

# ***Rreb1*** Cas9-KO Strategy

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# Project Overview

**Project Name**

***Rreb1***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rreb1* gene. The schematic diagram is as follows:



- The *Rreb1* gene has 11 transcripts. According to the structure of *Rreb1* gene, exon5-exon6 of *Rreb1*-207 (ENSMUST00000128570.8) transcript is recommended as the knockout region. The region contains 254bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rreb1* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Rreb1* gene is located on the Chr13. 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.



# Gene information (NCBI)

## Rreb1 ras responsive element binding protein 1 [Mus musculus (house mouse)]

Gene ID: 68750, updated on 31-Jan-2019

### Summary



<b>Official Symbol</b>	Rreb1 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	ras responsive element binding protein 1 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2443664</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000039087</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>	1110037N09Rik, AA414966, B930013M22Rik
<b>Expression</b>	Ubiquitous expression in adrenal adult (RPKM 5.6), colon adult (RPKM 5.2) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

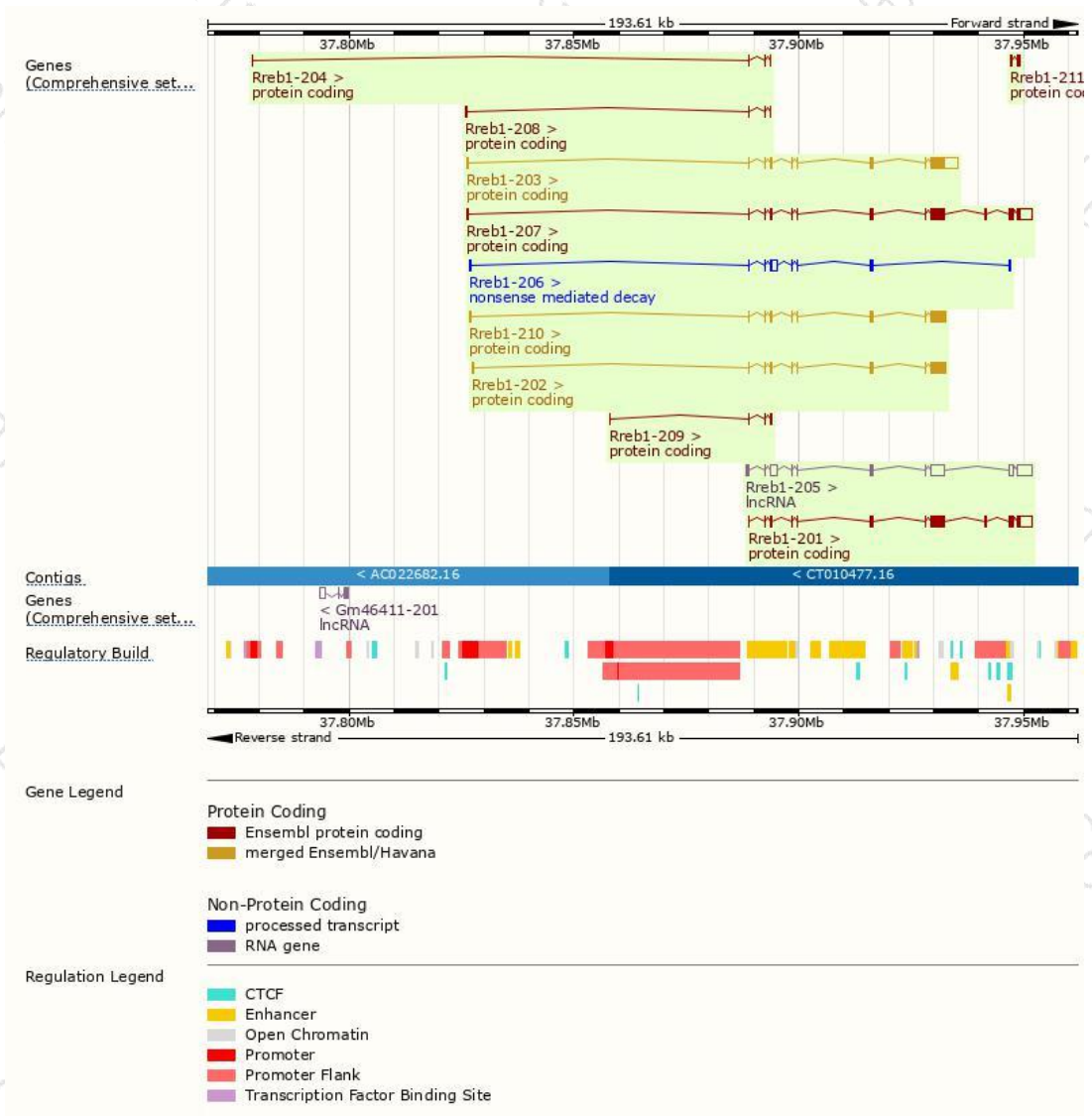
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Rreb1-207	<a href="#">ENSMUST00000128570.8</a>	8436	<a href="#">1754aa</a>	Protein coding	<a href="#">CCDS49238</a>	<a href="#">Q3UH06</a>	TSL:5 GENCODE basic APPRIS P1
Rreb1-201	<a href="#">ENSMUST00000037232.7</a>	8395	<a href="#">1754aa</a>	Protein coding	<a href="#">CCDS49238</a>	<a href="#">Q3UH06</a>	TSL:5 GENCODE basic APPRIS P1
Rreb1-203	<a href="#">ENSMUST00000110238.9</a>	7437	<a href="#">1291aa</a>	Protein coding	<a href="#">CCDS36634</a>	<a href="#">Q3UH06</a>	TSL:1 GENCODE basic
Rreb1-202	<a href="#">ENSMUST00000110237.8</a>	4617	<a href="#">1291aa</a>	Protein coding	<a href="#">CCDS36634</a>	<a href="#">Q3UH06</a>	TSL:1 GENCODE basic
Rreb1-210	<a href="#">ENSMUST00000149745.7</a>	4320	<a href="#">1291aa</a>	Protein coding	<a href="#">CCDS36634</a>	<a href="#">Q3UH06</a>	TSL:1 GENCODE basic
Rreb1-211	<a href="#">ENSMUST00000162849.1</a>	1053	<a href="#">320aa</a>	Protein coding	-	<a href="#">F6UB40</a>	CDS 5' incomplete TSL:2
Rreb1-209	<a href="#">ENSMUST00000138110.7</a>	512	<a href="#">33aa</a>	Protein coding	-	<a href="#">B8JJE4</a>	CDS 3' incomplete TSL:3
Rreb1-204	<a href="#">ENSMUST00000122842.7</a>	445	<a href="#">12aa</a>	Protein coding	-	<a href="#">B8JJE5</a>	CDS 3' incomplete TSL:3
Rreb1-208	<a href="#">ENSMUST00000138043.7</a>	342	<a href="#">4aa</a>	Protein coding	-	-	CDS 3' incomplete TSL:2
Rreb1-206	<a href="#">ENSMUST00000124373.7</a>	2376	<a href="#">67aa</a>	Nonsense mediated decay	-	<a href="#">Q3UHQ4</a>	TSL:5
Rreb1-205	<a href="#">ENSMUST00000124268.7</a>	9702	No protein	lncRNA	-	-	TSL:1

