

Clcc1 Cas9-KO Strategy

Designer:

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Project Overview

Project Name

Clcc1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Clcc1* gene. The schematic diagram is as follows:



- The *Clcc1* gene has 8 transcripts. According to the structure of *Clcc1* gene, exon5-exon7 of *Clcc1-203* (ENSMUST00000106613.1) transcript is recommended as the knockout region. The region contains 457bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Clcc1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a spontaneous mutation show strain-dependent cerebellar granule cell death and peripheral motor axon degeneration. The peripheral neuropathy, neurogenic muscular atrophy and mild truncal ataxia observed on the C57BL/6JGpt background are not found on the C3H/HeSnJ background.
- The *Clcc1* gene is located on the Chr3. 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)

Clcc1 chloride channel CLIC-like 1 [Mus musculus (house mouse)]

Gene ID: 229725, updated on 31-Jan-2019

Summary



Official Symbol	Clcc1 provided by MGI
Official Full Name	chloride channel CLIC-like 1 provided by MGI
Primary source	MGI:MGI:2385186
See related	Ensembl:ENSMUSG000000027884
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	Mclc
Expression	Ubiquitous expression in bladder adult (RPKM 9.9), limb E14.5 (RPKM 9.7) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

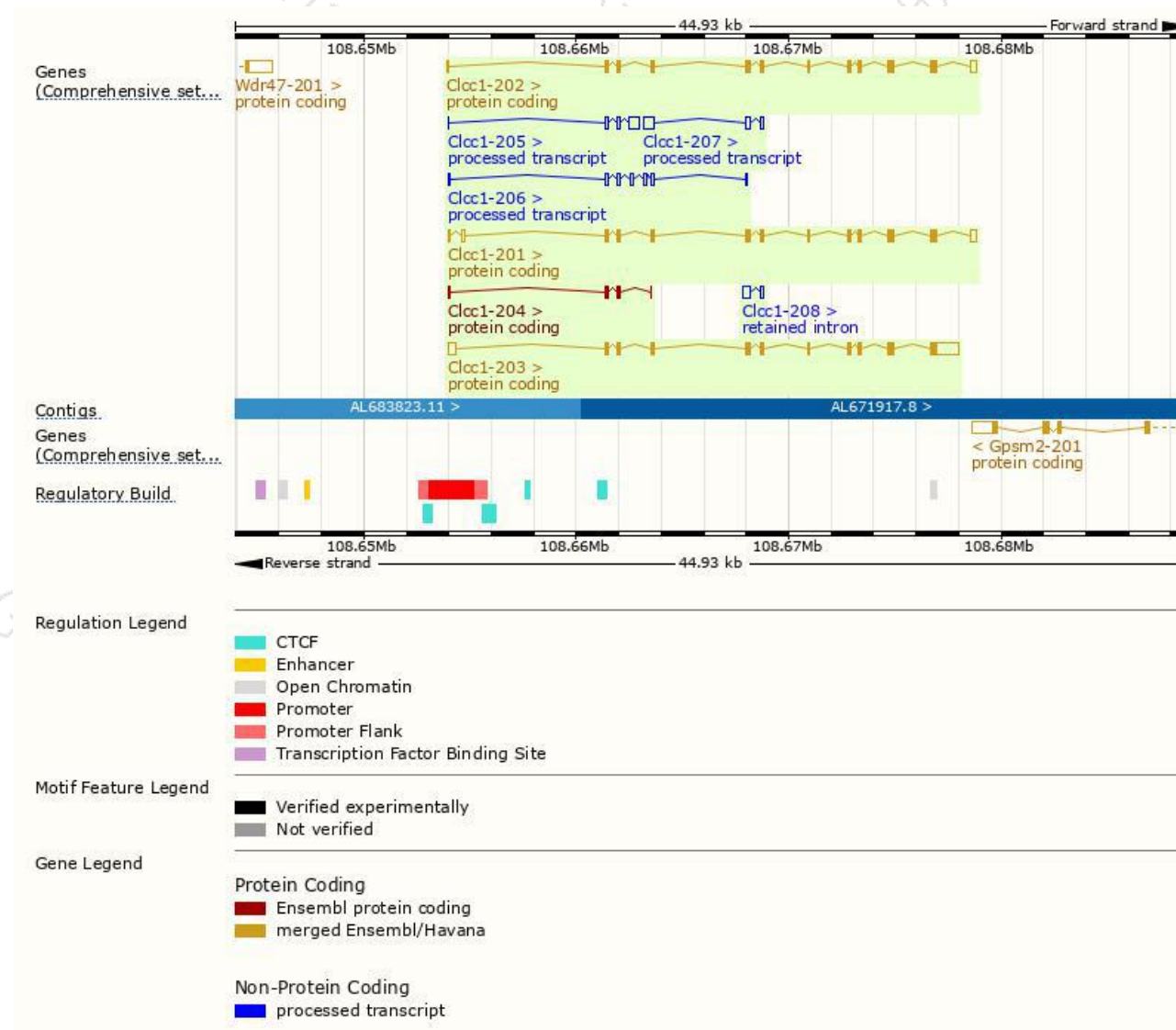
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Clcc1-203	ENSMUST00000106613.1	3064	544aa	Protein coding	CCDS51047	A2AEM2	TSL:1 GENCODE basic APPRIS ALT2
Clcc1-201	ENSMUST00000029483.14	2224	539aa	Protein coding	CCDS17766	Q99LI2	TSL:5 GENCODE basic APPRIS P3
Clcc1-202	ENSMUST00000106609.7	2043	539aa	Protein coding	CCDS17766	Q99LI2	TSL:1 GENCODE basic APPRIS P3
Clcc1-204	ENSMUST00000124384.7	358	84aa	Protein coding	-	Z4YMG1	CDS 3' incomplete TSL:3
Clcc1-206	ENSMUST00000130352.3	895	No protein	Processed transcript	-	-	TSL:3
Clcc1-207	ENSMUST00000139016.2	795	No protein	Processed transcript	-	-	TSL:3
Clcc1-205	ENSMUST00000125274.7	762	No protein	Processed transcript	-	-	TSL:3
Clcc1-208	ENSMUST00000156811.2	469	No protein	Retained intron	-	-	TSL:3

