

Phf14 Cas9-KO Strategy

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Project Overview

Project Name

Phf14

Project type

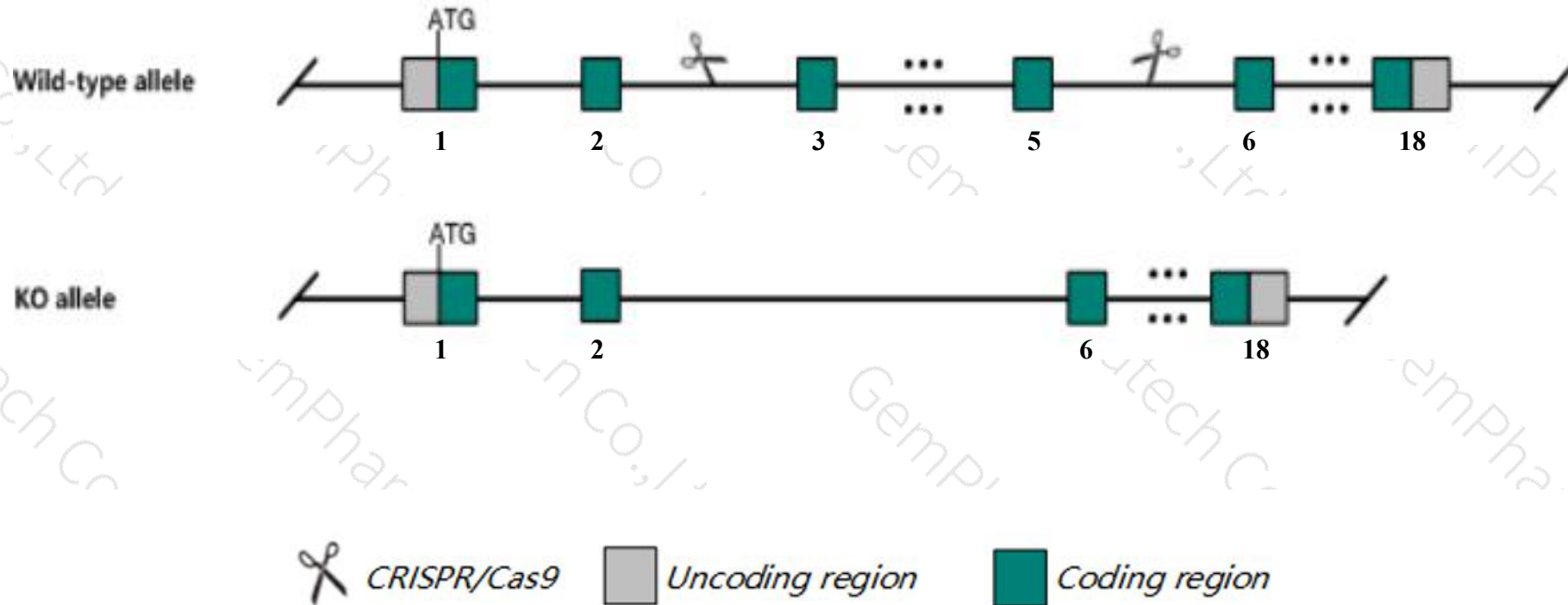
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Phf14* gene. The schematic diagram is as follows:



- The *Phf14* gene has 11 transcripts. According to the structure of *Phf14* gene, exon3-exon5 of *Phf14*-203(ENSMUST00000115511.8) transcript is recommended as the knockout region. The region contains 1072bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Phf14* gene. The brief process is as follows: CRISPR/Cas9 system 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.

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit complete neonatal lethality due to respiratory failure, pulmonary wall hypertrophy, abnormal sternum ossification, and increased proliferation of bone marrow-derived mesenchymal cells and mouse embryonic fibroblasts.
- Transcript 205 CDS 3' incomplete the influences is unknown.
- The *Phf14* gene is located on the Chr6. 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)

Phf14 PHD finger protein 14 [Mus musculus (house mouse)]

