

Alg14 Cas9-KO Strategy

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Project Overview

Project Name

Alg14

Project type

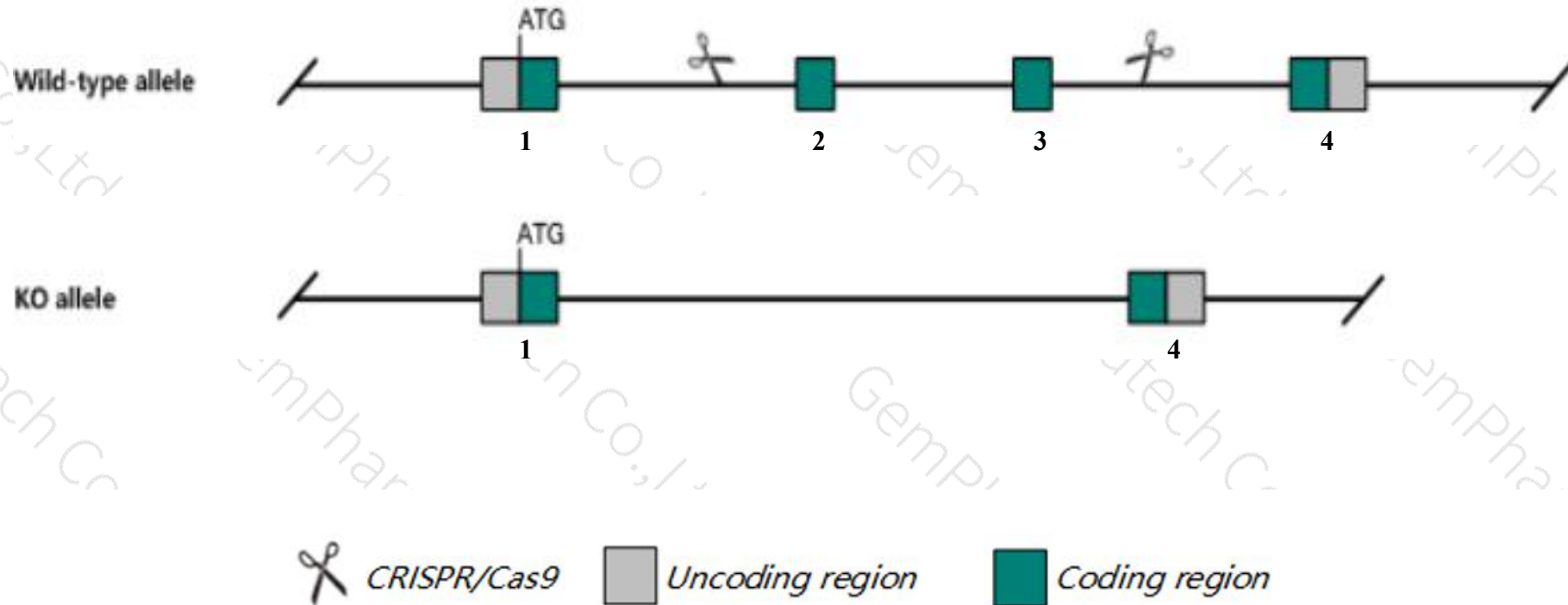
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Alg14* gene. The schematic diagram is as follows:



- The *Alg14* gene has 4 transcripts. According to the structure of *Alg14* gene, exon2-exon3 of *Alg14-201*(ENSMUST00000039442.11) transcript is recommended as the knockout region. The region contains 287bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Alg14* 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 homozygous for a knock-out allele show complete embryonic lethality between implantation and somite formation and failure of blastocysts to hatch from the zona pellucida with apparent necrosis during outgrowth culture.
- The *Alg14* gene is located on the Chr3. 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)

Alg14 asparagine-linked glycosylation 14 [Mus musculus (house mouse)]

Gene ID: 66789, updated on 13-Mar-2020

Summary



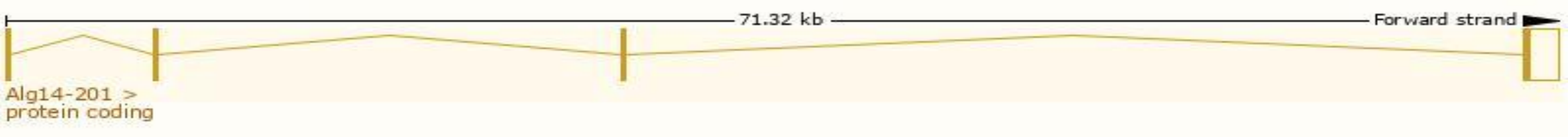
| | |
|---------------------------|---|
| Official Symbol | Alg14 provided by MGI |
| Official Full Name | asparagine-linked glycosylation 14 provided by MGI |
| Primary source | MGI:MGI:1914039 |
| See related | Ensembl:ENSMUSG00000039887 |
| Gene type | protein coding |
| RefSeq status | VALIDATED |
| Organism | Mus musculus |
| Lineage | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| Also known as | 5430428G01Rik, AI854024 |
| Expression | Ubiquitous expression in lung adult (RPKM 8.4), subcutaneous fat pad adult (RPKM 8.1) and 28 other tissues See more |
| Orthologs | human all |

