

Myd88 Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Myd88

Project type

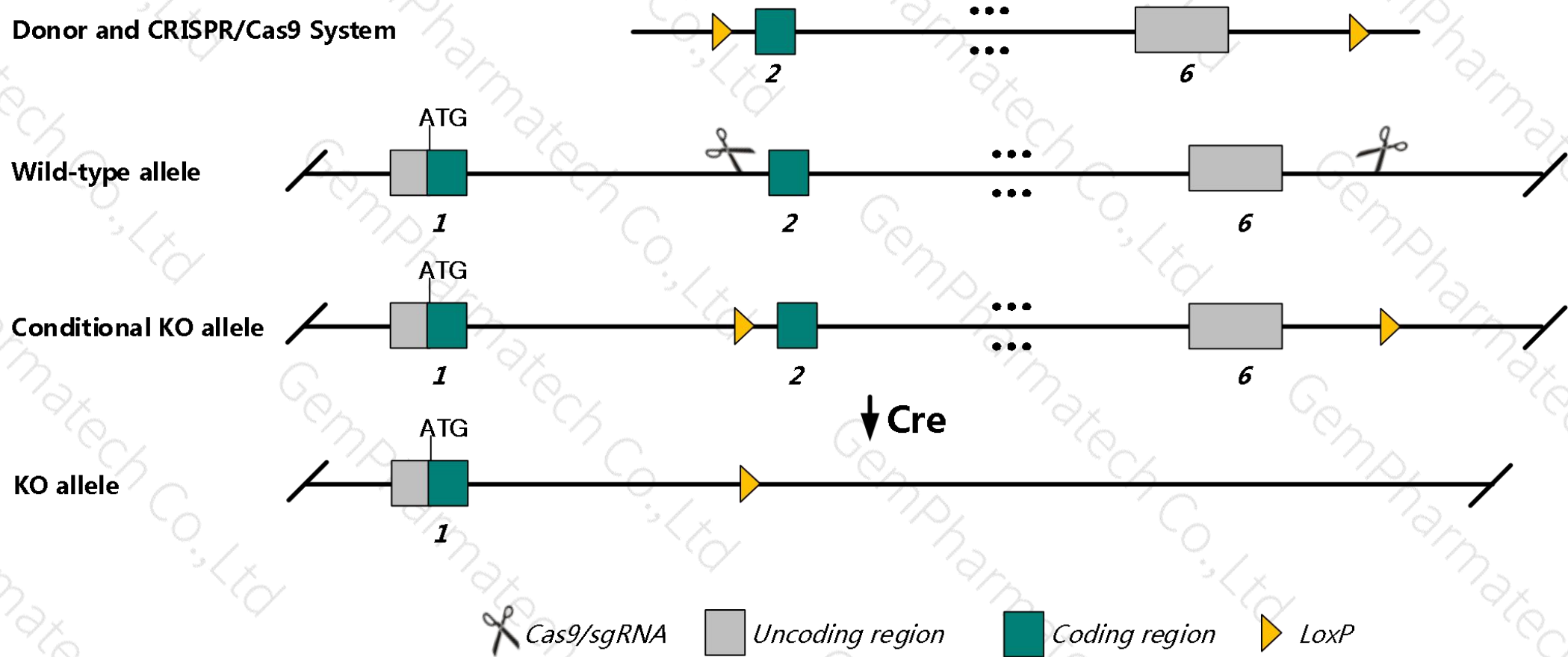
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Myd88* gene. The schematic diagram is as follows:



- The *Myd88* gene has 3 transcripts. According to the structure of *Myd88* gene, exon2-6 of *Myd88*-201 (ENSMUST00000035092.6) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Myd88* gene. The brief process is as follows: gRNA was transcribed in vitro, donor was constructed. Cas9, gRNA and Donor were microinjected into the fertilized eggs of C57BL/6J 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/6J 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 or cell types.

- According to the existing MGI data , Mice homozygous for a knock-out allele exhibit abnormal immune system morphology and physiology.
- Transcript *Myd88-202* may not be affected.
- The KO region contains functional region of the *Slc22a14* gene. Knockout the region may affect the function of *Slc22a14* gene.
- The KO region is 900bp away from *Acaala* gene. *Acaala* gene may be affected.
- The *Myd88* gene is located on the Chr9. 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)

Myd88 myeloid differentiation primary response gene 88 [*Mus musculus* (house mouse)]

