

Banp Cas9-CKO Strategy

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Project Overview

Project Name

Banp

Project type

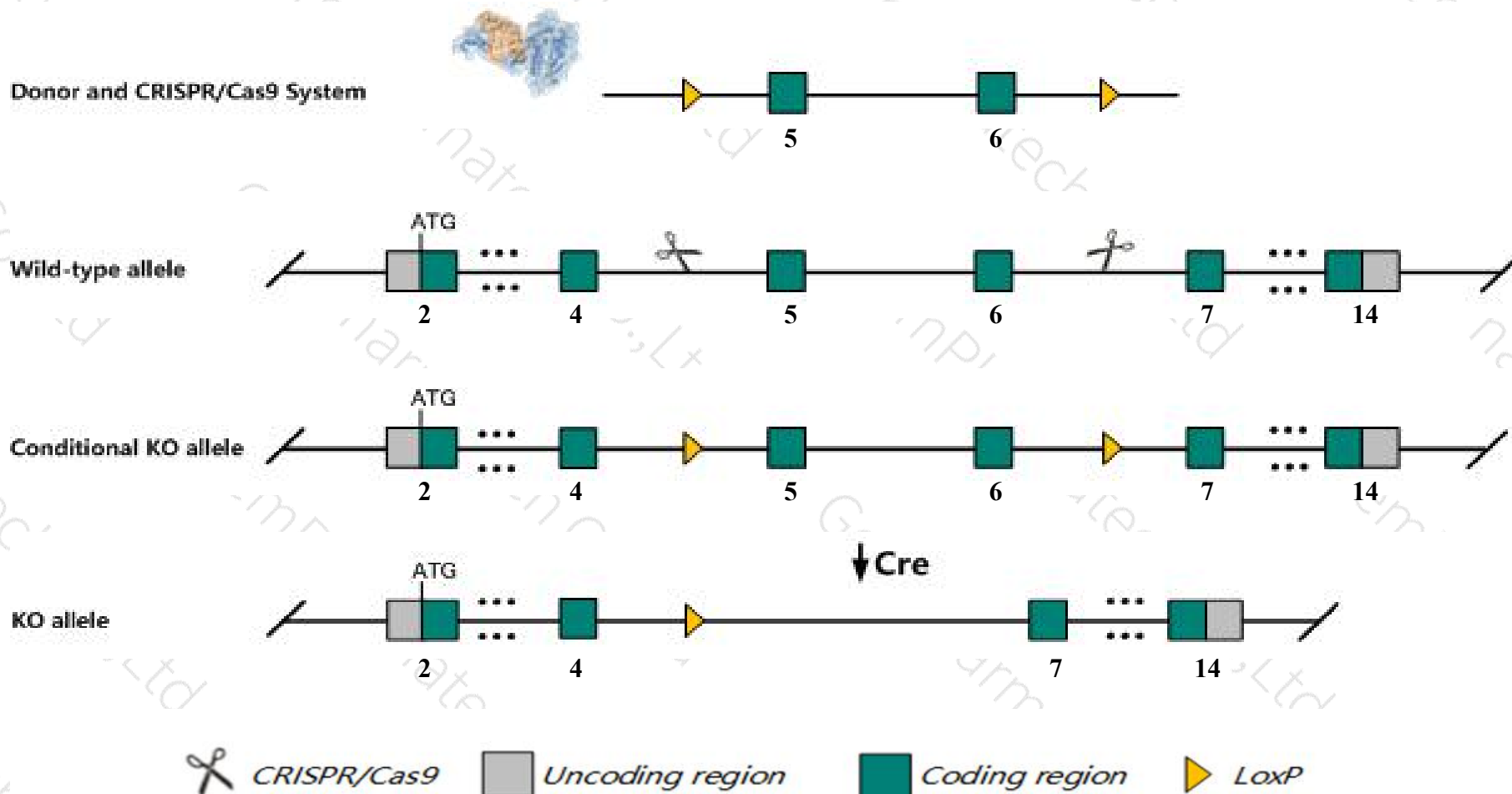
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



Technical routes

- The *Banp* gene has 16 transcripts. According to the structure of *Banp* gene, exon5-exon6 of *Banp*-204 (ENSMUST00000170857.7) transcript is recommended as the knockout region. The region contains 293bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Banp* 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 KO region contains partial intron of the *Gm20388* gene. Knockout the region may affect the function of *Gm20388* gene.
- The *Banp* gene is located on the Chr8. 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)

Banp BTG3 associated nuclear protein [Mus musculus (house mouse)]

