Fat1 Cas9-KO Strategy

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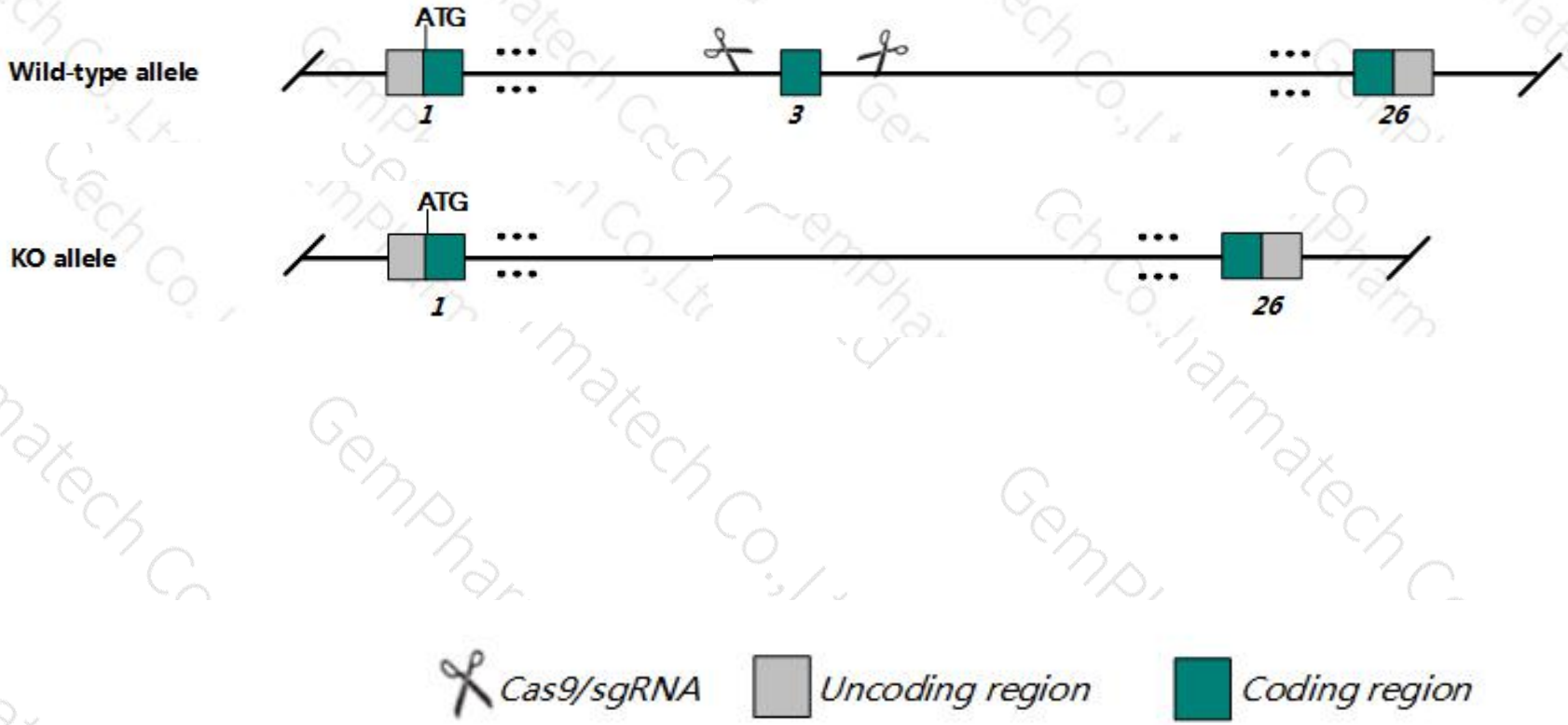
Design Date: 2019-7-17

Project Overview

Project Name	***Fat1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fat1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Fat1* gene has 6 transcripts. According to the structure of *Fat1* gene, exon4 of *Fat1-205* (ENSMUST00000191428.6) transcript is recommended as the knockout region.The region contains 62bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Fat1* gene. The brief process is as follows: CRISPR/Cas9 system v

Notice

- According to the existing MGI data,Homozygotes for a targeted null mutation exhibit holoprosencephaly, anophthalmia, kidney defects and perinatal lethality. Mice homozygous for a hypomorphic allele exhibit altered shoulder girdle and facial musculature, retinal defects, abnormal inner earpatterning and kidney defects.

