

Wapl Cas9-CKO Strategy

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Reviewer:

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Project Overview

Project Name

Wapl

Project type

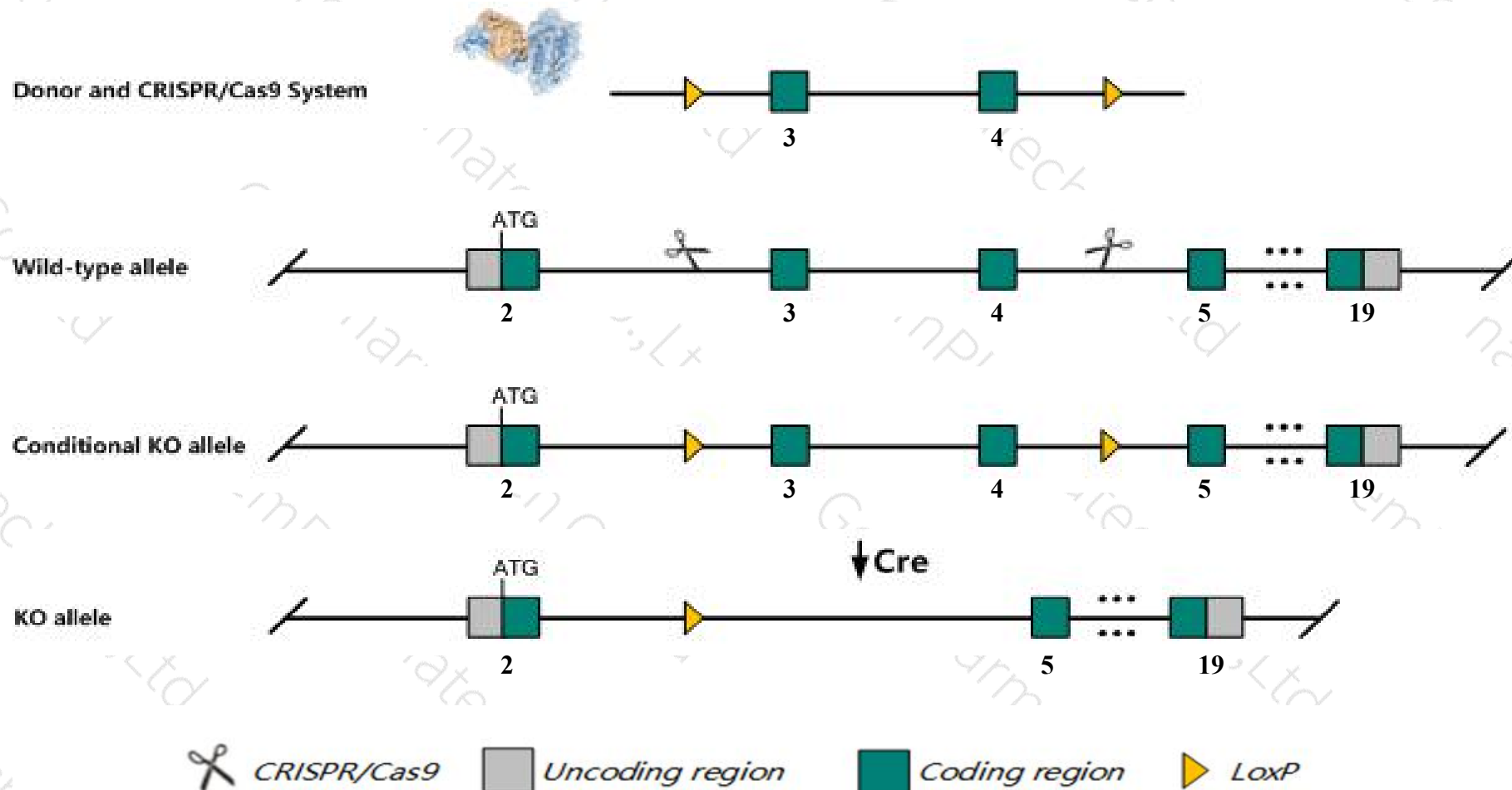
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

