# *Ift172* Cas9-KO Strategy

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**Reviewer:** Huan Wang

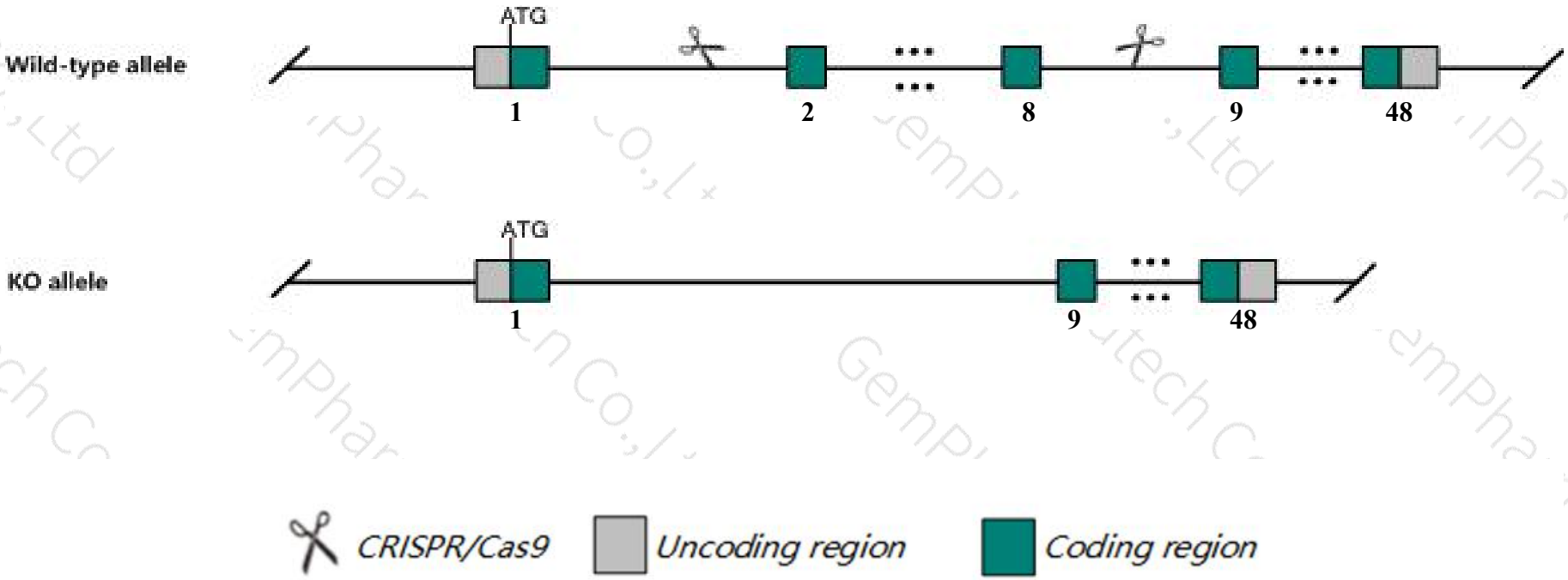
**Design Date:** 2019-12-16

# Project Overview

| | |
|---|---|
| **Project Name** | ***Ift172*** |
| **Project type** | **Cas9-KO** |
| **Strain background** | **C57BL/6JGpt** |

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ift172* gene. The schematic diagram is as follows:



# Technical routes

➢ The *Ift172* gene has 11 transcripts. According to the structure of *Ift172* gene, exon2-exon8 of *Ift172-201* (ENSMUST00000041565.10) transcript is recommended as the knockout region.The region contains 746bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Ift172* gene. The brief process is as follows: CRISPR/Cas9 system

# Notice

➢ According to the existing MGI data,Mice homozygous for disruptions in this gene display embryonic lethality during organogenesis, neural tube defects, and developmental patterning abnormalities. Mice homozygous for a conditional allele activated in the early limb bud exhibit polydactyly and short limbs.

➢Transcript-211,210 may not be affected.

