Wdr77 Cas9-KO Strategy

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Project Overview

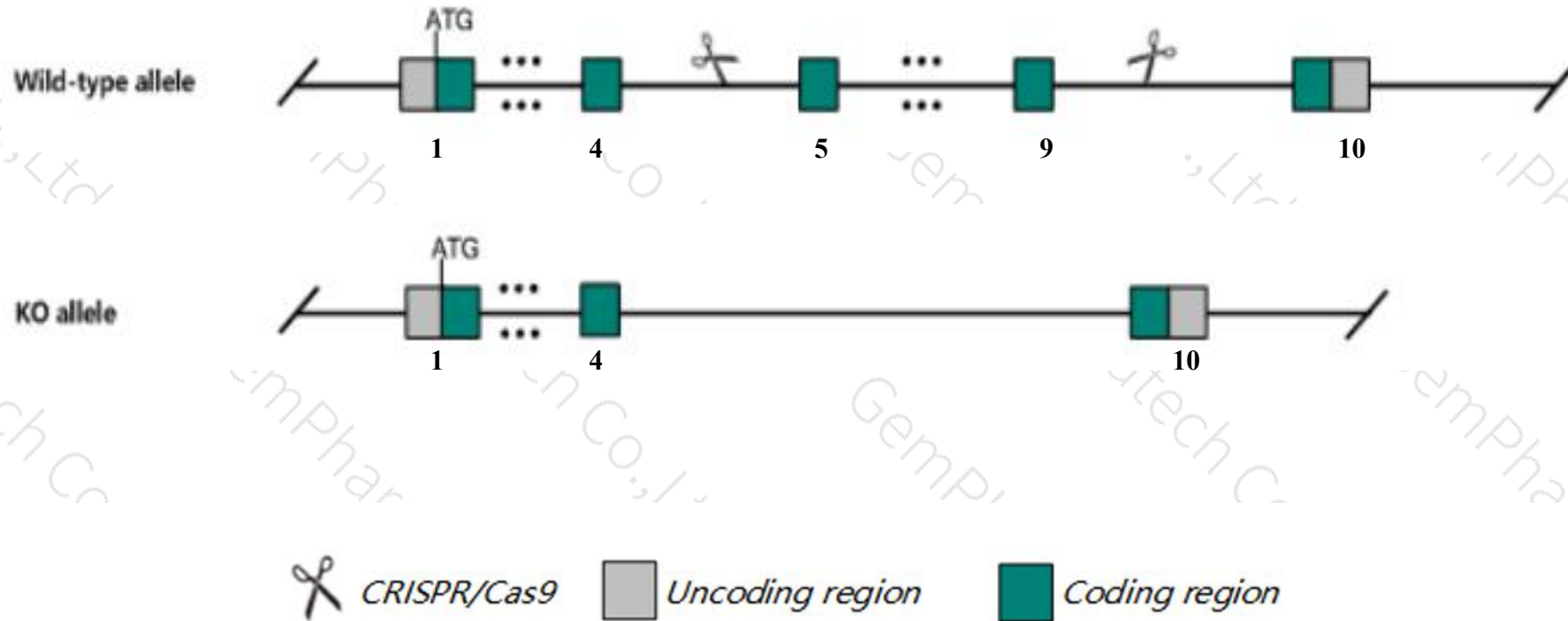|	
Project Name	*Wdr77*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Wdr77* gene. The schematic diagram is as follows:

Technical routes

➢ The *Wdr77* gene has 5 transcripts. According to the structure of *Wdr77* gene, exon5-exon9 of *Wdr77-201*(ENSMUST00000010278.11) transcript is recommended as the knockout region.The region contains 376bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Wdr77* gene. The brief process is as follows: CRISPR/Cas9 system 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.

Notice

➢ According to the existing MGI data,mice homozygous for a knock-out allele die prior to E8.5 for unknown reasons. Heterozygotes develop multifocal hyperplasia in the dorsal prostate; however, no prostate tumors are detected up to 12 months of age.

