Papln Cas9-CKO Strategy

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Project Overview

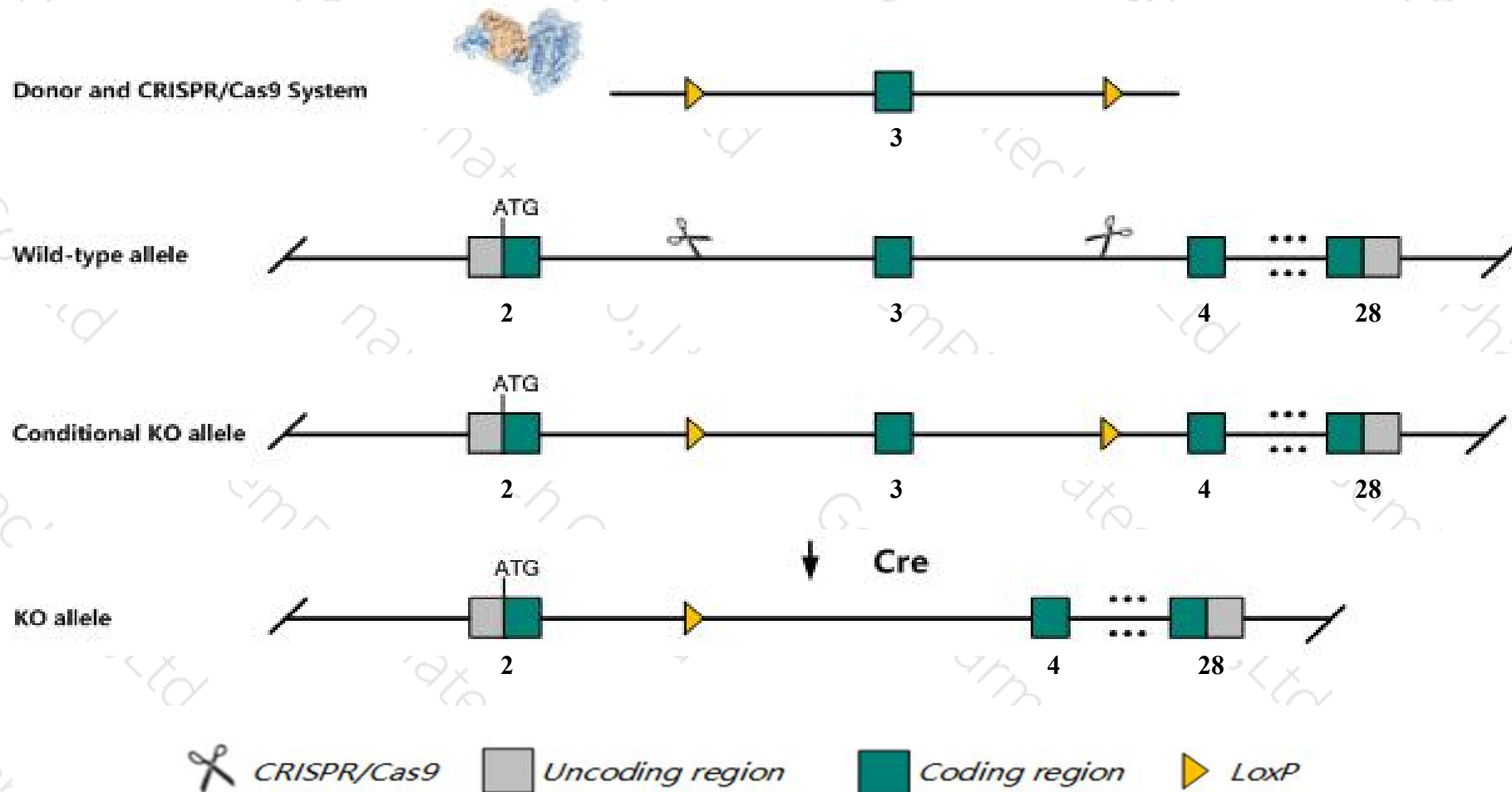|	
Project Name	*Papln*
Project type	**Cas9-CKO**
Strain background	**C57BL/6J**

Conditional Knockout strategy

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

Technical routes

➢ The *Papln* gene has 3 transcripts. According to the structure of *Papln* gene, exon3 of *Papln-202* (ENSMUST00000121733.7) transcript is recommended as the knockout region.The region contains Ens 116bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Papln* gene. The brief process is as follows:CRISPR/Cas9 system 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 and cell types.