- The *Fat1* gene is located on the Chr8. 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）

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Fat1 FAT atypical cadherin 1 [Mus musculus (house mouse)]

Gene ID: 14107, updated on 31-Jan-2019

Summary

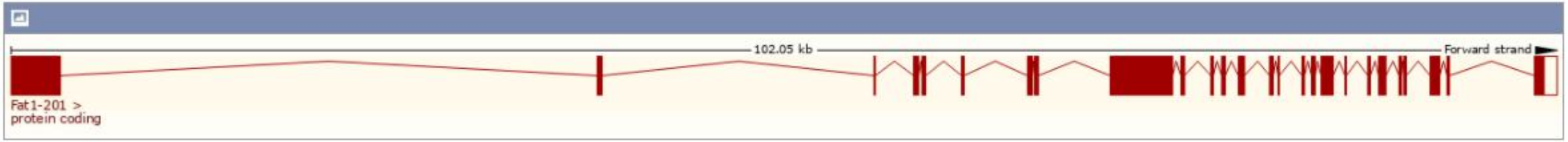
Official Symbol	Fat1 provided by MGI
Official Full Name	FAT atypical cadherin 1 provided by MGI
Primary source	MGI:MGI:109168
See related	Ensembl:ENSMUSG00000070047
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2310038E12Rik, AU023433, Fath, mFat1
Expression	Ubiquitous expression in limb E14.5 (RPKM 20.3), colon adult (RPKM 15.5) and 24 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

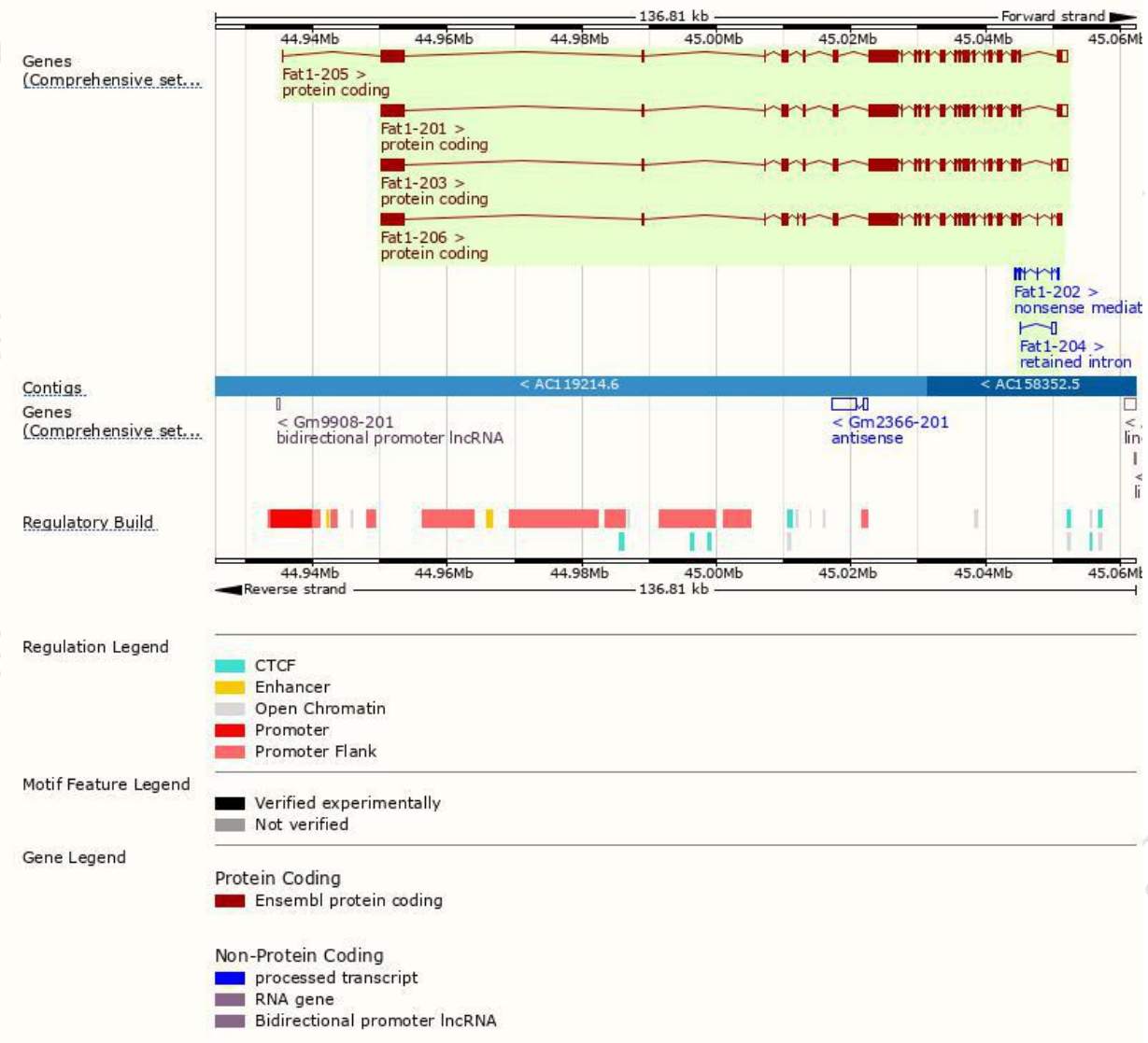
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fat1-205	ENSMUST00000191428.6	14814	4590aa	Protein coding	CCDS52547	F2Z4A3	TSL:5 GENCODE basic APPRIS P1
Fat1-201	ENSMUST00000098796.9	14627	4590aa	Protein coding	CCDS52547	F2Z4A3	TSL:5 GENCODE basic APPRIS P1
Fat1-203	ENSMUST00000189017.7	14651	4602aa	Protein coding	-	A0A087WRT4	TSL:5 GENCODE basic
Fat1-206	ENSMUST00000215588.1	13938	4645aa	Protein coding	-	A0A1L1SQU7	TSL:5 GENCODE basic
Fat1-202	ENSMUST00000186342.2	739	159aa	Nonsense mediated decay	-	A0A087WPU4	CDS 5' incomplete TSL:1
Fat1-204	ENSMUST00000189367.1	693	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Fat1-201* transcript,The transcription is shown below

