Atl1 Cas9-KO Strategy

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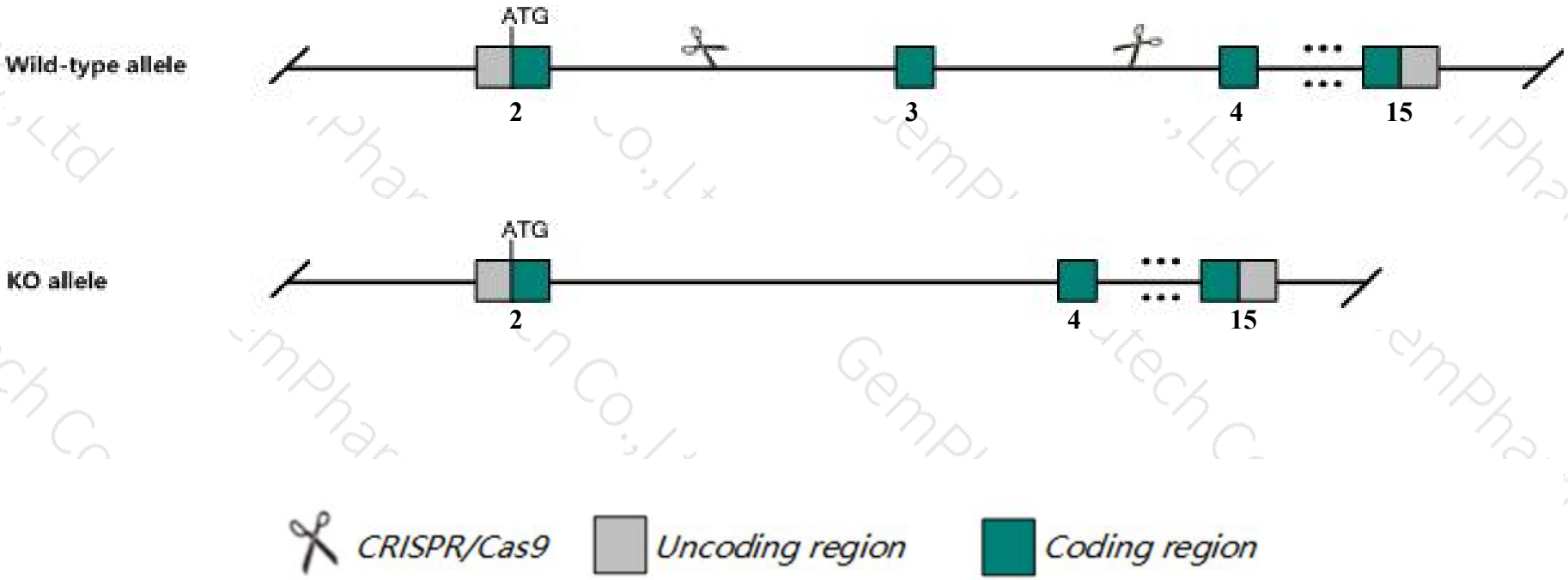
Project Overview

Project Name	***Atl1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atl1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Atl1* gene has 5 transcripts. According to the structure of *Atl1* gene, exon3 of *Atl1-201* (ENSMUST00000021466.9) transcript is recommended as the knockout region.The region contains 248bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Atl1* gene. The brief process is as follows: CRISPR/Cas9 system w

Notice

- According to the existing MGI data,Homozygous animals show a gait disturbance characterized by external rotation of the hind feet with footprint analysis.

