

# ***Wls Cas9-CKO Strategy***

**Designer: Jinling Wang**

**Reviewer: Longyun Hu**

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# Project Overview

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**Project Name**

*Wls*

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**Project type**

**Cas9-CKO**

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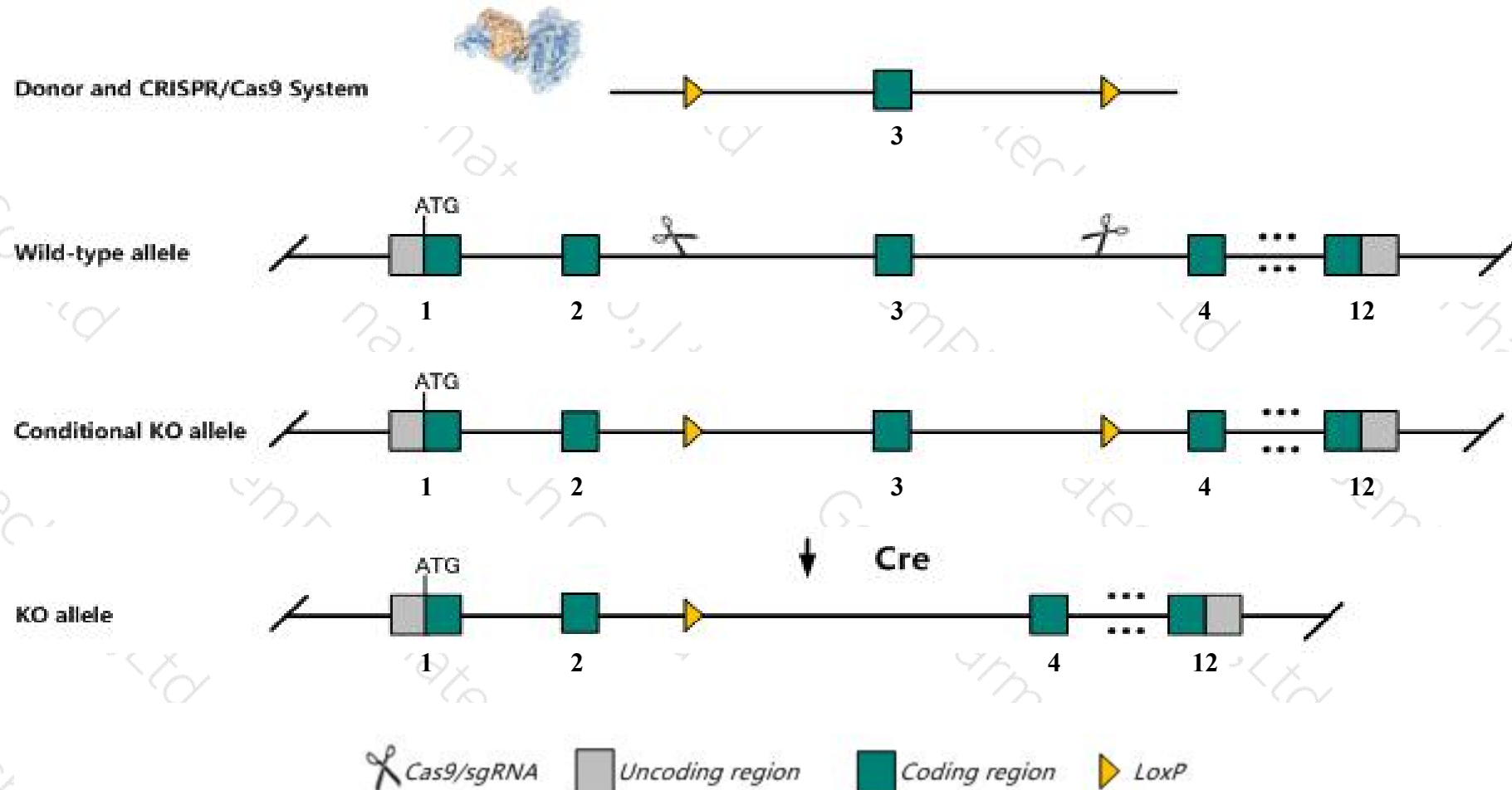
**Strain background**

**C57BL/6JGpt**

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# Conditional Knockout strategy

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



# Technical routes

- The *Wls* gene has 7 transcripts. According to the structure of *Wls* gene, exon3 of *Wls*-201(ENSMUST00000068952.9) transcript is recommended as the knockout region. The region contains 125bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Wls* 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 and cell types.

