

# *Far1* Cas9-CKO Strategy

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# Overview

## Target Gene Name

- *Far1*

## Project Type

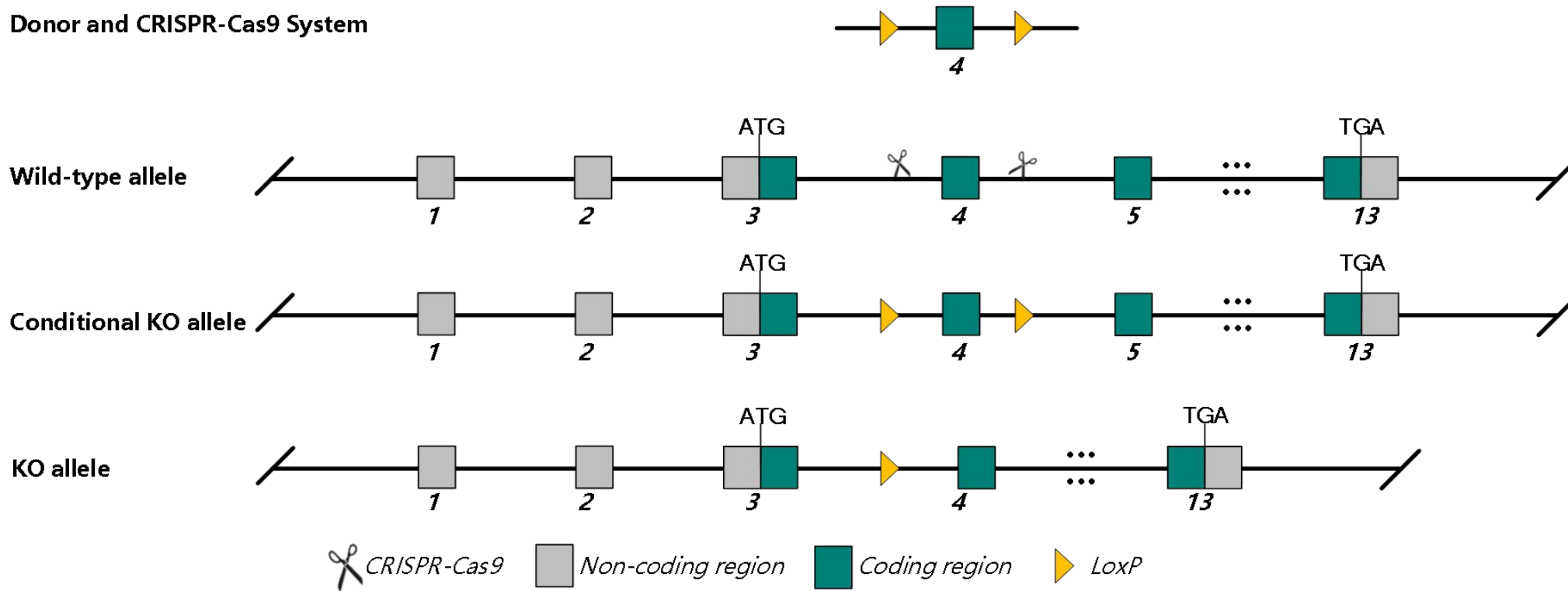
- Cas9-CKO

## Genetic Background

- C57BL/6JGpt

# Strain Strategy

## Donor and CRISPR-Cas9 System



Schematic representation of CRISPR-Cas9 engineering used to edit the *Far1* gene.

# Technical Information

- The *Far1* gene has 11 transcripts. According to the structure of *Far1* gene, exon 4 of *Far1*-201 (ENSMUST00000033018.15) is recommended as the knockout region. The region contains 176 bp of coding sequence. Knocking out the region will result in disruption of gene function.
- In this project we use CRISPR-Cas9 technology to modify *Far1* 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- 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.

