

C9orf72 Cas9-KO Strategy

Designer: Xueting Zhang

Reviewer: Yanhua Shen

Design Date: 2019-8-23

Project Overview



Project Name

C9orf72

Project type

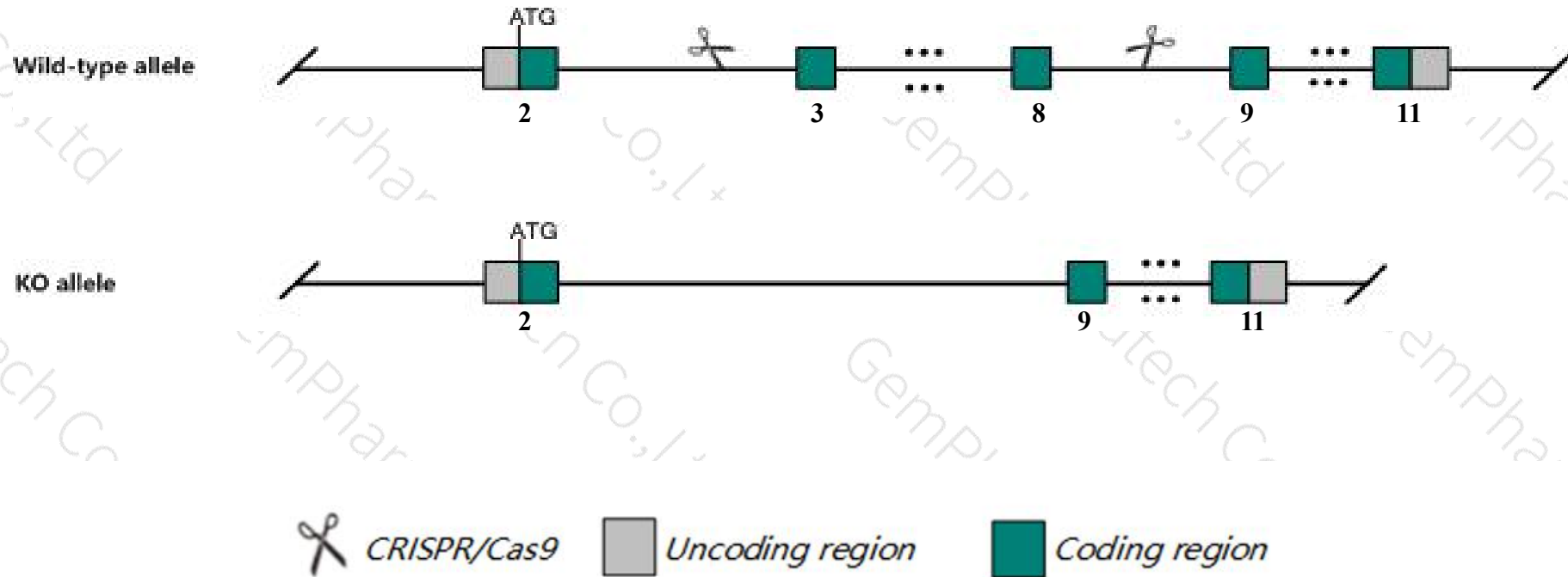
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *C9orf72* gene. The schematic diagram is as follows:



- The *C9orf72* gene has 7 transcripts. According to the structure of *C9orf72* gene, exon3-exon8 of *C9orf72-203* (ENSMUST00000108127.3) transcript is recommended as the knockout region. The region contains 647bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *C9orf72* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Nullizygous mice show splenomegaly and lymphadenopathy. Homozygotes for one allele show reduced body weight, hematocrit and hemoglobin content, lymphopenia, neutrophilia, social interaction deficits and premature death. Homozygotes for another allele show altered macrophage and microglia physiology.
- *Gm12366* gene will be deleted together in this strategy.
- The N-terminal of *C9orf72* gene will remain 148aa, it may remain the partial function of *C9orf72* gene.
- The *C9orf72* 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)

C9orf72 C9orf72, member of C9orf72-SMCR8 complex [*Mus musculus* (house mouse)]

Gene ID: 73205, updated on 12-Aug-2019

Summary

Official Symbol	C9orf72 provided by MGI
Official Full Name	C9orf72, member of C9orf72-SMCR8 complex provided by MGI
Primary source	MGI: MGI:1920455
See related	Ensembl: ENSMUSG00000028300
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	AI840585; 3110043O21Rik
Expression	Ubiquitous expression in subcutaneous fat pad adult (RPKM 12.1), CNS E18 (RPKM 11.9) and 26 other tissues See more
Orthologs	human all

Genomic context

Location: 4; 4 A5

See C9orf72 in [Genome Data Viewer](#)

Exon count: 13

Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	4	NC_000070.6 (35191285..35226153, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	4	NC_000070.5 (35138531..35173129, complement)

