

# ***Fgd1*** Cas9-CKO Strategy

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# Project Overview

**Project Name**

***Fgd1***

**Project type**

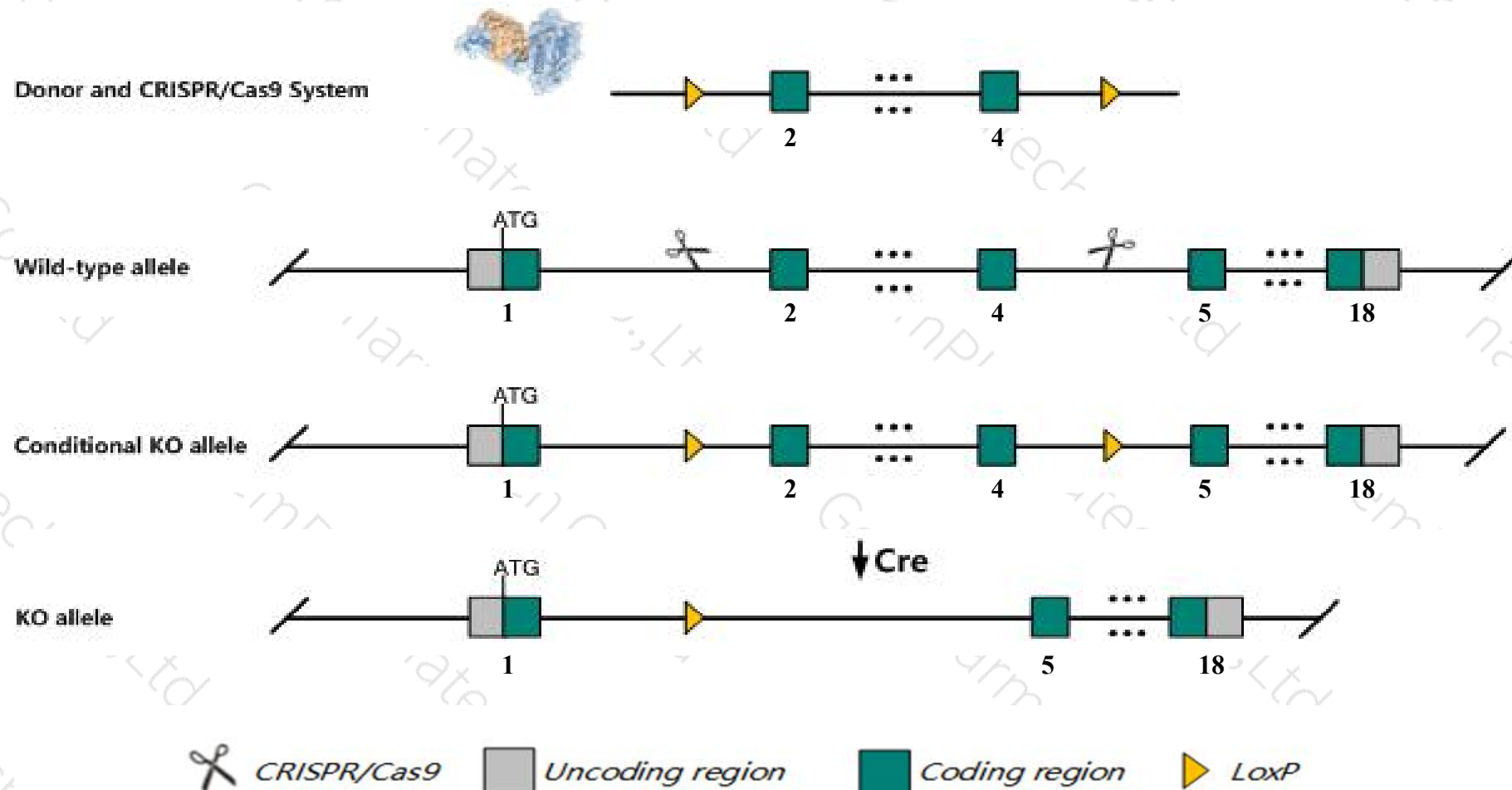
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

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



# Technical routes

- The *Fgd1* gene has 4 transcripts. According to the structure of *Fgd1* gene, exon2-exon4 of *Fgd1-201* (ENSMUST00000026296.7) transcript is recommended as the knockout region. The region contains 791bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fgd1* 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

- The *Fgd1* gene is located on the ChrX. 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.



