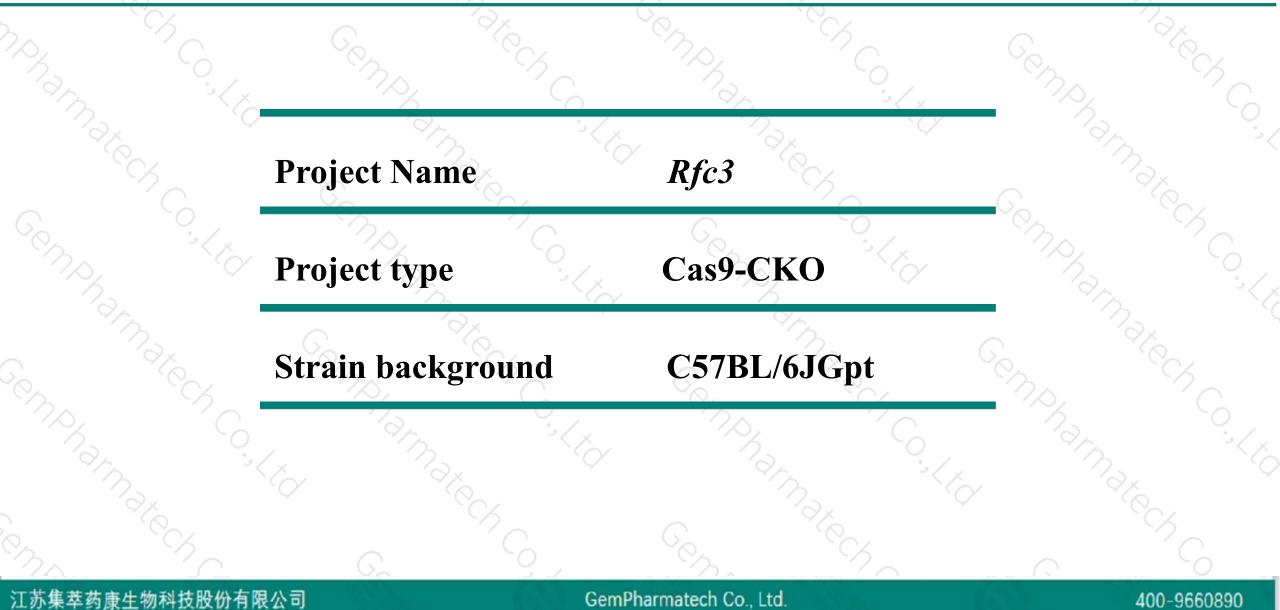


Rfc3 Cas9-CKO Strategy

Designer: Xueting Zhang Reviewer:Yanhua Shen Date:2020-03-16

Project Overview



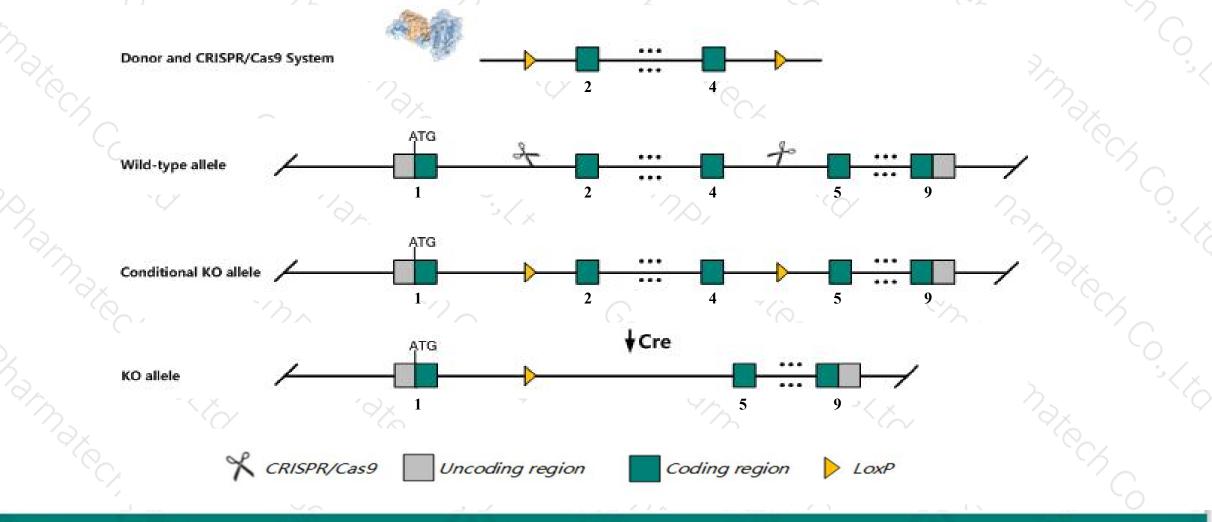


Conditional Knockout strategy



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This model will use CRISPR/Cas9 technology to edit the *Rfc3* gene. The schematic diagram is as follows:



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The *Rfc3* gene has 7 transcripts. According to the structure of *Rfc3* gene, exon2-exon4 of *Rfc3-201* (ENSMUST00000038131.9) transcript is recommended as the knockout region. The region contains 304bp coding sequence. Knock out the region will result in disruption of protein function.

In this project we use CRISPR/Cas9 technology to modify *Rfc3* 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.

Notice



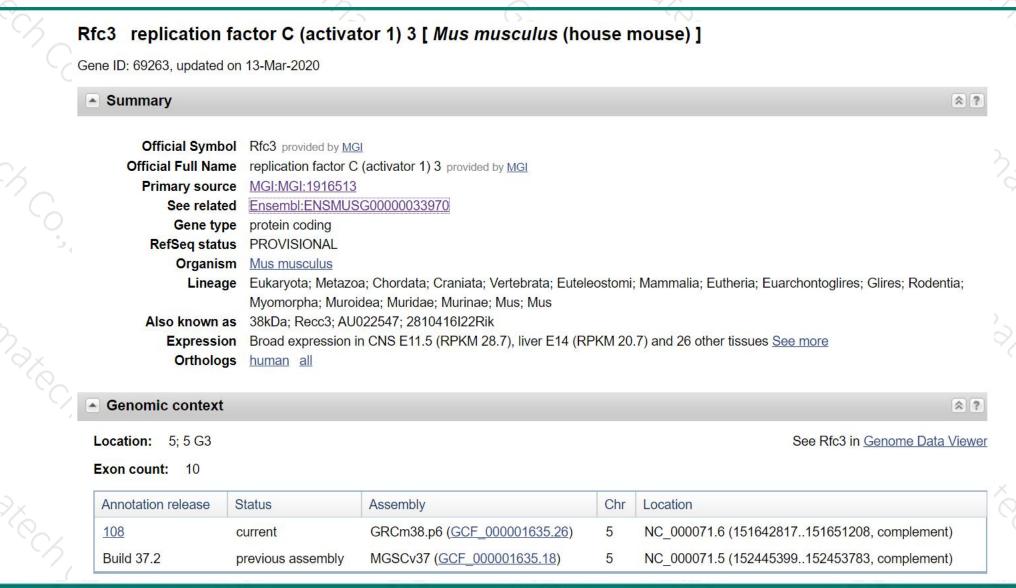
- Transcript *Rfc3*-202&207 may not be affected.
- The *Rfc3* gene is located on the Chr5. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This Strategy is designed based on genetic 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)

