

Oga Cas9-KO Strategy

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Project Overview

Project Name

Oga

Project type

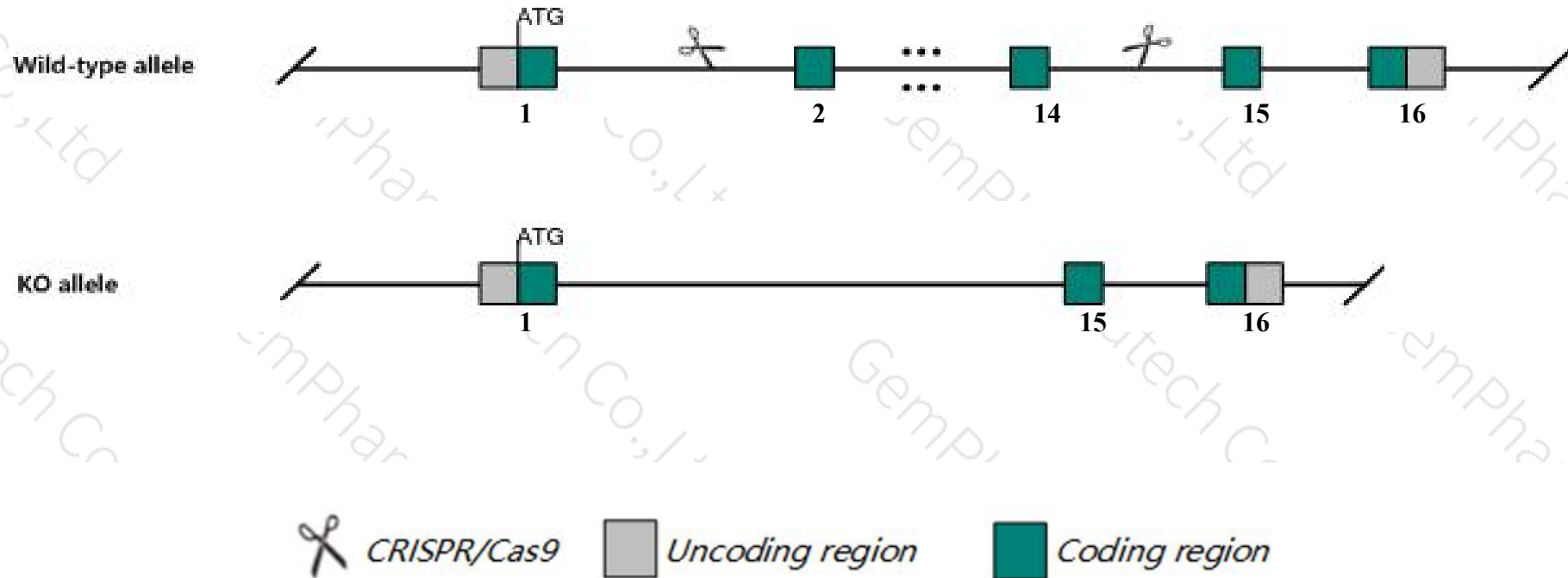
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Oga* gene has 6 transcripts. According to the structure of *Oga* gene, exon2-exon14 of *Oga-201* (ENSMUST00000026243.4) transcript is recommended as the knockout region. The region contains 2255bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Oga* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Mice homozygous for a gene-trapped allele exhibit perinatal lethality associated with a developmental delay and respiratory failure. Mouse embryonic fibroblasts exhibit proliferative and mitotic defects, frequent cytokinesis failure, and loss of genomic stability.
- The *Oga* gene is located on the Chr19. 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)

Oga O-GlcNAcase [Mus musculus (house mouse)]

Gene ID: 76055, updated on 19-Feb-2019

Summary



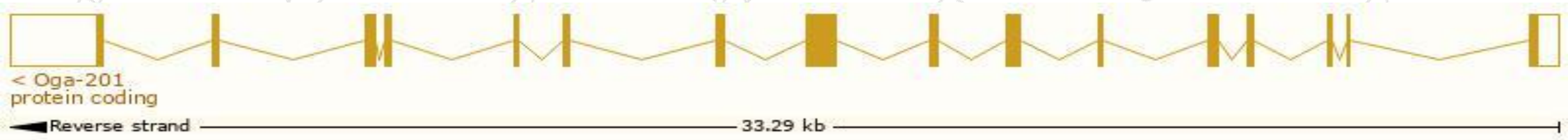
Official Symbol	Oga provided by MGI
Official Full Name	O-GlcNAcase provided by MGI
Primary source	MGI:MGI:1932139
See related	Ensembl:ENSMUSG00000025220
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Hy5, Mgea5, Ncoat
Expression	Ubiquitous expression in CNS E18 (RPKM 28.1), CNS E11.5 (RPKM 27.8) and 26 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

