

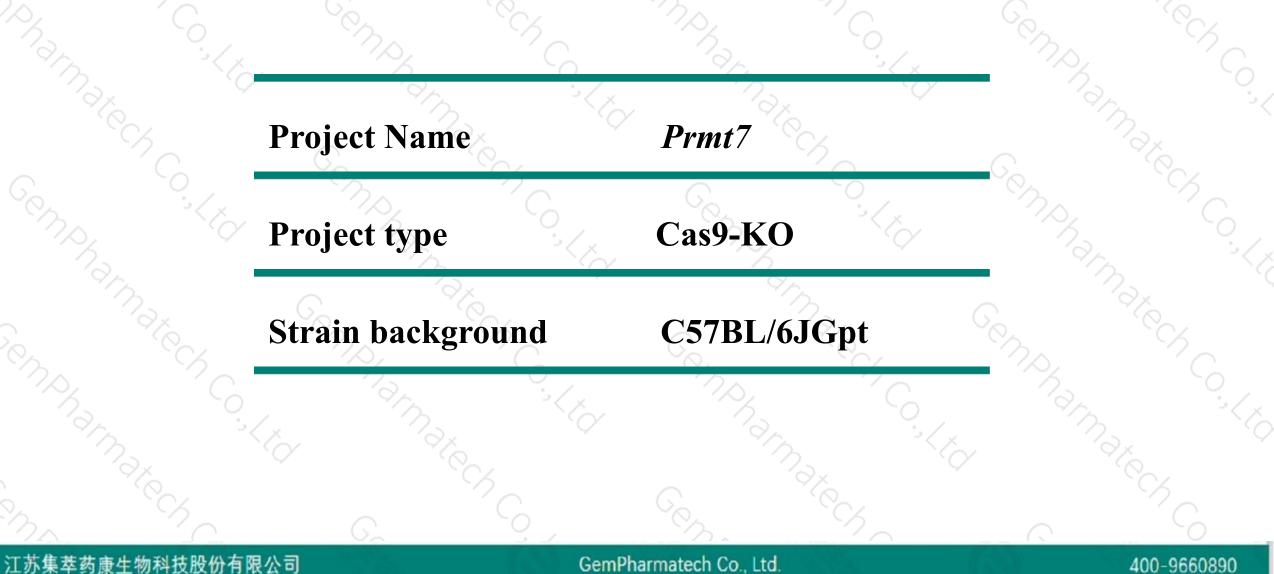
Prmt7 Cas9-KO Strategy

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Project Overview

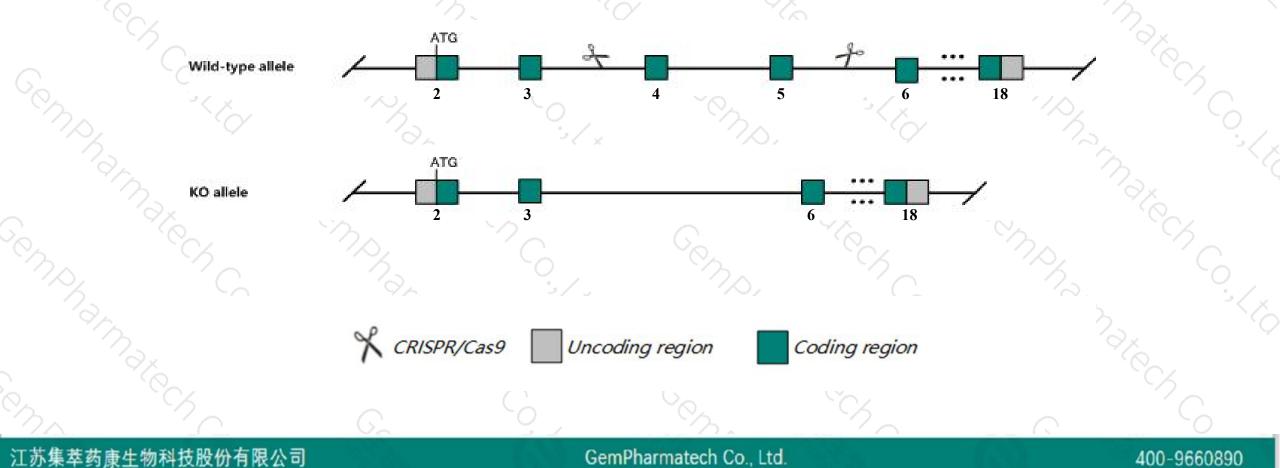




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Prmt7* gene. The schematic diagram is as follows:





