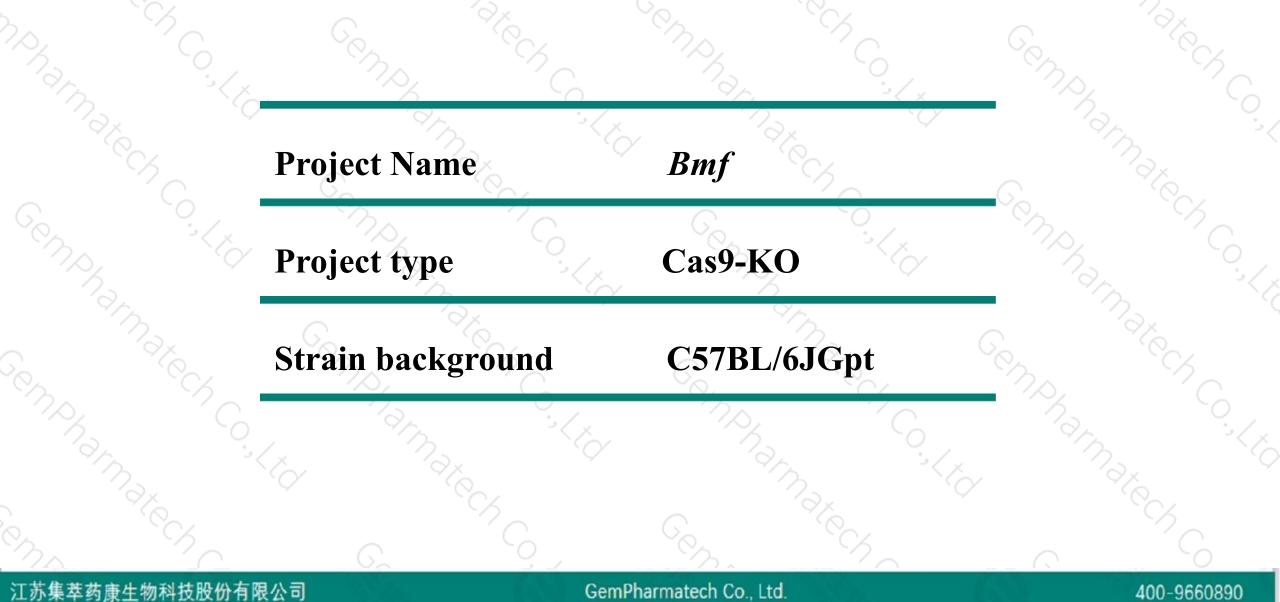


Bmf Cas9-KO Strategy

Designer:Xueting Zhang Reviewer:Yanhua Shen Date:2019-12-16

Project Overview

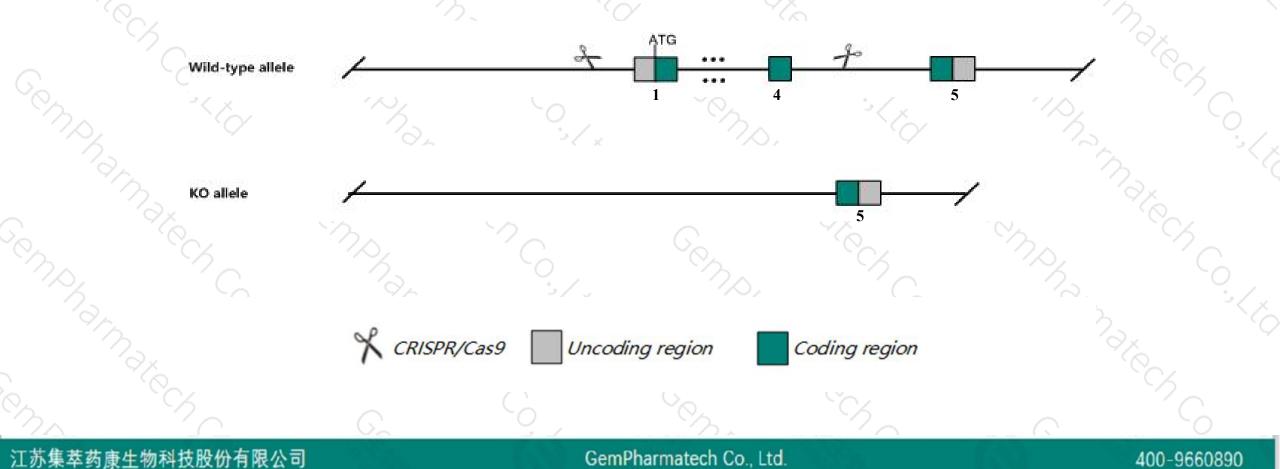




Knockout strategy



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





- The Bmf gene has 8 transcripts. According to the structure of Bmf gene, exon1-exon4 of Bmf-201 (ENSMUST00000090219.12) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify *Bmf* gene. The brief process is as follows: CRISPR/Cas9 system w

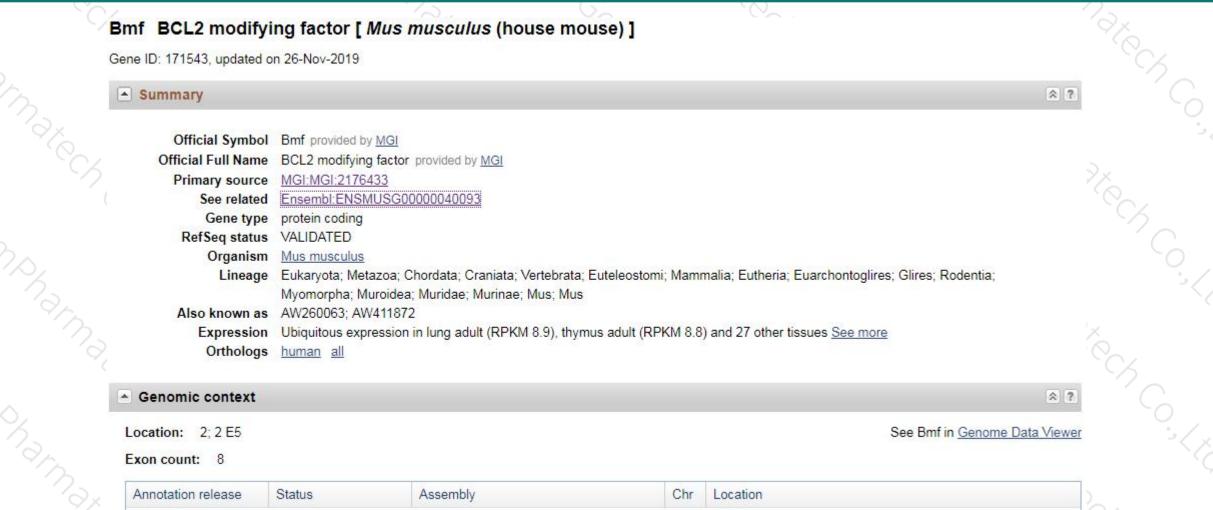
- According to the existing MGI data, Mice homozygous for targeted knockout mutations show enlarged spleen, increased B cells and CD8-positive T cells, decreased B cells and T cells apoptosis, vagina atresia and hydrometrocolpos.
- > The *Bmf* gene is located on the Chr2. If the knockout mice are crossed 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)

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Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	2	NC_000068.6 (11835449311837541	4, co <mark>mpl</mark> ement)
<u>108</u>	current	GRCm38.p6 (GCF_000001635.26)	2	NC_000068.7 (11852875711854968	6, complement)
Annotation release	Otatus	Assembly	On	Location	

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Transcript information (Ensembl)



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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Bmf-201	ENSMUST0000090219.12	4642	<u>271aa</u>	Protein coding	CCDS16578	A2AV75	TSL:1 GENCODE basic APPRIS P3
Bmf-202	ENSMUST00000110859.2	3078	<u>190aa</u>	Protein coding	CCDS79835	<u>A2AV74</u>	TSL:1 GENCODE basic APPRIS ALT2
Bmf-205	ENSMUST00000143583.1	905	No protein	IncRNA	-	1 2	TSL:3
Bmf-208	ENSMUST00000154521.1	840	No protein	IncRNA	12	20	TSL:1
Bmf-204	ENSMUST00000138342.1	447	No protein	IncRNA	7	50	TSL:2
Bmf-206	ENSMUST00000146962.1	411	No protein	IncRNA		-8	TSL:5
Bmf-203	ENSMUST00000125860.1	374	No protein	IncRNA	-	1 2	TSL:2
Bmf-207	ENSMUST00000152123.1	361	No protein	IncRNA	12	20	TSL:2

