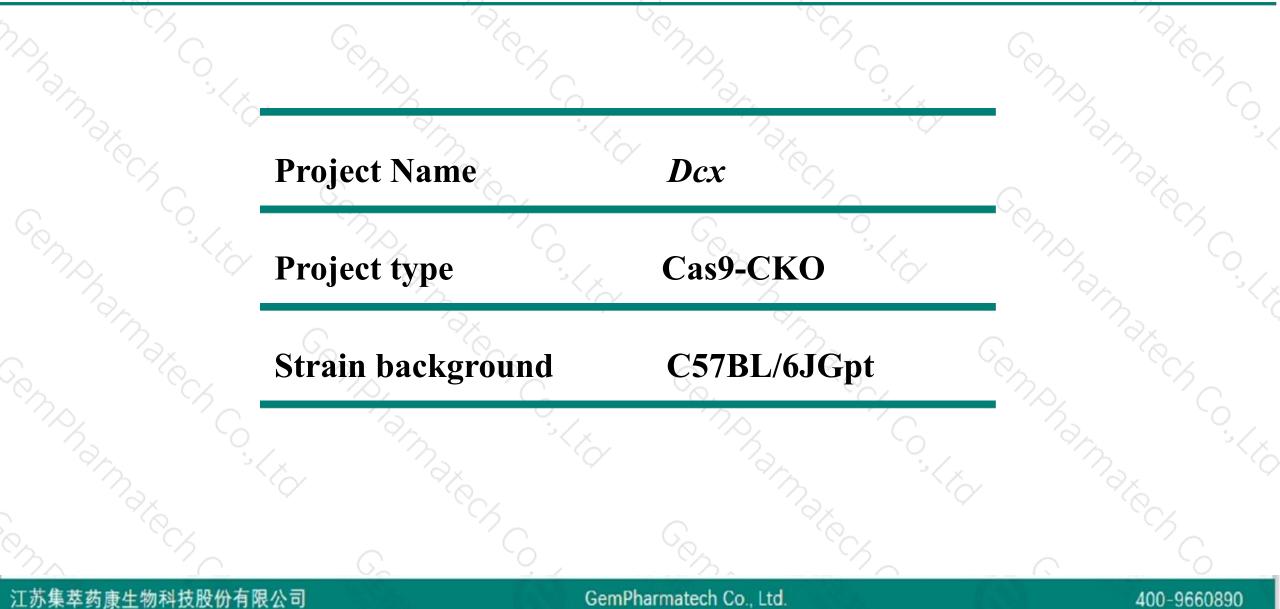


# **Dcx Cas9-CKO Strategy**

Designer: Reviewer: Design Date: Yang Zeng Xueting Zhang 2019-10-28

## **Project Overview**

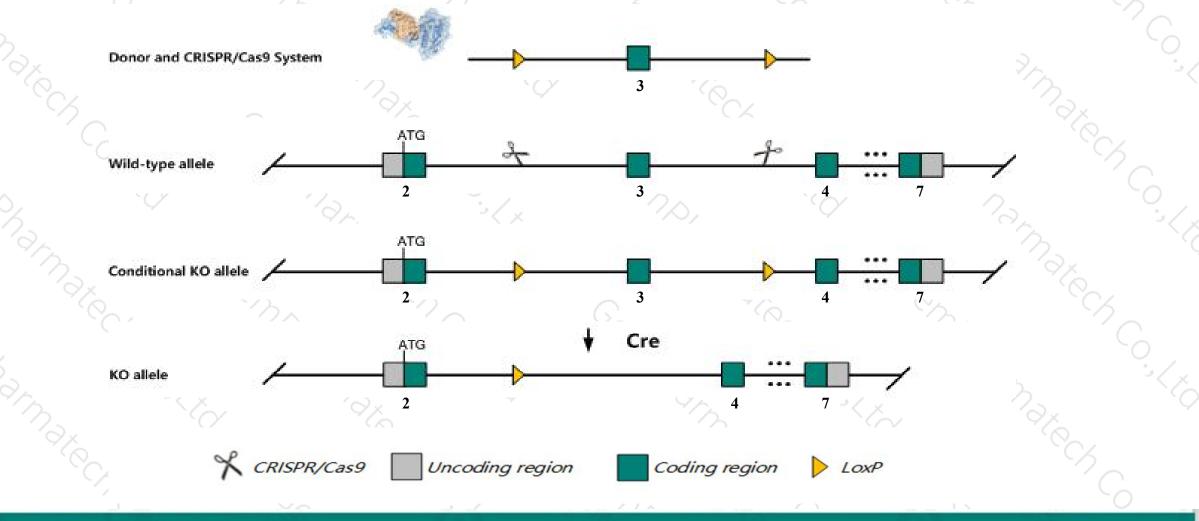




## **Conditional Knockout strategy**



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



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> The *Dcx* gene has 6 transcripts. According to the structure of *Dcx* gene, exon3 of *Dcx-201* (ENSMUST00000033642.9) transcript is recommended as the knockout region. The region contains 341bp coding sequence. Knock out the region will result in disruption of protein function.

