

***Babam2* Cas9-KO Strategy**

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Project Overview

Project Name

Babam2

Project type

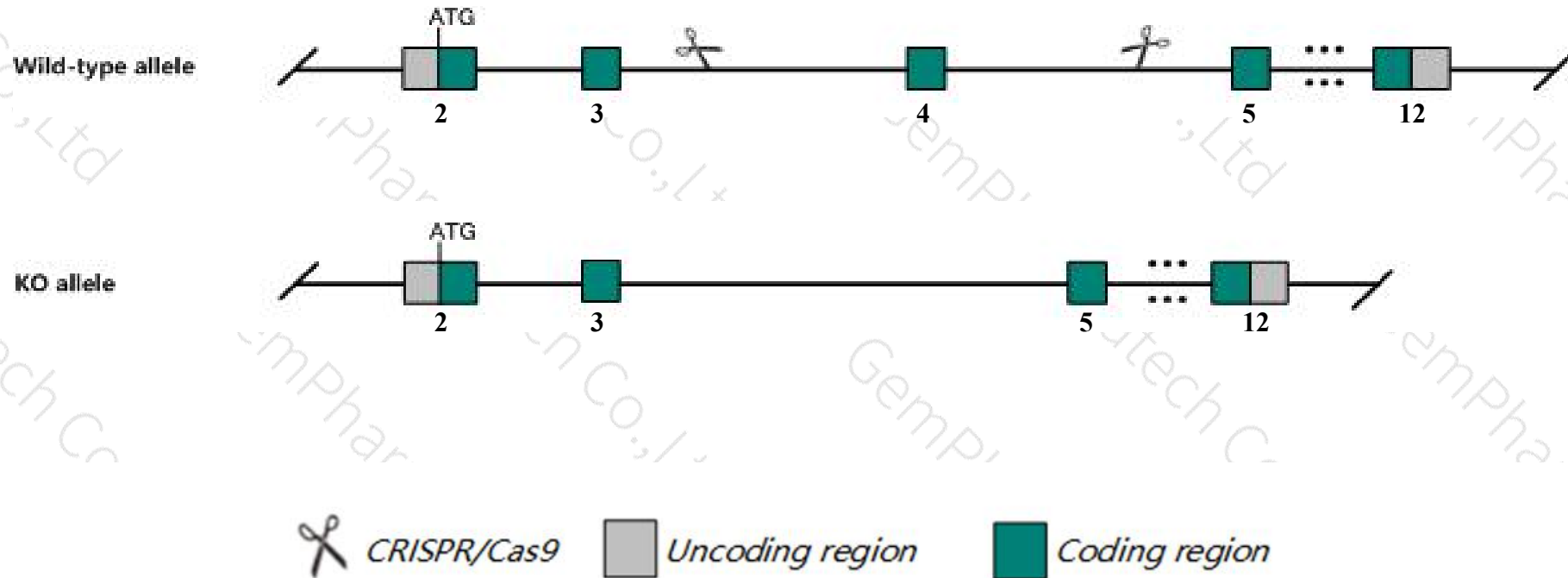
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Babam2* gene. The schematic diagram is as follows:



- The *Babam2* gene has 16 transcripts. According to the structure of *Babam2* gene, exon4 of *Babam2-209* (ENSMUST00000201352.3) transcript is recommended as the knockout region. The region contains 95bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Babam2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele are fertile. However, fibroblasts exhibit decreased proliferation and increased cellular replicative senescence in response to irradiation and hydrogen peroxide with impaired DNA damage repair.
- Transcript *Babam2*-207&208&210&211&212&214 may not be affected.
- The effect on transcript *Babam2*-216 is unknown.
- The N-terminal of *Babam2* gene will remain several amino acids, it may remain the partial function of *Babam2* gene.
- The *Babam2* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Babam2 BRISC and BRCA1 A complex member 2 [Mus musculus (house mouse)]