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Transcript information (Ensembl)



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

| Name 🖕 | Transcript ID 💧 | bp 🖕 | Protein 🖕 | Biotype 💧 | CCDS | UniProt 🖕 | Flags | \$ | |
|----------|----------------------|------|--------------|-----------------|--------------------|-----------------------------------|--------------------|-----------|--|
| Rfc3-201 | ENSMUST0000038131.9 | 1317 | <u>356aa</u> | Protein coding | <u>CCDS39413</u> & | <u>Q3TKD1</u> ៤7 <u>Q8R323</u> ៤7 | TSL:1 GENCODE basi | APPRIS P1 | |
| Rfc3-206 | ENSMUST00000145106.7 | 2726 | No protein | Retained intron | - | - | TSL:1 | | |
| Rfc3-205 | ENSMUST00000140067.7 | 1062 | No protein | Retained intron | - | | TSL:1 | | |
| Rfc3-203 | ENSMUST00000132709.1 | 906 | No protein | Retained intron | - | - | TSL:1 | | |
| Rfc3-202 | ENSMUST00000127366.1 | 706 | No protein | Retained intron | - | | TSL:2 | | |
| Rfc3-204 | ENSMUST00000136752.1 | 605 | No protein | Retained intron | - | - | TSL:2 | | |
| Rfc3-207 | ENSMUST00000156667.1 | 503 | No protein | Retained intron | - | | TSL:2 | | |

