

***Fam13b* Cas9-CKO Strategy**

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Project Overview

Project Name

Fam13b

Project type

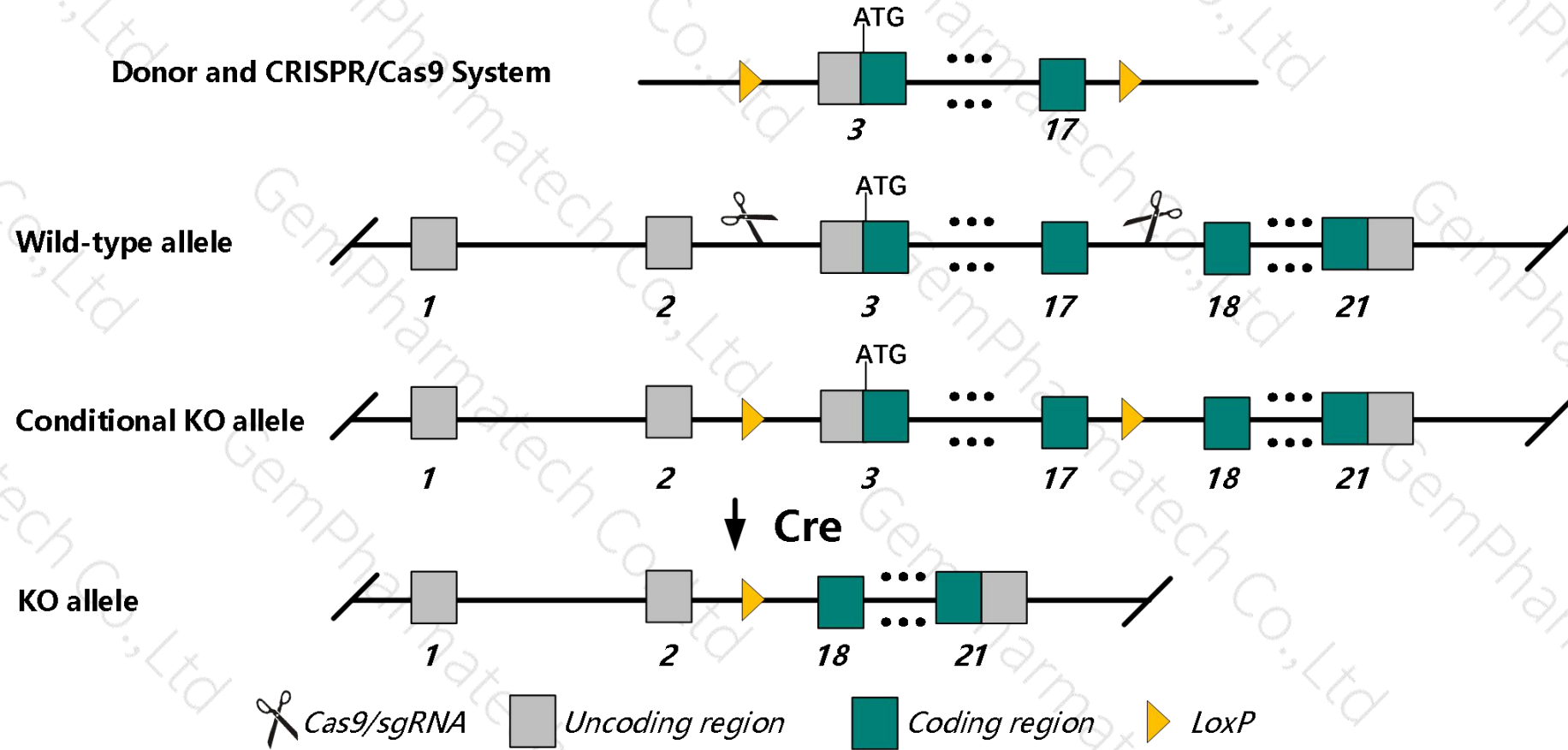
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fam13b* gene. The schematic diagram is as follows:



Technical routes

- The *Fam13b* gene has 13 transcripts. According to the structure of *Fam13b* gene, exon3-exon17 of *Fam13b-201*(ENSMUST00000040506.7) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fam13b* 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 *Fam13b* gene is located on the Chr18. 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.

