# *Pfas* Cas9-KO Strategy

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Reviewer:JiaYu
Design Date:2020-2-27

# Project Overview

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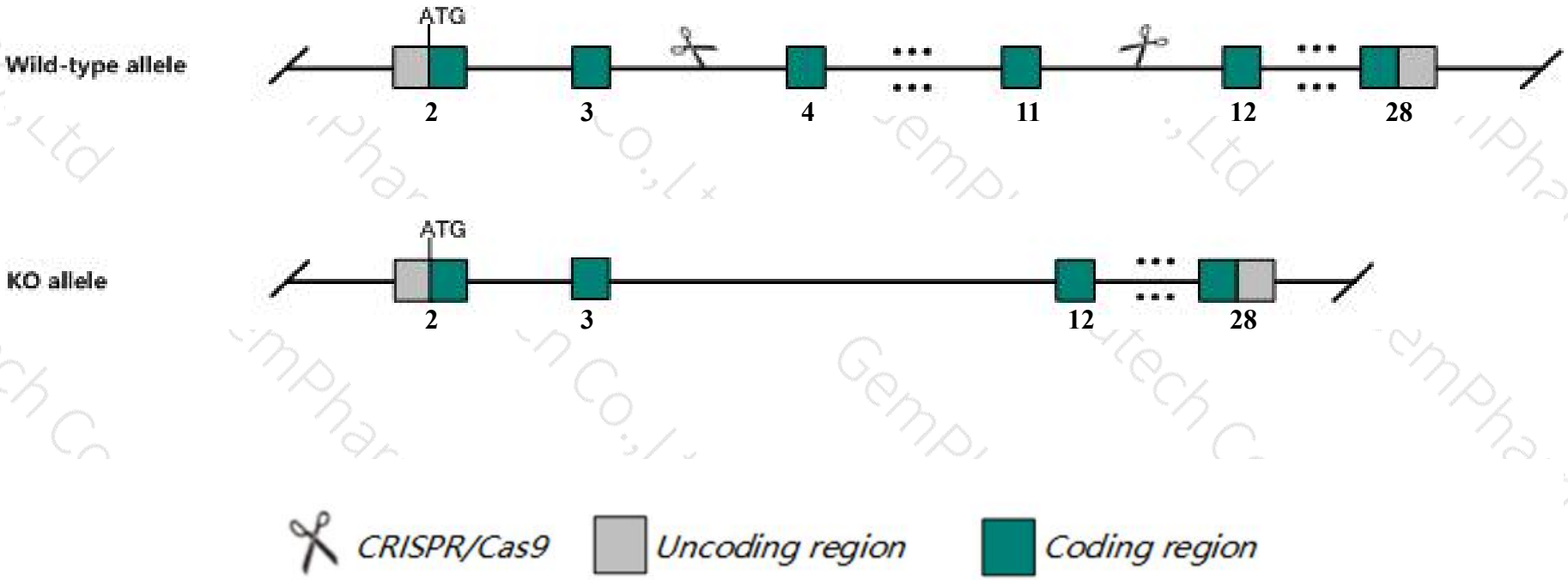
|---|---|
| **Project Name** | ***Pfas*** |
| **Project type** | **Cas9-KO** |
| **Strain background** | **C57BL/6JGpt** |

# Knockout strategy

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



# Technical routes

➢ The *Pfas* gene has 7 transcripts. According to the structure of *Pfas* gene, exon4-exon11 of *Pfas-201* (ENSMUST00000021282.11) transcript is recommended as the knockout region.The region contains 1058bp coding sequenc Knock out the region will result in disruption of protein function.

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

# Notice

- According to the existing MGI data,Mice heterozygous for spontaneous or ENU-induced mutations exhibit craniofacial abnormalities, most notably a domed cranium and short snout, variable white belly spots and white tail tips, and a range of eye defects including microphthalmia and anophthalmia.

