

Agbl2 Cas9-CKO Strategy

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Overview

Target Gene Name

- Agbl2

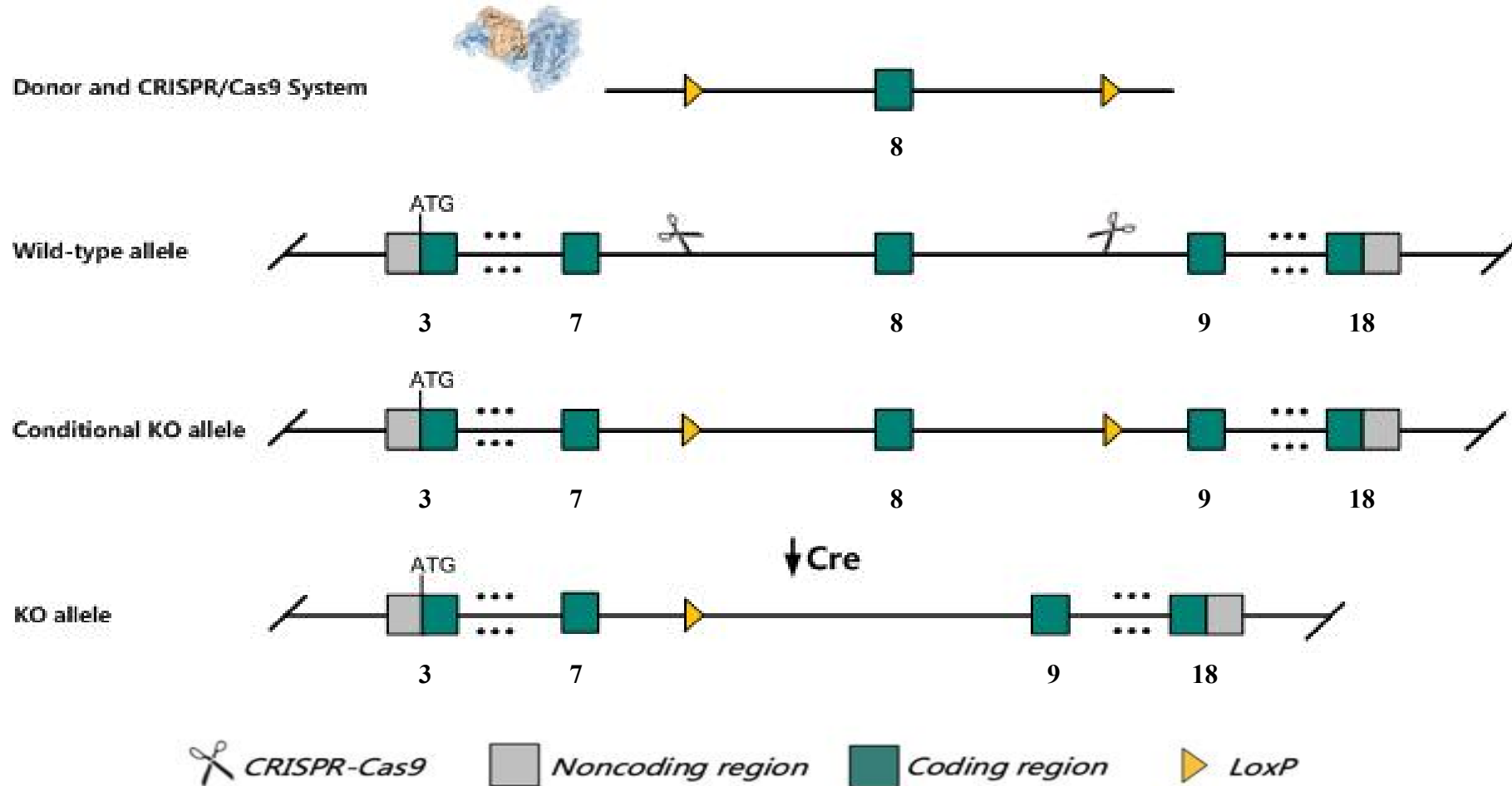
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Agbl2* gene.

