

Dync1i2 Cas9-KO Strategy

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Design Date:

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Project Overview

Project Name

Dync1i2

Project type

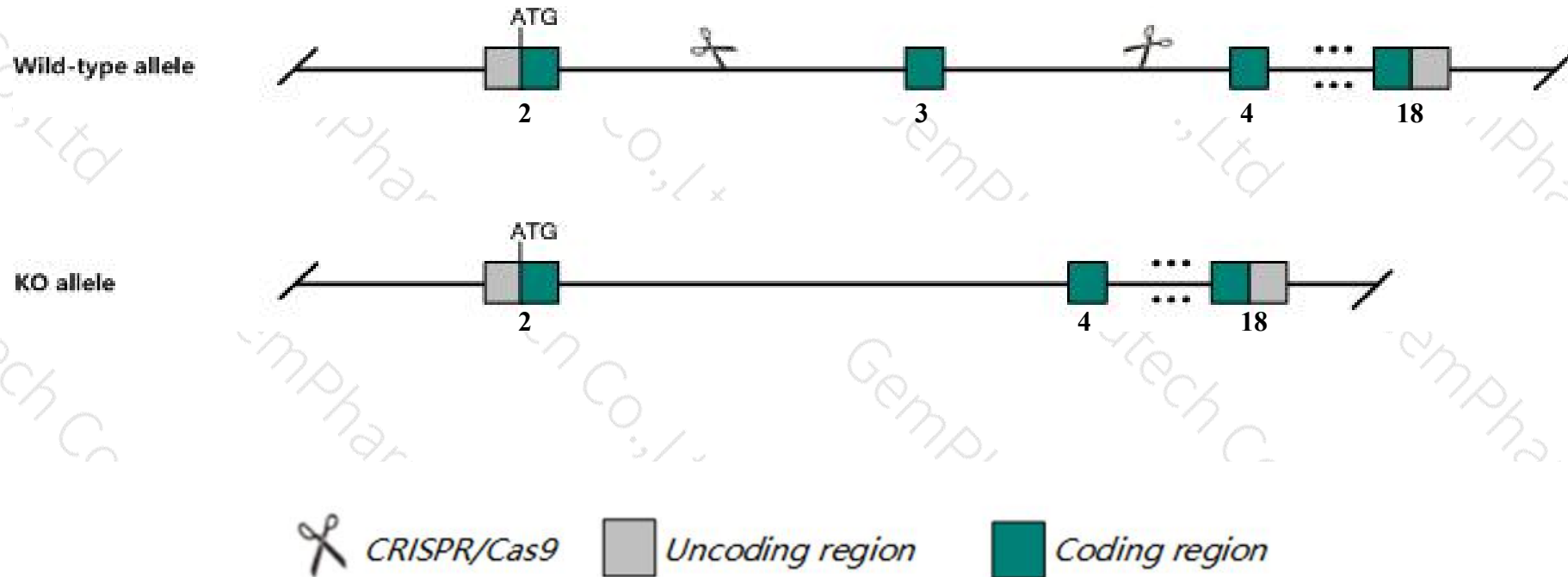
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Dync1i2* gene. The schematic diagram is as follows:



- The *Dync1i2* gene has 12 transcripts. According to the structure of *Dync1i2* gene, exon3 of *Dync1i2-206* (ENSMUST00000112140.7) transcript is recommended as the knockout region. The region contains 118bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Dync1i2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for an ENU-induced allele exhibit a trend towards slight locomotor deficit.
- The *Dync1i2* 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)

Dync1i2 dynein cytoplasmic 1 intermediate chain 2 [*Mus musculus* (house mouse)]

Gene ID: 13427, updated on 24-Dec-2019

Summary

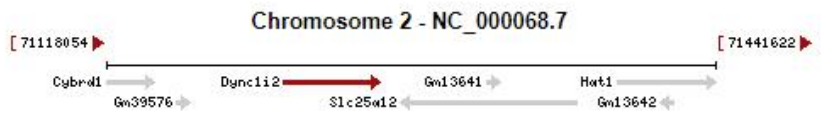
- Official Symbol** Dync1i2 provided by [MGI](#)
- Official Full Name** dynein cytoplasmic 1 intermediate chain 2 provided by [MGI](#)
- Primary source** [MGI:MGI:107750](#)
- See related** [Ensembl:ENSMUSG00000027012](#)
- Gene type** protein coding
- RefSeq status** VALIDATED
- Organism** [Mus musculus](#)
- Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
- Also known as** Dncic2; AW554389; 3110079H08Rik
- Expression** Broad expression in CNS E18 (RPKM 64.5), CNS E14 (RPKM 54.3) and 20 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 2 C2; 2 42.38 cM [See Dync1i2 in Genome Data Viewer](#)

Exon count: 20

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	2	NC_000068.7 (71211676..71263303)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	2	NC_000068.6 (71050070..71101351)