➢ The *Ift172* gene is located on the Chr5. 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）

集萃药康 GemPharmatech

## Ift172 intraflagellar transport 172 [Mus musculus (house mouse)]

Gene ID: 67661, updated on 17-Feb-2019

### Summary

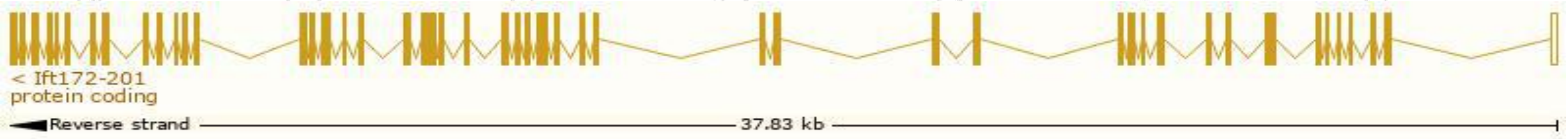
| | |
|---|---|
| **Official Symbol** | Ift172 provided by MGI |
| **Official Full Name** | intraflagellar transport 172 provided by MGI |
| **Primary source** | MGI:MGI:2682064 |
| **See related** | Ensembl:ENSMUSG00000038564 |
| **Gene type** | protein coding |
| **RefSeq status** | VALIDATED |
| **Organism** | Mus musculus |
| **Lineage** | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| **Also known as** | 4930553F24Rik, Slb, avc1, wim |
| **Expression** | Broad expression in testis adult (RPKM 50.1), cerebellum adult (RPKM 7.6) and 15 other tissues See more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

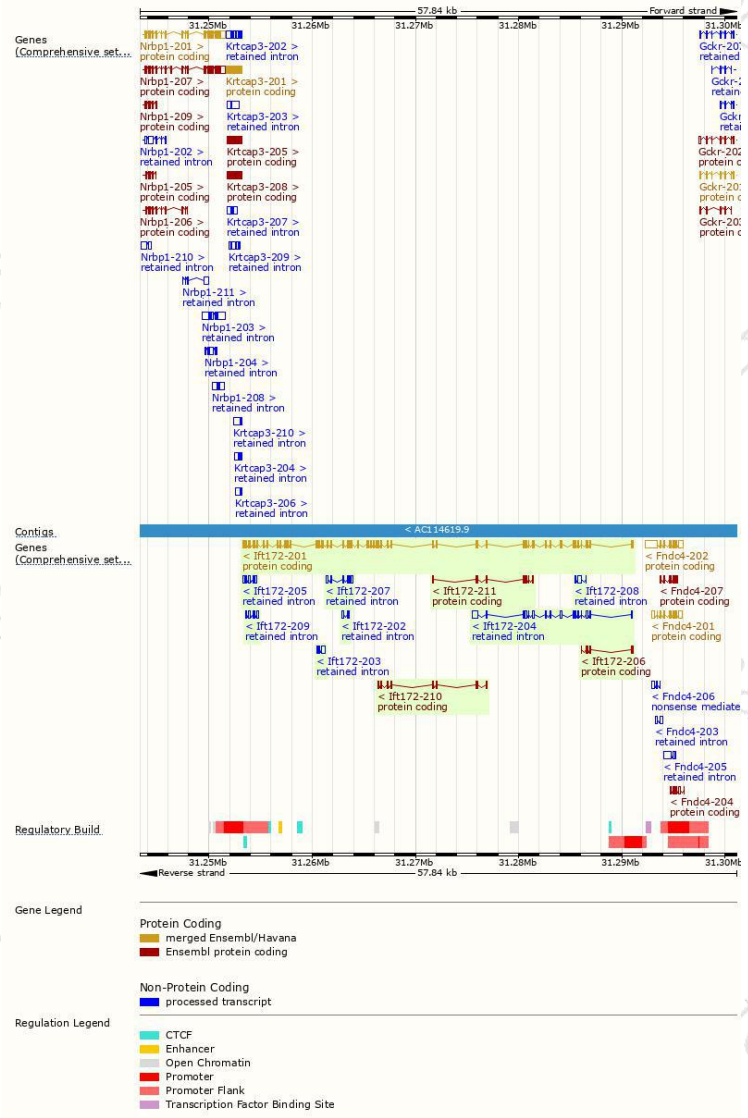
The gene has 11 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Ift172-201 | ENSMUST00000041565.10 | 5403 | 1749aa | Protein coding | CCDS39054 | Q6VH22 | TSL:1 GENCODE basic APPRIS P1 |
| Ift172-210 | ENSMUST00000202585.4 | 774 | 258aa | Protein coding | - | A0A0J9YUJ7 | 5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5 |
| Ift172-211 | ENSMUST00000202589.1 | 727 | 242aa | Protein coding | - | A0A0J9YU41 | CDS 5' incomplete TSL:3 |
| Ift172-206 | ENSMUST00000201809.1 | 405 | 83aa | Protein coding | - | A0A0J9YV04 | TSL:5 GENCODE basic |
| Ift172-204 | ENSMUST00000201274.1 | 2063 | No protein | Retained intron | - | - | TSL:1 |
| Ift172-207 | ENSMUST00000201953.3 | 785 | No protein | Retained intron | - | - | TSL:5 |
| Ift172-205 | ENSMUST00000201426.3 | 742 | No protein | Retained intron | - | - | TSL:1 |
| Ift172-209 | ENSMUST00000202560.1 | 563 | No protein | Retained intron | - | - | TSL:3 |
| Ift172-203 | ENSMUST00000201057.1 | 473 | No protein | Retained intron | - | - | TSL:3 |
| Ift172-208 | ENSMUST00000202410.2 | 435 | No protein | Retained intron | - | - | TSL:3 |
| Ift172-202 | ENSMUST00000200936.1 | 409 | No protein | Retained intron | - | - | TSL:3 |

