

Fam20a Cas9-KO Strategy

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Project Overview

Project Name

Fam20a

Project type

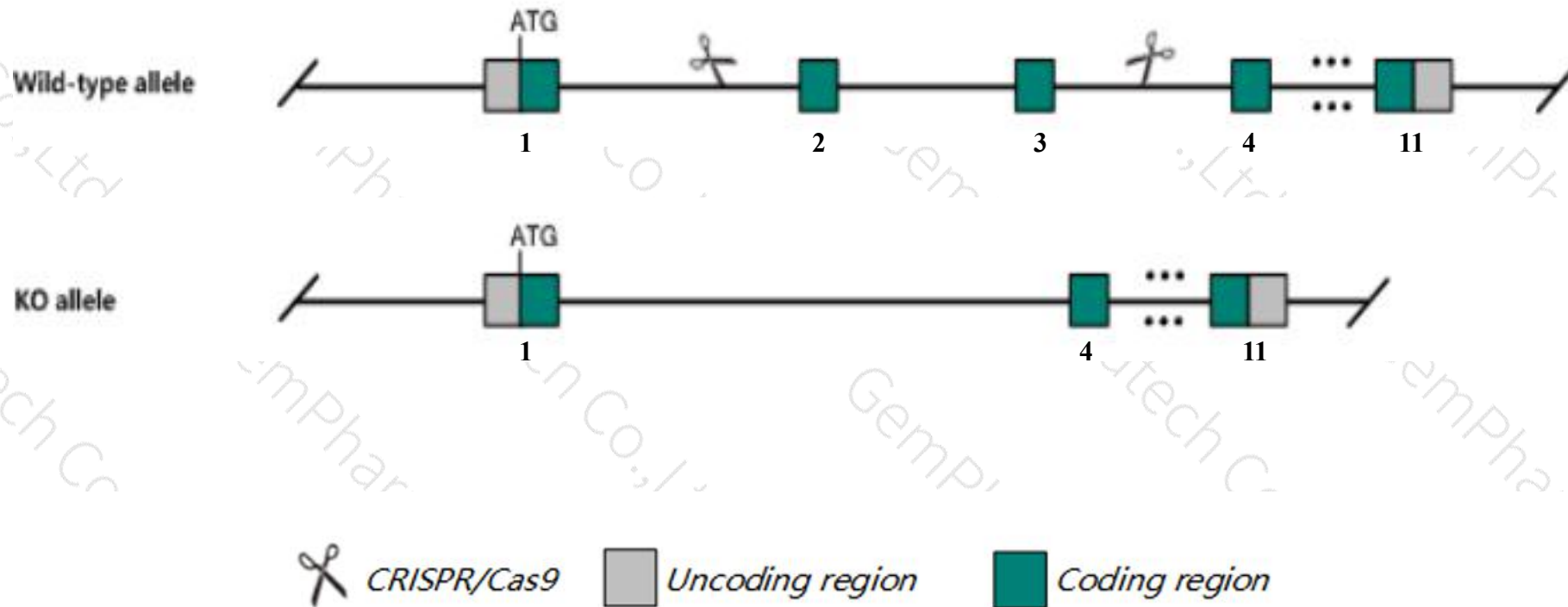
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fam20a* gene. The schematic diagram is as follows:



- The *Fam20a* gene has 4 transcripts. According to the structure of *Fam20a* gene, exon2-exon3 of *Fam20a-201* (ENSMUST00000020938.7) transcript is recommended as the knockout region. The region contains 236bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fam20a* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit abnormal ameloblast morphology, disrupted dental enamel formation in both incisor and molar teeth, abnormal kidney morphology, disseminated calcifications of muscular arteries, and intrapulmonary calcifications.
- The *Fam20a* 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)

Fam20a family with sequence similarity 20, member A [*Mus musculus* (house mouse)]

Gene ID: 208659, updated on 13-Mar-2020

Summary

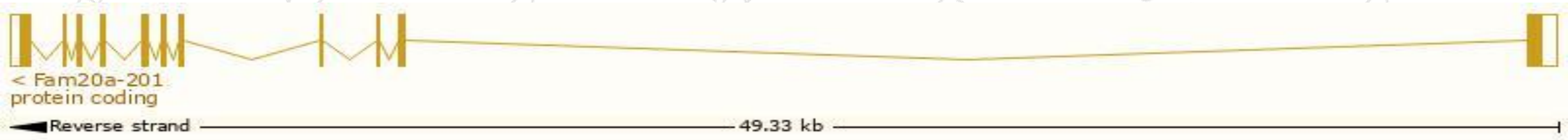
Official Symbol	Fam20a provided by MGI
Official Full Name	family with sequence similarity 20, member A provided by MGI
Primary source	MGI:MGI:2388266
See related	Ensembl:ENSMUSG00000020614
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI606893
Expression	Ubiquitous expression in testis adult (RPKM 14.5), duodenum adult (RPKM 11.5) and 26 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

