

# *Rhbdfl* Cas9-CKO Strategy

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**Reviewer: Shuang Zhang**

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# Project Overview

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**Project Name**

*Rhbdf1*

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**Project type**

**Cas9-CKO**

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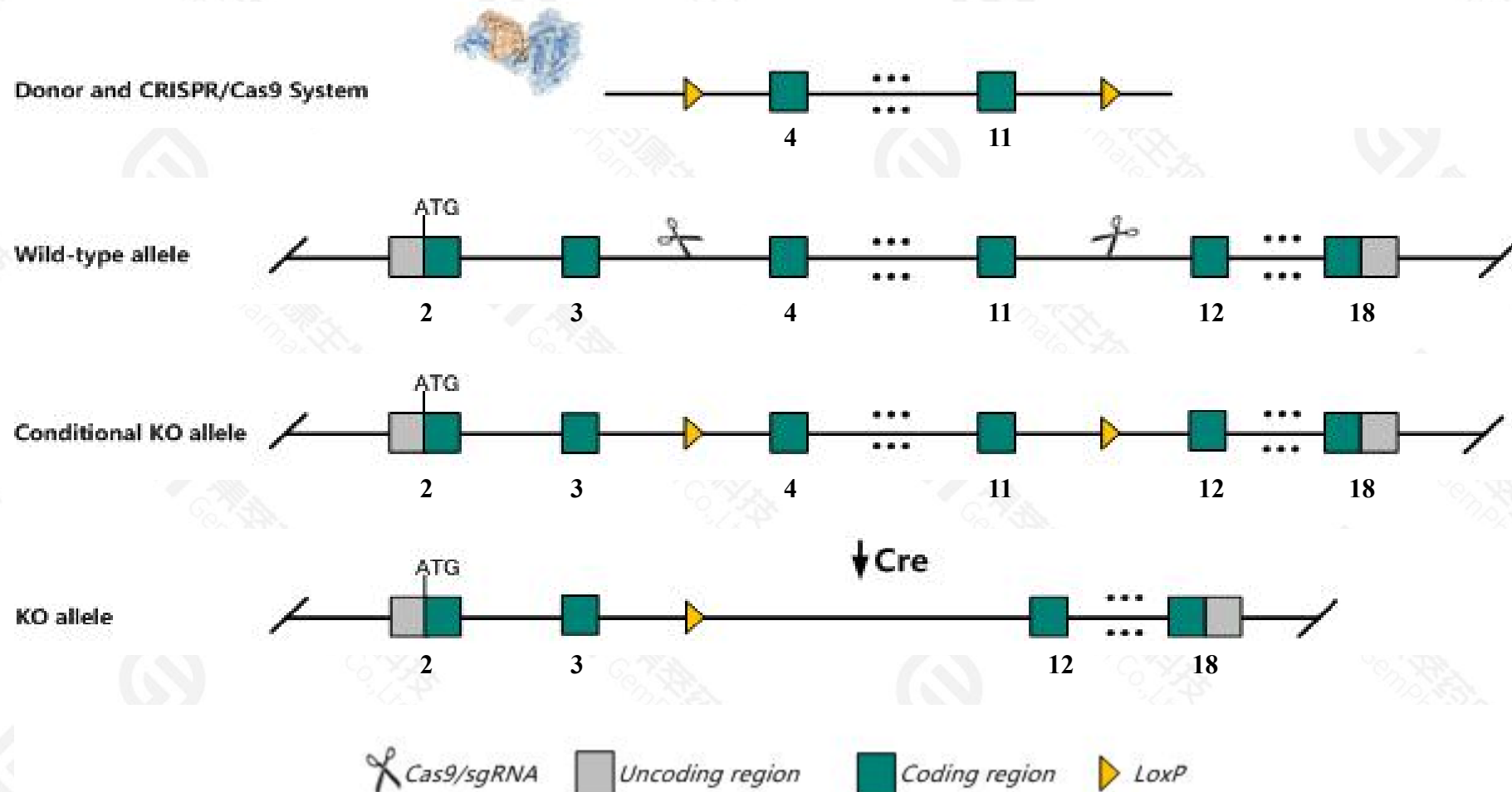
**Strain background**

**C57BL/6JGpt**

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# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rhbdf1* gene. The schematic diagram is as follows:



- The *Rhbdf1* gene has 9 transcripts. According to the structure of *Rhbdf1* gene, exon4-exon11 of *Rhbdf1*-201(ENSMUST00000020524.15) transcript is recommended as the knockout region. The region contains 1312bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rhbdf1* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor 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.