- The Prmt7 gene has 7 transcripts. According to the structure of Prmt7 gene, exon4-exon5 of Prmt7-201 (ENSMUST00000071592.11) transcript is recommended as the knockout region. The region contains 259bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Prmt7 gene. The brief process is as follows: CRISPR/Cas9 system

- The Prmt7 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.

Notice

Gene information (NCBI)



Prmt7 protein arginine N-methyltransferase 7 [Mus musculus (house mouse)]

Gene ID: 214572, updated on 10-Oct-2019

Summary

Official SymbolPrmt7 provided by MGIOfficial Full Nameprotein arginine N-methyltransferase 7 provided by MGIPrimary sourceMGI:MGI:2384879See relatedEnsembl:ENSMUSG0000060098Gene typeprotein codingRefSeq statusPROVISIONALOrganismMus musculusLineageEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Myomorpha; Muroidea; Murinae; Mus; MusAlso known asBC006705; 4933402B05RikExpressionUbiquitous expression in testis adult (RPKM 37.9), ovary adult (RPKM 19.4) and 28 other tissues See more
human_all

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Transcript information (Ensembl)



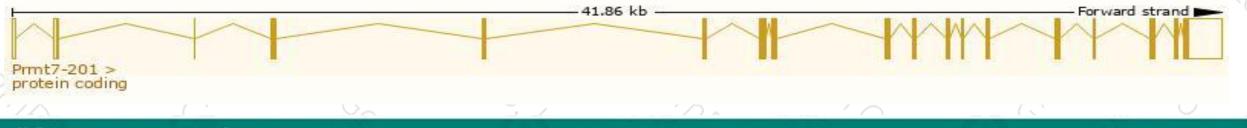
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The gene has 7 transcripts, all transcripts are shown below:

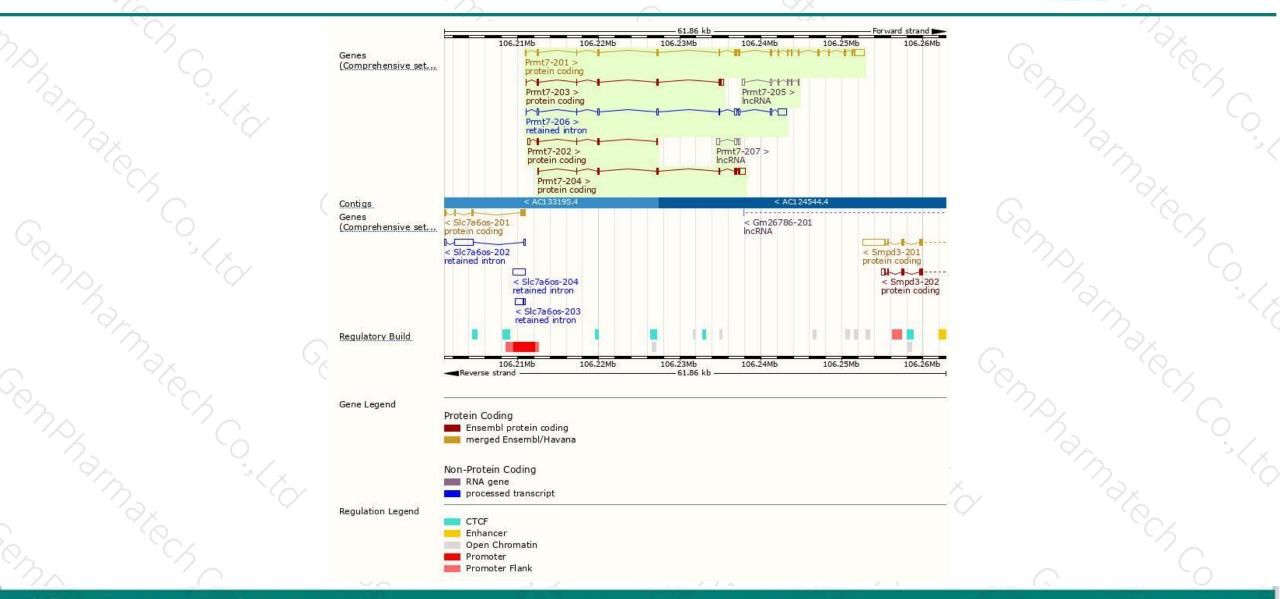
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| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-----------|-----------------------|------|--------------|-----------------|-----------|---------------|-------------------------------|
| Prmt7-201 | ENSMUST00000071592.11 | 3472 | <u>692aa</u> | Protein coding | CCDS22633 | <u>Q922X9</u> | TSL:1 GENCODE basic APPRIS P1 |
| Prmt7-204 | ENSMUST00000128201.1 | 1535 | <u>298aa</u> | Protein coding | - | F6RXJ8 | CDS 5' incomplete TSL:1 |
| Prmt7-203 | ENSMUST00000109297.7 | 1094 | <u>217aa</u> | Protein coding | 20 | D3Z1C9 | TSL:1 GENCODE basic |
| Prmt7-202 | ENSMUST00000109296.7 | 747 | <u>113aa</u> | Protein coding | 29 | D3Z1D0 | CDS 3' incomplete TSL:3 |
| Prmt7-206 | ENSMUST00000147063.7 | 2277 | No protein | Retained intron | 56 | - | TSL:1 |
| Prmt7-207 | ENSMUST00000153272.1 | 851 | No protein | IncRNA | - | - | TSL:2 |
| Prmt7-205 | ENSMUST00000134151.1 | 660 | No protein | IncRNA | - 29 | - | TSL:3 |

