

Bicra Cas9-CKO Strategy

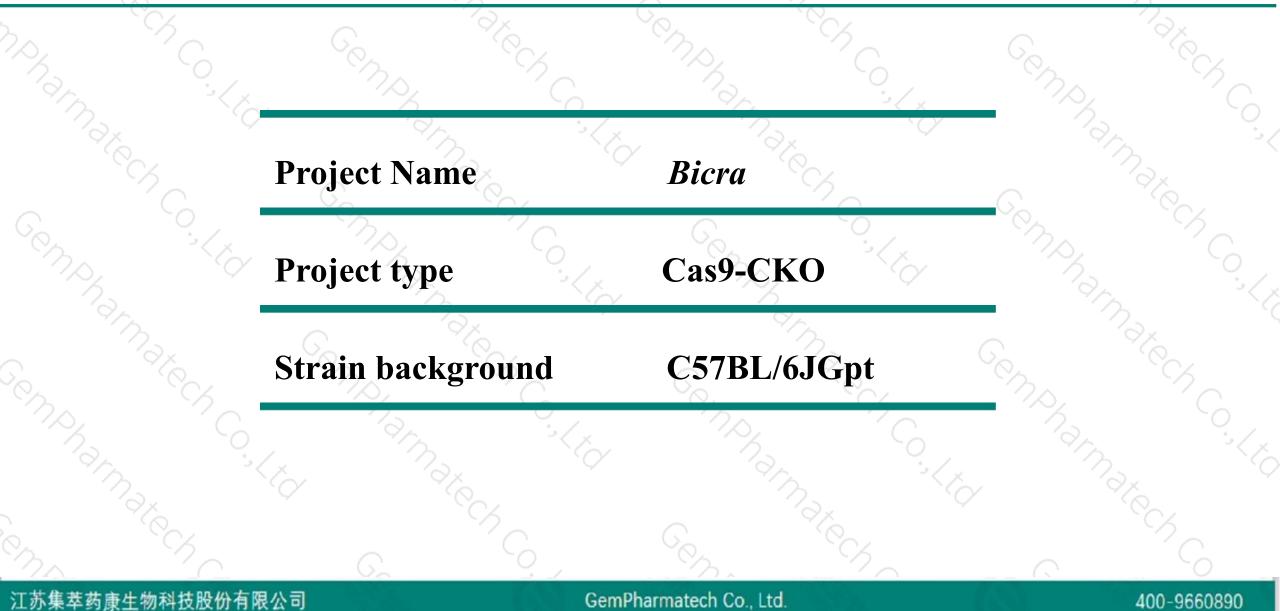
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Reviewer: Wenjing Li

