

Golga3 Cas9-KO Strategy

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Design Date: 2020-7-22

Project Overview

Project Name

Golga3

Project type

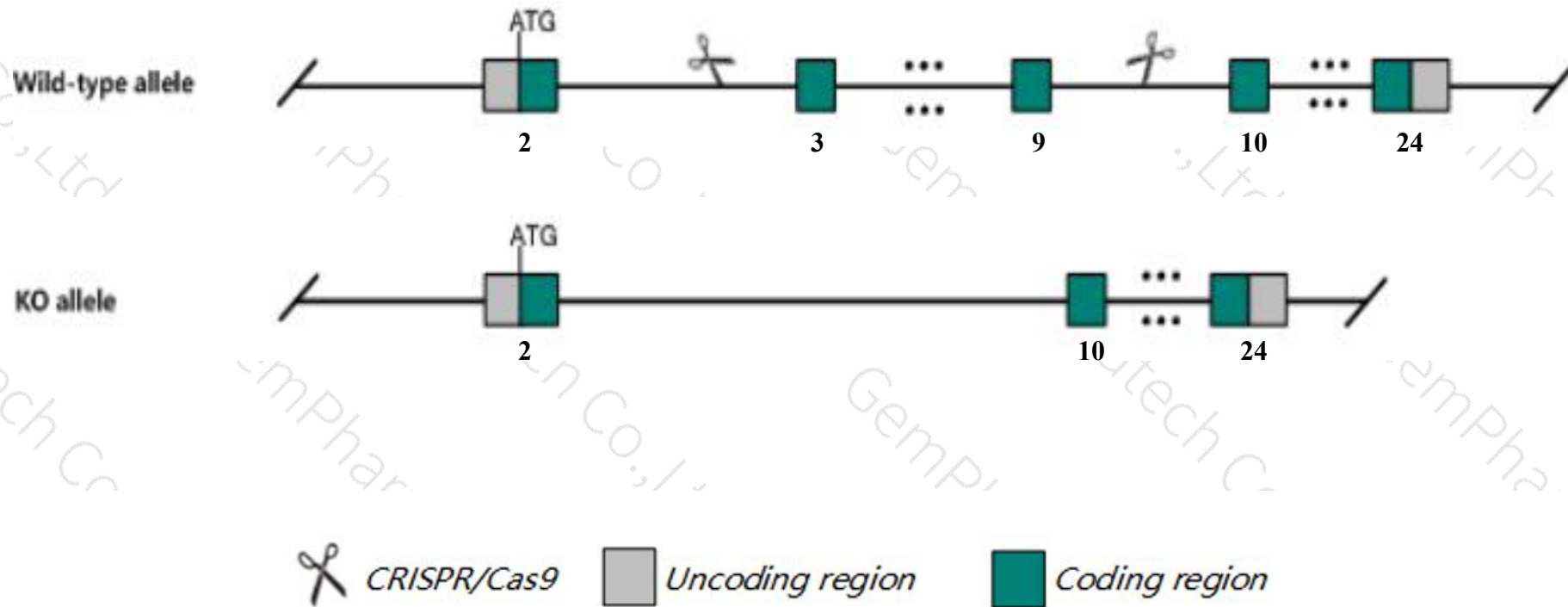
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Golga3* gene. The schematic diagram is as follows:



- The *Golga3* gene has 5 transcripts. According to the structure of *Golga3* gene, exon3-exon9 of *Golga3*-201(ENSMUST00000031477.8) transcript is recommended as the knockout region. The region contains 1790bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Golga3* 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, males homozygous for a hypomorphic transgenic insertional mutation exhibit impaired spermatogenesis involving loss of pachytene spermatocytes and are usually sterile. Male mice homozygous for an ENU-induced mutation exhibit infertility with low sperm concentration, poor motility and abnormal shape.
- The *Golga3* gene is located on the Chr5. 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)

Golga3 golgi autoantigen, golgin subfamily a, 3 [Mus musculus (house mouse)]

Gene ID: 269682, updated on 13-Mar-2020

Summary



Official Symbol [Golga3](#) provided by [MGI](#)

Official Full Name [golgi autoantigen, golgin subfamily a, 3](#) provided by [MGI](#)

Primary source [MGI:MGI:96958](#)

See related [Ensembl:ENSMUSG00000029502](#)

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 [5330413L04](#), [5430416E01Rik](#), [AI449376](#), [AW490576](#), [G1-499-14](#), [Mea-2](#), [Mea2](#), [Mea2/Golga3](#), [repro27](#)

Expression Ubiquitous expression in testis adult (RPKM 11.9), bladder adult (RPKM 5.9) and 28 other tissues [See more](#)

