

Fbxo44 Cas9-KO Strategy

Designer:

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Design Date:

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Project Overview

Project Name

Fbxo44

Project type

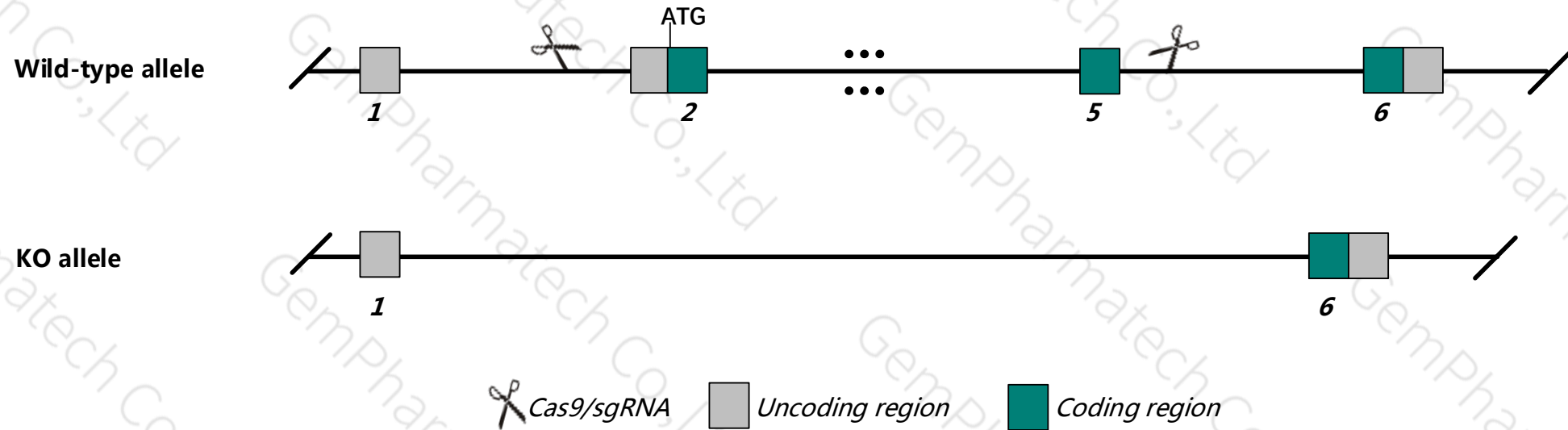
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Fbxo44* gene. The schematic diagram is as follows:



- The *Fbxo44* gene has 10 transcripts. According to the structure of *Fbxo44* gene, exon2~exon5 of *Fbxo44-201* (ENSMUST00000057907.9) transcript is recommended as the knockout region. The region contains the start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fbxo44* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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 *Fbxo44* gene is located on the Chr4. 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.
- The distance between exon2 of *Fbxo44* and *Fbxo2* is about 1.7kb, and the 5-terminal regulation of *Fbxo2* may be affect.
- 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)

Fbxo44 F-box protein 44 [*Mus musculus* (house mouse)]

Gene ID: 230903, updated on 14-Aug-2019

Summary

Official Symbol Fbxo44 provided by [MGI](#)
Official Full Name F-box protein 44 provided by [MGI](#)
Primary source [MGI:MGI:1354744](#)
See related [Ensembl:ENSMUSG00000029001](#)
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 FBG3; FBX30; Fbx6a; Fbxo6a; AV001623; 5730411K09
Expression Broad expression in testis adult (RPKM 49.7), cerebellum adult (RPKM 30.0) and 19 other tissues [See more](#)
Orthologs [human](#) [all](#)

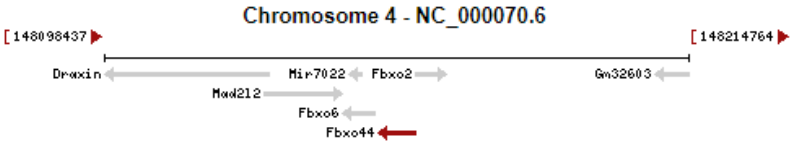
Genomic context

Location: 4; 4 E2

See Fbxo44 in [Genome Data Viewer](#)