Gene ID: 17874, updated on 4-Jan-2020




Summary



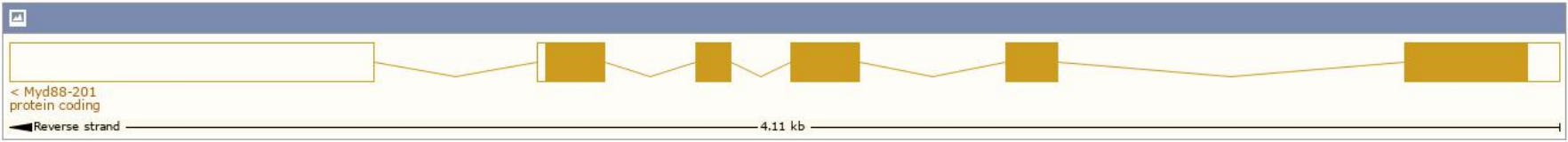
Official Symbol	Myd88 provided by MGI
Official Full Name	myeloid differentiation primary response gene 88 provided by MGI
Primary source	MGI:MGI:108005
See related	Ensembl:ENSMUSG00000032508
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Expression	Ubiquitous expression in lung adult (RPKM 14.9), spleen adult (RPKM 14.1) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

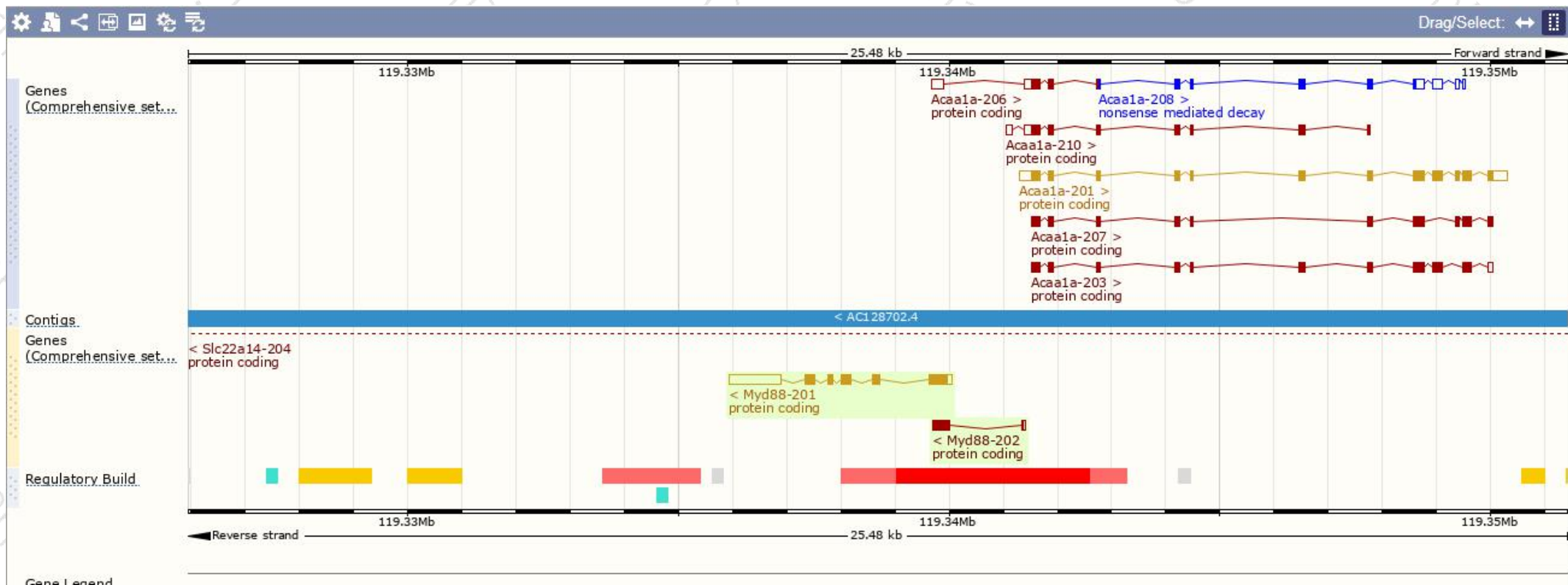
The gene has 3 transcripts, and all transcripts are shown below:

Show/hide columns (1 hidden)						Filter	
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Myd88-201	ENSMUST00000035092.6	1960	296aa	 Protein coding	CCDS23612	P22366 Q3U7M4	TSL:1 Gencode basic APPRIS P1
Myd88-202	ENSMUST00000139870.1	379	109aa	 Protein coding	-	F6SPW1	CDS 3' incomplete TSL:2
Myd88-203	ENSMUST00000150837.1	2458	No protein	 Retained intron	-	-	TSL:1