➢ Some amino acids will remain at the N-terminus and some functions may be retained.

➢ The *Wdr77* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information （NCBI）

Wdr77 WD repeat domain 77 [Mus musculus (house mouse)]

Gene ID: 70465, updated on 13-Mar-2020

Summary

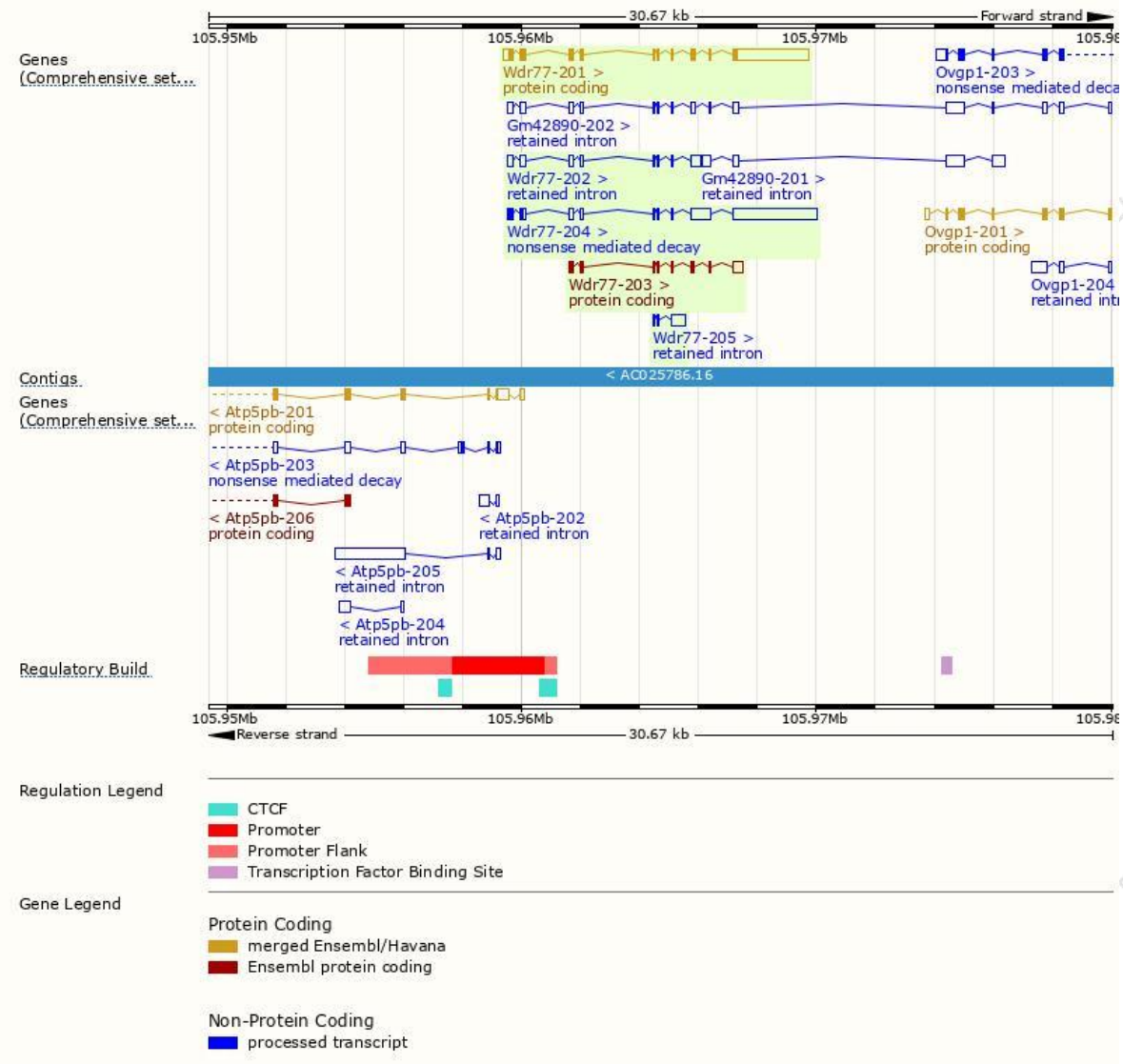|	
Official Symbol	Wdr77 provided by MGI
Official Full Name	WD repeat domain 77 provided by MGI
Primary source	MGI:MGI:1917715
See related	Ensembl:ENSMUSG0000000561
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2610003I18Rik, 2610312E17Rik, C79984, p44/MEP50
Expression	Ubiquitous expression in duodenum adult (RPKM 34.7), liver adult (RPKM 22.0) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Wdr77-201	ENSMUST00000010278.11	3682	342aa	Protein coding	CCDS17715	Q99J09	TSL:1 GENCODE basic APPRIS P1
Wdr77-203	ENSMUST00000128005.1	911	167aa	Protein coding	-	F7D5L2	CDS 5' incomplete TSL:3
Wdr77-204	ENSMUST00000130994.7	4286	60aa	Nonsense mediated decay	-	D6RIL4	TSL:1
Wdr77-202	ENSMUST00000127464.7	1095	No protein	Retained intron	-	-	TSL:1
Wdr77-205	ENSMUST00000151263.2	590	No protein	Retained intron	-	-	TSL:2

