

Gnai2 Cas9-KO Strategy

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Project Overview



Project Name

Gnai2

Project type

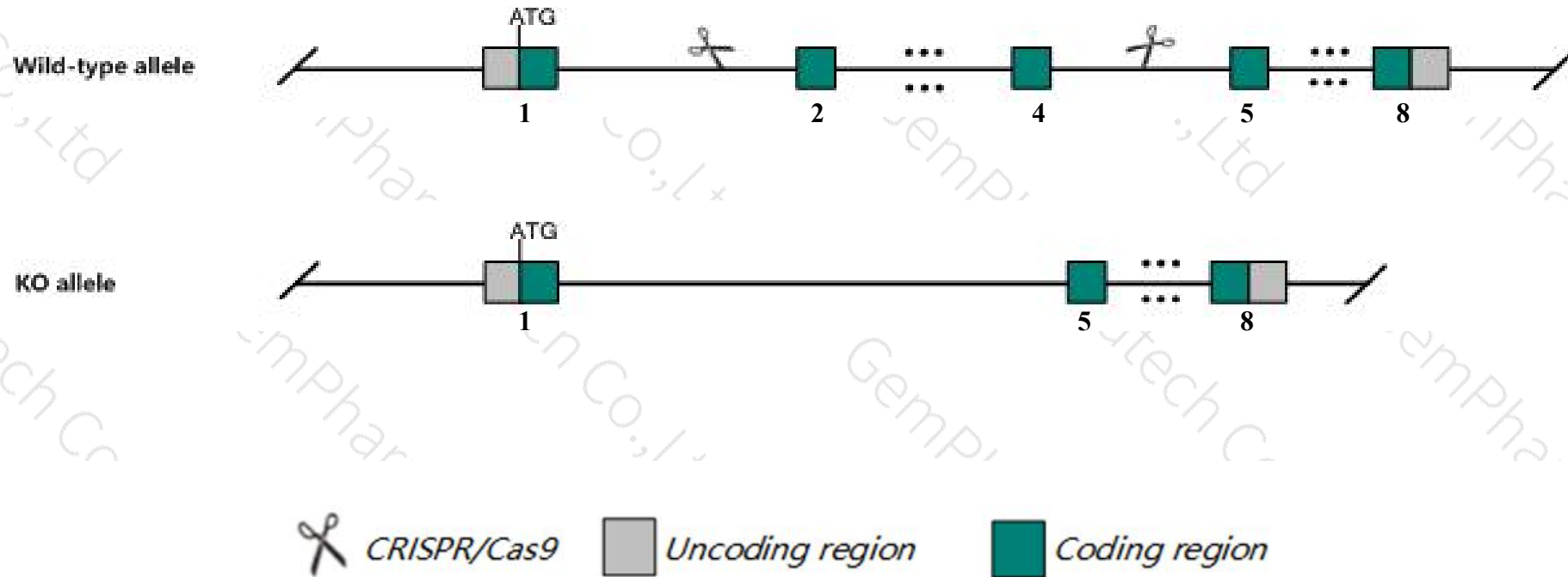
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Gnai2* gene. The schematic diagram is as follows:



- The *Gnai2* gene has 10 transcripts. According to the structure of *Gnai2* gene, exon2-exon4 of *Gnai2-201* (ENSMUST00000055704.11) transcript is recommended as the knockout region. The region contains 346bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Gnai2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Nullizygous mice exhibit growth retardation, lethal ulcerative colitis, colon adenocarcinomas, granulocytosis, altered thymocyte maturation and function and enhanced production of pro-inflammatory cytokines, and may show alterations in leukocyte physiology and susceptibility to parasitic infection.
- The *Gnai2* gene is located on the Chr9. 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)

Gnai2 guanine nucleotide binding protein (G protein), alpha inhibiting 2 [Mus musculus (house mouse)]

