

Myc Cas9-CKO Strategy

Designer:

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Design Date:

2019-7-17

Project Overview

Project Name

Myc

Project type

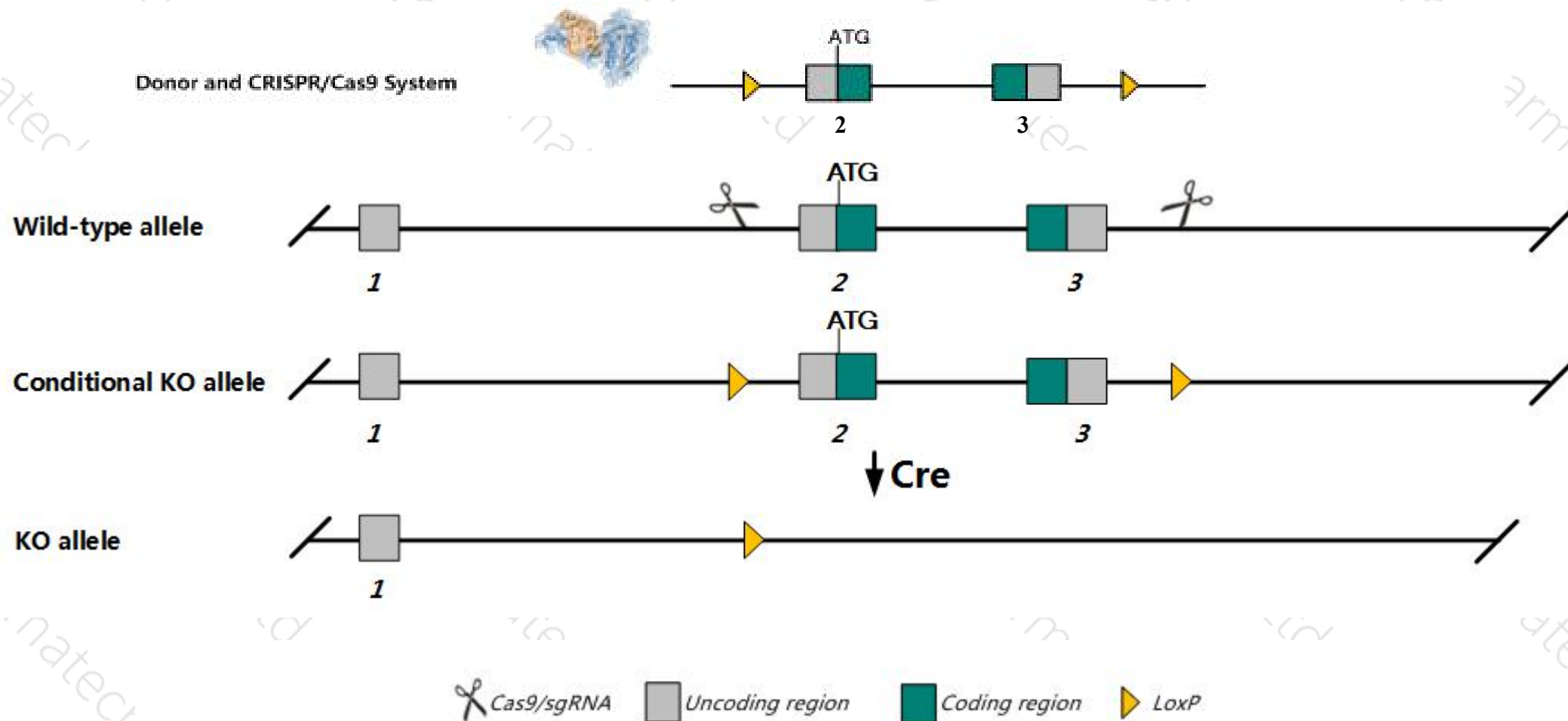
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- The *Myc* gene has 8 transcripts. According to the structure of *Myc* gene, exon2-exon3 of *Myc-201* (ENSMUST00000022971.7) transcript is recommended as the knockout region. The region contains all 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 *Myc* 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.

- According to the existing MGI data, Mutations affect growth and development of heart, pericardium, neural tube, vasculogenesis and erythropoiesis. Homozygous null mutants die by embryonic day 10.5. Heterozygotes have reduced body size and multiorgan hypoplasia; females have small litters.
- The *Myc* gene is located on the Chr15. 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)

Myc myelocytomatosis oncogene [Mus musculus (house mouse)]