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



- The *Wapl* gene has 7 transcripts. According to the structure of *Wapl* gene, exon3-exon4 of *Wapl*-201 (ENSMUST00000048263.13) transcript is recommended as the knockout region. The region contains 1172bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Wapl* 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, Mice homozygous for a targeted allele exhibit prenatal lethality.
- The *Wapl* gene is located on the Chr14. 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)

Wapl WAPL cohesin release factor [Mus musculus (house mouse)]

Gene ID: 218914, updated on 31-Jan-2019

Summary



Official Symbol Wapl provided by [MGI](#)

Official Full Name WAPL cohesin release factor provided by [MGI](#)

Primary source [MGI:MGI:2675859](#)

See related [Ensembl:ENSMUSG00000041408](#)

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 A530089A20Rik, BC037674, DIF-2, FOE, Wapal

Summary Studies suggest that the protein encoded by this gene is important for the release of cohesin from chromatin. This gene product is thought to be essential for development, and reduced expression of this gene in cells causes defects in chromatin structure. High levels of expression of the human ortholog of this gene are observed in cervical cancers, and expression of the human ortholog of this gene in mice results in tumor formation. Alternative splicing results in multiple transcript variants encoding different protein isoforms. [provided by RefSeq, Aug 2014]

Expression Ubiquitous expression in liver E14 (RPKM 13.4), placenta adult (RPKM 11.9) and 28 other tissues [See more](#)

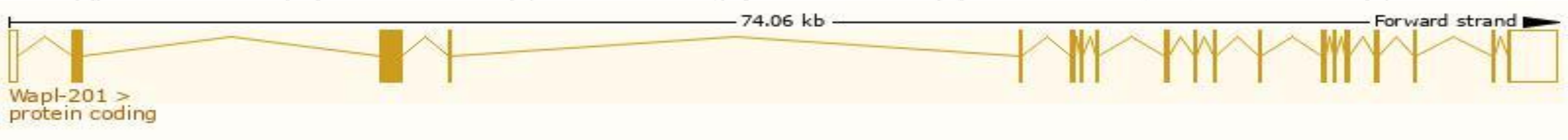
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

