

Aifl-CreERT2-PolyA Cas9-KI Strategy

Designer:

Design Date:

Reviewer

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2019-9-25

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Project Overview

Project Name

Aifl-CreERT2-PolyA

Project type

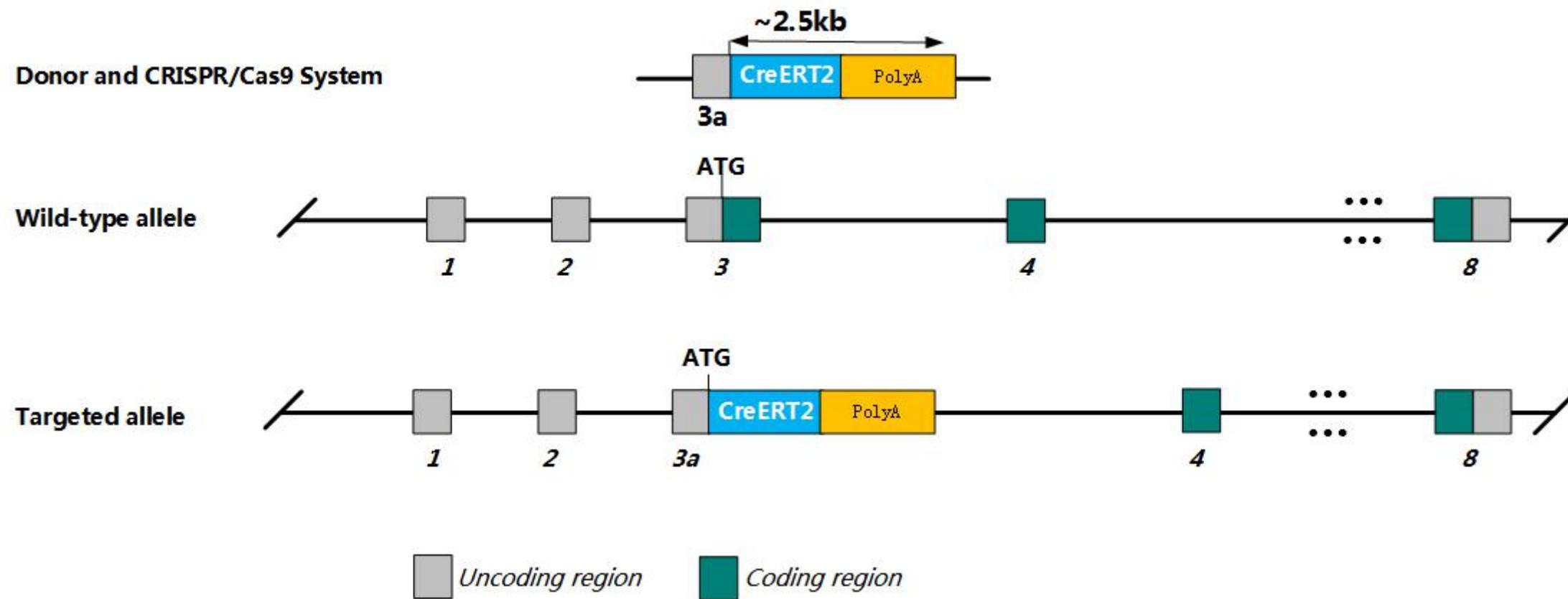
Cas9-KI

Strain background

C57BL/6J

Knockin strategy

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



Technical routes

- The *Aifl* gene has 7 transcripts. According to the structure of *Aifl* gene, *Aifl-206*(ENSMUST00000173324.7) is selected for presentation of the recommended strategy.
- *Aifl-206* gene has 8 exons, with the ATG start codon in exon3 and TGA stop codon in exon8.
- We make *Aifl-CreERT2* knockin mice via CRISPR/Cas9 system. Cas9 mRNA, sgRNA and donor will be co-injected into zygotes. sgRNA direct Cas9 endonuclease cleavage at exon 3 near the start codon ATG , and create a DSB(double-strand break). Such breaks will be repaired, and result in *CreERT2-polyA* inserted after the start codon ATG by homologous recombination. The pups will be genotyped by PCR, followed by sequence analysis.

Notice

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit decreased spleen weight, decreased platelet cell number and decreased susceptibility to induced arthritis.
- Insertion of CreERT2 may affect the regulation of the 5' end of the *Aifl* gene.
- The *Aifl* gene is located on the Chr17. If the knockin 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 gene transcription and translation processes, all risks cannot be predicted under existing information.