Gene ID: 75725, updated on 13-Mar-2020

Summary



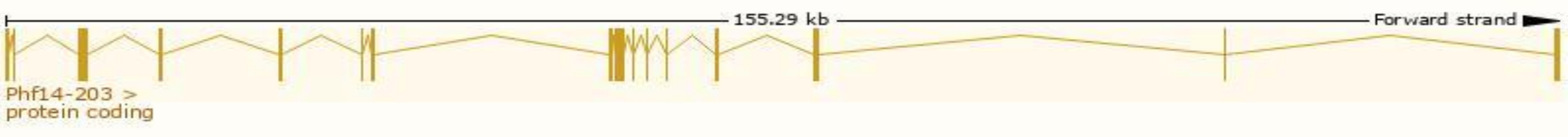
Official Symbol	Phf14 provided by MGI
Official Full Name	PHD finger protein 14 provided by MGI
Primary source	MGI:MGI:1923539
See related	Ensembl:ENSMUSG00000029629
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1110001C23Rik, 4932409F11Rik, 5730446A07Rik, AA623952, AV297001, mKIAA0783
Expression	Broad expression in CNS E11.5 (RPKM 8.4), CNS E14 (RPKM 6.2) and 19 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

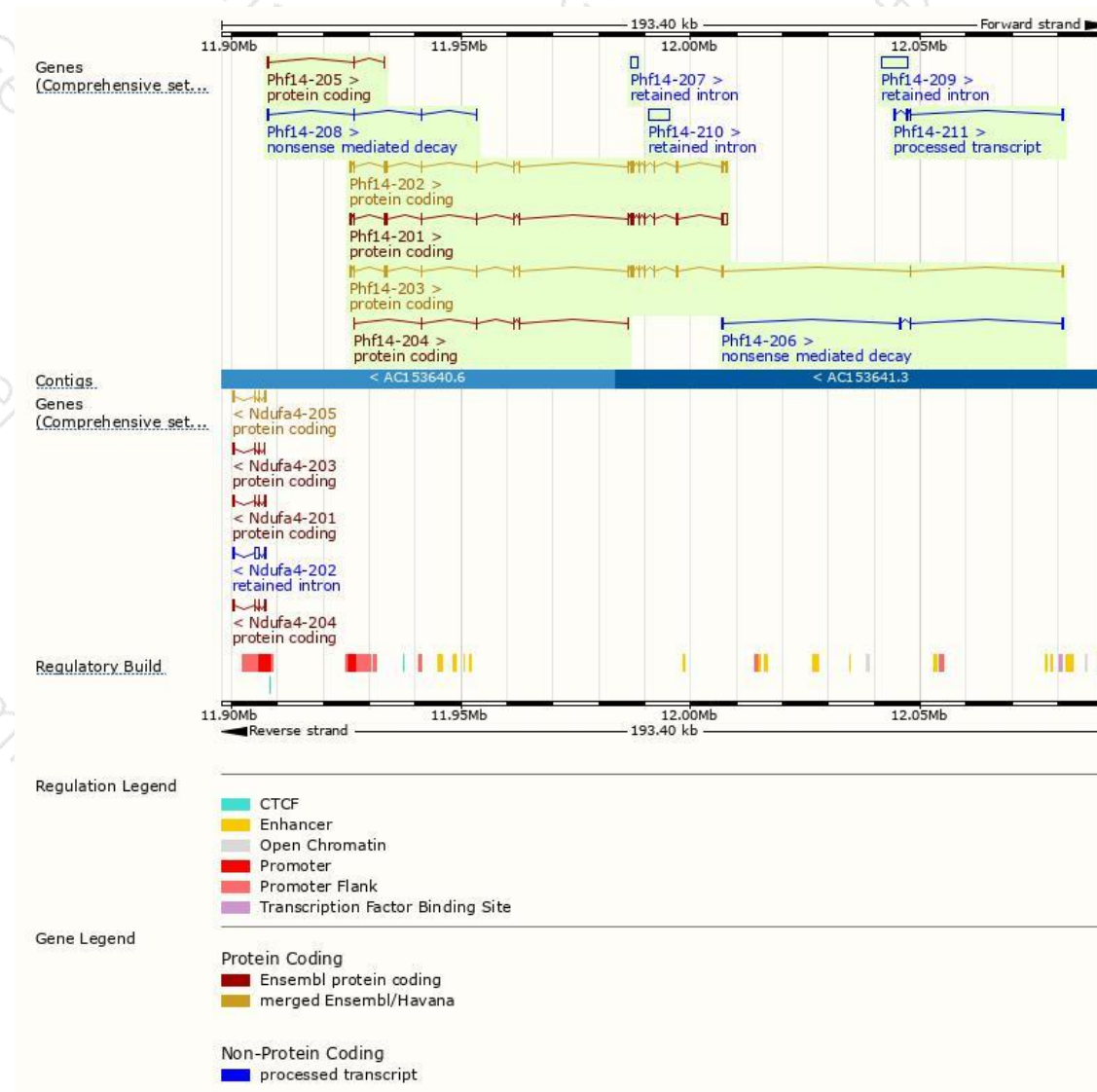
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Phf14-202	ENSMUST00000115510.7	3353	881aa	Protein coding	CCDS39428	G5E8S0	TSL:1 GENCODE basic
Phf14-203	ENSMUST00000115511.8	3336	941aa	Protein coding	CCDS51720	Q9D4H9	TSL:5 GENCODE basic APPRIS P1
Phf14-201	ENSMUST00000090632.10	3985	878aa	Protein coding	-	Q9D4H9	TSL:1 GENCODE basic
Phf14-204	ENSMUST00000133776.1	727	243aa	Protein coding	-	F6TN92	CDS 5' and 3' incomplete TSL:3
Phf14-205	ENSMUST00000155037.3	478	90aa	Protein coding	-	A0A0N4SV73	CDS 3' incomplete TSL:2
Phf14-206	ENSMUST00000203045.1	566	69aa	Nonsense mediated decay	-	A0A0N4SWI1	CDS 5' incomplete TSL:3
Phf14-208	ENSMUST00000203459.2	483	42aa	Nonsense mediated decay	-	A0A0N4SW36	TSL:3
Phf14-211	ENSMUST00000214543.1	462	No protein	Processed transcript	-	-	TSL:2
Phf14-209	ENSMUST00000204150.1	5905	No protein	Retained intron	-	-	TSL:NA
Phf14-210	ENSMUST00000204565.1	4438	No protein	Retained intron	-	-	TSL:NA
Phf14-207	ENSMUST00000203222.1	1592	No protein	Retained intron	-	-	TSL:NA