- The *Atl1* gene is located on the Chr12. 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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Atl1 atlastin GTPase 1 [Mus musculus (house mouse)]

Gene ID: 73991, updated on 31-Jan-2019

Summary

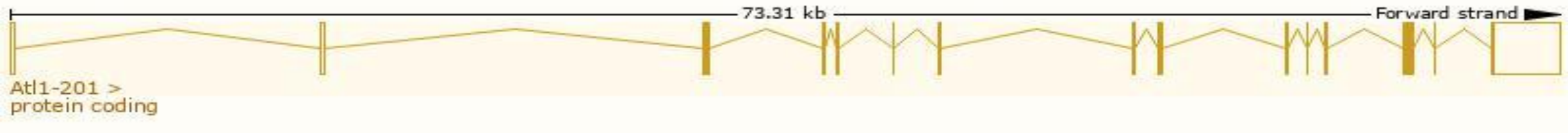
Official Symbol	Atl1 provided by MGI
Official Full Name	atlastin GTPase 1 provided byMGI
Primary source	MGI:MGI:1921241
See related	Ensembl:ENSMUSG00000021066
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	4930435M24Rik, Adfsp, Fsp1, Spg3, Spg3a
Summary	This gene encodes a member of the dynamin family of GTPases. The encoded protein interacts with tubule-shaping proteins of the endoplasmic reticulum. Mutations in the homologous human gene can cause hereditary spastic paraplegia. [provided by RefSeq, Feb 2010]
Expression	Biased expression in CNS E18 (RPKM 20.0), frontal lobe adult (RPKM 19.8) and 11 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

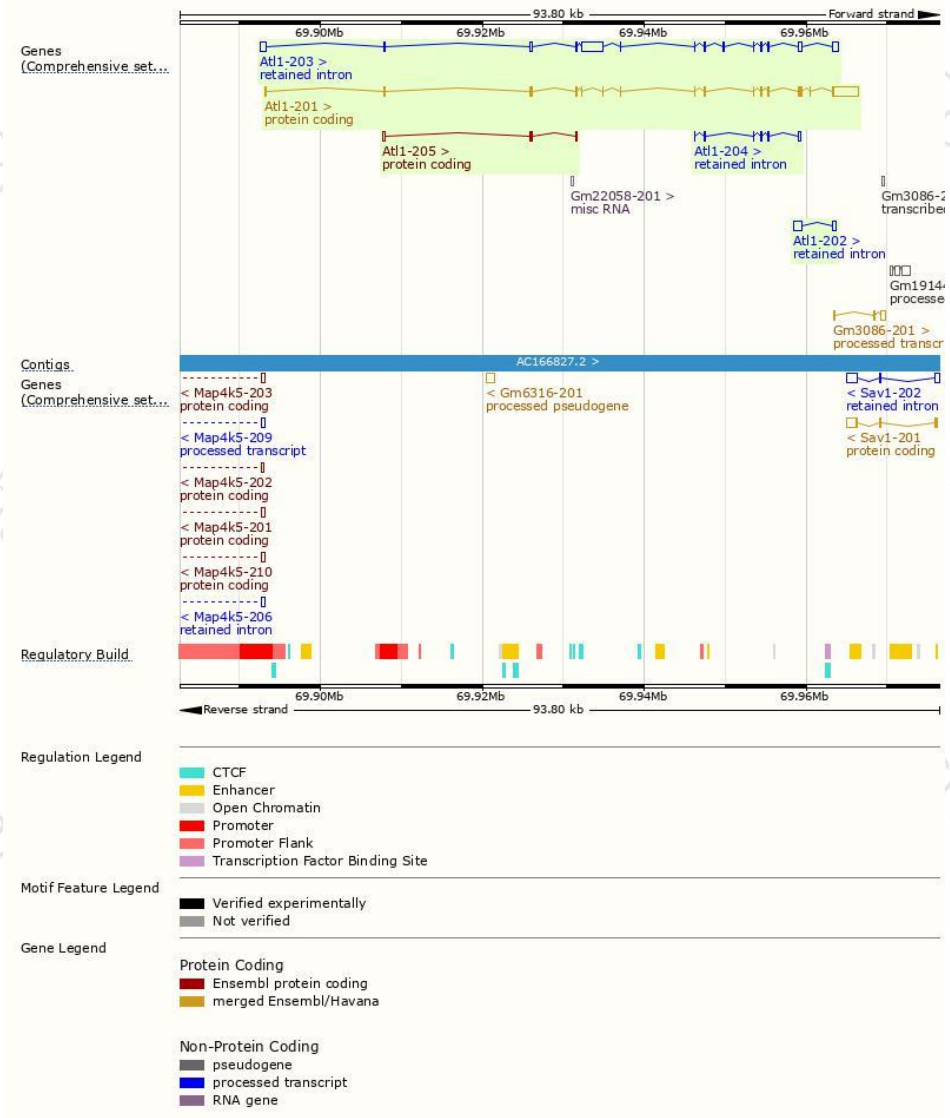
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atl1-201	ENSMUST00000021466.9	5150	558aa	Protein coding	CCDS36465	Q8BH66	TSL:1 GENCODE basic APPRIS P1
Atl1-205	ENSMUST00000223456.1	626	133aa	Protein coding	-	A0A1Y7VLD6	CDS 3' incomplete TSL:2
Atl1-203	ENSMUST00000222141.1	6025	No protein	Retained intron	-	-	TSL:5
Atl1-202	ENSMUST00000220935.1	1512	No protein	Retained intron	-	-	TSL:5
Atl1-204	ENSMUST00000222246.1	815	No protein	Retained intron	-	-	TSL:5

