Chd7 Cas9-KO Strategy

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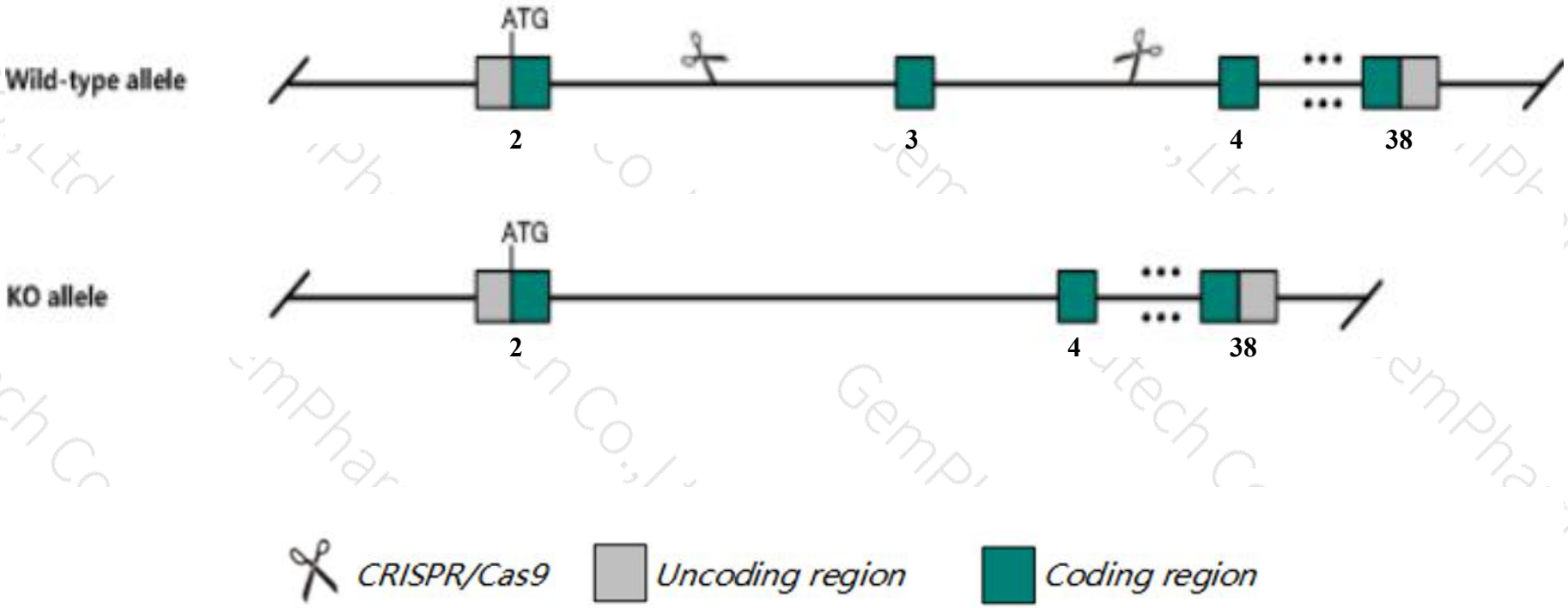
Project Overview

Project Name	***Chd7***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Chd7* gene. The schematic diagram is as follows:



Technical routes

➢ The *Chd7* gene has 8 transcripts. According to the structure of *Chd7* gene, exon3 of *Chd7-201*(ENSMUST00000039267.9) transcript is recommended as the knockout region.The region contains 422bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Chd7* 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.

Notice

➢ According to the existing MGI data,heterozygotes for mutations of this gene exhibit a variety of combinations of hyperactivity, circling, head-bobbing, semicircular canal defects, hearing loss, reduced size, and tail-kink.

➢ Transcript *Chd7*-204&208 may not be affected.

➢ The KO region will not result in frameshift of *Chd7*-206.