Transcript information (Ensembl)

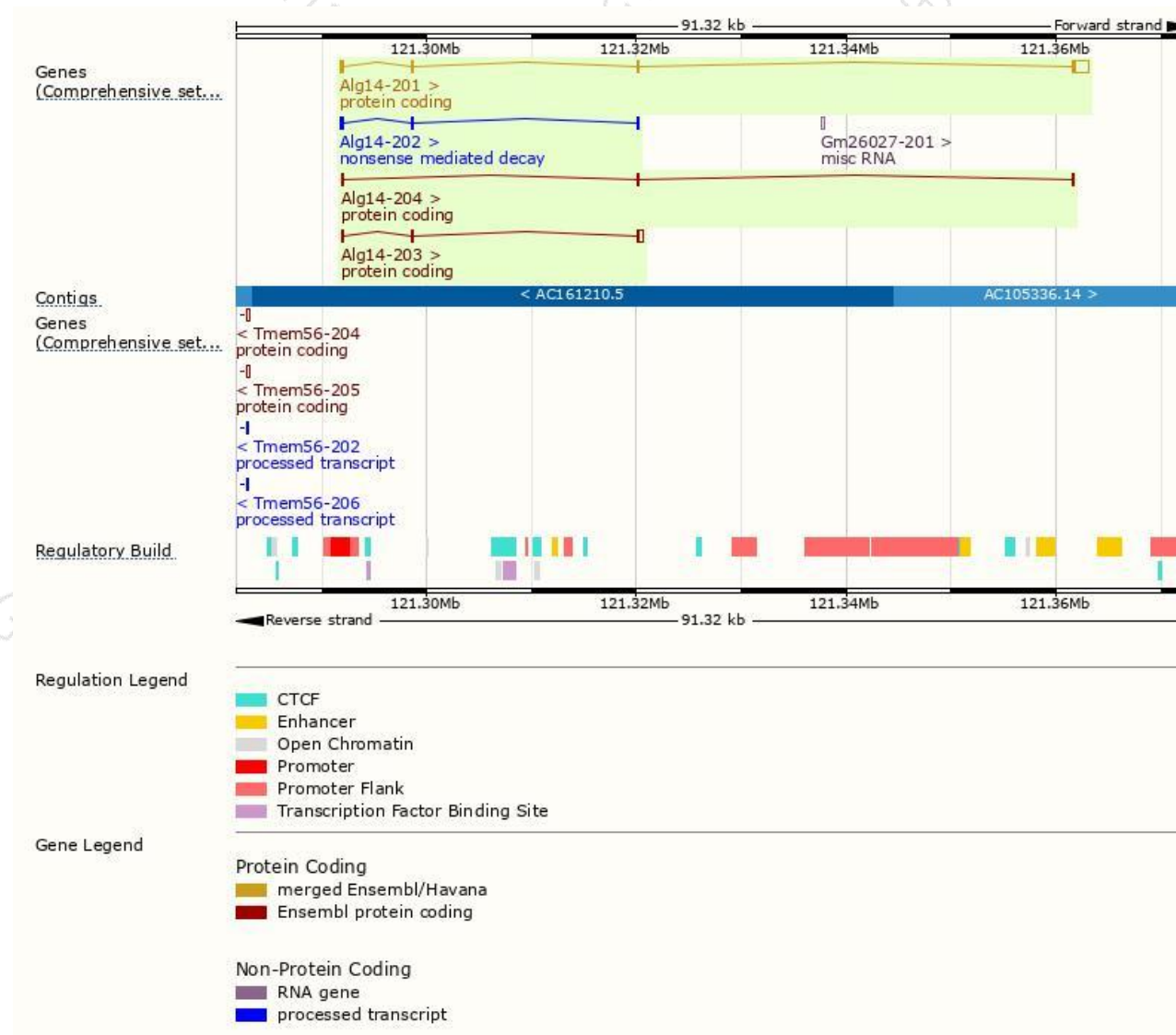
The gene has 4 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-----------|---------------------------------------|------|-----------------------|-------------------------|---------------------------|----------------------------|-------------------------------|
| Alg14-201 | ENSMUST00000039442.11 | 2037 | 217aa | Protein coding | CCDS17801 | Q9D081 | TSL:1 GENCODE basic APPRIS P1 |
| Alg14-203 | ENSMUST00000198341.1 | 831 | 133aa | Protein coding | - | A0A0G2JEH5 | CDS 5' incomplete TSL:2 |
| Alg14-204 | ENSMUST00000199554.1 | 441 | 92aa | Protein coding | - | A0A0G2JEQ0 | TSL:3 GENCODE basic |
| Alg14-202 | ENSMUST00000198235.1 | 474 | 60aa | Nonsense mediated decay | - | A0A0G2JF20 | TSL:3 |

