

Fam114a1 Cas9-KO Strategy

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Project Overview

Project Name

Fam114a1

Project type

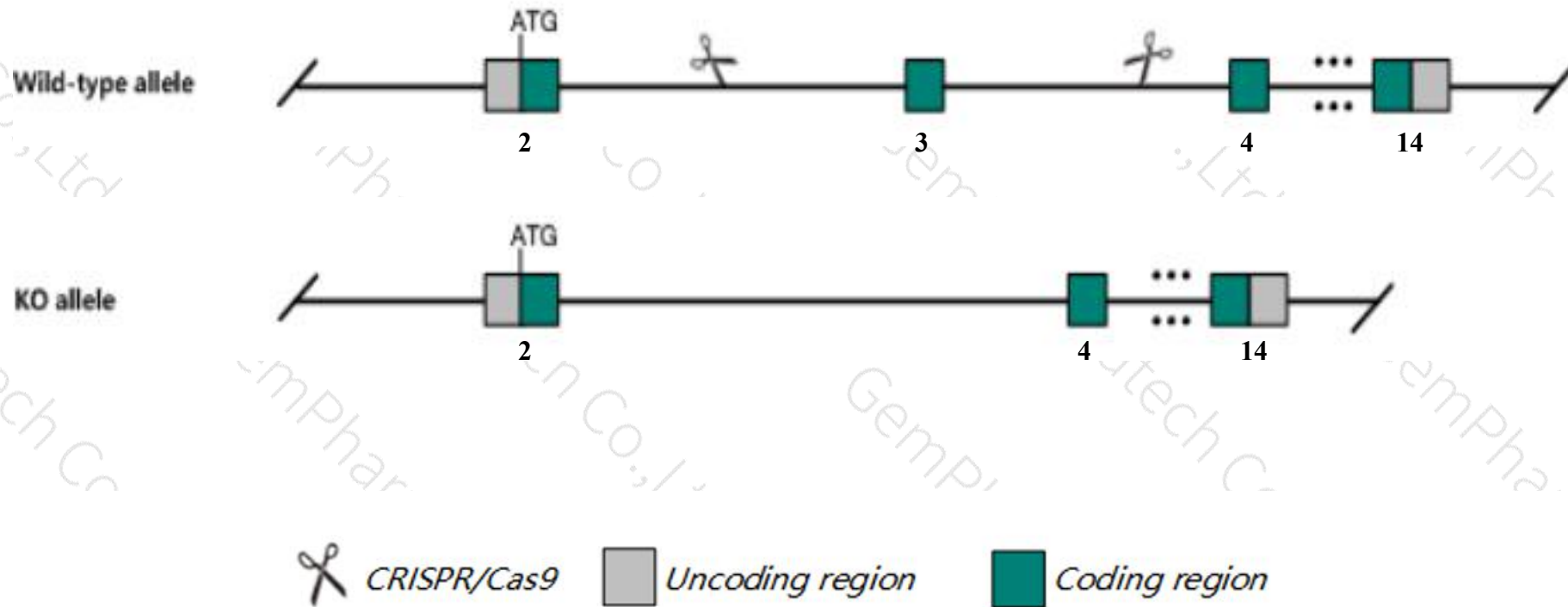
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fam114a1* gene. The schematic diagram is as follows:



- The *Fam114a1* gene has 2 transcripts. According to the structure of *Fam114a1* gene, exon3 of *Fam114a1-201*(ENSMUST00000031080.14) transcript is recommended as the knockout region. The region contains 88bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fam114a1* gene. The brief process is as follows: CRISPR/Cas9 system 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 *Fam114a1* 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)

Fam114a1 family with sequence similarity 114, member A1 [Mus musculus (house mouse)]

Gene ID: 68303, updated on 13-Mar-2020

Summary



Official Symbol [Fam114a1](#) provided by [MGI](#)

Official Full Name [family with sequence similarity 114, member A1](#) provided by [MGI](#)

Primary source [MGI:MGI:1915553](#)

See related [Ensembl:ENSMUSG00000029185](#)

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 [1190001N04Rik](#), [9130005N14Rik](#), [Noxp20](#)

Expression [Broad expression in bladder adult \(RPKM 26.5\), limb E14.5 \(RPKM 22.0\) and 26 other tissues](#)[See more](#)

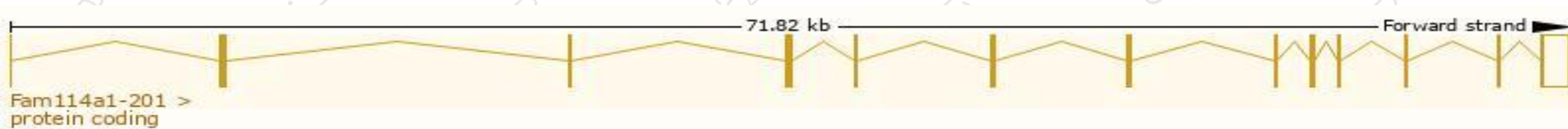
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

