

Dusp16 Cas9-KO Strategy

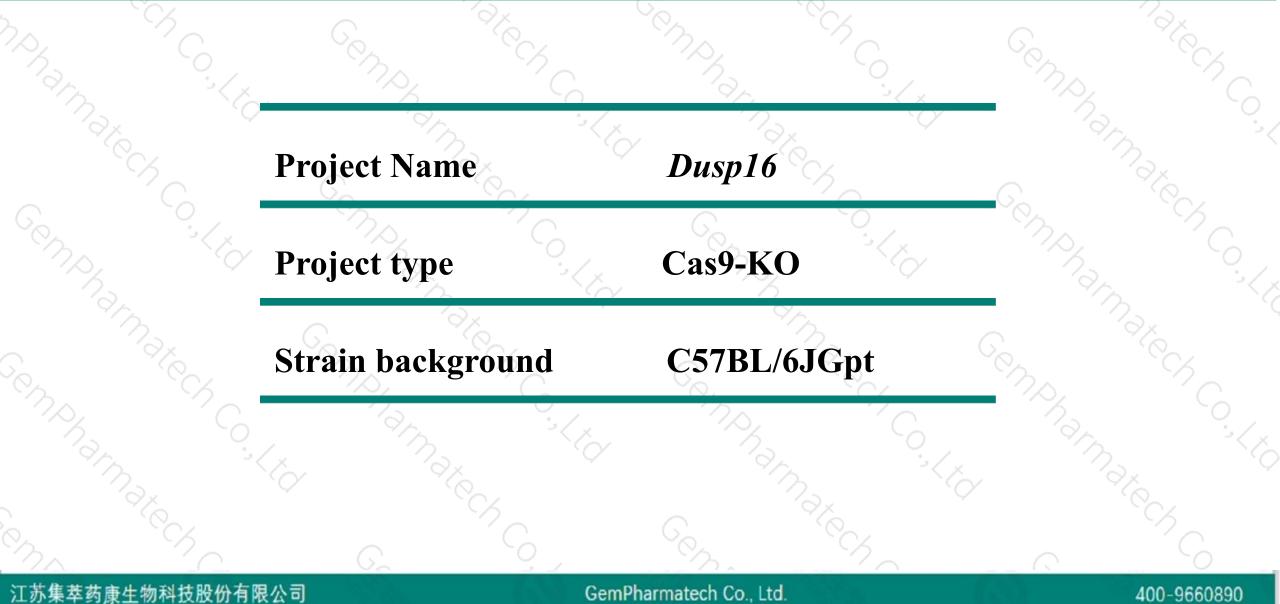
Designer: Huimin Su

Reviewer: Ruiuri Zhang

Design Date: 2020-7-21

Project Overview

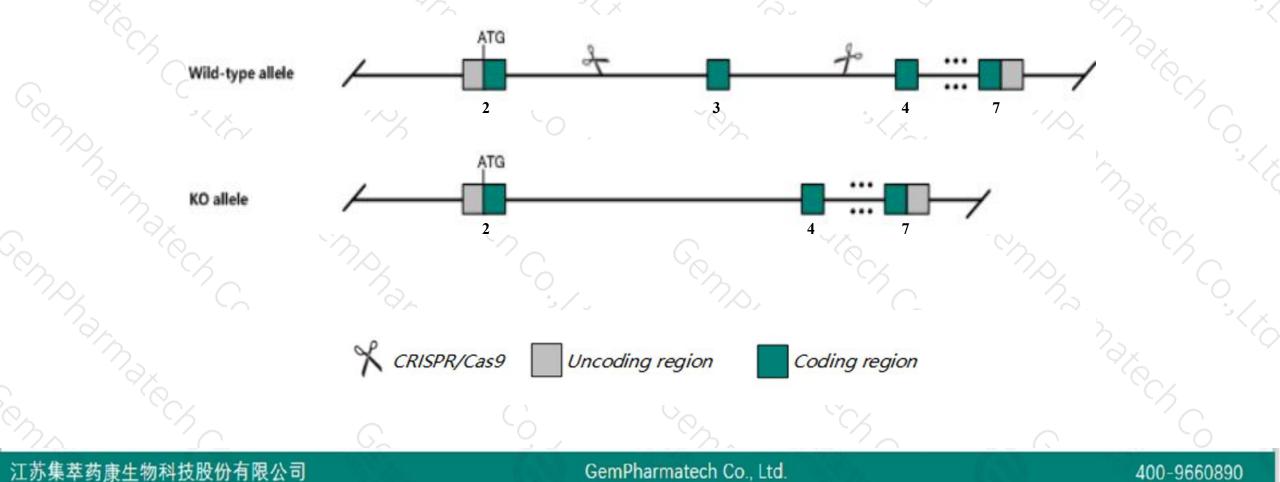




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the Dusp16 gene. The schematic diagram is as follows:





➤ The Dusp16 gene has 7 transcripts. According to the structure of Dusp16 gene, exon3 of Dusp16-201(ENSMUST00000100857.9) transcript is recommended as the knockout region. The region contains 139bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Dusp16* 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.

- > According to the existing MGI data, mice homozygous for a gene trap allele exhibit complete neonatal lethality and decreased birth weight.
- The *Dusp16* gene is located on the Chr6. 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)



Dusp16 dual specificity phosphatase 16 [Mus musculus (house mouse)]

Gene ID: 70686, updated on 11-Jul-2020

Summary

Official Symbol Dusp16 provided by MGI

Official Full Name dual specificity phosphatase 16 provided by MGI

Primary source MGI:MGI:1917936

See related Ensembl:ENSMUSG00000030203

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 MKP7; Mkpm; MKP-7; AW558566; D6Ertd213e; 3830417M17Rik