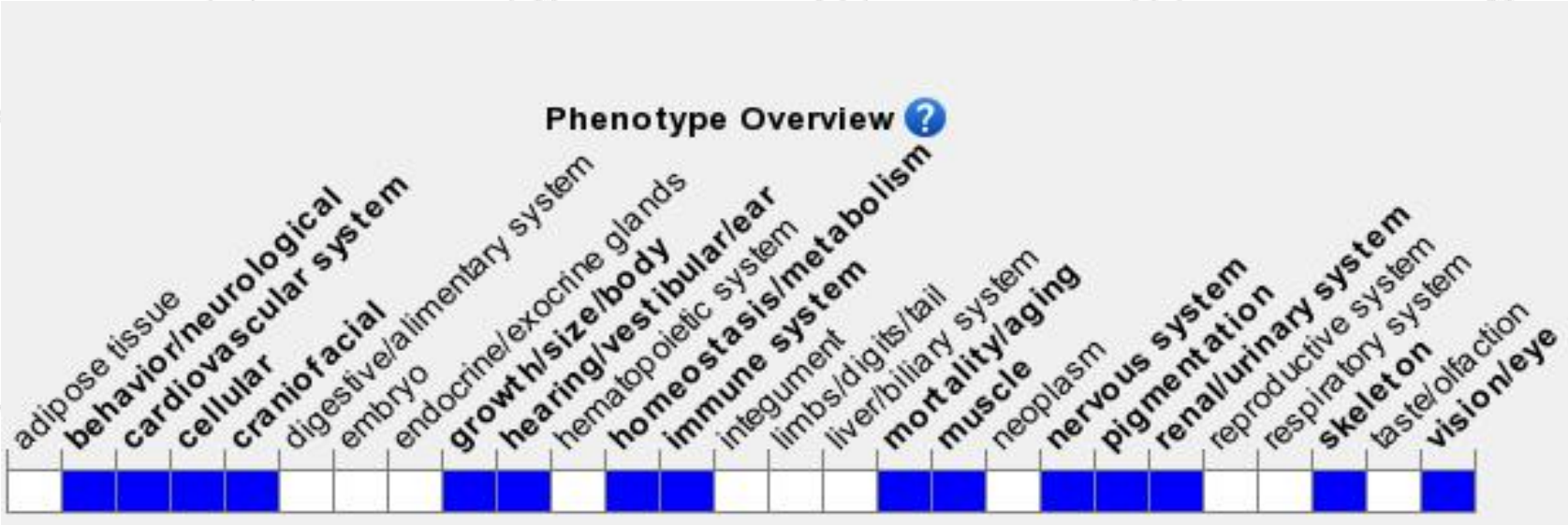


Genomic location distribution



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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