

# Alg13 Cas9-CKO Strategy

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# Overview

## Target Gene Name

- Alg13

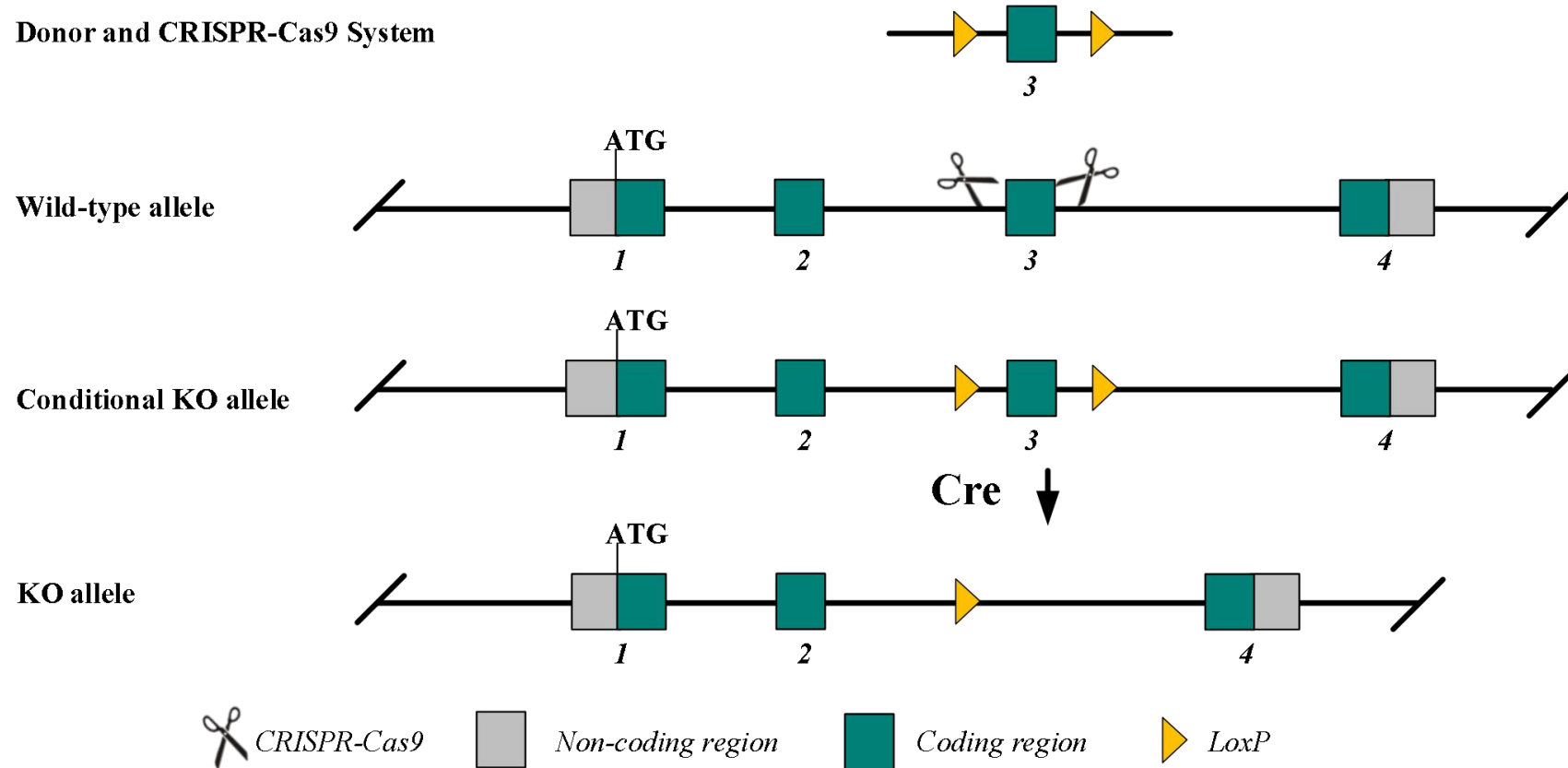
## Project Type

- Cas9-CKO

## Genetic Background

- C57BL/6JGpt

# Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Alg13* gene.