➢ The *Chd7* gene is located on the Chr4. 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）

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Chd7 chromodomain helicase DNA binding protein 7 [Mus musculus (house mouse)]

Gene ID: 320790, updated on 13-Mar-2020

Summary

Official Symbol	Chd7 provided by MGI
Official Full Name	chromodomain helicase DNA binding protein 7 provided by MGI
Primary source	MGI:MGI:2444748
See related	Ensembl:ENSMUSG00000041235
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	A730019I05Rik, Cycn, Cyn, Dz, Edy, Flo, GENA 47, GENA 60, Gena 52, Lda, Mt, Obt, Todo, WBE1, Whi, metis
Summary	This gene encodes a protein containing two chromodomains and an ATP-binding helicase domain that functions as a regulator of transcription. Mutations in this gene result in an array of development defects, including inner ear problems. Mice defective for this gene exhibit many of the clinical features of the CHARGE syndrome caused by mutations in the homologous gene in human. [provided by RefSeq, Sep 2015]
Expression	Broad expression in CNS E11.5 (RPKM 14.2), cerebellum adult (RPKM 11.8) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

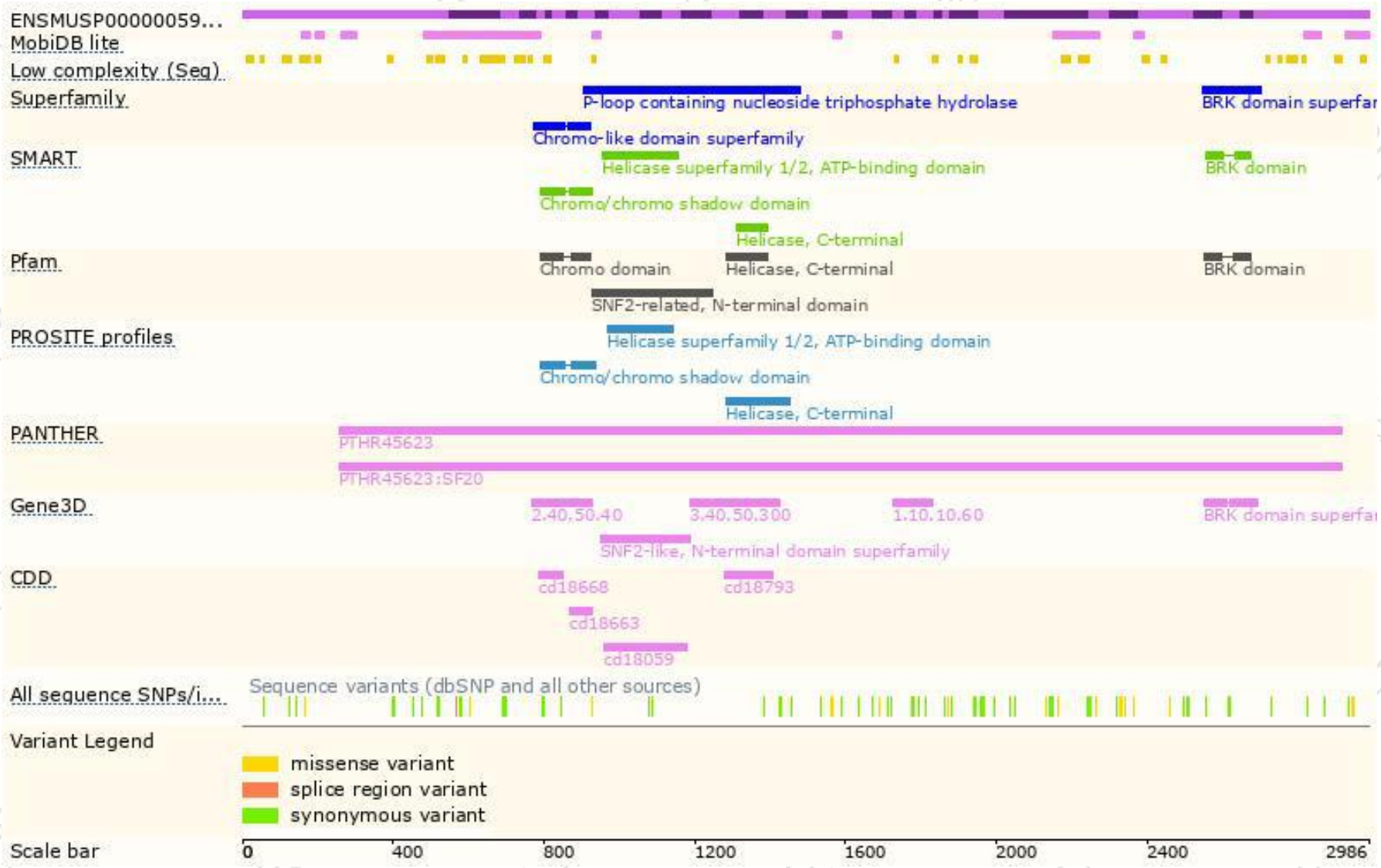
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Chd7-202	ENSMUST00000051558.9	10216	2986aa	Protein coding	CCDS38689	A2AJK6	TSL:5 GENCODE basic APPRIS P1
Chd7-201	ENSMUST00000039267.9	9444	2986aa	Protein coding	CCDS38689	A2AJK6	TSL:5 GENCODE basic APPRIS P1
Chd7-206	ENSMUST00000170391.1	3462	941aa	Protein coding	-	E9PV74	TSL:5 GENCODE basic
Chd7-203	ENSMUST00000127476.7	2381	631aa	Protein coding	-	A0A0R4J1U9	CDS 3' incomplete TSL:1
Chd7-208	ENSMUST00000222546.1	582	194aa	Protein coding	-	A0A1Y7VIV0	CDS 5' and 3' incomplete TSL:3
Chd7-204	ENSMUST00000129655.1	458	19aa	Protein coding	-	A2AJK7	CDS 3' incomplete TSL:3
Chd7-205	ENSMUST00000130709.1	741	No protein	Processed transcript	-	-	TSL:3
Chd7-207	ENSMUST00000170457.1	4953	No protein	Retained intron	-	-	TSL:2

