Mafk Cas9-CKO *Strategy*

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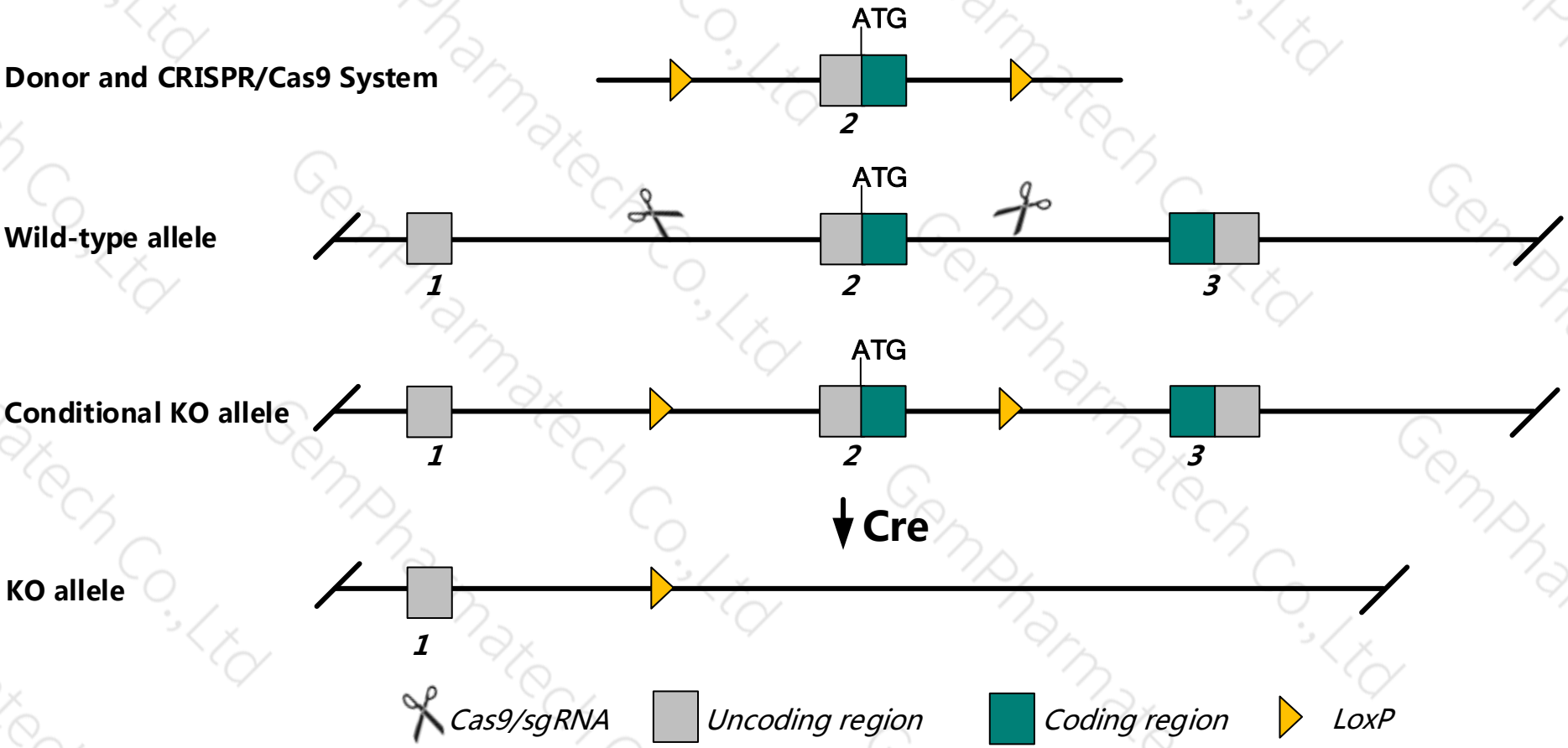
Project Overview

Project Name	***Mafk***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

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



Technical routes

- The *Mafk* gene has 3 transcripts.According to the structure of *Mafk* gene, exon2 of *Mafk*-201 (ENSMUST00000018287.9)transcript is recommended as the knockout region.The region contains the start codon ATG.Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Mafk* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed.Cas9, sgRNA 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 was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues or cell types.

