

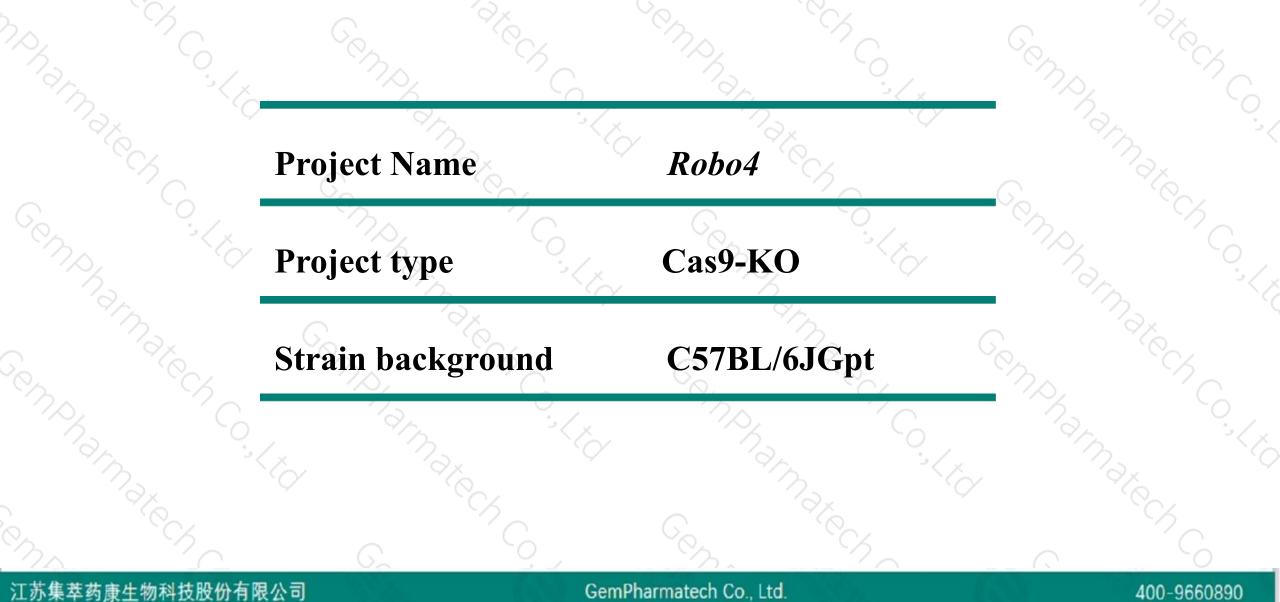
Robo4 Cas9-KO Strategy

Designer:Xueting Zhang Reviewer:Yanhua Shen Date:2020-1-15

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Project Overview

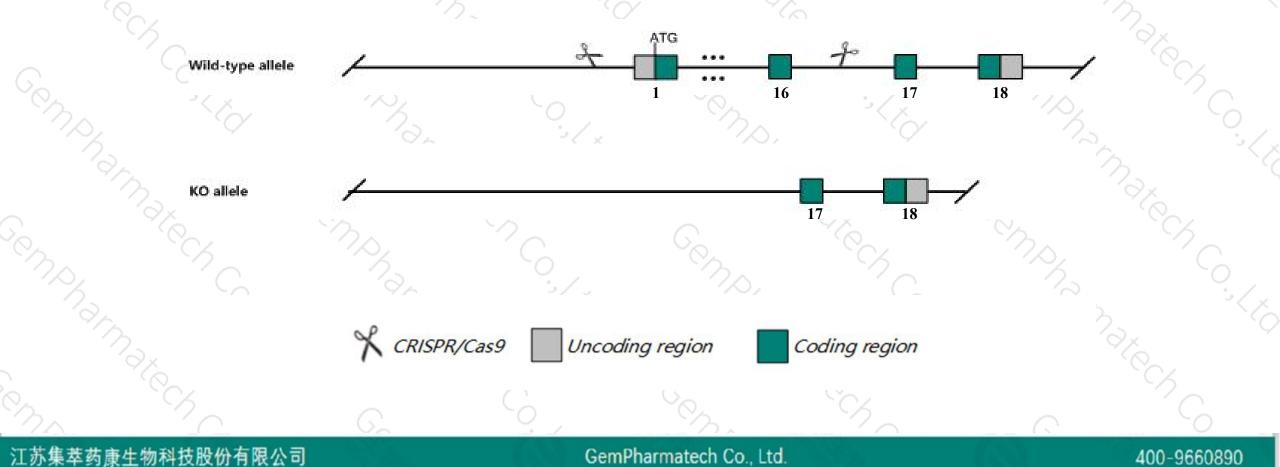




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Robo4 gene. The schematic diagram is as follows:





The Robo4 gene has 6 transcripts. According to the structure of Robo4 gene, exon1-exon16 of Robo4-205 (ENSMUST00000214185.1) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.

