

# ***Bfar Cas9-CKO Strategy***

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**Reviewer :**

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# Project Overview

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**Project Name**

***Bfar***

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**Project type**

**Cas9-CKO**

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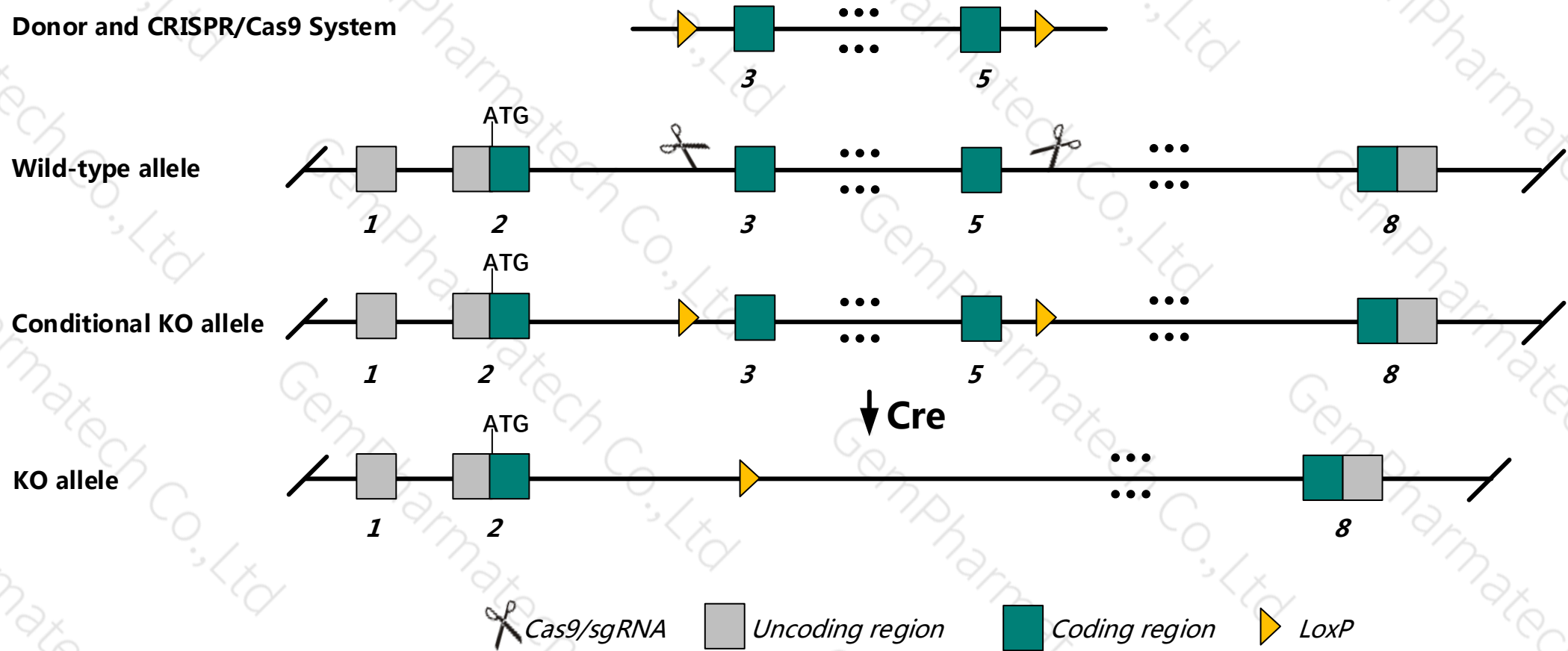
**Strain background**

**C57BL/6JGpt**

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# Conditional Knockout strategy

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



- The *Bfar* gene has 8 transcripts. According to the structure of *Bfar* gene, exon3-exon5 of *Bfar*-201 (ENSMUST00000023365.12) transcript is recommended as the knockout region. The region contains 520bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Bfar* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed. Cas9, sgRNA 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 was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues or cell types.

- The *Bfar* gene is located on the Chr16. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

# Gene information ( NCBI )



## Bfar bifunctional apoptosis regulator [ *Mus musculus* (house mouse) ]

Gene ID: 67118, updated on 12-Aug-2019

Summary

Official Symbol	Bfar provided by MGI
Official Full Name	bifunctional apoptosis regulator provided by MGI
Primary source	MGI:MGI:1914368
See related	Ensembl:ENSMUSG00000022684 Ensembl:ENSMUSG00000079737
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	Bar; Rnf47; AI666707; AW107665; 3010001A07Rik; 3110001I22Rik
Expression	Ubiquitous expression in bladder adult (RPKM 14.9), subcutaneous fat pad adult (RPKM 12.4) and 28 other tissues See more
Orthologs	human all

