

# Gem Cas9-KO Strategy

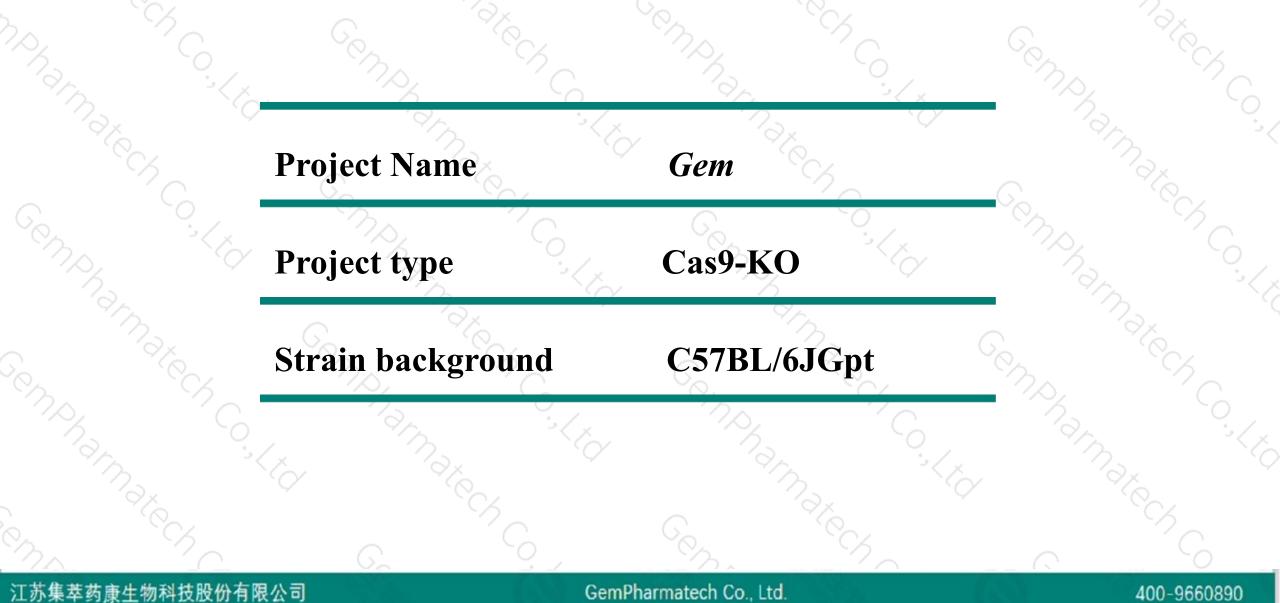
Designer: Reviewer: Design Date:

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JiaYu Xiaojing Li 2020-1-19

# **Project Overview**

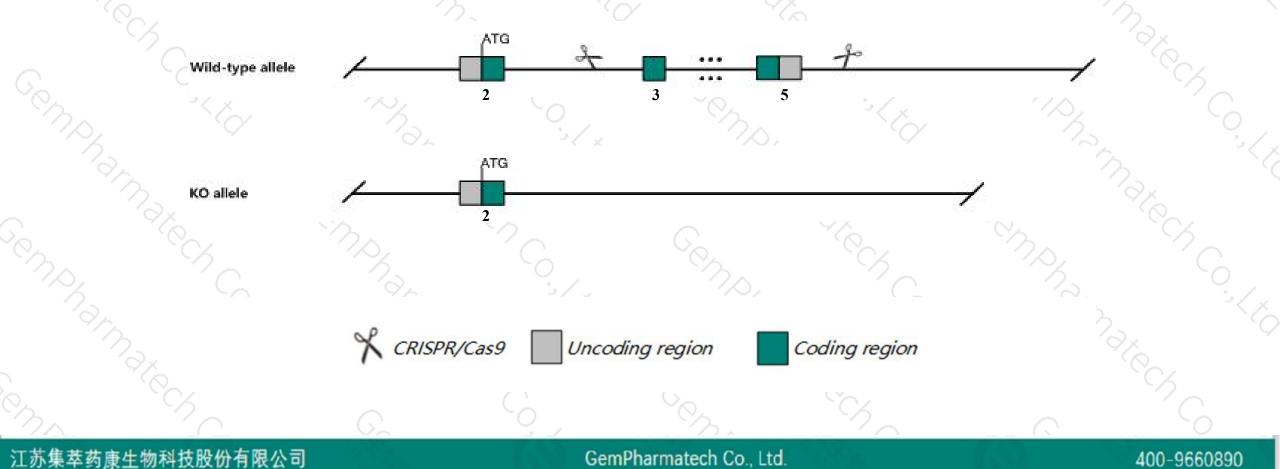




# **Knockout strategy**



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





- The Gem gene has 2 transcripts. According to the structure of Gem gene, exon3-exon5 of Gem-202 (ENSMUST00000108304.8) transcript is recommended as the knockout region. The region contains 560bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Gem gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit impaired glucose tolerance, decreased insulin secretion and abnormal calcium handling in pancreatic beta-cells.
- The Gem gene is located on the Chr4. 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.