Gene information (NCBI)

Aif1 allograft inflammatory factor 1 [*Mus musculus* (house mouse)]

Gene ID: 11629, updated on 21-Aug-2019

Summary

Official Symbol Aif1 provided by MGI

Official Full Name allograft inflammatory factor 1 provided by MGI

Primary source MGI: MGI:1343098

See related Ensembl: ENSMUSG00000024397

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 G1; Iba1; AIF-1; AI607846; D17H6S50E

Expression Biased expression in testis adult (RPKM 116.9) and liver E18 (RPKM 4.3) [See more](#)

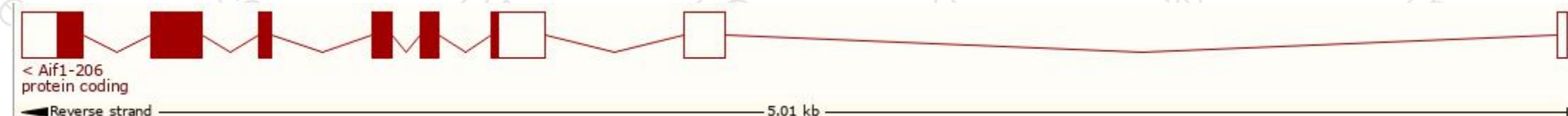
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

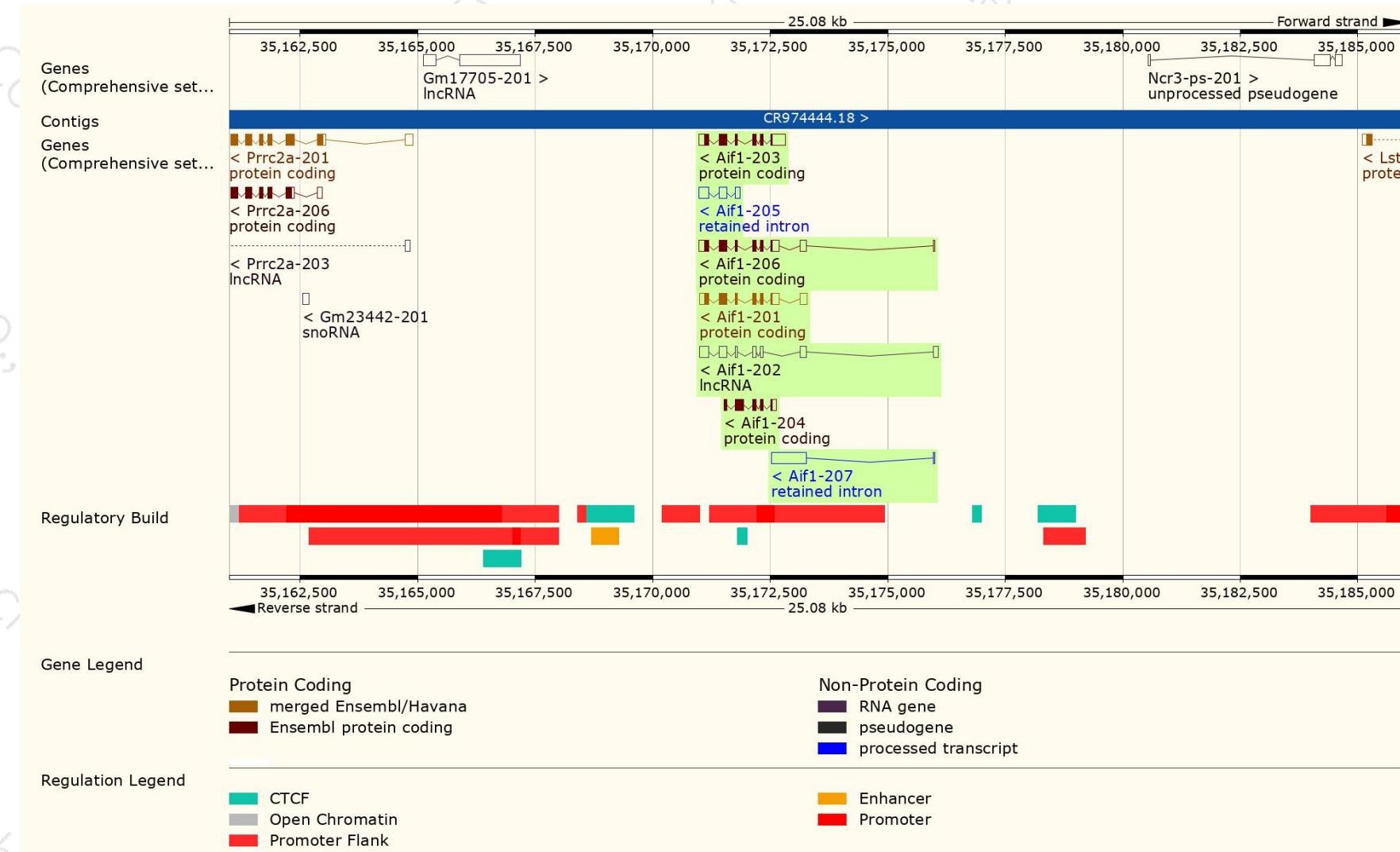
The gene has 7 transcripts, and all transcripts are shown below :