Expression Ubiquitous expression in bladder adult (RPKM 11.4), mammary gland adult (RPKM 7.2) and 28 other tissues See more Orthologs human all

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

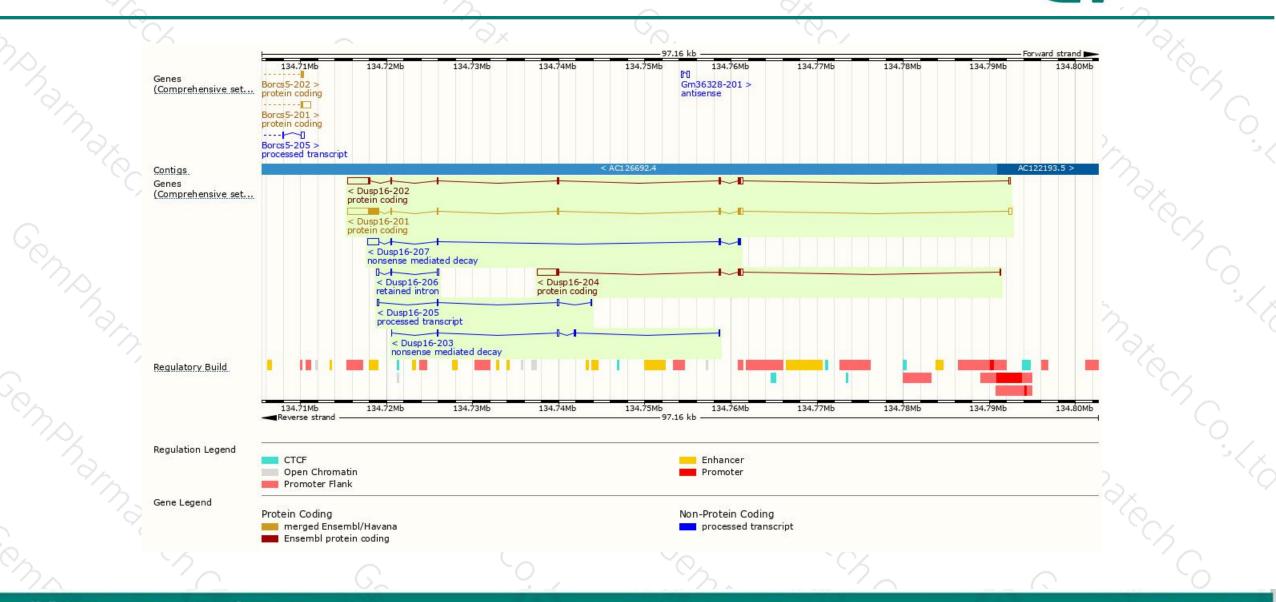
| Name 🍦 | Transcript ID 🕴 | bp 🛊 | Protein 🔺 | Biotype 🖕 | CCDS | UniProt 🖕 | Flags | |
|------------|----------------------|------|--------------|-------------------------|--------------------|-------------|---------------------------------|--|
| Dusp16-203 | ENSMUST00000148926.1 | 579 | <u>51aa</u> | Nonsense mediated decay | | A0A0N4SV20 | CDS 5' incomplete TSL:3 | |
| Dusp16-207 | ENSMUST00000204083.2 | 1915 | <u>143aa</u> | Nonsense mediated decay | | A0A0N4SUV2@ | TSL:5 | |
| Dusp16-204 | ENSMUST00000149776.2 | 3305 | <u>206aa</u> | Protein coding | 0-0 | Q8BZE4 6 | TSL:1 GENCODE basic | |
| Dusp16-202 | ENSMUST00000129433.3 | 3993 | <u>338aa</u> | Protein coding | <u>CCDS85175</u> 교 | F6UIK0@ | TSL:1 GENCODE basic APPRIS ALT2 | |
| Dusp16-201 | ENSMUST00000100857.9 | 5104 | <u>660aa</u> | Protein coding | <u>CCDS39679</u> 교 | Q6PCP3 | TSL:1 GENCODE basic APPRIS P3 | |
| Dusp16-205 | ENSMUST00000203452.2 | 553 | No protein | Processed transcript | 121 | 2 | TSL:5 | |
| Dusp16-206 | ENSMUST00000203651.1 | 629 | No protein | Retained intron | 1021 | <u>20</u> | TSL:2 | |

