

Rbm5 Cas9-CKO Strategy

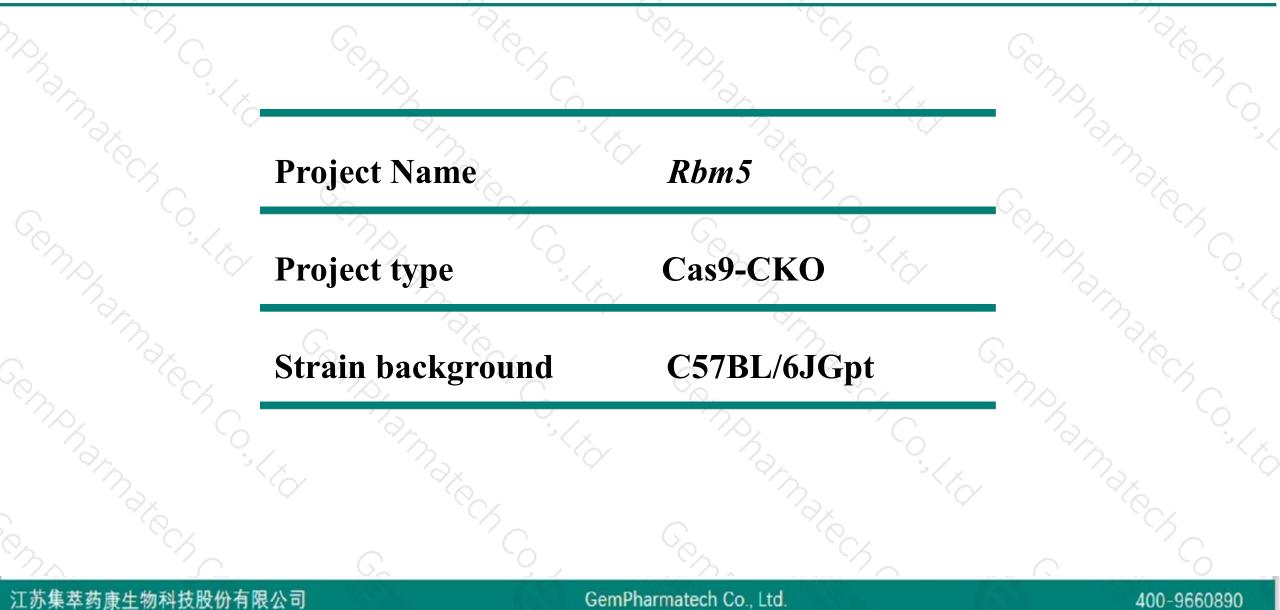
Designer: Lingyan Wu

Reviewer: Rui Xiong

Design Date: 2020-6-3

Project Overview



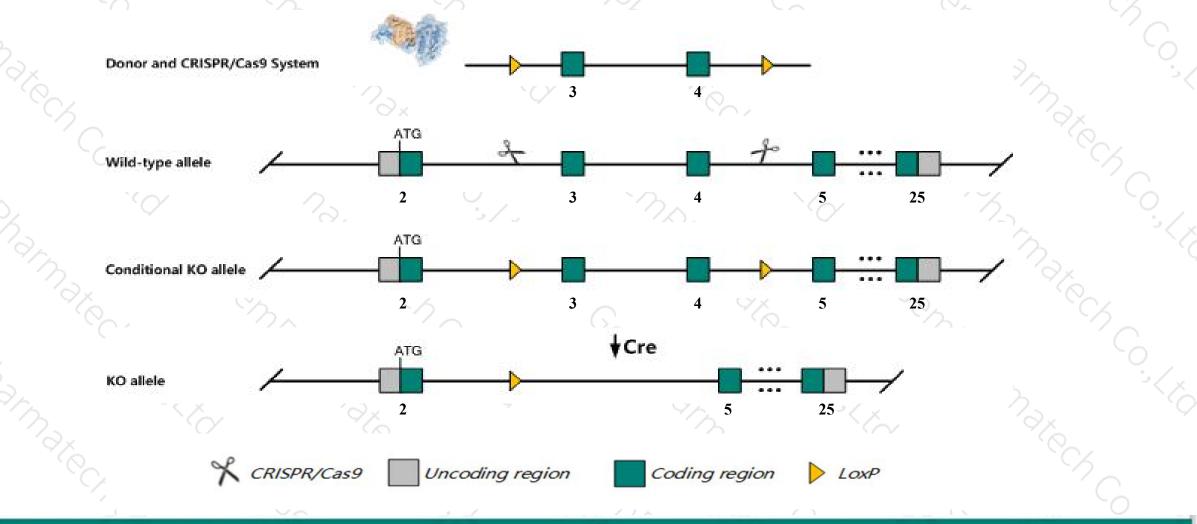


Conditional Knockout strategy



400-9660890

This model will use CRISPR/Cas9 technology to edit the *Rbm5* gene. The schematic diagram is as follows:



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The *Rbm5* gene has 24 transcripts. According to the structure of *Rbm5* gene, exon3-exon4 of *Rbm5-214* (ENSMUST00000182659.7) transcript is recommended as the knockout region. The region contains 322bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Rbm5* 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 an enu-induced allele exhibit male infertility with azoospermia, male germ cell apoptosis, round spermatid arrest and spermatid differentiation arrest.
- > Transcript *Rbm5-205&222* may not be affected.
- The *Rbm5* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)



\$?