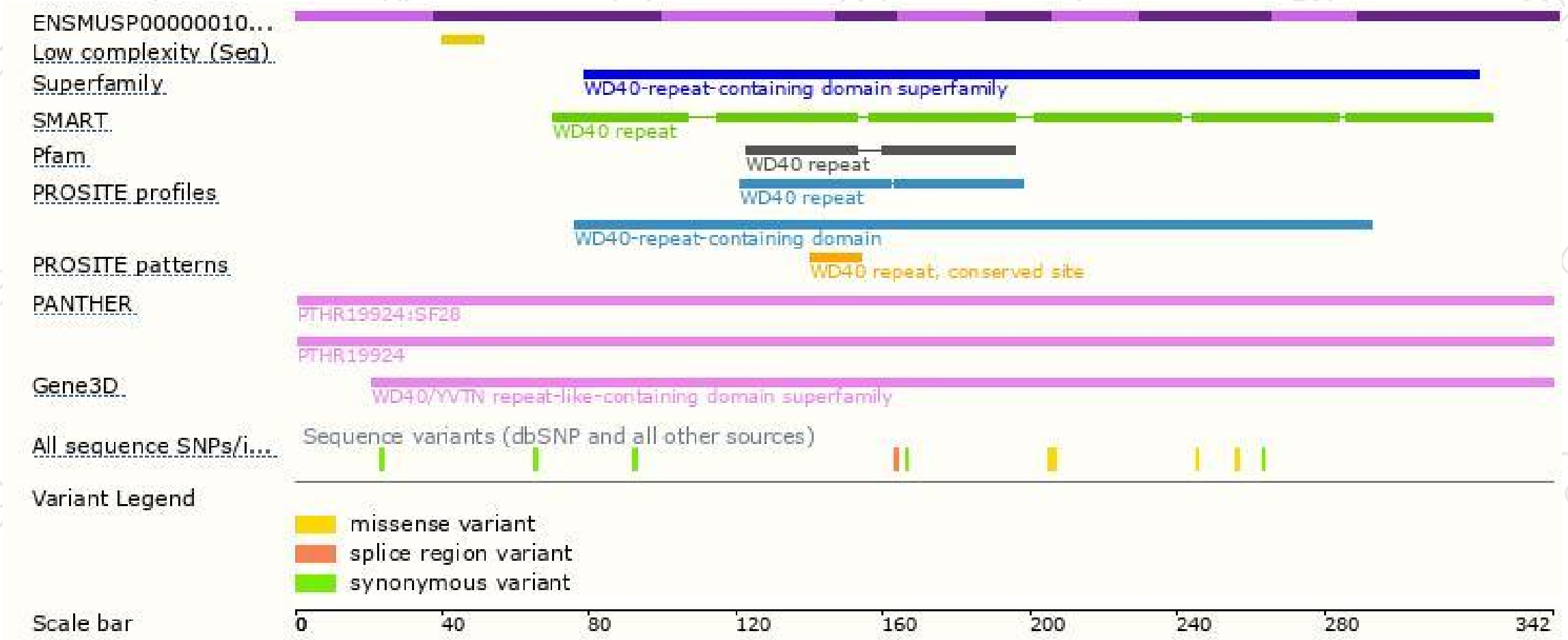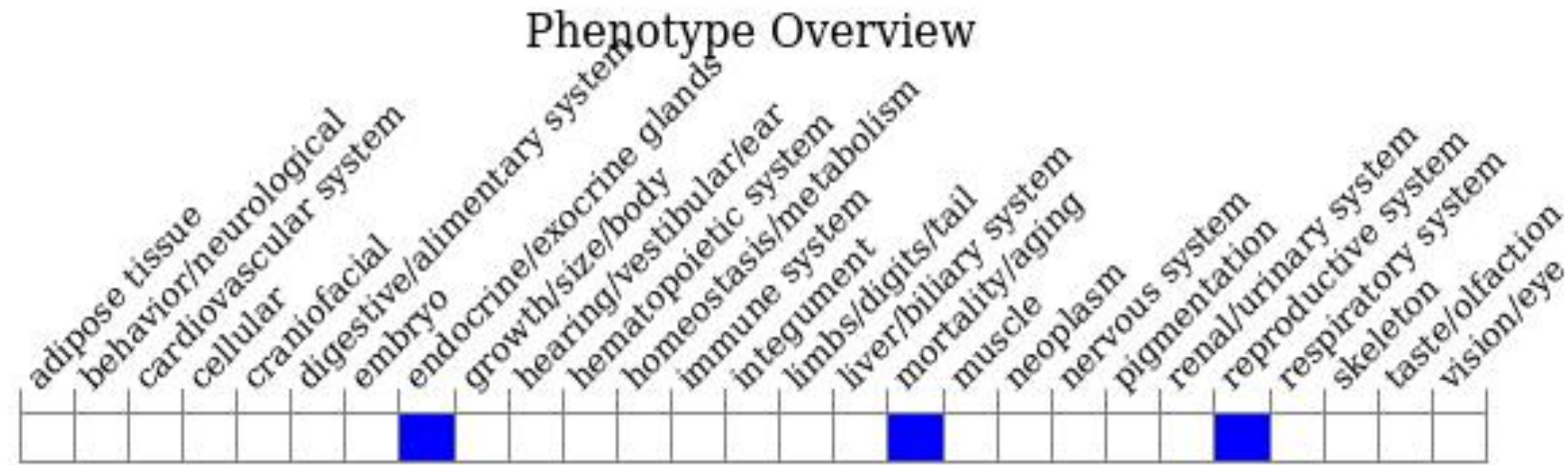The strategy is based on the design of *Wdr77-201* transcript,the transcription is shown below:

Genomic location distribution

Protein domain

ENSMUSP00000010...	
Low complexity (Seg)	
Superfamily	WD40-repeat-containing domain superfamily
SMART	WD40 repeat
Pfam	WD40 repeat
PROSITE profiles	WD40 repeat
	WD40-repeat-containing domain
PROSITE patterns	WD40 repeat, conserved site
PANTHER	PTHR19924:SF28
	PTHR19924
Gene3D	WD40/YVTN repeat-like-containing domain superfamily
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)
Variant Legend	missense variant splice region variant synonymous variant
Scale bar	0 40 80 120 160 200 240 280 342

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/).

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