

# *Gak* Cas9-KO Strategy

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# Project Overview

**Project Name**

***Gak***

**Project type**

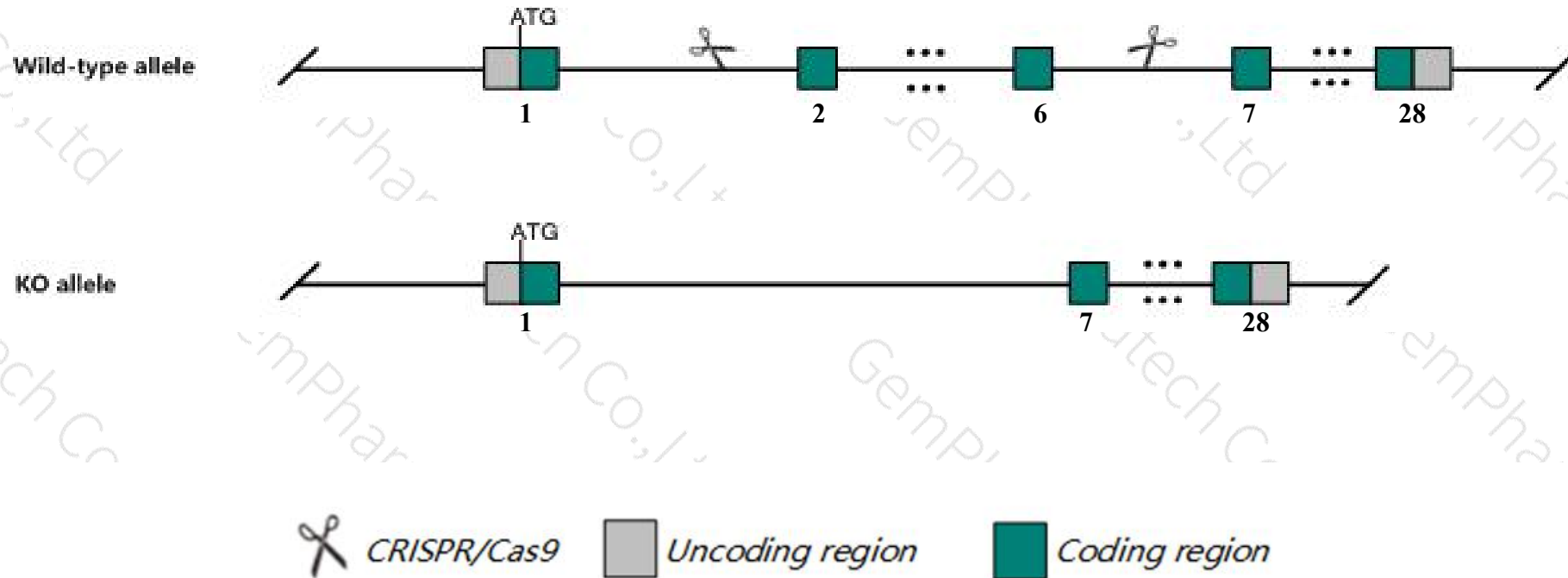
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- The *Gak* gene has 13 transcripts. According to the structure of *Gak* gene, exon2-exon6 of *Gak-201* (ENSMUST00000046603.14) transcript is recommended as the knockout region. The region contains 506bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Gak* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Mice homozygous for a deletion of the kinase domain display neonatal lethality with abnormal lung alveolar morphology and development. Mice homozygous for a knock-out allele exhibit lethality during early development.
- Transcript *Gak-202&209&210* may not be affected. And the effect on transcript *Gak-205&208&213* is unknown.
- The knockout region is near to the N-terminal of *Tmem175* gene, this strategy may influence the regulatory function of the N-terminal of *Tmem175* gene.
- The *Gak* 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)

