

# *Rbpms* Cas9-KO Strategy

**Designer:**

**Daohua Xu**

**Reviewer:**

**Huimin Su**

**Design Date:**

**2019-11-22**

# Project Overview

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**Project Name**

*Rbpms*

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**Project type**

**Cas9-KO**

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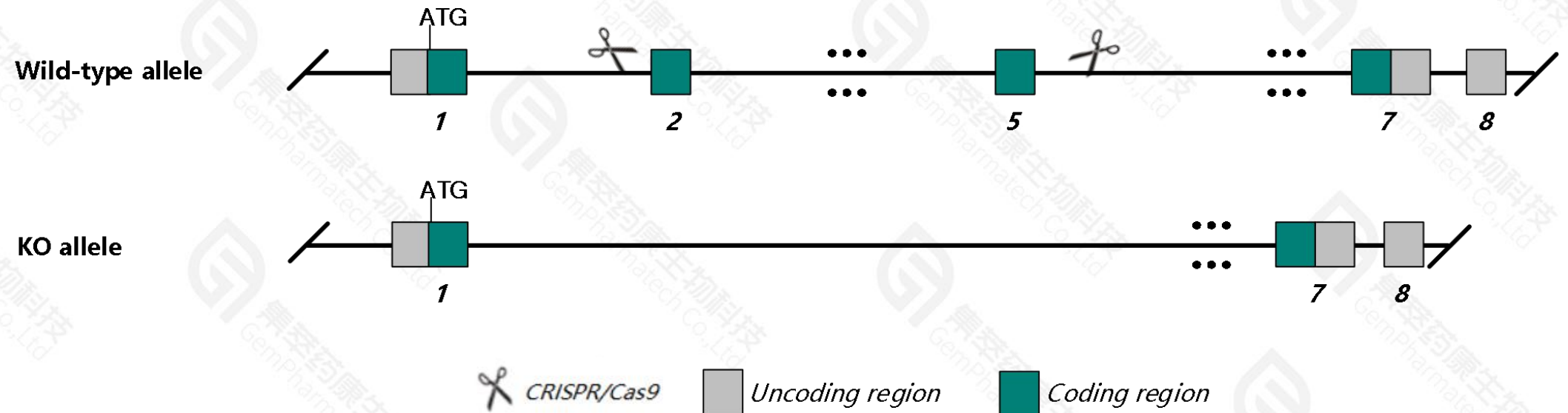
**Strain background**

**C57BL/6JGpt**

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# Knockout strategy

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



- The *Rbpms* gene has 15 transcripts. According to the structure of *Rbpms* gene, exon2-exon5 of *Rbpms*-203(ENSMUST00000053251.12) transcript is recommended as the knockout region. The region contains 331bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Rbpms* gene. The brief process is as follows: CRISPR/Cas9 system 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 *Rbpms* gene is located on the Chr8. 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.

## Rbpms RNA binding protein gene with multiple splicing [Mus musculus (house mouse)]

Gene ID: 19663, updated on 29-Jan-2021

### Summary



**Official Symbol** Rbpms provided by [MGI](#)

**Official Full Name** RNA binding protein gene with multiple splicing provided by [MGI](#)

**Primary source** [MGI:MGI:1334446](#)

**See related** [Ensembl:ENSMUSG00000031586](#)

**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** 2010300K22Rik, 2700019M19Rik, AU017537, RBP-MS, herm, hermes

**Expression** Broad expression in ovary adult (RPKM 24.2), bladder adult (RPKM 22.5) and 20 other tissues [See more](#)

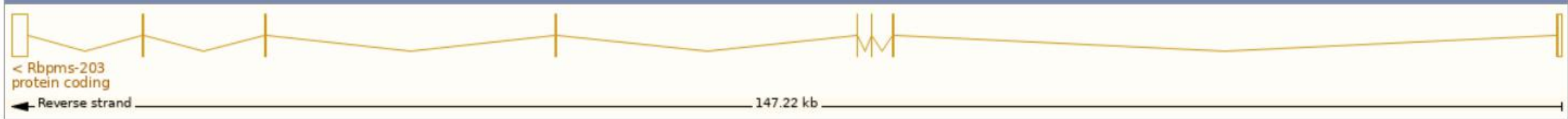
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