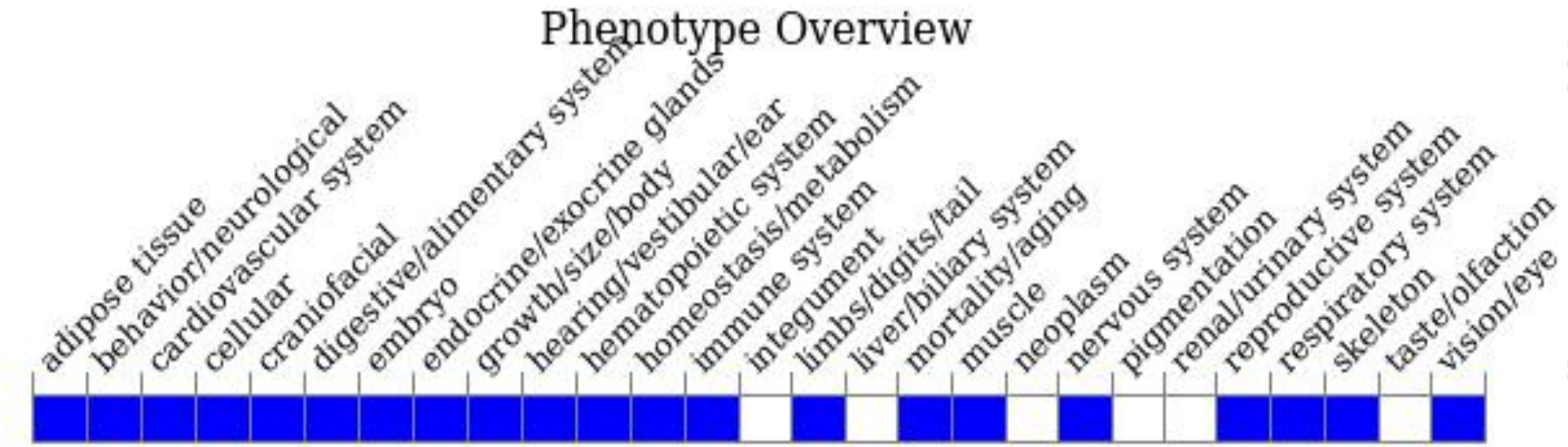
The strategy is based on the design of *Chd7-201* transcript,the transcription is shown below:

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,heterozygotes for mutations of this gene exhibit a variety of combinations of hyperactivity, circling, head-bobbing, semicircular canal defects, hearing loss, reduced size, and tail-kink.

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

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