Gene ID: 14678, updated on 7-Apr-2019

Summary



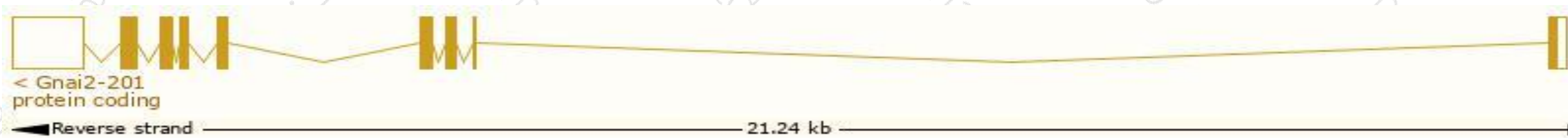
| | |
|---------------------------|---|
| Official Symbol | Gnai2 provided by MGI |
| Official Full Name | guanine nucleotide binding protein (G protein), alpha inhibiting 2 provided by MGI |
| Primary source | MGI:MGI:95772 |
| See related | Ensembl:ENSMUSG00000032562 |
| Gene type | protein coding |
| 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 | C76432, Galphai2, Gia, Gnai-2 |
| Expression | Ubiquitous expression in lung adult (RPKM 259.7), thymus adult (RPKM 238.6) and 28 other tissues See more |
| Orthologs | human all |

Transcript information (Ensembl)

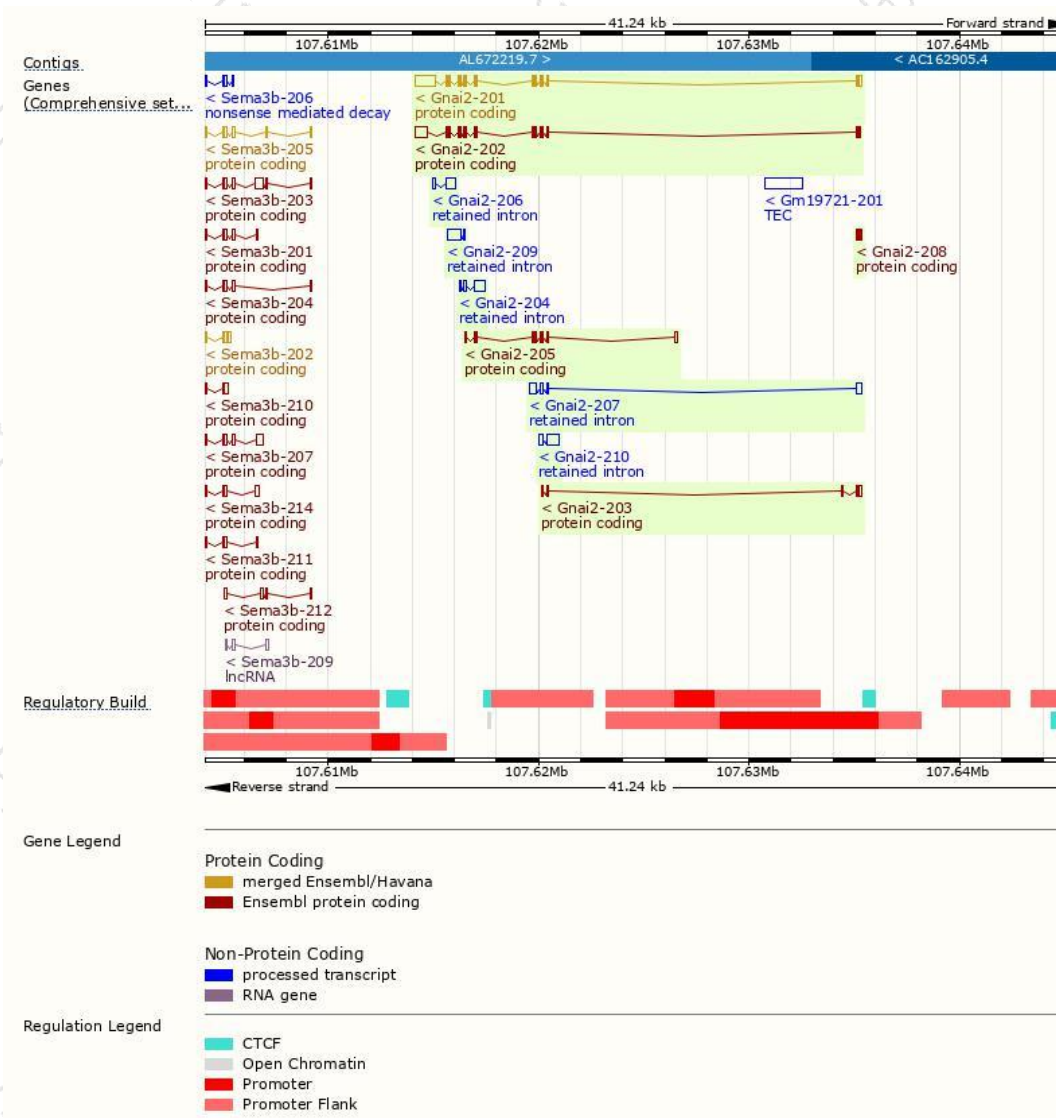
The gene has 10 transcripts, all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-----------|---------------------------------------|------|-----------------------|-----------------|---------------------------|----------------------------|-------------------------------|
| Gnai2-201 | ENSMUST00000055704.11 | 2215 | 355aa | Protein coding | CCDS23502 | P08752 | TSL:1 GENCODE basic APPRIS P1 |
| Gnai2-202 | ENSMUST00000192615.5 | 1777 | 355aa | Protein coding | CCDS23502 | P08752 | TSL:1 GENCODE basic APPRIS P1 |
| Gnai2-205 | ENSMUST00000193394.1 | 621 | 160aa | Protein coding | - | A0A0A6YWA9 | CDS 3' incomplete TSL:3 |
| Gnai2-203 | ENSMUST00000192837.1 | 421 | 85aa | Protein coding | - | A0A0A6YXC2 | TSL:5 GENCODE basic |
| Gnai2-208 | ENSMUST00000193876.1 | 197 | 39aa | Protein coding | - | A0A0A6YXN0 | CDS 3' incomplete TSL:5 |
| Gnai2-204 | ENSMUST00000193372.1 | 752 | No protein | Retained intron | - | - | TSL:2 |
| Gnai2-209 | ENSMUST00000195231.1 | 752 | No protein | Retained intron | - | - | TSL:3 |
| Gnai2-210 | ENSMUST00000195762.1 | 706 | No protein | Retained intron | - | - | TSL:3 |
| Gnai2-207 | ENSMUST00000193835.1 | 698 | No protein | Retained intron | - | - | TSL:1 |
| Gnai2-206 | ENSMUST00000193538.1 | 595 | No protein | Retained intron | - | - | TSL:1 |

