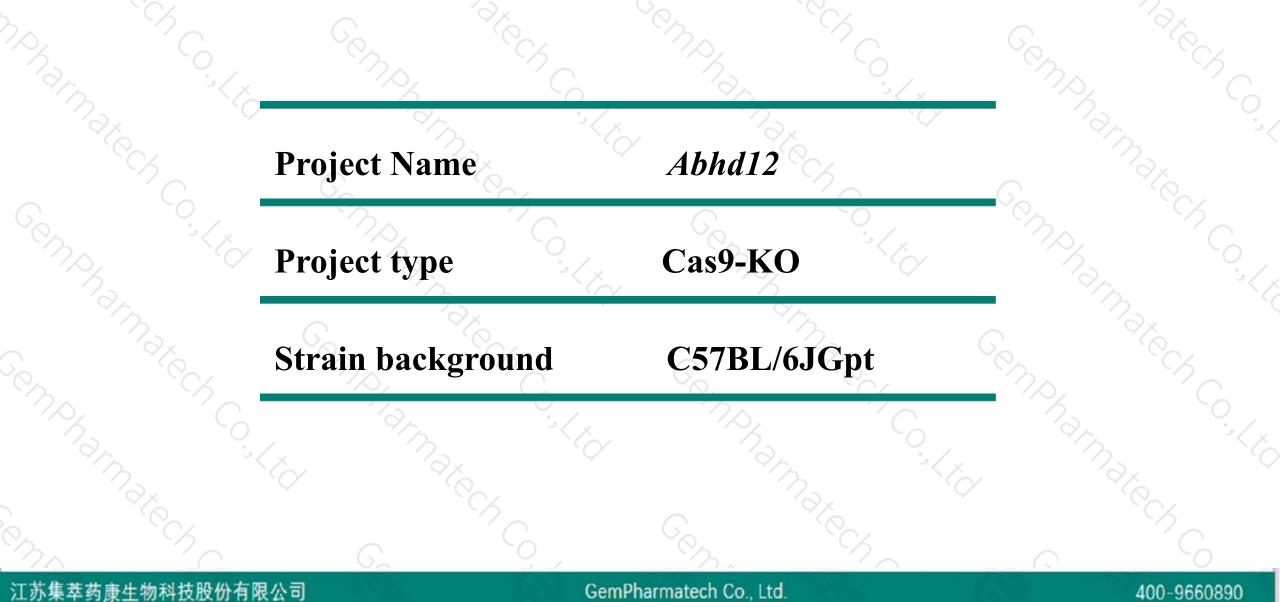


Abhd12 Cas9-KO Strategy

Designer: Reviewer: Design Date: JiaYu Xiaojing Li 2020-2-20

Project Overview

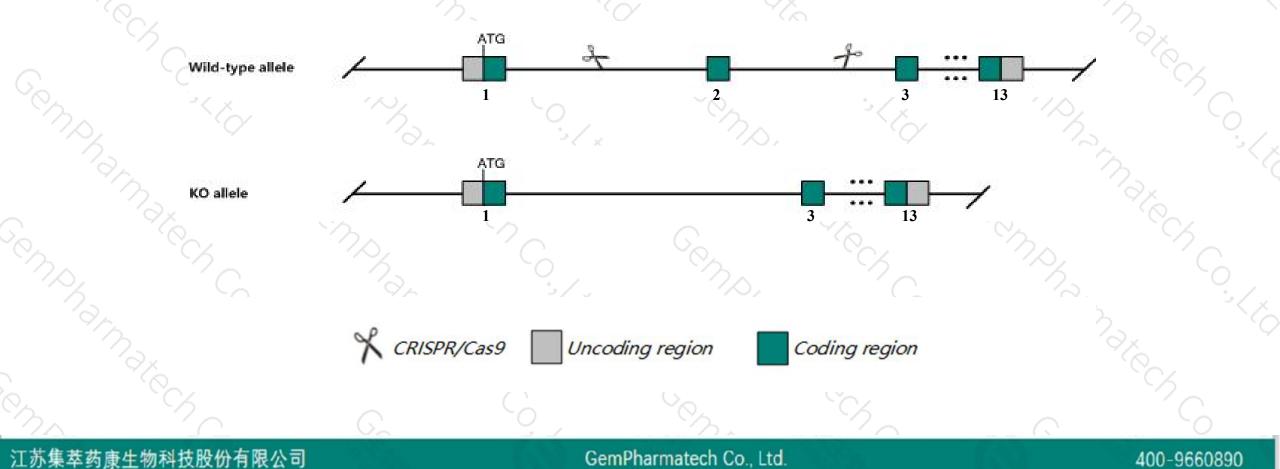




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Abhd12* gene. The schematic diagram is as follows:





- The Abhd12 gene has 7 transcripts. According to the structure of Abhd12 gene, exon2 of Abhd12-201 (ENSMUST00000056149.14) transcript is recommended as the knockout region. The region contains 125bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Abhd12 gene. The brief process is as follows: CRISPR/Cas9 system



- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit neurological symptoms of neurodegeneration, hearing loss, ataxia, microgliosis and reduced brain lysophosphatidylserine lipase activity.
- The Abhd12 gene is located on the Chr2. 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)



\$?