## Gak cyclin G associated kinase [Mus musculus (house mouse)]

Gene ID: 231580, updated on 7-Apr-2019

### Summary



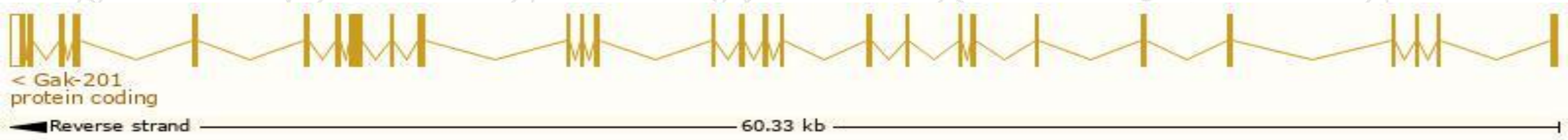
<b>Official Symbol</b>	Gak provided by <a href="#">MGI</a>
<b>Official Full Name</b>	cyclin G associated kinase provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2442153</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000062234</a>
<b>Gene type</b>	protein coding
<b>RefSeq 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>	D130045N16Rik
<b>Expression</b>	Ubiquitous expression in colon adult (RPKM 34.6), large intestine adult (RPKM 29.7) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

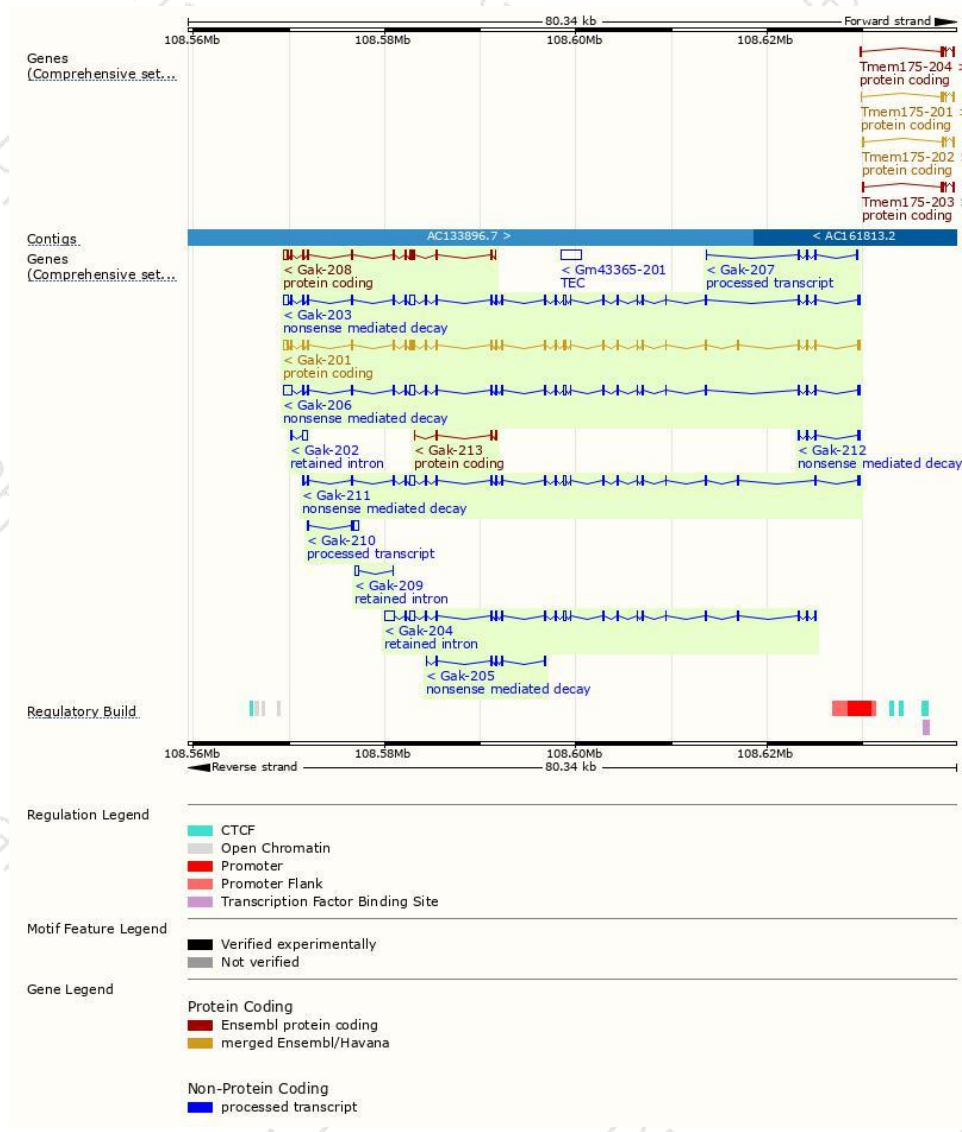
The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Gak-201	<a href="#">ENSMUST00000046603.14</a>	4453	<a href="#">1305aa</a>	Protein coding	<a href="#">CCDS19513</a>	<a href="#">A0A0R4J0F6</a>	TSL:1 GENCODE basic APPRIS P1
Gak-208	<a href="#">ENSMUST00000156110.7</a>	2269	<a href="#">608aa</a>	Protein coding	-	<a href="#">F6SLK1</a>	CDS 5' incomplete TSL:1
Gak-213	<a href="#">ENSMUST00000200204.1</a>	387	<a href="#">129aa</a>	Protein coding	-	<a href="#">A0A0G2JFZ0</a>	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:1