Gene information (NCBI)

Fam13b family with sequence similarity 13, member B [Mus musculus (house mouse)]

Gene ID: 225358, updated on 13-Mar-2020

Summary



Official Symbol Fam13b provided by [MGI](#)

Official Full Name family with sequence similarity 13, member B provided by [MGI](#)

Primary source [MGI:MGI:2447834](#)

See related [Ensembl:ENSMUSG00000036501](#)

Gene type protein coding

RefSeq status PROVISIONAL

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as 2610024E20Rik, AW060714, AW546153

Expression Ubiquitous expression in CNS E18 (RPKM 15.4), whole brain E14.5 (RPKM 11.7) and 28 other tissues [See more](#)

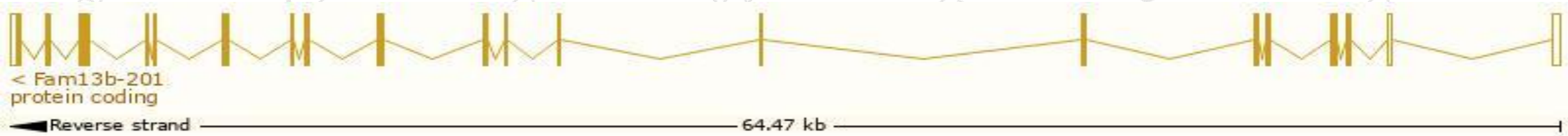
Orthologs [human all](#)

Transcript information (Ensembl)

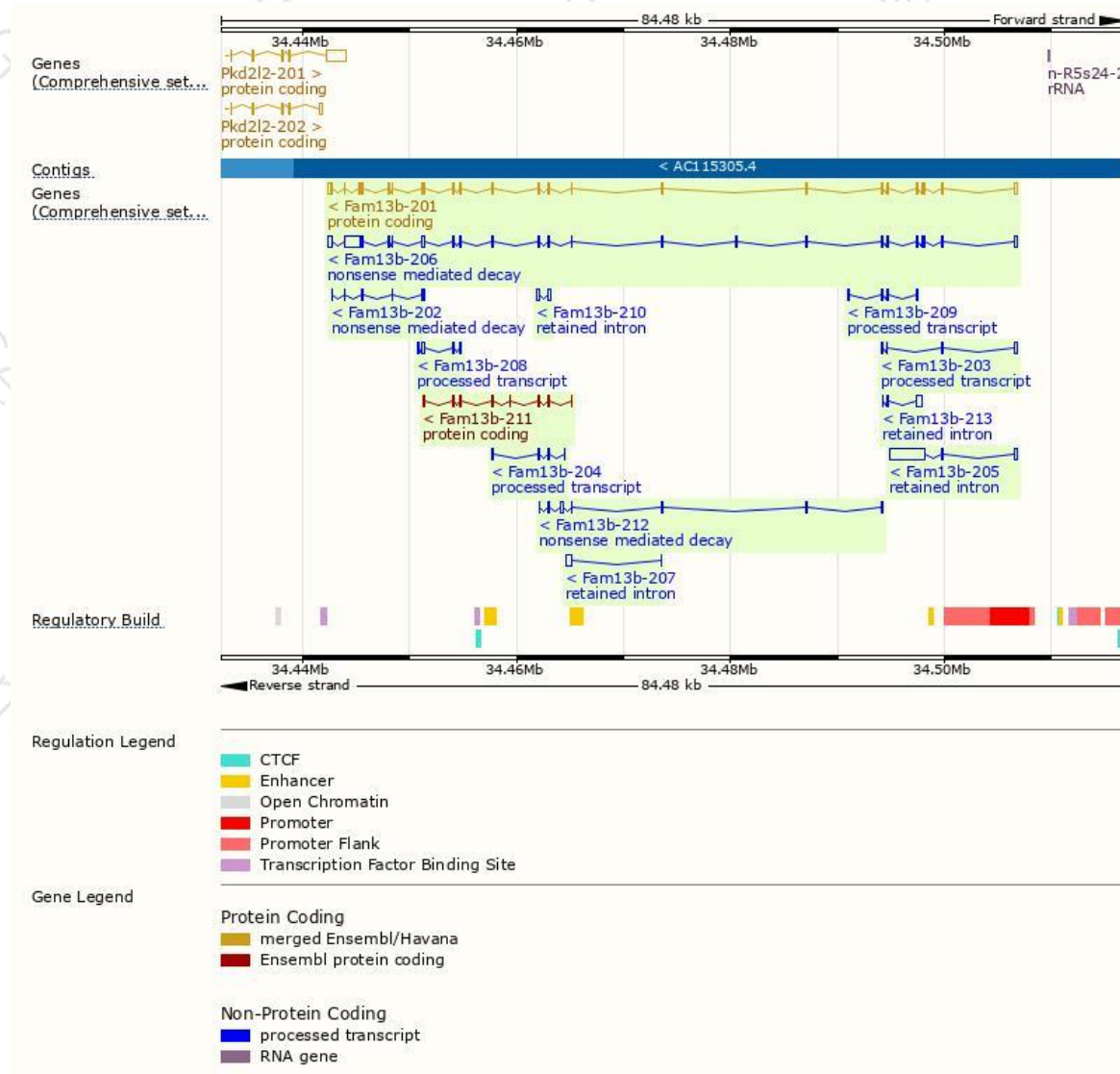
The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fam13b-201	ENSMUST00000040506.7	3344	851aa	Protein coding	CCDS29128	Q8K2H3	TSL:1 GENCODE basic APPRIS P1
