

# ***Gnao1* Cas9-KO Strategy**

**Designer: Yupeng Yang**

**Reviewer: Yun Li**

**Design Date: 2018-12-4**

# Project Overview

**Project Name**

***Gnao1***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Gnao1* gene. The schematic diagram is as follows:



- The *Gnao1* gene has 12 transcripts. According to the structure of *Gnao1* gene, exon3 of *Gnao1*-203(ENSMUST00000125716.7) transcript is recommended as the knockout region. The region contains 142bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Gnao1* gene. The brief process is as follows: CRISPR/Cas9 system 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 sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- According to the existing MGI data, mice lacking both isoforms exhibit reduced survival, sterility, low body weight, hyperalgesia, tremors, turning behavior, impaired locomotion, altered channel response and improved glucose tolerance. Isoform-specific deletion may lead to increased insulin release and abnormal eye electrophysiology.
- The *Gnao1* gene is located on the Chr8. 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)

## Gnao1 guanine nucleotide binding protein, alpha O [Mus musculus (house mouse)]

Gene ID: 14681, updated on 13-Mar-2020

### Summary

**Official Symbol** Gnao1 provided by [MGI](#)

**Official Full Name** guanine nucleotide binding protein, alpha O provided by [MGI](#)

**Primary source** [MGI:MGI:95775](#)

**See related** [Ensembl:ENSMUSG00000031748](#)

**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** AW050213, Galphao, Gnao, alphaO

**Expression** Broad expression in cortex adult (RPKM 40.0), frontal lobe adult (RPKM 39.2) and 16 other tissues [See more](#)

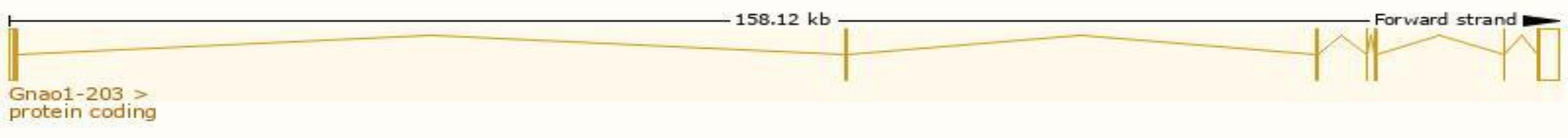
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