Gene ID: 107976, updated on 31-Jan-2019

Summary



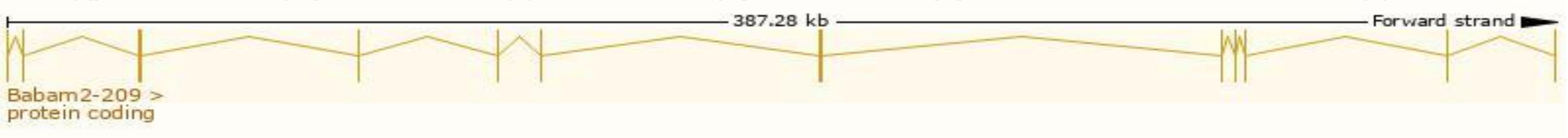
Official Symbol	Babam2 provided by MGI
Official Full Name	BRISC and BRCA1 A complex member 2 provided by MGI
Primary source	MGI:MGI:1333875
See related	Ensembl:ENSMUSG00000052139
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	6030405P19Rik, AI429776, B830038C02Rik, Bre
Expression	Ubiquitous expression in adrenal adult (RPKM 28.8), bladder adult (RPKM 19.0) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

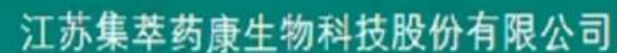
The gene has 16 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Babam2-209	ENSMUST00000201352.3	1888	383aa	Protein coding	CCDS19188	Q8K3W0	TSL:1 GENCODE basic APPRIS P1
Babam2-201	ENSMUST00000063813.10	1410	420aa	Protein coding	CCDS19189	Q8K3W0	TSL:1 GENCODE basic
Babam2-202	ENSMUST00000071531.11	1308	374aa	Protein coding	CCDS39058	Q8K3W0	TSL:1 GENCODE basic
Babam2-205	ENSMUST00000131995.6	1220	245aa	Protein coding	CCDS39059	Q8K3W0	TSL:1 GENCODE basic
Babam2-203	ENSMUST00000114507.9	1143	319aa	Protein coding	CCDS51461	Q8K3W0	TSL:1 GENCODE basic
Babam2-204	ENSMUST00000114515.8	1497	385aa	Protein coding	-	D3Z7P0	TSL:5 GENCODE basic
Babam2-216	ENSMUST00000202815.3	462	63aa	Protein coding	-	A0A0J9YV56	CDS 3' incomplete TSL:3
Babam2-206	ENSMUST00000200705.1	842	205aa	Nonsense mediated decay	-	E9Q0U3	TSL:5
Babam2-215	ENSMUST00000202293.3	668	43aa	Nonsense mediated decay	-	E9Q8Q1	TSL:5
Babam2-207	ENSMUST00000201107.3	2034	No protein	Retained intron	-	-	TSL:1
Babam2-210	ENSMUST00000201487.3	742	No protein	Retained intron	-	-	TSL:1
Babam2-208	ENSMUST00000201202.3	715	No protein	Retained intron	-	-	TSL:1
Babam2-211	ENSMUST00000201592.3	587	No protein	lncRNA	-	-	TSL:3
Babam2-213	ENSMUST00000202087.1	576	No protein	lncRNA	-	-	TSL:2
Babam2-212	ENSMUST00000202080.1	377	No protein	lncRNA	-	-	TSL:3
Babam2-214	ENSMUST00000202270.1	339	No protein	lncRNA	-	-	TSL:3