Exon count: 12

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	4	NC_000070.6 (148152799..148160183, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	4	NC_000070.5 (147526909..147534173, complement)

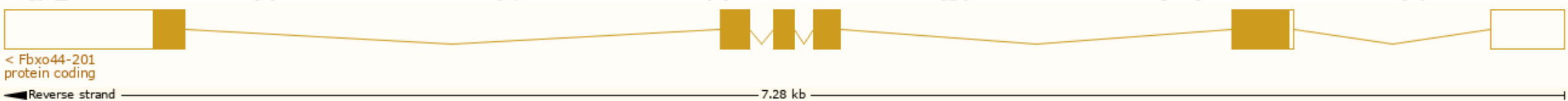


Transcript information (Ensembl)

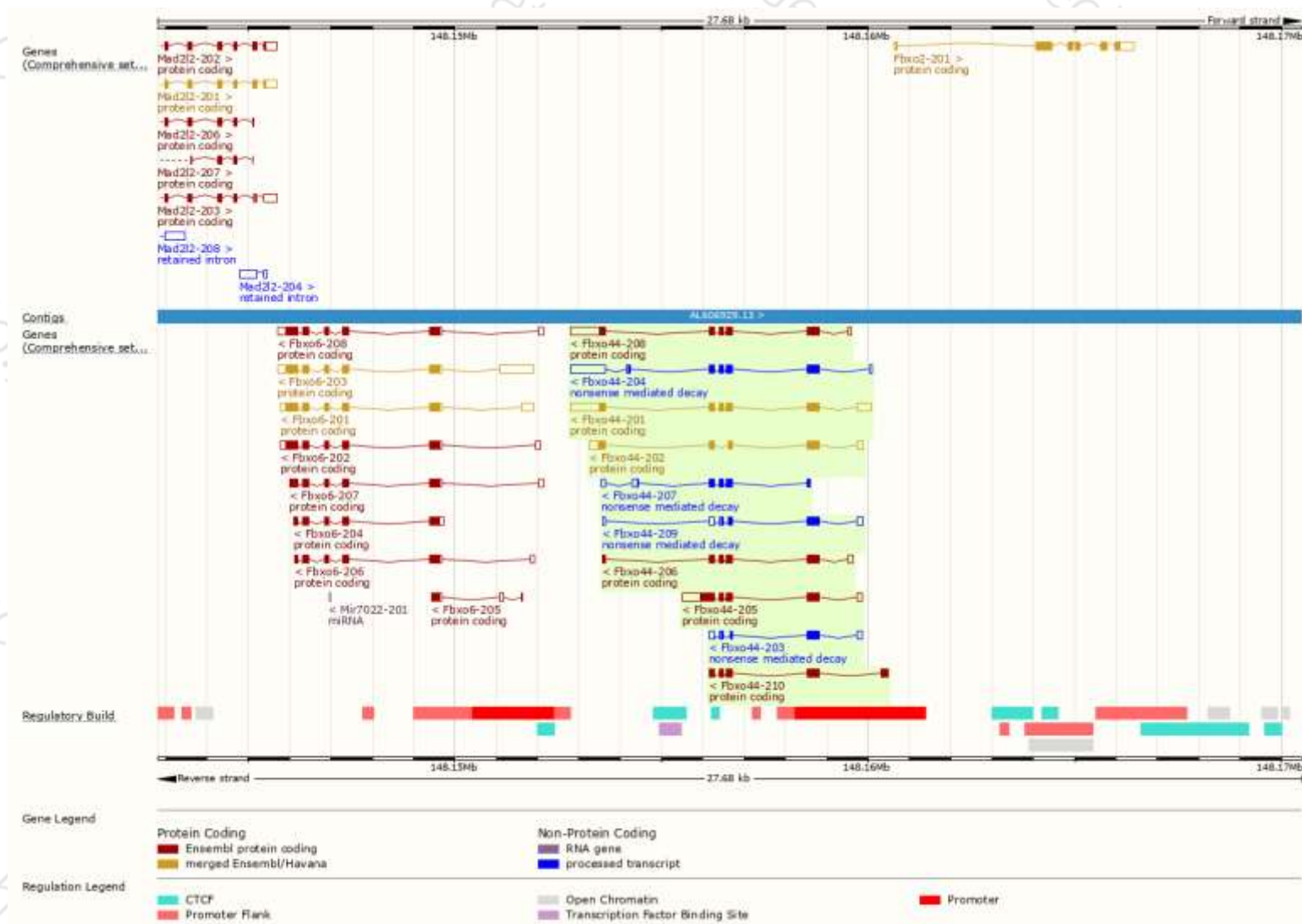
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fbxo44-201	ENSMUST00000057907.9	1829	255aa	Protein coding	CCDS18934	A2A7H5	TSL:1 GENCODE basic APPRIS P1
Fbxo44-208	ENSMUST00000167160.7	1572	255aa	Protein coding	CCDS18934	A2A7H5	TSL:5 GENCODE basic APPRIS P1
Fbxo44-202	ENSMUST00000105705.8	1034	224aa	Protein coding	CCDS51377	A2A7H6	TSL:2 GENCODE basic
Fbxo44-205	ENSMUST00000151127.7	1403	276aa	Protein coding	-	G3UYF5	TSL:1 GENCODE basic
Fbxo44-206	ENSMUST00000151246.7	854	232aa	Protein coding	-	A2A7H4	CDS 3' incomplete TSL:5
Fbxo44-210	ENSMUST00000173352.1	793	254aa	Protein coding	-	G3UZT3	CDS 3' incomplete TSL:3
Fbxo44-204	ENSMUST00000129253.7	1633	218aa	Nonsense mediated decay	-	E9PUJ0	TSL:1
Fbxo44-209	ENSMUST00000172472.7	823	133aa	Nonsense mediated decay	-	G3UY69	TSL:5
Fbxo44-207	ENSMUST00000153703.7	677	144aa	Nonsense mediated decay	-	F6UI76	CDS 5' incomplete TSL:3
Fbxo44-203	ENSMUST00000122913.2	676	117aa	Nonsense mediated decay	-	D6RHP0	TSL:5