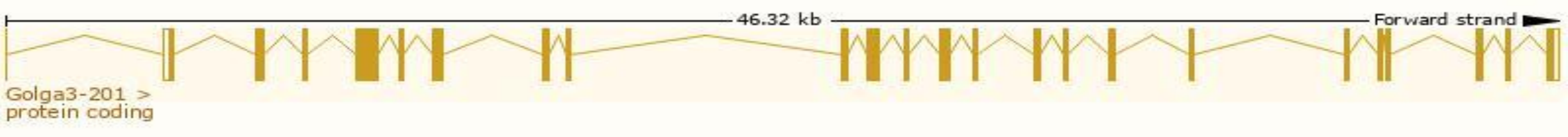
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

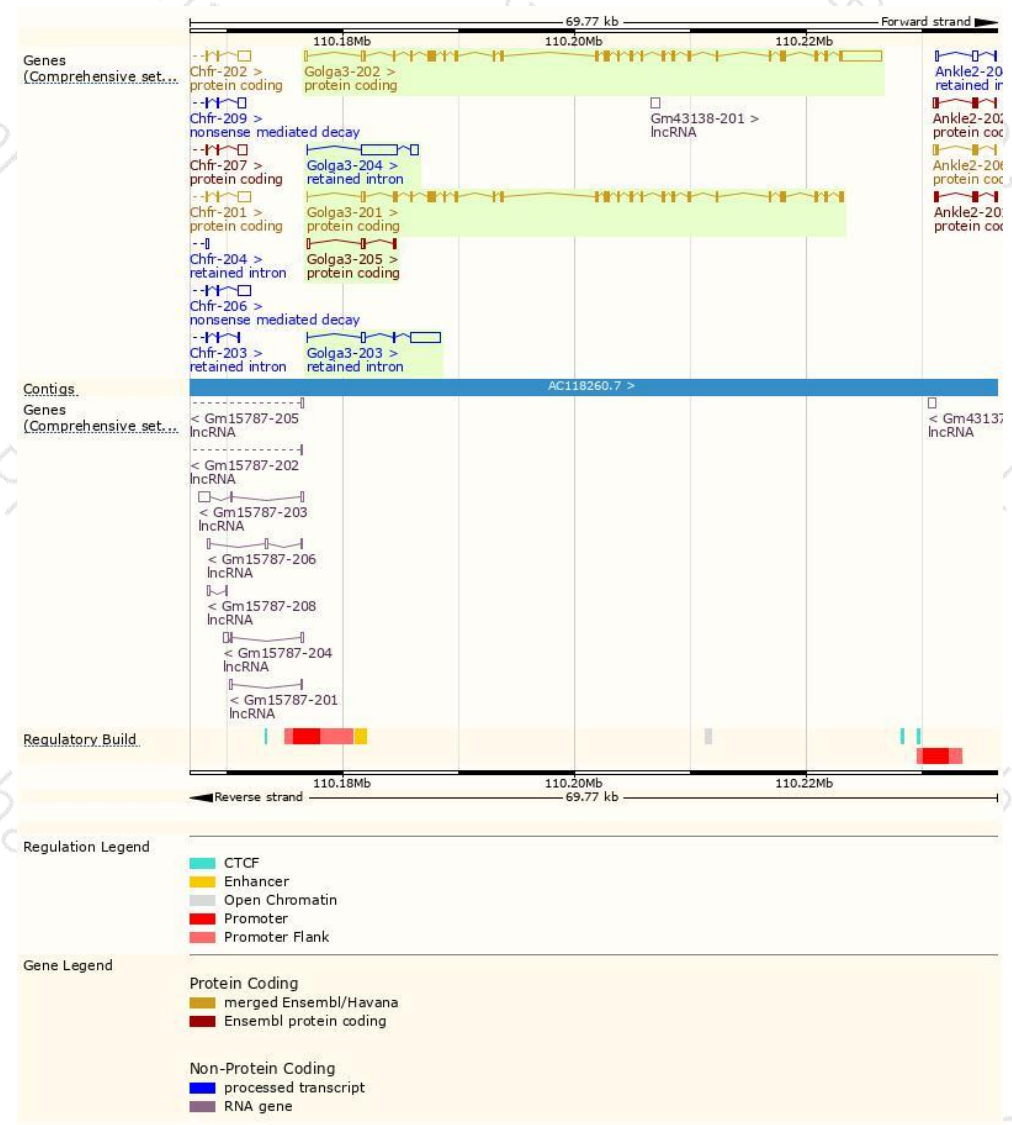
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Golga3-202	ENSMUST00000112512.7	8132	1447aa	Protein coding	CCDS39209	A0A0R4J1H6	TSL:1 GENCODE basic APPRIS P3
Golga3-201	ENSMUST00000031477.8	4805	1487aa	Protein coding	CCDS84928	E9QP99	TSL:5 GENCODE basic APPRIS ALT2
Golga3-205	ENSMUST00000139611.7	711	121aa	Protein coding	-	D3Z0Q8	CDS 3' incomplete TSL:2
Golga3-204	ENSMUST00000136900.1	3786	No protein	Retained intron	-	-	TSL:1
Golga3-203	ENSMUST00000125380.1	3115	No protein	Retained intron	-	-	TSL:1