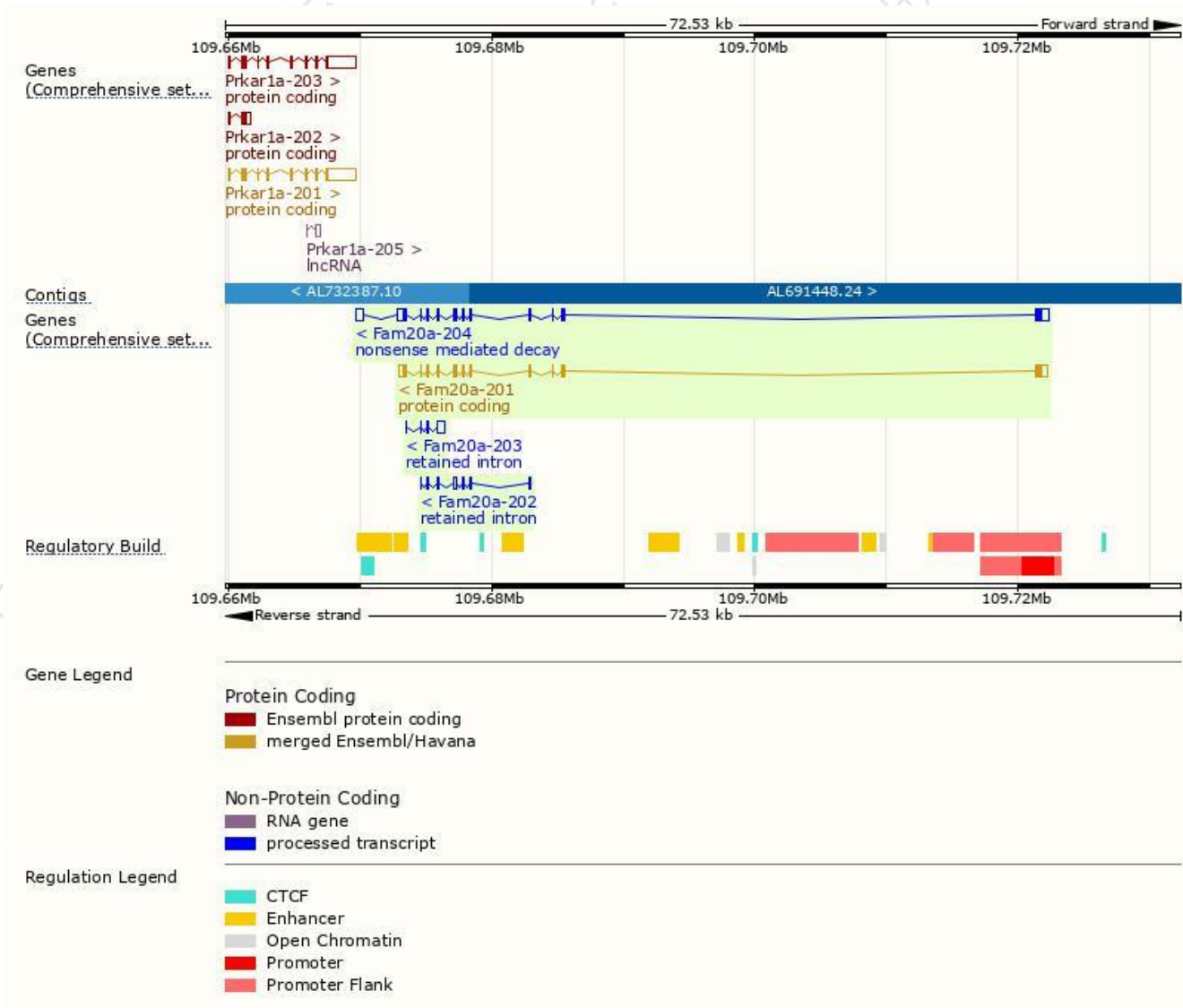
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fam20a-201	ENSMUST00000020938.7	2541	541aa	Protein coding	CCDS25584	Q8CID3	TSL:1 GENCODE basic APPRIS P1
Fam20a-204	ENSMUST00000155559.7	3085	541aa	Nonsense mediated decay	-	Q8CID3	TSL:1
Fam20a-203	ENSMUST00000146408.7	828	No protein	Retained intron	-	-	TSL:3
Fam20a-202	ENSMUST00000144972.1	794	No protein	Retained intron	-	-	TSL:3

