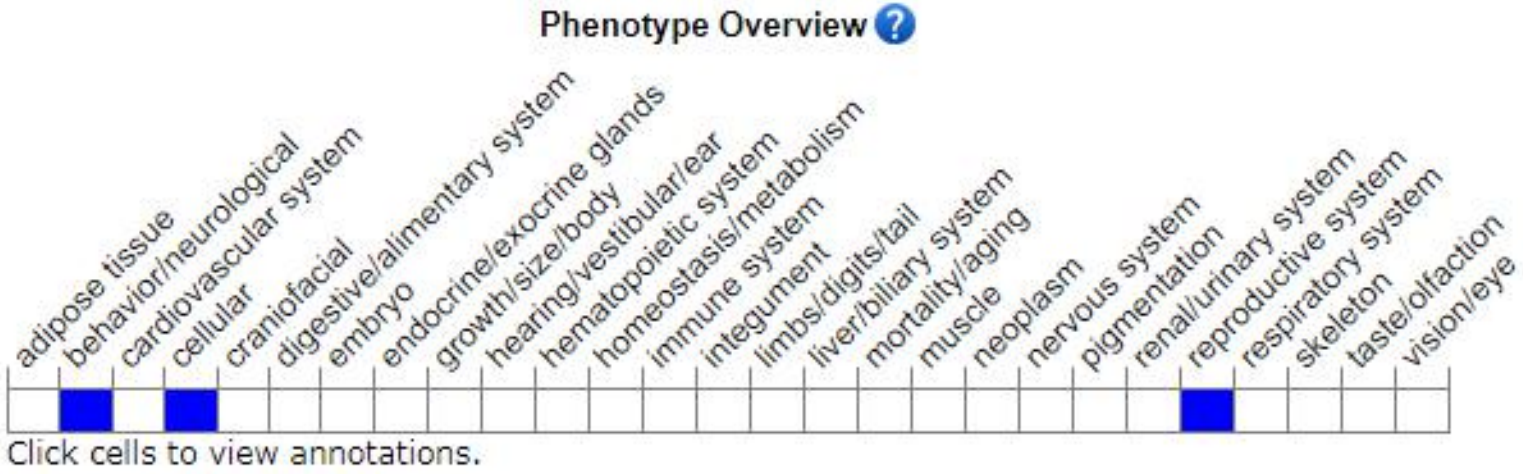
Genomic location distribution



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,Female mice homozygous for a knock-out allele display polyploid embryo formation, recurrent pregnancy loss, hypofertility, and inadequate nursing behavior.

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

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