Abhd12 abhydrolase domain containing 12 [Mus musculus (house mouse)]

Gene ID: 76192, updated on 31-Jan-2019

Summary

| Official Symbol | Abhd12 provided by MGI |
|-----------------------|--|
| Official Full Name | abhydrolase domain containing 12 provided byMGI |
| Primary source | MGI:MGI:1923442 |
| See related | Ensembl:ENSMUSG0000032046 |
| 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 | 1500011G07Rik, 6330583M11Rik, Al431047, AW547313 |
| Expression | Ubiquitous expression in cortex adult (RPKM 64.9), bladder adult (RPKM 63.9) and 28 other tissues See more |
| Orthologs | human all |

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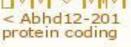
Transcript information (Ensembl)



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

| 1 Mar | I do | | | | | | | |
|------------|-----------------------|------|--------------|----------------------------------|-----------|---------|-------------------------------|--|
| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags | |
| Abhd12-201 | ENSMUST00000056149.14 | 1999 | <u>398aa</u> | Protein coding | CCDS50742 | Q99LR1 | TSL:1 GENCODE basic APPRIS P1 | |
| Abhd12-204 | ENSMUST00000141899.7 | 1969 | <u>298aa</u> | Nonsense mediated decay | -8 | D6RFU2 | TSL:1 | |
| Abhd12-202 | ENSMUST00000129228.1 | 597 | <u>70aa</u> | Nonsense mediated decay - D6RI21 | | D6RI21 | TSL:3 | |
| Abhd12-205 | ENSMUST00000145826.1 | 353 | <u>56aa</u> | Nonsense mediated decay | 29 | F7BHM8 | CDS 5' incomplete TSL:5 | |
| Abhd12-206 | ENSMUST00000155119.7 | 700 | No protein | Retained intron | 56 | 65 | TSL:3 | |
| Abhd12-203 | ENSMUST00000138608.7 | 1334 | No protein | IncRNA - | | 87 | TSL:1 | |
| Abhd12-207 | ENSMUST00000156641.7 | 1292 | No protein | IncRNA | 19 | 32 | TSL:1 | |

The strategy is based on the design of Abhd12-201 transcript, The transcription is shown below

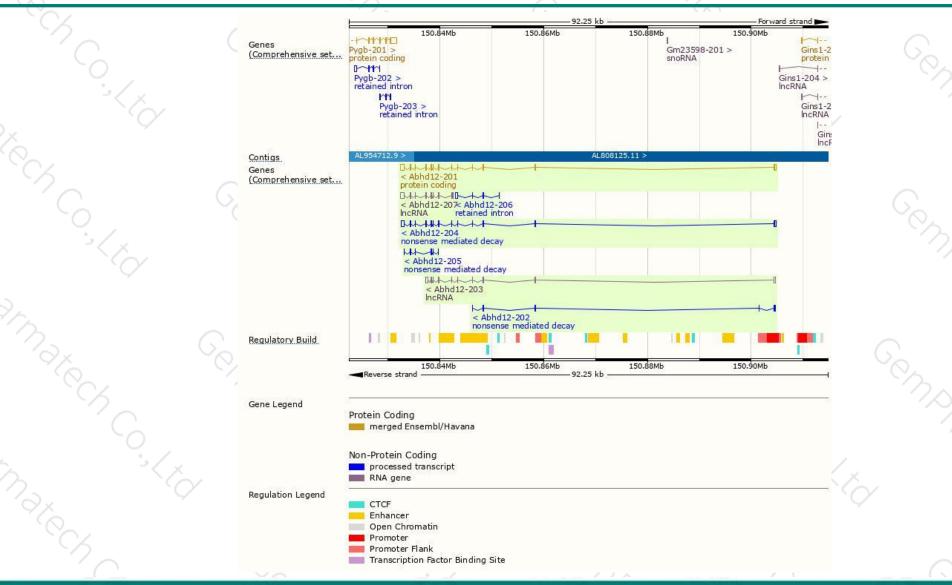


Reverse strand -

72.25 kb

Genomic location distribution





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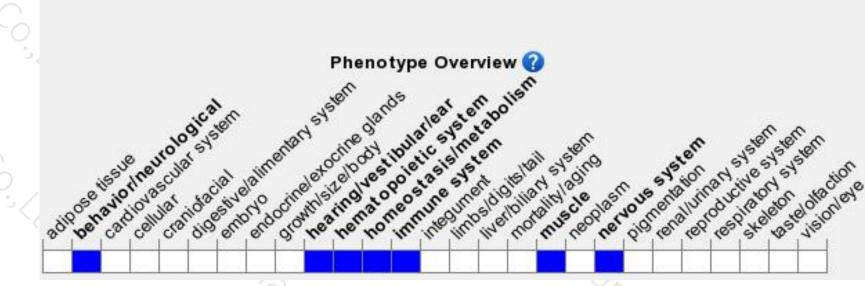
Protein domain



| 7317 | ENSMUSP00000053 | | 5 | ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ | | 9.915. | | < x | | < <u>~</u> ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ |
|---------|--|-------------------------------------|---------|--|---------------|--------------|----------|----------|---------|--|
| G | Transmembrane heli MobiDB lite Low complexity (Seg) Superfamily | | | ; | Alpha/Beta hy | drolase fold | | | | |
| \sim | Pfam | | | | Serine | aminopeptid | ase, S33 | 10 57 | | 2 |
| 1 - I - | PANTHER | PE | R12277 | | | | | | | |
| Sent | All sequence SNPs/i Variant Legend | Mo Sequence variar missense v | ariant | | | ſ | | | nine of | |
| | Scale bar | o 40 | 80 | 120 | 160 | 200 | 240 | 280 | 320 | 398 |
| | Mare H | C. | d te ch | | Ser. | | ate ch | | | ALC C |
| 江苏集萃 | 药康生物科技股份有限公 | 23 | | Gem | Pharmatech | h Co., Ltd. | | 1 | 3 | 400-9660890 |

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 knock-out allele exhibit neurological symptoms of neurodegeneration, hearing loss, ataxia, microgliosis and reduced brain lysophosphatidylserine lipase activity.



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