Gene ID: 17869, updated on 9-Apr-2019

Summary

Official Symbol	Myc provided by MGI
Official Full Name	myelocytomatosis oncogene provided by MGI
Primary source	MGI:MGI:97250
See related	Ensembl:ENSMUSG00000022346
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AU016757, Myc2, Niard, Nird, bHLHe39
Summary	The protein encoded by this gene is a multifunctional, nuclear phosphoprotein that plays a role in cell cycle progression, apoptosis and cellular transformation. It functions as a transcription factor that regulates transcription of specific target genes. Mutations, overexpression, rearrangement and translocation of this gene have been associated with a variety of hematopoietic tumors, leukemias and lymphomas, including Burkitt lymphoma, in human. There is evidence to show that alternative translation initiations from an upstream, in-frame non-AUG (CUG) and a downstream AUG start site result in the production of two isoforms with distinct N-termini, in human and mouse. Under conditions of stress, such as high cell densities and methionine deprivation, there is a specific and dramatic increase in the synthesis of the non-AUG initiated protein, suggesting its importance in times of adversity. Alternative splicing results in multiple transcript variants. [provided by RefSeq, Apr 2010]
Expression	Broad expression in ovary adult (RPKM 36.6), thymus adult (RPKM 28.3) and 22 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

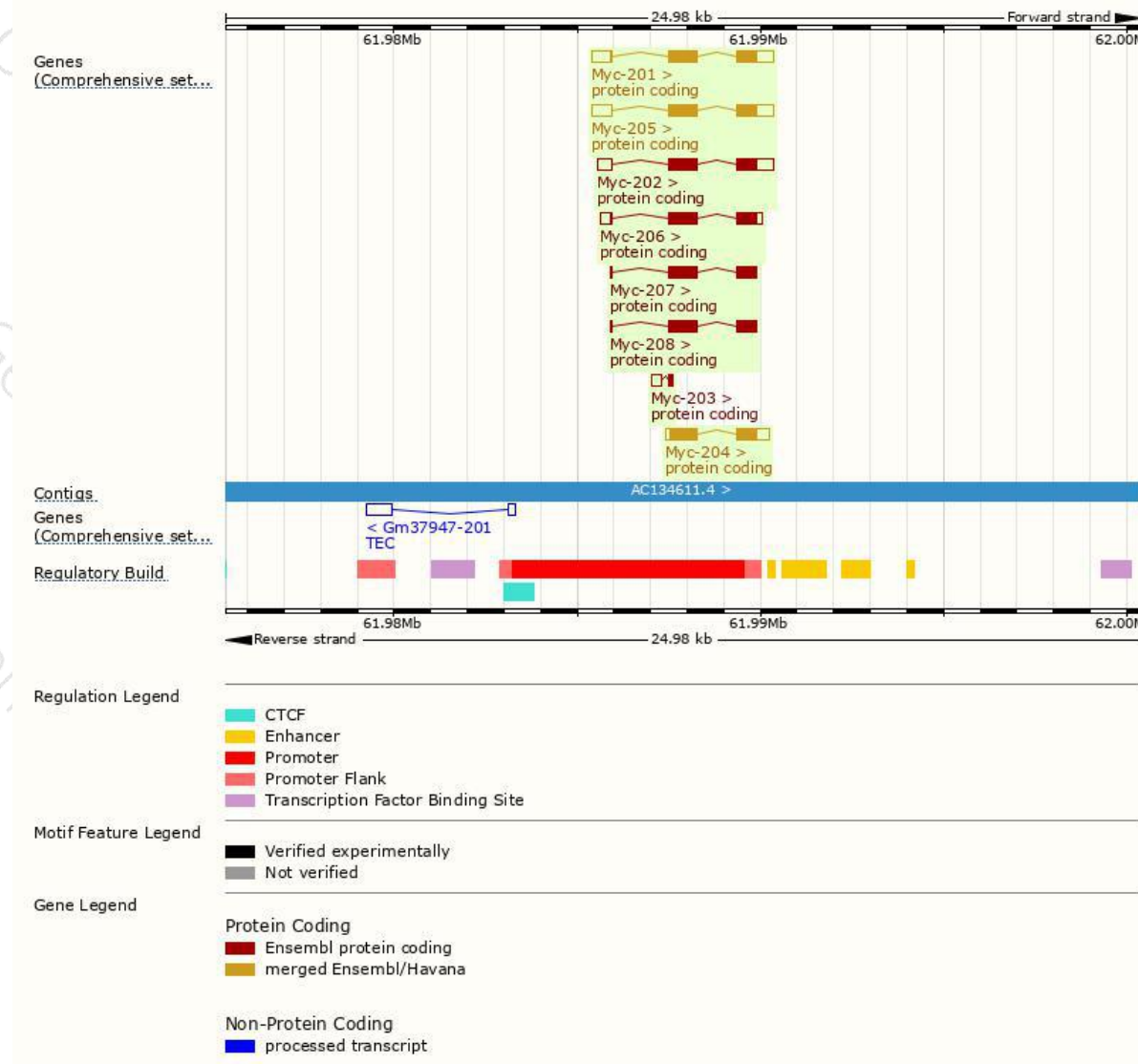
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Myc-205	ENSMUST00000161976.7	2338	439aa	Protein coding	CCDS49615	P01108	TSL:1 GENCODE basic
Myc-202	ENSMUST00000159327.1	2186	439aa	Protein coding	CCDS49615	P01108	TSL:1 GENCODE basic
Myc-204	ENSMUST00000160009.1	1765	439aa	Protein coding	CCDS49615	P01108	TSL:1 GENCODE basic
Myc-207	ENSMUST00000188482.7	1365	454aa	Protein coding	CCDS27504	B2RSN1	TSL:1 GENCODE basic APPRIS P2
Myc-208	ENSMUST00000191178.1	1362	453aa	Protein coding	CCDS49614	A0A087WSQ0	TSL:1 GENCODE basic
Myc-201	ENSMUST00000022971.7	2338	454aa	Protein coding	-	F8WID3	TSL:1 GENCODE basic APPRIS ALT1
Myc-206	ENSMUST00000167731.7	1821	453aa	Protein coding	-	F6PX41	TSL:1 GENCODE basic
Myc-203	ENSMUST00000159338.1	381	32aa	Protein coding	-	E0CZD1	CDS 3' incomplete TSL:2