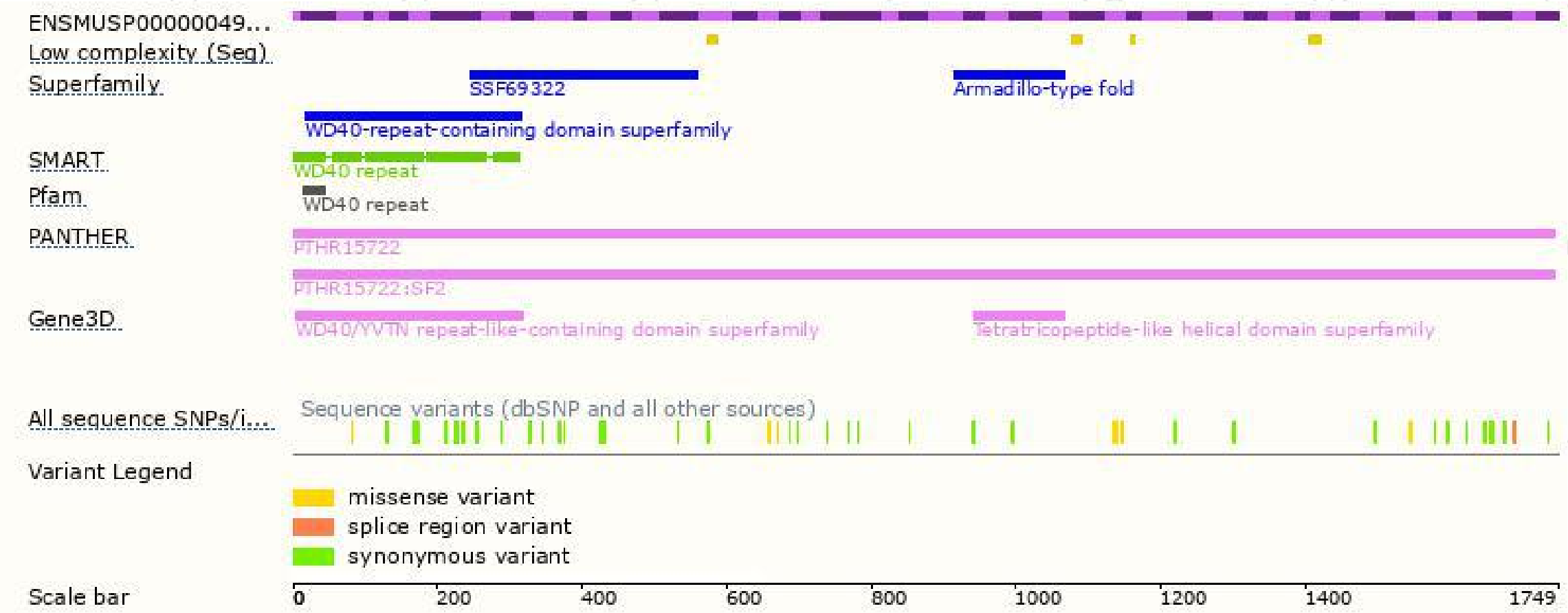
The strategy is based on the design of *Ift172-201* transcript,The transcription is shown below



