

Odf2 Cas9-KO Strategy

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Reviewer:

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Design Date:

2019-9-9

Project Overview



Project Name

Odf2

Project type

Cas9-KO

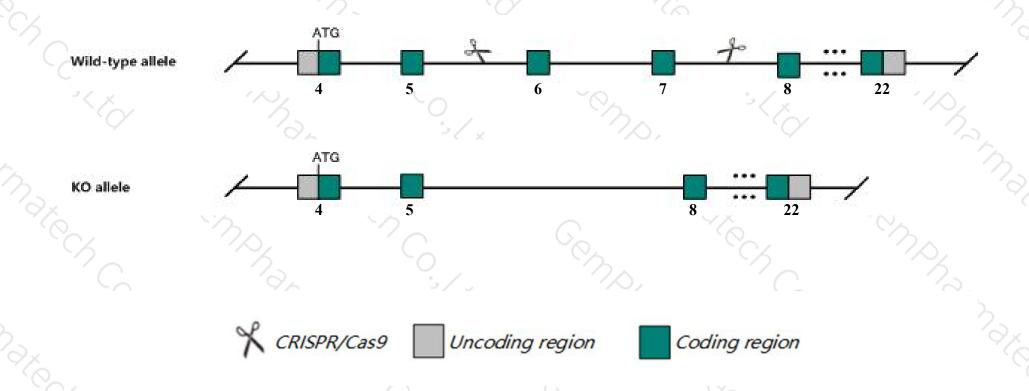
Strain background

C57BL/6JGpt

Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Odf2 gene. The schematic diagram is as follows:



Technical routes



- ➤ The *Odf2* gene has 25 transcripts. According to the structure of *Odf2* gene, exon6-exon7 of *Odf2-202*(ENSMUST00000046571.13) transcript is recommended as the knockout region. The region contains 332bp coding sequence Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Odf2* gene. The brief process is as follows: CRISPR/Cas9 system v

Notice



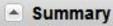
- ➤ According to the existing MGI data, Mice homozygous for a gene trapped allele exhibit embryonic lethality before implantation and transmission ratio distortion while all heterozygous males display normal development and fertility. Males heterozygous for other alleles are either infertile orshow reduced fertility.
- > The *Odf2* gene is located on the Chr2. 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)



Odf2 outer dense fiber of sperm tails 2 [Mus musculus (house mouse)]

Gene ID: 18286, updated on 14-Aug-2019





Official Symbol Odf2 provided by MGI

Official Full Name outer dense fiber of sperm tails 2 provided by MGI

Primary source MGI:MGI:1098824

See related Ensembl:ENSMUSG00000026790

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 Al848335; MMTEST29

Expression Biased expression in testis adult (RPKM 224.3), cerebellum adult (RPKM 22.9) and 4 other tissues See more

Orthologs human all

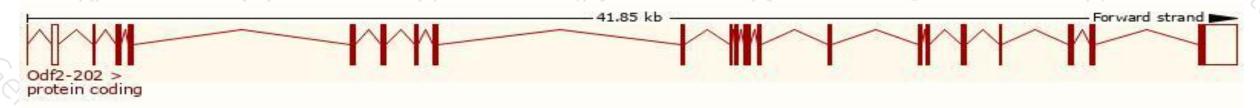
Transcript information (Ensembl)



The gene has 25 transcripts, all transcripts are shown below:

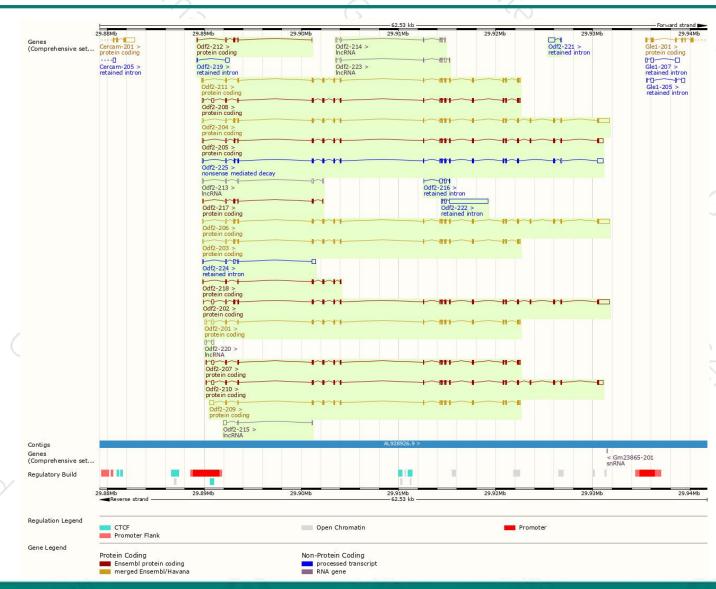
Name	Transcript ID	bp 🍦	Protein	Biotype	CCDS	UniProt	Flags
Odf2-202	ENSMUST00000046571.13	3959	825aa	Protein coding	CCDS50556 Ø	<u>A3KGV1</u> ₽	TSL:2 GENCODE basic APPRIS ALT
Odf2-204	ENSMUST00000113756.7	3826	825aa	Protein coding	CCDS50556₽	<u>A3KGV1</u> ₽	TSL:1 GENCODE basic APPRIS ALT
Odf2-206	ENSMUST00000113759.8	3807	826aa	Protein coding	CCDS50555@	<u>A3KGV1</u> ₽	TSL:1 GENCODE basic APPRIS ALT
Odf2-209	ENSMUST00000113764.3	2450	638aa	Protein coding	CCDS15861₽	A3KGV1₽	TSL:5 GENCODE basic APPRIS P3
Odf2-201	ENSMUST00000028128.12	2376	<u>638aa</u>	Protein coding	CCDS15861@	<u>A3KGV1</u> ₽	TSL:1 GENCODE basic APPRIS P3
Odf2-208	ENSMUST00000113763.7	2364	638aa	Protein coding	CCDS15861@	A3KGV1₽	TSL:5 GENCODE basic APPRIS P3
Odf2-203	ENSMUST00000113755.7	2305	652aa	Protein coding	CCDS50557₽	A3KGV1₽	TSL:1 GENCODE basic
Odf2-211	ENSMUST00000113767.7	2249	701aa	Protein coding	CCDS50554₽	<u>A3KGW0</u> ₽	TSL:1 GENCODE basic APPRIS ALT
Odf2-210	ENSMUST00000113765.7	3188	830aa	Protein coding	-	A3KGV1₽	TSL:5 GENCODE basic APPRIS ALT
Odf2-205	ENSMUST00000113757.7	3082	806aa	Protein coding	55	A3KGV1₽	TSL:5 GENCODE basic
Odf2-207	ENSMUST00000113762.7	2353	657aa	Protein coding	12	A3KGV9₽	TSL:5 GENCODE basic
Odf2-218	ENSMUST00000137558.7	814	<u>271aa</u>	Protein coding	-	F6Y325@	CDS 5' and 3' incomplete TSL:3
Odf2-217	ENSMUST00000133233.7	658	<u>138aa</u>	Protein coding	22	A3KGV3₽	CDS 3' incomplete TSL:2
Odf2-212	ENSMUST00000123335.7	403	69aa	Protein coding		<u>A3KGV2</u> ₽	CDS 3' incomplete TSL:3
Odf2-225	ENSMUST00000184845.7	3035	680aa	Nonsense mediated decay		V9GXZ0₽	TSL:5
Odf2-222	ENSMUST00000152503.1	4291	No protein	Retained intron	- 0		TSL:1
Odf2-224	ENSMUST00000153216.7	828	No protein	Retained intron		-	TSL:2
Odf2-221	ENSMUST00000152026.1	673	No protein	Retained intron	55	-	TSL:3
Odf2-216	ENSMUST00000131165.7	553	No protein	Retained intron	12	2	TSL:5
Odf2-219	ENSMUST00000148883.1	437	No protein	Retained intron	-	-	TSL:2
Odf2-223	ENSMUST00000152932.7	793	No protein	IncRNA	2	2	TSL:5
Odf2-214	ENSMUST00000129960.7	674	No protein	IncRNA	-	- 20	TSL:3
Odf2-213	ENSMUST00000126103.7	589	No protein	IncRNA		- 1	TSL:2
Odf2-215	ENSMUST00000130899.1	395	No protein	IncRNA	2	2	TSL:3
Odf2-220	ENSMUST00000150827.1	349	No protein	IncRNA	-	-	TSL:3
0.0		4	1			0 1	

The strategy is based on the design of *Odf2-202* transcript, The transcription is shown below



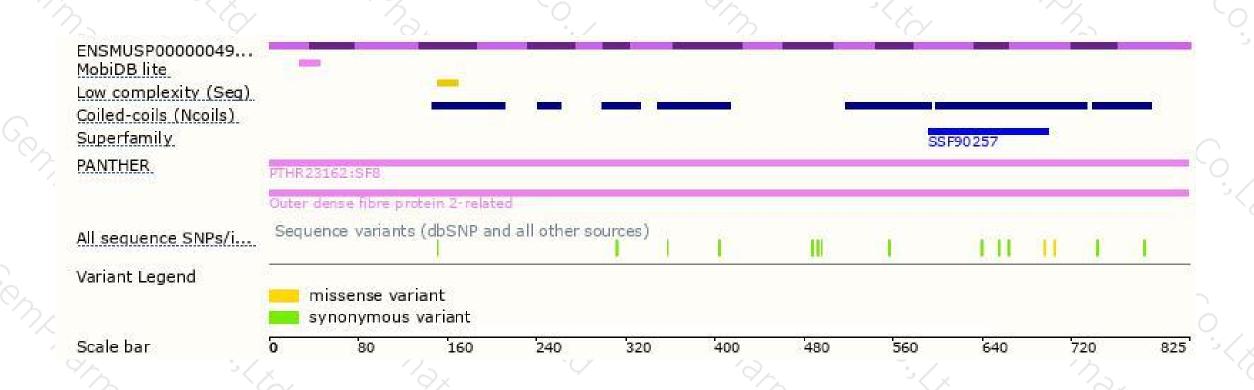
Genomic location distribution





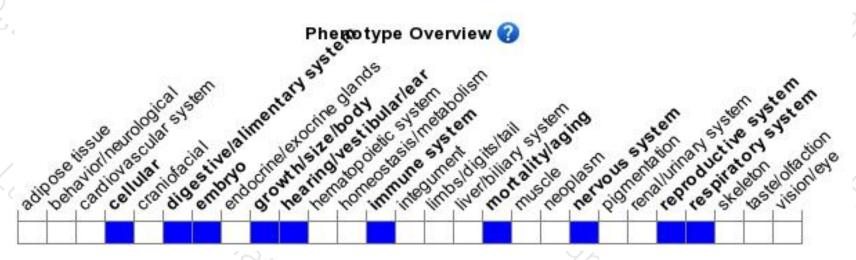
Protein domain





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, Mice homozygous for a gene trapped allele exhibit embryonic lethality before implantation and transmission ratio distortion while all heterozygous males display normal development and fertility. Males heterozygous for other alleles are either infertile orshow reduced fertility.



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