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



Genomic location distribution



Protein domain

ENSMUSP00000022...

[MobiDB lite](#)

[Low complexity \(Seg\)](#)

[Conserved Domains](#)

[Coiled-coils \(Ncoils\)](#)

[hmmpanther](#)

PTHR11514:SF2

PTHR11514

[Superfamily domains](#)

[SMART domains](#)

[Prints domain](#)

[Pfam domain](#)

Transcription regulator Myc

Transcription regulator Myc, N-terminal

Helix-loop-helix DNA-binding

Myc-type, basic helix-loop

Leucine zipper

Myc-type, basic helix-loop

Myc-type, basic helix-loop

[PROSITE profiles](#)

[PIRSF domain](#)

Transcription regulator Myc

[Gene3D](#)

Helix-loop-helix DNA-binding

[All sequence SNPs/indels](#)

Sequence variants (dbSNP and all other sources)

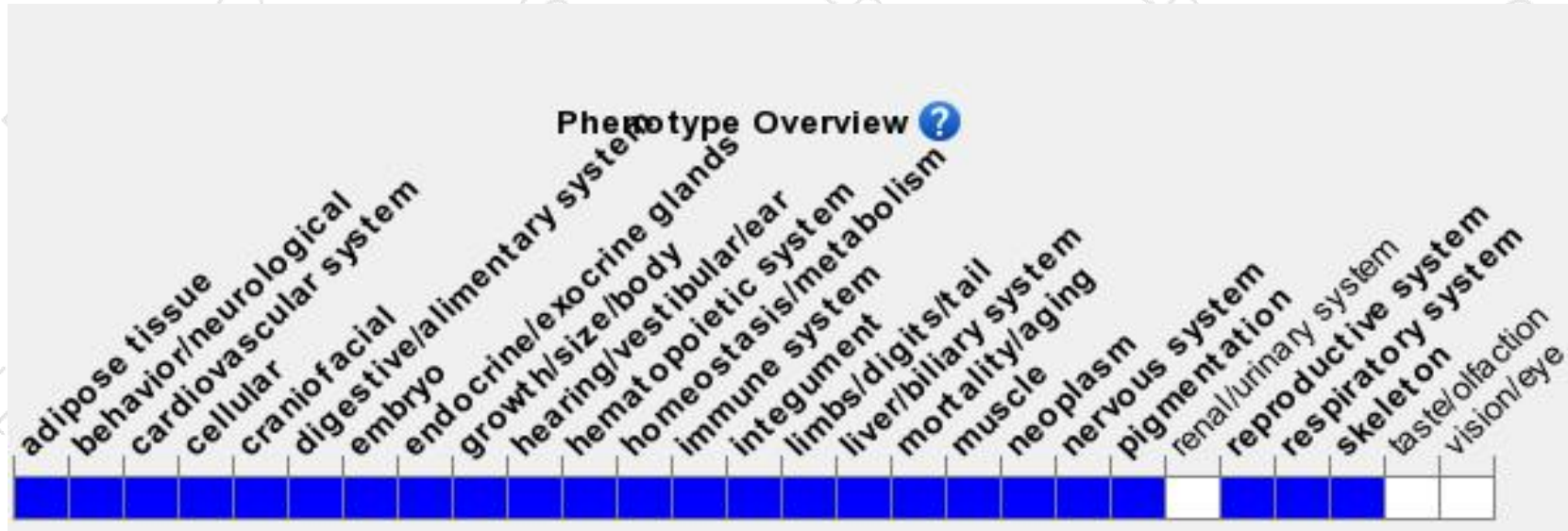
[Variant Legend](#)

- stop gained
- missense variant
- synonymous variant

[Scale bar](#)

0 40 80 120 160 200 240 280 320 360 400 454

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 affect growth and development of heart, pericardium, neural tube, vasculogenesis and erythropoiesis. Homozygous null mutants die by embryonic day 10.5. Heterozygotes have reduced body size and multiorgan hypoplasia; females have small litters.

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

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