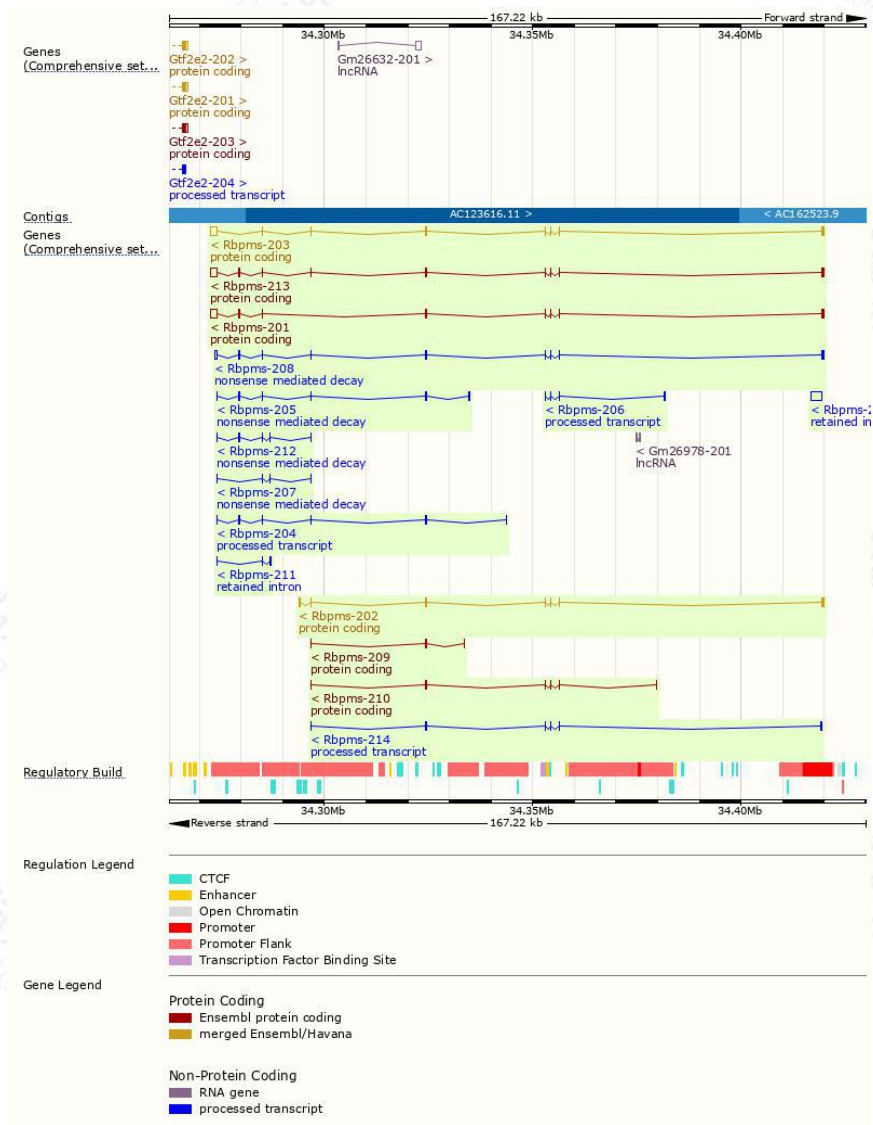
The gene has 15 transcripts,all transcripts are shown below:

| Name      | Transcript ID                         | bp   | Protein               | Biotype                 | CCDS                      | UniProt | Flags                                 |
|-----------|---------------------------------------|------|-----------------------|-------------------------|---------------------------|---------|---------------------------------------|
| Rbpms-213 | <a href="#">ENSMUST00000191473.7</a>  | 2547 | <a href="#">197aa</a> | Protein coding          | <a href="#">CCDS40317</a> |         | TSL:1 , GENCODE basic , APPRIS ALT1 , |
| Rbpms-203 | <a href="#">ENSMUST00000053251.12</a> | 2466 | <a href="#">197aa</a> | Protein coding          | <a href="#">CCDS40317</a> |         | TSL:1 , GENCODE basic , APPRIS ALT1 , |
| Rbpms-201 | <a href="#">ENSMUST00000033994.15</a> | 2375 | <a href="#">191aa</a> | Protein coding          | <a href="#">CCDS72112</a> |         | TSL:1 , GENCODE basic ,               |
| Rbpms-202 | <a href="#">ENSMUST00000033995.14</a> | 1039 | <a href="#">220aa</a> | Protein coding          | <a href="#">CCDS40318</a> |         | TSL:1 , GENCODE basic , APPRIS P4 ,   |
| Rbpms-210 | <a href="#">ENSMUST00000183088.2</a>  | 592  | <a href="#">159aa</a> | Protein coding          | -                         |         | CDS 3' incomplete , TSL:5 ,           |
| Rbpms-209 | <a href="#">ENSMUST00000183062.2</a>  | 459  | <a href="#">64aa</a>  | Protein coding          | -                         |         | CDS 3' incomplete , TSL:3 ,           |
| Rbpms-208 | <a href="#">ENSMUST00000182987.8</a>  | 1385 | <a href="#">197aa</a> | Nonsense mediated decay | <a href="#">CCDS40317</a> |         | TSL:1 ,                               |
| Rbpms-205 | <a href="#">ENSMUST00000182256.8</a>  | 865  | <a href="#">93aa</a>  | Nonsense mediated decay | -                         |         | TSL:3 ,                               |
| Rbpms-212 | <a href="#">ENSMUST00000183336.8</a>  | 549  | <a href="#">70aa</a>  | Nonsense mediated decay | -                         |         | CDS 5' incomplete , TSL:3 ,           |
| Rbpms-207 | <a href="#">ENSMUST00000182926.8</a>  | 405  | <a href="#">58aa</a>  | Nonsense mediated decay | -                         |         | CDS 5' incomplete , TSL:3 ,           |
| Rbpms-204 | <a href="#">ENSMUST00000182184.8</a>  | 643  | No protein            | Processed transcript    | -                         |         | TSL:1 ,                               |
| Rbpms-214 | <a href="#">ENSMUST00000231786.2</a>  | 516  | No protein            | Processed transcript    | -                         |         |                                       |
| Rbpms-206 | <a href="#">ENSMUST00000182871.2</a>  | 317  | No protein            | Processed transcript    | -                         |         | TSL:3 ,                               |
| Rbpms-215 | <a href="#">ENSMUST00000231942.2</a>  | 2534 | No protein            | Retained intron         | -                         |         |                                       |
| Rbpms-211 | <a href="#">ENSMUST00000183122.2</a>  | 525  | No protein            | Retained intron         | -                         |         | TSL:2 ,                               |