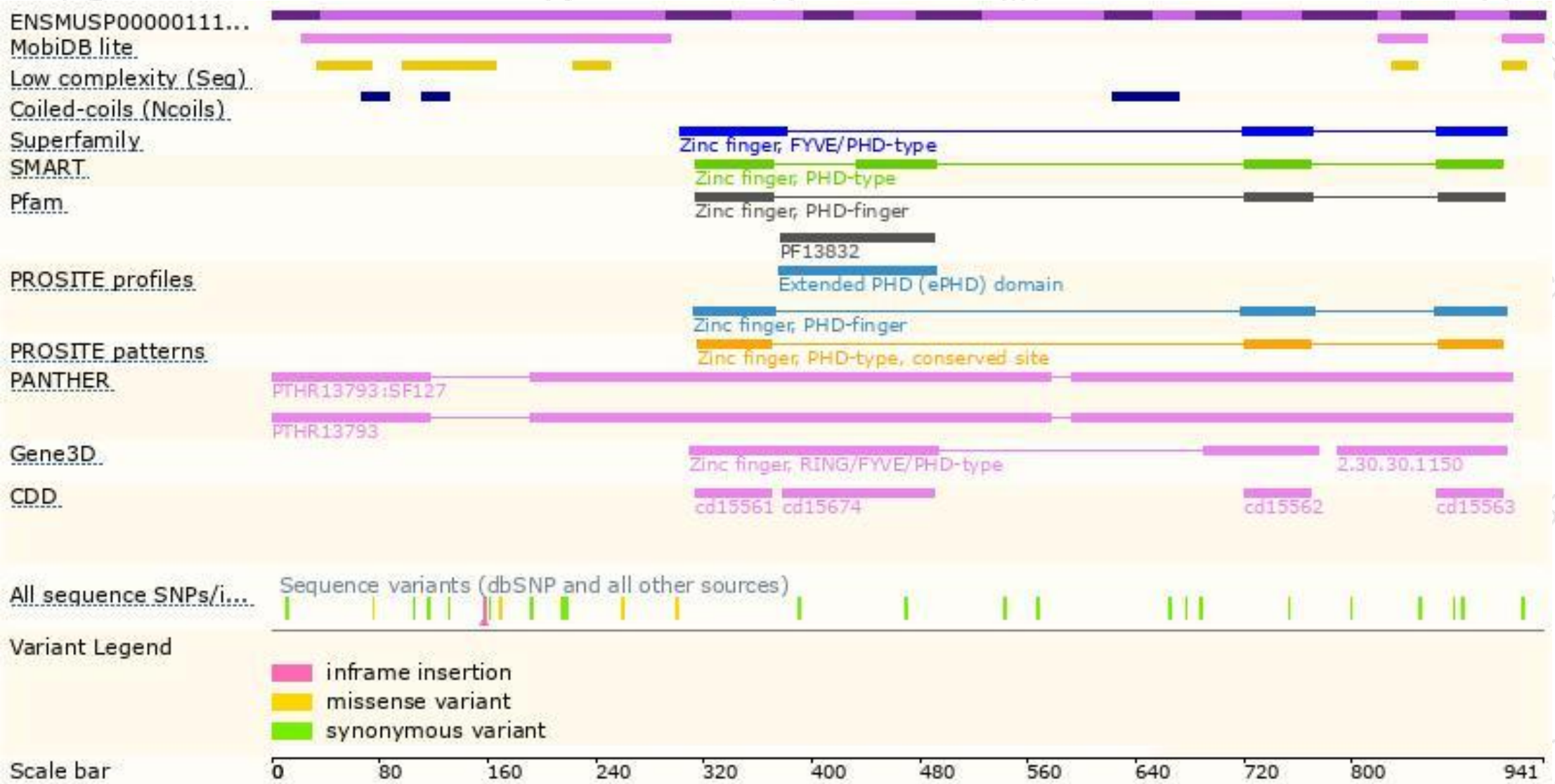
The strategy is based on the design of *Phf14-203* transcript,the transcription is shown below:



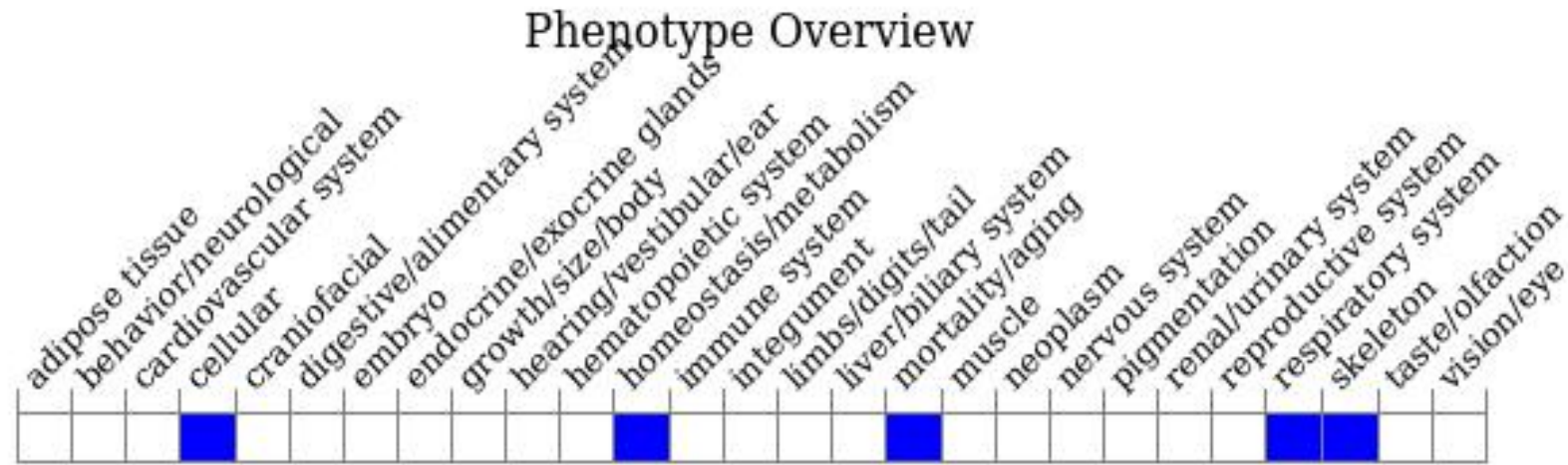
Genomic location distribution



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 exhibit complete neonatal lethality due to respiratory failure, pulmonary wall hypertrophy, abnormal sternum ossification, and increased proliferation of bone marrow-derived mesenchymal cells and mouse embryonic fibroblasts.

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

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