

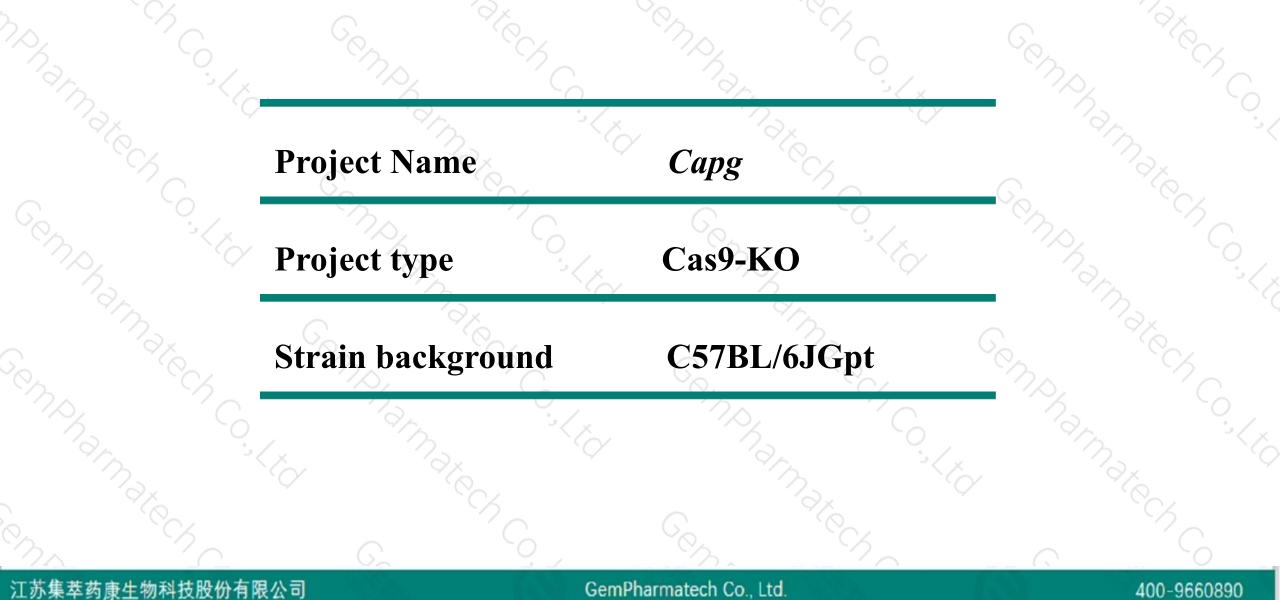
Capg Cas9-KO Strategy

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Project Overview

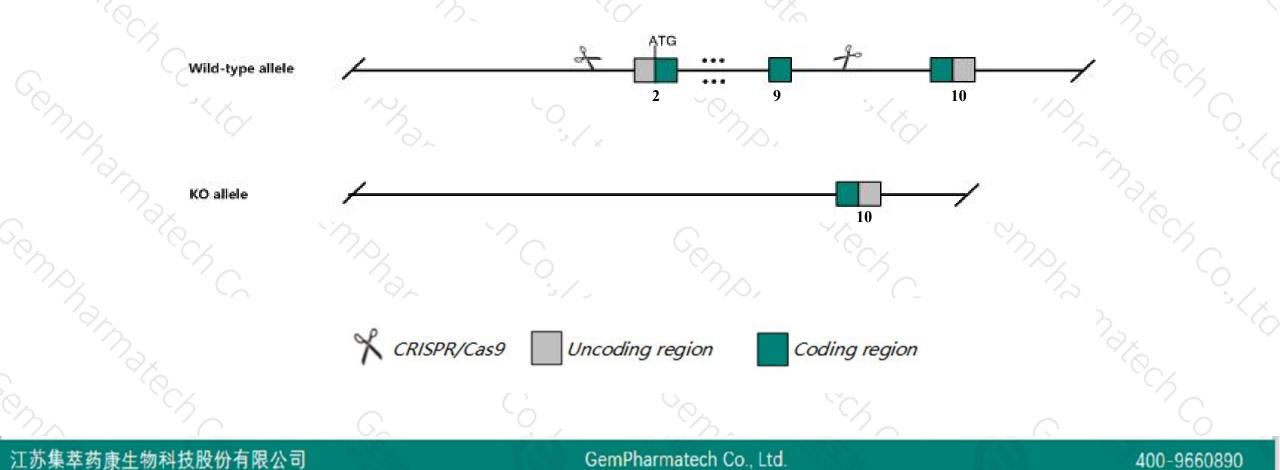




Knockout strategy



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





- The Capg gene has 11 transcripts. According to the structure of Capg gene, exon2-exon9 of Capg-202 (ENSMUST00000114071.7) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify *Capg* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Inactivation of this loci results in impaired immune cell motility which manifests in homozygous mutant mice as increased susceptibility to some bacterial infections.
- The Capg gene is located on the Chr6. 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)



Capg capping protein (actin filament), gelsolin-like [Mus musculus (house mouse)]

Gene ID: 12332, updated on 12-Aug-2019

Summary

 Official Symbol
 Capg provided by MGI

 Official Full Name
 capping protein (actin filament), gelsolin-like provided by MGI

 Primary source
 MGI:MGI:1098259

 See related
 Ensembl:ENSMUSG00000056737

 Gene type
 protein coding

 RefSeq status
 VALIDATED

 Organism
 Mus musculus

 Lineage
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Murinae; Mus; Mus

 Also known as
 mbh1; gCap39

 Expression
