

Abl2 Cas9-KO Strategy

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Project Overview

Project Name

Abl2

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Abl2* gene. The schematic diagram is as follows:



- The *Abl2* gene has 4 transcripts. According to the structure of *Abl2* gene, exon2-exon4 of *Abl2-202* (ENSMUST00000166172.8) transcript is recommended as the knockout region. The region contains 530bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Abl2* gene. The brief process is as follows: CRISPR/Cas9 system will

- According to the existing MGI data, Mice homozygous for targeted mutations that inactivate the gene display multiple behavioral abnormalities indicating neuronal defects.
- The *Abl2* gene is located on the Chr1. 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.

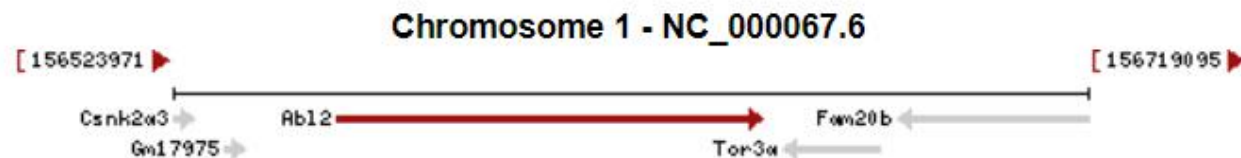
Gene information (NCBI)

Abl2 v-abl Abelson murine leukemia viral oncogene 2 (arg, Abelson-related gene) [*Mus musculus* (house mouse)]

Gene ID: 11352, updated on 14-Nov-2019

Summary

Official Symbol	Abl2 provided by MGI
Official Full Name	v-abl Abelson murine leukemia viral oncogene 2 (arg, Abelson-related gene) provided by MGI
Primary source	MGI:MGI:87860
See related	Ensembl:ENSMUSG00000026596
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	Arg; Abll; AA536808
Expression	Ubiquitous expression in frontal lobe adult (RPKM 5.8), whole brain E14.5 (RPKM 3.4) and 28 other tissues See more
Orthologs	human all

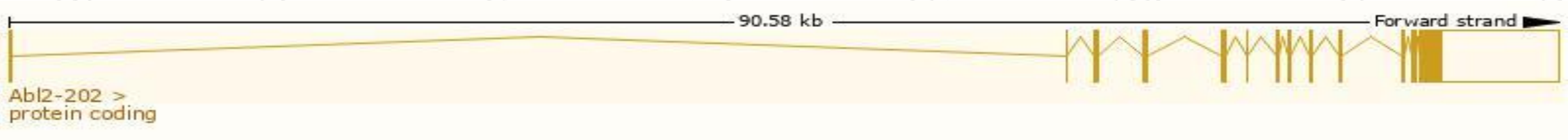


Transcript information (Ensembl)

