Golga1 Cas9-KO Strategy

Designer: Xueting Zhang
Reviewer:Yanhua Shen
Date:2020-03-03

Project Overview

Project Name	*Golga1*
Project type	Cas9-KO
Strain background	C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Golga1* gene. The schematic diagram is as follows:

Technical routes

➢ The *Golga1* gene has 11 transcripts. According to the structure of *Golga1* gene, exon4-exon5 of *Golga1-201* (ENSMUST00000039165.14) transcript is recommended as the knockout region.The region contains 166bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Golga1* gene. The brief process is as follows: CRISPR/Cas9 system

➢ According to the existing MGI data,Homozygous mice exhibit tremors and limb grasping behavior at two months of age. A variable severity of hearing loss was also seen.

➢ The effect on transcript *Golga1*-206 is unknown.

➢ Transcript *Golga1*-203&207&209&211 may not be affected.

➢ The *Golga1* gene is located on the Chr2. 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）

Golga1   golgi autoantigen, golgin subfamily a, 1 [*Mus musculus* (house mouse)]

Gene ID: 76899, updated on 12-Aug-2019

▲ Summary

Official Symbol	Golga1 provided by MGI
Official Full Name	golgi autoantigen, golgin subfamily a, 1 provided by MGI
Primary source	MGI:MGI:1924149
See related	Ensembl:ENSMUSG00000026754
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	awag; Golgi97; AW107649; golgin-97; 0710001G09Rik; 2210418B03Rik
Expression	Ubiquitous expression in CNS E14 (RPKM 8.2), whole brain E14.5 (RPKM 7.4) and 28 other tissues See more
Orthologs	human all

▲ Genomic context

Location: 2; 2 B
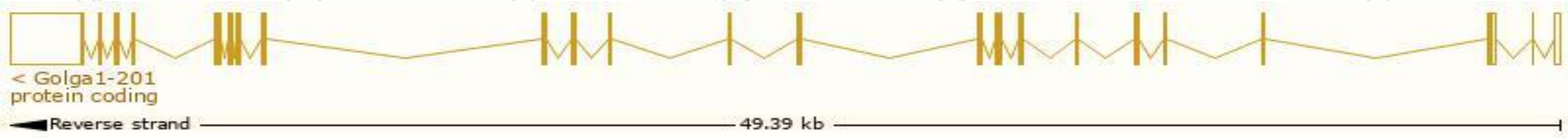
See Golga1 in Genome Data Viewer

Exon count: 25

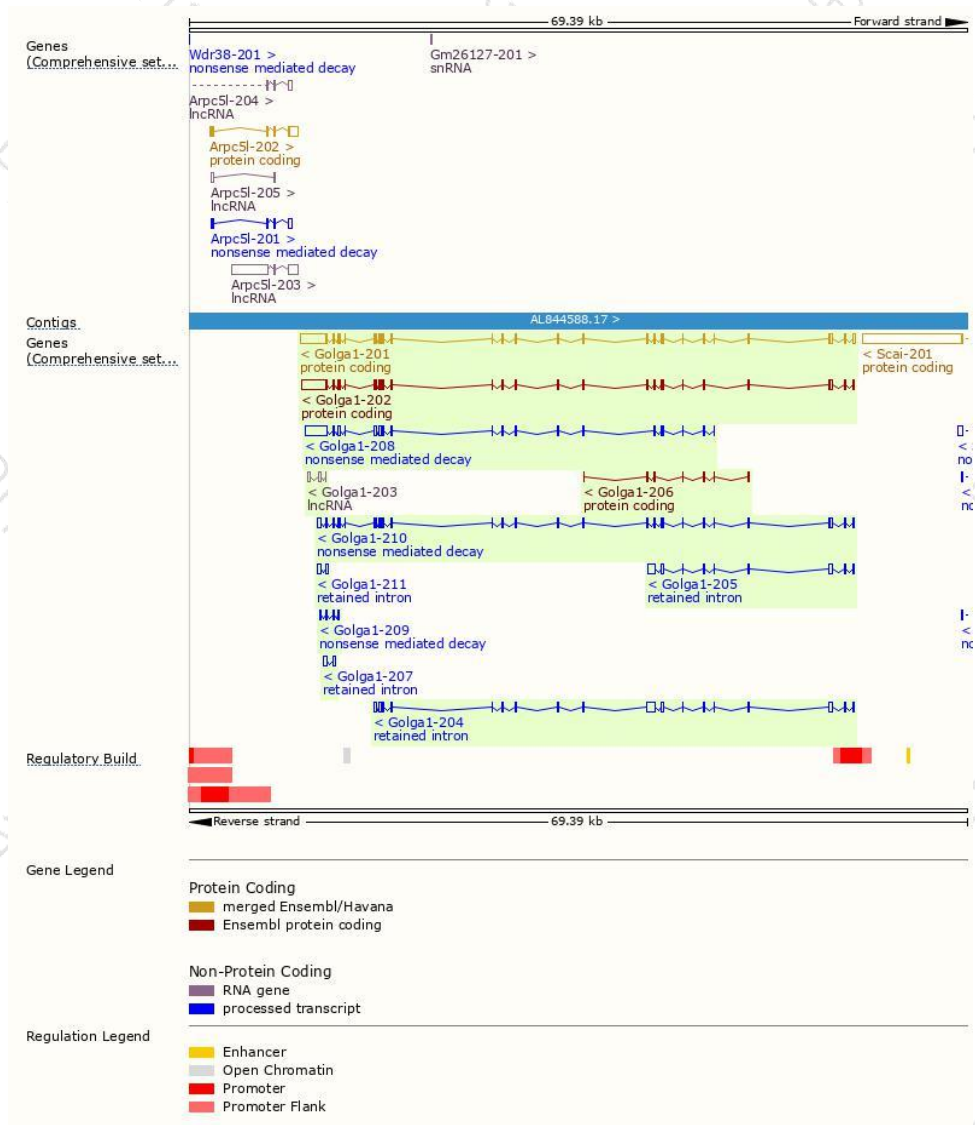| Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	2	NC_000068.7 (39016155..39065551, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	2	NC_000068.6 (38872023..38920926, complement)

