

# ***Wdr59 Cas9-CKO Strategy***

**Designer:**

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**Design Date:**

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# Project Overview

**Project Name**

***Wdr59***

**Project type**

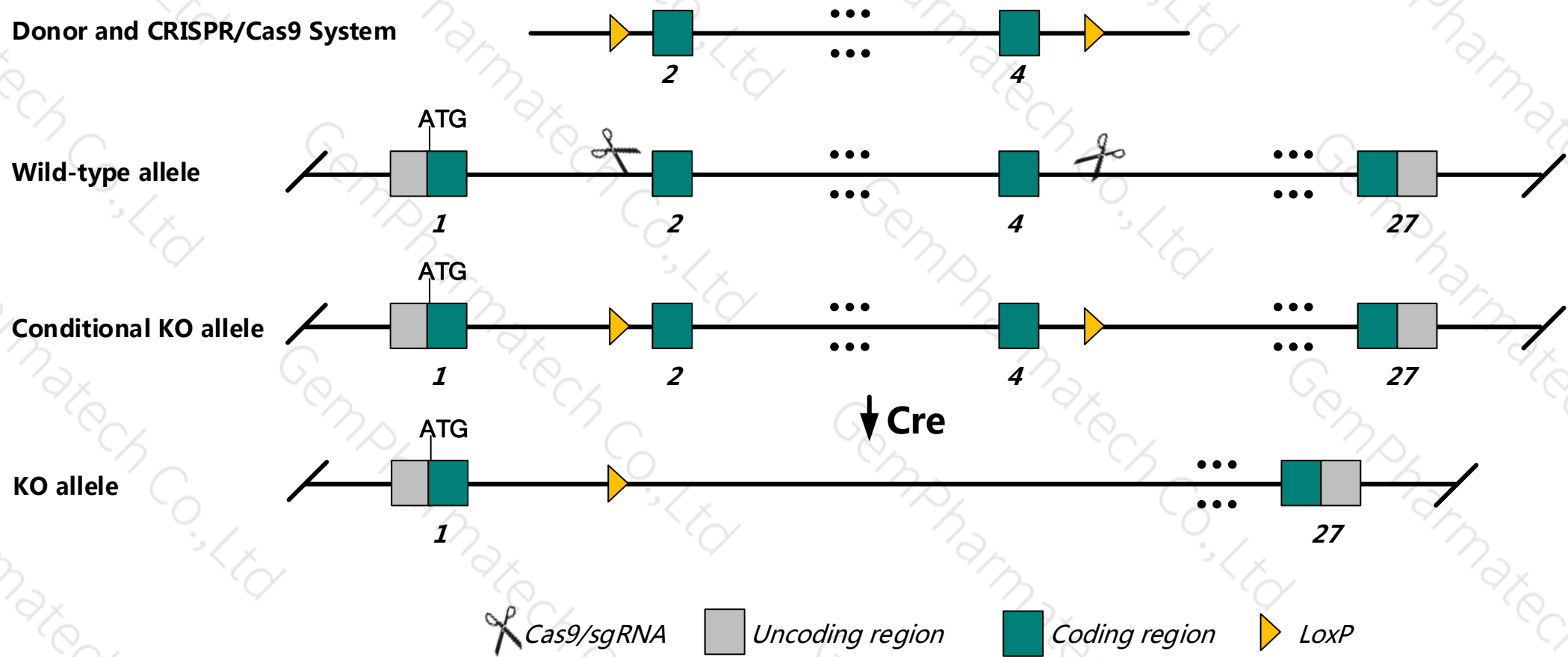
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Wdr59* gene. The schematic diagram is as follows:



- The *Wdr59* gene has 4 transcripts. According to the structure of *Wdr59* gene, exon2-exon4 of *Wdr59*-201 (ENSMUST00000034437.7) transcript is recommended as the knockout region. The region contains 272bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Wdr59* 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 or cell types.

