

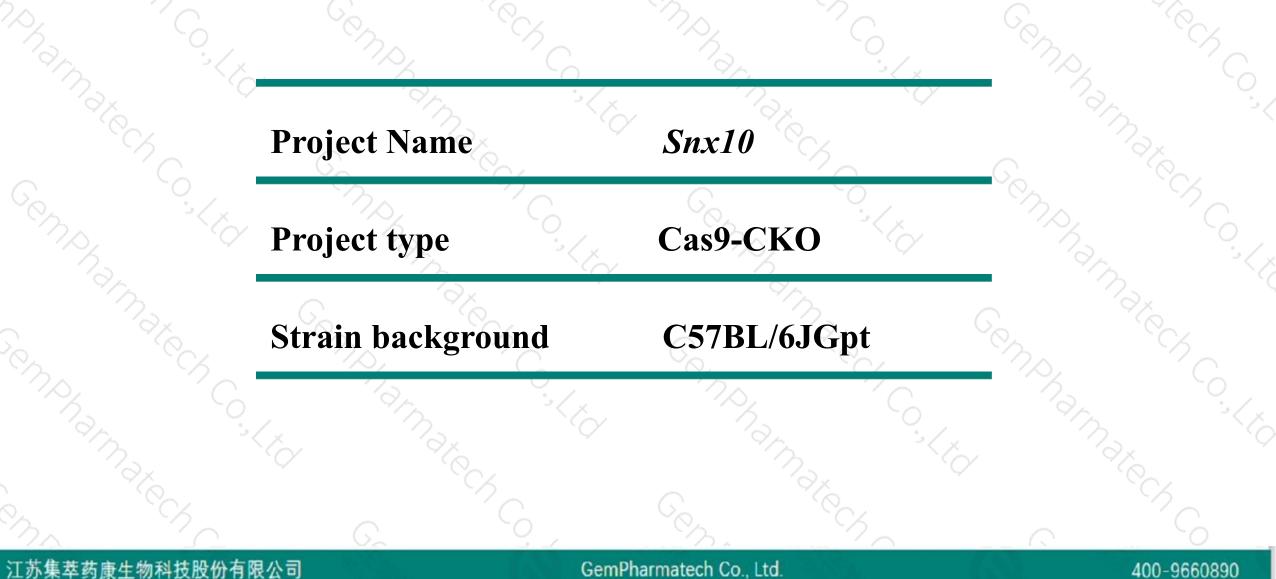
Companyated Snx10 Cas9-CKO Strategy Romphamater Control

Comphannater Co Designer: Shilei Zhu Semphamatech Co

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Project Overview



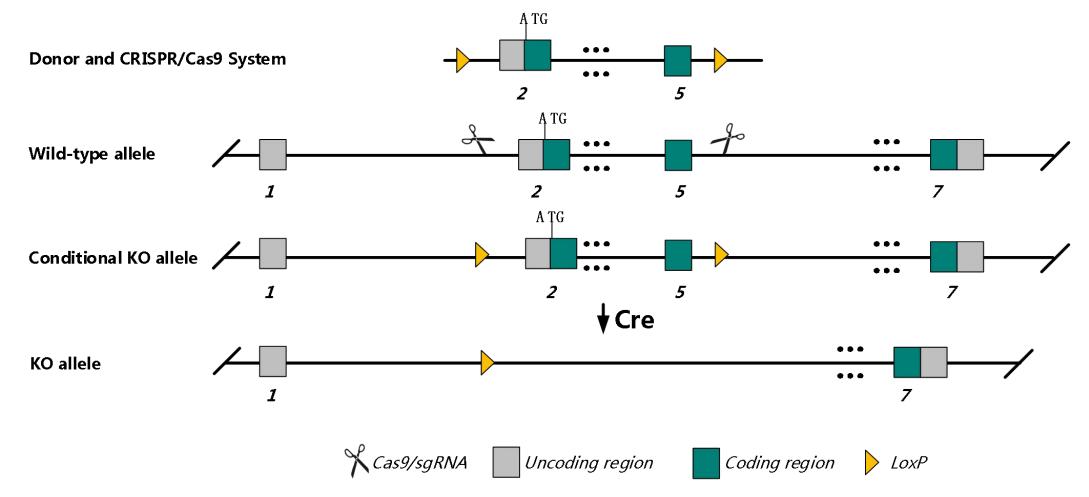


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Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Snx10 gene. The schematic diagram is as follows:





The Snx10 gene has 7 transcripts. According to the structure of Snx10 gene, exon2-exon5 of Snx10-201 (ENSMUST00000049152.14) 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 *Snx10* gene. The brief process is as follows:CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice.Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.



- According to the existing MGI data, Mice homozygous for a hypomorphic allele show postnatal growth retardation, failure of tooth eruption, impaired skeleton development, and osteopetrorickets associated with failed osteoclast activity, high stomach pH, low calcium availability, impaired bone mineralization, and premature death.
- The Snx10 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

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Gene information (NCBI)



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Snx10 sorting nexin 10 [Mus musculus (house mouse)]

Gene ID: 71982, updated on 31-Jan-2019

Summary

Official Symbol	Snx10 provided by MGI
Official Full Name	sorting nexin 10 provided by MGI
Primary source	MGI:MGI:1919232
See related	Ensembl:ENSMUSG0000038301
Gene type	protein coding
RefSeq status	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	2410004M09Rik
Expression	Broad expression in frontal lobe adult (RPKM 11.5), cortex adult (RPKM 10.9) and 17 other tissues See more
Orthologs	human all

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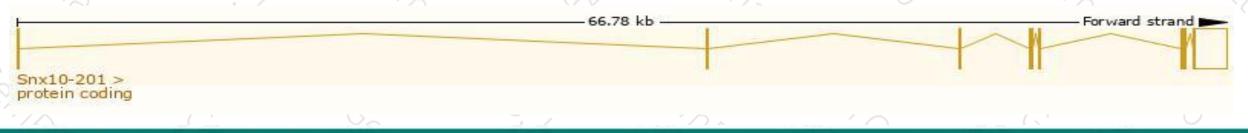
Transcript information (Ensembl)



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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Snx10-201	ENSMUST00000049152.14	2480	<u>201aa</u>	Protein coding	CCDS20136	Q4FJX6 Q9CWT3	TSL:1 GENCODE basic APPRIS P1
Snx10-207	ENSMUST00000179365.7	2464	<u>201aa</u>	Protein coding	CCDS20136	Q4FJX6 Q9CWT3	TSL:1 GENCODE basic APPRIS P1
Snx10-202	ENSMUST00000114439.7	968	<u>201aa</u>	Protein coding	CCDS20136	Q4FJX6 Q9CWT3	TSL:1 GENCODE basic APPRIS P1
Snx10-203	ENSMUST00000137212.7	809	<u>177aa</u>	Protein coding	62	D3YW62	CDS 3' incomplete TSL:3
Snx10-204	ENSMUST00000140560.7	433	<u>96aa</u>	Protein coding	17	D3Z4P6	CDS 3' incomplete TSL:5
Snx10-205	ENSMUST00000149024.1	693	<u>44aa</u>	Nonsense mediated decay	87	<u>S4R1A0</u>	TSL:3
Snx10-206	ENSMUST00000155724.2	6512	No protein	Retained intron	2 -	-	TSL:1

The strategy is based on the design of Snx10-201 transcript, The transcription is shown below