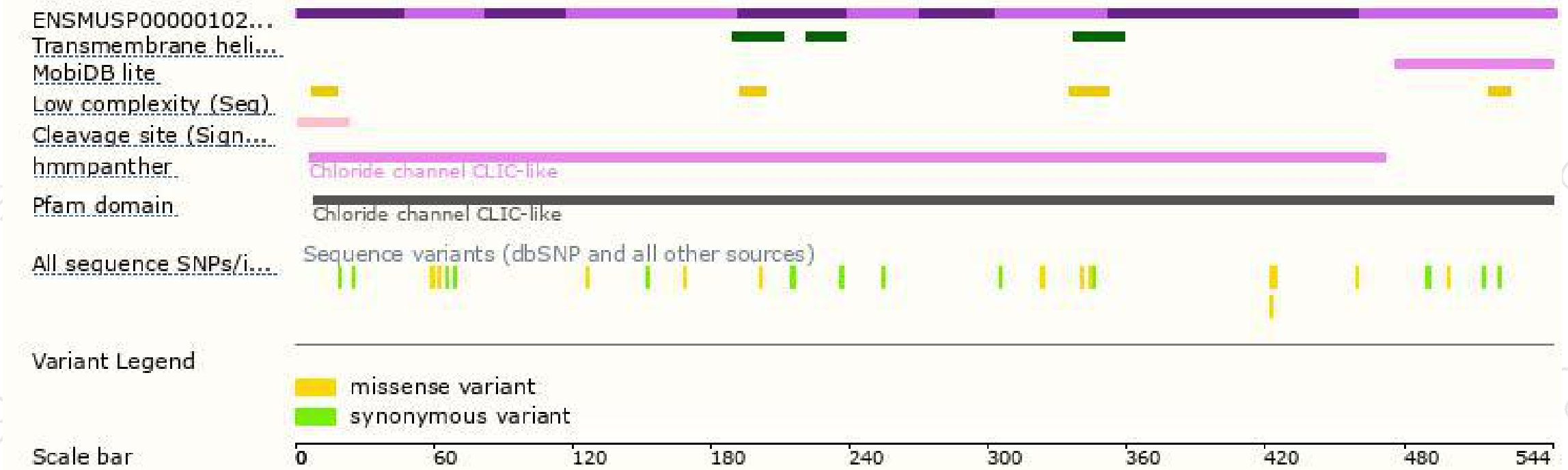
The strategy is based on the design of *Clcc1-203* transcript,The transcription is shown below