# Gene Information

**Far1** fatty acyl CoA reductase 1 [ *Mus musculus* (house mouse) ]

[Download Datasets](#)

Gene ID: 67420, updated on 23-Nov-2023

## Summary

<b>Official Symbol</b>	Far1 <small>provided by MGI</small>
<b>Official Full Name</b>	fatty acyl CoA reductase 1 <small>provided by MGI</small>
<b>Primary source</b>	<a href="#">MGI:MGI:1914670</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000030759</a> <a href="#">AllianceGenome:MGI:1914670</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	Mlstd2; 2600011M19Rik; 2900034E22Rik; 3732409C05Rik
<b>Summary</b>	Enables fatty-acyl-CoA reductase (alcohol-forming) activity. Involved in wax biosynthetic process. Located in peroxisome. Orthologous to human FAR1 (fatty acyl-CoA reductase 1). [provided by Alliance of Genome Resources, Apr 2022]
<b>Expression</b>	Broad expression in bladder adult (RPKM 22.8), CNS E18 (RPKM 14.0) and 22 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>
<b>NEW</b>	Try the new <a href="#">Gene table</a> Try the new <a href="#">Transcript table</a>

## Genomic context

**Location:** 7 F1; 7 59.21 cM

See Far1 in [Genome Data Viewer](#)

**Exon count:** 15

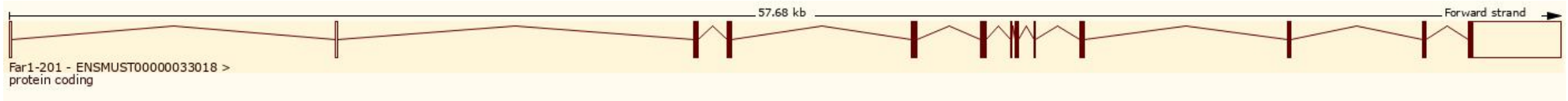
<https://www.ncbi.nlm.nih.gov/gene/67420>

# Transcript Information

The gene has 11 transcripts, all transcripts are shown below:

Show/hide columns (1 hidden)							Filter	
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags	
<a href="#">ENSMUST00000033018.15</a>	Far1-201	4962	<a href="#">515aa</a>	Protein coding	<a href="#">CCDS40093</a>	<a href="#">Q922J9</a>	Ensembl Canonical	GENCODE basic APPRIS P3 TSL:1
<a href="#">ENSMUST00000067929.15</a>	Far1-202	4935	<a href="#">515aa</a>	Protein coding	<a href="#">CCDS72024</a>	<a href="#">Q922J9-3</a>	GENCODE basic	APPRIS ALT1 TSL:1
<a href="#">ENSMUST00000122890.2</a>	Far1-203	445	<a href="#">37aa</a>	Protein coding		<a href="#">D3Z072</a>	TSL:3	CDS 3' incomplete
<a href="#">ENSMUST00000123591.2</a>	Far1-204	1674	No protein	Retained intron		-	TSL:1	
<a href="#">ENSMUST00000123845.8</a>	Far1-205	1218	No protein	Retained intron		-	TSL:1	
<a href="#">ENSMUST00000129087.8</a>	Far1-206	769	<a href="#">181aa</a>	Protein coding		<a href="#">D3Z5W6</a>	TSL:3	CDS 3' incomplete
<a href="#">ENSMUST00000136158.8</a>	Far1-207	733	<a href="#">206aa</a>	Protein coding		<a href="#">D3Z4N9</a>	TSL:3	CDS 3' incomplete
<a href="#">ENSMUST00000151133.2</a>	Far1-208	524	No protein	Retained intron		-	TSL:2	
<a href="#">ENSMUST00000155183.2</a>	Far1-209	775	No protein	Retained intron		-	TSL:2	
<a href="#">ENSMUST00000156554.2</a>	Far1-210	413	No protein	Retained intron		-	TSL:2	
<a href="#">ENSMUST00000164745.8</a>	Far1-211	3972	<a href="#">515aa</a>	Protein coding	<a href="#">CCDS40093</a>	<a href="#">Q922J9</a>	GENCODE basic	APPRIS P3 TSL:5

