

***Hdac7* Cas9-KO Strategy**

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Project Overview

Project Name

Hdac7

Project type

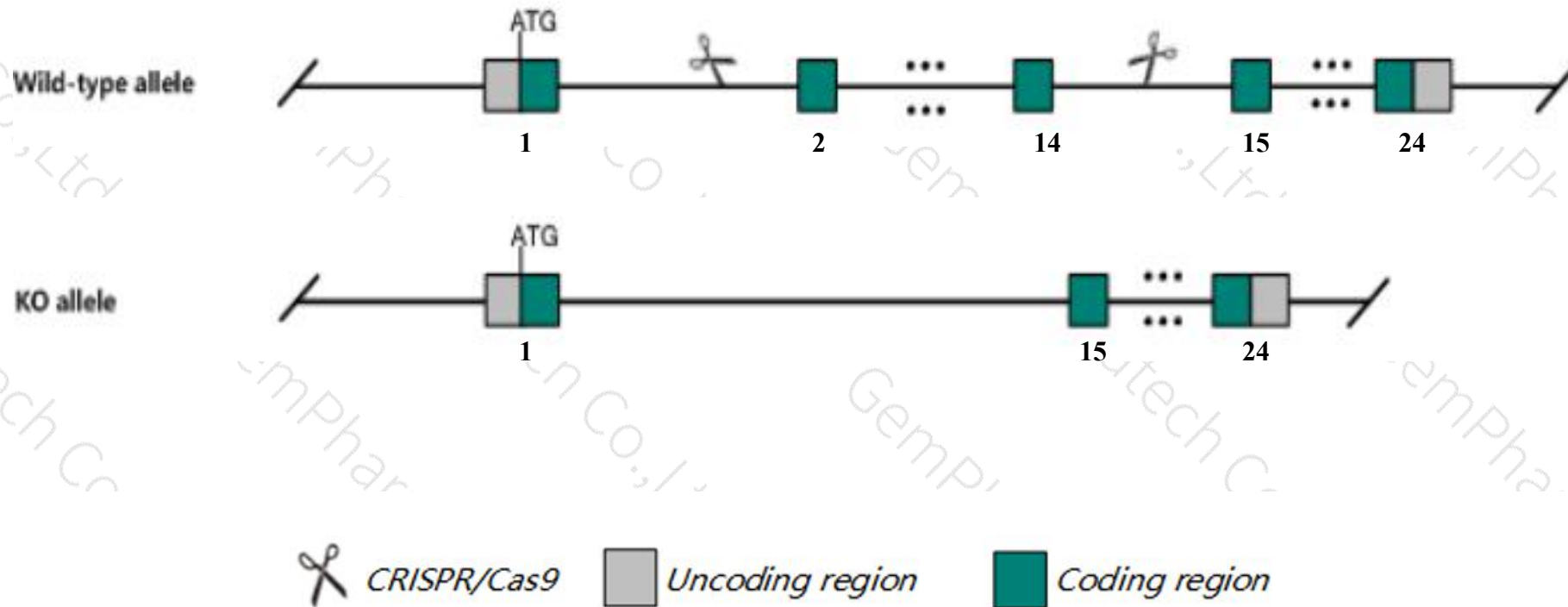
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Hdac7* gene. The schematic diagram is as follows:



- The *Hdac7* gene has 13 transcripts. According to the structure of *Hdac7* gene, exon2-exon14 of *Hdac7*-202(ENSMUST00000088402.11) transcript is recommended as the knockout region. The region contains 1808bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Hdac7* 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.

- According to the existing MGI data, deletion of this gene result in embryonic lethality by E11, due to vascular defects which are due to endothelial cell adhesion defects.
- Transcript 209 and 210 may not be affected.
- The *Hdac7* gene is located on the Chr15. 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)

Hdac7 histone deacetylase 7 [Mus musculus (house mouse)]