Notice

# **Gene information (NCBI)**



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## Gem GTP binding protein (gene overexpressed in skeletal muscle) [Mus musculus (house mouse)]

Gene ID: 14579, updated on 31-Jan-2019

### Summary

Official Symbol	Gem provided by MGI
Official Full Name	GTP binding protein (gene overexpressed in skeletal muscle) provided by MGI
<b>Primary source</b>	MGI:MGI:99844
See related	Ensembl:ENSMUSG0000028214
Gene type	protein coding
<b>RefSeq status</b>	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	AV020497
Expression	Broad expression in ovary adult (RPKM 36.0), lung adult (RPKM 14.1) and 16 other tissues See more
Orthologs	human all

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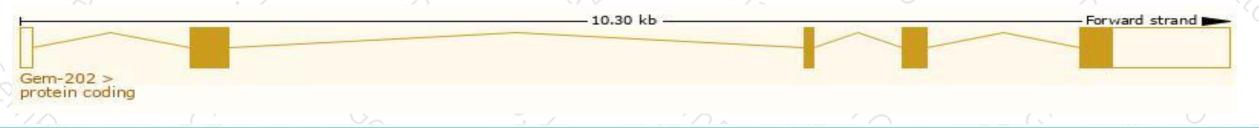
# **Transcript information (Ensembl)**



The gene has 2 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Gem-202	ENSMUST00000108304.8	2006	<u>295aa</u>	Protein coding	CCDS17971	P55041 Q3TH76	TSL:1 GENCODE basic APPRIS P1
Gem-201	ENSMUST0000029868.6	1994	<u>295aa</u>	Protein coding	CCDS17971	P55041 Q3TH76	TSL:2 GENCODE basic APPRIS P1

The strategy is based on the design of Gem-202 transcript, The transcription is shown below

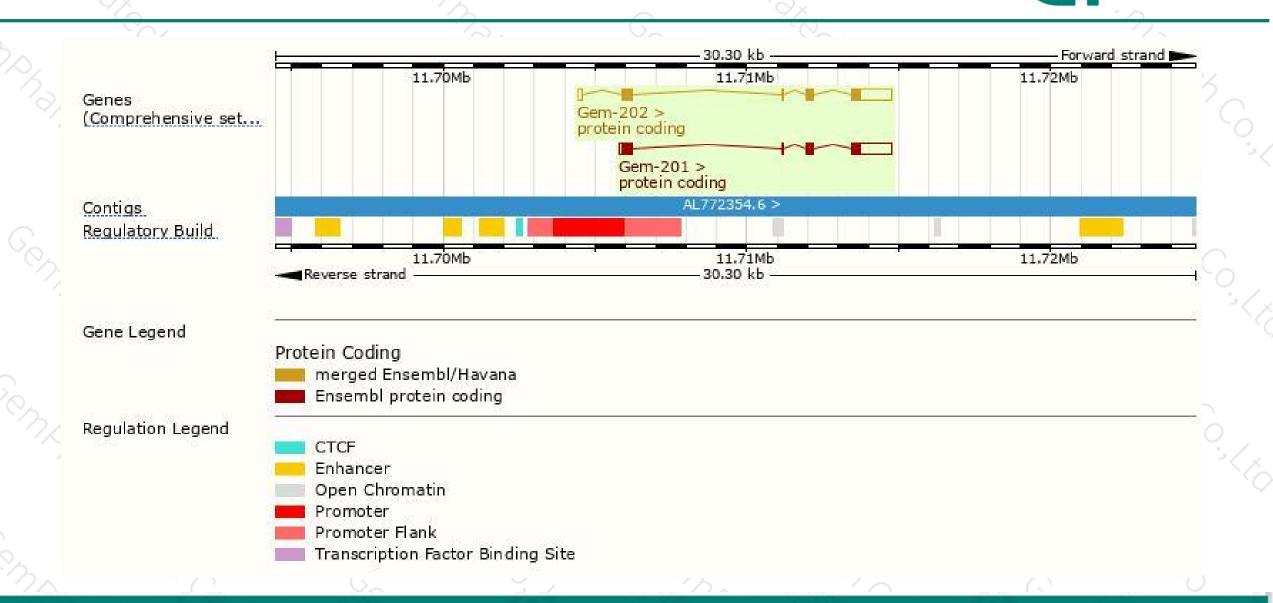


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# **Genomic location distribution**



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# **Protein domain**

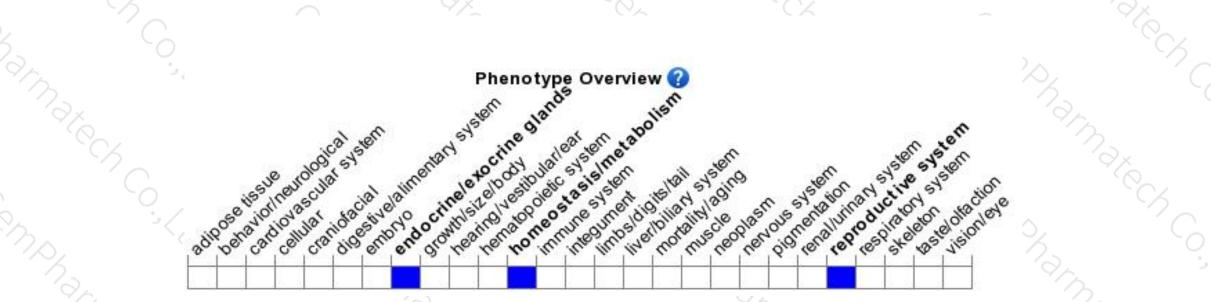
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47	Superfamily			P-loop contain	ning nucleoside trip	hosphate hydrolas	e .			
	SMART			SM00173						
				SM00175						
				SM00174						
	Prints			PR00449						
	<u>Pfam</u>			Small GTPas	se					
$\gamma_{\lambda}$	PROSITE profiles			Small GTPase s	superfamily, Ras-typ	pe				0
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# 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 exhibit impaired glucose tolerance, decreased insulin secretion and abnormal calcium handling in pancreatic beta-cells.



If you have any questions, you are welcome to inquire. Tel: 400-9660890