Notice

➢ The *Papln* gene is located on the Chr12. 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）

Papln papilin, proteoglycan-like sulfated glycoprotein [Mus musculus (house mouse)]
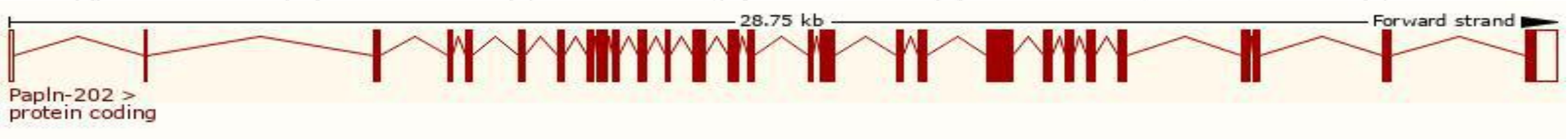
Gene ID: 170721, updated on 13-Mar-2020

Summary

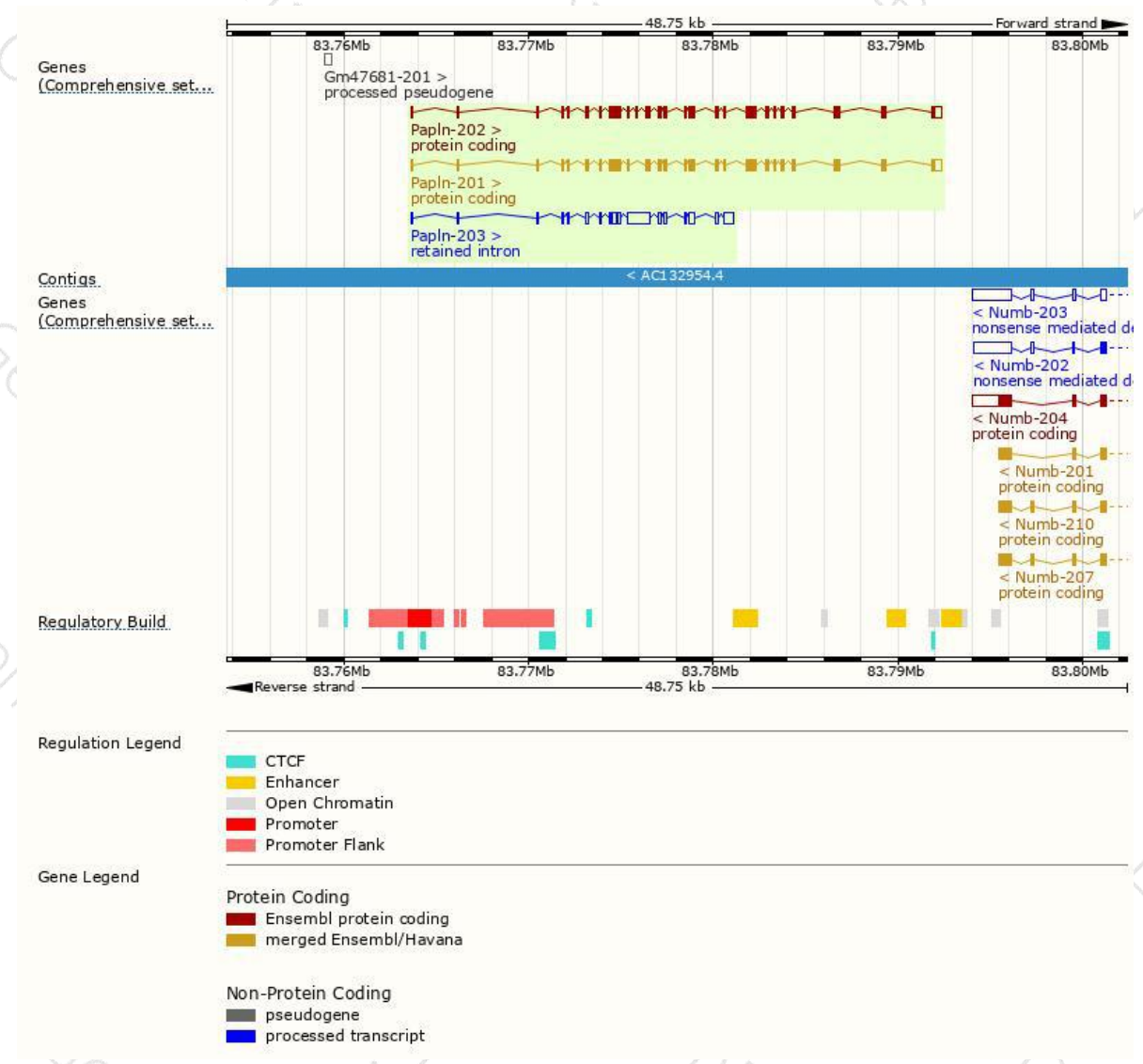|	
Official Symbol	Papln provided by MGI
Official Full Name	papilin, proteoglycan-like sulfated glycoprotein provided byMGI
Primary source	MGI:MGI:2386139
See related	Ensembl:ENSMUSG00000021223
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	E030033C16Rik
Expression	Ubiquitous expression in mammary gland adult (RPKM 17.7), ovary adult (RPKM 6.3) and 26 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Papln-202	ENSMUST00000121733.7	4373	1302aa	Protein coding	CCDS56847	B7ZN28	TSL:1 GENCODE basic
Papln-201	ENSMUST00000021646.5	4260	1280aa	Protein coding	CCDS26031	Q9EPX2	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P1
Papln-203	ENSMUST00000152904.1	3622	No protein	Retained intron	-	-	TSL:5