 Broad expression in genital fat pad adult (RPKM 25.9), bladder adult (RPKM 25.4) and 19 other tissues See more or human all

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Transcript information (Ensembl)



Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Capg-202	ENSMUST00000114071.7	1400	<u>349aa</u>	Protein coding	CCDS39516	Q99LB4	TSL:1 GENCODE basic APPRIS P1
Capg-203	ENSMUST00000114072.7	1388	<u>349aa</u>	Protein coding	CCDS39516	<u>Q99LB4</u>	TSL:1 GENCODE basic APPRIS P1
Capg-201	ENSMUST00000071044.12	1247	<u>349aa</u>	Protein coding	CCDS39516	<u>Q99LB4</u>	TSL:1 GENCODE basic APPRIS P1
Capg-204	ENSMUST00000126101.2	857	<u>254aa</u>	Protein coding	2	D3YTL5	CDS 3' incomplete TSL:5
Capg-205	ENSMUST00000126124.7	679	<u>193aa</u>	Protein coding		D3YU77	CDS 3' incomplete TSL:3
Capg-209	ENSMUST00000155188.7	605	<u>173aa</u>	Protein coding		D3YZN3	CDS 3' incomplete TSL:5
Capg-210	ENSMUST00000155705.7	515	<u>104aa</u>	Protein coding	-	D3Z4K5	CDS 3' incomplete TSL:3
Capg-207	ENSMUST00000134809.7	500	<u>90aa</u>	Protein coding	2	D3Z014	CDS 3' incomplete TSL:2
Capg-208	ENSMUST00000137435.1	734	No protein	Retained intron	-	-	TSL:3
Capg-206	ENSMUST00000127770.1	411	No protein	Retained intron		-8	TSL:5
Capg-211	ENSMUST00000156168.1	407	No protein	Retained intron	-	- 22	TSL:3
	111	/	1		2	1.1.1.1.	

The gene has 11 transcripts, all transcripts are shown below:

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

Capg-202 > protein coding

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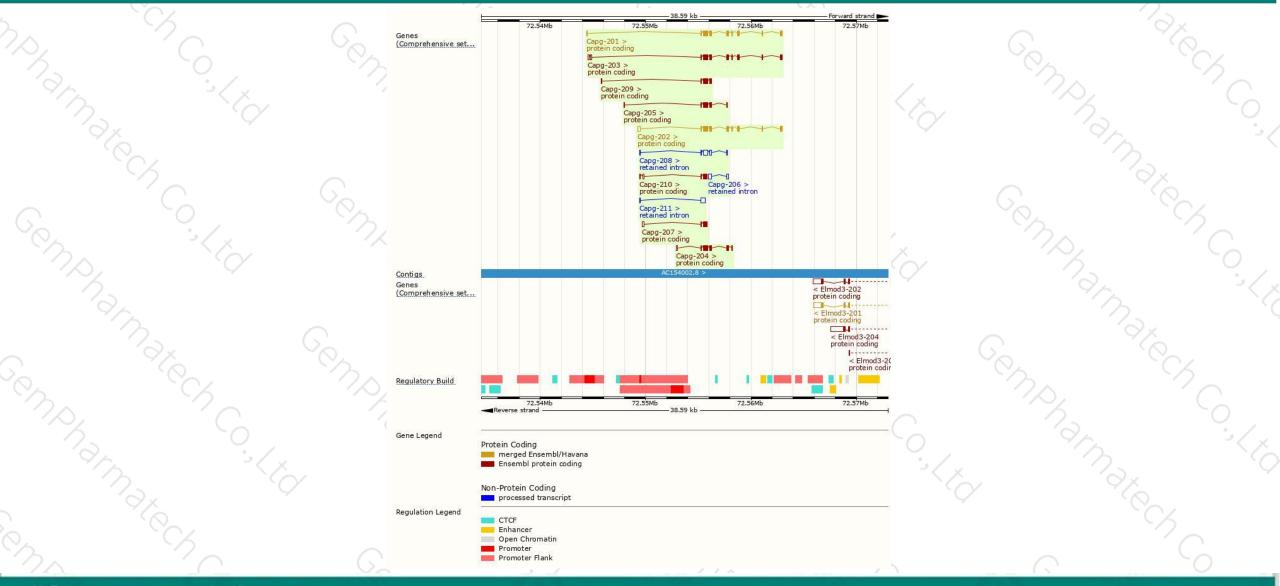
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Forward strand

Genomic location distribution





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Protein domain



ENSMUSP00000109			1	-					
Superfamily SMART	SSF55				-11				
Prints	Villin/	Gelsolin Villin/Gelso	lin						
Pfam		ielsolin-like d	Contraction of the second s						
PANTHER	Villin/Gelsolir	1							
	Macrophage	capping prof	ein .						- C.
Gene3D			main superfami						
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CDD All sequence SNPs/i	Sequence v	variants (db nse variant	SNP and all ot	cd		200	cd1129	280	349
<u>CDD</u> All sequence SNPs/i Variant Legend	Sequence v	variants (db nse variant ymous vari	SNP and all ot	her sources)		200			349

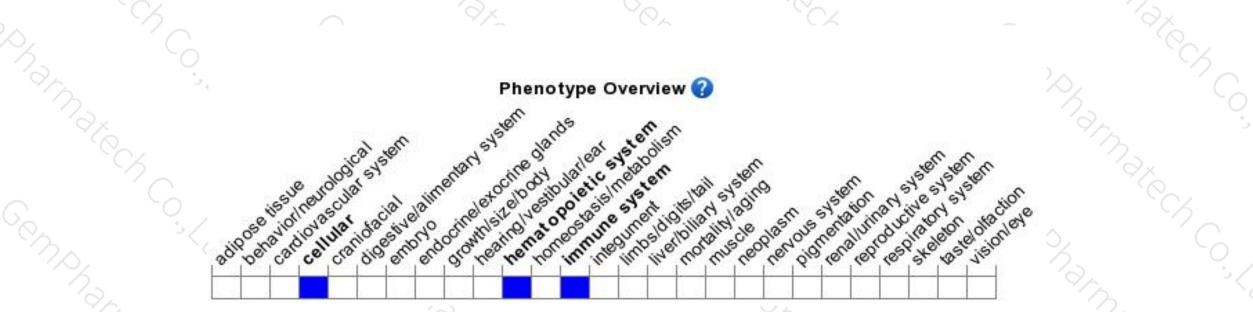
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Mouse phenotype description(MGI)





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, Inactivation of this loci results in impaired immune cell motility which manifests in homozygous mutant mice as increased susceptibility to some bacterial infections.



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