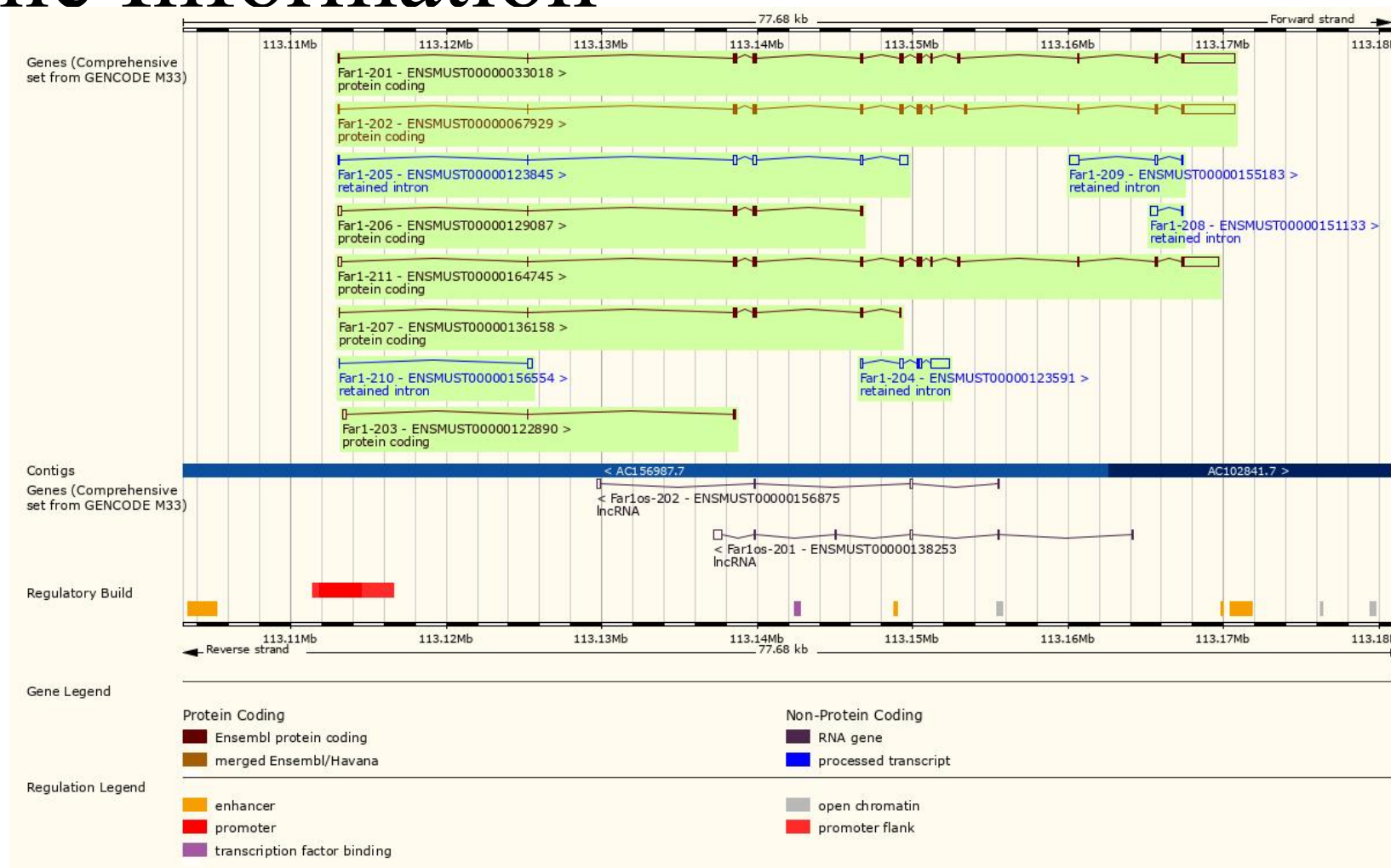
The strategy is based on the design of *Far1*-201 transcript, the transcription is shown below:



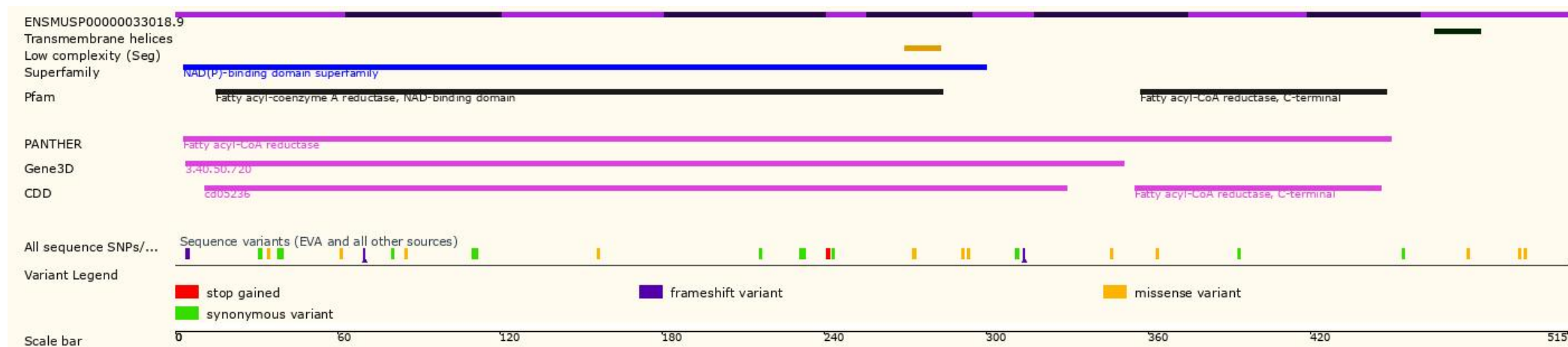
Source: <http://asia.ensembl.org/>



# Genomic Information

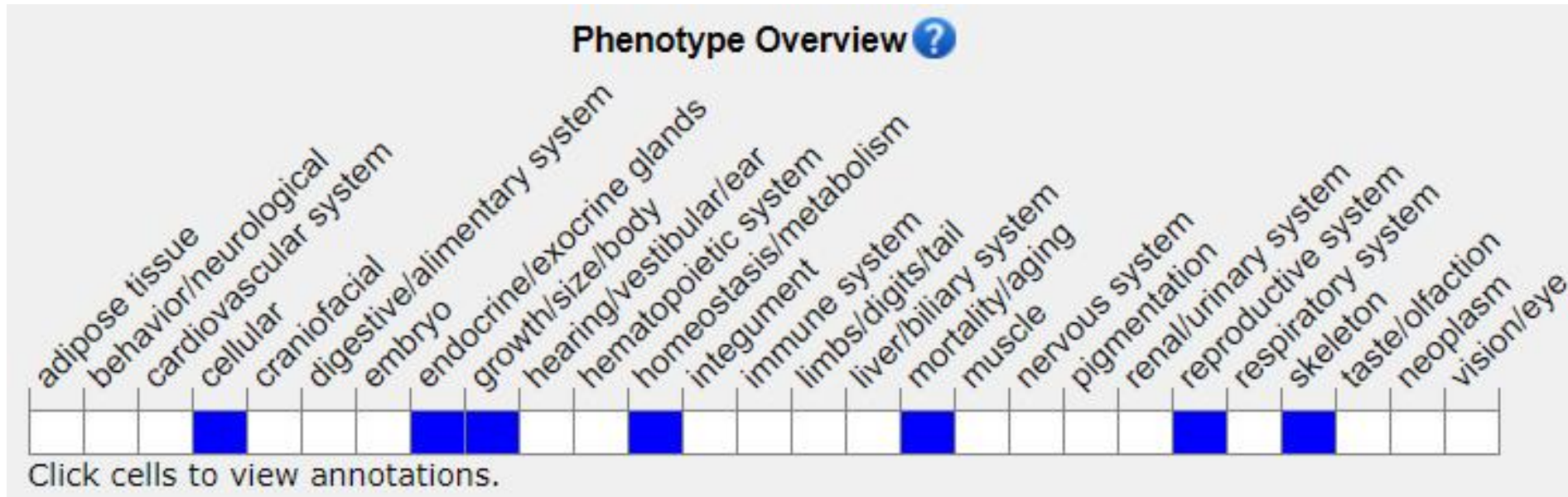


# Protein Information





# Mouse Phenotype Information (MGI)



Mice homozygous for a null allele show partial preweaning lethality, postnatal growth retardation, small testes, and male infertility associated with azoospermia, spermatogenesis arrest, disrupted intercellular bridge formation, multinucleated giant germ cells, and increased male germ cell apoptosis.

# Important Information

- The knockout region overlaps with *Far1os* gene, which may affect the function of this gene.
- This strategy may not affect *Far1-203*, *Far1-204*, *Far1-208* and *Far1-209* transcript.
- *Far1* is located on Chr 7. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 the existing technology level.