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Aif1-201	ENSMUST0000025257.11	847	147aa	Protein coding	CCDS28689	O70200 Q4FJL9	TSL:2 GENCODE basic APPRIS P1
Aif1-202	ENSMUST00000172679.1	763	No protein	lncRNA	-	-	TSL:3
Aif1-203	ENSMUST00000172693.7	842	147aa	Protein coding	CCDS28689	O70200 Q4FJL9	TSL:1 GENCODE basic APPRIS P1
Aif1-204	ENSMUST00000173106.1	477	128aa	Protein coding	-	G3UYJ2	CDS 3' incomplete TSL:3
Aif1-205	ENSMUST00000173281.7	462	No protein	Retained intron	-	-	TSL:2
Aif1-206	ENSMUST00000173324.7	875	147aa	Protein coding	CCDS28689	O70200 Q4FJL9	TSL:1 GENCODE basic APPRIS P1
Aif1-207	ENSMUST00000174044.1	775	No protein	Retained intron	-	-	TSL:5

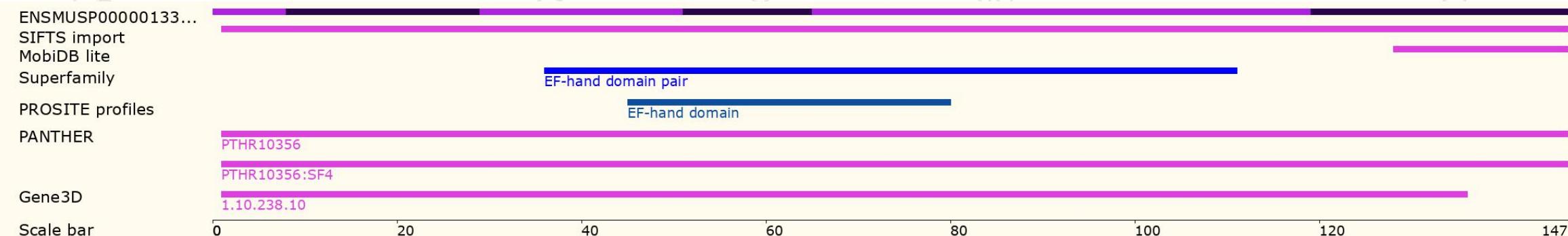
The strategy is based on the design of *Aif1-206* transcript, The transcription is shown below



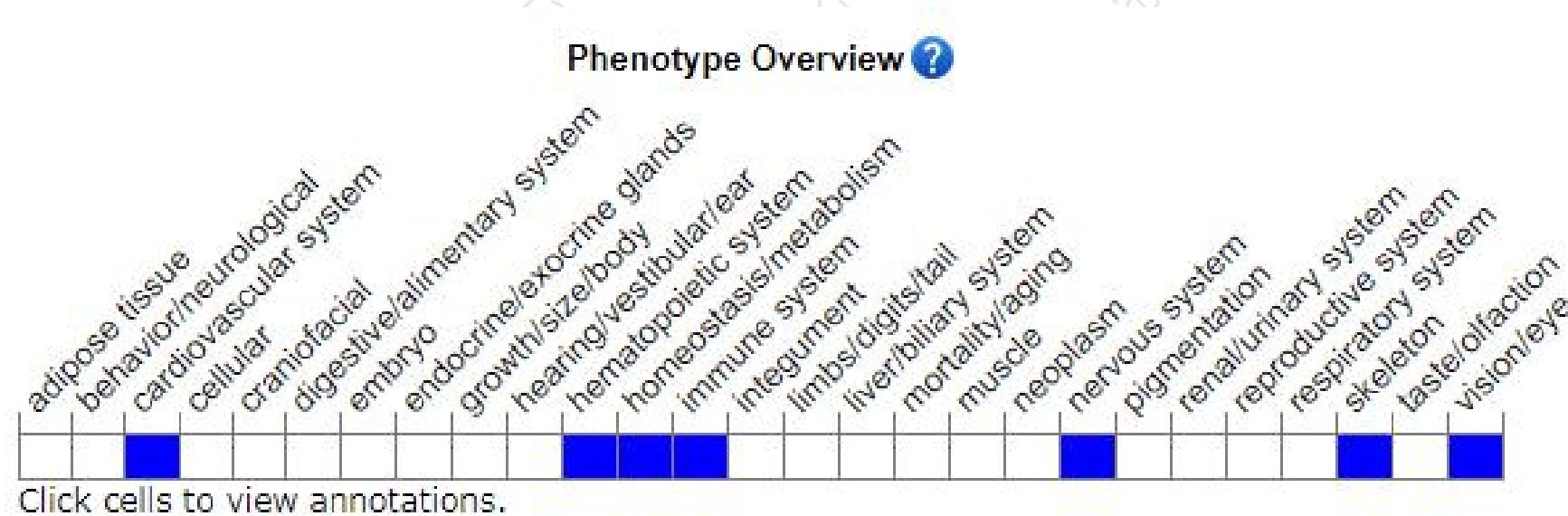
Genomic location distribution



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/marker/MGI:2179326>) .

Mice homozygous for a knock-out allele exhibit decreased spleen weight, decreased platelet cell number and decreased susceptibility to induced arthritis.

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

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