

Wdr12 Cas9-CKO Strategy

Designer:

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Project Overview

Project Name

Wdr12

Project type

Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

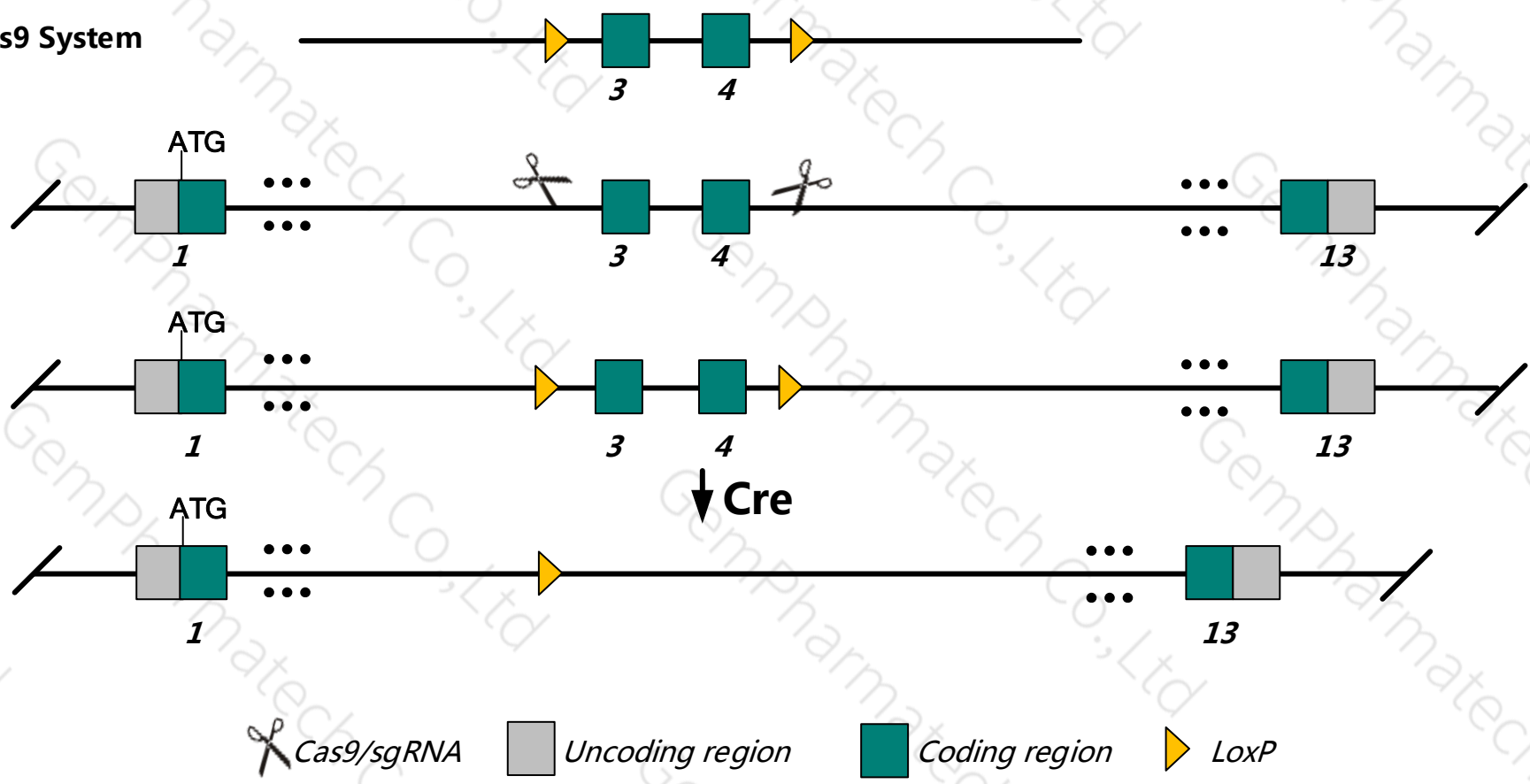
This model will use CRISPR/Cas9 technology to edit the *Wdr12* gene. The schematic diagram is as follows:

Donor and CRISPR/Cas9 System

Wild-type allele

Conditional KO allele

KO allele



- The *Wdr12* gene has 8 transcripts. According to the structure of *Wdr12* gene, exon3-exon4 of *Wdr12*-201 (ENSMUST00000027173.14) transcript is recommended as the knockout region. The region contains 202bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Wdr12* 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 *Wdr12* gene is located on the Chr1. 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)

Wdr12 WD repeat domain 12 [*Mus musculus* (house mouse)]

Gene ID: 57750, updated on 12-Aug-2018

Summary

Official Symbol Wdr12 provided by [MGI](#)

Official Full Name WD repeat domain 12 provided by [MGI](#)

Primary source [MGI:MGI:1927241](#)

See related [Ensembl:ENSMUSG00000026019](#) [Vega:OTTMUSG00000021598](#)