The strategy is based on the design of *Papln-202* transcript,the transcription is shown below:
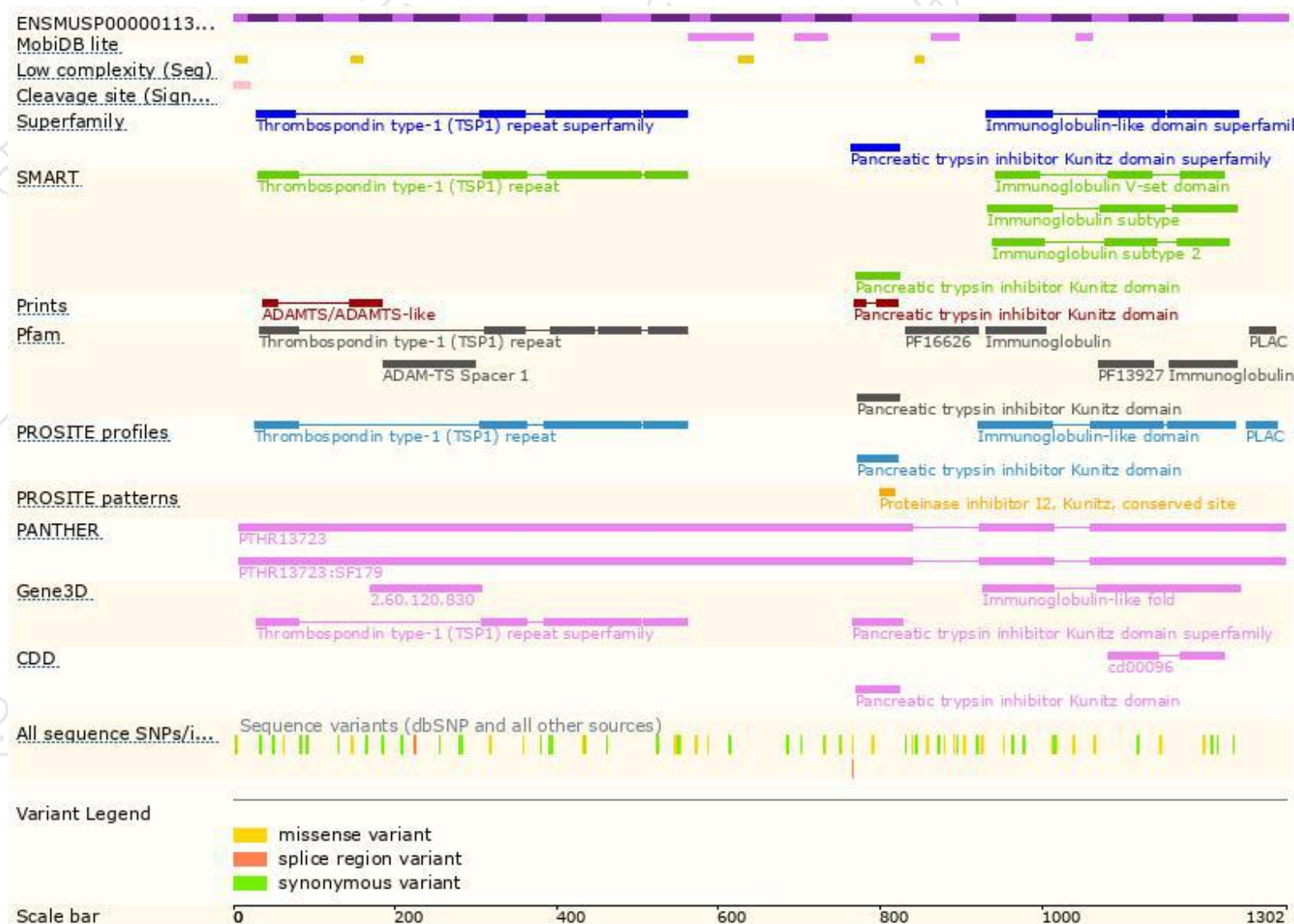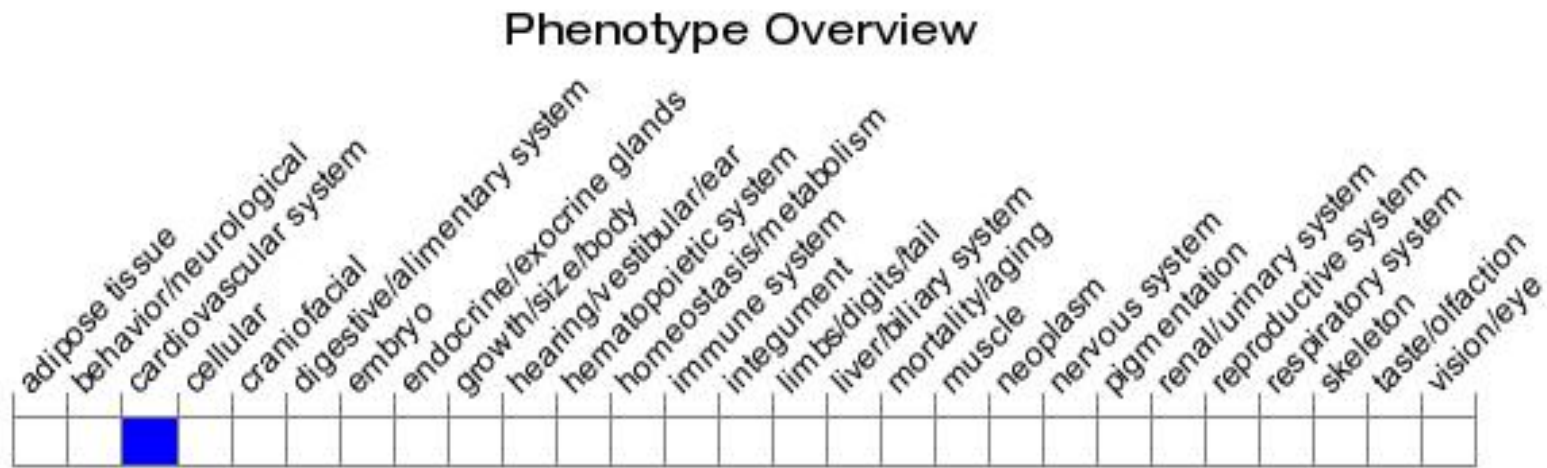
Genomic location distribution