Technical Information

- The *Agbl2* gene has 8 transcripts. According to the structure of *Agbl2* gene, exon8 of *Agbl2*-202 (ENSMUST00000037219.12) transcript is recommended as the knockout region. The region contains 154bp coding sequence. Knocking out the region will result in disruption of protein function.
- In this project we use CRISPR-Cas9 technology to modify *Agbl2* 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

Agbl2 ATP/GTP binding protein-like 2 [Mus musculus (house mouse)]

Gene ID: 271813, updated on 15-Apr-2023

Summary

Official Symbol	Agbl2 provided by MGI
Official Full Name	ATP/GTP binding protein-like 2 provided by MGI
Primary source	MGI:MGI:2443254
See related	Ensembl:ENSMUSG00000040812
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	4930524K04, A430081C19Rik, CCP2
Summary	Enables metallocarboxypeptidase activity. Involved in protein side chain deglutamylation. Located in cytosol. Is expressed in brain. Orthologous to human AGBL2 (AGBL carboxypeptidase 2). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Biased expression in testis adult (RPKM 15.6), cerebellum adult (RPKM 1.1) and 1 other tissue See more
Orthologs	human all

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

Transcript Information

The gene has 8 transcripts, all transcripts are shown below:

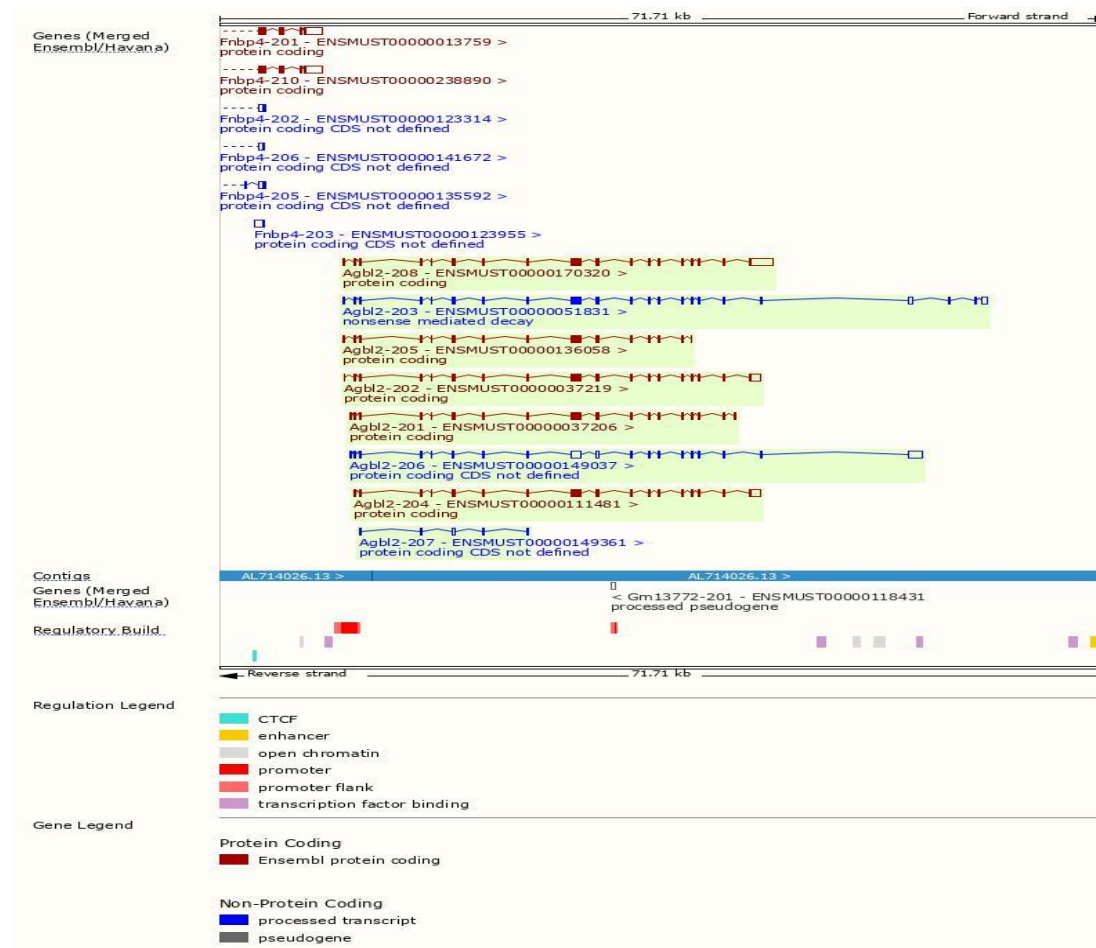
Show/hide columns (1 hidden)							Filter	
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags	
ENSMUST00000037206.11	Agbl2-201	2763	809aa	Protein coding		Q8CDK2-6	GENCODE basic	APPRIS P4 TSL:1
ENSMUST00000037219.12	Agbl2-202	3462	862aa	Protein coding	CCDS38177	Q8CDK2-1	GENCODE basic	APPRIS ALT2 TSL:1
ENSMUST00000051831.13	Agbl2-203	3778	836aa	Nonsense mediated decay		Q8CDK2-3	TSL:1	
ENSMUST00000111481.2	Agbl2-204	3448	862aa	Protein coding	CCDS38177	Q8CDK2-1	GENCODE basic	APPRIS ALT2 TSL:5
ENSMUST00000136058.8	Agbl2-205	2226	711aa	Protein coding		A0A0B4J1L6	TSL:1	CDS 3' incomplete
ENSMUST00000149037.8	Agbl2-206	3838	No protein	Protein coding CDS not defined		-	TSL:2	
ENSMUST00000149361.2	Agbl2-207	622	No protein	Protein coding CDS not defined		-	TSL:3	
ENSMUST00000170320.8	Agbl2-208	4507	862aa	Protein coding	CCDS38177	Q8CDK2-1	Ensembl Canonical	GENCODE basic APPRIS ALT2 TSL:1

