

Pex14 Cas9-KO Strategy

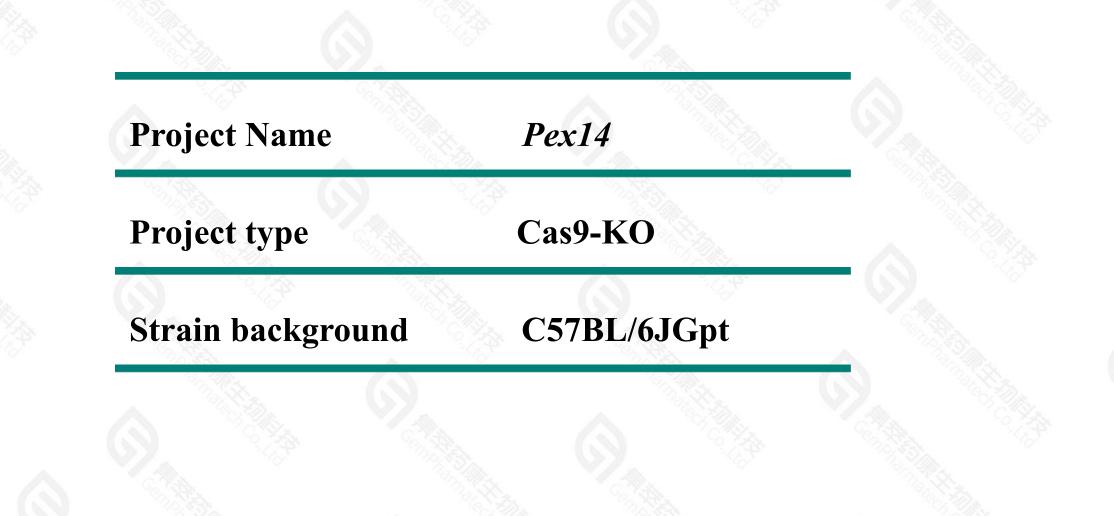
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Reviewer: Rui Xiong

Design Date: 2021-3-2

Project Overview





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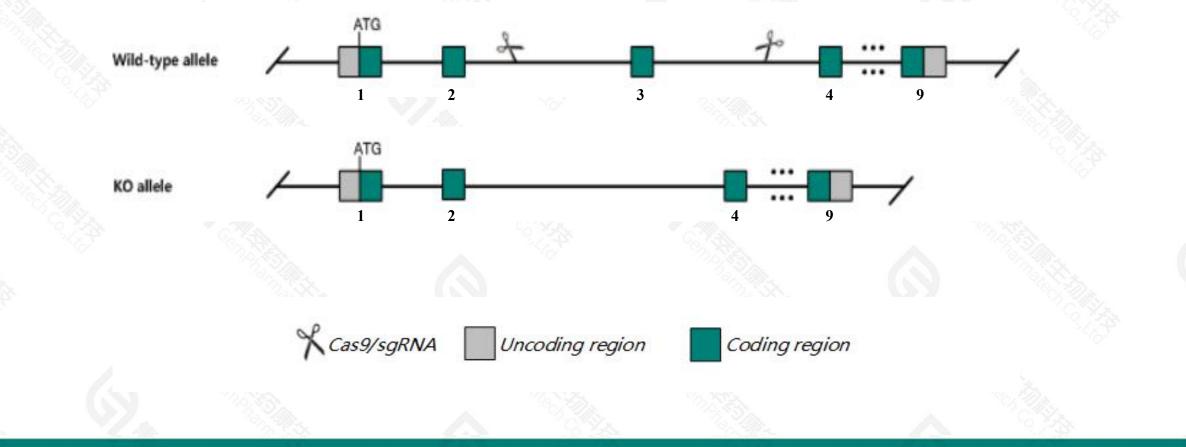
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Knockout strategy



400-9660890

This model will use CRISPR/Cas9 technology to edit the *Pex14* gene. The schematic diagram is as follows:



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> The *Pex14* gene has 5 transcripts. According to the structure of *Pex14* gene, exon3 of *Pex14*-201(ENSMUST00000103217.10) transcript is recommended as the knockout region. The region contains 85bp coding sequence. Knock out the region will result in disruption of protein function.