Transcript information（Ensembl）

The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Golga1-201	ENSMUST00000039165.14	4869	758aa	Protein coding	CCDS16016	Q9CW79	TSL:1 GENCODE basic APPRIS P3
Golga1-202	ENSMUST00000112850.8	4635	733aa	Protein coding	CCDS71049	Q9CW79	TSL:1 GENCODE basic APPRIS ALT2
Golga1-206	ENSMUST00000149810.6	560	186aa	Protein coding	-	A0A0N4SVQ8	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Golga1-210	ENSMUST00000184996.7	2894	758aa	Nonsense mediated decay	CCDS16016	Q9CW79	TSL:1
Golga1-208	ENSMUST00000153914.7	3834	168aa	Nonsense mediated decay	-	A0A0N4SVV1	CDS 5' incomplete TSL:1
Golga1-209	ENSMUST00000154210.2	386	82aa	Nonsense mediated decay	-	A0A0N4SVD1	CDS 5' incomplete TSL:3
Golga1-204	ENSMUST00000126520.7	2614	No protein	Retained intron	-	-	TSL:1
Golga1-205	ENSMUST00000136261.1	1494	No protein	Retained intron	-	-	TSL:1
Golga1-207	ENSMUST00000149842.1	588	No protein	Retained intron	-	-	TSL:3
Golga1-211	ENSMUST00000204127.1	457	No protein	Retained intron	-	-	TSL:3
Golga1-203	ENSMUST00000124463.1	408	No protein	lncRNA	-	-	TSL:3

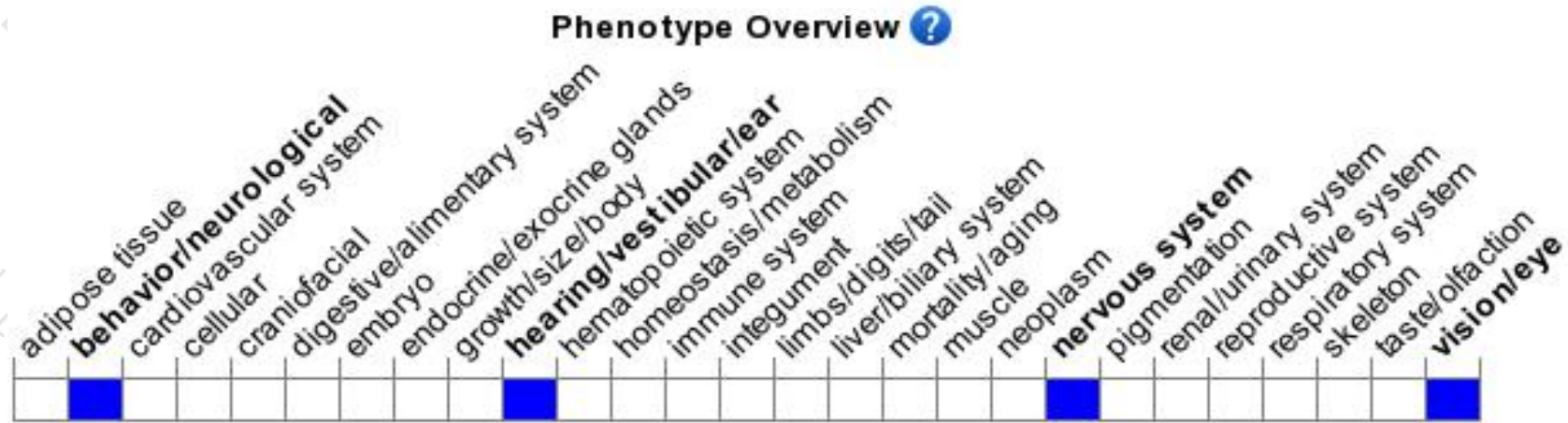The strategy is based on the design of *Golga1-201* transcript,The transcription is shown below