The strategy is based on the design of *Atl1-201* transcript,The transcription is shown below

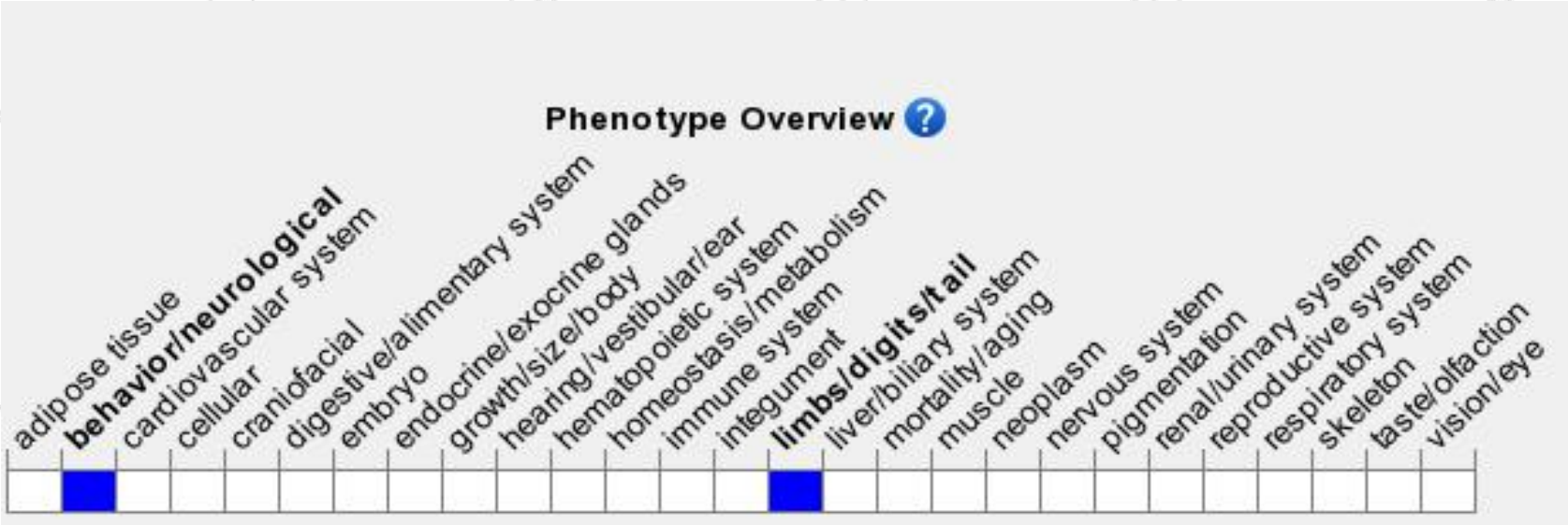


Genomic location distribution



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/).

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

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