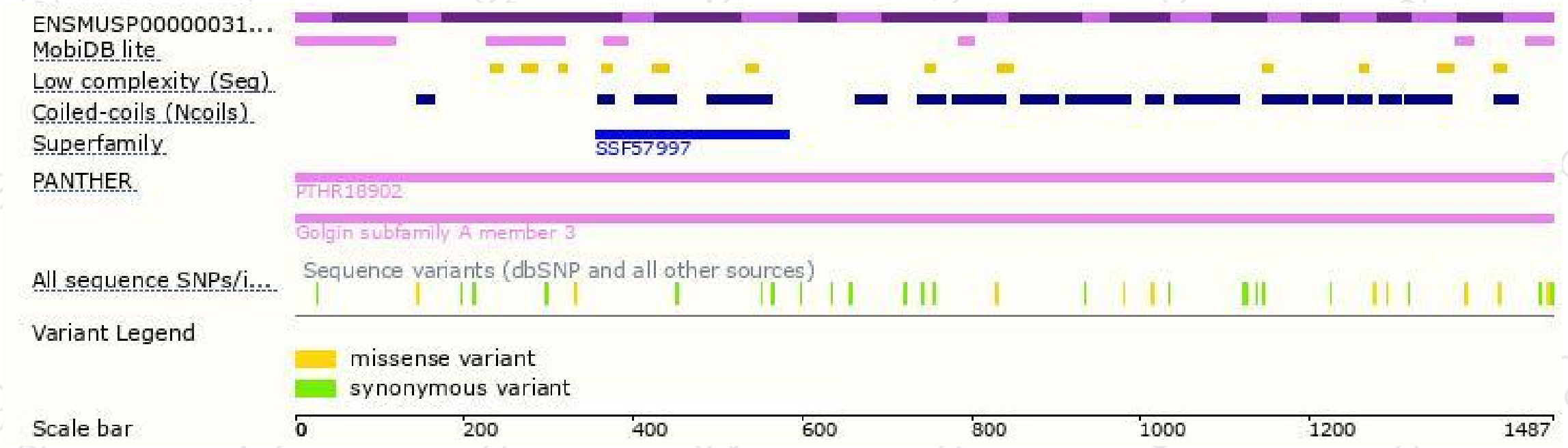
The strategy is based on the design of *Golga3-201* transcript,the transcription is shown below:



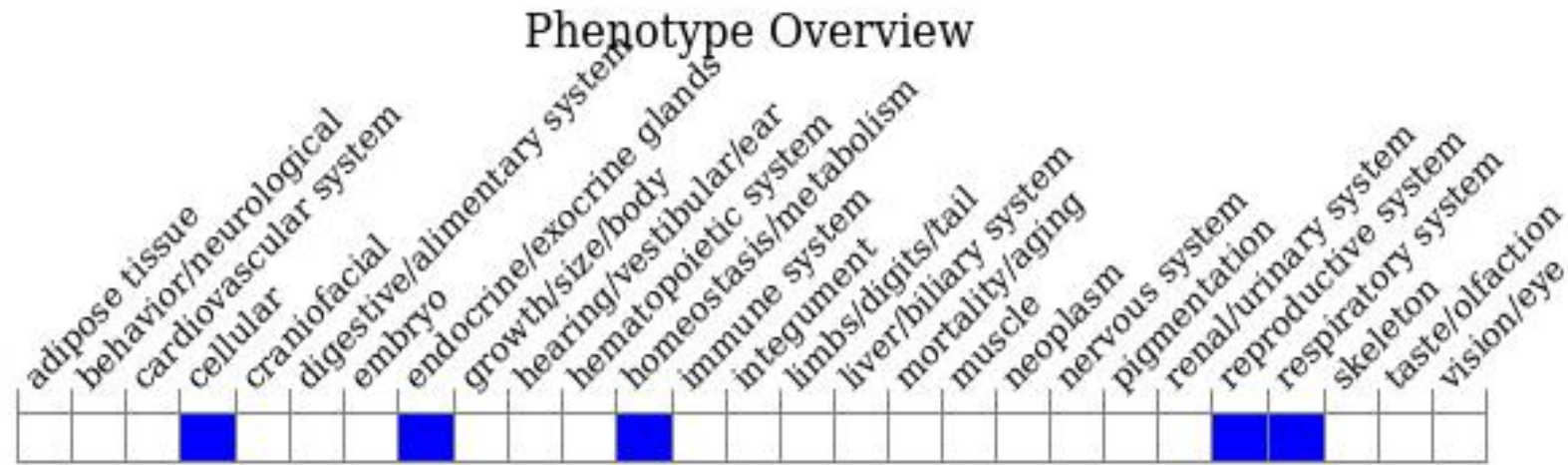
Genomic location distribution



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/>).

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

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