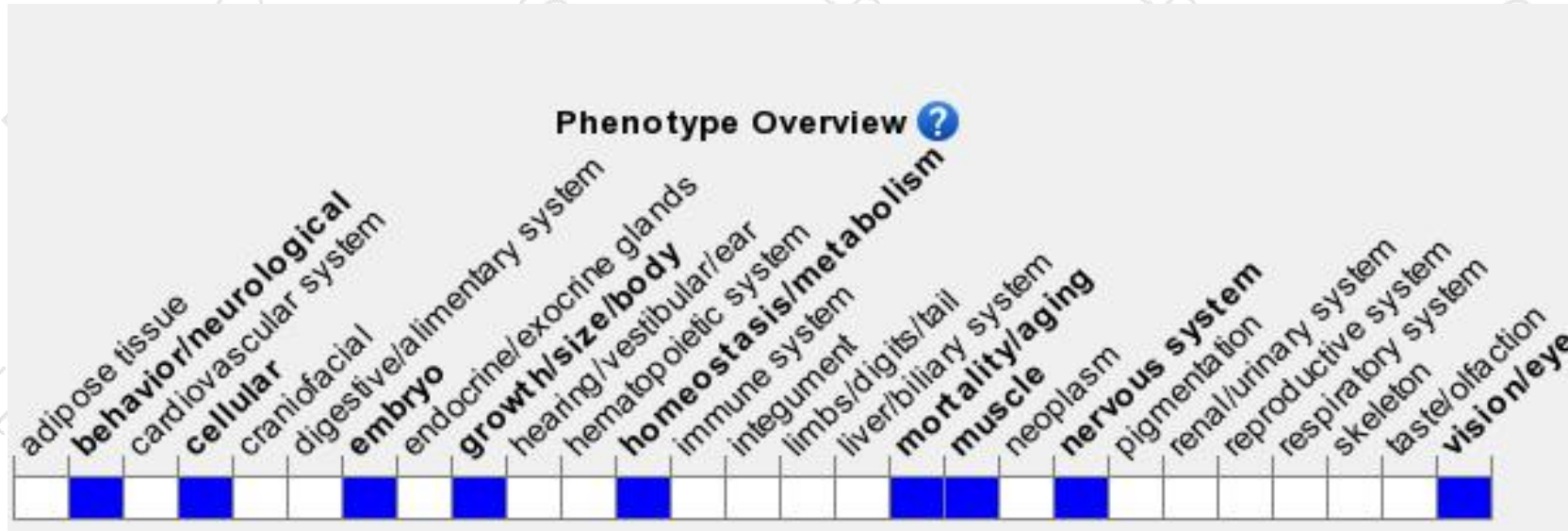
Genomic location distribution



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 spontaneous mutation show strain-dependent cerebellar granule cell death and peripheral motor axon degeneration. The peripheral neuropathy, neurogenic muscular atrophy and mild truncal ataxia observed on the C57BL/6JGpt background are not found on the C3H/HeSnJ background.

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

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