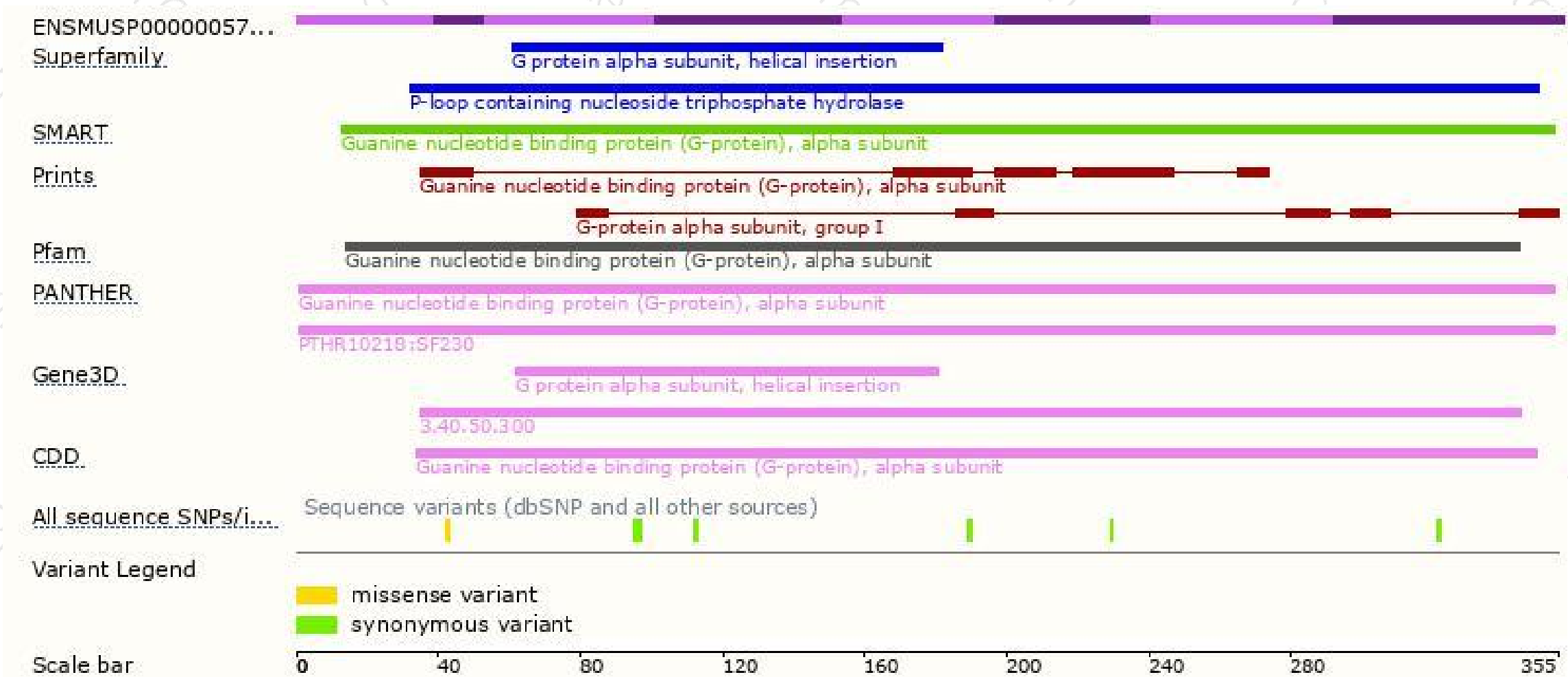
The strategy is based on the design of *Gnai2-201* transcript, The transcription is shown below