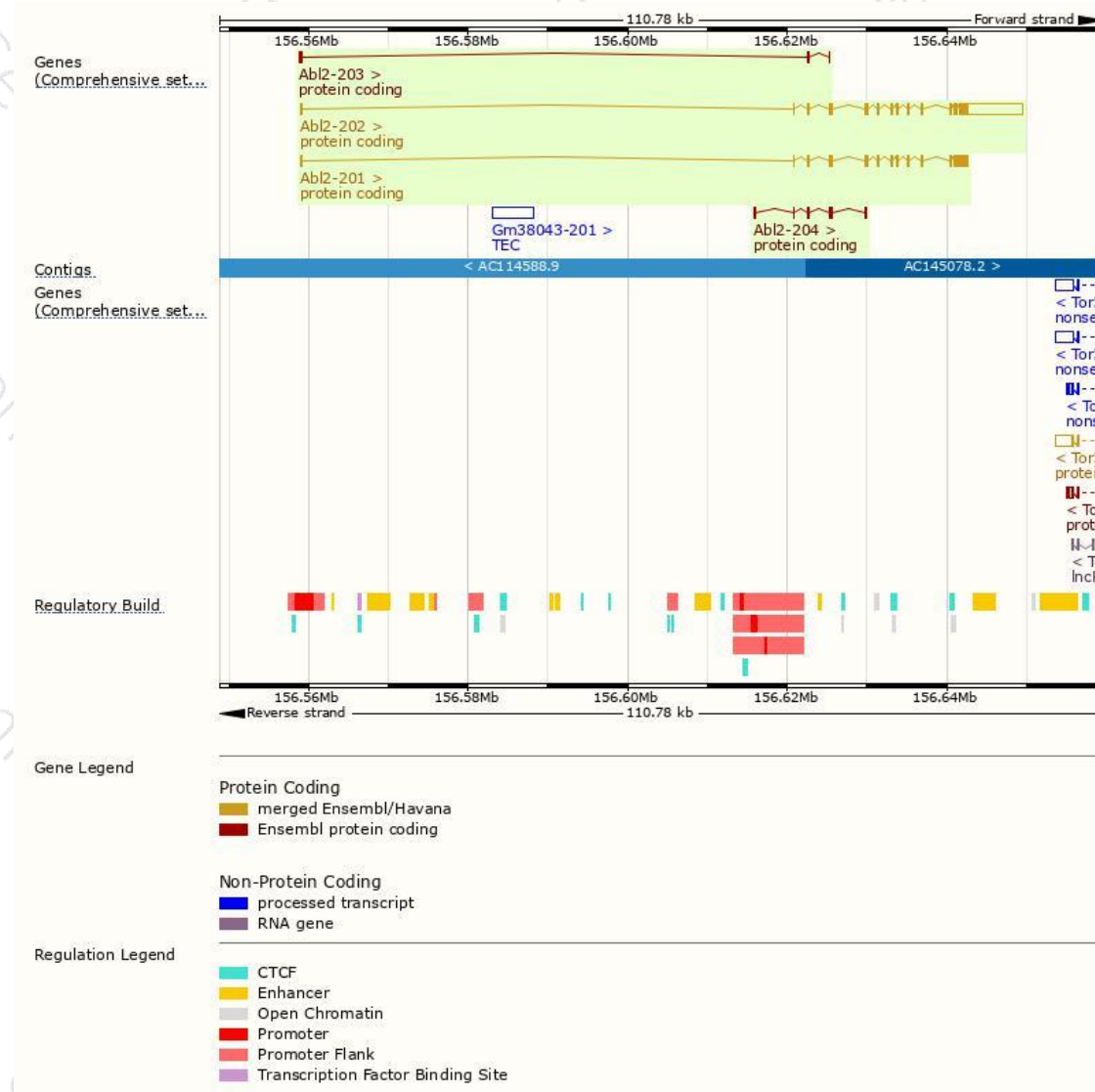
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Abl2-202	ENSMUST00000166172.8	10151	1078aa	Protein coding	CCDS48404	B2RQ57	TSL:1 GENCODE basic APPRIS ALT 1
Abl2-201	ENSMUST00000027888.12	3549	1182aa	Protein coding	CCDS15393	F8VQH0	TSL:1 GENCODE basic APPRIS P3
Abl2-204	ENSMUST00000190749.1	807	269aa	Protein coding	-	A0A087WQB7	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Abl2-203	ENSMUST00000173929.7	680	139aa	Protein coding	-	G3UWQ2	CDS 3' incomplete TSL:3

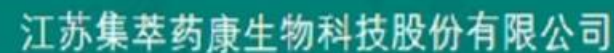
The strategy is based on the design of *Abl2-202* transcript,The transcription is shown below



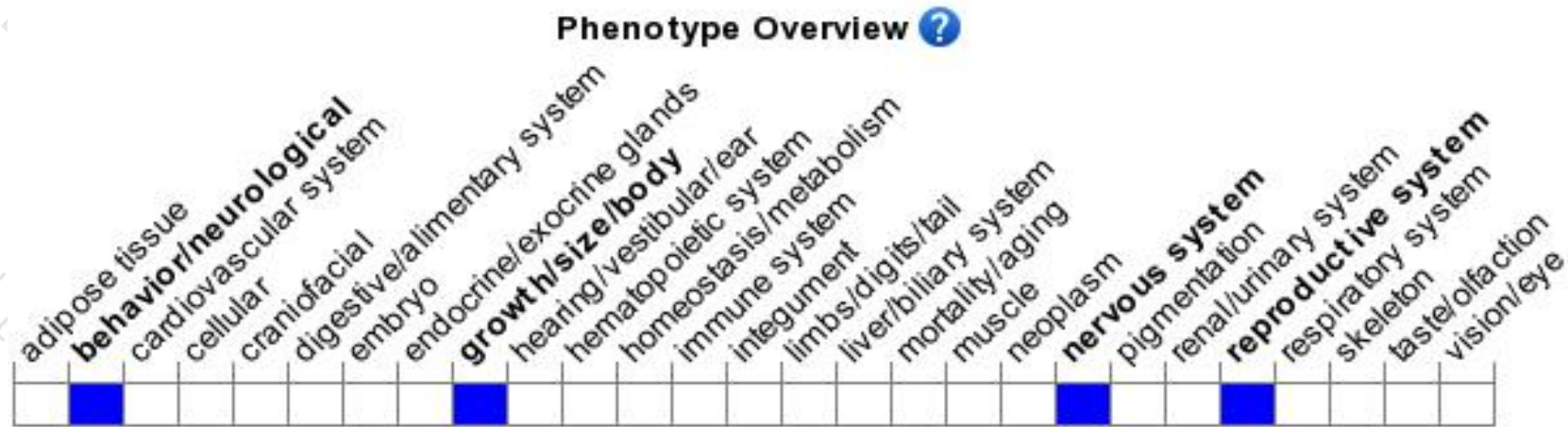
Genomic location distribution



集萃药康
GemPharmatech



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 targeted mutations that inactivate the gene display multiple behavioral abnormalities indicating neuronal defects.

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

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