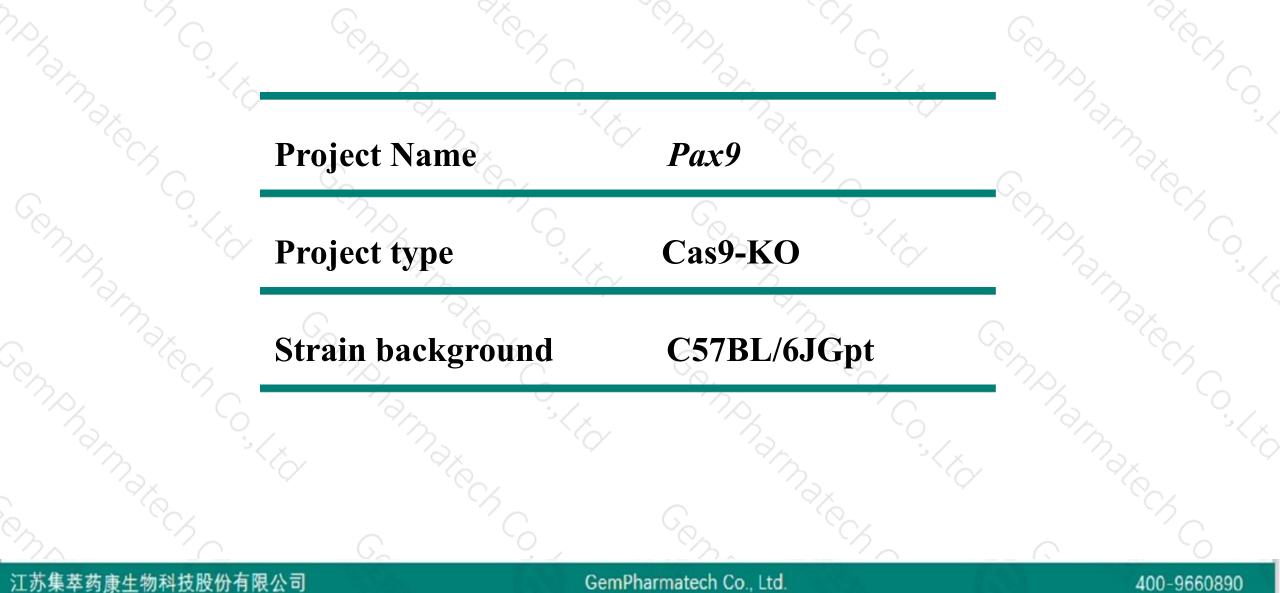


Pax9 Cas9-KO Strategy

Designer:Xiaojing Li Reviewer:JiaYu Design Date:2020-3-12

Project Overview

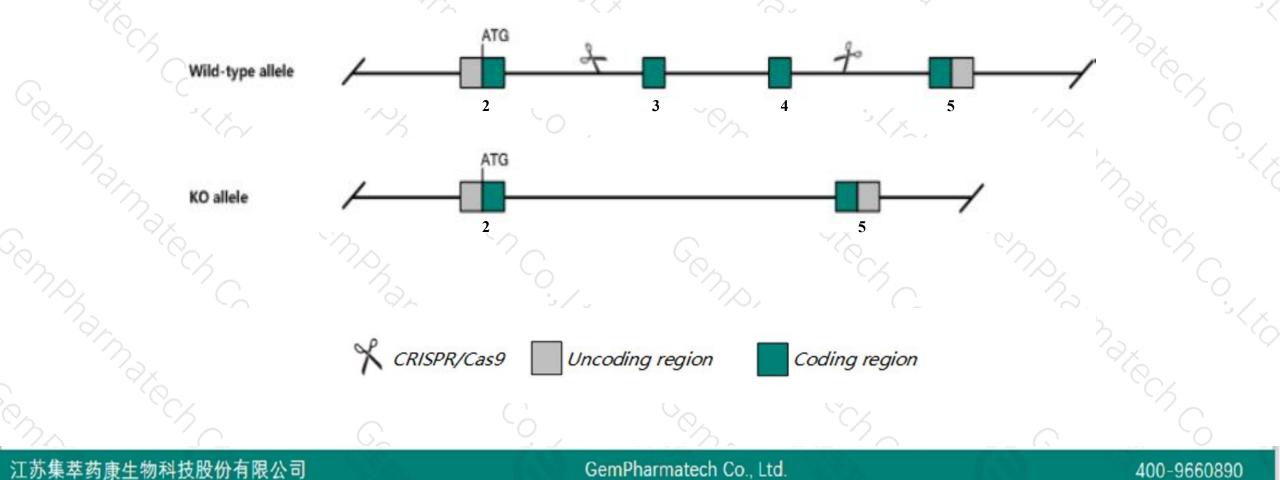




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Pax9 gene. The schematic diagram is as follows:





- The Pax9 gene has 3 transcripts. According to the structure of Pax9 gene, exon3-exon4 of Pax9-203 (ENSMUST00000153250.8) transcript is recommended as the knockout region. The region contains 770bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Pax9 gene. The brief process is as follows: CRISPR/Cas9 system



- According to the existing MGI data, Homozygous inactivation of this gene results in abnormal tooth development and absent teeth and may lead to lack of pharyngeal pouch derivatives, athymia, craniofacial and limb anomalies, a small tympanic ring, various defects of the skeleton and musculature, and neonatal lethality.
- > The knockout region is about 3KB from the 5-terminal of Gm15524 gene, which may affect its 5-terminal regulatory function.
- The Pax9 gene is located on the Chr12. 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.

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Gene information (NCBI)



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Pax9 paired box 9 [Mus musculus (house mouse)]

Gene ID: 18511, updated on 10-Mar-2020

Summary

Official Symbol	Pax9 provided by MGI						
Official Full Name	paired box 9 provided by MGI						
Primary source	MGI:MGI:97493						
See related	Ensembl:ENSMUSG0000001497						