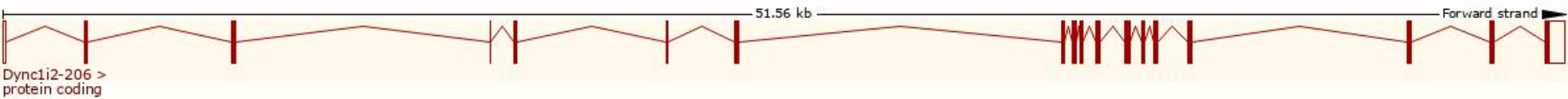


Transcript information (Ensembl)

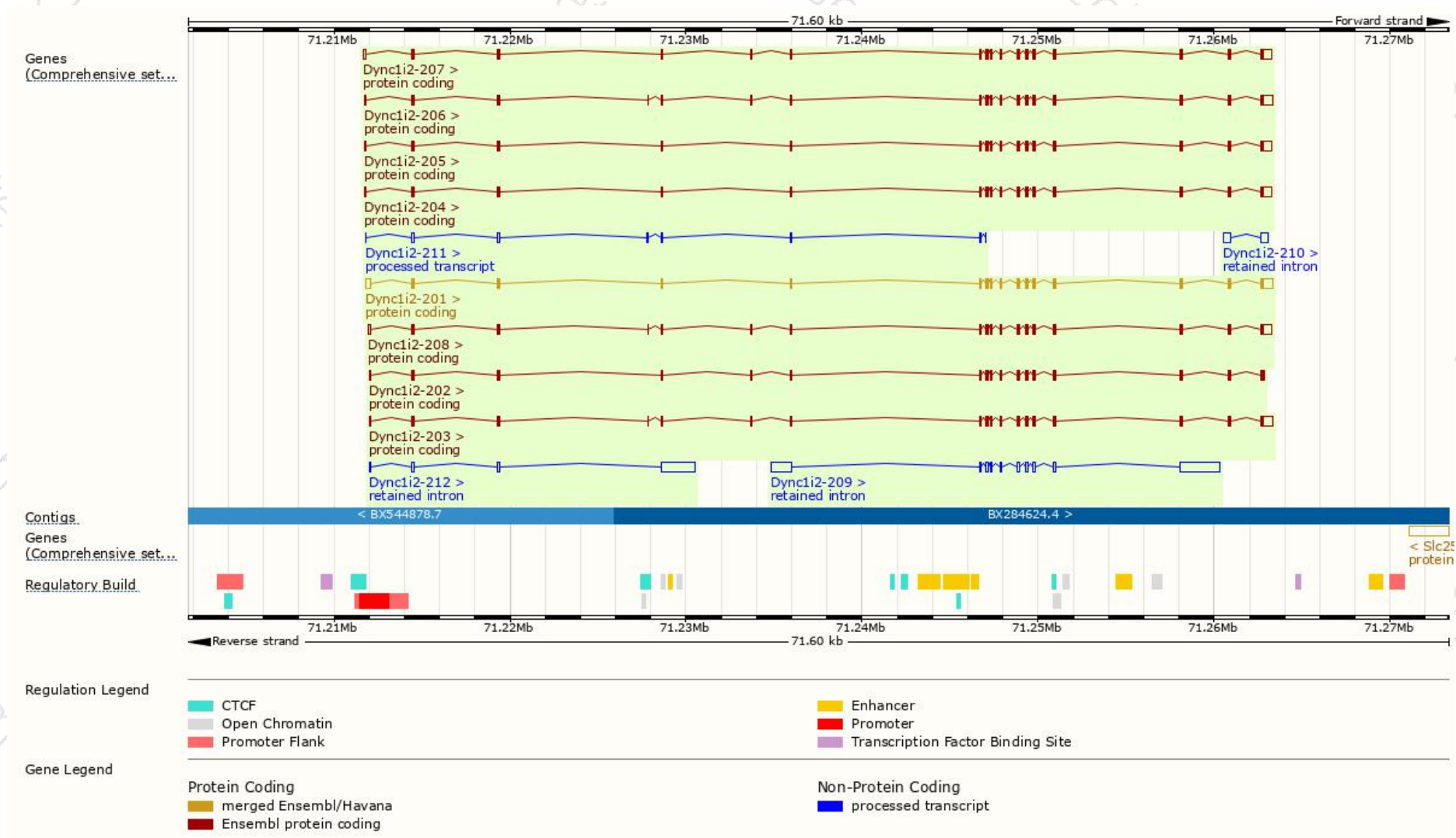
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dync1i2-201	ENSMUST00000081710.11	2631	612aa	Protein coding	CCDS16112	A2BFF7 Q88487	TSL:1 GENCODE basic APPRIS P3
Dync1i2-207	ENSMUST00000112142.7	2585	632aa	Protein coding	CCDS57175	Q3TPJ8	TSL:1 GENCODE basic APPRIS ALT1
Dync1i2-206	ENSMUST00000112140.7	2573	638aa	Protein coding	CCDS84536	A2BFF9	TSL:5 GENCODE basic APPRIS ALT1
Dync1i2-208	ENSMUST00000112144.8	2565	638aa	Protein coding	CCDS84536	A2BFF9	TSL:5 GENCODE basic APPRIS ALT1
Dync1i2-204	ENSMUST00000112138.7	2466	612aa	Protein coding	CCDS16112	A2BFF7 Q88487	TSL:1 GENCODE basic APPRIS P3
Dync1i2-202	ENSMUST00000100028.9	2097	632aa	Protein coding	CCDS57175	Q3TPJ8	TSL:5 GENCODE basic APPRIS ALT1
Dync1i2-203	ENSMUST00000112136.1	2548	637aa	Protein coding	-	A2BFF5	TSL:5 GENCODE basic APPRIS ALT1
Dync1i2-205	ENSMUST00000112139.7	2483	611aa	Protein coding	-	A2BFF8	TSL:5 GENCODE basic APPRIS ALT1
Dync1i2-211	ENSMUST00000141619.7	679	No protein	Processed transcript	-	-	TSL:5
Dync1i2-209	ENSMUST00000137683.1	4523	No protein	Retained intron	-	-	TSL:1
Dync1i2-212	ENSMUST00000149735.1	2248	No protein	Retained intron	-	-	TSL:1
Dync1i2-210	ENSMUST00000138613.1	812	No protein	Retained intron	-	-	TSL:2