- The *Pfas* gene is located on the Chr11. 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

## Pfas phosphoribosylformylglycinamidine synthase (FGAR amidotransferase) [ *Mus musculus* (house mouse) ]

Gene ID: 237823, updated on 25-Feb-2020

### Summary

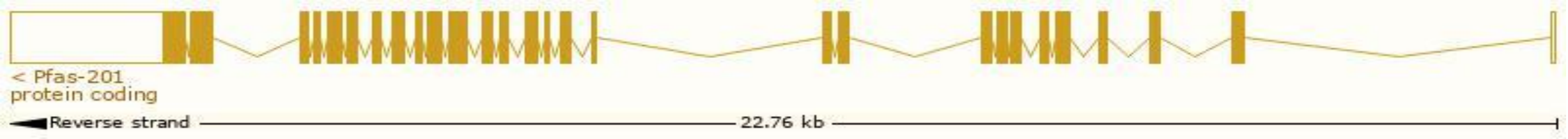
| | |
|---|---|
| **Official Symbol** | Pfas provided by MGI |
| **Official Full Name** | phosphoribosylformylglycinamidine synthase (FGAR amidotransferase) provided by MGI |
| **Primary source** | MGI:MGI:2684864 |
| **See related** | Ensembl:ENSMUSG00000020899 |
| **Gene type** | protein coding |
| **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** | Gm18; PURL; Sofa; FGAMS; FGARAT; FGAR-AT; 4432409B16Rik |
| **Expression** | Ubiquitous expression in CNS E11.5 (RPKM 10.9), ovary adult (RPKM 10.3) and 28 other tissues See more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

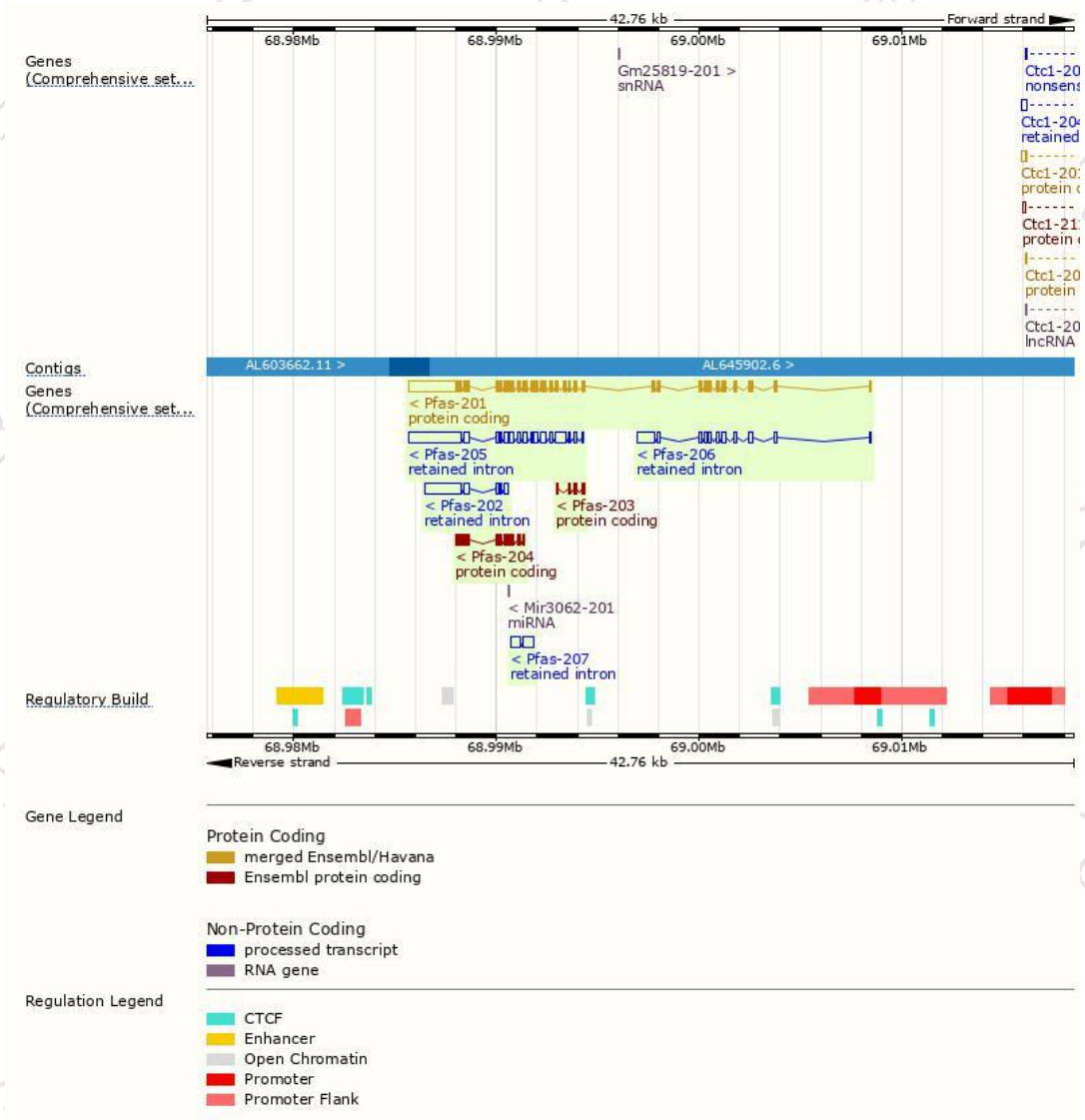
The gene has 7 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Pfas-201 | ENSMUST00000021282.11 | 6373 | 1337aa | Protein coding | CCDS48823 | Q5SUR0 | TSL:5 GENCODE basic APPRIS P1 |
| Pfas-204 | ENSMUST00000152964.2 | 1421 | 473aa | Protein coding | - | F6RUL9 | CDS 5' incomplete TSL:3 |
| Pfas-203 | ENSMUST00000149703.3 | 350 | 117aa | Protein coding | - | G3UY86 | 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 |
| Pfas-205 | ENSMUST00000172915.7 | 5144 | No protein | Retained intron | - | - | TSL:5 |
| Pfas-202 | ENSMUST00000146490.1 | 2584 | No protein | Retained intron | - | - | TSL:1 |
| Pfas-206 | ENSMUST00000172987.1 | 2129 | No protein | Retained intron | - | - | TSL:1 |
| Pfas-207 | ENSMUST00000173410.1 | 927 | No protein | Retained intron | - | - | TSL:2 |