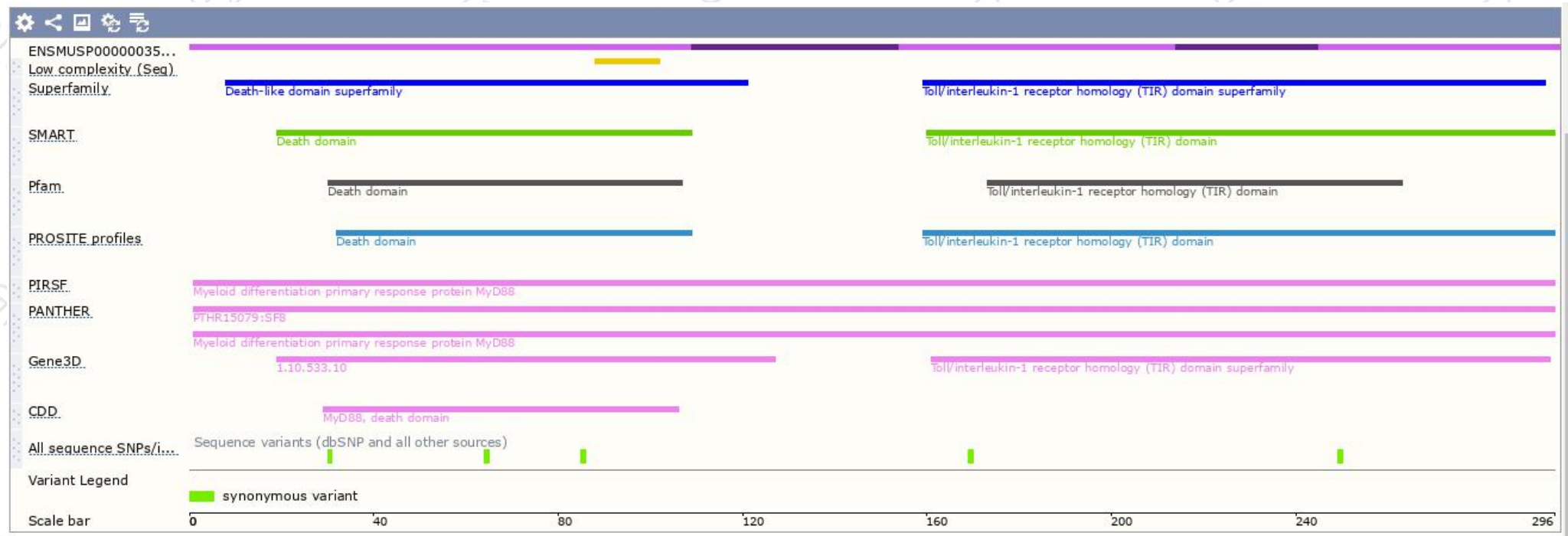
The strategy is based on the design of *Myd88-201* transcript, The transcription is shown below



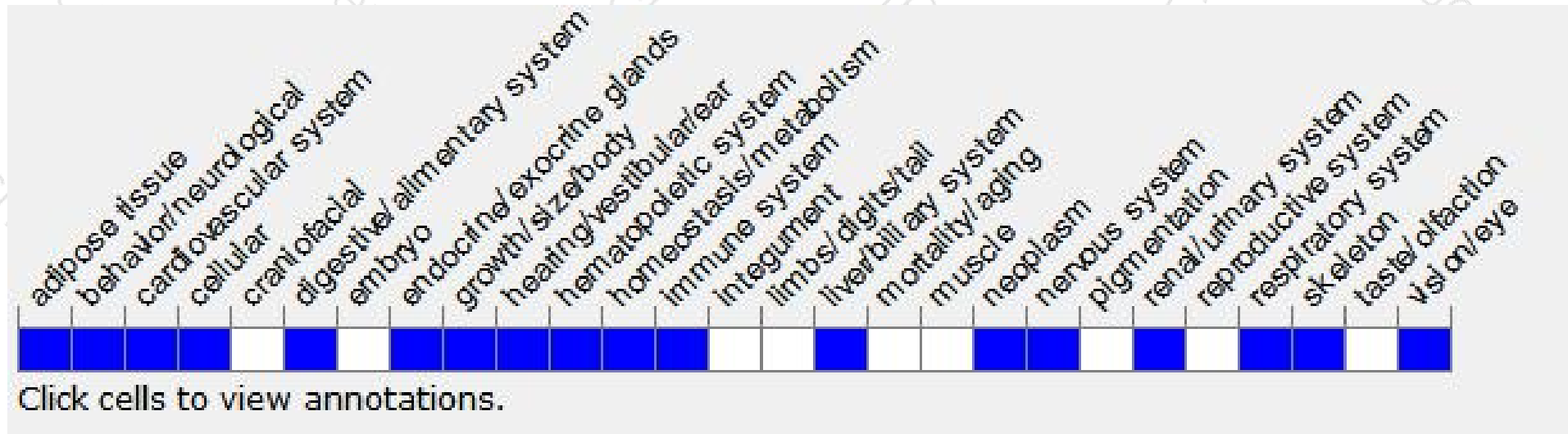
Genomic location distribution



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, Mutations in this locus affect cell-cycle regulation and apoptosis. Null homozygotes show high, early-onset tumor incidence; some have persistent hyaloid vasculature and cataracts. Truncated or temperature-sensitive alleles cause early aging phenotypes.

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