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 Ytm1; Ytm1p; 4933402C23Rik

Expression Broad expression in testis adult (RPKM 14.9), liver E14 (RPKM 8.3) and 22 other tissues [See more](#)

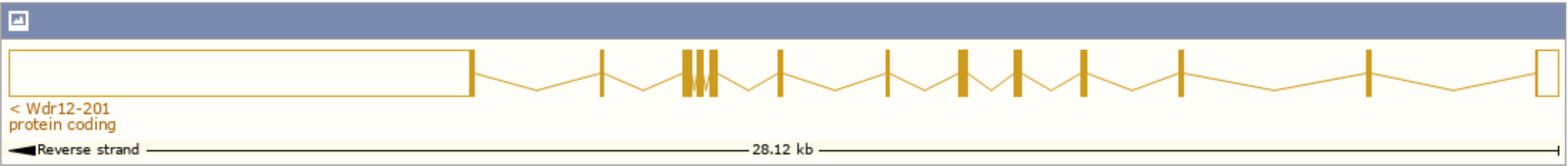
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

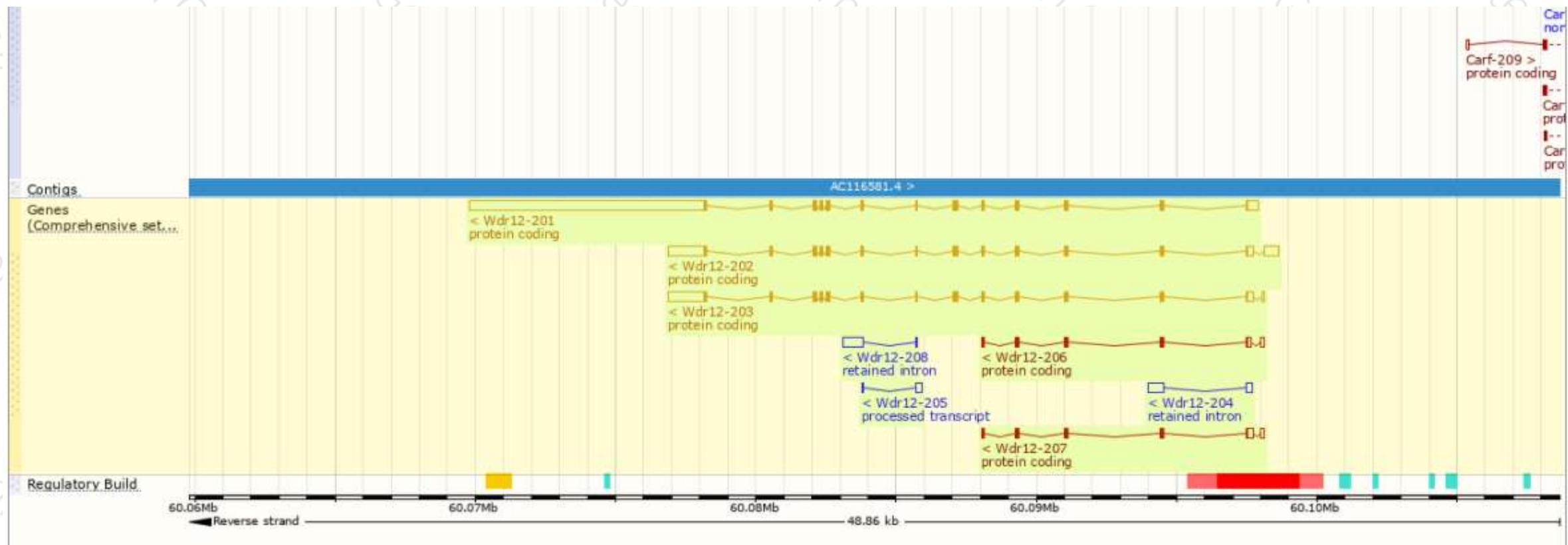
The gene has 8 transcripts, and all transcripts are shown below:

Show/hide columns (1 hidden)								Filter	
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	RefSeq	Flags	
Wdr12-201	ENSMUST00000027173.14	10012	423aa	Protein coding	CCDS14988	Q4V9X1 Q9JJA4	NM_021312 NP_067287	TSL:1	GENCODE basic APPRIS P1
Wdr12-202	ENSMUST00000117438.7	3251	423aa	Protein coding	CCDS14988	Q4V9X1 Q9JJA4	NM_001199060 NP_001185989	TSL:1	GENCODE basic APPRIS P1
Wdr12-203	ENSMUST00000122038.7	2850	423aa	Protein coding	CCDS14988	Q4V9X1 Q9JJA4	NM_001199061 NP_001185990	TSL:1	GENCODE basic APPRIS P1
Wdr12-207	ENSMUST00000143342.7	770	151aa	Protein coding	-	D3Z369	-	CDS 3' incomplete	TSL:5
Wdr12-206	ENSMUST00000141417.2	720	151aa	Protein coding	-	D3Z369	-	CDS 3' incomplete	TSL:5
Wdr12-205	ENSMUST00000136461.1	275	No protein	Processed transcript	-	-	-	TSL:3	
Wdr12-208	ENSMUST00000147413.1	808	No protein	Retained intron	-	-	-	TSL:3	
Wdr12-204	ENSMUST00000133767.1	720	No protein	Retained intron	-	-	-	TSL:2	