Transcript information (Ensembl)

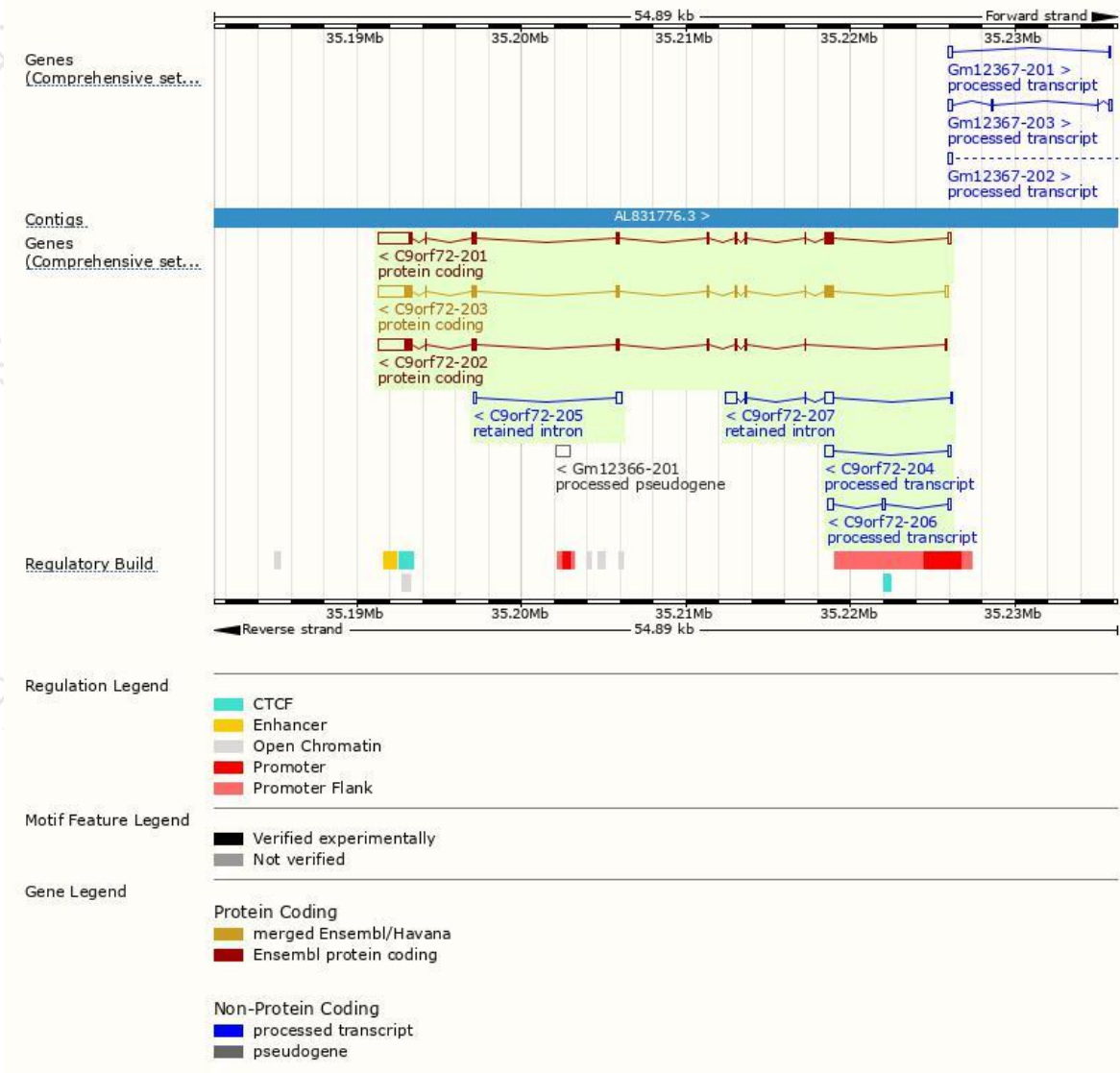
The gene has 7 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
C9orf72-203	ENSMUST00000108127.3	3193	481aa	Protein coding	CCDS38708	Q6DFW0	TSL:1 GENCODE basic APPRIS P1
C9orf72-201	ENSMUST00000084724.9	3413	420aa	Protein coding	-	Q6DFW0	TSL:1 GENCODE basic
C9orf72-202	ENSMUST00000108126.7	2644	317aa	Protein coding	-	A2ANZ2	TSL:1 GENCODE basic
C9orf72-206	ENSMUST00000149138.1	727	No protein	Processed transcript	-	-	TSL:3
C9orf72-204	ENSMUST00000130538.7	703	No protein	Processed transcript	-	-	TSL:3
C9orf72-207	ENSMUST00000156472.1	1370	No protein	Retained intron	-	-	TSL:5
C9orf72-205	ENSMUST00000142628.1	528	No protein	Retained intron	-	-	TSL:3