- According to the existing MGI data, homozygotes for a null allele show pleiotropic phenotypes and postnatal lethality largely dependent on the genetic background. Observed defects range from small size, reduced fat mass, and brain haemorrhages to small lymph organs, thrombosis, abnormal pancreatic acini, and behavioral deficits.
- The *Rhbdf1* gene is located on the Chr11. 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.
- Transcripts 206 and 207 will not be disrupted.
- 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)

## Rhbdf1 rhomboid 5 homolog 1 [Mus musculus (house mouse)]

Gene ID: 13650, updated on 7-Mar-2021

### Summary



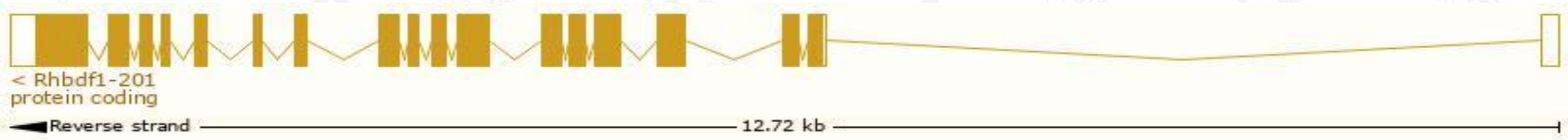
<b>Official Symbol</b>	Rhbdf1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	rhomboid 5 homolog 1 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:104328</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000020282</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	C16ORF8, Di, Dis, Dist, Dist1, Egfr, Egfr-rs, mKIAA4242
<b>Expression</b>	Ubiquitous expression in ovary adult (RPKM 45.8), lung adult (RPKM 41.4) and 26 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

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

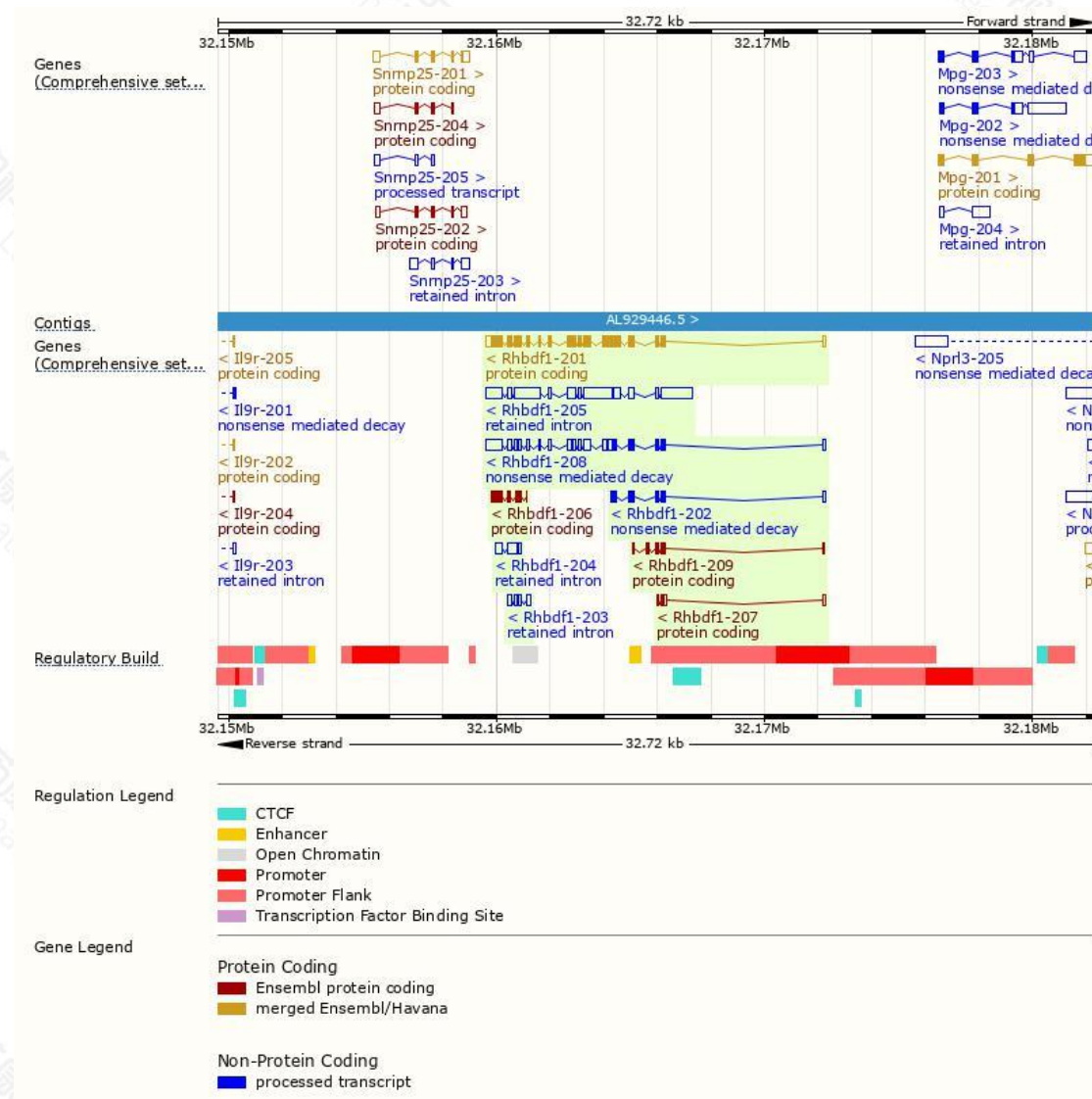
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rhbdf1-201	<a href="#">ENSMUST00000020524.15</a>	2946	<a href="#">856aa</a>	Protein coding	<a href="#">CCDS24519</a>		TSL:1 , GENCODE basic , APPRIS P1 ,
Rhbdf1-206	<a href="#">ENSMUST00000143988.2</a>	696	<a href="#">231aa</a>	Protein coding	-		CDS 5' incomplete , TSL:5 ,
Rhbdf1-209	<a href="#">ENSMUST00000150381.2</a>	509	<a href="#">136aa</a>	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Rhbdf1-207	<a href="#">ENSMUST00000144902.2</a>	353	<a href="#">57aa</a>	Protein coding	-		CDS 3' incomplete , TSL:3 ,
Rhbdf1-208	<a href="#">ENSMUST00000146179.8</a>	2805	<a href="#">168aa</a>	Nonsense mediated decay	-		TSL:1 ,
Rhbdf1-202	<a href="#">ENSMUST00000132578.8</a>	708	<a href="#">168aa</a>	Nonsense mediated decay	-		TSL:5 ,
Rhbdf1-205	<a href="#">ENSMUST00000143036.8</a>	5089	No protein	Retained intron	-		TSL:2 ,
Rhbdf1-204	<a href="#">ENSMUST00000142274.2</a>	709	No protein	Retained intron	-		TSL:3 ,
Rhbdf1-203	<a href="#">ENSMUST00000137125.2</a>	490	No protein	Retained intron	-		TSL:5 ,