## Fgd1 FYVE, RhoGEF and PH domain containing 1 [Mus musculus (house mouse)]

Gene ID: 14163, updated on 31-Jan-2019

### Summary



<b>Official Symbol</b>	Fgd1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	FYVE, RhoGEF and PH domain containing 1 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:104566</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000025265</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	REVIEWED
<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>	ZFYVE3
<b>Summary</b>	This gene encodes a member of family of Rho-specific guanine nucleotide exchange factors. Rho-specific guanine nucleotide exchange factors catalyze the exchange of GDP for GTP and activate small GTPases, which function as molecular switches in signaling. This protein specifically binds cell division cycle 42, a Rho (Ras homology) GTPase. Investigations in mouse suggest that this protein is important for skeletal mineralization and for regulating the actin cytoskeleton. In humans, mutations in this gene are associated with faciogenital dysplasia, also known as Aarskog-Scott syndrome. [provided by RefSeq, Mar 2014]
<b>Expression</b>	Broad expression in limb E14.5 (RPKM 14.2), whole brain E14.5 (RPKM 11.1) and 26 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information

# Ensembl



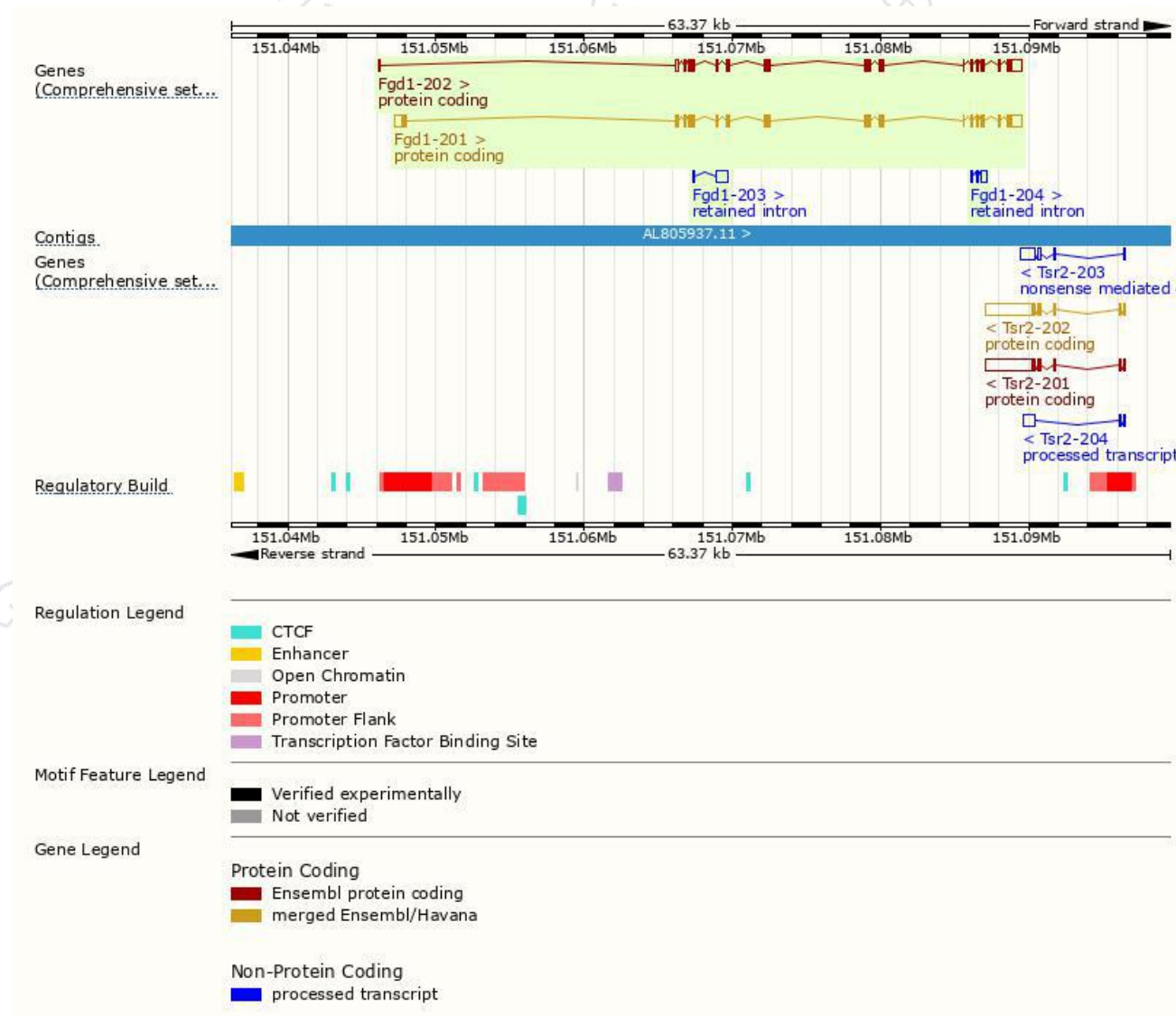
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fgd1-201	<a href="#">ENSMUST00000026296.7</a>	4001	<a href="#">960aa</a>	Protein coding	<a href="#">CCDS30467</a>	<a href="#">P52734</a>	TSL:1 GENCODE basic APPRIS P1
Fgd1-202	<a href="#">ENSMUST00000112685.7</a>	3240	<a href="#">791aa</a>	Protein coding	-	<a href="#">A2ALP5</a>	TSL:5 GENCODE basic
Fgd1-203	<a href="#">ENSMUST00000124882.1</a>	861	No protein	Retained intron	-	-	TSL:3
Fgd1-204	<a href="#">ENSMUST00000125620.1</a>	594	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Fgd1-201* 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/>).*

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

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