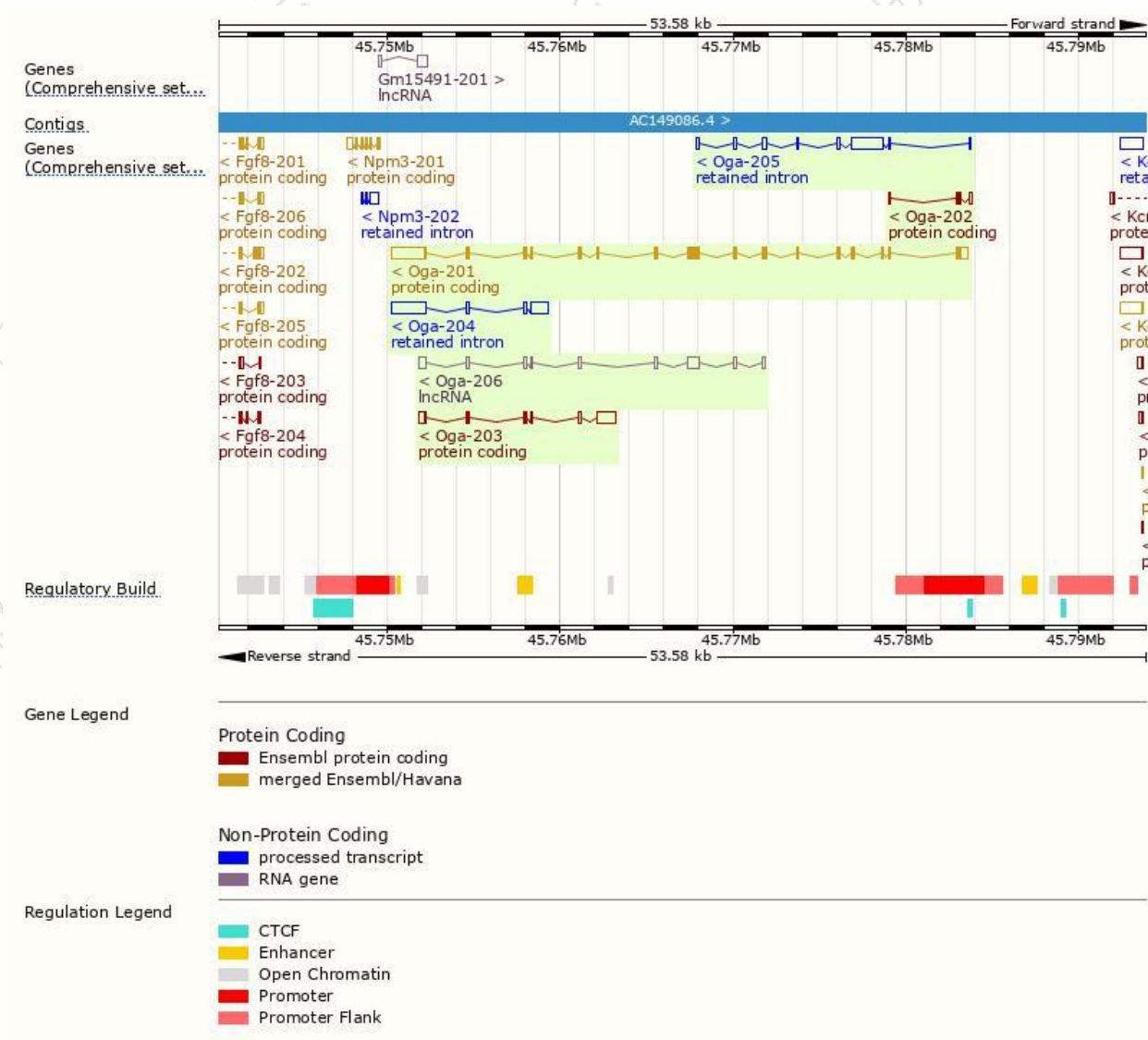
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Oga-201	ENSMUST00000026243.4	5057	916aa	Protein coding	CCDS29866	Q9EQQ9	TSL:1 GENCODE basic APPRIS P1
Oga-203	ENSMUST00000235508.1	2045	182aa	Protein coding	-	-	GENCODE basic
Oga-202	ENSMUST00000235448.1	457	84aa	Protein coding	-	-	CDS 3' incomplete
Oga-204	ENSMUST00000235865.1	3315	No protein	Retained intron	-	-	
Oga-205	ENSMUST00000235936.1	2812	No protein	Retained intron	-	-	
Oga-206	ENSMUST00000236960.1	2148	No protein	lncRNA	-	-	

