

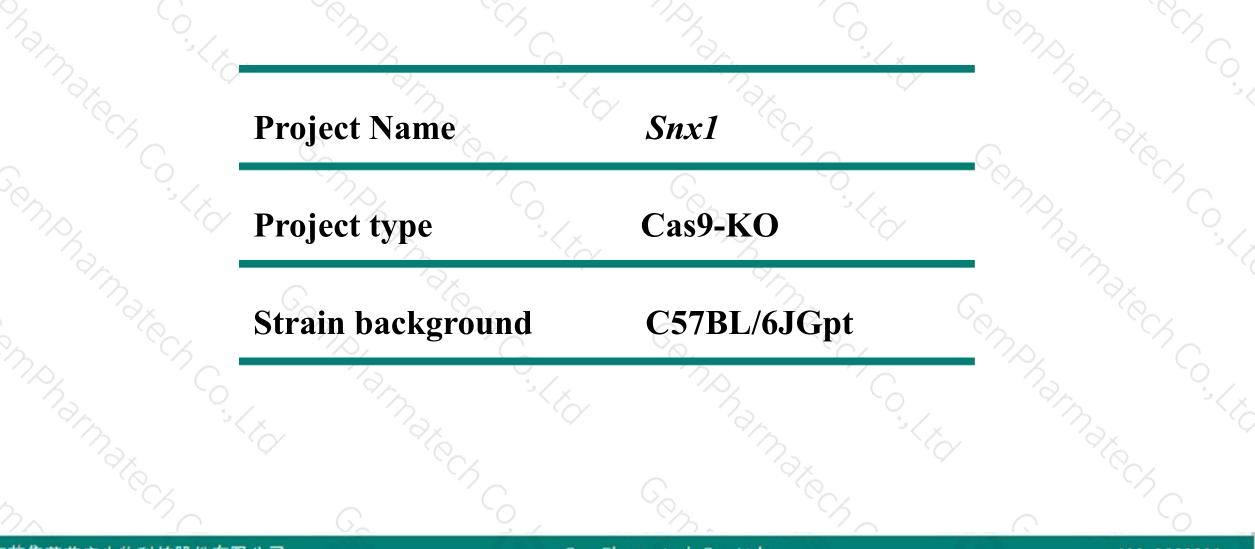
Snx1 Cas9-KO Strategy

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Project Overview





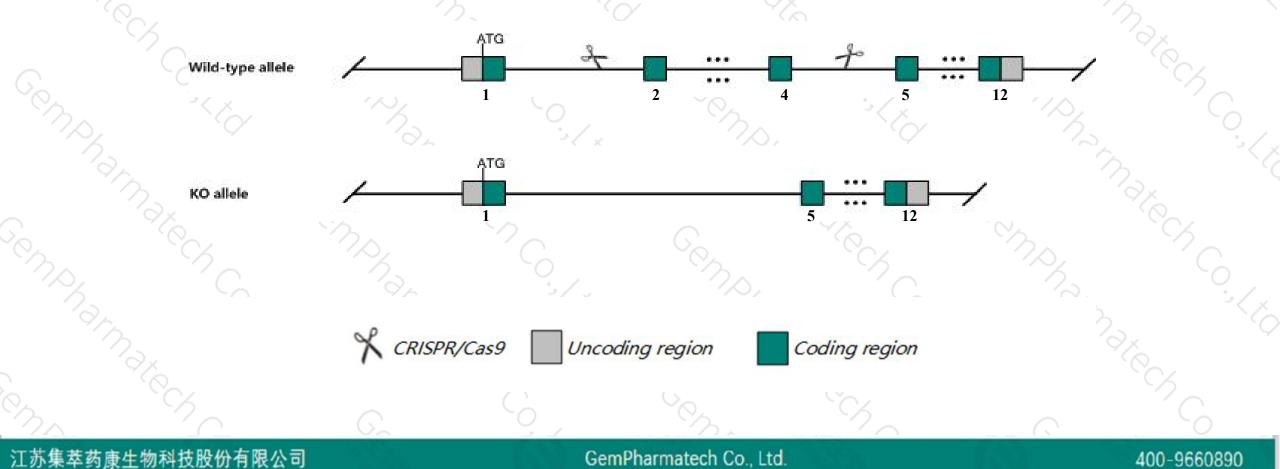
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Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Snx1 gene. The schematic diagram is as follows:





- The Snx1 gene has 7 transcripts. According to the structure of Snx1 gene, exon2-exon4 of Snx1-201 (ENSMUST00000027488.10) transcript is recommended as the knockout region. The region contains 547bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Snx1 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 resistance to ryanodine- and palmitate-induced pancreatic apoptosis. Mice homozygous for a different knock-out allele exhibit increased adiposity, body and organ weights, and leptin serum levels on background containing LG/J.
- > 9430060103Rik gene may be destroyed in this strategy.
- ➤ Transcript *Capn10*-203&204&206 may not be affected.
- The Capn10 gene is located on the Chr1. 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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C	Capn10 calpain 10	[Mus musculus	s (house mouse)]			2			
G	Gene ID: 23830, updated on	5-Nov-2019							
	Summary					* ?			
	Official Symbol	Capn10 provided by MG	l			200			
	Official Full Name	calpain 10 provided by N							
u.	Primary source	MGI:MGI:1344392							
	See related	in the second							
		protein coding							
	RefSeq status								
		Mus musculus Fullemente Materiae Oberniete Vietebrete Futbleesterni Menneelie Futberie Fuerebenterlinee Olinee Derlentie							
	Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus							
	Also known as								
	Expression								
	Orthologs	human all	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~						
	Genomic context								
	Location: 1; 1 D				See Capn10 in Genome Data	Viewer			
	Exon count: 12								
	Annotation release	Status	Assembly	Chr	Location				
	108	current	GRCm38.p6 (GCF_000001635.26)	1	NC_000067.6 (9293440892947948)				
	Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	1	NC_000067.5 (9483098594844525)	(

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Transcript information (Ensembl)



The gene has 7 transcripts, all transcripts are shown below:

	\/ Y						2	States a
Name 🍦	Transcript ID 🖕	bp 🍦	Protein 🖕	Biotype 🖕	CCDS 🖕	UniProt 🖕	Flags	
Capn10-201	ENSMUST0000027488.10	2902	<u>666aa</u>	Protein coding	<u>CCDS15181</u> &	Q9ESK3 ₆ 과	TSL:1 GENCO	DE basic APPRIS P1
Capn10-202	ENSMUST00000117814.7	1268	<u>264aa</u>	Protein coding	-	<u>Q9CPY2</u> &	TSL:1	GENCODE basic
Capn10-205	ENSMUST00000152983.7	2171	<u>507aa</u>	Nonsense mediated decay	-	D6RGR0 &		TSL:5
Capn10-207	ENSMUST00000187342.1	752	<u>179aa</u>	Nonsense mediated decay	()	<u>A0A087WSM6</u> &	CDS 5' inc	complete TSL:5
Capn10-206	ENSMUST00000153828.1	317	No protein	Processed transcript	-	-		TSL:2
Capn10-203	ENSMUST00000128429.1	829	No protein	Retained intron		19 <u>9</u>		TSL:3
Capn10-204	ENSMUST00000136598.1	458	No protein	Retained intron	-	p -		TSL:2

The strategy is based on the design of Capn10-201 transcript, The transcription is shown below