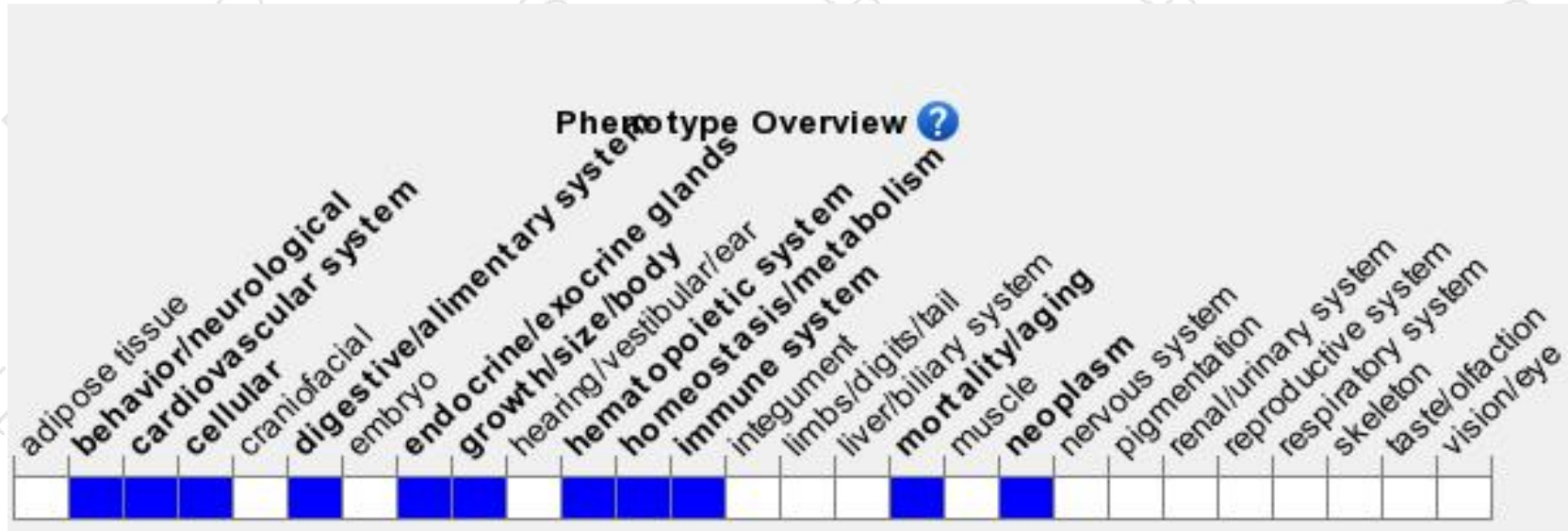
Genomic location distribution



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, Nullizygous mice exhibit growth retardation, lethal ulcerative colitis, colon adenocarcinomas, granulocytosis, altered thymocyte maturation and function and enhanced production of pro-inflammatory cytokines, and may show alterations in leukocyte physiology and susceptibility to parasitic infection.

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

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