

# Rfx3 Cas9-KO Strategy

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**Design Date:** 2019-7-30

## **Project Overview**



**Project Name** 

Rfx3

**Project type** 

Cas9-KO

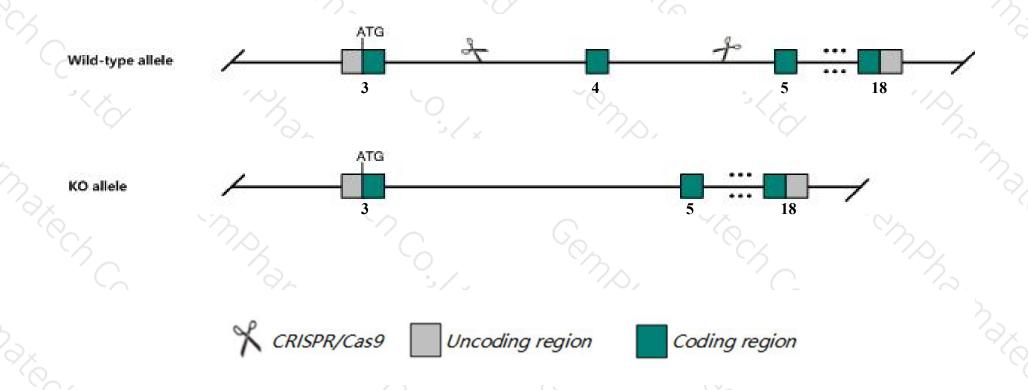
Strain background

C57BL/6JGpt

## **Knockout strategy**



This model will use CRISPR/Cas9 technology to edit the *Rfx3* gene. The schematic diagram is as follows:



### **Technical routes**



- ➤ The *Rfx3* gene has 8 transcripts. According to the structure of *Rfx3* gene, exon4 of *Rfx3-202*(ENSMUST00000165566.7) transcript is recommended as the knockout region. The region contains 98bp coding sequence.

  Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Rfx3* gene. The brief process is as follows: CRISPR/Cas9 system v

### **Notice**



- ➤ According to the existing MGI data, Homozygous null mice display embryonic and perinatal lethality, impaired development of cilia on the embryonic node, abnormal left-right patterning, meso- and dextrocardia, and situs inversus in surviving adults.
- > The *Rfx3* gene is located on the Chr19. 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)



#### Rfx3 regulatory factor X, 3 (influences HLA class II expression) [Mus musculus (house mouse)]

Gene ID: 19726, updated on 31-Jan-2019

#### Summary

☆ ?

Official Symbol Rfx3 provided by MGI

Official Full Name regulatory factor X, 3 (influences HLA class II expression) provided by MGI

Primary source MGI:MGI:106582

See related Ensembl:ENSMUSG00000040929

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 C230093O12Rik, MRFX3

Expression Broad expression in CNS E18 (RPKM 4.6), whole brain E14.5 (RPKM 4.4) and 22 other tissuesSee more

Orthologs <u>human</u> all

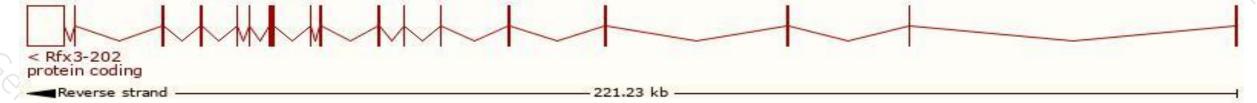
## Transcript information (Ensembl)



The gene has 8 transcripts, all transcripts are shown below:

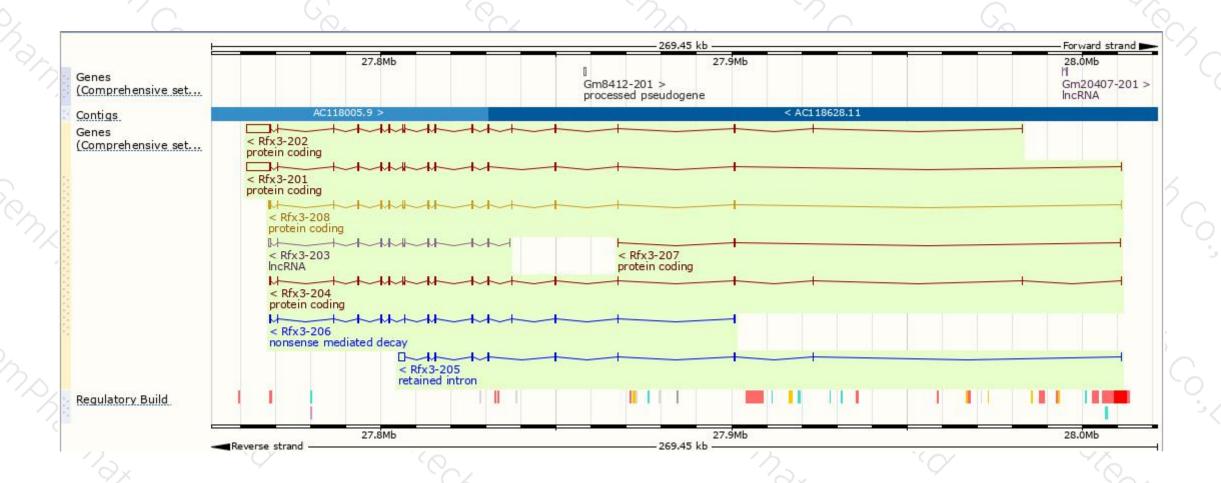
Transcript ID	bp 🍦	Protein 🍦	Biotype	CCDS 🍦	UniProt #	Flags
ENSMUST00000165566.7	9146	749aa	Protein coding	CCDS29725 ₽	<u>P48381</u> ₽	TSL:5 GENCODE basic APPRIS P1
ENSMUST00000174850.7	2743	749aa	Protein coding	CCDS29725 ₺	P48381 ₽	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000172907.7	2621	749aa	Protein coding	CCDS29725 ₺	P48381@	TSL:1 GENCODE basic APPRIS P1
ENSMUST00000046898.16	8988	724aa	Protein coding	-	<u>G5E890</u> ₽	TSL:1 GENCODE basic
ENSMUST00000174420.1	343	<u>71aa</u>	Protein coding	-	G3UZZ6₽	CDS 3' incomplete TSL:2
ENSMUST00000173863.1	2053	458aa	Nonsense mediated decay	-	G3UWP0₽	TSL:5
ENSMUST00000173161.1	3039	No protein	Retained intron	-	22	TSL:1
ENSMUST00000172498.7	2091	No protein	IncRNA	-	ā	TSL:2
	ENSMUST00000165566.7 ENSMUST00000174850.7 ENSMUST00000172907.7 ENSMUST00000046898.16 ENSMUST00000174420.1 ENSMUST00000173863.1 ENSMUST00000173161.1	ENSMUST00000165566.7 9146 ENSMUST00000174850.7 2743 ENSMUST00000172907.7 2621 ENSMUST00000046898.16 8988 ENSMUST00000174420.1 343 ENSMUST00000173863.1 2053 ENSMUST00000173161.1 3039	ENSMUST00000165566.7         9146         749aa           ENSMUST00000174850.7         2743         749aa           ENSMUST00000172907.7         2621         749aa           ENSMUST00000046898.16         8988         724aa           ENSMUST00000174420.1         343         71aa           ENSMUST00000173863.1         2053         458aa           ENSMUST00000173161.1         3039         No protein	ENSMUST00000165566.7         9146         749aa         Protein coding           ENSMUST00000174850.7         2743         749aa         Protein coding           ENSMUST00000172907.7         2621         749aa         Protein coding           ENSMUST00000046898.16         8988         724aa         Protein coding           ENSMUST00000174420.1         343         71aa         Protein coding           ENSMUST00000173863.1         2053         458aa         Nonsense mediated decay           ENSMUST00000173161.1         3039         No protein         Retained intron	ENSMUST00000165566.7         9146         749aa         Protein coding         CCDS29725 №           ENSMUST00000174850.7         2743         749aa         Protein coding         CCDS29725 №           ENSMUST00000172907.7         2621         749aa         Protein coding         CCDS29725 №           ENSMUST00000046898.16         8988         724aa         Protein coding         -           ENSMUST00000174420.1         343         71aa         Protein coding         -           ENSMUST00000173863.1         2053         458aa         Nonsense mediated decay         -           ENSMUST00000173161.1         3039         No protein         Retained intron         -	ENSMUST00000165566.7         9146         749aa         Protein coding         CCDS29725 ©         P48381 ©           ENSMUST00000174850.7         2743         749aa         Protein coding         CCDS29725 ©         P48381 ©           ENSMUST00000172907.7         2621         749aa         Protein coding         CCDS29725 ©         P48381 ©           ENSMUST00000046898.16         8988         724aa         Protein coding         -         G5E890 ©           ENSMUST00000174420.1         343         71aa         Protein coding         -         G3UZZ6 ©           ENSMUST00000173863.1         2053         458aa         Nonsense mediated decay         -         G3UWP0 ©           ENSMUST00000173161.1         3039         No protein         Retained intron         -         -