The strategy is based on the design of *Agbl2*-202 transcript, the transcription is shown below:



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

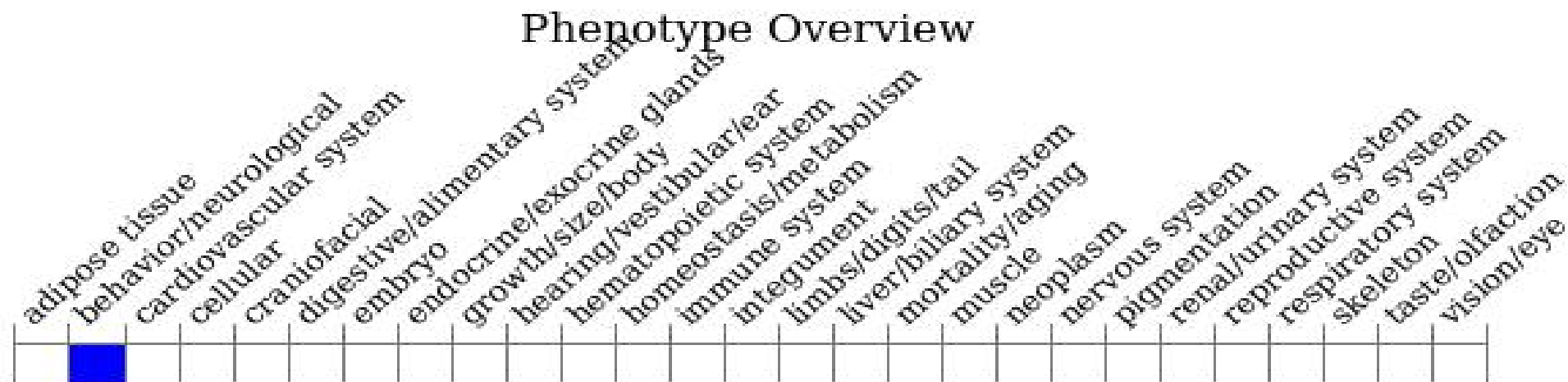
Genomic Information



Protein Information



Mouse Phenotype Information (MGI)



- Homozygous mice for a targeted allele are viable and fertile. Mice exhibit normal response to herpes simplex virus (HSV) and vaccinia virus (VACV) infection.

Important Information

- *Agbl2* is located on Chr2. 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.