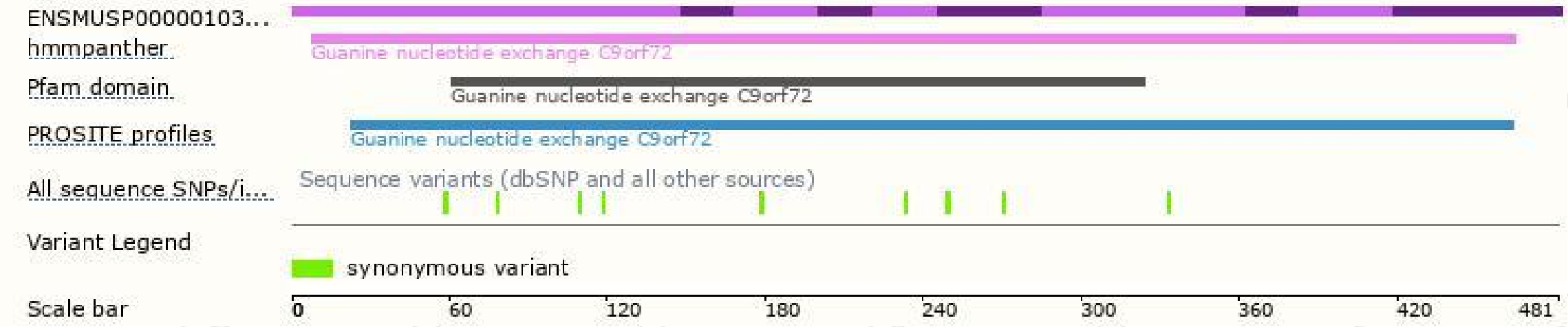
The strategy is based on the design of *C9orf72-203* transcript, The transcription is shown below



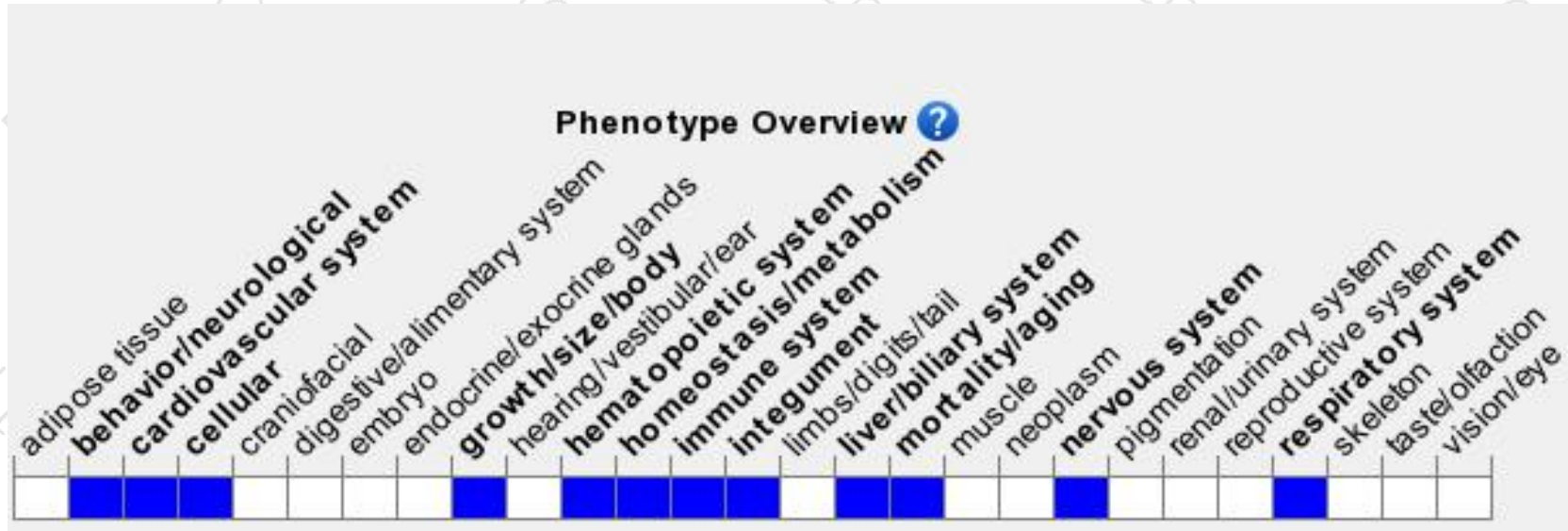
Genomic location distribution



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, Nullizygous mice show splenomegaly and lymphadenopathy. Homozygotes for one allele show reduced body weight, hematocrit and hemoglobin content, lymphopenia, neutrophilia, social interaction deficits and premature death. Homozygotes for another allele show altered macrophage and microglia physiology.

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

Tel: 400-9660890