Gak-206	<a href="#">ENSMUST00000145467.7</a>	4487	<a href="#">128aa</a>	Nonsense mediated decay	-	<a href="#">D6RHK5</a>	TSL:2
Gak-203	<a href="#">ENSMUST00000135225.7</a>	4310	<a href="#">128aa</a>	Nonsense mediated decay	-	<a href="#">D6RHK5</a>	TSL:1
Gak-211	<a href="#">ENSMUST00000199048.4</a>	3532	<a href="#">90aa</a>	Nonsense mediated decay	-	<a href="#">A0A0G2JEW6</a>	TSL:1
Gak-205	<a href="#">ENSMUST00000139303.1</a>	710	<a href="#">187aa</a>	Nonsense mediated decay	-	<a href="#">F7BG02</a>	CDS 5' incomplete TSL:5
Gak-212	<a href="#">ENSMUST00000199662.1</a>	444	<a href="#">51aa</a>	Nonsense mediated decay	-	<a href="#">A0A0G2JGP6</a>	TSL:5
Gak-210	<a href="#">ENSMUST00000199010.1</a>	644	No protein	Processed transcript	-	-	TSL:5
Gak-207	<a href="#">ENSMUST00000145935.5</a>	339	No protein	Processed transcript	-	-	TSL:5
Gak-204	<a href="#">ENSMUST00000137872.7</a>	3846	No protein	Retained intron	-	-	TSL:5
Gak-202	<a href="#">ENSMUST00000133745.1</a>	625	No protein	Retained intron	-	-	TSL:3
Gak-209	<a href="#">ENSMUST00000196010.1</a>	402	No protein	Retained intron	-	-	TSL:1

