

***Chd2* Cas9-KO Strategy**

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Project Overview

Project Name

Chd2

Project type

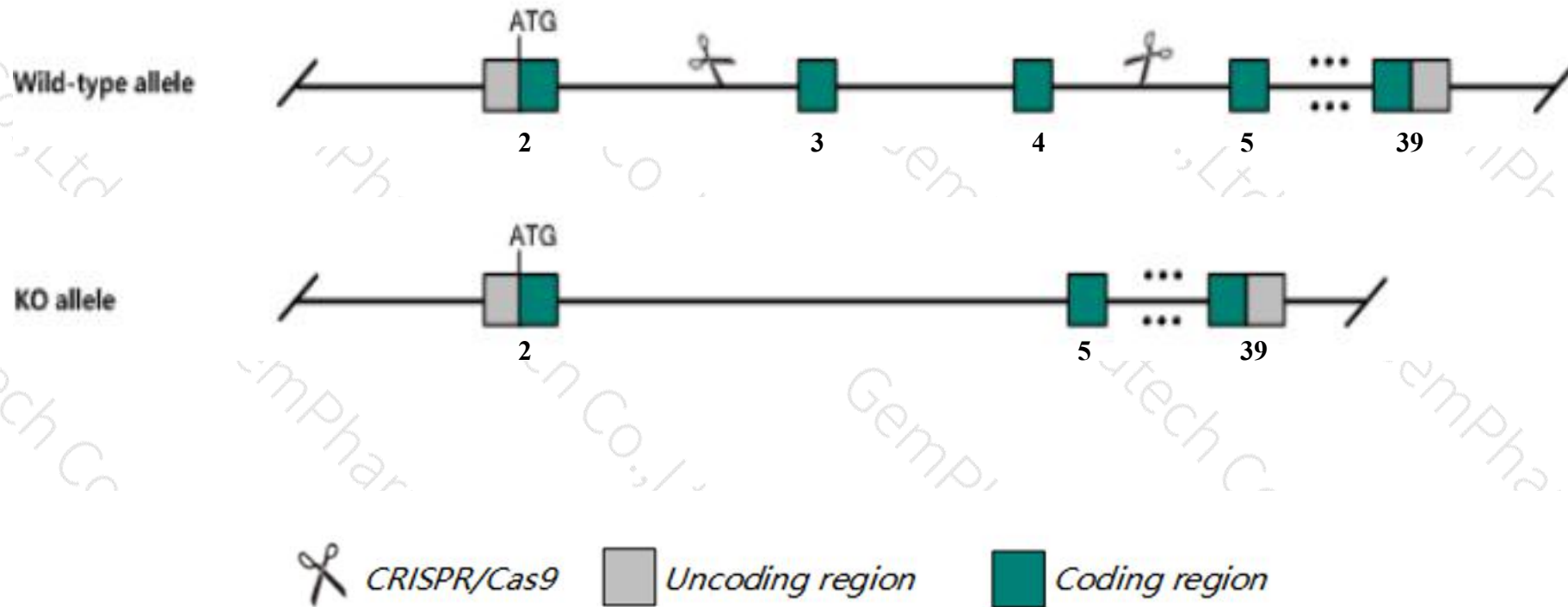
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Chd2* gene. The schematic diagram is as follows:



- The *Chd2* gene has 18 transcripts. According to the structure of *Chd2* gene, exon3-exon4 of *Chd2*-203(ENSMUST00000169922.8) transcript is recommended as the knockout region. The region contains 319bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Chd2* 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, mice homozygous for a gene trap allele exhibit early postnatal lethality associated with fetal growth retardation. Mice heterozygous for a gene trap allele exhibit postnatal lethality and premature death after weaning associated with growth retardation and multi-organ defects.
- The *Chd2* gene is located on the Chr7. 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)

Chd2 chromodomain helicase DNA binding protein 2 [*Mus musculus* (house mouse)]

Gene ID: 244059, updated on 26-Jun-2020

Summary

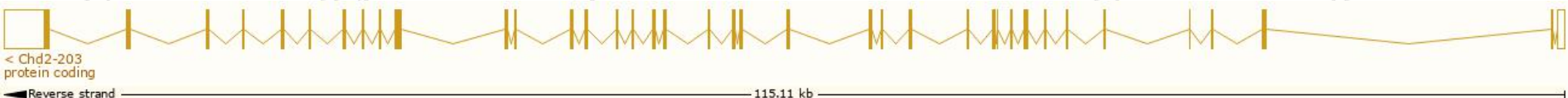
Official Symbol	Chd2 provided by MGI
Official Full Name	chromodomain helicase DNA binding protein 2 provided by MGI
Primary source	MGI:MGI:2448567
See related	Ensembl:ENSMUSG00000078671
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	CHD-2; AI851092; BC029703; 2810013C04Rik; 2810040A01Rik; 5630401D06Rik
Expression	Ubiquitous expression in CNS E11.5 (RPKM 9.7), limb E14.5 (RPKM 9.5) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

