GemPharmatech™

Amigo2 Cas9-CKO Strategy

Designer: Xiangli Bian

Reviewer: Jing Chen

Design Date: 2024-4-8

Overview

Target Gene Name

- *Amigo2*

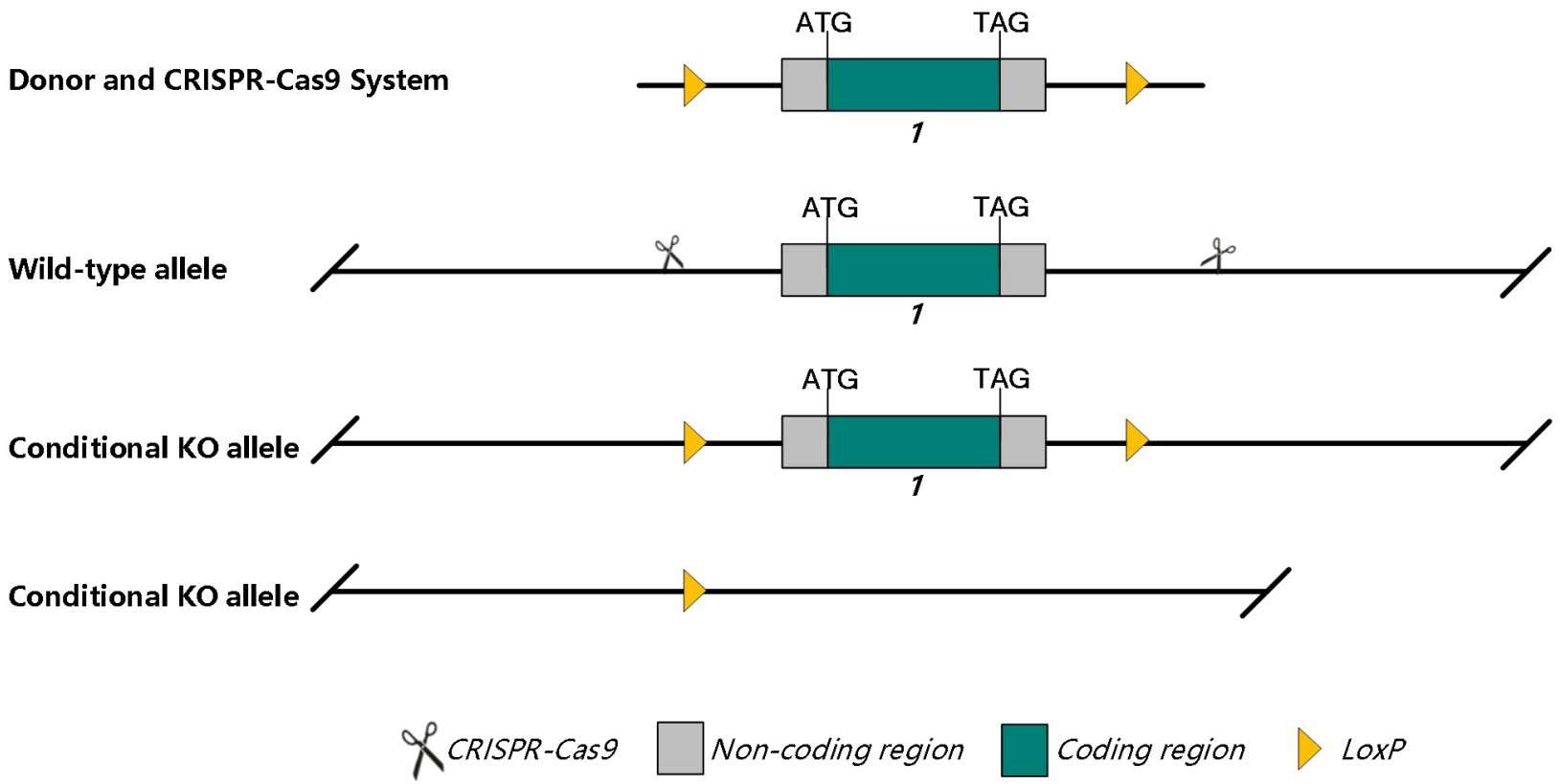
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Amigo2* gene.

Technical Information

- The *Amigo2* gene has 2 transcripts. According to the structure of *Amigo2* gene, exon 1 of *Amigo2*-202 (ENSMUST00000229890.2) is recommended as the knockout region. The region contains all of coding sequence. Knocking out the region will result in disruption of gene function.
- In this project we use CRISPR-Cas9 technology to modify *Amigo2* gene. The brief process is as follows: CRISPR-Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Gene Information

Amigo2 adhesion molecule with Ig like domain 2 [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 105827, updated on 5-Mar-2024

