

# *Cog5* Cas9-KO Strategy

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# Project Overview



**Project Name**

***Cog5***

**Project type**

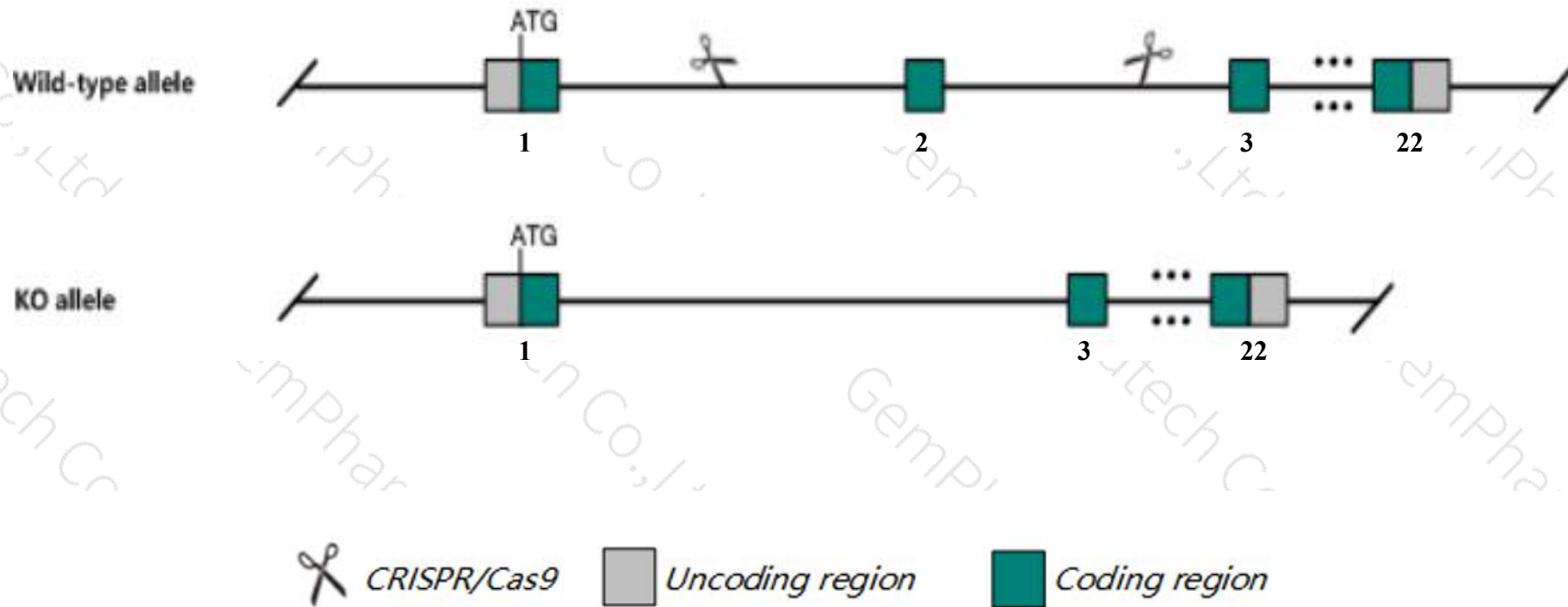
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cog5* gene. The schematic diagram is as follows:



- The *Cog5* gene has 4 transcripts. According to the structure of *Cog5* gene, exon2 of *Cog5-201* (ENSMUST00000036862.4) transcript is recommended as the knockout region. The region contains 140bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Cog5* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Cog5* gene is located on the Chr12. 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.
- The effect on transcript *Cog5-202* is unknown.
- Transcript *Cog5-203&204* may not be affected.
- The knockout region is near to the N-terminal of *Dus4l* gene, this strategy may influence the regulatory function of the N-terminal of *Dus4l* gene.
- 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)

## Cog5 component of oligomeric golgi complex 5 [Mus musculus (house mouse)]

Gene ID: 238123, updated on 13-Mar-2020

### Summary



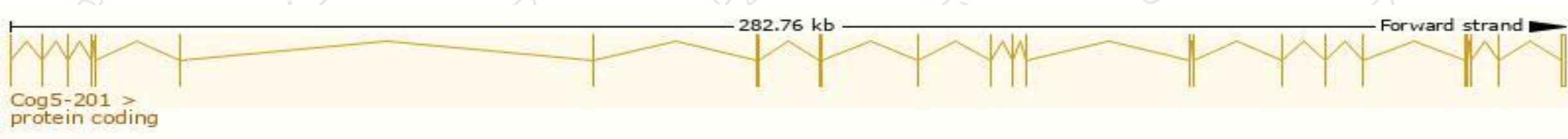
<b>Official Symbol</b>	Cog5 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	component of oligomeric golgi complex 5 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2145130</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000035933</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	5430405C01Rik, C87247, D18362, GOLTC1, GTC90
<b>Expression</b>	Ubiquitous expression in ovary adult (RPKM 11.7), mammary gland adult (RPKM 11.4) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