Gene ID: 56233, updated on 18-Mar-2020

Summary



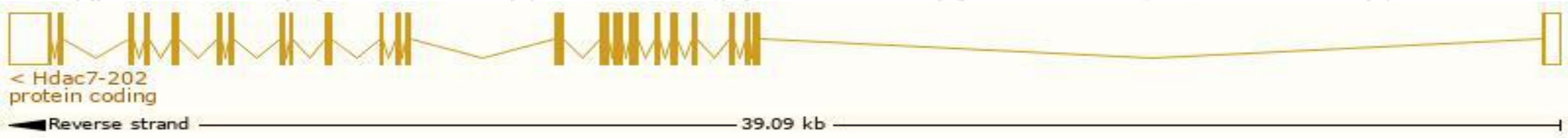
Official Symbol	Hdac7 provided by MGI
Official Full Name	histone deacetylase 7 provided by MGI
Primary source	MGI:MGI:1891835
See related	Ensembl:ENSMUSG00000022475
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	5830434K02Rik, HD7, HD7a, Hdac7a, mFLJ00062
Expression	Broad expression in thymus adult (RPKM 141.4), lung adult (RPKM 54.7) and 16 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

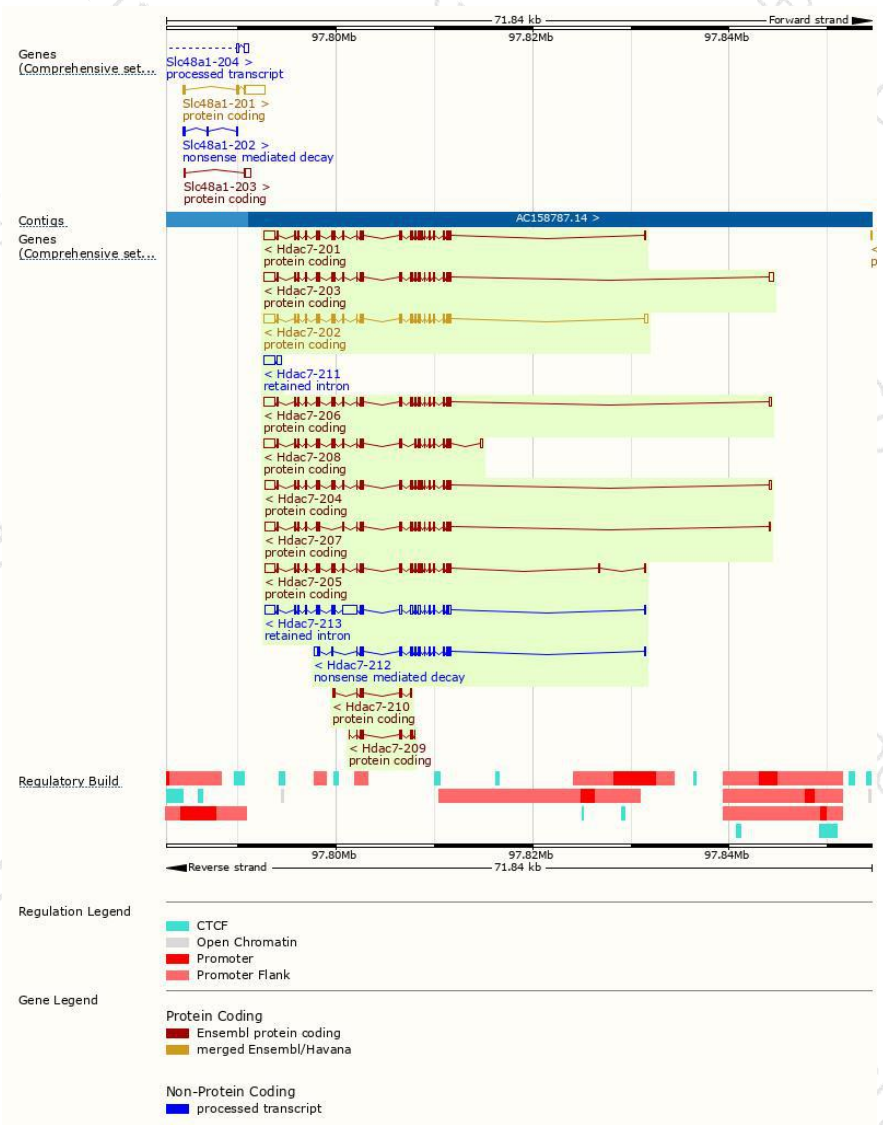
The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Hdac7-203	ENSMUST00000116408.8	4226	916aa	Protein coding	CCDS57004	Q8C2B3	TSL:1 GENCODE basic APPRIS ALT2
Hdac7-202	ENSMUST00000088402.11	4223	938aa	Protein coding	CCDS37188	Q8C2B3	TSL:1 GENCODE basic APPRIS P3
Hdac7-204	ENSMUST00000116409.8	4113	953aa	Protein coding	CCDS57006	Q8C2B3	TSL:1 GENCODE basic APPRIS ALT2
Hdac7-205	ENSMUST00000118294.7	4069	946aa	Protein coding	CCDS57005	Q8C2B3	TSL:1 GENCODE basic APPRIS ALT2
Hdac7-201	ENSMUST00000079838.13	3985	944aa	Protein coding	CCDS57007	Q8C2B3	TSL:1 GENCODE basic APPRIS ALT2
Hdac7-206	ENSMUST00000119670.7	3899	892aa	Protein coding	CCDS57001	E9PXW1	TSL:1 GENCODE basic APPRIS ALT2
Hdac7-208	ENSMUST00000121514.7	3767	851aa	Protein coding	CCDS57002	E9PX62	TSL:1 GENCODE basic APPRIS ALT2
Hdac7-207	ENSMUST00000120683.7	3701	868aa	Protein coding	CCDS57003	E9PXW8	TSL:1 GENCODE basic
Hdac7-209	ENSMUST00000134258.1	770	257aa	Protein coding	-	F6VIB5	CDS 5' and 3' incomplete TSL:3
Hdac7-210	ENSMUST00000135651.7	639	213aa	Protein coding	-	F6RY11	CDS 5' and 3' incomplete TSL:3
Hdac7-212	ENSMUST00000156045.7	2367	636aa	Nonsense mediated decay	-	E9PZG4	TSL:1
Hdac7-213	ENSMUST00000228466.1	5179	No protein	Retained intron	-	-	
Hdac7-211	ENSMUST00000151334.1	1572	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Hdac7-202* transcript,the transcription is shown below:



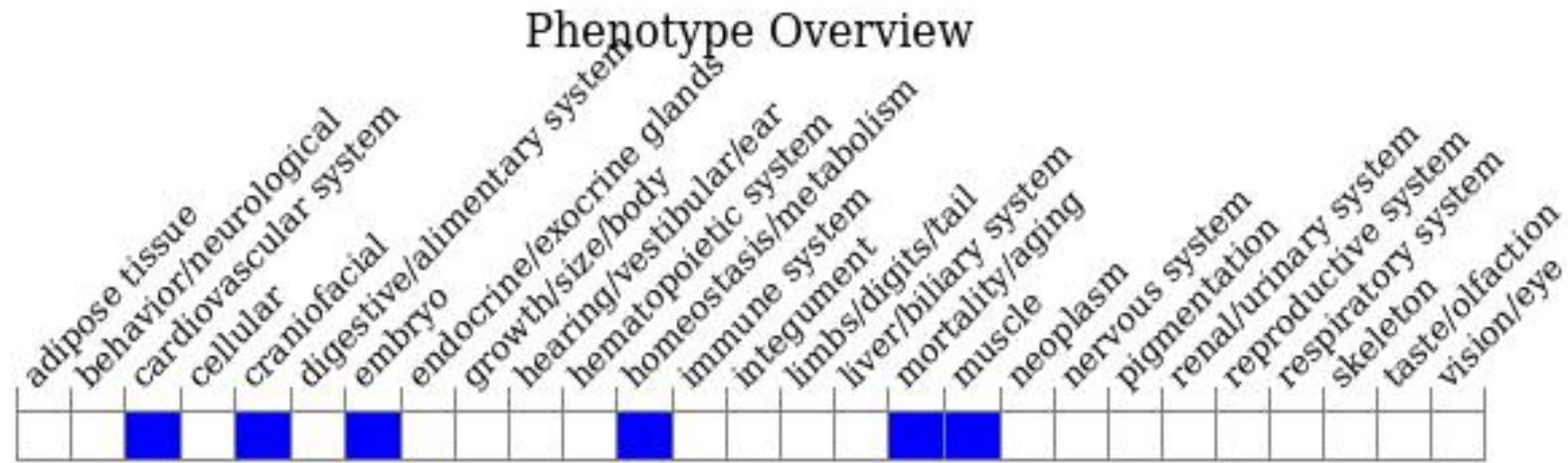
Genomic location distribution



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, deletion of this gene result in embryonic lethality by E11, due to vascular defects which are due to endothelial cell adhesion defects.

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

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