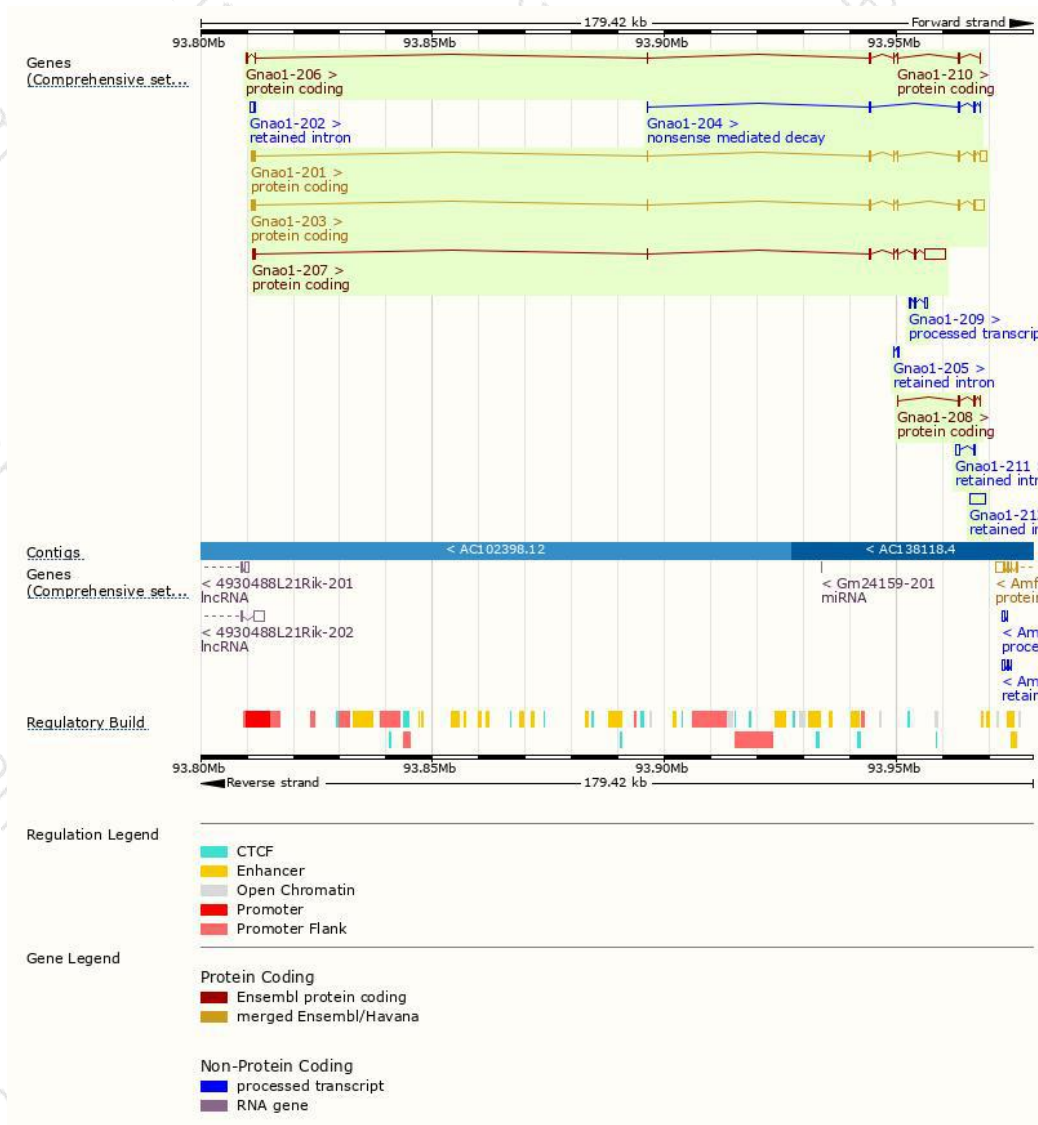
The gene has 12 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Gnao1-207	<a href="#">ENSMUST00000138659.8</a>	5526	<a href="#">354aa</a>	Protein coding	<a href="#">CCDS85585</a>	<a href="#">P18872</a>	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT1
Gnao1-203	<a href="#">ENSMUST00000125716.7</a>	3462	<a href="#">354aa</a>	Protein coding	<a href="#">CCDS22532</a>	<a href="#">P18872 Q543S2</a>	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P3
Gnao1-201	<a href="#">ENSMUST00000034198.14</a>	2948	<a href="#">354aa</a>	Protein coding	<a href="#">CCDS22532</a>	<a href="#">P18872 Q543S2</a>	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P3
Gnao1-206	<a href="#">ENSMUST00000137202.7</a>	741	<a href="#">179aa</a>	Protein coding	-	<a href="#">D3Z2M7</a>	CDS 3' incomplete TSL:3
Gnao1-208	<a href="#">ENSMUST00000142466.1</a>	332	<a href="#">109aa</a>	Protein coding	-	<a href="#">F6WC15</a>	CDS 5' incomplete TSL:5
Gnao1-210	<a href="#">ENSMUST00000149530.7</a>	231	<a href="#">74aa</a>	Protein coding	-	<a href="#">F6W1B2</a>	CDS 5' incomplete TSL:5
Gnao1-204	<a href="#">ENSMUST00000127900.1</a>	805	<a href="#">101aa</a>	Nonsense mediated decay	-	<a href="#">F7BLT7</a>	CDS 5' incomplete TSL:5
Gnao1-209	<a href="#">ENSMUST00000144451.1</a>	748	No protein	Processed transcript	-	-	TSL:3
Gnao1-212	<a href="#">ENSMUST00000212008.1</a>	3415	No protein	Retained intron	-	-	TSL:NA
Gnao1-202	<a href="#">ENSMUST00000125695.2</a>	938	No protein	Retained intron	-	-	TSL:1
Gnao1-211	<a href="#">ENSMUST00000155245.1</a>	848	No protein	Retained intron	-	-	TSL:2
Gnao1-205	<a href="#">ENSMUST00000130974.1</a>	402	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Gnao1-203* transcript,the transcription is shown below:

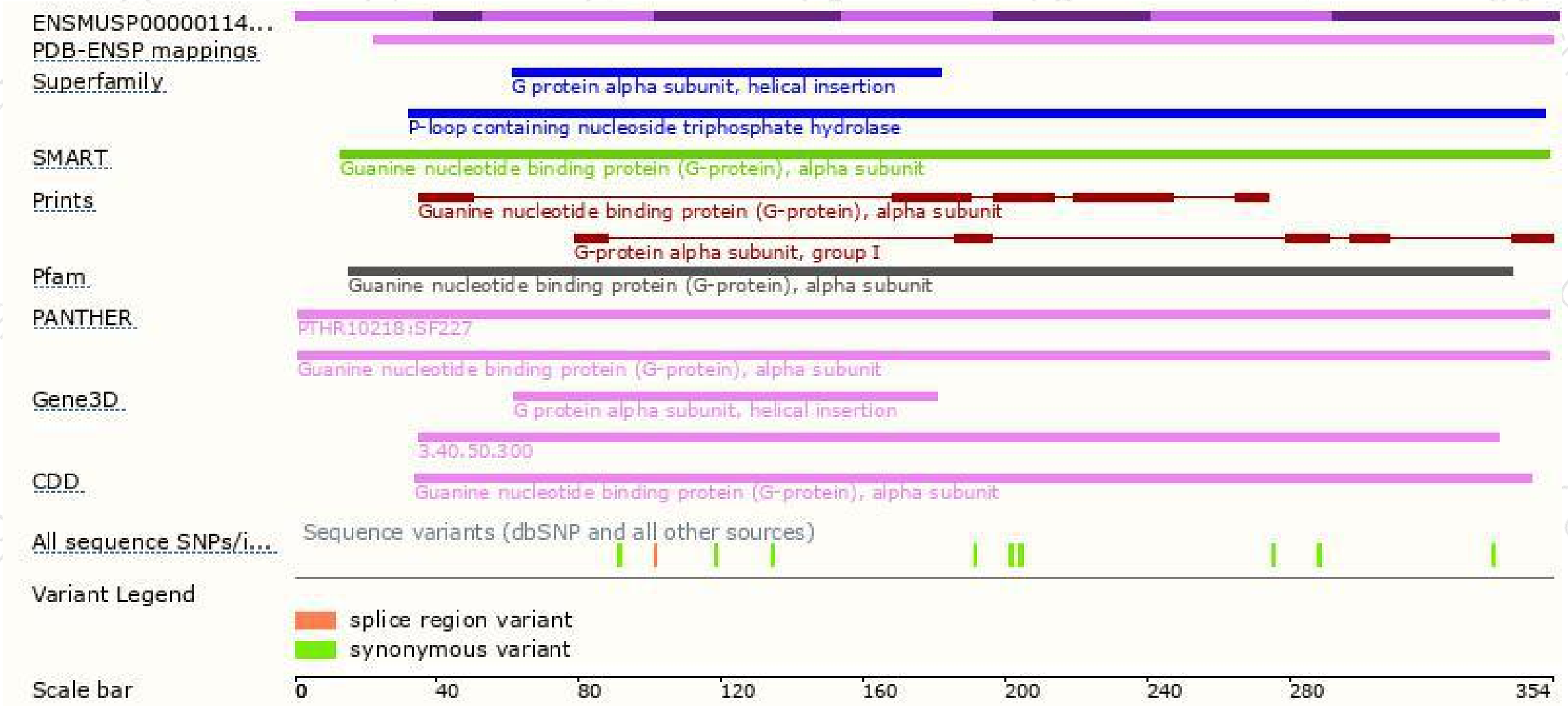


# Genomic location distribution

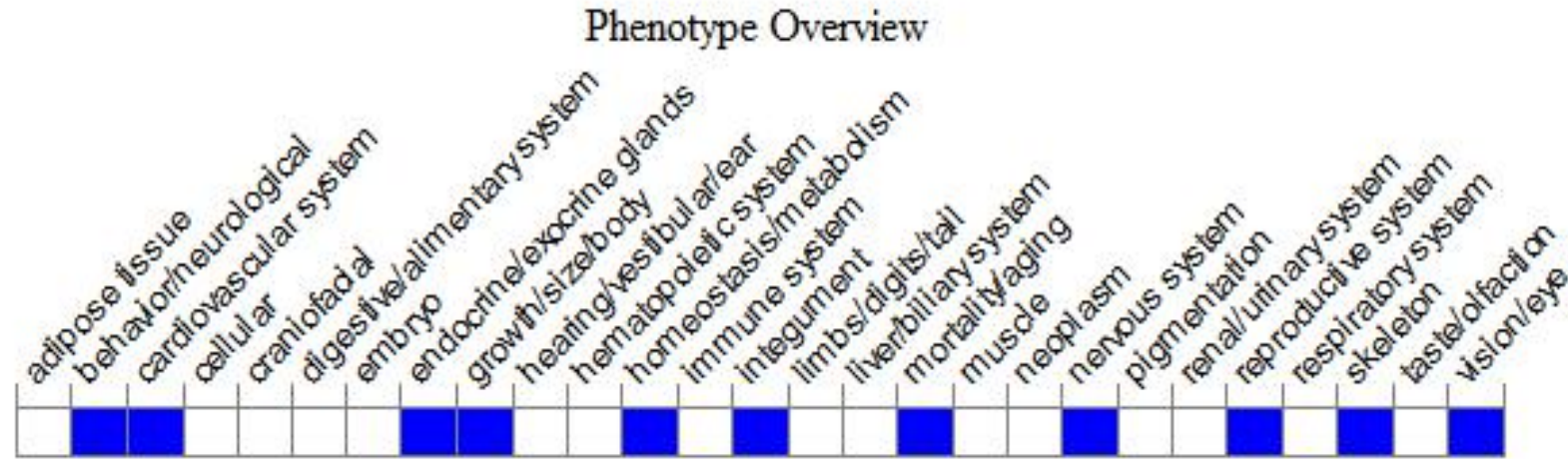




# Protein domain



# 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 lacking both isoforms exhibit reduced survival, sterility, low body weight, hyperalgesia, tremors, turning behavior, impaired locomotion, altered channel response and improved glucose tolerance. Isoform-specific deletion may lead to increased insulin release and abnormal eye electrophysiology.

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

Tel: 400-9660890