Gene ID: 53325, updated on 31-Jan-2019

Summary



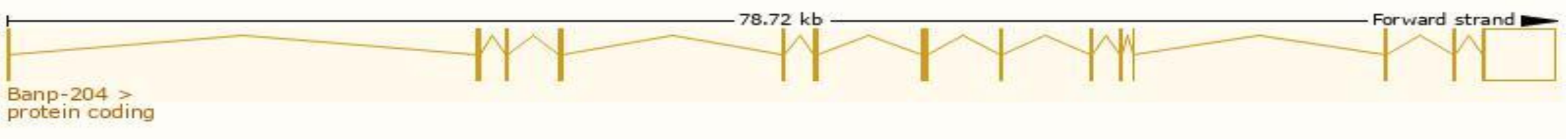
Official Symbol	Banp provided by MGI
Official Full Name	BTG3 associated nuclear protein provided by MGI
Primary source	MGI:MGI:1889023
See related	Ensembl:ENSMUSG00000025316
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AA408158, SMAR1
Expression	Ubiquitous expression in ovary adult (RPKM 15.5), thymus adult (RPKM 13.6) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

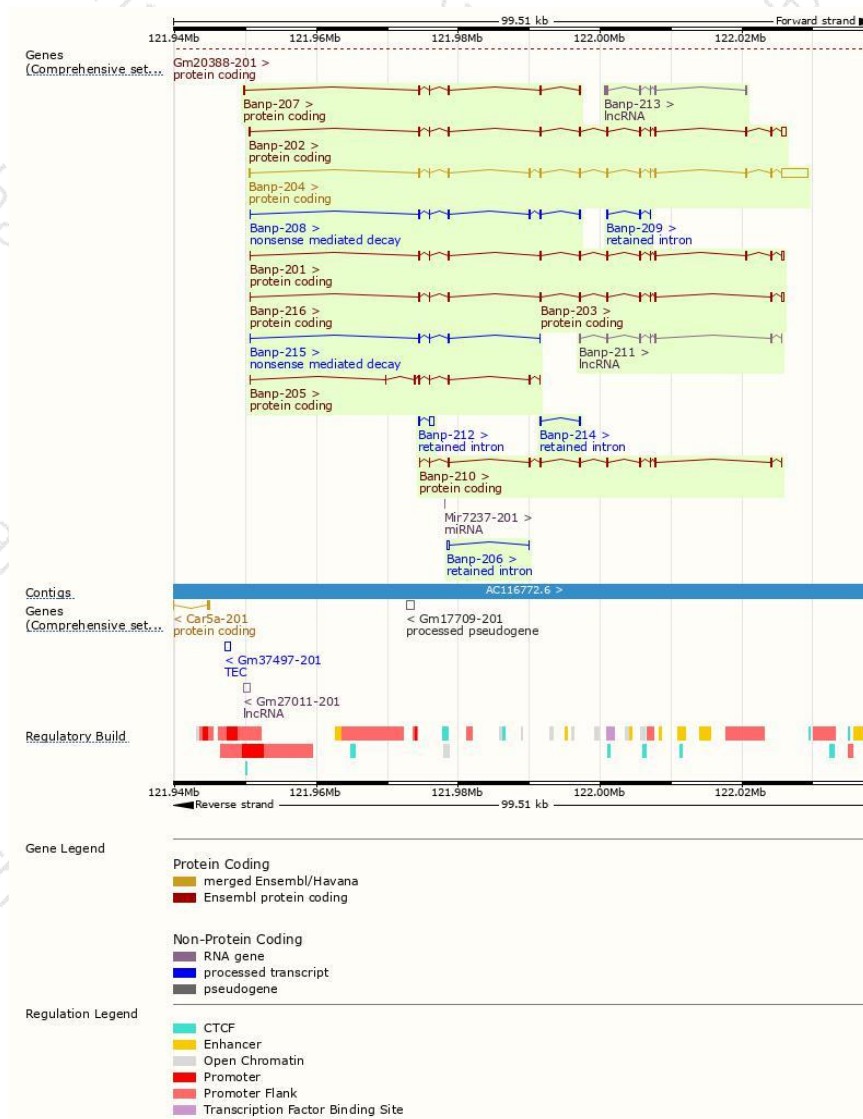
The gene has 16 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Banp-204	ENSMUST00000170857.7	5444	548aa	Protein coding	CCDS40502	Q8VBU8	TSL:1 GENCODE basic APPRIS P3
Banp-202	ENSMUST00000093078.12	2289	506aa	Protein coding	CCDS72177	Q8VBU8	TSL:1 GENCODE basic APPRIS ALT2
Banp-201	ENSMUST00000026354.14	1970	509aa	Protein coding	CCDS72176	Q8VBU8	TSL:1 GENCODE basic APPRIS ALT2
Banp-210	ENSMUST00000173254.7	1521	506aa	Protein coding	-	Q8VBU8	TSL:5 GENCODE basic APPRIS ALT2
Banp-203	ENSMUST00000167711.8	1289	321aa	Protein coding	-	F6V6B6	CDS 5' incomplete TSL:5
Banp-207	ENSMUST00000172628.7	849	265aa	Protein coding	-	G3UWM0	CDS 3' incomplete TSL:5
Banp-205	ENSMUST00000172511.7	699	179aa	Protein coding	-	G3UWN8	CDS 3' incomplete TSL:5
Banp-216	ENSMUST00000174753.7	513	126aa	Protein coding	-	G3UYF0	CDS 3' incomplete TSL:3
Banp-208	ENSMUST00000172681.7	893	55aa	Nonsense mediated decay	-	G3UZ43	TSL:5
Banp-215	ENSMUST00000174445.7	470	55aa	Nonsense mediated decay	-	G3UZ43	TSL:3
Banp-212	ENSMUST00000173753.1	706	No protein	Retained intron	-	-	TSL:2
Banp-206	ENSMUST00000172513.1	481	No protein	Retained intron	-	-	TSL:2
Banp-209	ENSMUST00000173201.1	457	No protein	Retained intron	-	-	TSL:5
Banp-214	ENSMUST00000174327.1	445	No protein	Retained intron	-	-	TSL:3
Banp-211	ENSMUST00000173396.1	780	No protein	lncRNA	-	-	TSL:3
Banp-213	ENSMUST00000173925.7	609	No protein	lncRNA	-	-	TSL:5