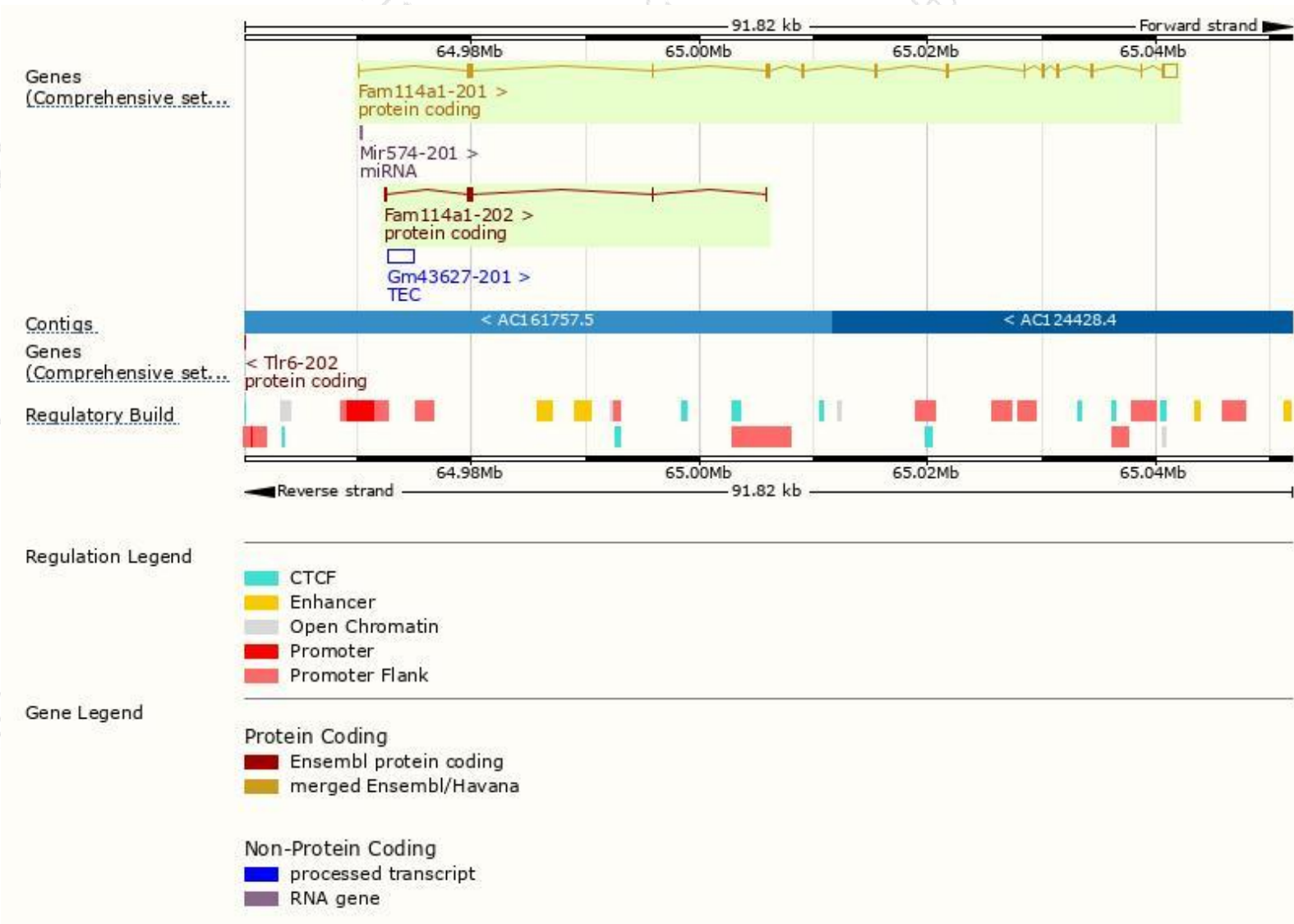
The gene has 2 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fam114a1-201	ENSMUST00000031080.14	2938	569aa	Protein coding	CCDS19304	Q9D281	TSL:1 GENCODE basic APPRIS P1
Fam114a1-202	ENSMUST00000139366.1	576	176aa	Protein coding	-	D3Z2J2	CDS 3' incomplete TSL:5