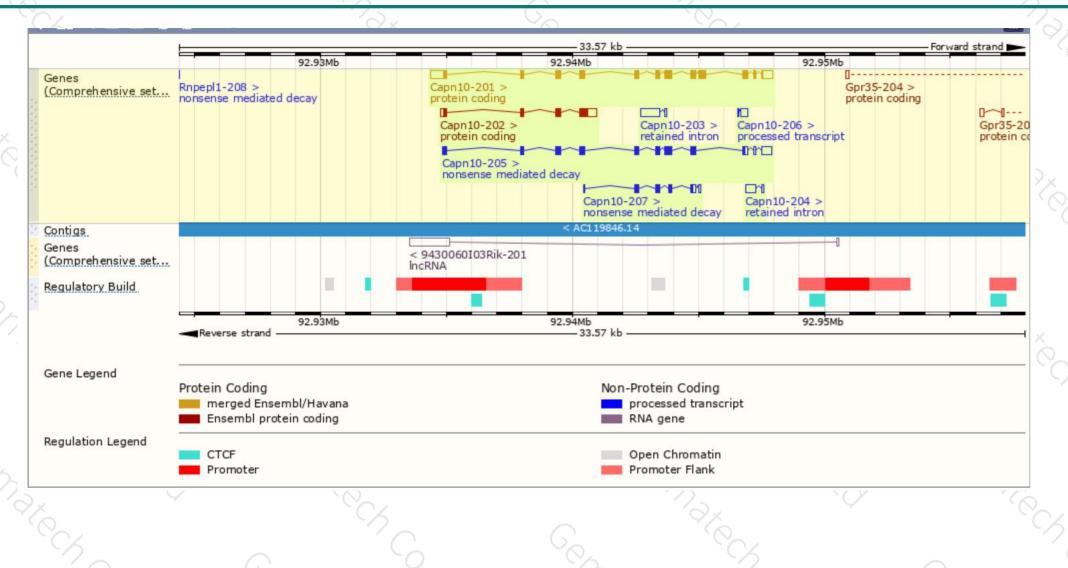
Capn10-201 > protein coding			13.57 kb		Forwar	rd strand
	1	0		10.	1 100	6

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Genomic location distribution





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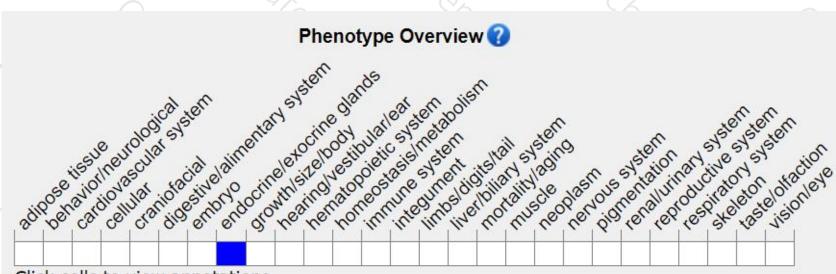
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Protein domain



		6		(2000	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	5	G.		737. 27.
harnax	ENSMUSP00000027 Low complexity (Seg) Superfamily	Papain-like cysteine pe	ptidase superfamily			alpain large subunit, do	nain III superfamily	_		30
D'A	SMART Prints	Peptidase C2, calpain, ca Peptidase C2,				eptidase C2, calpain, do	main III			
~ (]	Pfam PROSITE profiles	Peptidase C2, calpain, Peptidase C2, calpain,	catalytic domain			Peptidase C2, calpain, la	arge subunit, domain III			2×
Comphan Man	PROSITE patterns PANTHER	Calpain-10	e peptidase, cysteine active s	ite						~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
100 A	Gene3D CDD	PTHR10183		3.90.70.10		.60.120.380				~O
(97).	All sequence SNPs/i	Peptidase C2, calpain, o Sequence variants (db	SNP and all other sources	1	1	alpain subdomain III	i i	0.10	I.	×
Sep.	Variant Legend	stop gained synonymous vari	iant			nissense variant				`Ч _С
	Scale bar	0 60	120 180	240	300	360 420	480	540 600	666	-0
			Nate Ch	$\sim \phi$		narmare			Naxe	، م
<u></u>	10	G.	~ _	/	- Ýs	A	2			0
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Mouse phenotype description(MGI)



Click cells to view annotations.

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 resistance to ryanodine- and palmitate-induced pancreatic apoptosis. Mice homozygous for a different knock-out allele exhibit increased adiposity, body and organ weights, and leptin serum levels on background containing LG/J.

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