> In this project we use CRISPR/Cas9 technology to modify Dcx gene. The brief process is as follows:CRISPR/Cas9 system

and Donor 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 flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.



- According to the existing MGI data, Males hemizygous for a null allele are fertile but show branching and nucleokinesis defects in migrating interneurons. Males hemizygous for a reporter allele show severe postnatal lethality and variable fertility; both female and male mutants display hippocampal dyslamination and behavioral defects.
- The Dcx gene is located on the ChrX. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

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## Gene information (NCBI)



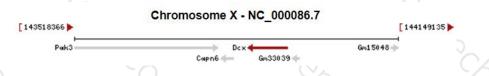
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## Dcx doublecortin [ Mus musculus (house mouse) ]

Gene ID: 13193, updated on 15-Oct-2019

Summary

| Official Symbol    | Dcx provided by MGI  |             |
|--------------------|--|-------------|
| Official Full Name | doublecortin provided by MGI   |             |
| Primary source     | MGI:MGI:1277171  |             |
| See related        | Ensembl:ENSMUSG00000031285   |             |
| Gene type          | protein coding   |             |
| RefSeq status      | REVIEWED   |             |
| Organism           | Mus musculus   |             |
| Lineage            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;   |             |
|                    | Muroidea; Muridae; Murinae; Mus; Mus   |             |
| Also known as      | Dbct   |             |
| Summary            | This gene encodes a member of the doublecortin family. The protein encoded by this gene is a cytoplasmic protein and contains two doublecortin domains, which bind microtubules. In the developing cortex, cortical neurons must migrate over long distances to reach the site of their final differentiation. The encoded protein appears to direct neuronal migration by regulating the organization and stability of microtubules. In addition, the encoded protein interacts with LIS1, the regulatory gamma subunit of platelet activating factor acetylhydrolase. Studies in knockout mice lacking this gene and the LIS1 gene suggest that the molecular interaction of these two genes is important in both in neuronal migration and neurogenesis, and there is a cortical role of this gene in nuclear translocation and positioning of the mitotic spindle in radial glial mitotic division. Multiple transcript variants encoding three different isoforms have been found for this gene. [provided by RefSeq, Sep 2010] |             |
| Expression         | Biased expression in whole brain E14.5 (RPKM 80.1), CNS E18 (RPKM 75.8) and 3 other tissues See more   | - fine<br>J |
| Orthologs          | human all  | 1           |
|                    |  |             |



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## Transcript information (Ensembl)



| Name 🖕  | Transcript ID        | bp 🍦 | Protein 🖕    | Translation ID       | Biotype 💧       | CCDS 🖕             | UniProt 🖕       | Flags                        |
|---------|----------------------|------|--------------|----------------------|-----------------|--------------------|-----------------|------------------------------|
| Dcx-201 | ENSMUST0000033642.9  | 9074 | <u>366aa</u> | ENSMUSP0000033642.3  | Protein coding  | <u>CCDS53209</u> r | <u>088809</u> & | TSL:1 GENCODE basic APPRIS A |
| Dcx-203 | ENSMUST00000112851.7 | 4095 | <u>365aa</u> | ENSMUSP00000108472.1 | Protein coding  | <u>CCDS53210</u> & | <u>Q6PGI2</u> ₽ | TSL:1 GENCODE basic APPRIS A |
| Dcx-202 | ENSMUST0000087313.9  | 3120 | <u>366aa</u> | ENSMUSP0000084570.3  | Protein coding  | <u>CCDS53209</u> & | <u>088809</u> & | TSL:1 GENCODE basic APPRIS A |
| Dcx-204 | ENSMUST00000112856.2 | 1333 | <u>360aa</u> | ENSMUSP00000108477.2 | Protein coding  | <u>CCDS41157</u>   | <u>Q9CXL6</u> & | TSL:1 GENCODE basic APPRIS F |
| Dcx-205 | ENSMUST00000125768.1 | 3194 | No protein   | 21                   | Retained intron |                    | 2               | TSL:2                        |
| Dcx-206 | ENSMUST00000139920.7 | 2617 | No protein   | -                    | Retained intron | <u>_</u>           | 2               | TSL:2                        |

