

Lasp1 Cas9-KO Strategy

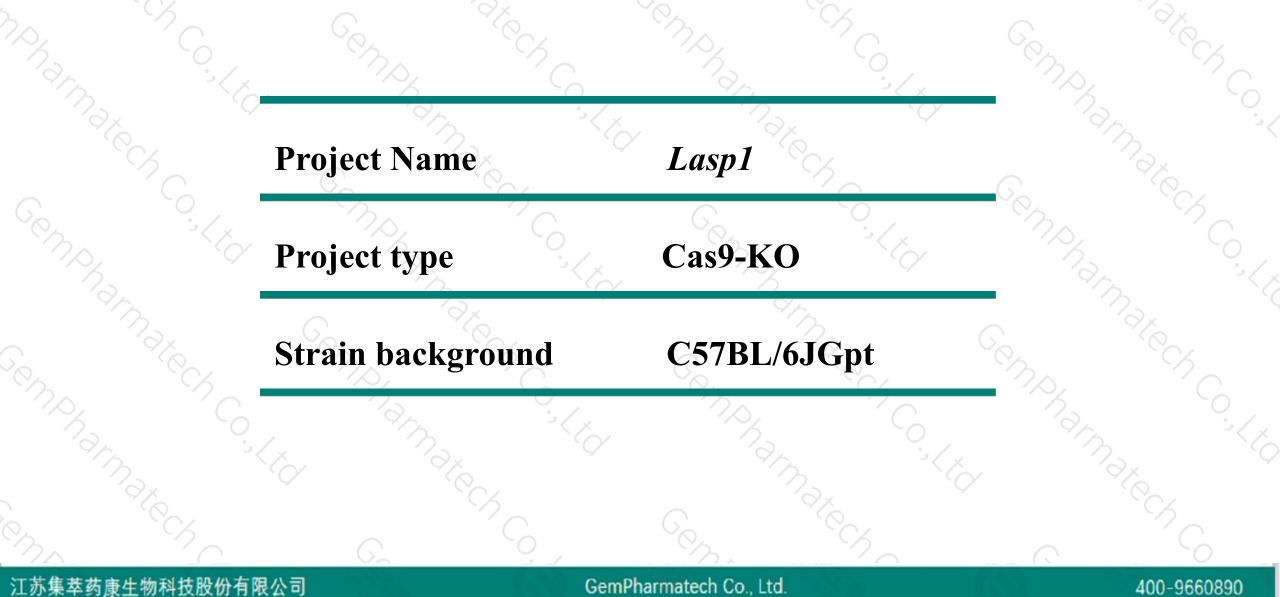
Designer: Reviewer:

Design Date:

Daohua Xu Huimin Su 2020-2-18

Project Overview

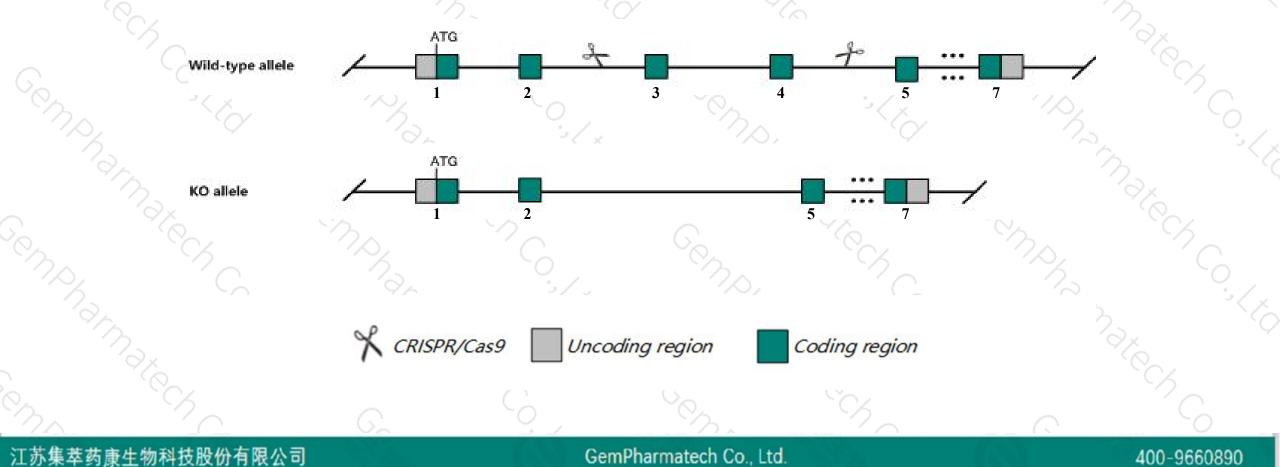




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Lasp1 gene. The schematic diagram is as follows:





- The Lasp1 gene has 16 transcripts. According to the structure of Lasp1 gene, exon3-exon4 of Lasp1-201 (ENSMUST00000043843.11) transcript is recommended as the knockout region. The region contains 193bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Lasp1 gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit reduced histamine-stimulated gastric acid secretion and enlarged heart and testes on a mixed background. Mice homozygous for a transgene insertion exhibit abnormal tail vertebrae with scoliosis, transient spina bifida occulta, and a bent tail.
 Transcript Lasp1-210 and Lasp1-211 may not be affected.
- The Lasp1 gene is located on the Chr11. 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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Lasp1 LIM and SH3 protein 1 [Mus musculus (house mouse)]

Gene ID: 16796, updated on 7-Apr-2019

Summary

Official SymbolLasp1 provided by MGIOfficial Full NameLIM and SH3 protein 1 provided by MGIPrimary sourceMGI:MGI:109656See relatedEnsembl:ENSMUSG0000038366Gene typeprotein codingprotein codingVALIDATEDOrganismMus musculusLineageEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;
Muroidea; Murinae; Mus; MusAlso knownasA4408629, Def-4, LASP-1, MLN 50, SH3P6, Tg(Col1a1-lacZ)1NgmaBurgerssionUbiquitous expression in large intestine adult (RPKM 112.9), duodenum adult (RPKM 108.0) and 28 other tissues

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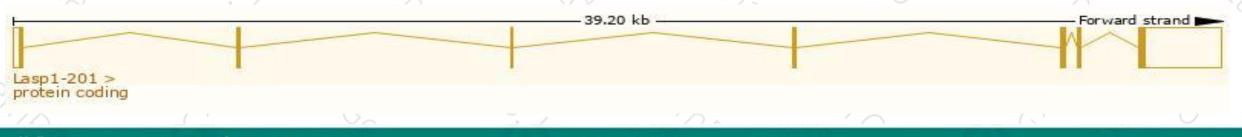
Transcript information (Ensembl)



Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Lasp1-201	ENSMUST00000043843.11	3540	<u>263aa</u>	Protein coding	CCDS25332	Q543N3 Q61792	TSL:1 GENCODE basic APPRIS P1
Lasp1-207	ENSMUST00000129828.7	1207	<u>129aa</u>	Protein coding		<u>A2A6G9</u>	CDS 3' incomplete TSL:3
Lasp1-213	ENSMUST00000148280.2	686	<u>186aa</u>	Protein coding	-	A2A6H0	CDS 3' incomplete TSL:3
Lasp1-215	ENSMUST00000153520.2	503	<u>47aa</u>	Protein coding	-	<u>A2A6G4</u>	CDS 3' incomplete TSL:1
Lasp1-206	ENSMUST00000129558.7	487	<u>103aa</u>	Protein coding		<u>A2A6G8</u>	CDS 3' incomplete TSL:2
Lasp1-214	ENSMUST00000152962.7	433	<u>99aa</u>	Protein coding		A2A6G7	CDS 3' incomplete TSL:3
Lasp1-211	ENSMUST00000143571.1	429	<u>28aa</u>	Protein coding	-	<u>A2A6G0</u>	CDS 3' incomplete TSL:5
Lasp1-204	ENSMUST00000127033.8	386	<u>70aa</u>	Protein coding	-	E9Q0N6	CDS 3' incomplete TSL:3
Lasp1-212	ENSMUST00000146572.7	376	<u>89aa</u>	Protein coding	5	<u>A2A6G6</u>	CDS 3' incomplete TSL:5
Lasp1-208	ENSMUST00000134428.1	337	<u>18aa</u>	Protein coding		<u>A2A6G3</u>	CDS 3' incomplete TSL:3
Lasp1-209	ENSMUST00000136723.7	322	<u>69aa</u>	Protein coding	-	A2A6G5	CDS 3' incomplete TSL:5
Lasp1-216	ENSMUST00000155762.2	310	<u>56aa</u>	Protein coding	-	A2A6H1	CDS 3' incomplete TSL:3
Lasp1-210	ENSMUST00000138919.1	112	<u>12aa</u>	Protein coding		<u>A2A6G2</u>	CDS 3' incomplete TSL:3
Lasp1-205	ENSMUST00000127575.1	758	No protein	Retained intron	-	1.	TSL:2
Lasp1-203	ENSMUST00000107569.2	686	No protein	Retained intron	-	(a <u>r</u>)	TSL:2
Lasp1-202	ENSMUST00000107568.1	580	No protein	Retained intron	-	120	TSL:1