Fam13b-211	ENSMUST00000238047.1	919	306aa	Protein coding	-	A0A494B9P7	CDS 5' and 3' incomplete
Fam13b-206	ENSMUST00000236786.1	4731	289aa	Nonsense mediated decay	-	A0A494B944	
Fam13b-212	ENSMUST00000238059.1	736	137aa	Nonsense mediated decay	-	A0A494BBL2	CDS 5' incomplete
Fam13b-202	ENSMUST00000235364.1	510	134aa	Nonsense mediated decay	-	A0A494BBP0	CDS 5' incomplete
Fam13b-203	ENSMUST00000235499.1	680	No protein	Processed transcript	-	-	
Fam13b-209	ENSMUST00000237576.1	621	No protein	Processed transcript	-	-	
Fam13b-208	ENSMUST00000237302.1	598	No protein	Processed transcript	-	-	
Fam13b-204	ENSMUST00000235529.1	463	No protein	Processed transcript	-	-	
Fam13b-205	ENSMUST00000236598.1	3757	No protein	Retained intron	-	-	
Fam13b-213	ENSMUST00000238068.1	794	No protein	Retained intron	-	-	
Fam13b-207	ENSMUST00000237051.1	658	No protein	Retained intron	-	-	
Fam13b-210	ENSMUST00000237676.1	525	No protein	Retained intron	-	-	