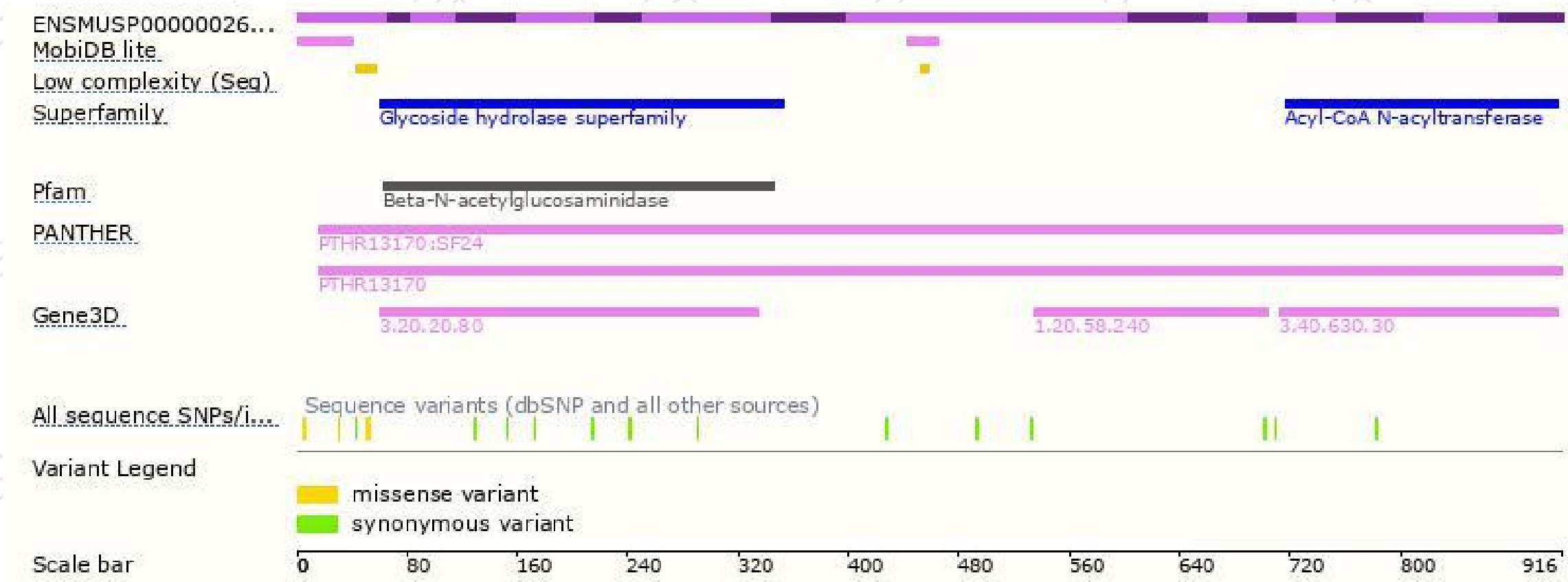
The strategy is based on the design of *Oga-201* transcript,The transcription is shown below



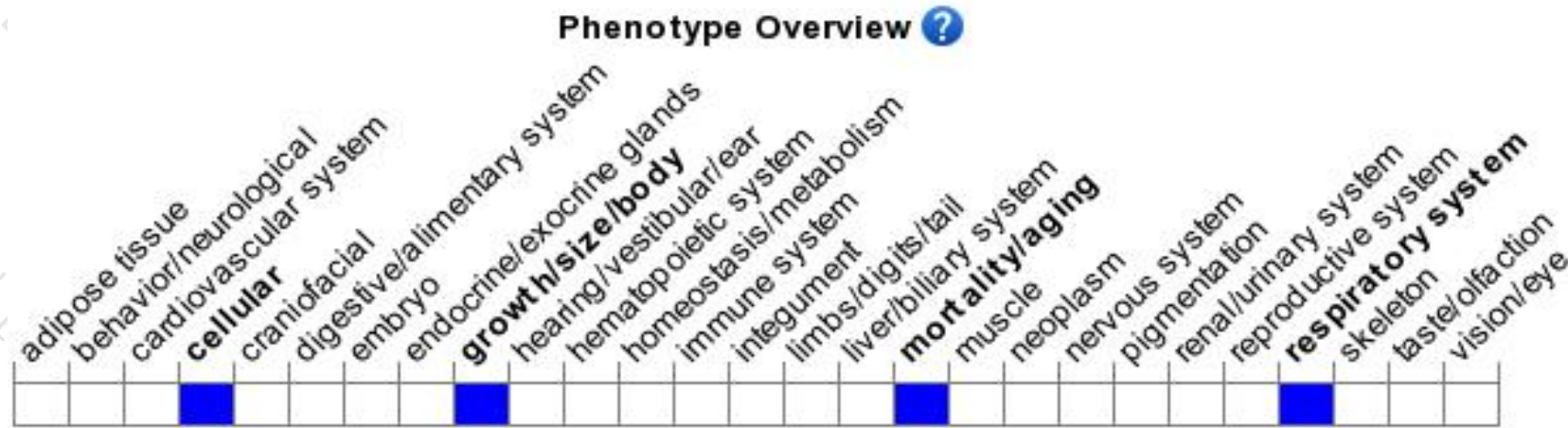
Genomic location distribution



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 gene-trapped allele exhibit perinatal lethality associated with a developmental delay and respiratory failure. Mouse embryonic fibroblasts exhibit proliferative and mitotic defects, frequent cytokinesis failure, and loss of genomic stability.

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

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