

# Mex3d Cas9-KO Strategy

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Design Date: 2023-10-18

### Overview

### Target Gene Name

• Mex3d

**Project Type** 

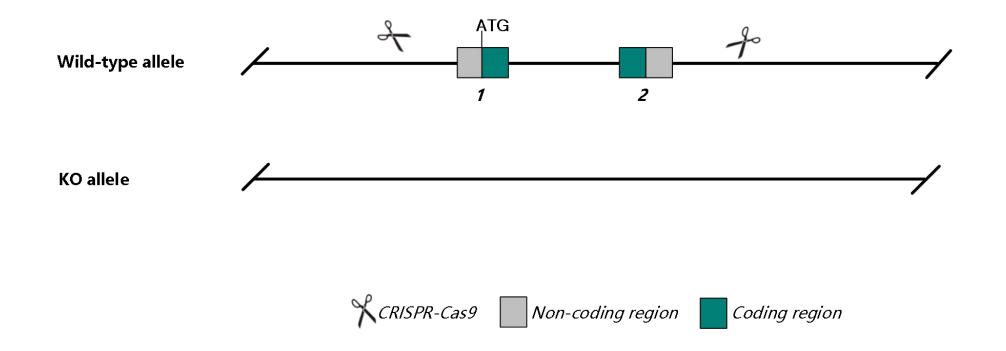
• Cas9-KO

**Genetic Background** 

• C57BL/6JGpt



## Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the Mex3d gene.

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### **Technical Information**

- The *Mex3d* gene has 2 transcripts. According to the structure of *Mex3d* gene, exon1-exon2 of *Mex3d* -201(ENSMUST00000105350.3) transcript is recommended as the knockout region. The region contains all coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Mex3d* gene. The brief process is as follows: CRISPR-Cas9 system 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.



### Gene Information

#### Mex3d mex3 RNA binding family member D [ Mus musculus (house mouse) ]

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Gene ID: 237400, updated on 7-Sep-2023

#### Summary

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Official Symbol	Mex3d provided by MGI	
Official Full Name	mex3 RNA binding family member D provided by MGI	
Primary source	MGI:MGI:2681847	
See related	Ensembl:ENSMUSG00000048696 AllianceGenome:MGI:2681847	
Gene type	protein coding	
<b>RefSeq status</b>	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	Rkhd1	
Summary	Predicted to enable mRNA 3'-UTR AU-rich region binding activity. Predicted to act upstream of or within RNA destabilization	22
	and mRNA catabolic process. Predicted to be located in nucleus and perinuclear region of cytoplasm. Orthologous to human	
	MEX3D (mex-3 RNA binding family member D). [provided by Alliance of Genome Resources, Apr 2022]	31
Expression	Biased expression in testis adult (RPKM 193.1), ovary adult (RPKM 36.0) and 7 other tissues See more	
Orthologs	human all	
NEW	Try the new Gene table	

Try the new Transcript table

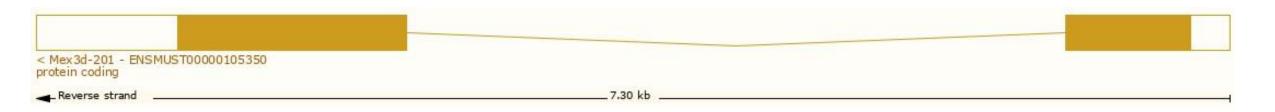
https://www.ncbi.nlm.nih.gov/gene/237400

### **Transcript Information**

The gene has 2 transcripts, all transcripts are shown below:

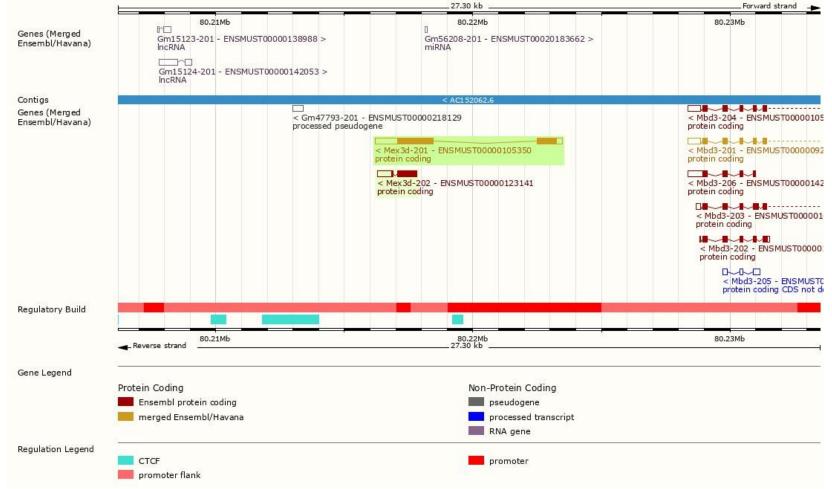
Show/hide columns (	Filter							
Transcript ID	÷	Name 🖕	bp 💧	Protein 💧	Biotype 🝦	CCDS 🍦	UniProt Match	Flags 🔶
ENSMUST0000010535	0.3	Mex3d-201	3266	<u>718aa</u>	Protein coding	<u>CCDS48629</u> &	D3YTR3 &	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1
ENSMUST0000012314	1.2	Mex3d-202	1358	<u>268aa</u>	Protein coding		F6TY75	TSL:2 CDS 5' incomplete

The strategy is based on the design of *Mex3d* -201 transcript, the transcription is shown below:





## Genomic Information



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### Protein Information

ENSMUSP00000100987 MobiDB lite Low complexity (Seg)	.3	-															
AFDB-ENSP mappings Superfamily			K Hor	nology d	iomain, ty	pe 1 sup	pertamily								SSF57	850	
SMART Pfam				ology da nology d	main omain, ty	pe 1									PF13	920	
PROSITE profiles			255	0084		-									Zinc	tinger, RIN	
PANTHER	RNA-binding protein	1 MEX3														_	
Gene3D			K Hom	ology do	main, typ	e 1 supe	ertamily	Ē.							Zinc finge	r, RING/FY	
CDD		RNA-binding protein MEX-3, second type I KH domain RNA-binding protein MEX-3, first type I KH domain															
All sequence SNPs/	Sequence variants (EVA an	id all other sources)	i – ji	0.0	11-1		Ш	• •	11	1	I.	1	1.1	J.	M1		
Variant Legend	frameshift variant						mis	sense	/ariant	ŝ							
Scale bar	0 '60	120 180	240		300		360	'4	20	48	0	540		600		718	



### **Important Information**

- The knockout region will delete *Gm56208*, the risk is unknown.
- The knockout region is 2.5kb away from the 5' of *Gm47793*, which may affect the 5' regulation of *Gm47793*.
- The *Mex3d* gene is located on the Chr10. 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.

