Wdr19 Cas9-KO Strategy

Designer: JiaYu

Reviewer: Xiaojing Li

Design Date: 2020-8-13

Project Overview

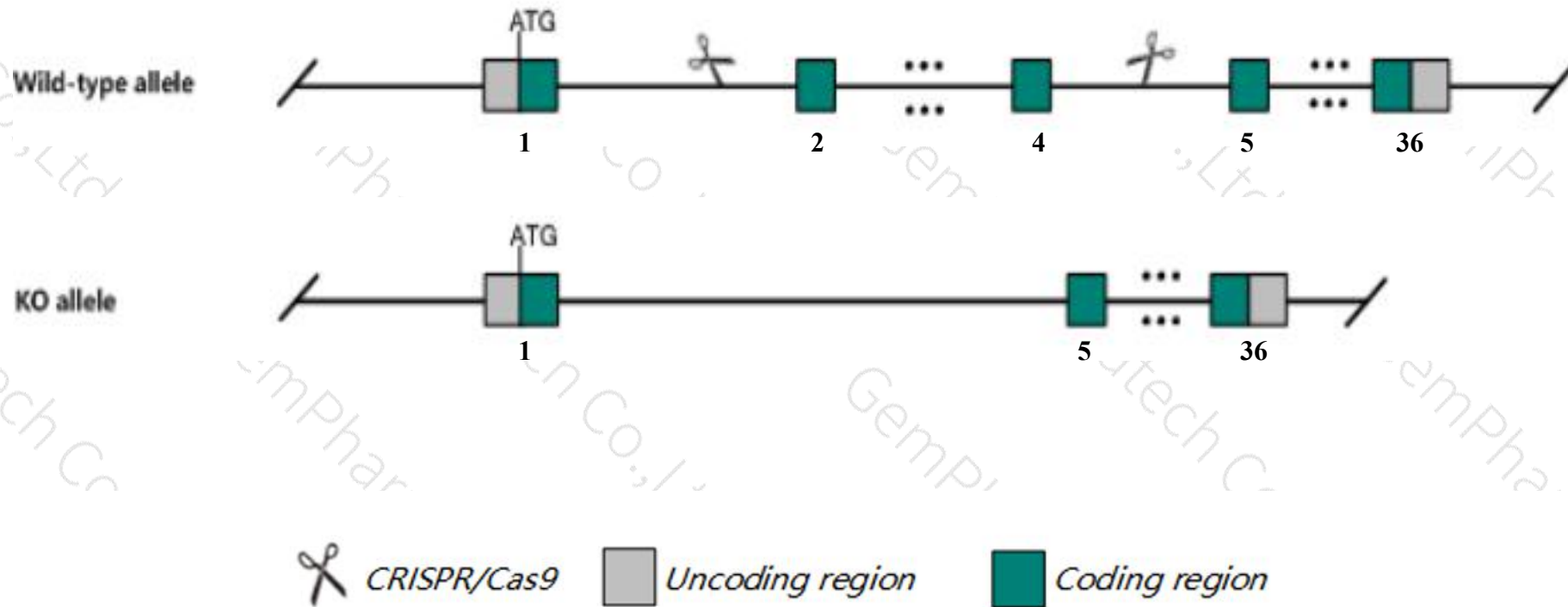|	
Project Name	*Wdr19*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Wdr19* gene. The schematic diagram is as follows:

Technical routes

➢ The *Wdr19* gene has 8 transcripts. According to the structure of *Wdr19* gene, exon2-exon4 of *Wdr19-204*(ENSMUST00000203653.2) transcript is recommended as the knockout region.The region contains 284bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Wdr19* 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 transgenic gene disruption exhibit embryonic lethality at E10.

➢Transcript 203 CDS 5' incomplete the influences is unknown.

➢ The *Wdr19* gene is located on the Chr5. 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）

Wdr19 WD repeat domain 19 [Mus musculus (house mouse)]
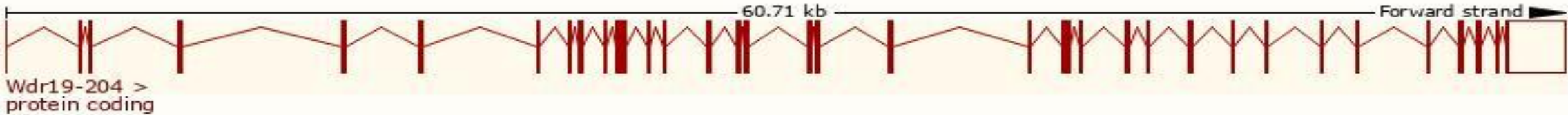
Gene ID: 213081, updated on 20-Mar-2020