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

< Bmf-201 protein coding

Reverse strand

- 20.93 kb --

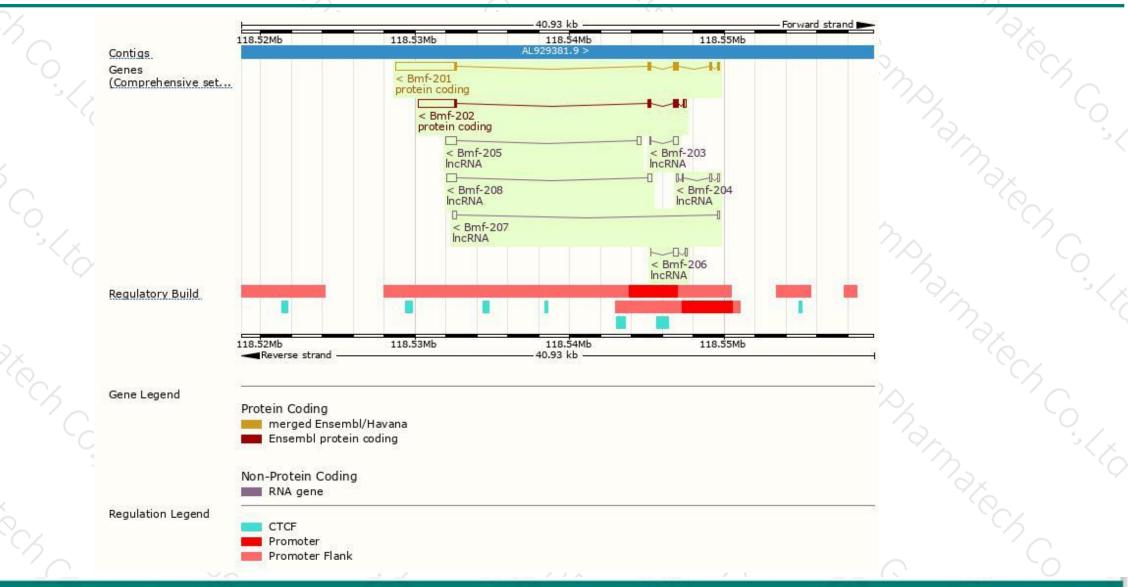
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Genomic location distribution





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Protein domain



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Pfam. PANTHER				nodifying factor				
All sequence SNPs/	Sequenc	e variants (dbSNP a				E.	1	
Variant Legend		sense variant onymous variant						
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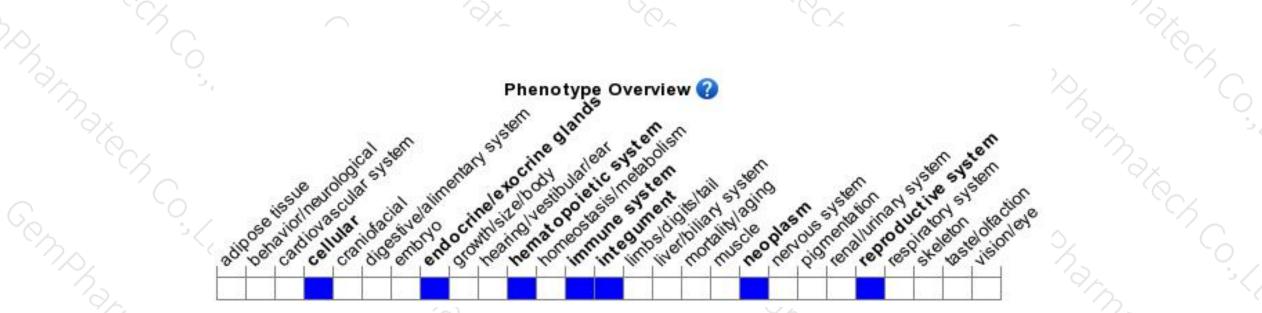
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Mouse phenotype description(MGI)





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, Mice homozygous for targeted knockout mutations show enlarged spleen, increased B cells and CD8-positive T cells, decreased B cells and T cells apoptosis, vagina atresia and hydrometrocolpos.



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