- According to the existing MGI data, mice homozygous for null alleles exhibit impaired body axis and triploblastic development dying prior to E10.5. Mice homozygous for a floxed allele activated in keratinocytes exhibit a psoriasiform dermatitis-like phenotype.
- The *Wls* gene is located on the Chr3. 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)

## Wls wntless WNT ligand secretion mediator [Mus musculus (house mouse)]

Gene ID: 68151, updated on 5-Mar-2019

### Summary



<b>Official Symbol</b>	Wls provided by <a href="#">MGI</a>
<b>Official Full Name</b>	wntless WNT ligand secretion mediator provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1915401</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000028173</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	5031439A09Rik, AI173978, AI987742, EVI, Gpr177
<b>Expression</b>	Broad expression in bladder adult (RPKM 41.9), limb E14.5 (RPKM 30.9) and 21 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

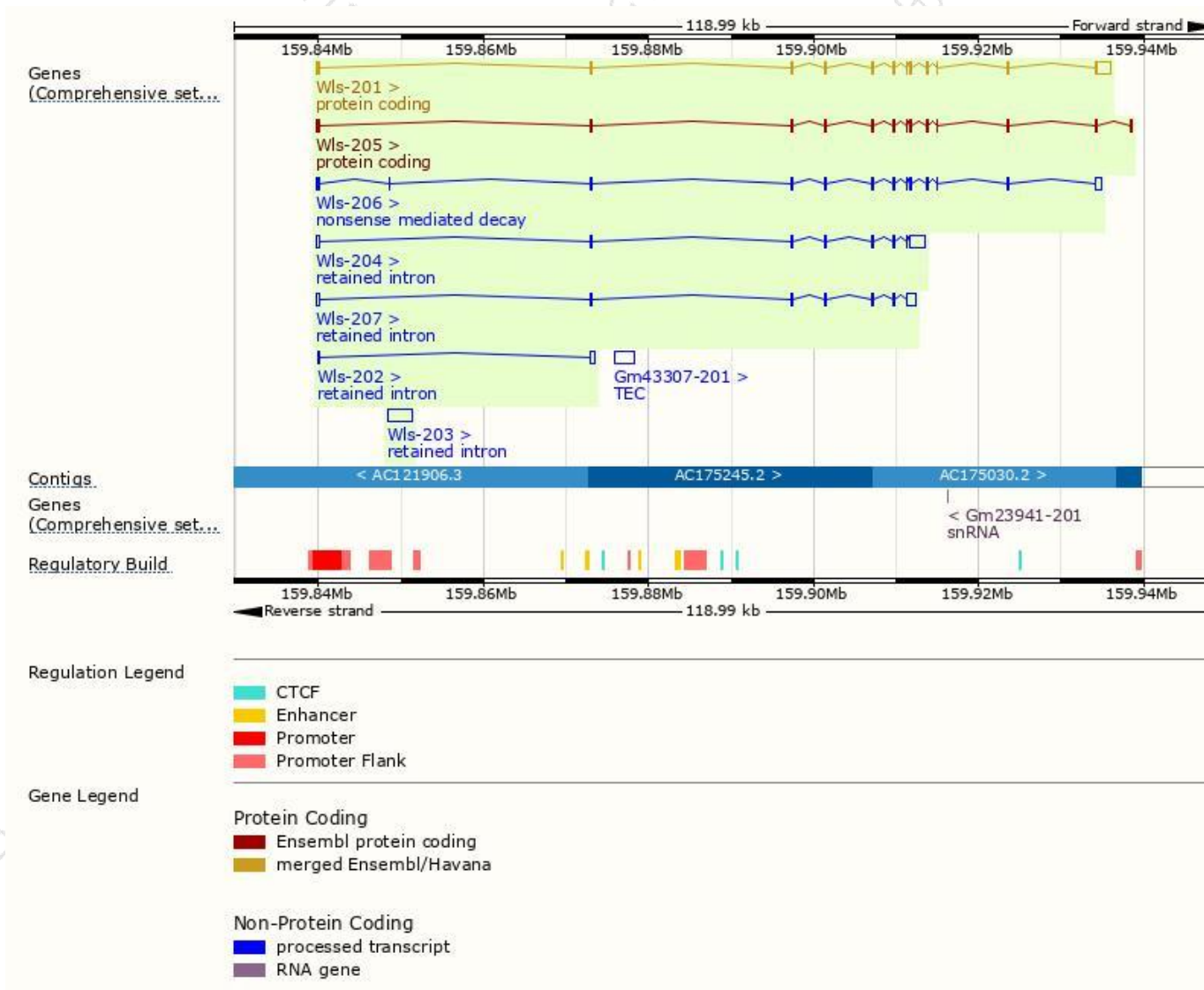
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Wls-201	<a href="#">ENSMUST00000068952.9</a>	3559	<a href="#">541aa</a>	Protein coding	<a href="#">CCDS38684</a>	<a href="#">Q6DID7</a>	TSL:1 GENCODE basic APPRIS P1
Wls-205	<a href="#">ENSMUST00000198878.1</a>	2050	<a href="#">541aa</a>	Protein coding	<a href="#">CCDS38684</a>	<a href="#">Q6DID7</a>	TSL:1 GENCODE basic APPRIS P1
Wls-206	<a href="#">ENSMUST00000200191.1</a>	2453	<a href="#">37aa</a>	Nonsense mediated decay	-	<a href="#">A0A0G2JEH4</a>	TSL:1
Wls-204	<a href="#">ENSMUST00000197328.4</a>	2949	No protein	Retained intron	-	-	TSL:1
Wls-203	<a href="#">ENSMUST00000196782.1</a>	2824	No protein	Retained intron	-	-	TSL:NA
Wls-207	<a href="#">ENSMUST00000200571.4</a>	2338	No protein	Retained intron	-	-	TSL:1
Wls-202	<a href="#">ENSMUST00000196276.1</a>	634	No protein	Retained intron	-	-	TSL:1