Gene type	protein coding						
RefSeq status	REVIEWED						
Organism	Mus musculus						
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;						
	Myomorpha; Muroidea; Muridae; Mus; Mus; Mus						
Also known as	Pax-9						
Summary	This gene is a member of the paired box (PAX) family of transcription factors. Members of this gene family typically contain a paired box						
	domain, an octapeptide, and a paired-type homeodomain. These genes play critical roles during fetal development and cancer growth.	25					
	Mice lacking this gene exhibit impaired development of organs, musculature and the skeleton, including absent and abnormally	100					
	developed teeth, and neonatal lethality. Mutations in the human gene are associated with selective tooth agenesis-3. [provided by						
	RefSeq, Sep 2015]						
Expression Biased expression in thymus adult (RPKM 3.2), lung adult (RPKM 2.8) and 5 other tissues See more							
Orthologs	human all						
í O x							

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Transcript information (Ensembl)



The gene has 3 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pax9-203	ENSMUST00000153250.8	4232	<u>342aa</u>	Protein coding	CCDS25924	P47242 Q3V1K1	TSL:5 GENCODE basic APPRIS P1
Pax9-201	ENSMUST0000001538.9	4166	<u>342aa</u>	Protein coding	CCDS25924	P47242 Q3V1K1	TSL:1 GENCODE basic APPRIS P1
Pax9-202	ENSMUST00000152848.1	2309	No protein	Retained intron	2 4	2	TSL:1

The strategy is based on the design of *Pax9-203* transcript, The transcription is shown below