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



# Genomic location distribution

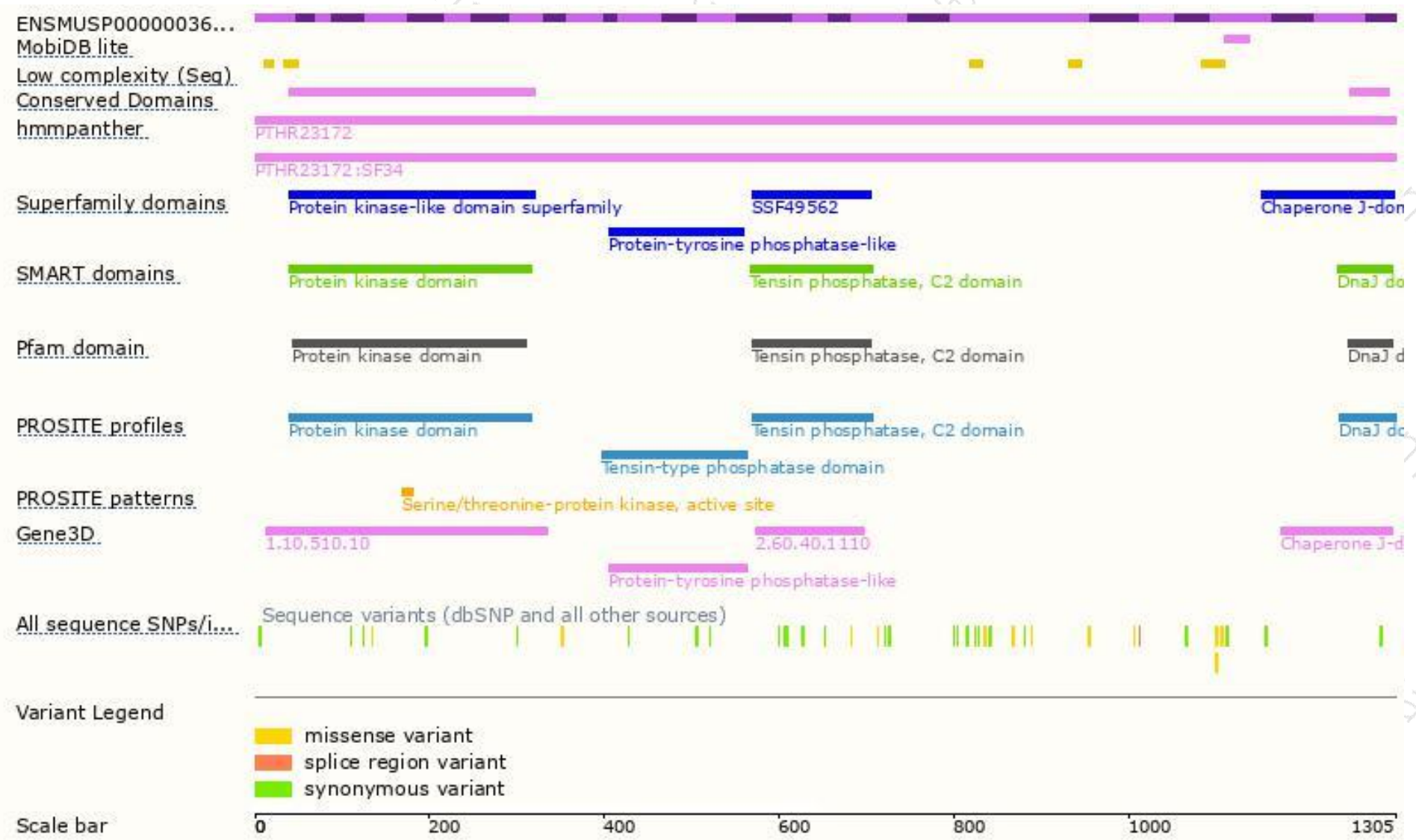




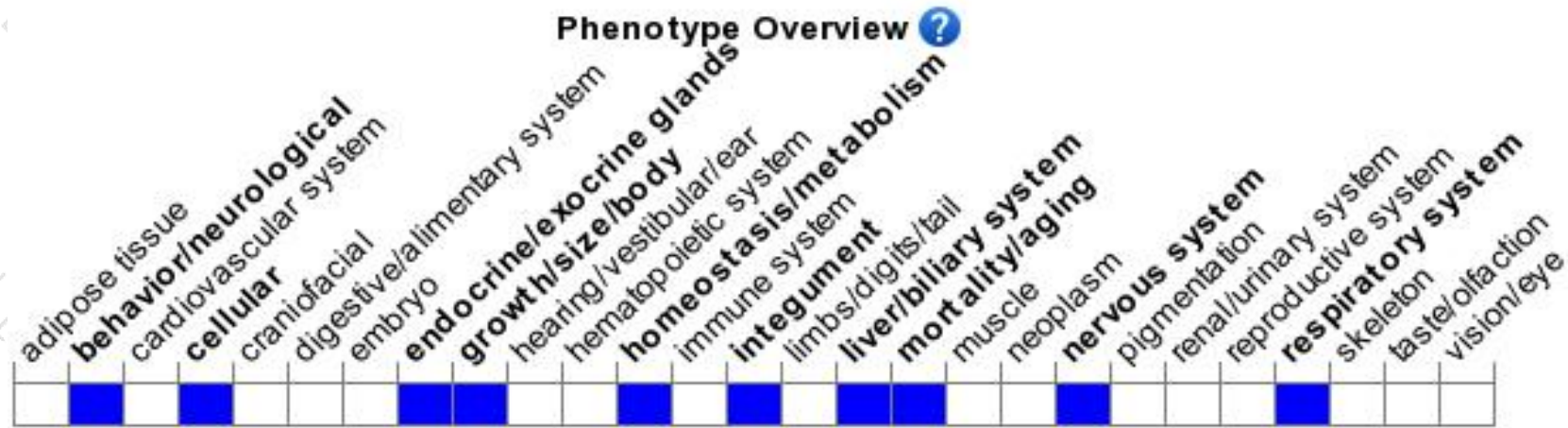
# Protein domain



集萃药康  
GemPharmatech



# 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 deletion of the kinase domain display neonatal lethality with abnormal lung alveolar morphology and development. Mice homozygous for a knock-out allele exhibit lethality during early development.

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

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