Summary

Official Symbol	Amigo2 provided by MGI
Official Full Name	adhesion molecule with Ig like domain 2 provided by MGI
Primary source	MGI:MGI:2145995
See related	Ensembl:ENSMUSG00000048218 AllianceGenome:MGI:2145995
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	Ali1; AMIGO-2
Summary	Acts upstream of or within positive regulation of synapse assembly. Predicted to be located in nucleus and plasma membrane. Predicted to be integral component of membrane. Is expressed in several structures, including brain; branchial arch; cranial ganglion; genitourinary system; and retina. Orthologous to human AMIGO2 (adhesion molecule with Ig like domain 2). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in frontal lobe adult (RPKM 2.9), lung adult (RPKM 2.6) and 28 other tissues See more
Orthologs	human all

NEW **Try the new Gene table**
Try the new Transcript table

Genomic context

Location: 15 F1; 15 52.91 cM — See Amigo2 in Genome Data Viewer

Exon count: 2

https://www.ncbi.nlm.nih.gov/gene/105827

Transcript Information

The gene has 2 transcripts, all transcripts are shown below:

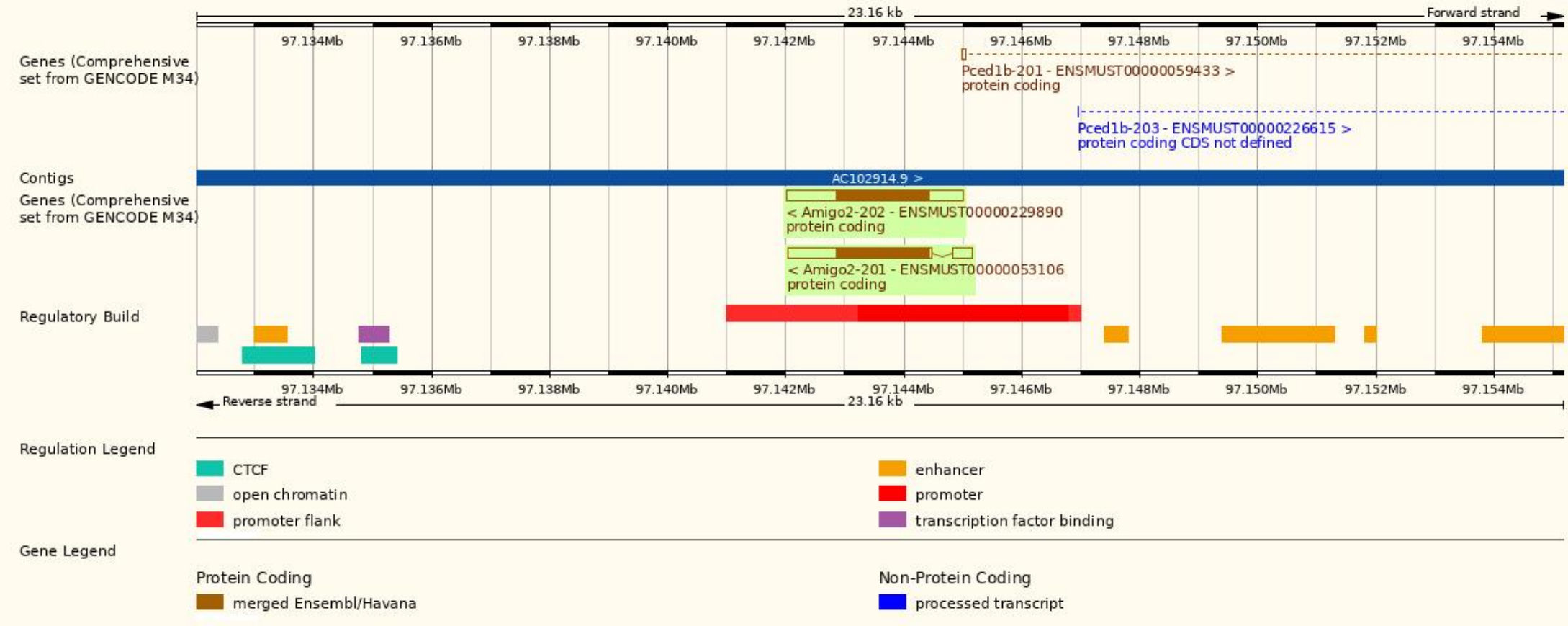
Show/hide columns (1 hidden) Filter

Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000229890.2	Amigo2-202	2998	519aa	Protein coding	CCDS27780	Q4VBE6 Q80ZD9	Ensembl Canonical GENCODE basic APPRIS P1
ENSMUST00000053106.7	Amigo2-201	2801	519aa	Protein coding	CCDS27780	Q4VBE6 Q80ZD9	GENCODE basic APPRIS P1 TSL:1

The strategy is based on the design of *Amigo2*-202 transcript, the transcription is shown below:

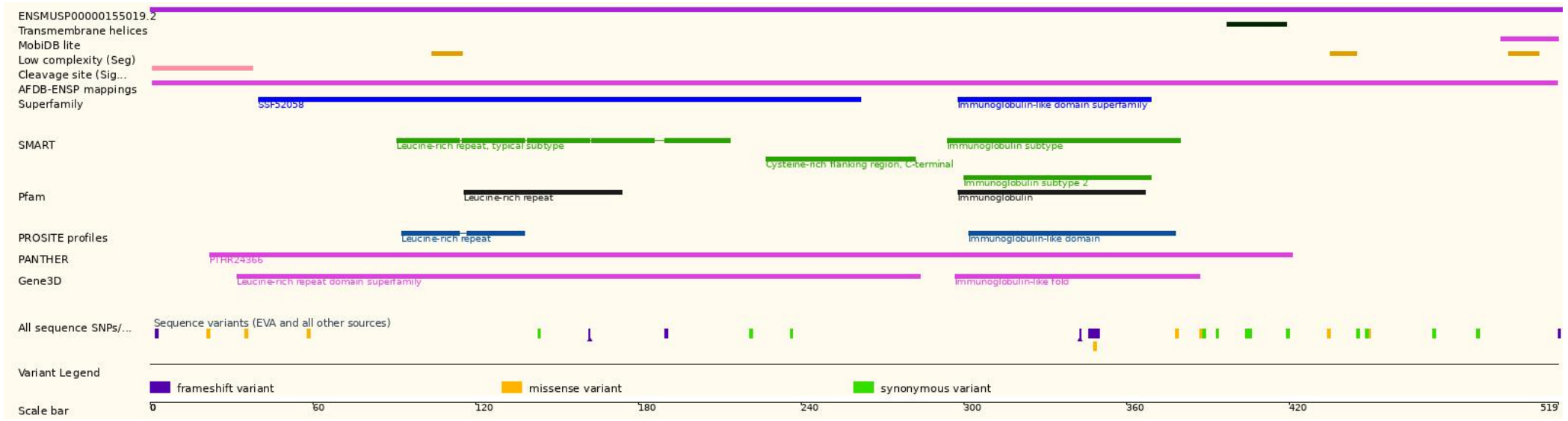
Source: http://asia.ensembl.org/

Genomic Information



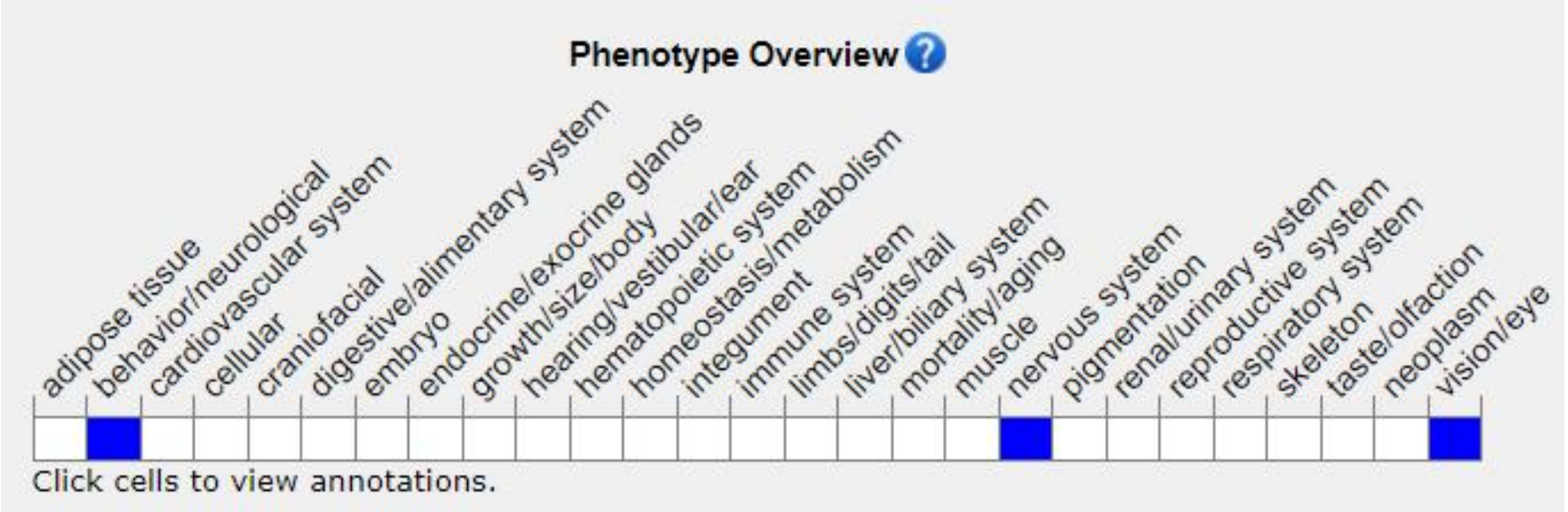
Source: http://asia.ensembl.org/

Protein Information



Source: https://www.ensembl.org

Mouse Phenotype Information (MGI)



Homozygous null mice exhibit starburst amacrine cell and rod bipolar cell dendrite arbor expansion and enhanced direction selectivity of direction-selective ganglion cell responses to starburst amacrine cell signals.

Source: https://www.informatics.jax.org

Important Information

- The knockout region overlaps with *Pced1b* gene, which may affect the function of this gene.
- *Amigo2* is located on Chr 15. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.