The strategy is based on the design of *Dusp16-201* transcript, the transcription is shown below:

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Genomic location distribution



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Protein domain



| 9 | ENSMUSP00000098 | G _{RA} | 7 X C/ | Cons. | ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ | Groom Construction | | |
|---|-----------------------------|---|--|--|--|--------------------|---------|--|
| | MobiDB lite Superfamily | Rhodanese-like domain superfamily | Protein-tyrosine phosphatase-like | | | | | |
| | SMART | Rhodanese-like domain | Dual specificity protein phosp | natase domain | | | 0 | |
| 3 | Prints Pfam | <mark>Mitogen-activated protein (MAP)</mark> Rhodanese-like domain | kinase phosphatase Dual specificity phosphatase | e, catalytic domain | | | Nate of | |
| | PROSITE profiles | Rhodanese-like domain | | e specific protein phosphatases domain | | | | |
| | PROSITE patterns PANTHER | PTHR10159:SF343 | Dual specificity protein phospl | natase domain otein-tyrosine phosphatase, active site | | | | |
| | Gene3D | PTHR10159 Rhodanese-like domain superfamily | Protein-tyrosine phosphatase- | like | | | | |
| 2 | CDD. | cd01446 | cd14646 | | | | No. | |
| ~ | All sequence SNPs/i | Sequence variants (dbSNP and all ot | ther sources) | ř ř | 1.1.1.1.111.1 | i. | | |
| | Variant Legend | inframe deletion synonymous variant | | missen: | missense variant | | | |
| | Scale bar | 0 60 12 | 20 180 240 | o '300 '360 | 420 480 | 540 600 | | |
| 6 | 3 3 | G_ | | George a | | | | |

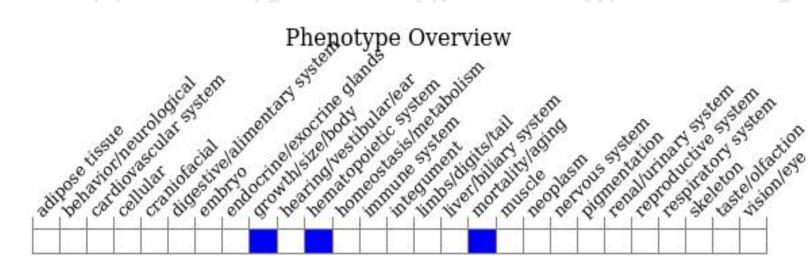
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Mouse phenotype description(MGI)





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 a gene trap allele exhibit complete neonatal lethality and decreased birth weight.



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



