

Utrn Cas9-KO Strategy

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Project Overview

Project Name

Utrn

Project type

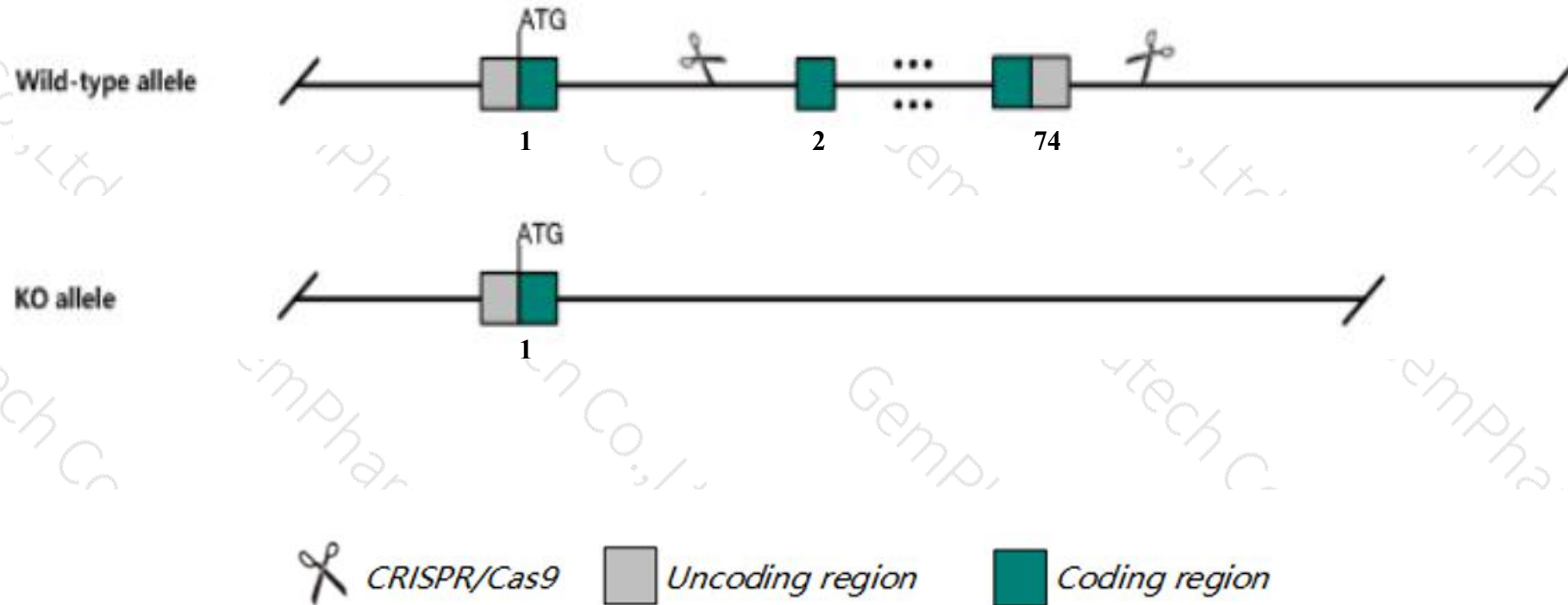
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Utrn* gene has 13 transcripts. According to the structure of *Utrn* gene, exon2-exon74 of *Utrn-201* (ENSMUST00000076817.4) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Utrn* gene. The brief process is as follows: CRISPR/Cas9 system were

- According to the existing MGI data, homozygous null mutants have reduced density of acetylcholine receptors and reduced number of junctional folds at neuromuscular junctions. mice homozygous for utrophin and dystrophin knockouts die prematurely with severe, progressive muscular dystrophy.
- The *Utrn* gene is located on the Chr10. 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)

Utrn utrophin [Mus musculus (house mouse)]

Gene ID: 22288, updated on 24-Feb-2019

Summary



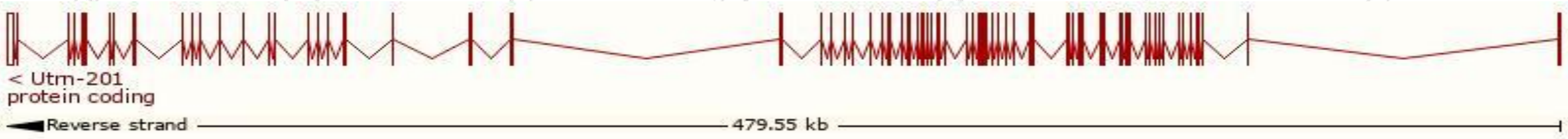
Official Symbol	Utrn provided by MGI
Official Full Name	utrophin provided by MGI
Primary source	MGI:MGI:104631
See related	Ensembl:ENSMUSG00000019820
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AA589569, DRP, Dmdl
Expression	Ubiquitous expression in lung adult (RPKM 10.2), bladder adult (RPKM 7.8) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