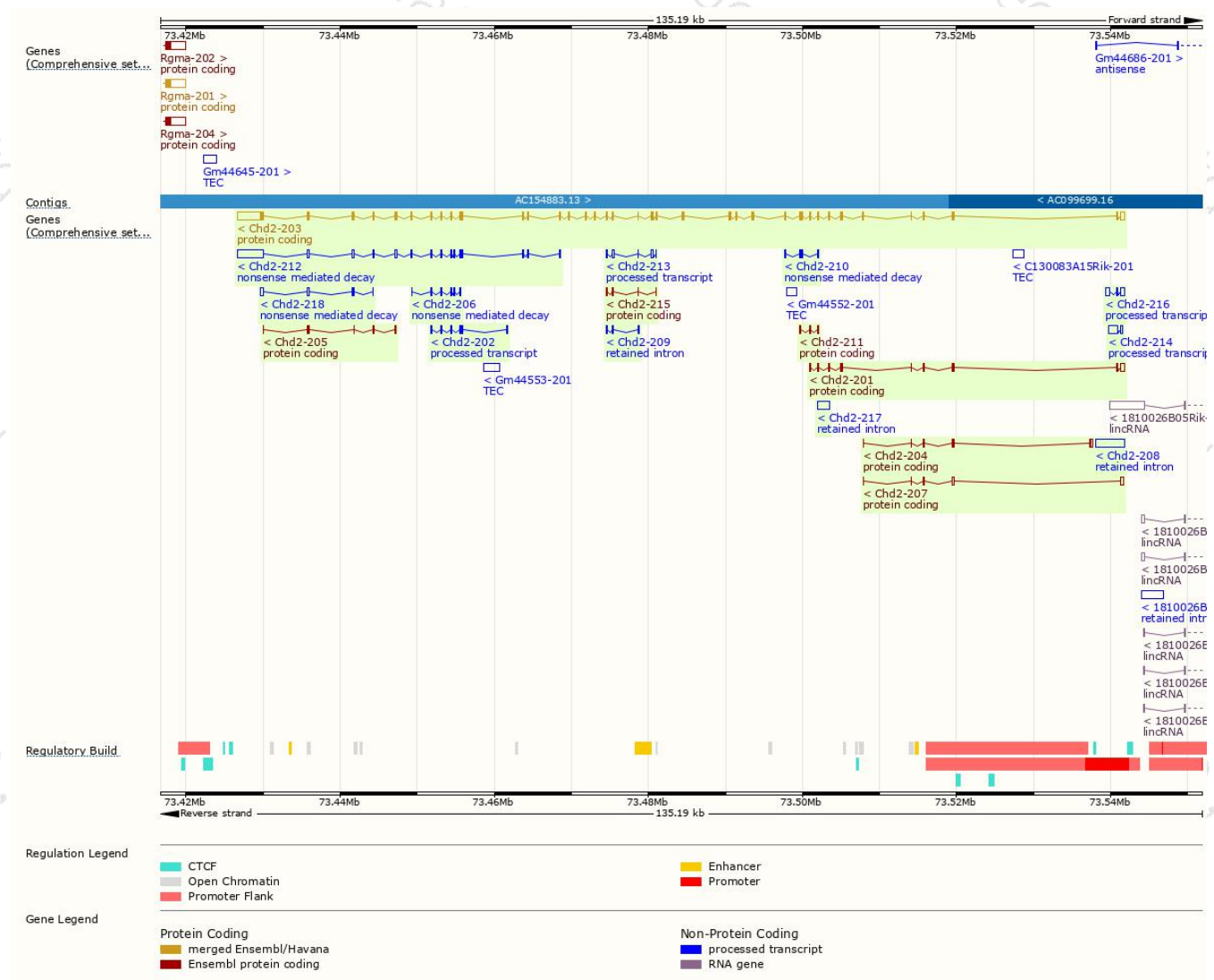
The gene has 18 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Chd2-218	ENSMUST00000208458.1	745	34aa	Nonsense mediated decay	-	A0A140LJE4	CDS 5' incomplete TSL:5
Chd2-206	ENSMUST00000181971.5	667	35aa	Nonsense mediated decay	-	M0QWT0	CDS 5' incomplete TSL:5
Chd2-207	ENSMUST00000197642.1	896	57aa	Protein coding	-	A0A0G2JDK8	CDS 3' incomplete TSL:5
Chd2-210	ENSMUST00000199601.1	558	74aa	Nonsense mediated decay	-	A0A0G2JFK1	CDS 5' incomplete TSL:5
Chd2-215	ENSMUST00000200423.1	339	113aa	Protein coding	-	A0A0G2JES5	CDS 5' and 3' incomplete TSL:5
Chd2-211	ENSMUST00000199641.1	360	120aa	Protein coding	-	A0A0G2JEP1	CDS 5' and 3' incomplete TSL:5
Chd2-205	ENSMUST00000173785.1	487	163aa	Protein coding	-	G3UXJ4	CDS 5' and 3' incomplete TSL:5
Chd2-204	ENSMUST00000172704.5	748	178aa	Protein coding	-	G3UZG2	CDS 3' incomplete TSL:5
Chd2-212	ENSMUST00000199809.4	5289	220aa	Nonsense mediated decay	-	A0A0G2JEZ3	CDS 5' incomplete TSL:5
Chd2-201	ENSMUST0000026895.13	1571	333aa	Protein coding	-	F7CDZ7	CDS 3' incomplete TSL:5
Chd2-203	ENSMUST00000169922.8	9085	1827aa	Protein coding	CCDS52274	E9PZM4	TSL:5 GENCODE basic APPRIS P1
Chd2-214	ENSMUST00000200218.1	1387	No protein	Processed transcript	-	-	TSL:1
Chd2-216	ENSMUST00000200492.1	1196	No protein	Processed transcript	-	-	TSL:5
Chd2-202	ENSMUST00000038366.8	755	No protein	Processed transcript	-	-	TSL:1
Chd2-213	ENSMUST00000199831.1	582	No protein	Processed transcript	-	-	TSL:5
Chd2-208	ENSMUST00000197800.1	3741	No protein	Retained intron	-	-	TSL:NA
Chd2-217	ENSMUST00000206665.1	1632	No protein	Retained intron	-	-	TSL:NA
Chd2-209	ENSMUST00000198225.1	392	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Chd2-203* transcript,the transcription is shown below:



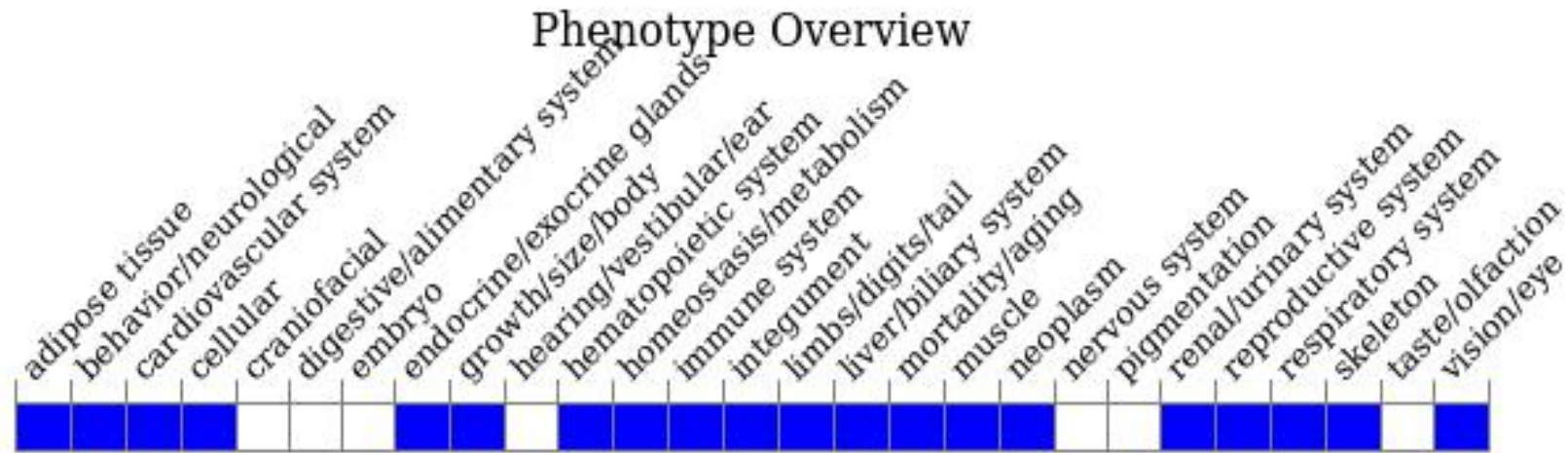
Genomic location distribution



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 trap allele exhibit early postnatal lethality associated with fetal growth retardation. Mice heterozygous for a gene trap allele exhibit postnatal lethality and premature death after weaning associated with growth retardation and multi-organ defects.

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

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