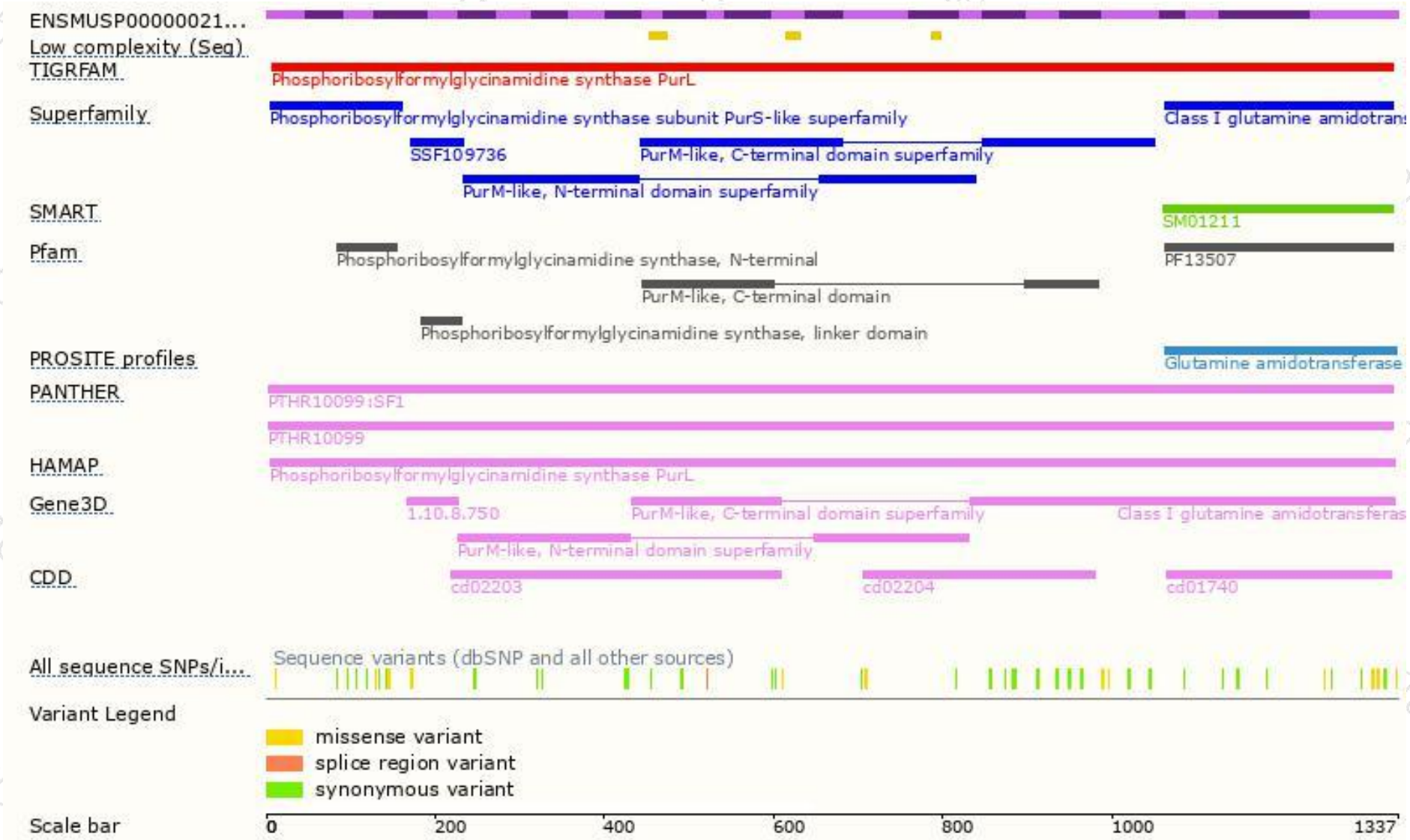
The strategy is based on the design of *Pfas-201* transcript,The transcription is shown below