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

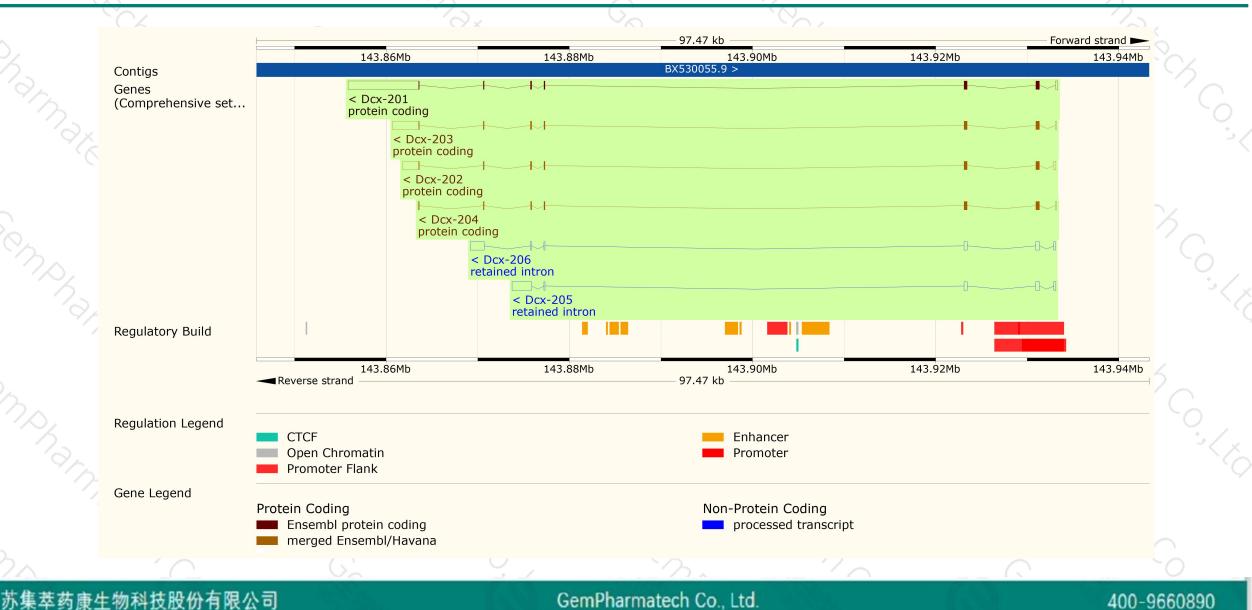


## **Genomic location distribution**

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## **Protein domain**



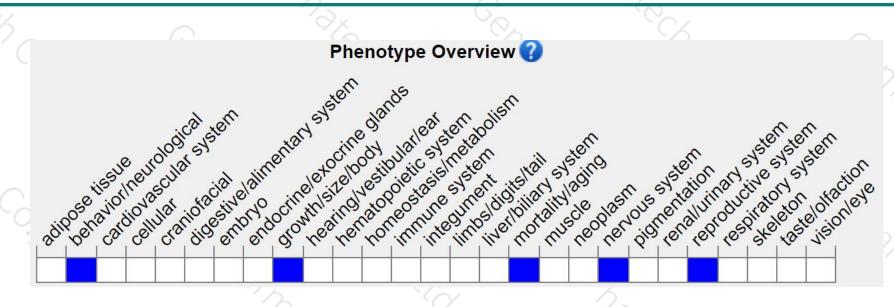
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| ENSMUSP0000033<br>MobiDB lite<br>Low complexity (Seg)<br>Superfamily<br>SMART |                  |                                      | omain superfamily |  |     |            |          | -     |         | —    |
|---|------------------|--------------------------------------|-------------------|--|-----|------------|----------|-------|---------|------|
| Pfam  |                  | Doublecortin d                       |                   |  |     |            |          |       |         | ر د' |
| PROSITE profiles<br>PIRSF   |                  | Doublecortin<br>protein doublecortin |                   |  |     |            |          |       |         |      |
| PANTHER   |                  |                                      | , choruata        |  |     |            |          |       |         | 1    |
|   | PTHR23005        |                                      |                   |  |     |            |          |       |         | L    |
| Gene3D  | RP1/RP1L1/       | DCX<br>Doublecortin domai            | n superfamily     |  |     |            |          |       |         |      |
| CDD   |                  | cd16112                              | in superiority    |  | cd  | 17069      |          |       |         |      |
| All sequence SNPs/i<br>Variant Legend   | Sequence variant | ts (dbSNP and all c                  | other sources)    |  | I   | synonymous | variant  | 1     |         |      |
| Scale bar   | 0                | 40                                   | 80                | 120                                    | 160 | 200        | 240      | 280   | 320     | 366  |
|   | Col X            | - Adr                                |                   | ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ |     | Dharmar    | S Co L X | Y Not | Mare Ch |      |
| Č.  |                  | G_                                   | 2                 |  | Con | · · ·      | Ч        | 0     |         | 0    |

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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, Males hemizygous for a null allele are fertile but show branching and nucleokinesis defects in migrating interneurons. Males hemizygous for a reporter allele show severe postnatal lethality and variable fertility; both female and male mutants display hippocampal dyslamination and behavioral defects.

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