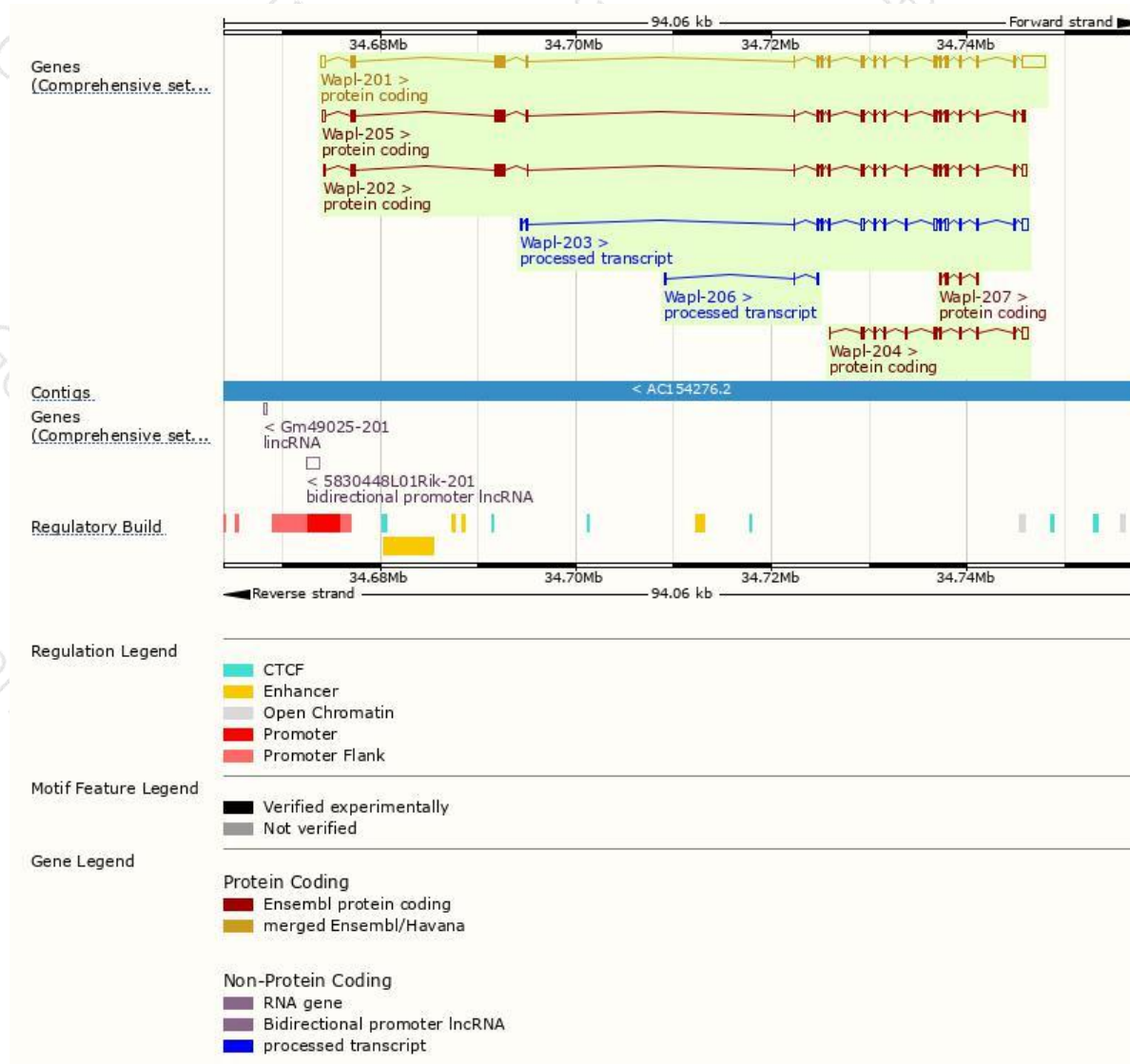
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Wapl-201	ENSMUST00000048263.13	6351	1200aa	Protein coding	CCDS36880	Q65Z40	TSL:1 GENCODE basic APPRIS P3
Wapl-202	ENSMUST00000090027.10	4185	1194aa	Protein coding	CCDS79296	B7ZP47	TSL:5 GENCODE basic APPRIS ALT2
Wapl-205	ENSMUST00000169910.7	4066	1200aa	Protein coding	CCDS36880	Q65Z40	TSL:1 GENCODE basic APPRIS P3
Wapl-204	ENSMUST00000151285.7	1820	430aa	Protein coding	-	F6YCH1	CDS 5' incomplete TSL:5
Wapl-207	ENSMUST00000174559.2	479	160aa	Protein coding	-	G3UXQ2	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Wapl-203	ENSMUST00000111895.7	2688	No protein	Processed transcript	-	-	TSL:1
Wapl-206	ENSMUST00000172658.1	382	No protein	Processed transcript	-	-	TSL:3