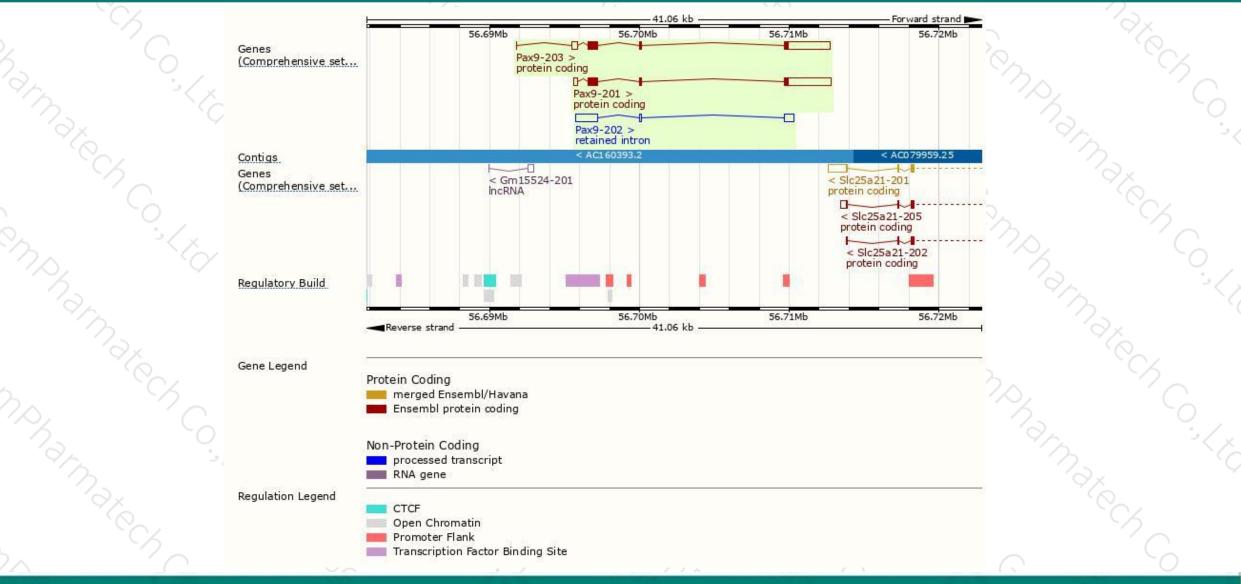
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Genomic location distribution



400-9660890



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Protein domain



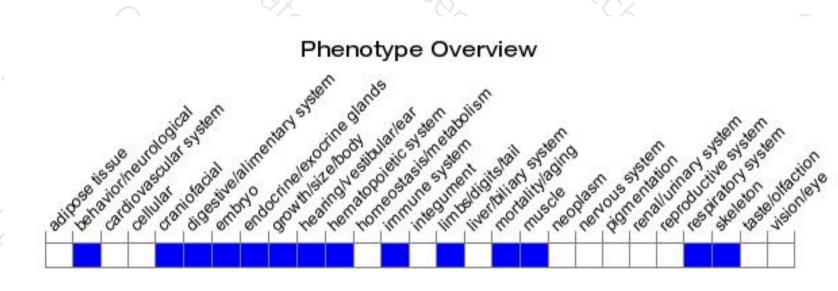
Z,	ENSMUSP00000117 Low complexity (Seg) Superfamily	Homeobax-like don	nain superfamily				20
	SMART	Paired domain					
	Prints Pfam	Paired domain Paired domain					
	PROSITE profiles	Paired domain					
2	PROSITE patterns	Paired	domain				
	PANTHER	Paired box protein PA	x.9				
	Gene3D CDD	PTHR45636 Winged helix-like DI Paired domain	VA-binding domain	superfamily			
2	All sequence SNPs/i	Sequence variants	(dbSNP and all o	ther sources)	ne ac		ò
	Variant Legend	missense vari					
	Scale bar	0 40	80	120 160	200	240 280	342
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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, Homozygous inactivation of this gene results in abnormal tooth development and absent teeth and may lead to lack of pharyngeal pouch derivatives, athymia, craniofacial and limb anomalies, a small tympanic ring, various defects of the skeleton and musculature, and neonatal lethality.

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