Notice

- According to the existing MGI data，mice homozygous for a knock-out allele are viable, fertile, healthy and phenotypically normal with no detectable erythroid deficiencies.

- The *Mafk* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information （NCBI）

集萃药康 GemPharmatech

Mafk v-maf musculoaponeurotic fibrosarcoma oncogene family, protein K (avian) [*Mus musculus* (house mouse)]

Gene ID: 17135, updated on 10-Oct-2019

Summary

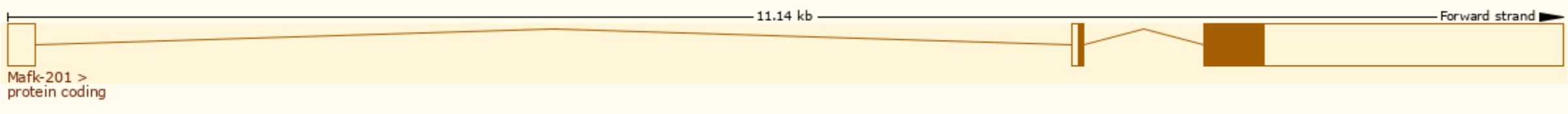
Official Symbol	Mafk provided by MGI
Official Full Name	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein K (avian) provided by MGI
Primary source	MGI:MGI:99951
See related	Ensembl:ENSMUSG00000018143
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	NF-E2; Nfe2u; AW061068
Expression	Ubiquitous expression in small intestine adult (RPKM 16.9), colon adult (RPKM 16.7) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

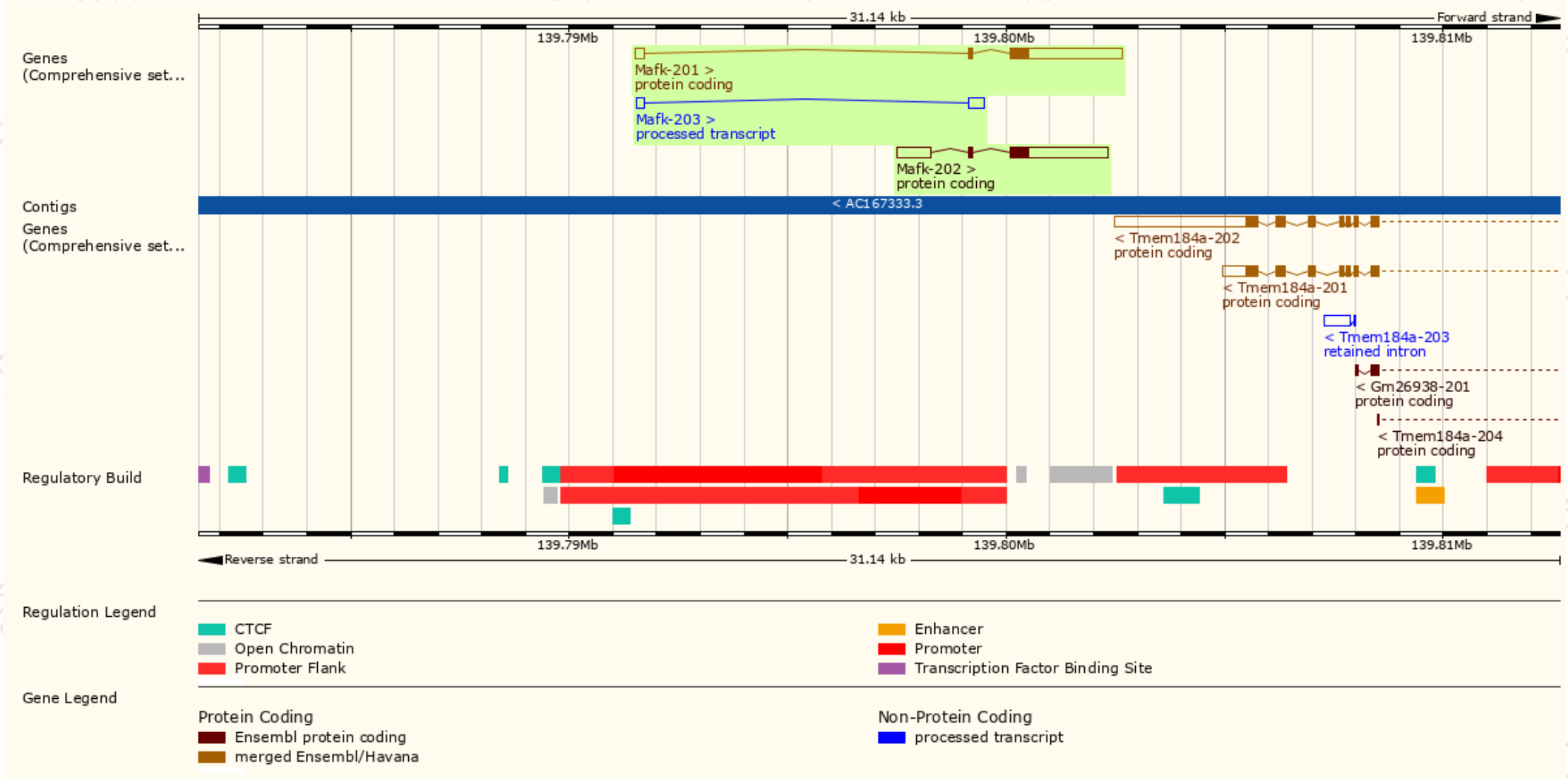
The gene has 3 transcripts, and all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Mafk-202	ENSMUST00000110836.1	3097	156aa	Protein coding	CCDS19814	Q3UP84 Q61827	TSL:5 GENCODE basic APPRIS P1
Mafk-201	ENSMUST00000018287.9	2849	156aa	Protein coding	CCDS19814	Q3UP84 Q61827	TSL:1 GENCODE basic APPRIS P1
Mafk-203	ENSMUST00000151577.1	541	No protein	Processed transcript	-	-	TSL:2