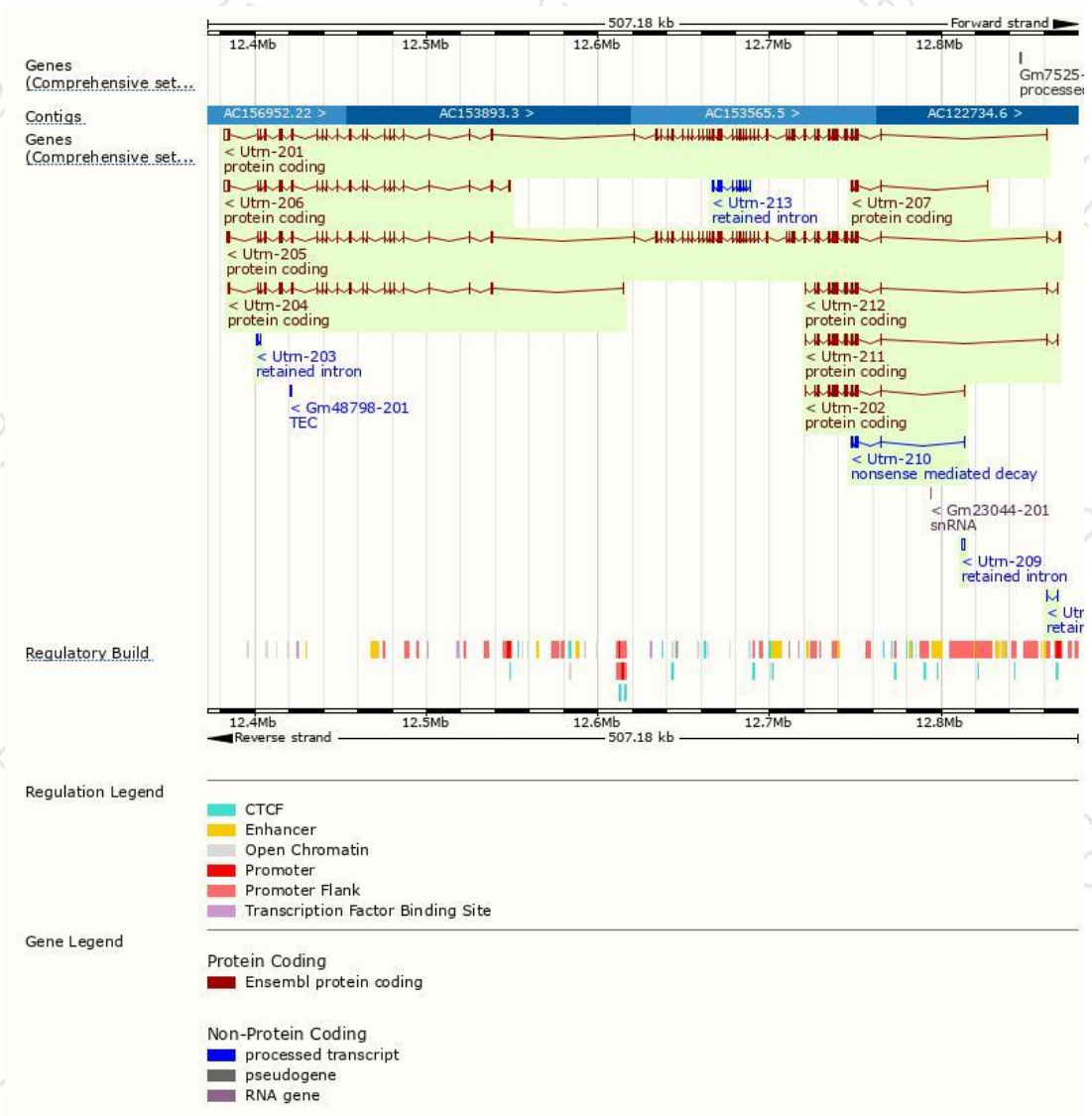
The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Utrn-201	ENSMUST00000076817.4	12382	3430aa	Protein coding	CCDS35841	E9Q6R7	TSL:1 GENCODE basic APPRIS P1
Utrn-205	ENSMUST00000218635.1	11801	3430aa	Protein coding	CCDS35841	E9Q6R7	TSL:5 GENCODE basic APPRIS P1
Utrn-206	ENSMUST00000219003.1	5751	956aa	Protein coding	-	A0A1W2P7C0	TSL:5 GENCODE basic
Utrn-204	ENSMUST00000217994.1	3161	987aa	Protein coding	-	Q61636	TSL:1 GENCODE basic
Utrn-212	ENSMUST00000219660.1	2468	730aa	Protein coding	-	A0A1W2P8G5	CDS 3' incomplete TSL:1
Utrn-211	ENSMUST00000219584.1	2328	730aa	Protein coding	-	A0A1W2P8G5	CDS 3' incomplete TSL:1
Utrn-202	ENSMUST00000217899.1	2272	732aa	Protein coding	-	A0A1W2P8A5	CDS 3' incomplete TSL:1
Utrn-207	ENSMUST00000219130.1	660	186aa	Protein coding	-	A0A1W2P6L4	CDS 3' incomplete TSL:3
Utrn-210	ENSMUST00000219163.1	648	62aa	Nonsense mediated decay	-	A0A1W2P6H3	TSL:3
Utrn-213	ENSMUST00000219724.1	2565	No protein	Retained intron	-	-	TSL:1
Utrn-209	ENSMUST00000219145.1	1139	No protein	Retained intron	-	-	TSL:NA
Utrn-203	ENSMUST00000217938.1	531	No protein	Retained intron	-	-	TSL:3
Utrn-208	ENSMUST00000219135.1	430	No protein	Retained intron	-	-	TSL:3