Rbm5 RNA binding motif protein 5 [Mus musculus (house mouse)]

Gene ID: 83486, updated on 20-Mar-2020

Summary

Rbm5 provided by MGI
RNA binding motif protein 5 provided by <u>MGI</u>
MGI:MGI:1933204
Ensembl:ENSMUSG0000032580
protein coding
VALIDATED
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
D030069N10Rik
Ubiquitous expression in CNS E14 (RPKM 44.1), CNS E11.5 (RPKM 42.8) and 28 other tissuesSee more
human all

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Transcript information (Ensembl)



The gene has 24 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags	
Rbm5-214	ENSMUST00000182659.7	3205	<u>815aa</u>	Protein coding	CCD523506	Q91YE7	TSL:1 GENCODE basic APPRIS P2	
Rbm5-201	ENSMUST0000035199.12	3064	<u>814aa</u>	Protein coding	1940	<u>Q91YE7</u>	TSL:5 GENCODE basic APPRIS ALT1	
Rbm5-204	ENSMUST00000182022.7	869	<u>137aa</u>	Protein coding	121	<u>S4R1V5</u>	CDS 3' incomplete TSL:5	
Rbm5-208	ENSMUST00000182304.7	850	<u>251aa</u>	Protein coding		<u>S4R1U7</u>	CDS 3' incomplete TSL:3	
Rbm5-205	ENSMUST00000182026.1	835	<u>154aa</u>	Protein coding	(1 -)	<u>S4R273</u>	CDS 5' incomplete TSL:2	
Rbm5-218	ENSMUST00000183248.2	781	<u>115aa</u>	Protein coding	152	<u>S4R1N4</u>	CDS 3' incomplete TSL:5	
Rbm5-222	ENSMUST00000194400.1	322	<u>101aa</u>	Protein coding		A0A0A6YY86	CDS 5' incomplete TSL:3	
Rbm5-210	ENSMUST00000182371.7	2986	<u>150aa</u>	Nonsense mediated decay	-	<u>54R184</u>	TSL:1	
Rbm5-211	ENSMUST00000182421.7	1704	<u>115aa</u>	Nonsense mediated decay	-	<u>S4R2T4</u>	TSL:1	
Rbm5-221	ENSMUST00000193342.5	896	<u>175aa</u>	Nonsense mediated decay	1.4	A0A0A6YX44	CDS 5' incomplete TSL:3	
Rbm5-220	ENSMUST00000192130.5	784	<u>150aa</u>	Nonsense mediated decay	121	<u>S4R184</u>	TSL:3	
Rbm5-219	ENSMUST00000183307.7	6321	No protein	Retained intron		-	TSL:1	
Rbm5-215	ENSMUST00000182792.1	4718	No protein	Retained intron	(1 4)	×	TSL:NA	
Rbm5-224	ENSMUST00000194801.5	2691	No protein	Retained intron	152		TSL:1	
Rbm5-203	ENSMUST00000182007.7	1939	No protein	Retained intron			TSL:1	
Rbm5-202	ENSMUST00000181993.1	1775	No protein	Retained intron	12	-	TSL:NA	
Rbm5-213	ENSMUST00000182518.1	1272	No protein	Retained intron	1.51		TSL:1	
Rbm5-206	ENSMUST00000182073.7	897	No protein	Retained intron	-	-	TSL:2	
Rbm5-209	ENSMUST00000182332.1	793	No protein	Retained intron	121	2	TSL:2	
Rbm5-207	ENSMUST00000182215.1	631	No protein	Retained intron		-	TSL:3	
Rbm5-212	ENSMUST00000182422.6	600	No protein	Retained intron	1940	2	TSL:2	
Rbm5-217	ENSMUST00000182856.7	539	No protein	Retained intron	151		TSL:3	
Rbm5-223	ENSMUST00000194682.1	502	No protein	Retained intron	1.00		TSL:3	
Rbm5-216	ENSMUST00000182836.1	500	No protein	Retained intron	121	2	TSL:3	

The strategy is based on the design of *Rbm5-214* transcript, the transcription is shown below:

< Rbm5-214 protein coding

Reverse strand -

— 30.63 kb -

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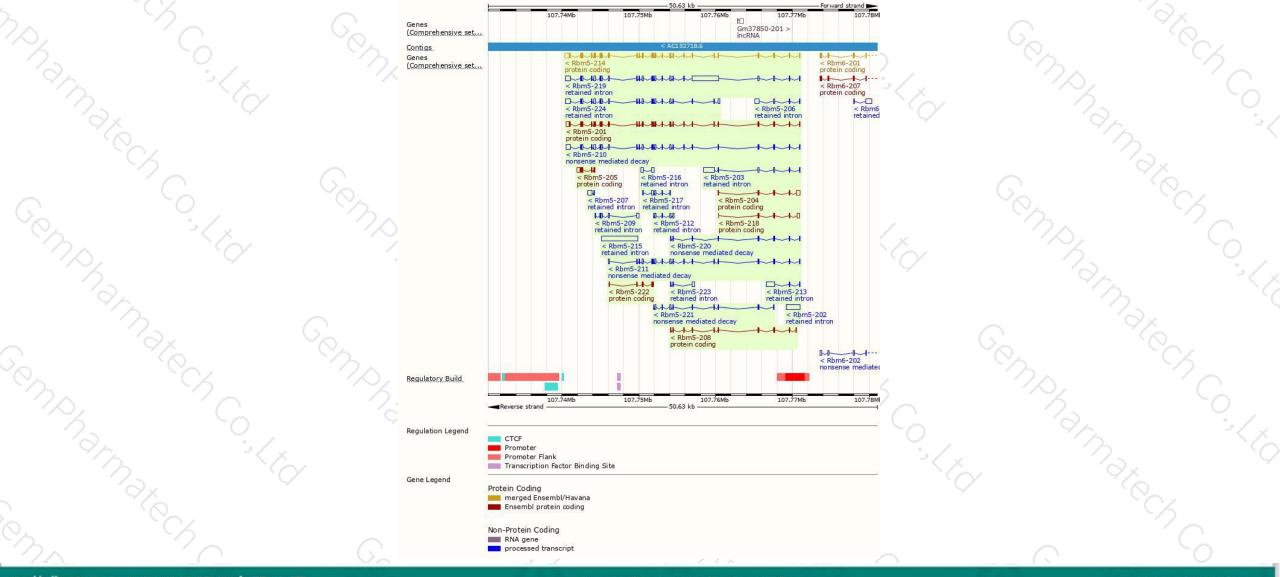
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Genomic location distribution



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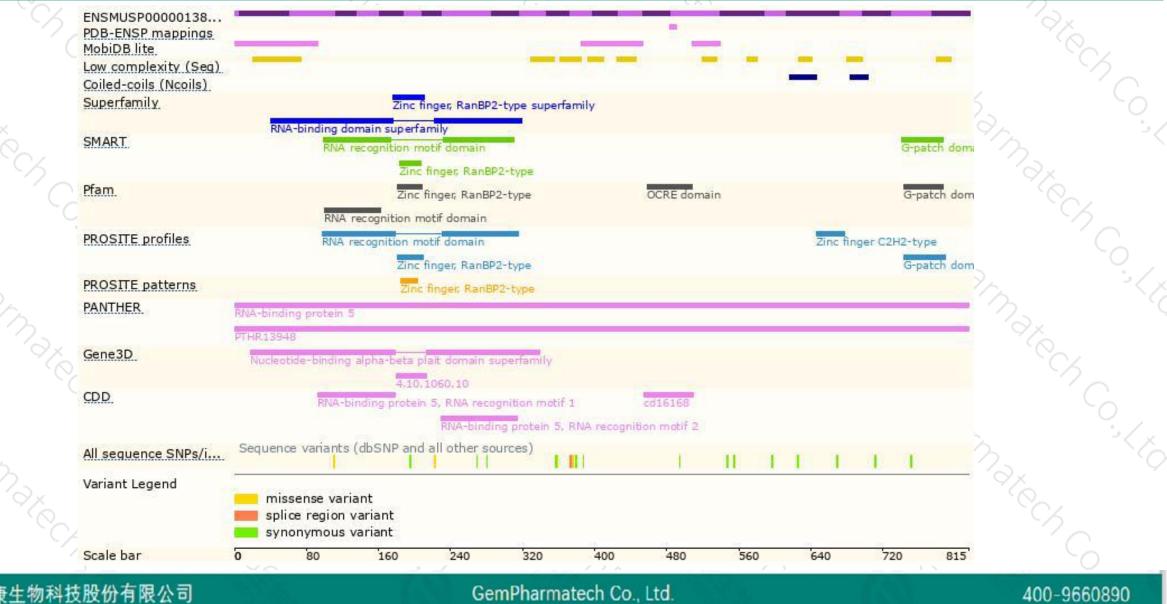


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Protein domain

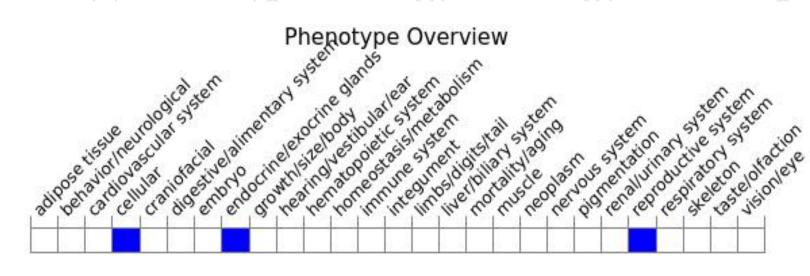




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Mouse phenotype description(MGI)





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 an ENU-induced allele exhibit male infertility with azoospermia, male germ cell apoptosis, round spermatid arrest and spermatid differentiation arrest.



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



