

# ***Fzr1* Cas9-CKO Strategy**

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# Project Overview

**Project Name**

*Fzr1*

**Project type**

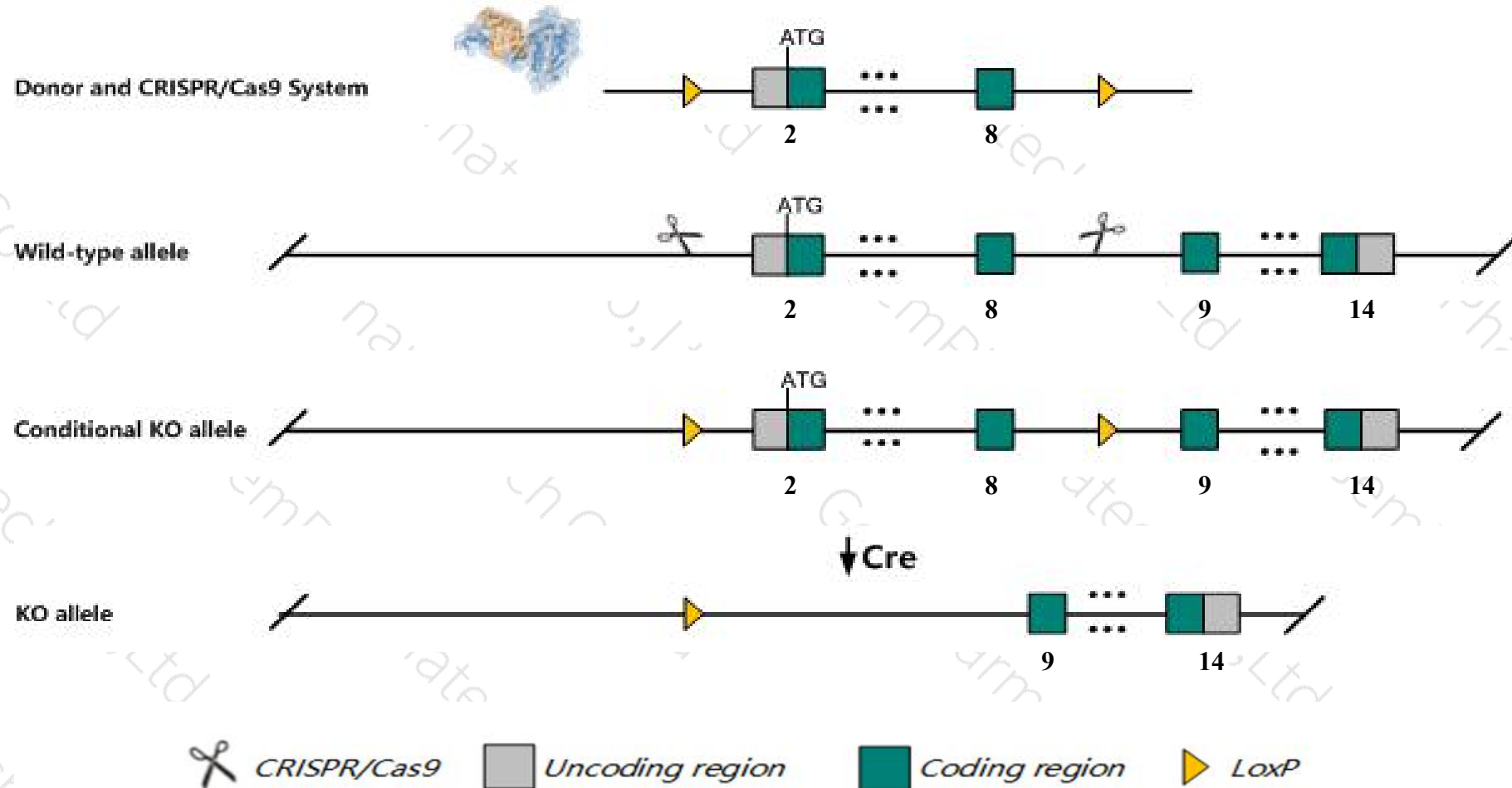
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fzr1* gene. The schematic diagram is as follows:



# Technical routes

- The *Fzr1* gene has 6 transcripts. According to the structure of *Fzr1* gene, exon2-exon8 of *Fzr1*-205(ENSMUST00000140901.7) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fzr1* 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.

