

Plekhg3 Cas9-CKO Strategy

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Project Overview



Project Name

Plekhg3

Project type

Cas9-CKO

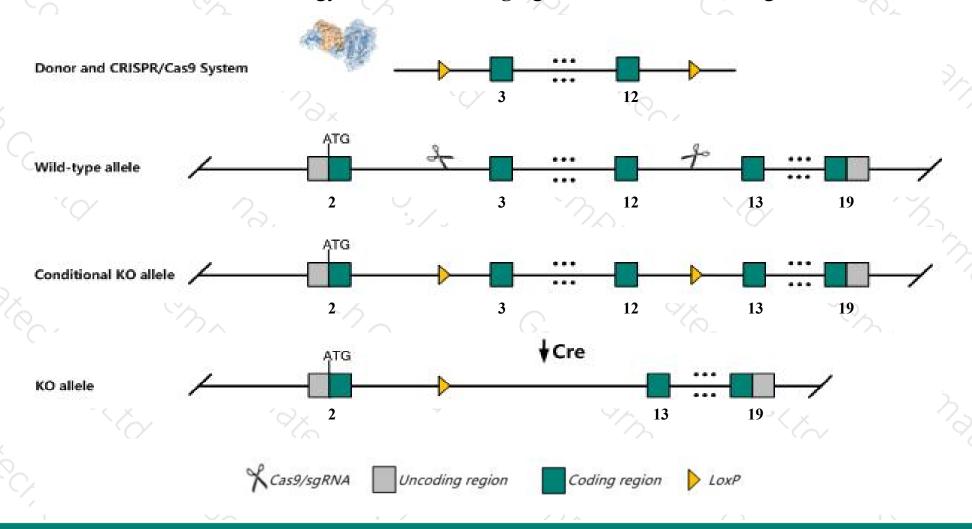
Strain background

C57BL/6JGpt

Conditional Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Plekhg3* gene. The schematic diagram is as follows:



Technical routes



- The *Plekhg3* gene has 9 transcripts. According to the structure of *Plekhg3* gene, exon3-exon12 of *Plekhg3*201(ENSMUST00000075249.5) transcript is recommended as the knockout region. The region contains 994bp coding sequence.

 Knock out the region will result in disruption of protein function.
- ➤ In this project we use CRISPR/Cas9 technology to modify *Plekhg3* gene. The brief process is as follows:sgRNA was transcribed in vitro, donor vector was constructed.Cas9, sgRNA 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 was 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.

Notice



- > The *Plekhg3* 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.
- > Transcript *Plekhg3*-205&208 may not be affected.
- ➤ The effect on transcript *Plekhg3*-202&204&209 is unknown.
- 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.

Gene information (NCBI)



Plekhg3 pleckstrin homology domain containing, family G (with RhoGef domain) member 3 [Mus musculus (house mouse)]

Gene ID: 263406, updated on 20-Mar-2020

Summary



Official Symbol Plekhq3 provided by MGI

Official Full Name pleckstrin homology domain containing, family G (with RhoGef domain) member 3 provided by MGI

Primary source MGI:MGI:2388284

See related Ensembl:ENSMUSG00000052609

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 BC030417

Expression Ubiquitous expression in kidney adult (RPKM 15.9), bladder adult (RPKM 13.1) and 25 other tissuesSee more

Orthologs <u>human</u> all

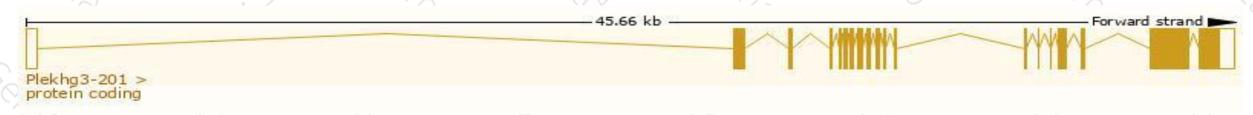
Transcript information (Ensembl)



The gene has 9 transcripts, all transcripts are shown below:

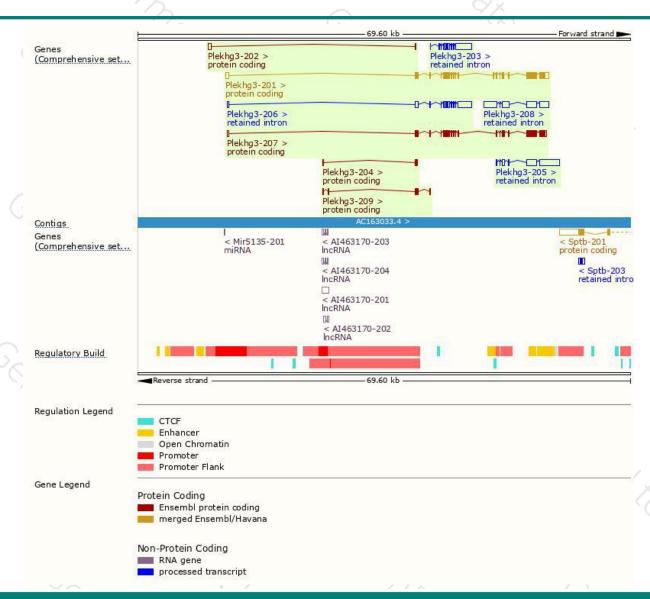
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Plekhg3-201	ENSMUST00000075249.5	5138	<u>1341aa</u>	Protein coding	CCDS25994	Q4VAC9	TSL:1 GENCODE basic APPRIS P2
Plekhg3-207	ENSMUST00000219063.1	4535	<u>1340aa</u>	Protein coding	-	Q4VAC9	TSL:5 GENCODE basic APPRIS ALT2
Plekhg3-209	ENSMUST00000219751.1	693	<u>143aa</u>	Protein coding	828	A0A1W2P7L9	CDS 3' incomplete TSL:3
Plekhg3-204	ENSMUST00000218380.1	474	<u>91aa</u>	Protein coding	-	A0A1W2P7Z4	CDS 3' incomplete TSL:3
Plekhg3-202	ENSMUST00000217730.1	449	<u>9aa</u>	Protein coding		A0A1W2P798	CDS 3' incomplete TSL:2
Plekhg3-208	ENSMUST00000219426.1	5641	No protein	Retained intron	(28)	2	TSL:1
Plekhg3-205	ENSMUST00000218427.1	4815	No protein	Retained intron	-	-	TSL:1
Plekhg3-206	ENSMUST00000218461.1	3434	No protein	Retained intron	020	2	TSL:1
Plekhg3-203	ENSMUST00000218357.1	3152	No protein	Retained intron		2	TSL:1
	* / 1 / 1	7 7 3			N 17 11		

The strategy is based on the design of *Plekhg3-201* transcript, the transcription is shown below:



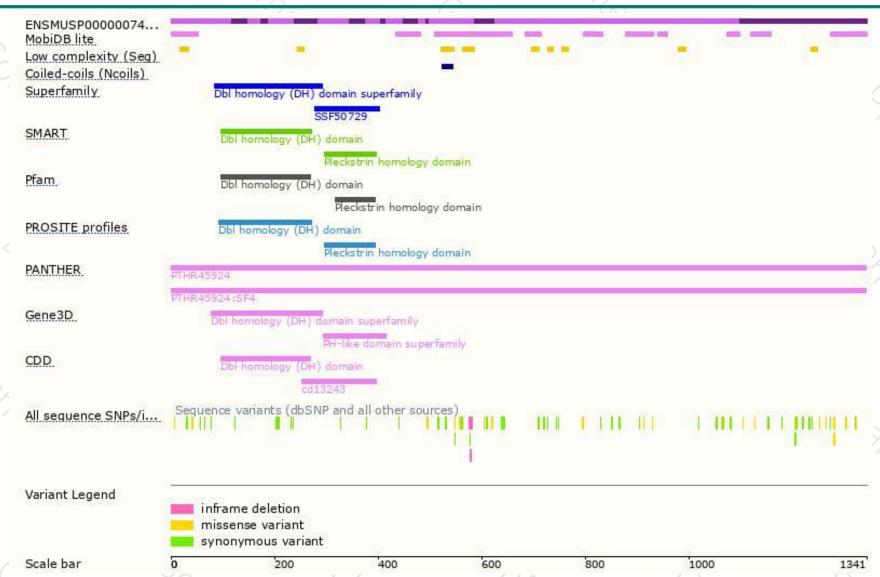
Genomic location distribution





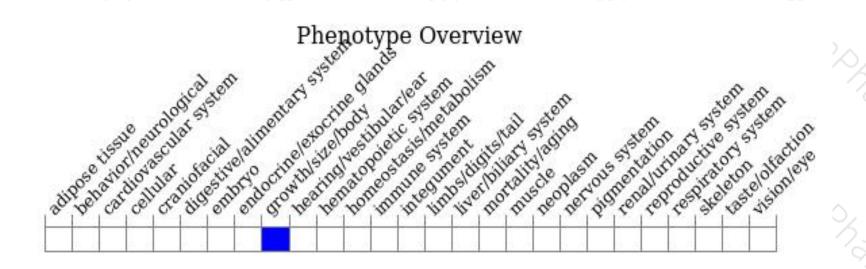
Protein domain





Mouse phenotype description(MGI)





Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).



If you have any questions, you are welcome to inquire.

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