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

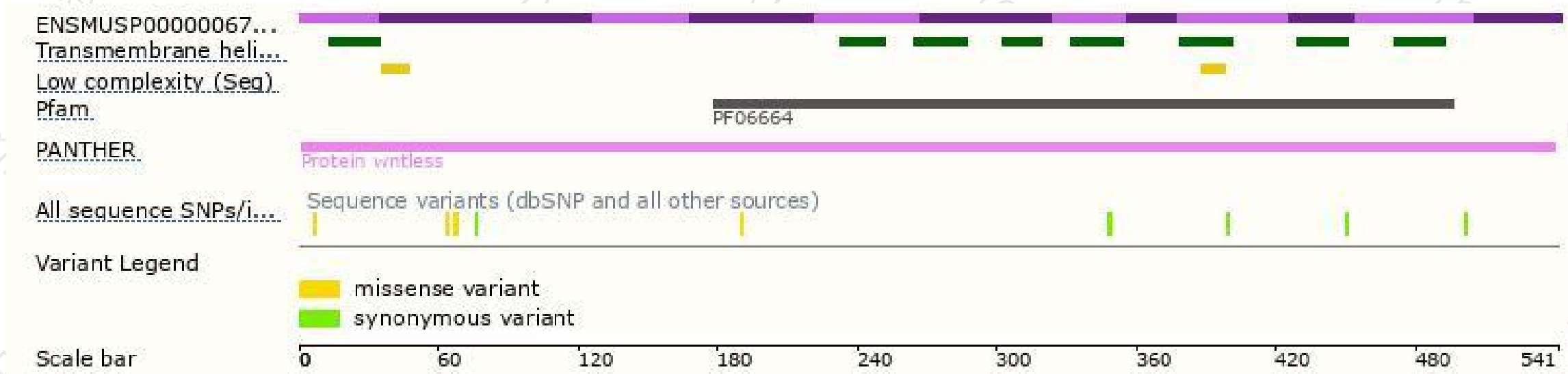


# Genomic location distribution





# 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 null alleles exhibit impaired body axis and triploblastic development dying prior to E10.5. Mice homozygous for a floxed allele activated in keratinocytes exhibit a psoriasiform dermatitis-like phenotype.

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

Tel: 025-5864 1534