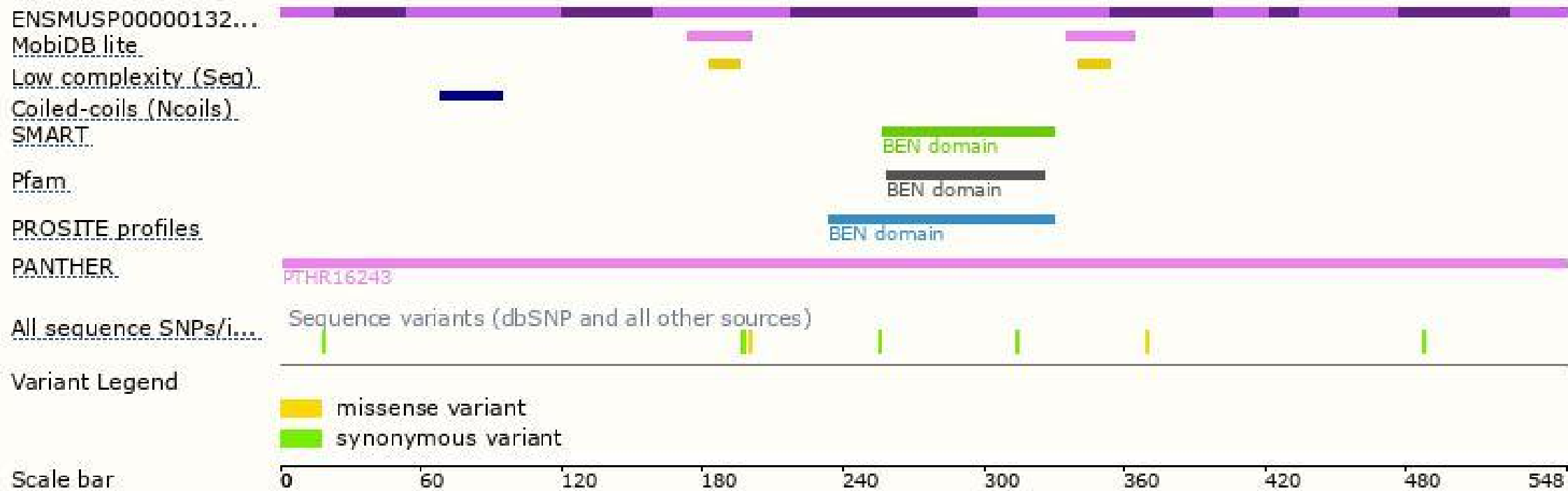
The strategy is based on the design of *Banp-204* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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