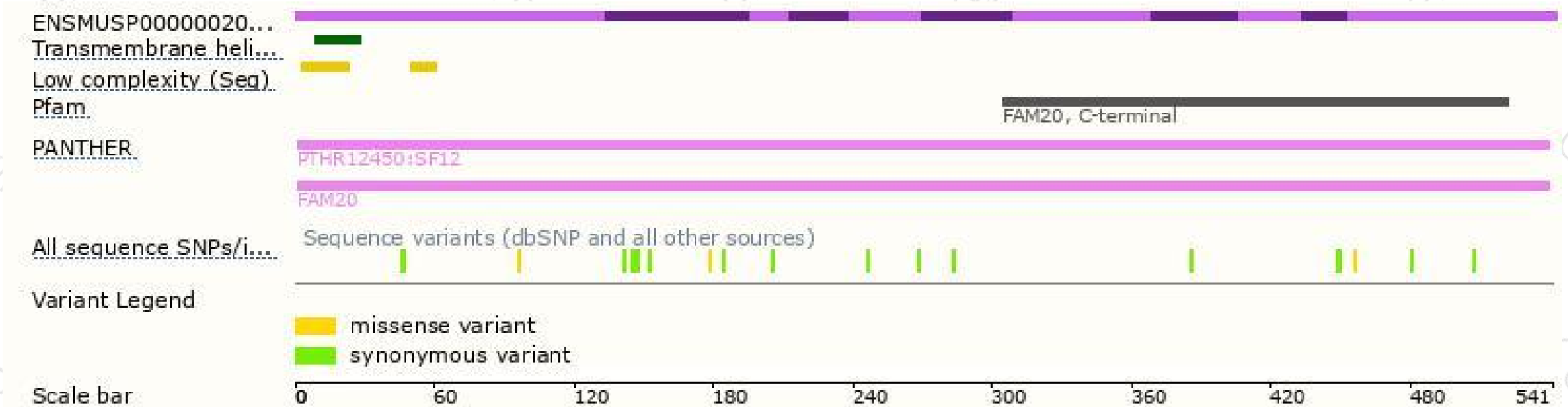
The strategy is based on the design of *Fam20a-201* transcript,The transcription is shown below



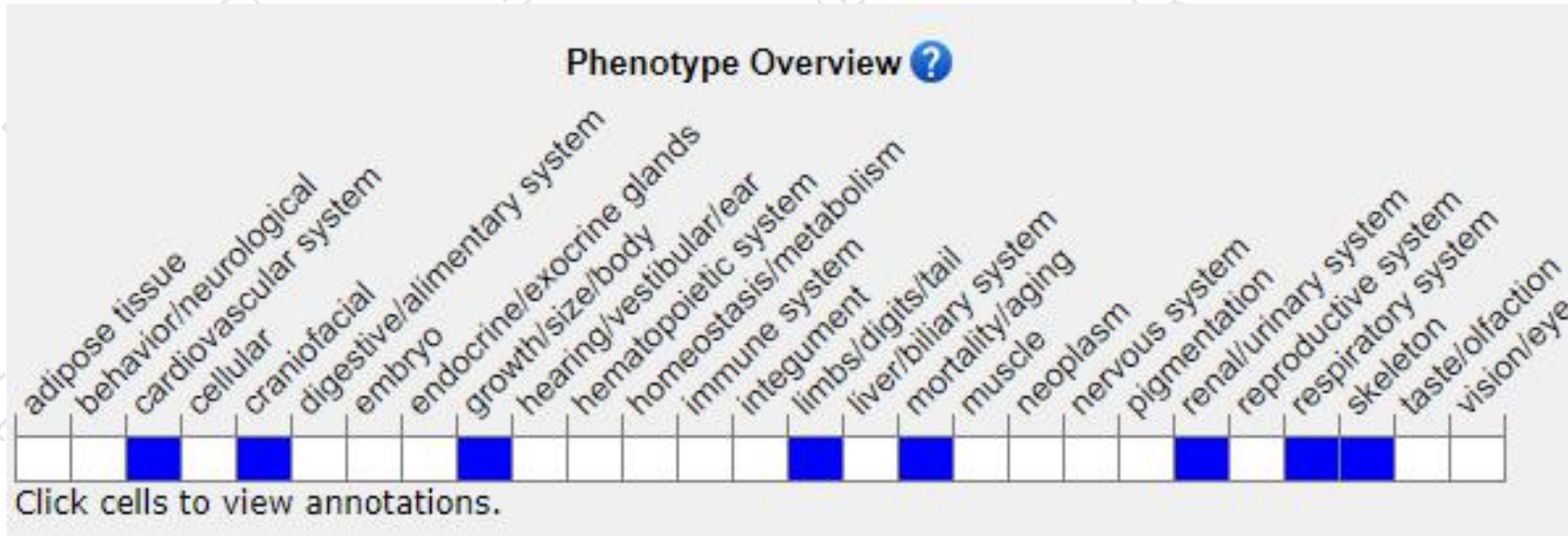
Genomic location distribution



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 a knock-out allele exhibit abnormal ameloblast morphology, disrupted dental enamel formation in both incisor and molar teeth, abnormal kidney morphology, disseminated calcifications of muscular arteries, and intrapulmonary calcifications.

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

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