> In this project we use CRISPR/Cas9 technology to modify *Pex14* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA 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.



- According to the existing MGI data, homozygous disruption of this locus results in embryonic lethality.
 The *Pex14* gene is located on the Chr4. 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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Devil 4

Official Symbol	Pex14 provided by MGI
Official Full Name	peroxisomal biogenesis factor 14 provided by MGI
Primary source	MGI:MGI:1927868
See related	Ensembl:ENSMUSG0000028975
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	Pex14p, R75137
Expression	Ubiquitous expression in adrenal adult (RPKM 52.9), duodenum adult (RPKM 28.4) and 28 other tissuesSee more
Orthologs	human all

Gene information (NCBI)



Gene ID: 56273, updated on 13-Mar-2020

Summary

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Transcript information (Ensembl)



The gene has 5 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags	
Pex14-201	ENSMUST00000103217.10	2006	<u>376aa</u>	Protein coding	CCDS18950	<u>Q9R0A0</u>	TSL:1 GENCODE basic APPRIS P1	
Pex14-203	ENSMUST00000134747.1	358	<u>78aa</u>	Nonsense mediated decay	H	D6RH82	TSL:3	
Pex14-205	ENSMUST00000154860.7	989	No protein	Processed transcript	<u>2</u> 7	023	TSL:2	
Pex14-204	ENSMUST00000148203.1	514	No protein	Processed transcript	R	8. 7 8	TSL:3	
Pex14-202	ENSMUST00000128067.7	3819	No protein	Retained intron	¥.	343	TSL:1	

The strategy is based on the design of *Pex14-201* transcript, the transcription is shown below:



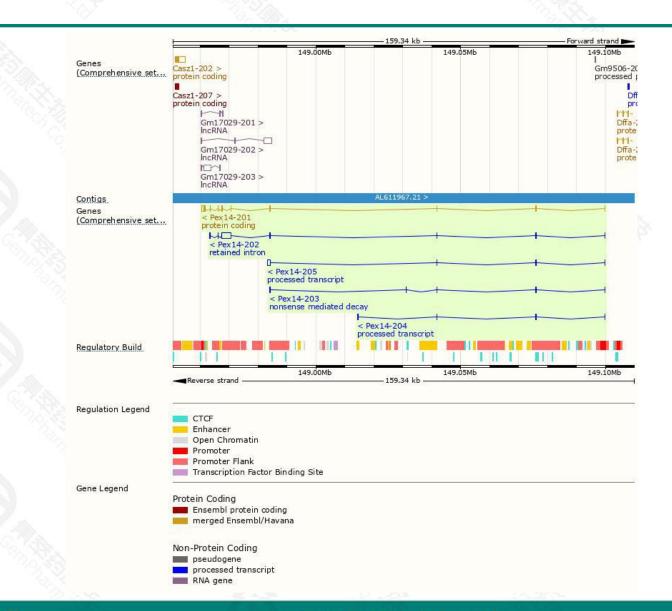
< Pex14-201 protein coding

- 139.34 kb -

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Genomic location distribution





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Protein domain

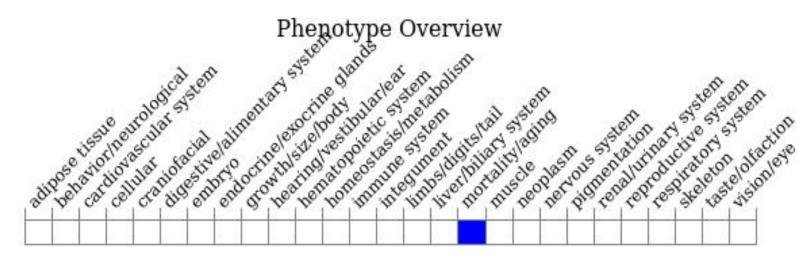


ENSMUSP00000099		k,		-		C2 44	b.			8.
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Gene3D			e protein 14 DNA-binding d	lomain superfa						
All sequence SNPs/i	Sequeno	e variants ((dbSNP and a	all other soun			1	п	10	
/ariant Legend	sync	onymous v	variant							
		40	80	120	160	200	240	280	320	37

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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 disruption of this locus results in embryonic lethality.

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If you have any questions, you are welcome to inquire. Tel: 025-5864 1534