Design Date: 2018/12/4

Project Overview



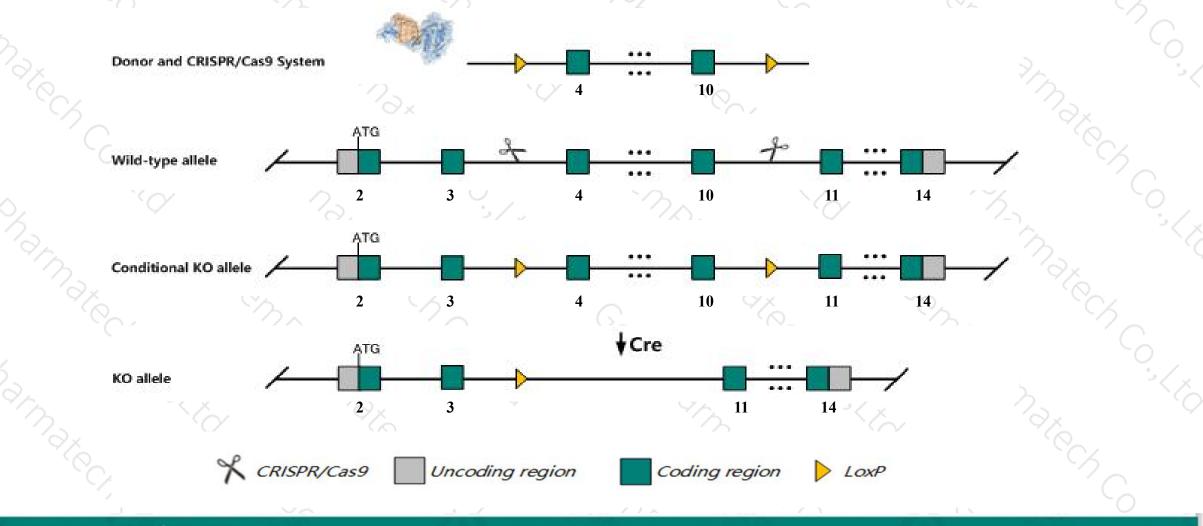


Conditional Knockout strategy



400-9660890

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



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The Bicra gene has 4 transcripts. According to the structure of Bicra gene, exon4-exon10 of Bicra-201(ENSMUST0000094821.3) transcript is recommended as the knockout region. The region contains 3194bp coding sequence. Knock out the region will result in disruption of protein function.

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



The flox region overlaps with Gm38948-201 and destroys the gene at the same time.
The *Bicra* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)



Bicra BRD4 interacting chromatin remodeling complex associated protein [Mus musculus (house mouse)]

Gene ID: 243842, updated on 13-Mar-2020

Summary

Official SymbolBicra provided by MGIOfficial Full NameBRD4 interacting chromatin remodeling complex associated protein provided byMGIPrimary sourceMGI:MGI:2154263See relatedEnsembl:ENSMUSG0000070808Gene typeprotein codingRefSeq statusPROVISIONALOrganismMus musculusLineageEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Myomorpha; Muroidea; Murinae; Mus; MusAlso known asGltscr1ExpressionUbiquitous expression in thymus adult (RPKM 18.0), spleen adult (RPKM 18.0) and 27 other tissues
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Transcript information (Ensembl)



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The gene has 4 transcripts, all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|-----------|----------------------|---------|---------------|----------------------|------------|---------|-------------------------------|
| Bicra-204 | ENSMUST00000210781.1 | 5975 | <u>1578aa</u> | Protein coding | CCD539780 | F8VPZ9 | TSL:5 GENCODE basic APPRIS P1 |
| Bicra-201 | ENSMUST0000094821.3 | 5360 | <u>1578aa</u> | Protein coding | CCDS39780 | F8VPZ9 | TSL:5 GENCODE basic APPRIS P1 |
| Bicra-202 | ENSMUST00000209251.1 | 665 | No protein | Processed transcript | <u>5</u> 0 | - | TSL:3 |
| Bicra-203 | ENSMUST00000210713.1 | 6623 | No protein | Retained intron | - | - | TSL:1 |
| C Pring | No series a | Streep. | | | | × × | |