The strategy is based on the design of *Rfc3-201* transcript, The transcription is shown below

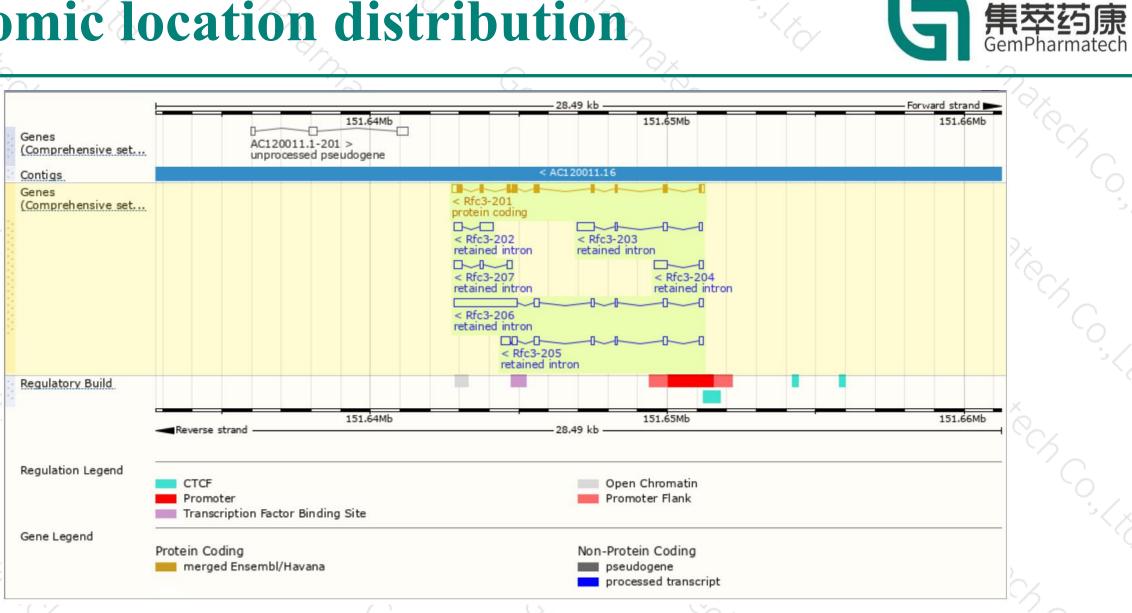


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Genomic location distribution



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Protein domain



| non | ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ | Con a | A Star | | Mp. | ~ () | S. Co | G _O | 5. | ALC CH |
|----------|--|------------------------------|---|----------------------|------|------------------|-------------|-----------------------|-------------------|---|
| hannar. | ENSMUSP00000039 Superfamily | P-loop containing nucleoside | triphosphate hydrolase | 2 | | | DNA polyme | rase III, clamp loade | r complex, gamma/ | |
| . 6 | SMART | AAA+ ATPase (| domain | | | | | | | ~ |
| | Pfam. | PF13177 | | | | | | | | |
| | PANTHER | PTHR11669:SF1 | | | | | | | | |
| Conphan, | Gene3D | PTHR11669 3.40.50.300 | | | | 1.10.8.60 | 1.20.272.10 | 2 | | ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ |
| 1 North | CDD | cd00009 | | | | cd18140 | | | | |
| | All sequence SNPs/i Variant Legend | Sequence variants (dbSNP | and all other sources <mark> </mark> | 5) | 1 | synonymous varia | . I | | | X. Rock |
| | Scale bar | 0 40 | 80 | 120 | 160 | 200 | 240 | 280 | 356 | 20 |
| | - Co - < / ¿ | y ann | | , (₍ ,) | | hann. | | | | |
| | ° K | G. | S. | 1 | Gen. | | 3 | | | т Су Су |

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



