

# **Dyrk1b** Cas9-KO Strategy

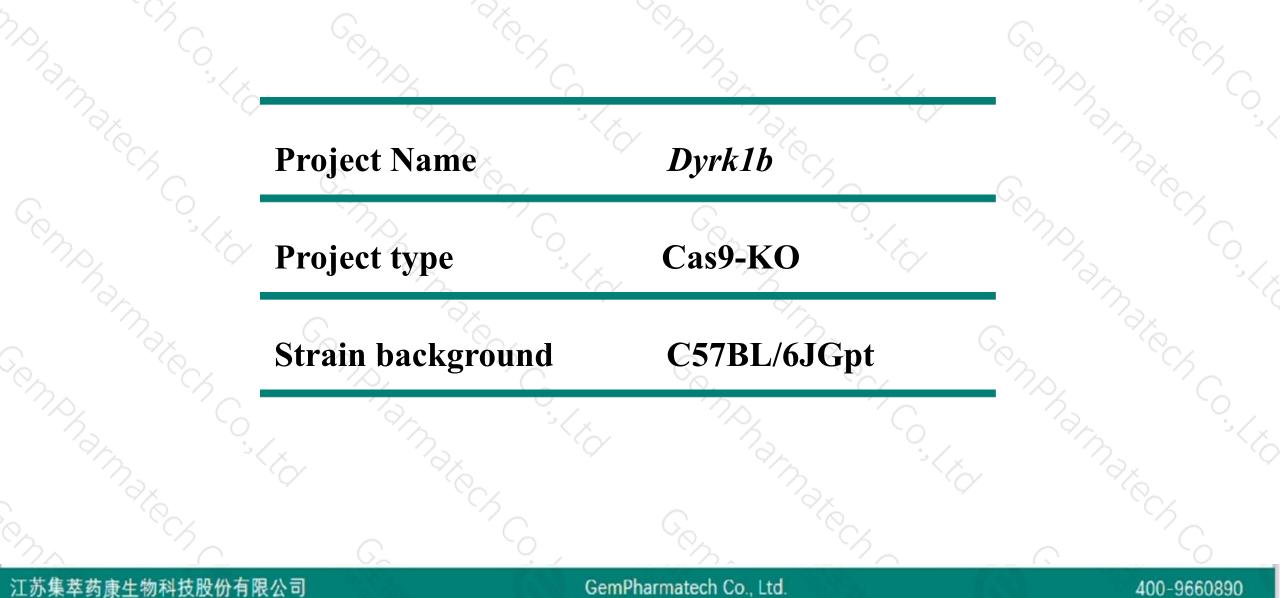
**Designer: Jinlong Zhao** 

**Reviewer: Shilei Zhu** 

Design Date: 2020-8-11

### **Project Overview**

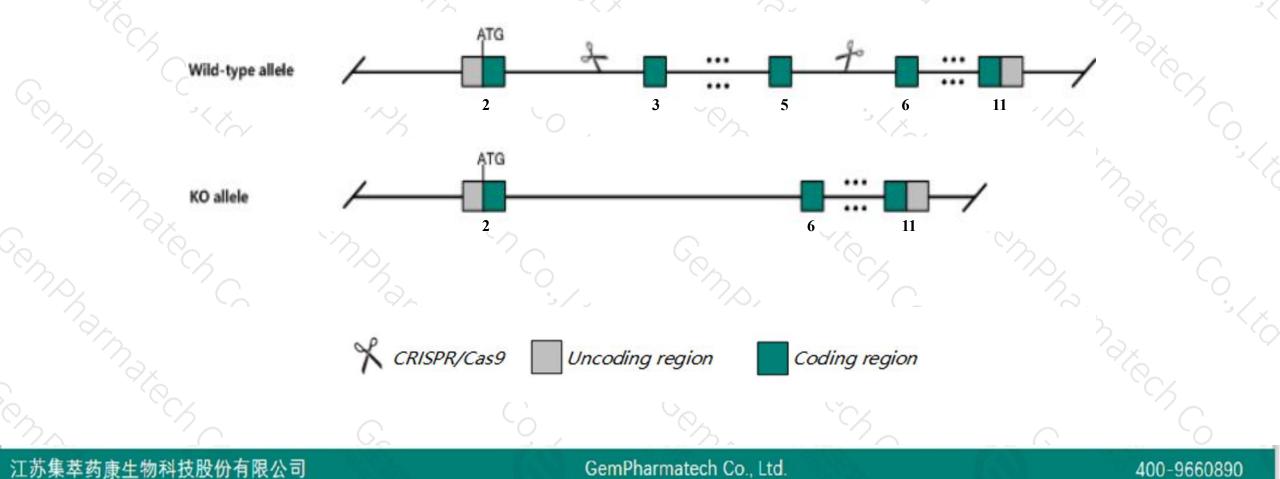




# **Knockout** strategy



This model will use CRISPR/Cas9 technology to edit the Dyrk1b gene. The schematic diagram is as follows:





➤ The Dyrk1b gene has 3 transcripts. According to the structure of Dyrk1b gene, exon3-exon5 of Dyrk1b-201(ENSMUST00000085901.12) transcript is recommended as the knockout region. The region contains 457bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Dyrk1b* 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 *Dyrk1b* gene is located on the Chr7. 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)**



☆ ?

Dyrk1b dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1b [Mus musculus (house mouse)]

Gene ID: 13549, updated on 13-Mar-2020

#### - Summary

Official SymbolDyrk1b provided by MGIOfficial Full Namedual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1b provided by MGIPrimary soureMGI:MGI:1330302See relatedEnsembl:ENSMUSG0000002409Gene typeprotein codingRefSeq statusVALIDATEDOrganismMus musculusLineageEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Rodentia; Myomorpha;<br/>Muroidea; Murinae; Mus; MusAlso known asMirkExpressionUbiquitous expression in testis adult (RPKM 39.4), thymus adult (RPKM 16.2) and 24 other tissues<br/>Muna all

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### GemPharmatech Co., Ltd.

#### 400-9660890

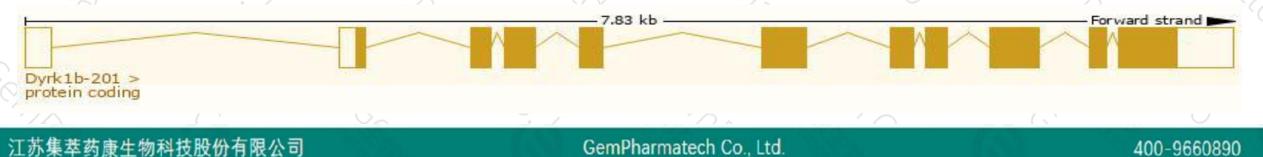
### **Transcript information (Ensembl)**



### The gene has 3 transcripts, all transcripts are shown below:

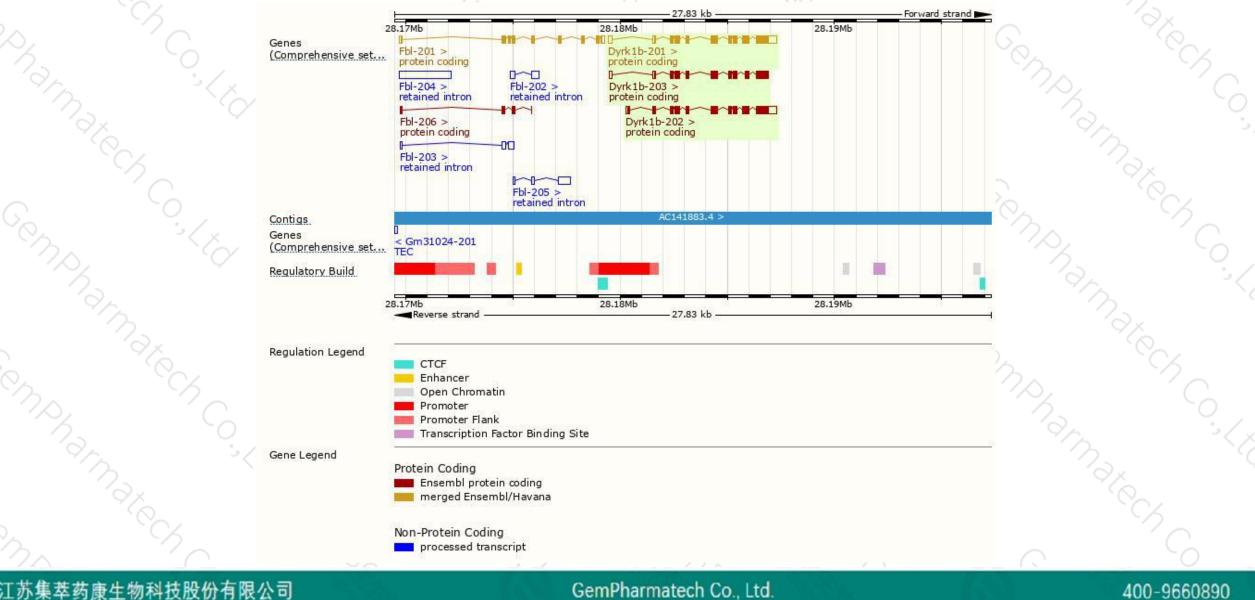
| Name       | Transcript ID        | bp   | Protein      | Biotype        | CCDS      | UniProt       | Flags   |
|------------|----------------------|------|--------------|----------------|-----------|---------------|---|
| Dyrk1b-201 | ENSMUST0000085901.12 | 2534 | <u>629aa</u> | Protein coding | CCDS21037 | <u>Q9Z188</u> | TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1 |
| Dyrk1b-202 | ENSMUST00000172467.7 | 2523 | <u>689aa</u> | Protein coding | CCDS85251 | <u>Q9Z188</u> | TSL:1 GENCODE basic   |
| Dyrk1b-203 | ENSMUST00000172761.7 | 2018 | <u>589aa</u> | Protein coding | CCDS57532 | Q9Z188        | TSL:1 GENCODE basic   |