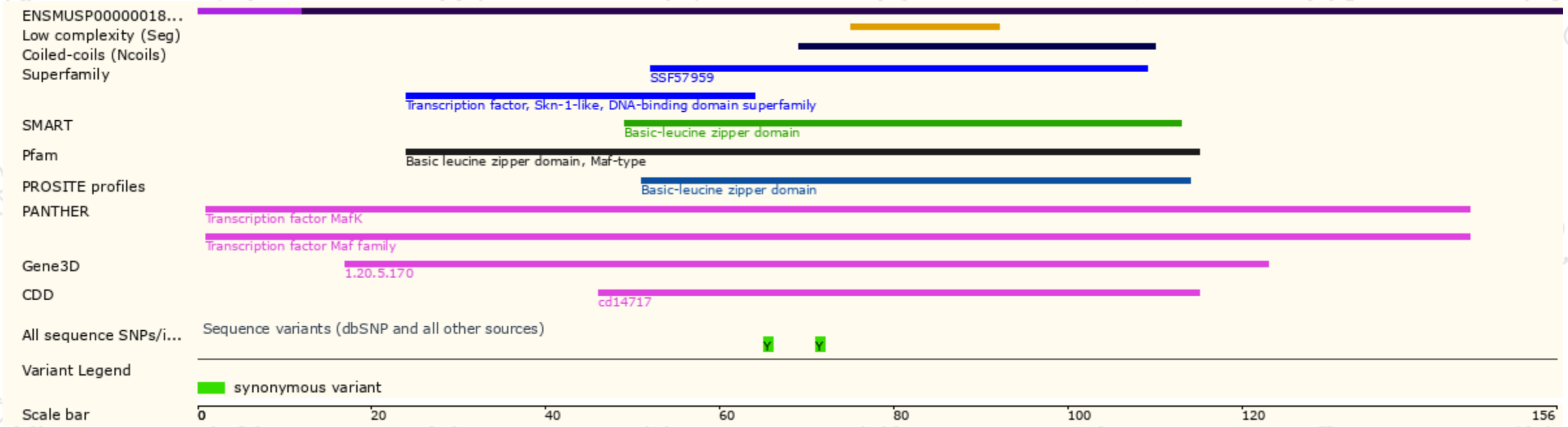
The strategy is based on the design of *Mafk-201* transcript,the transcription is shown below:



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 are viable, fertile, healthy and phenotypically normal with no detectable erythroid deficiencies.

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

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