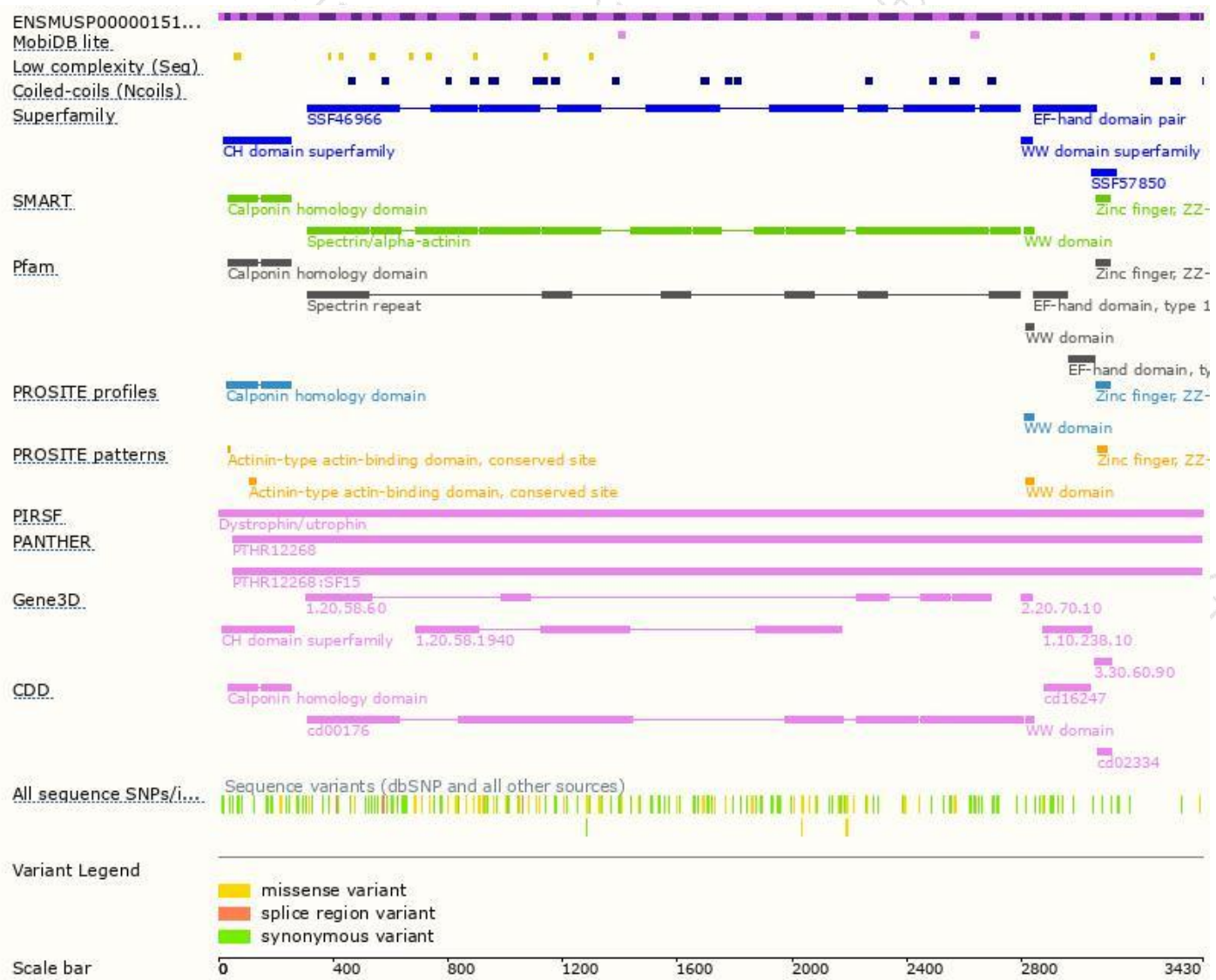
The strategy is based on the design of *Utrn-201* transcript,the transcription is shown below:



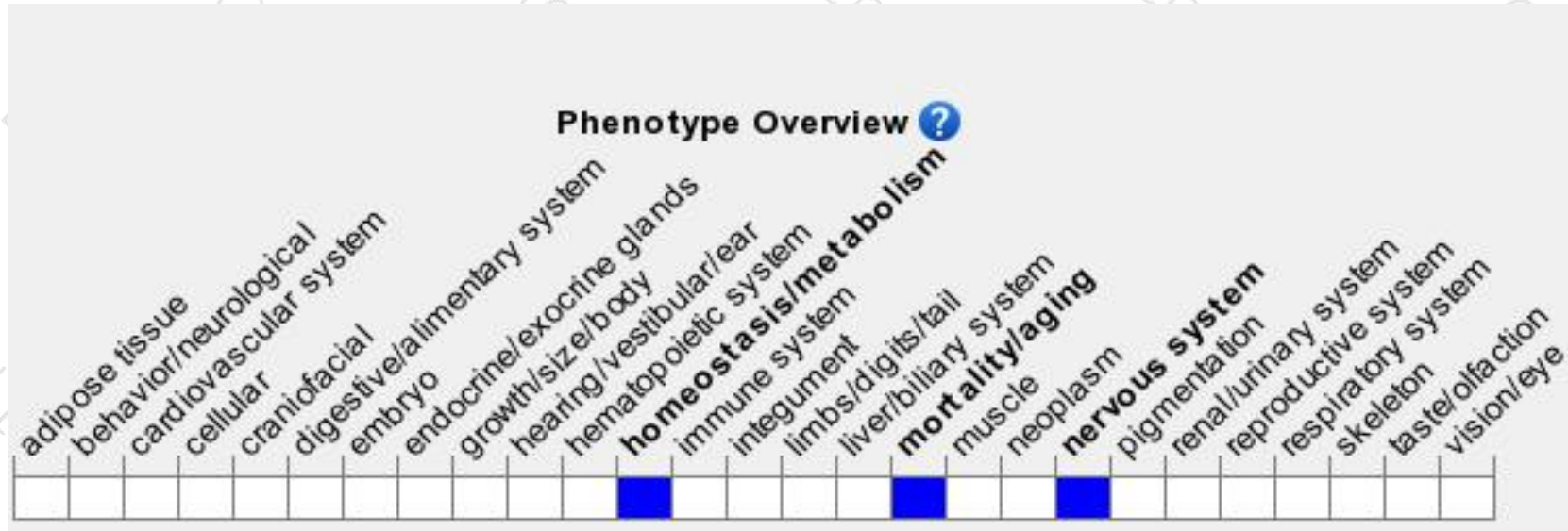
Genomic location distribution



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, homozygous null mutants have reduced density of acetylcholine receptors and reduced number of junctional folds at neuromuscular junctions. Mice homozygous for utrophin and dystrophin knockouts die prematurely with severe, progressive muscular dystrophy.

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

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