< Golga1-201
protein coding

◄— Reverse strand ——————————————————— 49.39 kb ————————————————————

Genomic location distribution

Protein domain

ENSMUSP00000037...	
MobiDB lite	
Low complexity (Seg)	
Coiled-coils (Ncoils)	
SMART	GRIP domain
Pfam	GRIP domain
PROSITE profiles	GRIP domain
PANTHER	PTHR23157
	PTHR23157:SF24
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)

Variant Legend

- 🟥 stop gained
- 🟨 missense variant
- 🟩 synonymous variant

Scale bar

0   80   160   240   320   400   480   560   640   758
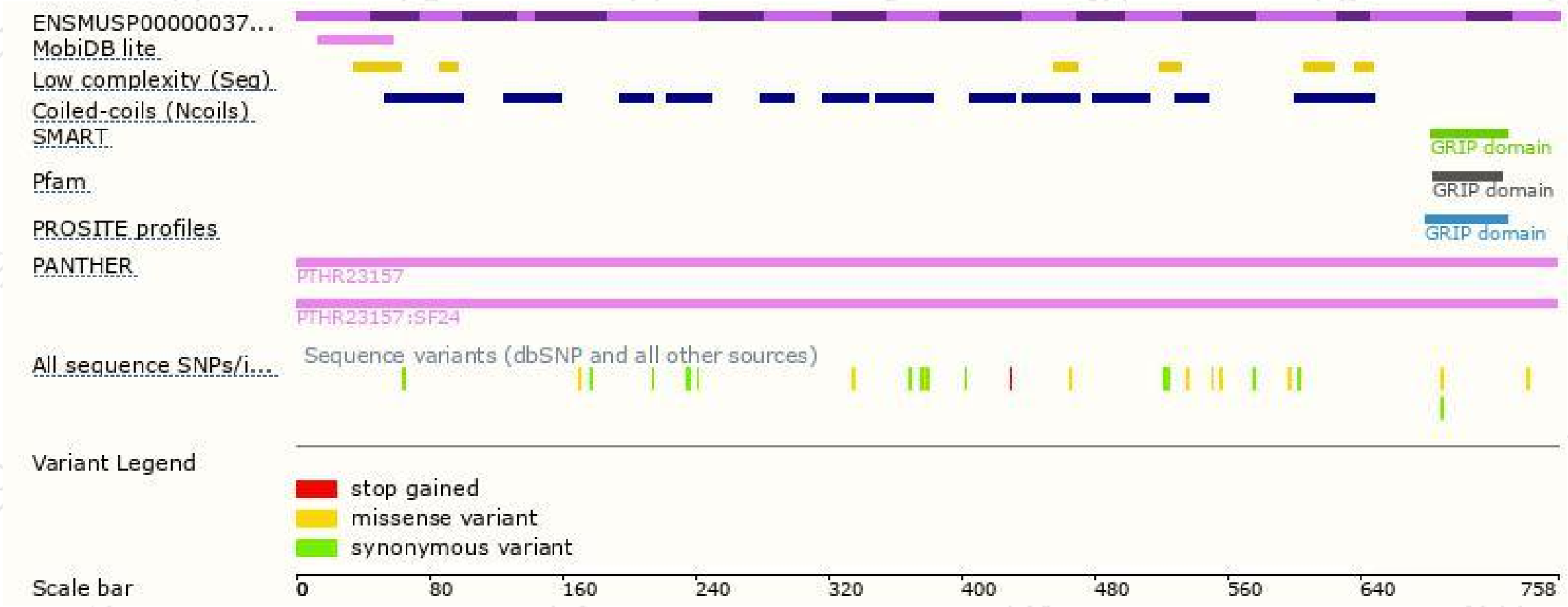
Mouse phenotype description(MGI)

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,Homozygous mice exhibit tremors and limb grasping behavior at two months of age. A variable severity of hearing loss was also seen.

If you have any questions, you are welcome to inquire.
Tel: 400-9660890

集萃药康生物科技
GemPharmatech Co.,Ltd