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

< Bicra-201 protein coding

Reverse strand -

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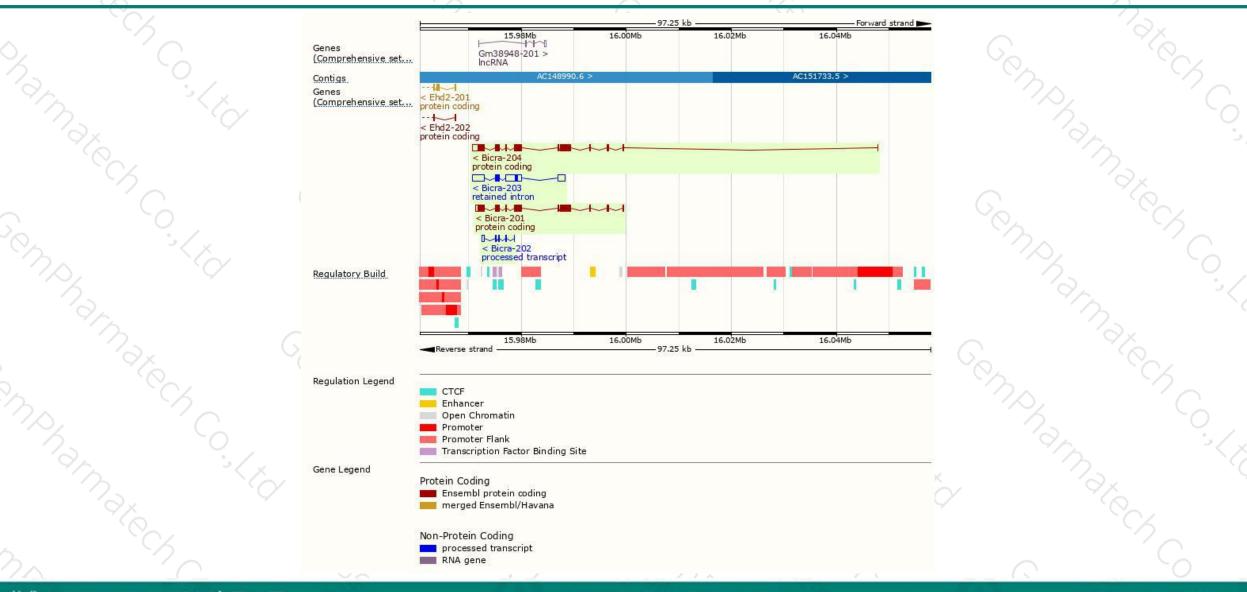
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28.23 kb

Genomic location distribution



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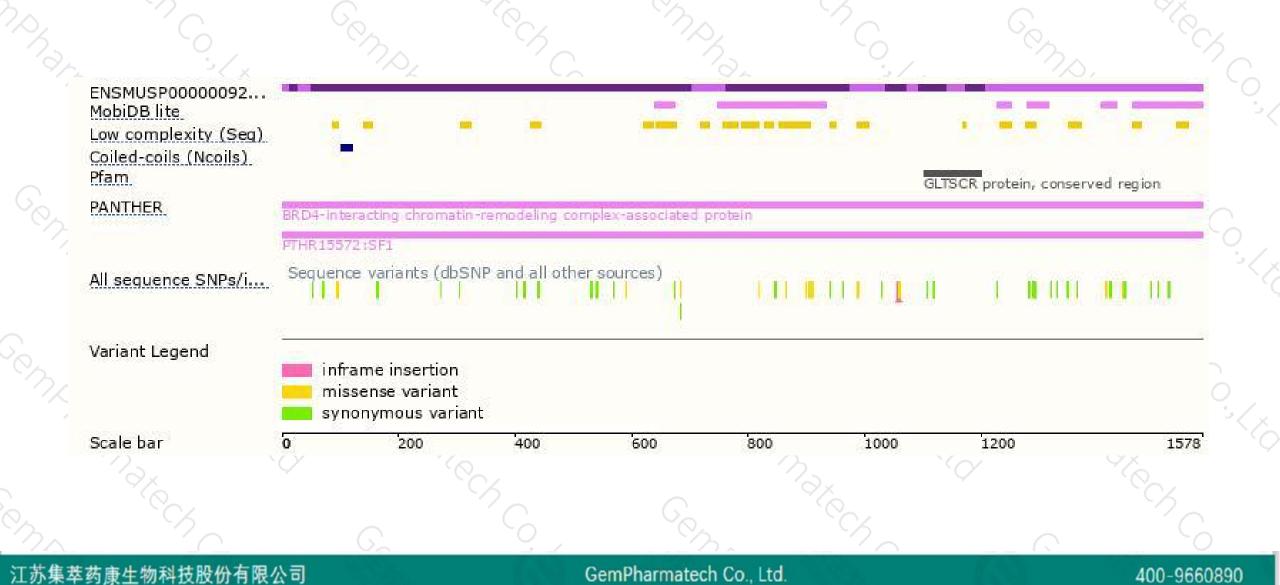


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Protein domain







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