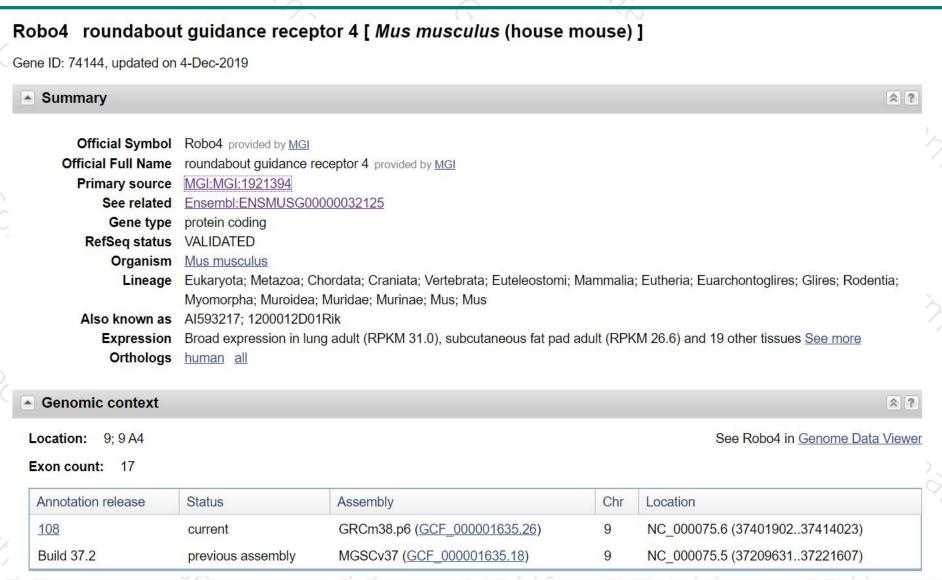
> In this project we use CRISPR/Cas9 technology to modify Robo4 gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a reporter/null allele display enhanced VEGF-induced endothelial migration, tube formation and vascular permeability, and show increased pathologic angiogenesis and vascular leak in models of oxygen-induced retinopathy and choroidal neovascularization.
 Transcript *Robo4*-204 may not be affected.
- The Robo4 gene is located on the Chr9. 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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Transcript information (Ensembl)



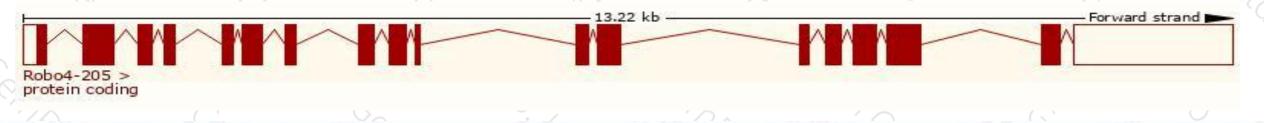
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The gene has 6 transcripts, all transcripts are shown below:

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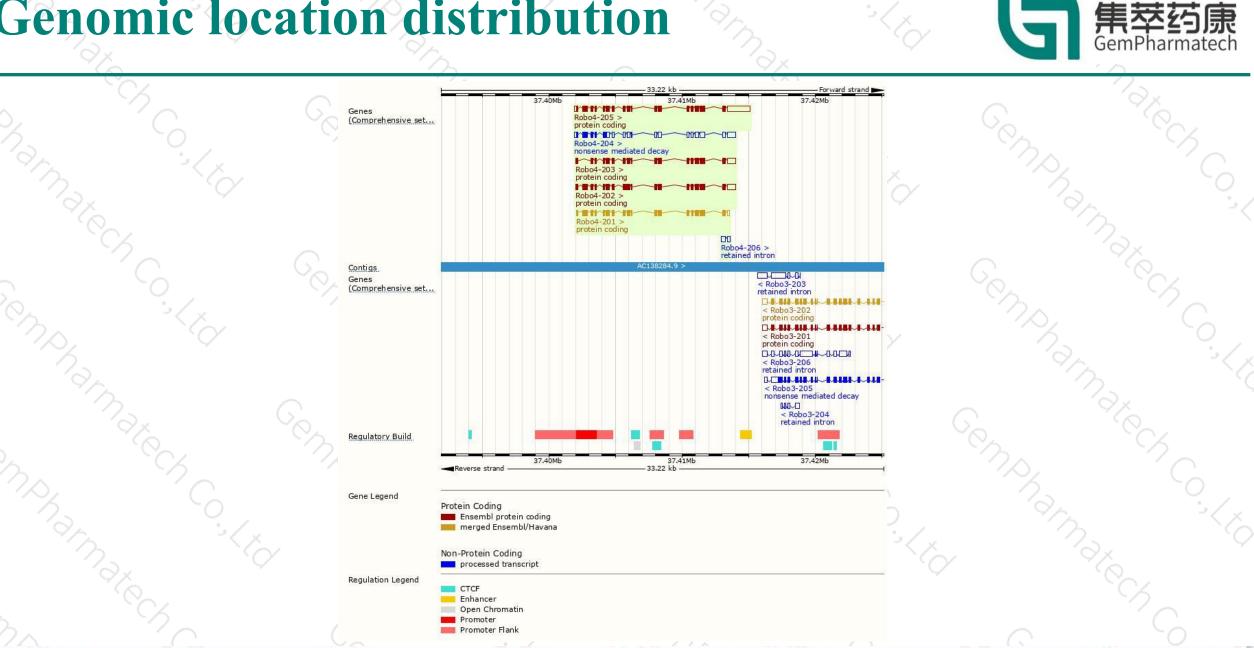
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Robo4-205	ENSMUST00000214185.1	4952	<u>1022aa</u>	Protein coding	CCDS80976	A0A1L1SUF8	TSL:1 GENCODE basic APPRIS ALT2
Robo4-201	ENSMUST00000102895.5	3226	<u>1015aa</u>	Protein coding	CCDS22977	A0A0R4J197	TSL:1 GENCODE basic APPRIS P3
Robo4-202	ENSMUST00000115046.7	3878	<u>1074aa</u>	Protein coding	2	D3Z4M4	TSL:2 GENCODE basic APPRIS ALT2
Robo4-203	ENSMUST00000115048.8	3392	<u>911aa</u>	Protein coding	2 2	E9QN68	TSL:1 GENCODE basic
Robo4-204	ENSMUST00000156972.1	3947	<u>318aa</u>	Nonsense mediated decay	-	A0A1L1SSV2	TSL:2
Robo4-206	ENSMUST00000215777.1	530	No protein	Retained intron			TSL:2

The strategy is based on the design of Robo4-205 transcript, The transcription is shown below



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Genomic location distribution



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Protein domain

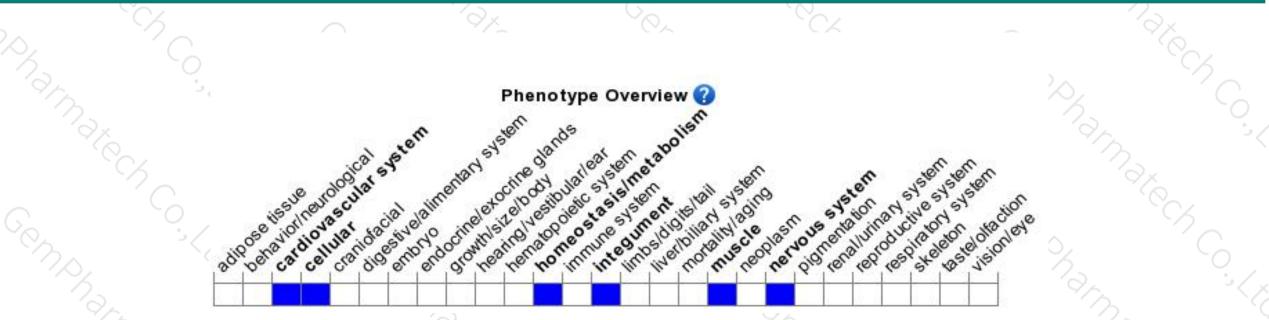


noparmater.	ENSMUSP00000150 MobiDB lite Low complexity (Seg) Cleavage site (Sign Superfamily	Fibronectin type III superfamily	
n na k	SMART	Immunoglobulin-like domain superfamily Immunoglobulin subtype 2) '''\
	Pfam	Immunoglobulin subtype Fibronectin type III PF13927 Immunoglobulin I-set Fibronectin type III	
Cemphan	PROSITE profiles	Immunoglobulin-like domain	
n show	PANTHER	Fibronectin type III	
a and	Gene3D CDD	PTHR44170 :SF11 Immunoglobulin-like fold Fibronectin type III	
Sons,	All sequence SNPs/i	Sequence variants (dbSNP and all other sources)	
Chipharnare Received	Variant Legend	frameshift variant missense variant splice region variant synonymous variant	
	Scale bar	0 100 200 300 400 500 600 700 800 900 1022	
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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 reporter/null allele display enhanced VEGF-induced endothelial migration, tube formation and vascular permeability, and show increased pathologic angiogenesis and vascular leak in models of oxygen-induced retinopathy and choroidal neovascularization.

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