Protein domain

ENSMUSP00000113...		
MobiDB lite		
Low complexity (Seg)		
Cleavage site (Sign...		
Superfamily	Thrombospondin type-1 (TSP1) repeat superfamily	Immunoglobulin-like domain superfamily
		Pancreatic trypsin inhibitor Kunitz domain superfamily
SMART	Thrombospondin type-1 (TSP1) repeat	Immunoglobulin V-set domain
		Immunoglobulin subtype
		Immunoglobulin subtype 2
		Pancreatic trypsin inhibitor Kunitz domain
Prints	ADAMTS/ADAMTS-like	Pancreatic trypsin inhibitor Kunitz domain
Pfam	Thrombospondin type-1 (TSP1) repeat	PF16626 Immunoglobulin / PLAC
	ADAM-TS Spacer 1	PF13927 Immunoglobulin
		Pancreatic trypsin inhibitor Kunitz domain
PROSITE profiles	Thrombospondin type-1 (TSP1) repeat	Immunoglobulin-like domain / PLAC
		Pancreatic trypsin inhibitor Kunitz domain
PROSITE patterns		Proteinase inhibitor I2, Kunitz, conserved site
PANTHER	PTHR13723	
	PTHR13723:SF179	
Gene3D	2.60.120.830	Immunoglobulin-like fold
	Thrombospondin type-1 (TSP1) repeat superfamily	Pancreatic trypsin inhibitor Kunitz domain superfamily
CDD		cd00096
		Pancreatic trypsin inhibitor Kunitz domain
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)	

Variant Legend

- missense variant
- splice region variant
- synonymous variant

Scale bar   0   200   400   600   800   1000   1302

Mouse phenotype description(MGI)

Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

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