- The *Wdr59* gene is located on the Chr8. 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 )

## Wdr59 WD repeat domain 59 [ *Mus musculus* (house mouse) ]

Gene ID: 319481, updated on 27-Jan-2018

### Summary

Official Symbol	Wdr59 provided by <a href="#">MGI</a>
Official Full Name	WD repeat domain 59 provided by <a href="#">MGI</a>
Primary source	<a href="#">MGI:MGI:2442115</a>
See related	<a href="#">Ensembl:ENSMUSG000000031959</a> <a href="#">Vega:OTTMUSG000000061792</a>
Gene type	protein coding
RefSeq status	VALIDATED
Organism	<a href="#">Mus musculus</a>
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Cdw12; 5430401O09Rik
Expression	Ubiquitous expression in ovary adult (RPKM 7.6), CNS E18 (RPKM 5.7) and 28 other tissues <a href="#">See more</a>
Orthologs	<a href="#">human</a> <a href="#">all</a>

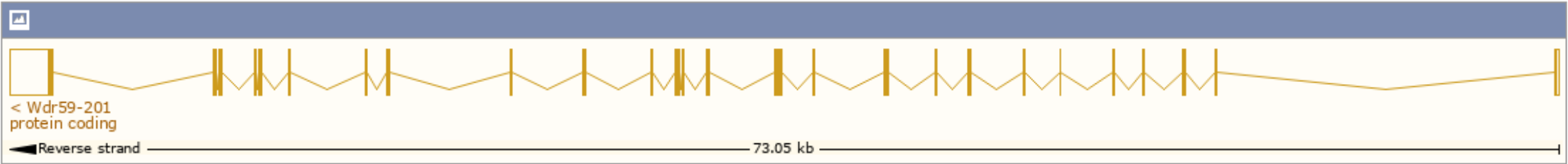


# Transcript information ( Ensembl )

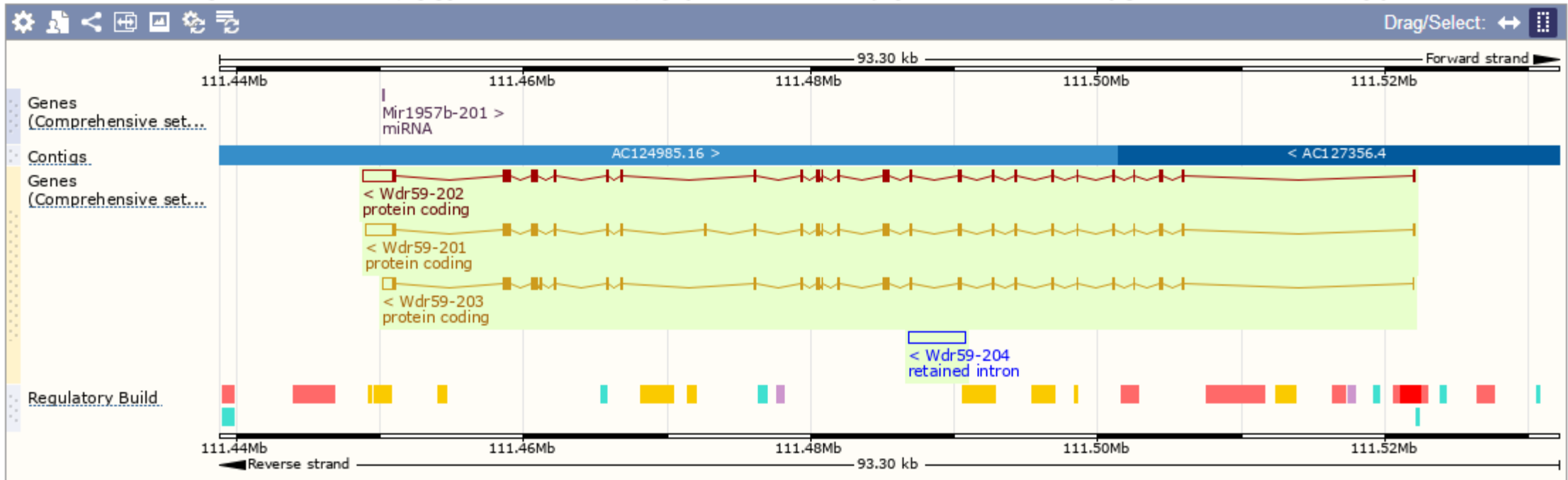
The gene has 4 transcripts, and all transcripts are shown below:

Show/hide columns (1 hidden)								Filter	
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	RefSeq	Flags	
Wdr59-202	<a href="#">ENSMUST00000038193.14</a>	5083	<a href="#">974aa</a>	<div></div> Protein coding	<a href="#">CCDS85613</a>	<a href="#">Q8C0M0</a>	<a href="#">NM_001170742</a> <a href="#">NP_001164213</a>	<a href="#">TSL:1</a>	<a href="#">GENCODE basic</a> <a href="#">APPRIS ALT1</a>
Wdr59-201	<a href="#">ENSMUST00000034437.7</a>	4896	<a href="#">993aa</a>	<div></div> Protein coding	<a href="#">CCDS52672</a>	<a href="#">D3Z1F9</a> <a href="#">Q8C0M0</a>	<a href="#">NM_001170743</a> <a href="#">NP_001164214</a>	<a href="#">TSL:1</a>	<a href="#">GENCODE basic</a> <a href="#">APPRIS P3</a>
Wdr59-203	<a href="#">ENSMUST00000211981.1</a>	3618	<a href="#">991aa</a>	<div></div> Protein coding	<a href="#">CCDS22675</a>	<a href="#">A0A1D5RLJ8</a>	<a href="#">NM_176923</a> <a href="#">NP_795897</a>	<a href="#">TSL:1</a>	<a href="#">GENCODE basic</a>
Wdr59-204	<a href="#">ENSMUST00000212327.1</a>	3902	No protein	<div></div> Retained intron	-	-	-	<a href="#">TSL:NA</a>	

The strategy is based on the design of Wdr59-201 transcript,The transcription is shown below



# Genomic location distribution

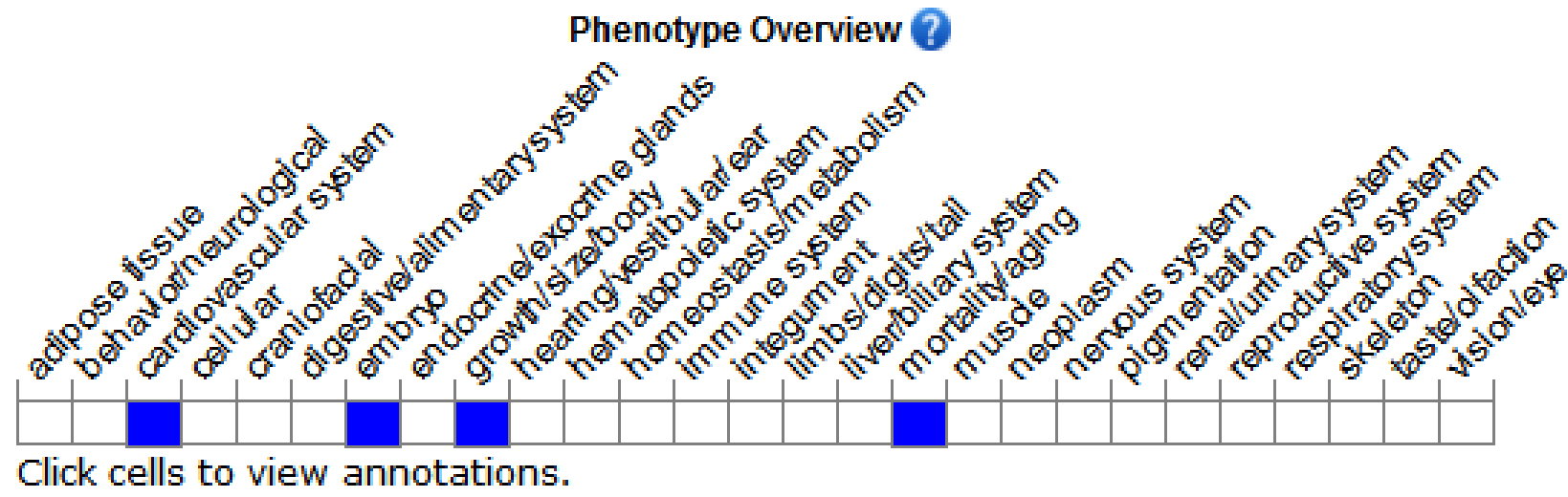




# Protein domain



# Mouse phenotype description(MGI)



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

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