The strategy is based on the design of Prmt7-201 transcript, The transcription is shown below



Genomic location distribution



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Protein domain



| | | C_{1} C_{1} C_{2} C_{2} | |
|---|---------------------------------|--|----------|
| | ENSMUSP00000071 SIFTS import | | - X_ |
| 4 | Superfamily Pfam | S-adenosyl-L-methionine-dependent methyltransferase PF06325 | |
| | PROSITE profiles | Protein arginine N-methyltransferase | |
| | PIRSF | Protein arginine N-methyltransferase PRMT7 | |
| | PANTHER | PTHR11006 | |
| | | PTHR11006:SF4 | |
| | Gene3D | 2.70.160.11 | |
| | CDD | 3.40.50,150 cd02440 | |
| | All sequence SNPs/i | Sequence variants (dbSNP and all other sources) | 10001 |
| | | | <u> </u> |
| | Variant Legend | missense variant synonymous variant | 3<2 |
| | Scale bar | 0 60 120 180 240 300 360 420 480 540 60 | 0 692 |
| 2 | N C | C_{1} | 6 |

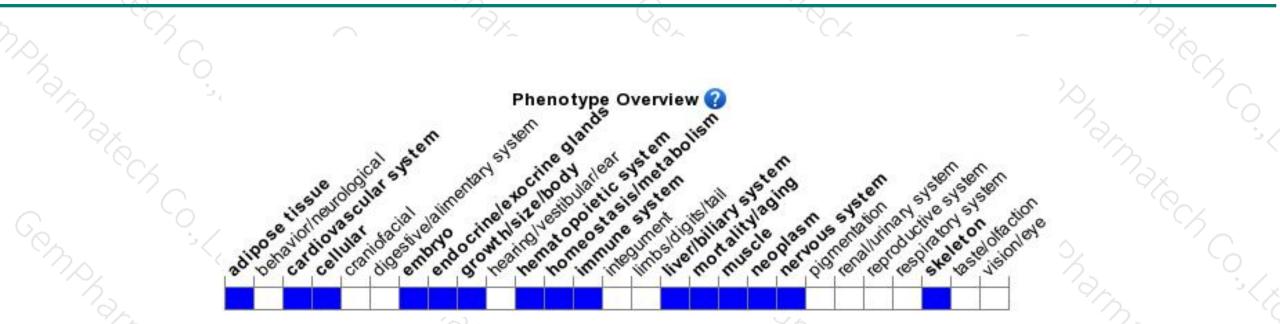
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Mouse phenotype description(MGI)





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



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