The strategy is based on the design of *Fam13b-201* transcript,the transcription is shown below:



Genomic location distribution



Protein domain

ENSMUSP000000038...

MobiDB lite

Low complexity (Seg)

Coiled-coils (Ncoils)

Superfamily

SMART

Pfam

PROSITE profiles

PANTHER

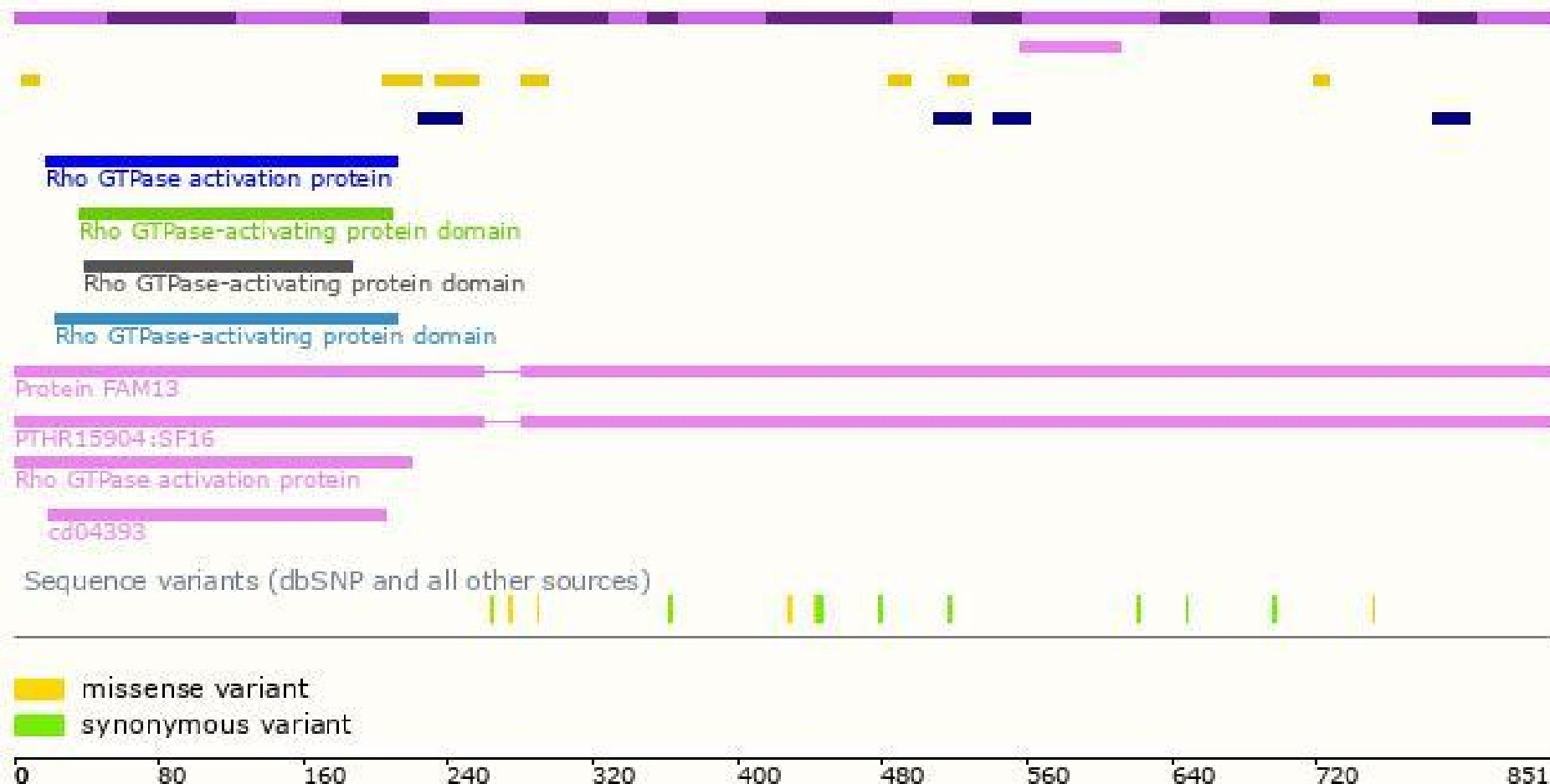
Gene3D

CDD

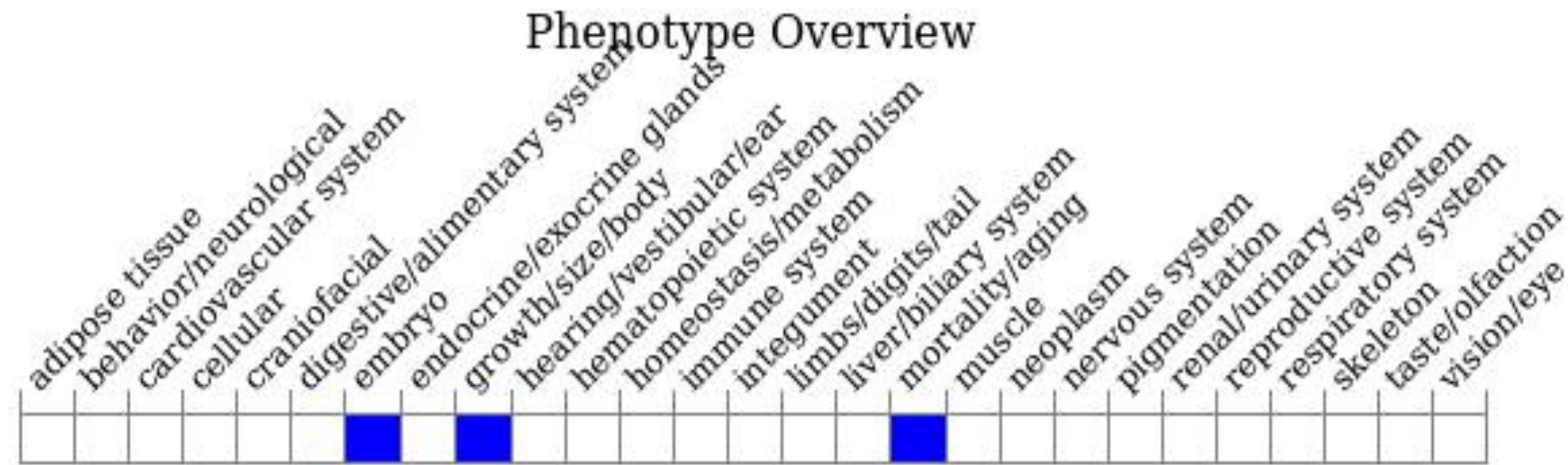
All sequence SNPs/i...

Variant Legend

Scale bar



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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