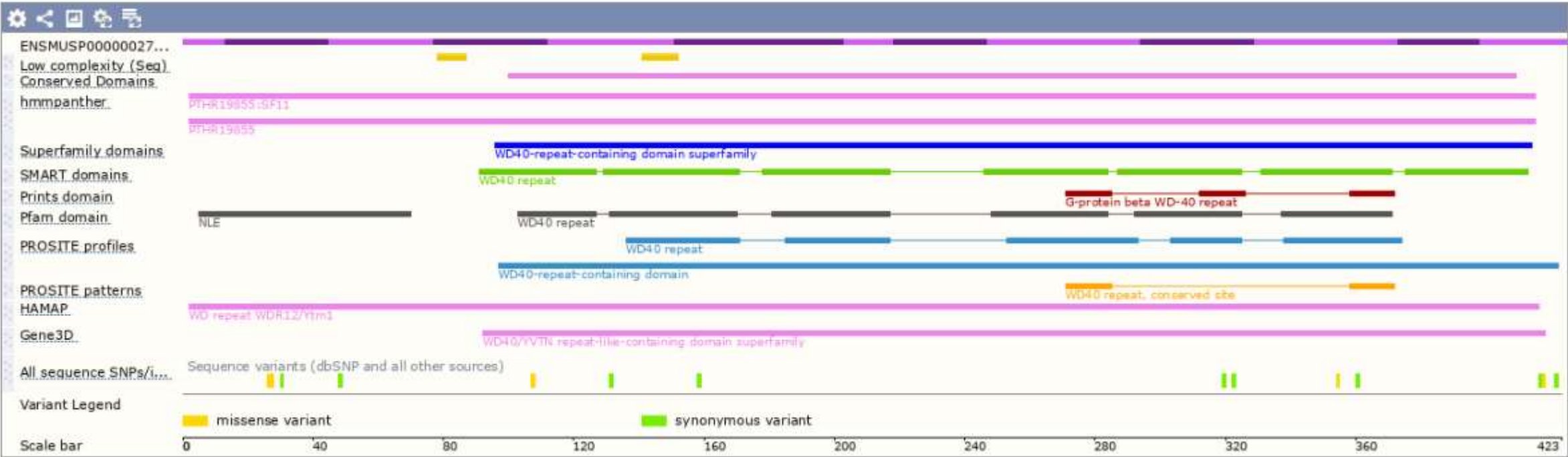
The strategy is based on the design of *Wdr12-201* transcript, The transcription is shown below



Genomic location distribution

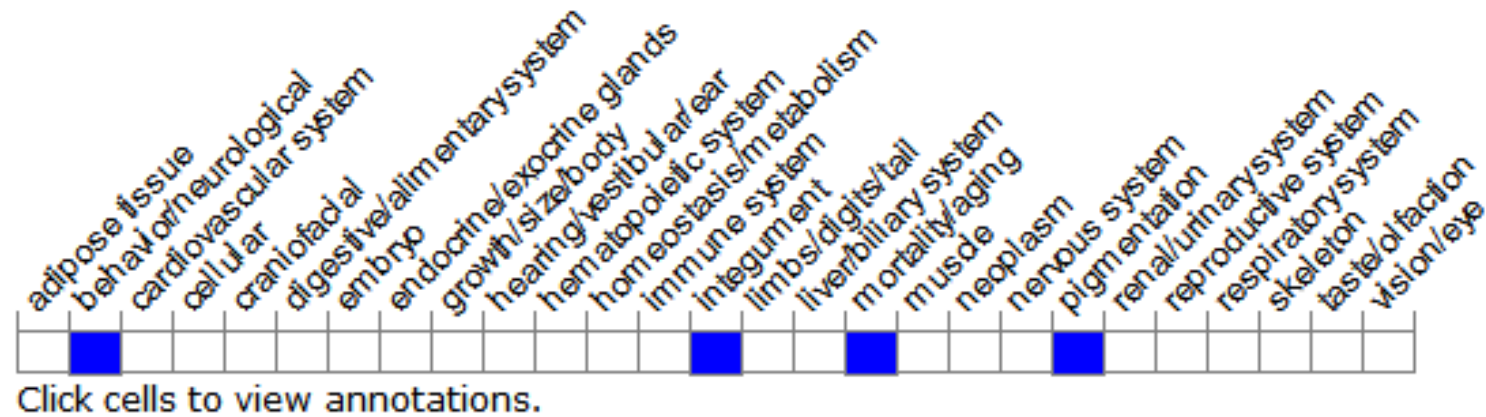


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview ?



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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