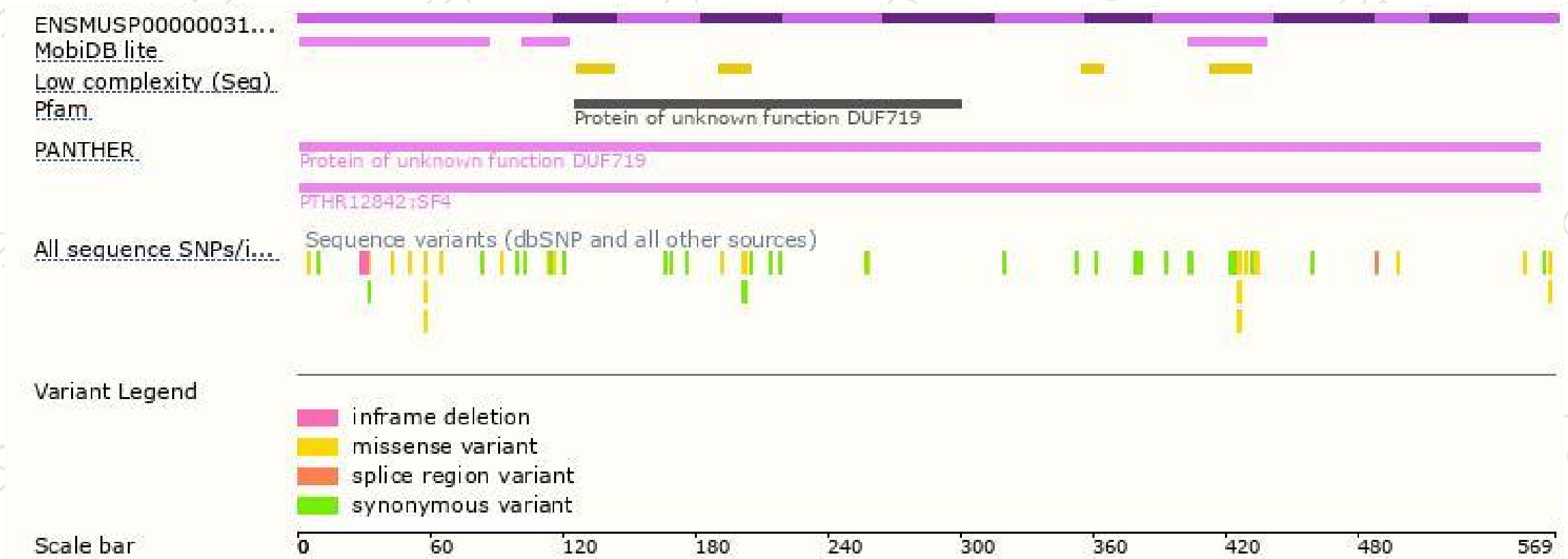
The strategy is based on the design of *Fam114a1-201* transcript, the transcription is shown below:



Genomic location distribution

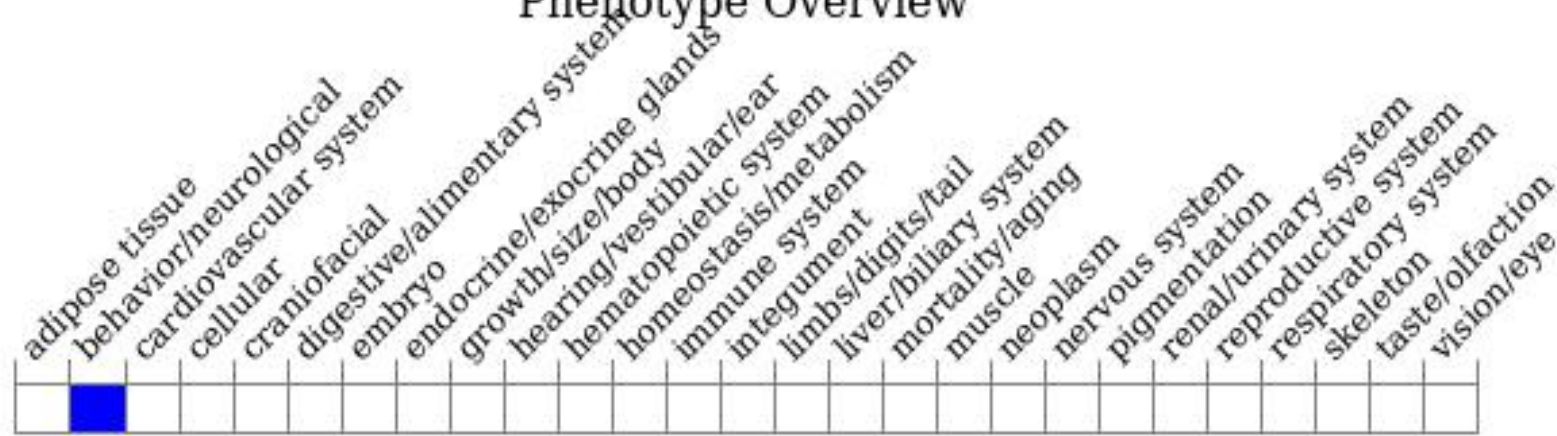


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview



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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