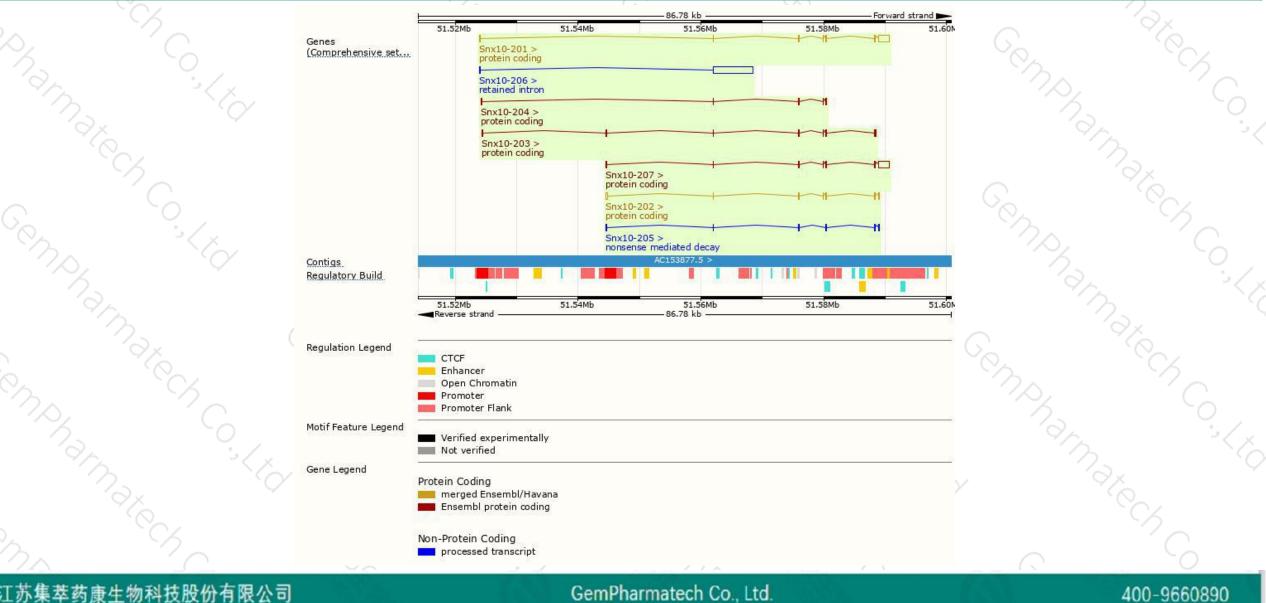


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Genomic location distribution





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Protein domain



ENSMUSP00000044... MobiDB lite Low complexity (Seq) Conserved Domains hmmpanther. Sorting ne PTHR1055 Superfamily domains SMART domains Pfam domain Phox PROSITE profiles

Gene3D

Scale bar

All sequence SNPs/i... Variant Legend

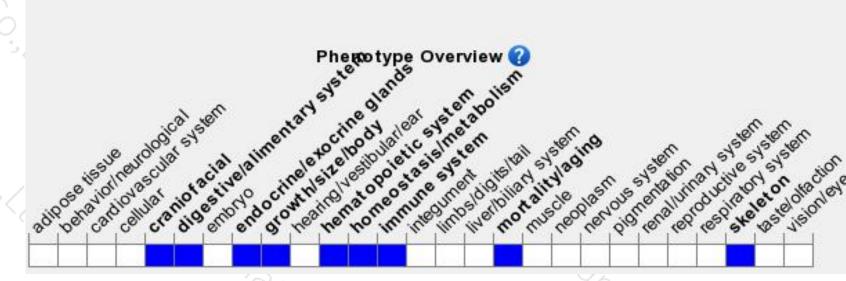
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and the second sec	0555:SF128						
PX	domain superfa	mily					
P	nox homologous	domain					
	Phox homolog	ous domain					
	Phox homologo	is domain				_	
	main superfamil						
Sequence variants (dbSNP and all other sources)				1			
n n	nissense varia synonymous v						
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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 hypomorphic allele show postnatal growth retardation, failure of tooth eruption, impaired skeleton development, and osteopetrorickets associated with failed osteoclast activity, high stomach pH, low calcium availability, impaired bone mineralization, and premature death.

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