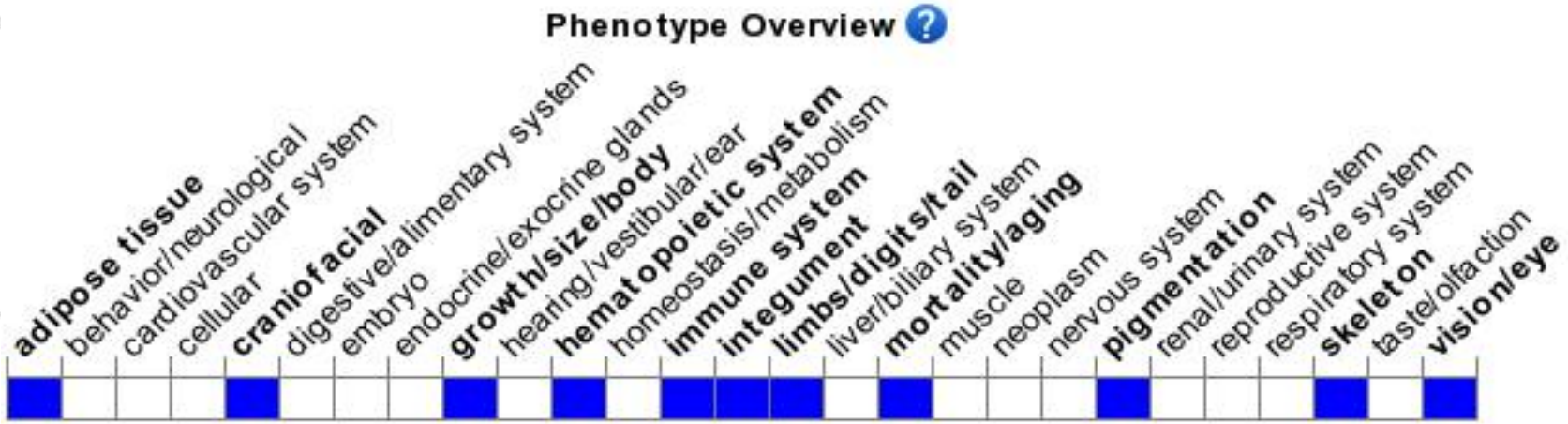
# Genomic location distribution



# 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/).*

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

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