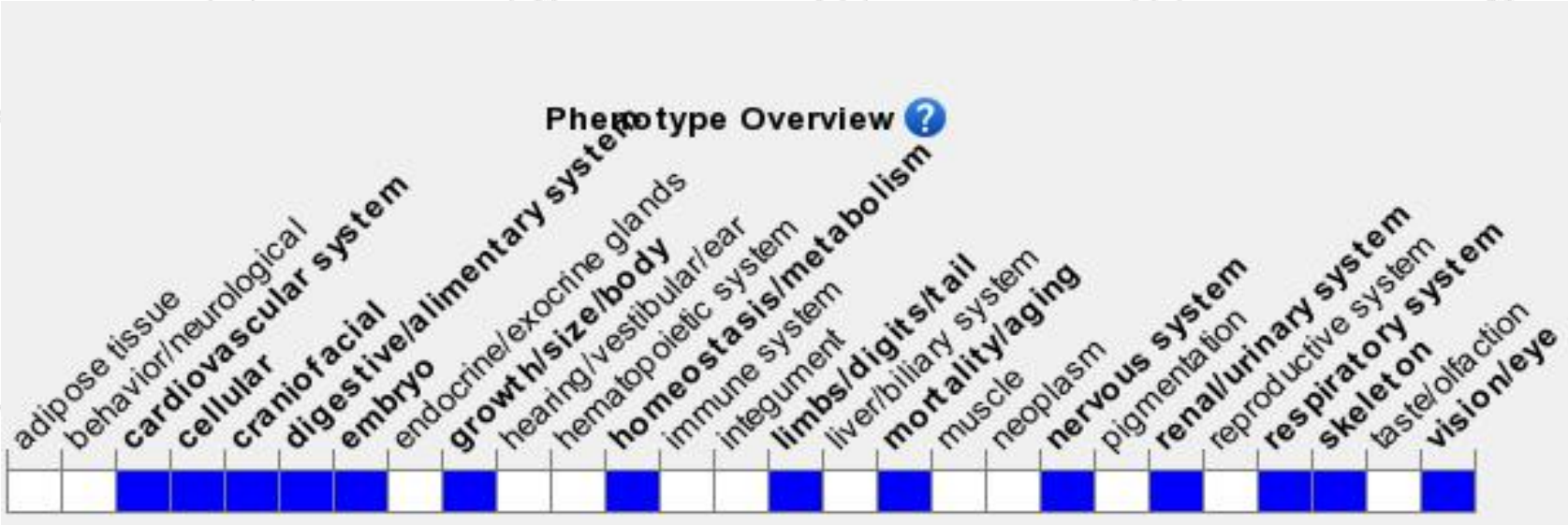
# Genomic location distribution



# 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,Mice homozygous for disruptions in this gene display embryonic lethality during organogenesis, neural tube defects, and developmental patterning abnormalities. Mice homozygous for a conditional allele activated in the early limb bud exhibit polydactyly and short limbs.

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

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