The gene has 16 transcripts, all transcripts are shown below:

The strategy is based on the design of Lasp1-201 transcript, The transcription is shown below

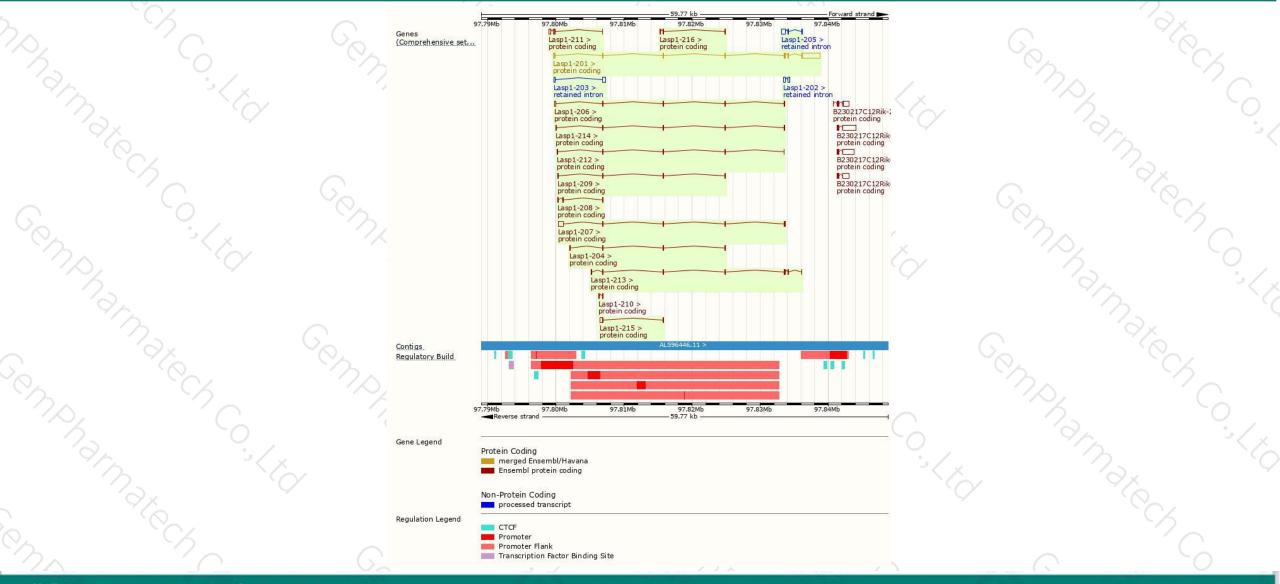


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Genomic location distribution





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Protein domain





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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 reduced histamine-stimulated gastric acid secretion and enlarged heart and testes on a mixed background. Mice homozygous for a transgene insertion exhib abnormal tail vertebrae with scoliosis, transient spina bifida occulta, and a bent tail.

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