The strategy is based on the design of *Fbxo44-201* transcript,The transcription is shown below



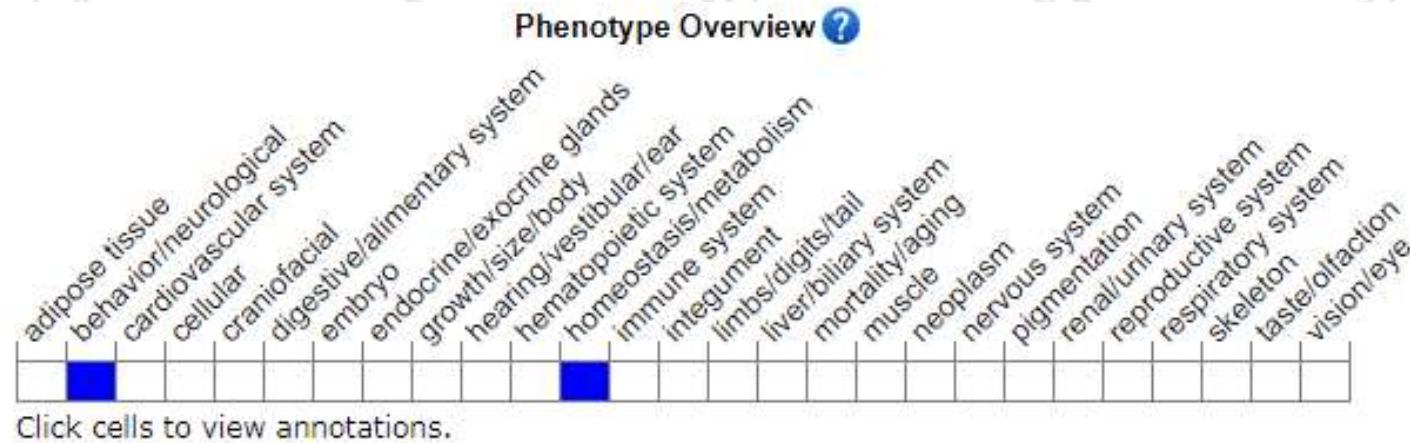
Genomic location distribution



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/>).

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

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