The strategy is based on the design of *Rreb1-207* transcript,The transcription is shown below



# Genomic location distribution

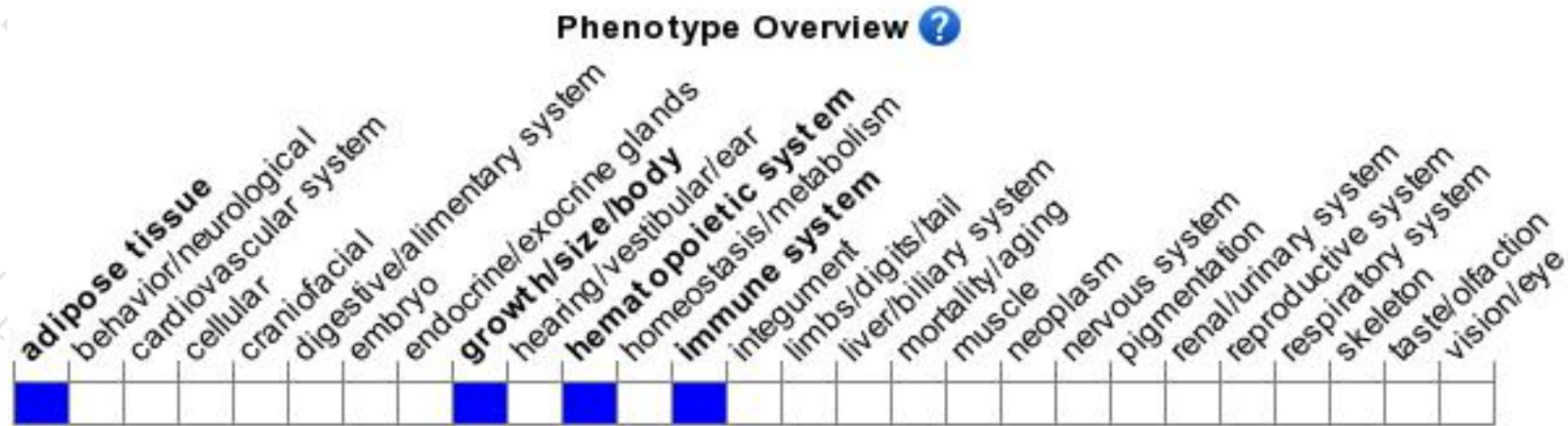




# Protein domain



# 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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