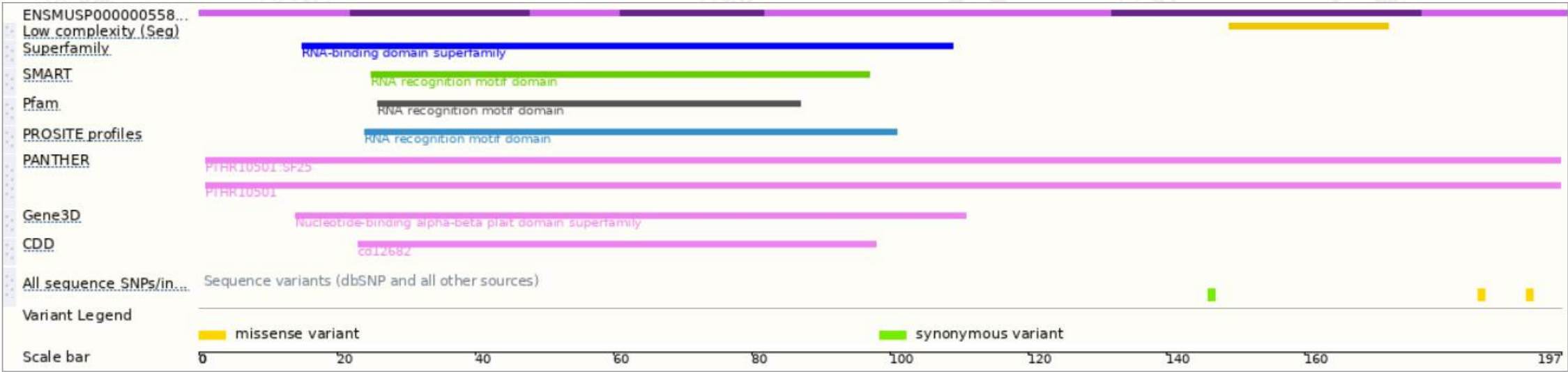
The strategy is based on the design of *Rbpms-203* transcript,the transcription is shown below:



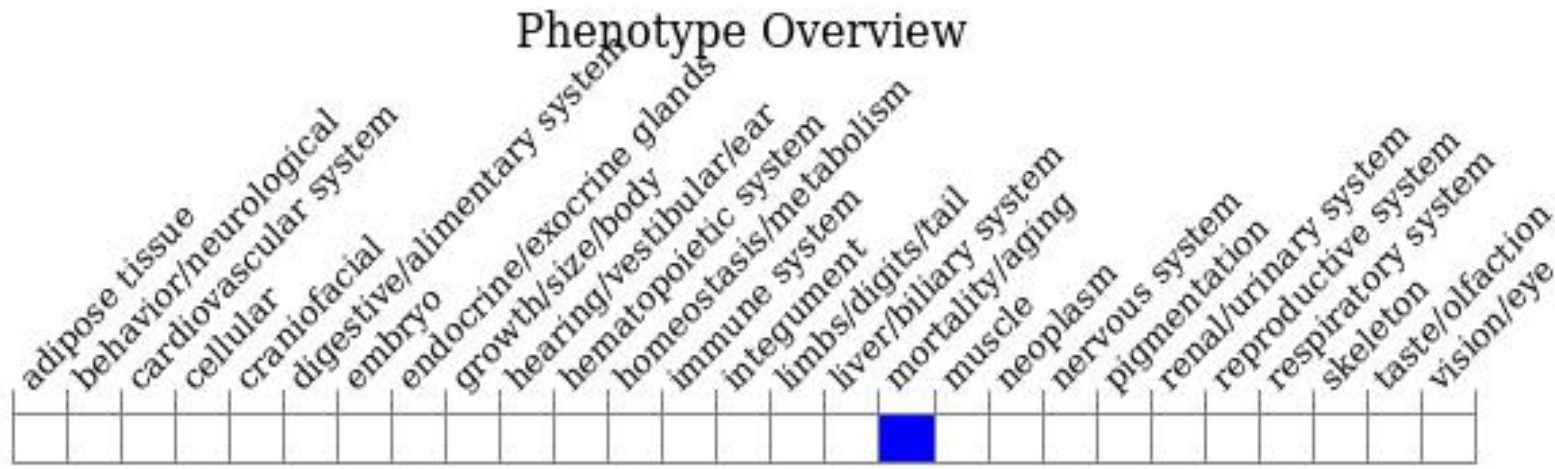
# Genomic location distribution



# 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.  
Tel: 400-9660890