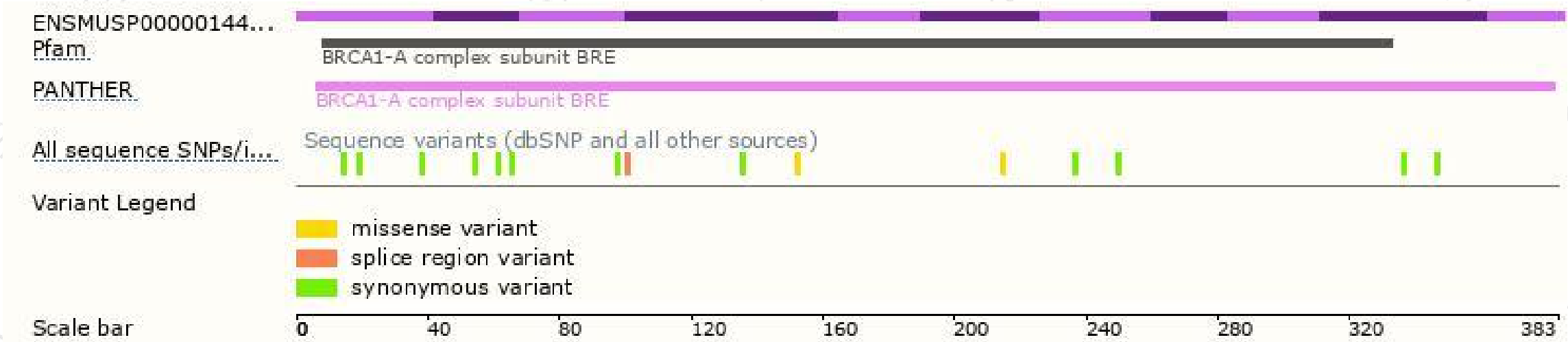
The strategy is based on the design of *Babam2-209* transcript,The transcription is shown below



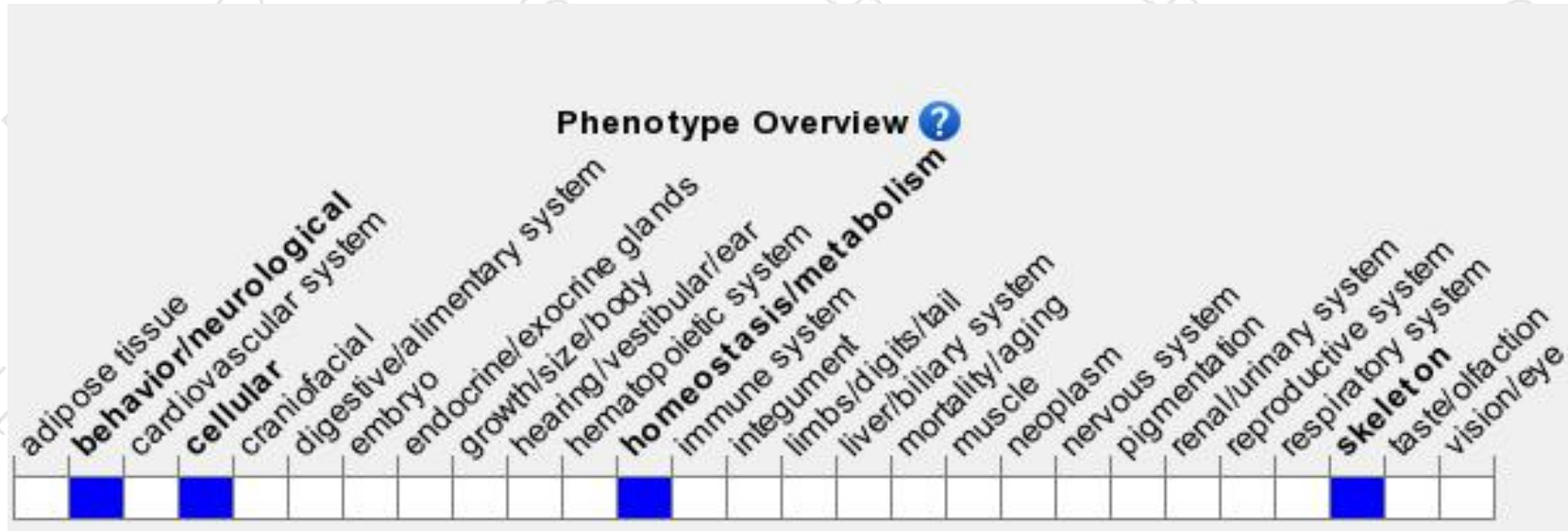
集萃药康
GemPharmatech



Protein domain



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 a knock-out allele are fertile. However, fibroblasts exhibit decreased proliferation and increased cellular replicative senescence in response to irradiation and hydrogen peroxide with impaired DNA damage repair.

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

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