# Technical Information

- The *Alg13* gene has 15 transcripts. According to the structure of *Alg13* gene, exon 3 of *Alg13*-202 (ENSMUST00000070801.11) transcript is recommended as the knockout region. The region contains 139 bp of coding sequences. Knocking out the region may result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Alg13* 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

## Alg13 asparagine-linked glycosylation 13 [ *Mus musculus* (house mouse) ]

Gene ID: 67574, updated on 5-Mar-2024

[Download Datasets](#)

### Summary

<b>Official Symbol</b>	Alg13 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	asparagine-linked glycosylation 13 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1914824</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000041718</a> <a href="#">AllianceGenome:MGI:1914824</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	MDS031; Glt28d1; 2810046O15Rik; 4833435D08Rik
<b>Summary</b>	Predicted to enable N-acetylglucosaminylidiphosphodolichol N-acetylglucosaminyltransferase activity and thiol-dependent deubiquitinase. Acts upstream of or within negative regulation of TORC1 signaling; negative regulation of neuron death; and regulation of synaptic plasticity. Located in cytoplasm. Is expressed in several structures, including forelimb bud; nervous system; and respiratory system. Human ortholog(s) of this gene implicated in developmental and epileptic encephalopathy 36. Orthologous to human ALG13 (ALG13 UDP-N-acetylglucosaminyltransferase subunit). [provided by Alliance of Genome Resources, Apr 2022]
<b>Expression</b>	Ubiquitous expression in testis adult (RPKM 4.3), limb E14.5 (RPKM 4.0) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>
<b>NEW</b>	Try the new <a href="#">Gene table</a> Try the new <a href="#">Transcript table</a>

### Genomic context

**Location:** X F2; X 65.42 cM

See Alg13 in [Genome Data Viewer](#)

**Exon count:** 28

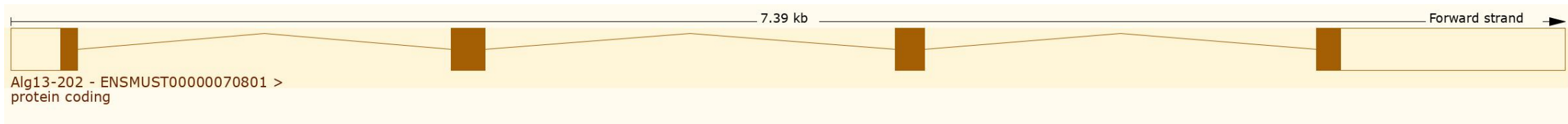
Source: <https://www.ncbi.nlm.nih.gov/>

# Transcript Information

The gene has 15 transcripts, all transcript are shown below:

Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
<a href="#">ENSMUST00000238864.2</a>	Alg13-215	4191	<a href="#">969aa</a>	Protein coding		<a href="#">A0A5F8MPZ7</a>	Ensembl Canonical Gencode basic
<a href="#">ENSMUST00000070801.11</a>	Alg13-202	1802	<a href="#">165aa</a>	Protein coding	<a href="#">CCDS30456</a>	<a href="#">Q9D8C3-2</a>	Gencode basic APPRIS P1 TSL:1
<a href="#">ENSMUST00000123710.8</a>	Alg13-203	604	<a href="#">61aa</a>	Protein coding		<a href="#">E9Q161</a>	Gencode basic TSL:1
<a href="#">ENSMUST00000149330.8</a>	Alg13-207	479	<a href="#">61aa</a>	Protein coding		<a href="#">E9Q161</a>	Gencode basic TSL:2
<a href="#">ENSMUST00000154827.8</a>	Alg13-210	4168	<a href="#">155aa</a>	Nonsense mediated decay		<a href="#">E9PX10</a>	TSL:1
<a href="#">ENSMUST00000197316.5</a>	Alg13-212	3839	<a href="#">51aa</a>	Nonsense mediated decay		<a href="#">A0A0G2JEZ0</a>	TSL:5
<a href="#">ENSMUST00000198039.5</a>	Alg13-213	3307	<a href="#">48aa</a>	Nonsense mediated decay		<a href="#">A0A0G2JFD0</a>	TSL:5
<a href="#">ENSMUST00000145724.7</a>	Alg13-206	859	<a href="#">81aa</a>	Nonsense mediated decay		<a href="#">E9Q2P6</a>	TSL:5
<a href="#">ENSMUST00000149427.8</a>	Alg13-208	2996	No protein	Protein coding CDS not defined		-	TSL:5
<a href="#">ENSMUST00000132416.8</a>	Alg13-204	2608	No protein	Protein coding CDS not defined		-	TSL:5
<a href="#">ENSMUST00000149811.3</a>	Alg13-209	619	No protein	Protein coding CDS not defined		-	TSL:5
<a href="#">ENSMUST00000040338.9</a>	Alg13-201	508	No protein	Protein coding CDS not defined		-	TSL:5
<a href="#">ENSMUST00000144185.5</a>	Alg13-205	476	No protein	Protein coding CDS not defined		-	TSL:5
<a href="#">ENSMUST00000197138.5</a>	Alg13-211	877	No protein	Retained intron		-	TSL:5
<a href="#">ENSMUST00000199040.2</a>	Alg13-214	719	No protein	Retained intron		-	TSL:5