The strategy is based on the design of *Rhbdf1-201* transcript,the transcription is shown below:





# Genomic location distribution

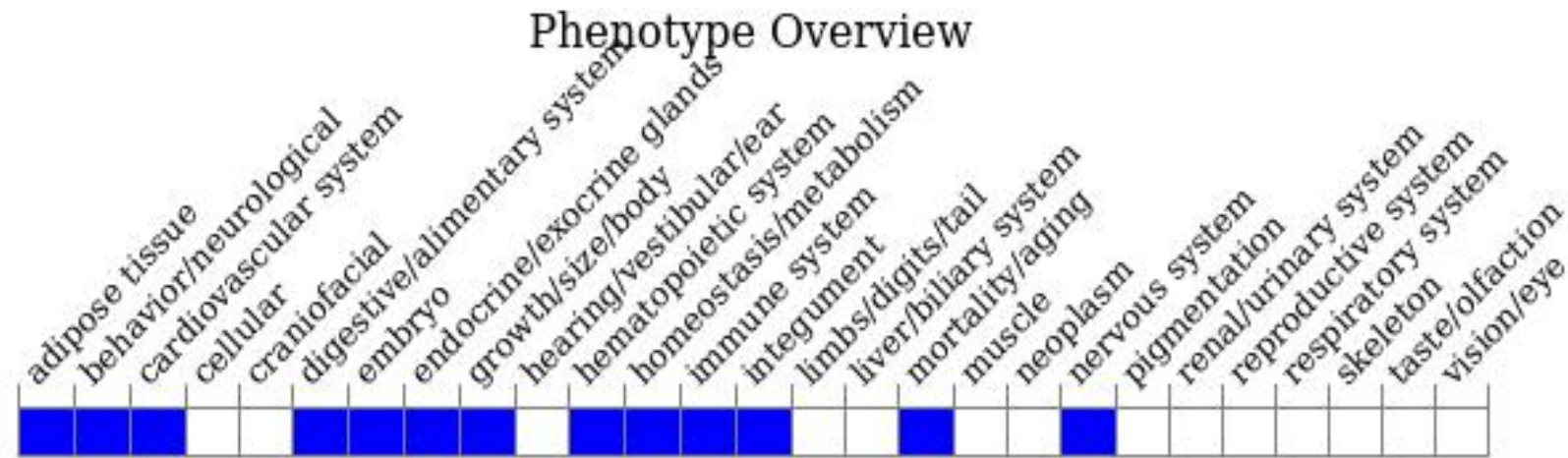




# Protein domain



# Mouse phenotype description(MGI )



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

According to the existing MGI data, homozygotes for a null allele show pleiotropic phenotypes and postnatal lethality largely dependent on the genetic background. Observed defects range from small size, reduced fat mass, and brain haemorrhages to small lymph organs, thrombosis, abnormal pancreatic acini, and behavioral deficits.

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

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