- According to the existing MGI data, homozygous null mutants die embryonically at around E9.5-E12.5 with poorly developed placentae, no placental giant cells and/or erythroblast deficiency. Homozygous MEFs undergo premature senescence. Heterozygotes exhibit learning/memory defects and/or elevated spontaneous epithelial tumor incidence.
- The *Fzr1* gene is located on the Chr10. 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.
- The deletion region in this strategy is less than 5K from the 5' end of gene *4930404N11Rik*.
- The intron8-9 is only 530bp, loxp insertion may affect mRNA splicing.
- The 3' loxp will be placed on exon 8 of transcript *Fzr1*-204.
- The 3' loxp may be placed on exon 1 of transcript *Fzr1*-206.



# Gene information (NCBI)

## Fzr1 fizzy and cell division cycle 20 related 1 [Mus musculus (house mouse)]

Gene ID: 56371, updated on 13-Mar-2020

### Summary



**Official Symbol** Fzr1 provided by [MGI](#)

**Official Full Name** fizzy and cell division cycle 20 related 1 provided by [MGI](#)

**Primary source** [MGI:MGI:1926790](#)

**See related** [Ensembl:ENSMUSG00000020235](#)

**Gene type** protein coding

**RefSeq status** PROVISIONAL

**Organism** [Mus musculus](#)

**Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

**Also known as** AW108046, Cdh1, FZR, FZR2, Fyr, HCDH, HCDH1

**Expression** Ubiquitous expression in ovary adult (RPKM 80.2), testis adult (RPKM 77.0) and 28 other tissues [See more](#)

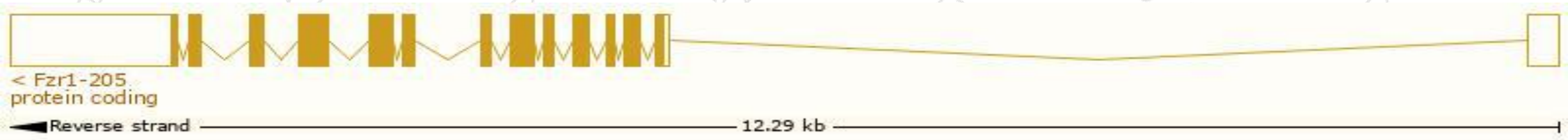
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

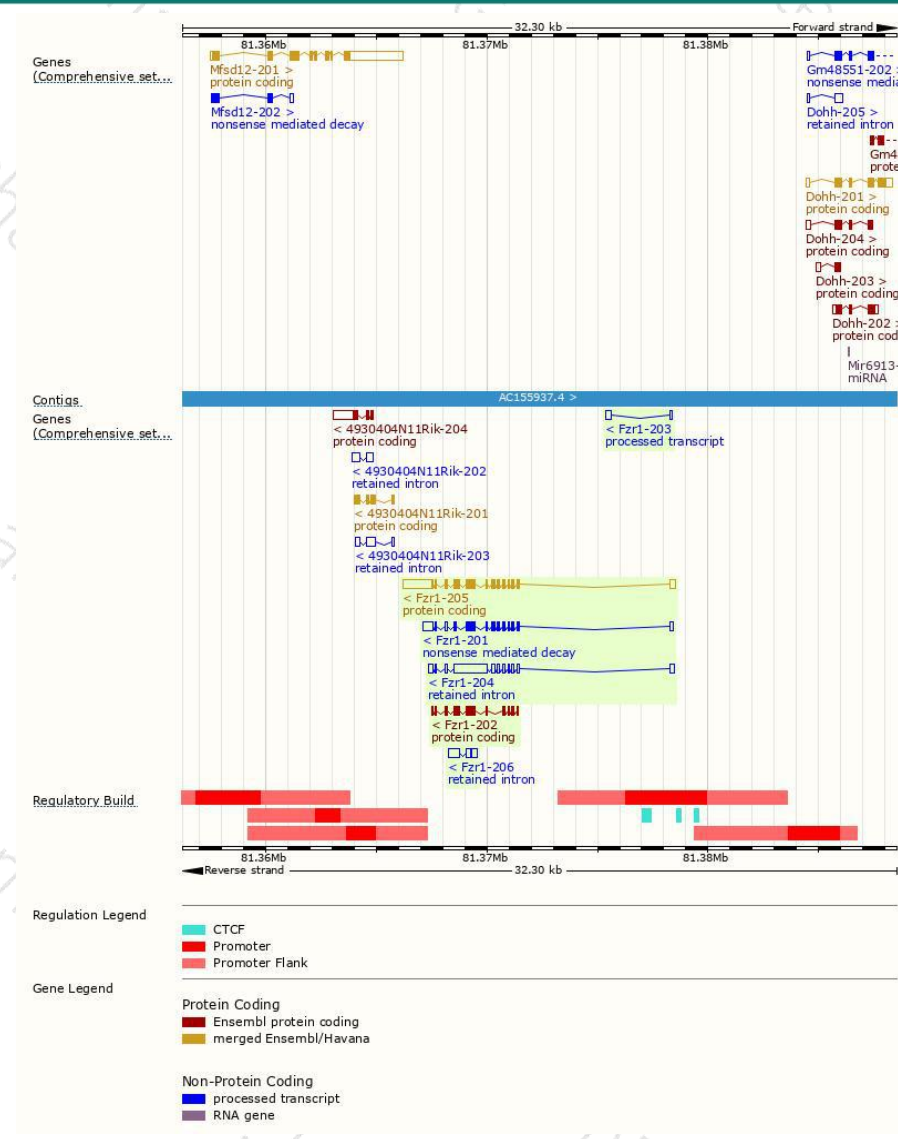
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fzr1-205	<a href="#">ENSMUST00000140901.7</a>	3057	<a href="#">493aa</a>	Protein coding	<a href="#">CCDS24057</a>	<a href="#">Q3U3D4 Q9R1K5</a>	TSL:1 GENCODE basic APPRIS P1
Fzr1-202	<a href="#">ENSMUST00000118812.1</a>	1215	<a href="#">404aa</a>	Protein coding	-	<a href="#">D3YTV2</a>	TSL:5 GENCODE basic
Fzr1-201	<a href="#">ENSMUST00000020457.13</a>	1956	<a href="#">361aa</a>	Nonsense mediated decay	-	<a href="#">F8WJ80</a>	TSL:1
Fzr1-203	<a href="#">ENSMUST00000127203.1</a>	369	No protein	Processed transcript	-	-	TSL:3
Fzr1-204	<a href="#">ENSMUST00000138343.1</a>	2780	No protein	Retained intron	-	-	TSL:1
Fzr1-206	<a href="#">ENSMUST00000150824.1</a>	870	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Fzr1-205* transcript,the transcription is shown below:



# Genomic location distribution

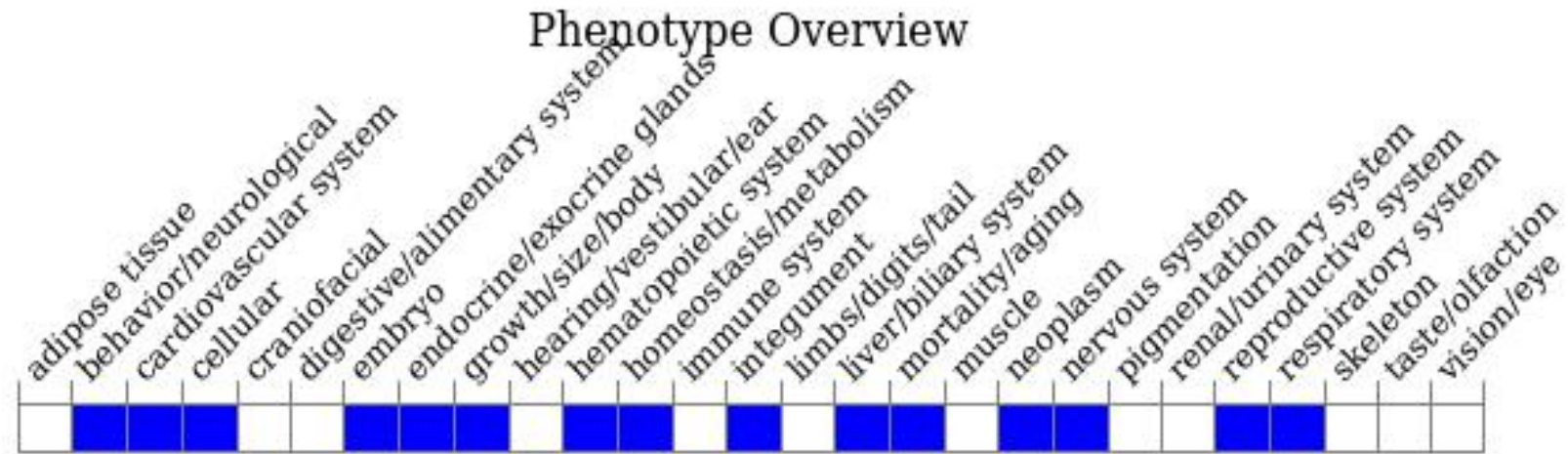




# Protein domain



# 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, homozygous null mutants die embryonically at around E9.5-E12.5 with poorly developed placentae, no placental giant cells and/or erythroblast deficiency. Homozygous MEFs undergo premature senescence. Heterozygotes exhibit learning/memory defects and/or elevated spontaneous epithelial tumor incidence.

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

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