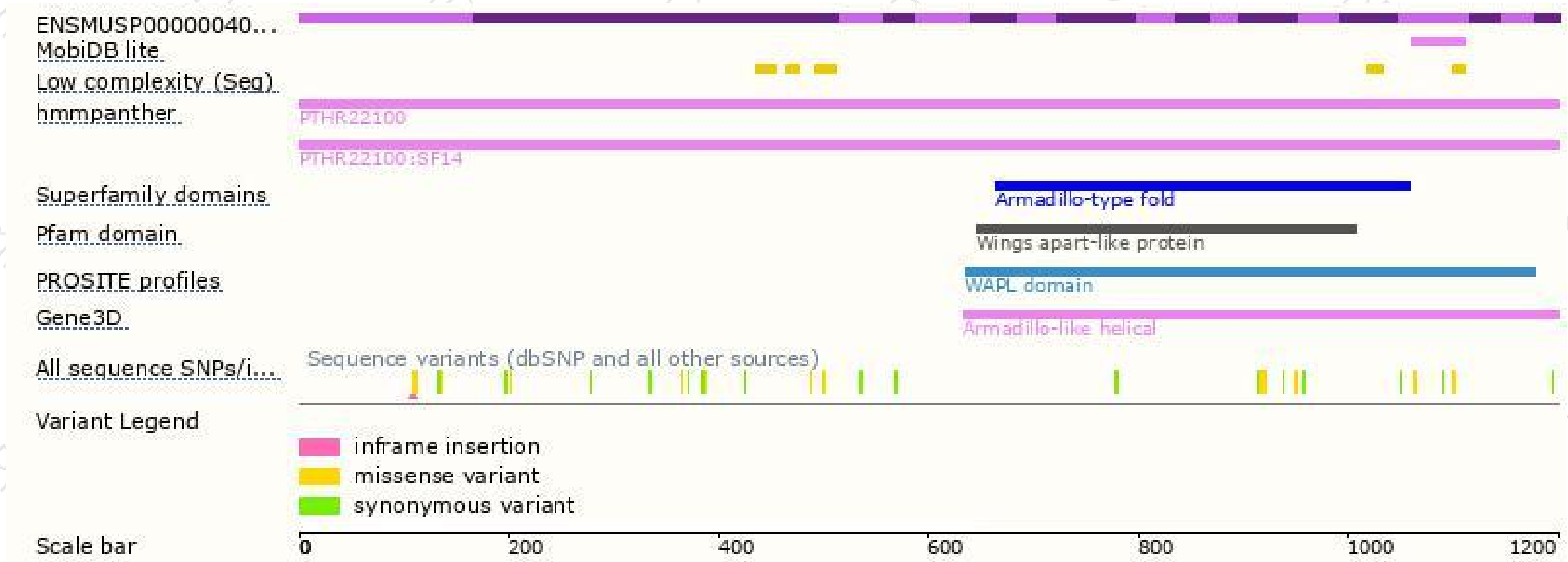
The strategy is based on the design of *Wapl-201* transcript,The transcription is shown below



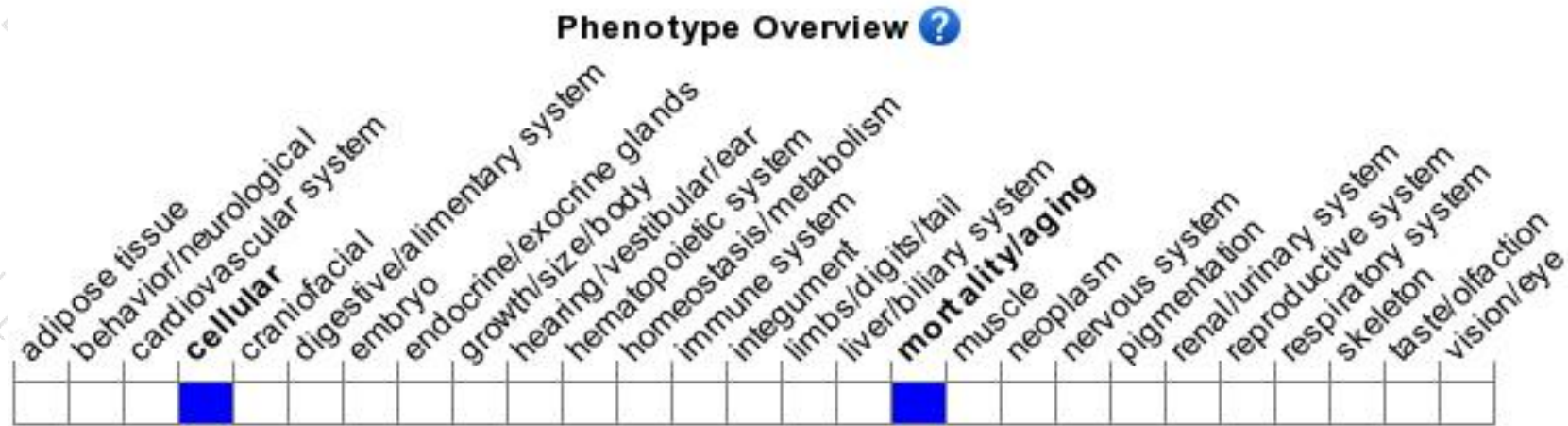
Genomic location distribution



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 targeted allele exhibit prenatal lethality.

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

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