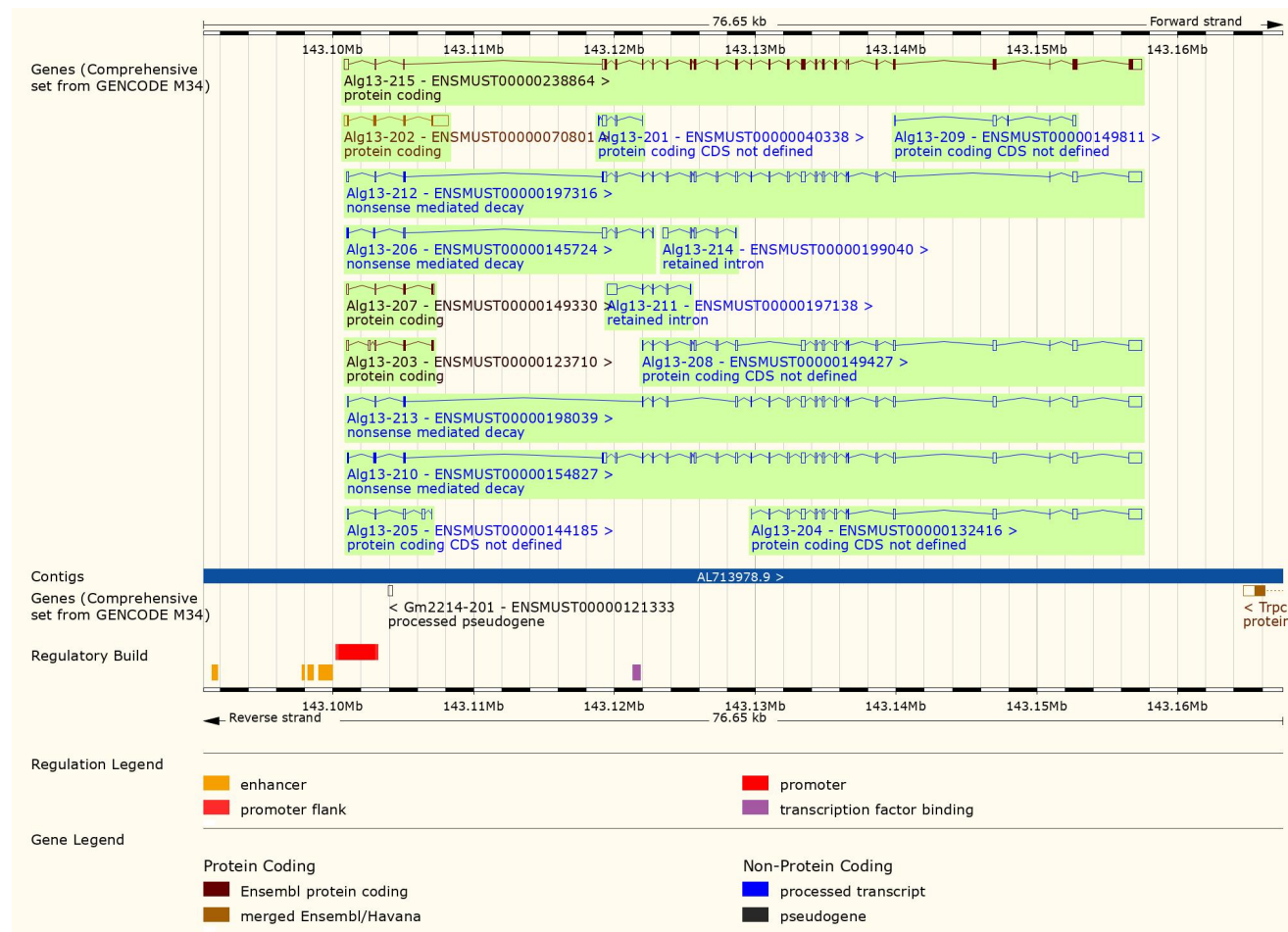
The strategy is based on the design of *Alg13-202* transcript, the transcription is shown below:



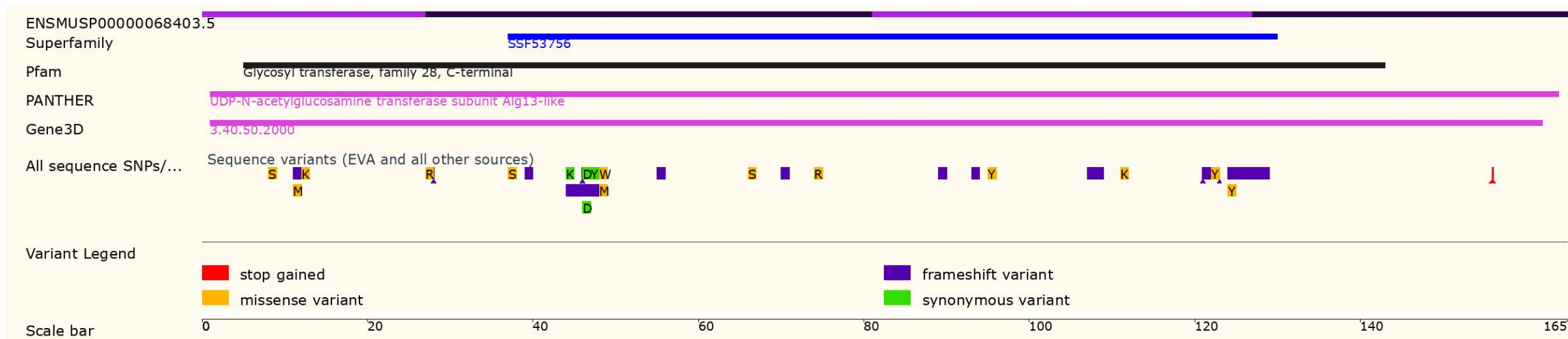
Source: <https://www.ensembl.org>



# Genomic Information



# Protein Information

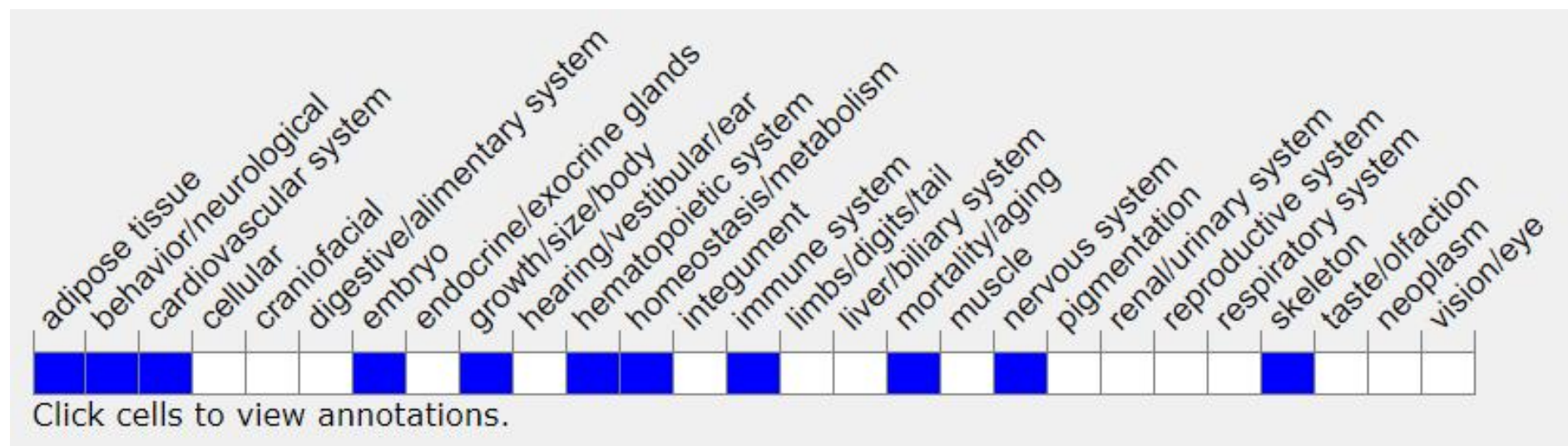




# Important Information

- According to the existing MGI data, males hemizygous for a null allele exhibit environmentally induced seizures and increased susceptibility to pharmacologically induced seizures. Homozygous females for a different null allele show increased body fat and decreased lean body mass, decreased bone mineral density, decreased granulocyte numbers and increased leukocyte numbers.
- *Gm2214-201* gene may be destroyed.
- The effect of other transcripts is unknown.
- *Alg13* is located on Chr X. 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.

# Mouse phenotype description(MGI )



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>)

Males hemizygous for a null allele exhibit environmentally induced seizures and increased susceptibility to pharmacologically induced seizures. Homozygous females for a different null allele show increased body fat and decreased lean body mass, decreased bone mineral density, decreased granulocyte numbers and increased leukocyte numbers.