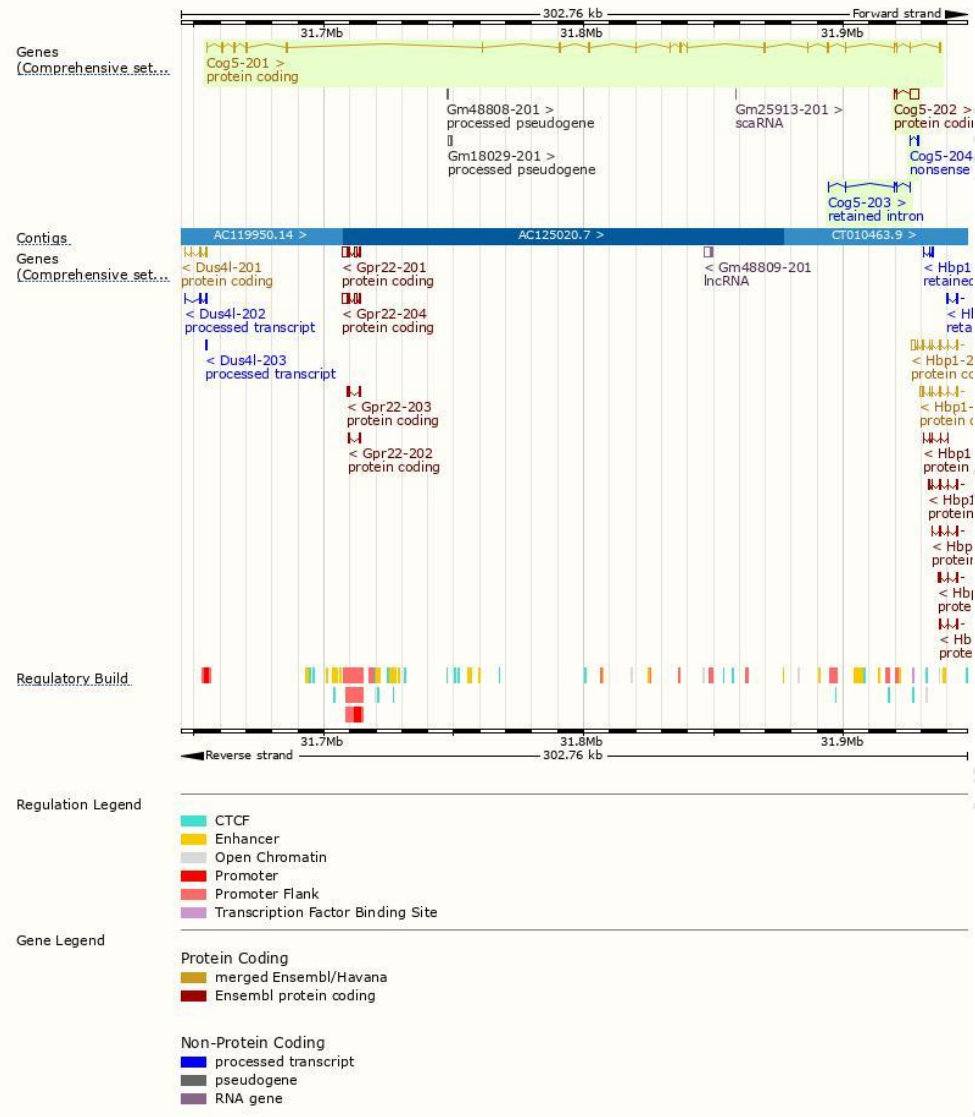
The gene has 4 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cog5-201	<a href="#">ENSMUST00000036862.4</a>	2997	<a href="#">829aa</a>	Protein coding	<a href="#">CCDS49046</a>	<a href="#">Q8C0L8</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 P1
Cog5-202	<a href="#">ENSMUST00000218428.1</a>	3610	<a href="#">99aa</a>	Protein coding	-	<a href="#">A0A1W2P7M6</a>	CDS 5' incomplete TSL:3
Cog5-204	<a href="#">ENSMUST00000219837.1</a>	372	<a href="#">21aa</a>	Nonsense mediated decay	-	<a href="#">A0A1W2P822</a>	CDS 5' incomplete TSL:5
Cog5-203	<a href="#">ENSMUST00000219672.1</a>	750	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Cog5-201* transcript, the transcription is shown below:

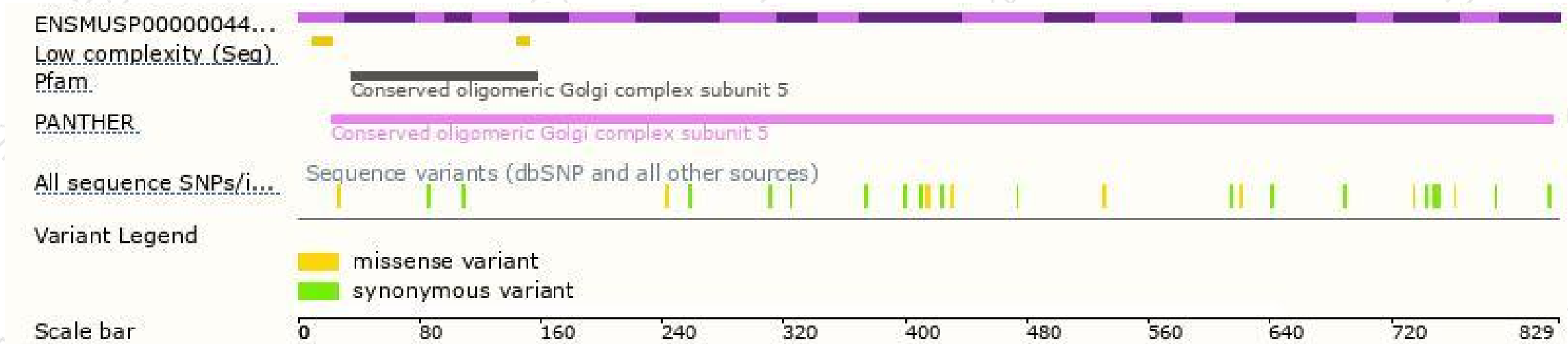


# Genomic location distribution





# Protein domain



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

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