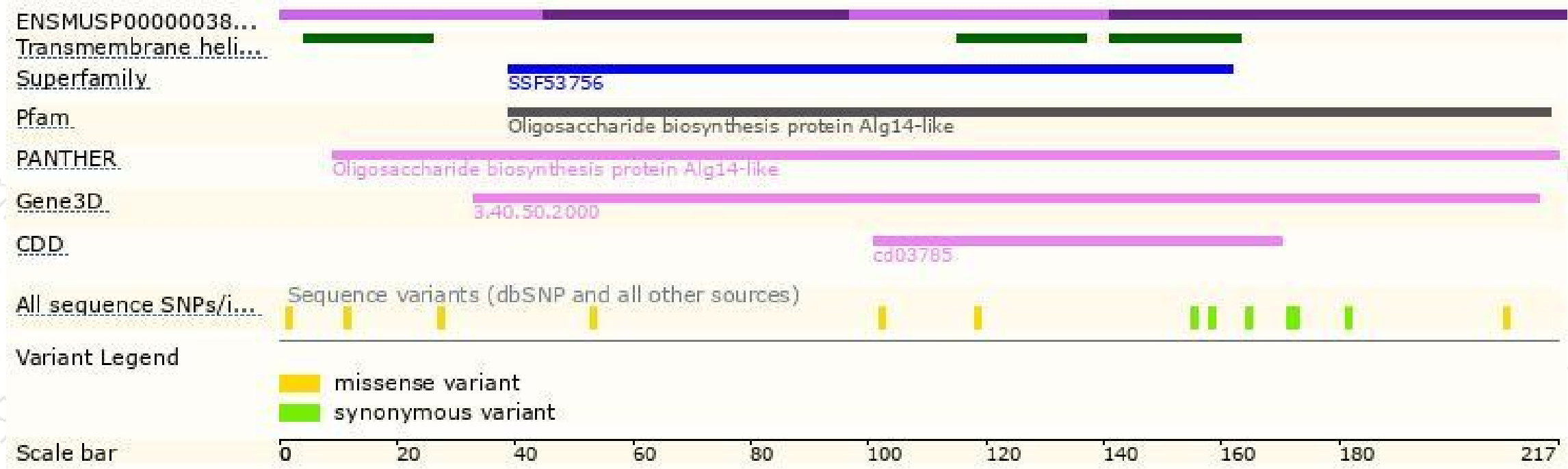
The strategy is based on the design of *Alg14-201* transcript,the transcription is shown below:



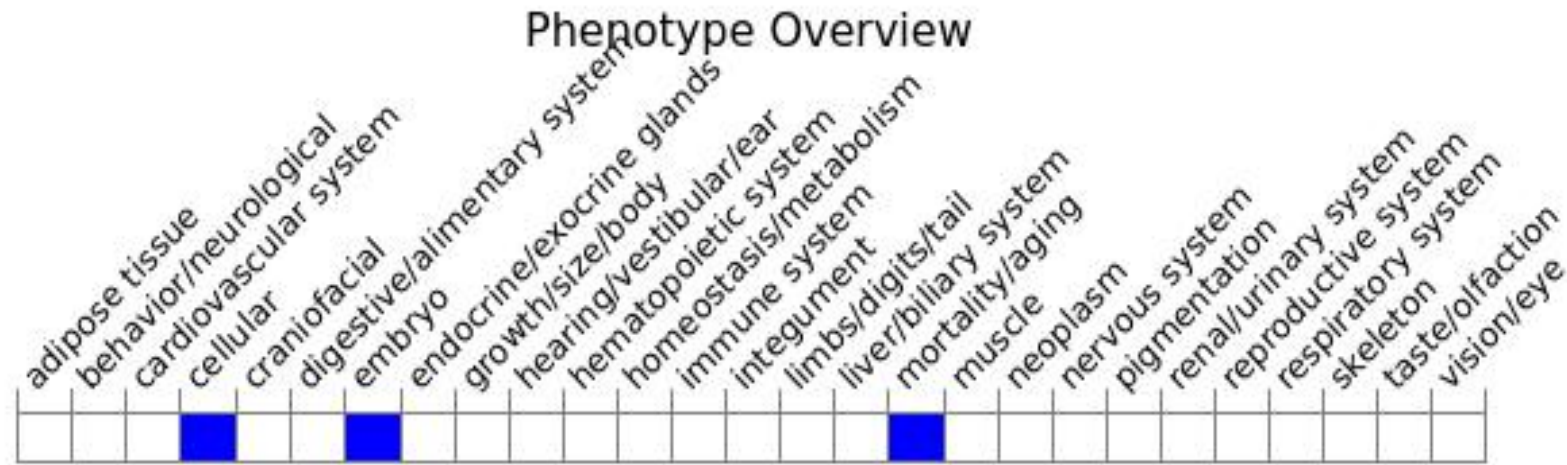
Genomic location distribution



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, mice homozygous for a knock-out allele show complete embryonic lethality between implantation and somite formation and failure of blastocysts to hatch from the zona pellucida with apparent necrosis during outgrowth culture.

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

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