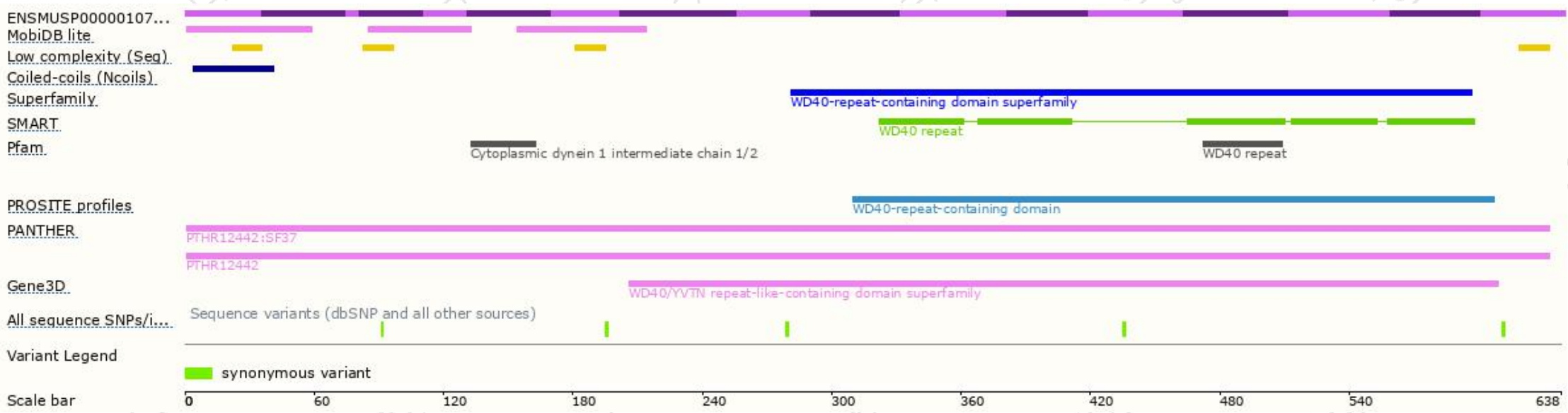
The strategy is based on the design of *Dync1i2-206* transcript, the transcription is shown below:



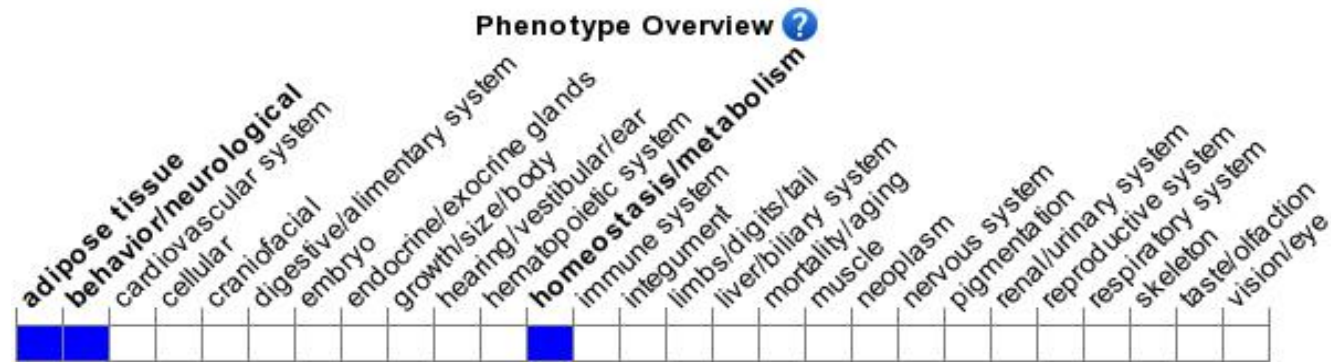
Genomic location distribution



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 an ENU-induced allele exhibit a trend towards slight locomotor deficit.

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

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