The strategy is based on the design of Rfx3-202 transcript, The transcription is shown below



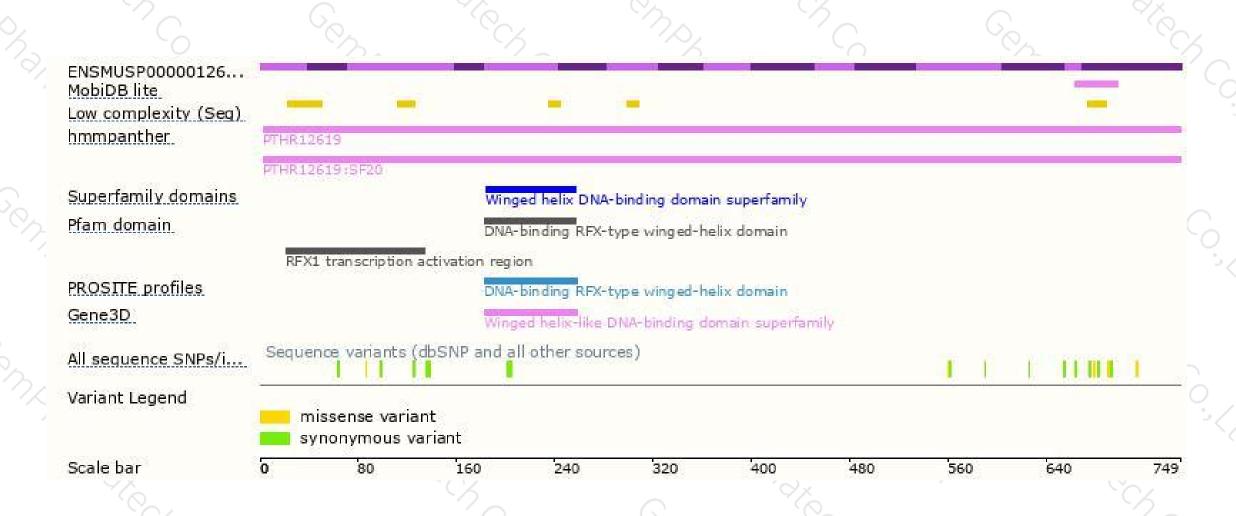
### Genomic location distribution





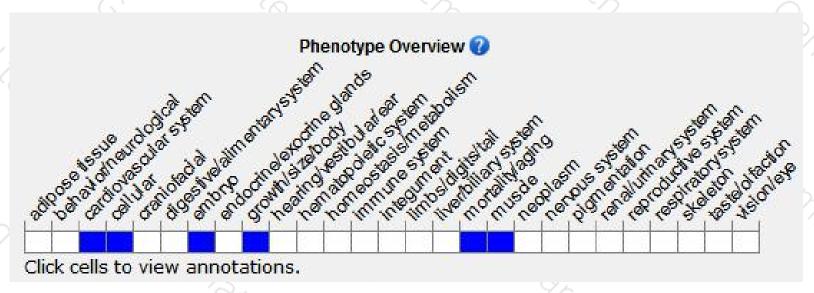
### Protein domain





## 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, Homozygous null mice display embryonic and perinatal lethality, impaired development of cilia on the embryonic node, abnormal left-right patterning, meso- and dextrocardia, and situs inversus in surviving adults.



If you have any questions, you are welcome to inquire. Tel: 400-9660890