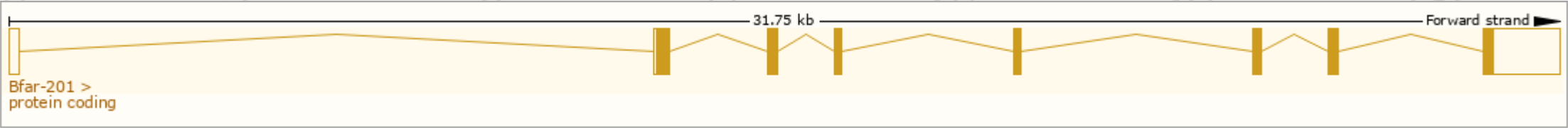


# Transcript information ( Ensembl )

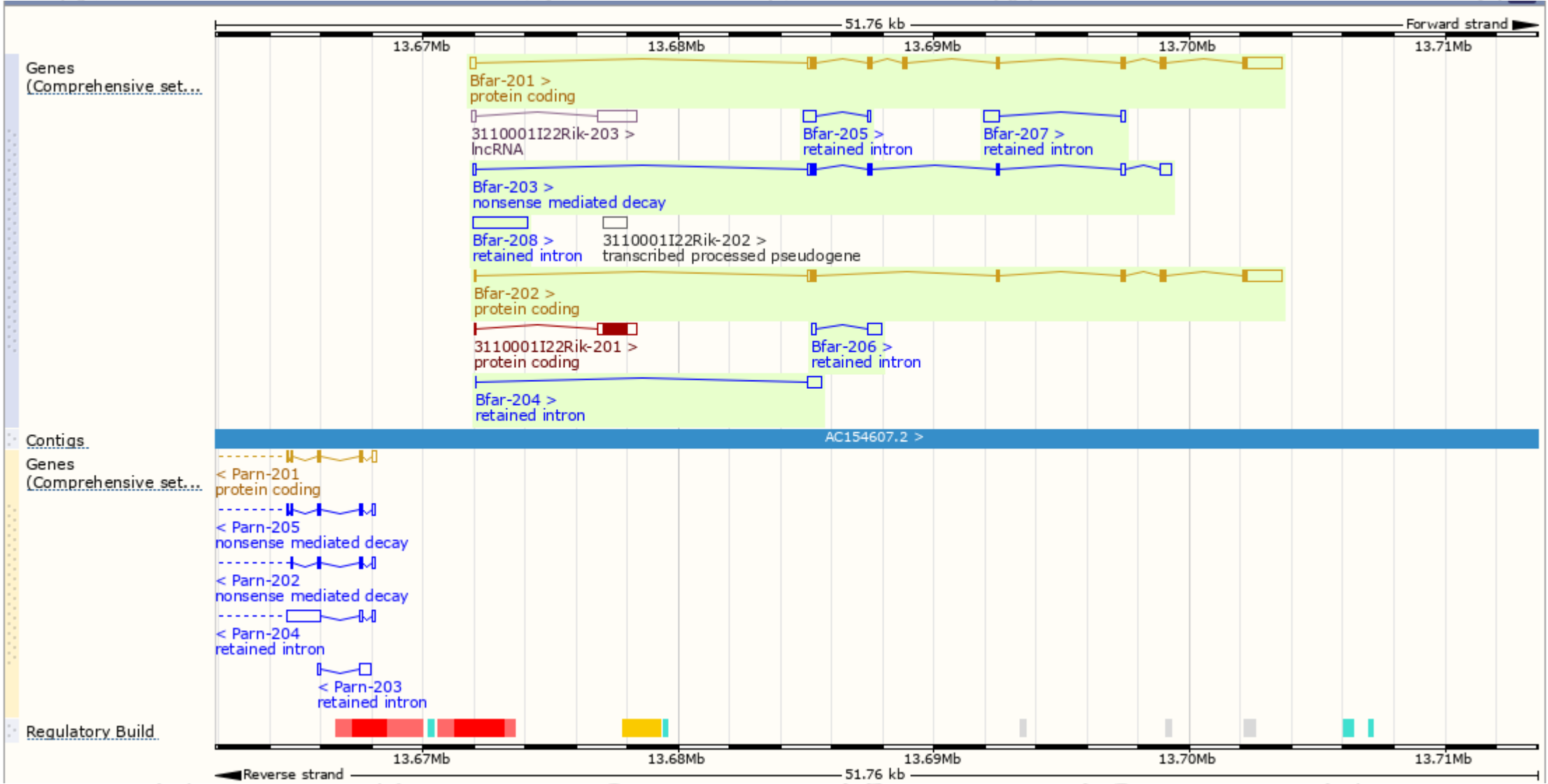
The gene has 8 transcripts, and all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Bfar-201	<a href="#">ENSMUST00000023365.12</a>	3003	<a href="#">450aa</a>	Protein coding	<a href="#">CCDS27966</a>	<a href="#">A0A0R4J040</a>	TSL:1 GENCODE basic APPRIS P1
Bfar-202	<a href="#">ENSMUST00000069281.7</a>	2456	<a href="#">325aa</a>	Protein coding	<a href="#">CCDS49769</a>	<a href="#">Q8R079</a>	TSL:1 GENCODE basic
Bfar-203	<a href="#">ENSMUST00000127973.7</a>	1407	<a href="#">176aa</a>	Nonsense mediated decay	-	<a href="#">D6RG73</a>	TSL:1
Bfar-208	<a href="#">ENSMUST00000230905.1</a>	2121	No protein	Retained intron	-	-	-
Bfar-207	<a href="#">ENSMUST00000154568.1</a>	787	No protein	Retained intron	-	-	TSL:2
Bfar-206	<a href="#">ENSMUST00000148079.1</a>	750	No protein	Retained intron	-	-	TSL:1
Bfar-205	<a href="#">ENSMUST00000144804.1</a>	659	No protein	Retained intron	-	-	TSL:1
Bfar-204	<a href="#">ENSMUST00000132349.1</a>	572	No protein	Retained intron	-	-	TSL:2

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



# Genomic location distribution





# Protein domain



If you have any questions, you are welcome to inquire.  
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