The strategy is based on the design of *Dyrk1b-201* transcript, the transcription is shown below:



### **Genomic location distribution**





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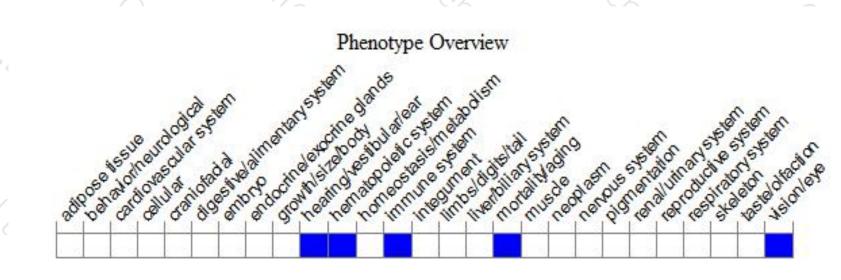
### **Protein domain**



|                    | ENSMUSP0000083                      | -  |                       | 143       |               | 0                          | 14            | · \\           |           |       |     |          |      |
|--------------------|-------------------------------------|--|-----------------------|-----------|---------------|----------------------------|---------------|----------------|-----------|-------|-----|----------|------|
| 7.0 <sub>7.3</sub> | MobiDB lite<br>Low complexity (Seg) |  | -                     |           |               | 16                         |               |                |           | -     |     |          |      |
| ×1.                | Superfamily                         | Protein kinase-like domain superfamily   |                       |           |               |                            |               |                |           |       |     |          |      |
|                    | SMART                               |  | Protein kinase domain |           |               |                            |               |                |           |       |     |          |      |
|                    | <u>Pfam</u>                         | Protein kinase domain  |                       |           |               |                            |               |                |           |       |     |          |      |
|                    | PROSITE profiles                    | Protein kinase domain  |                       |           |               |                            |               |                |           |       |     |          |      |
| Go.                | PROSITE patterns                    |  |                       | Protein k | inase, ATP b  | 100                        |               |                |           |       |     |          |      |
|                    | PANTHER                             | PTHR240  |                       |           |               | All America I for Lines of | ireonine-prot | ein kinase, ao | tive site |       |     |          |      |
|                    | Gene3D                              | Dual specificity tyrosine-phosphorylation-regulated kinase 1A/B<br>3.30.200.20 |                       |           |               |                            |               |                |           |       |     |          |      |
|                    | <u>CDD</u>                          |  |                       | cd14226   | 1.10.510.1    | .0                         |               |                |           |       |     |          | 0    |
|                    | All sequence SNPs/i                 | Sequen   | ce variants           | (dbSNP an | d all other s | sources)                   | 1             | 3              | 1         |       | 11  |          |      |
| <u></u>            | Variant Legend                      | missense variant<br>synonymous variant   |                       |           |               |                            |               |                |           |       |     |          |      |
|                    | Scale bar                           | 0  | 60                    | 120       | 180           | 240                        | 300           | 360            | 420       | 480   | 540 | 629      |      |
| 江苏集团               | 萃药康生物科技股份有限                         | <b></b> 【公司  |                       |           |               | GemPharm                   | atech Co., L  | td.            |           | - 633 |     | 400-9660 | 0890 |

### 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