Summary

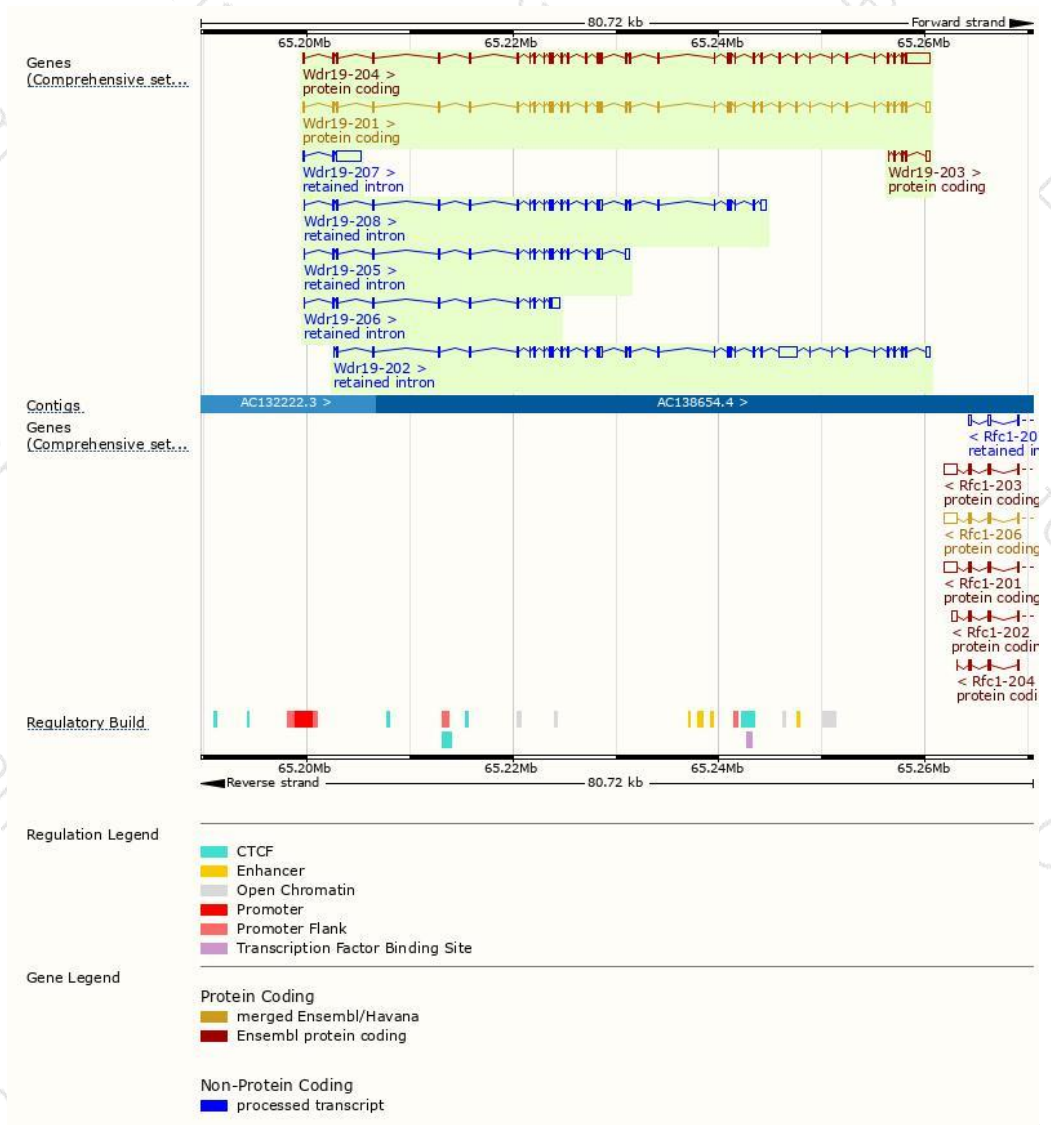|	
Official Symbol	Wdr19 provided by MGI
Official Full Name	WD repeat domain 19 provided byMGI
Primary source	MGI:MGI:2443231
See related	Ensembl:ENSMUSG00000037890
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	C330027H04Rik, D330023L08Rik, DYF2, Ift144, PWDMP, mKIAA1638
Expression	Broad expression in testis adult (RPKM 6.3), frontal lobe adult (RPKM 3.9) and 21 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Wdr19-204	ENSMUST00000203653.2	6279	1341aa	Protein coding	CCDS51509	Q3UGF1	TSL:1 GENCODE basic APPRIS P1
Wdr19-201	ENSMUST00000041892.12	4401	1341aa	Protein coding	CCDS51509	Q3UGF1	TSL:1 GENCODE basic APPRIS P1
Wdr19-203	ENSMUST00000203554.1	625	105aa	Protein coding	-	A0A0N4SUU5	CDS 5' incomplete TSL:5
Wdr19-202	ENSMUST00000203359.1	5830	No protein	Retained intron	-	-	TSL:2
Wdr19-208	ENSMUST00000204647.2	3381	No protein	Retained intron	-	-	TSL:1
Wdr19-207	ENSMUST00000204582.2	2516	No protein	Retained intron	-	-	TSL:1
Wdr19-205	ENSMUST00000203676.2	2305	No protein	Retained intron	-	-	TSL:1
Wdr19-206	ENSMUST00000204375.2	1924	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Wdr19-204* transcript,the transcription is shown below:
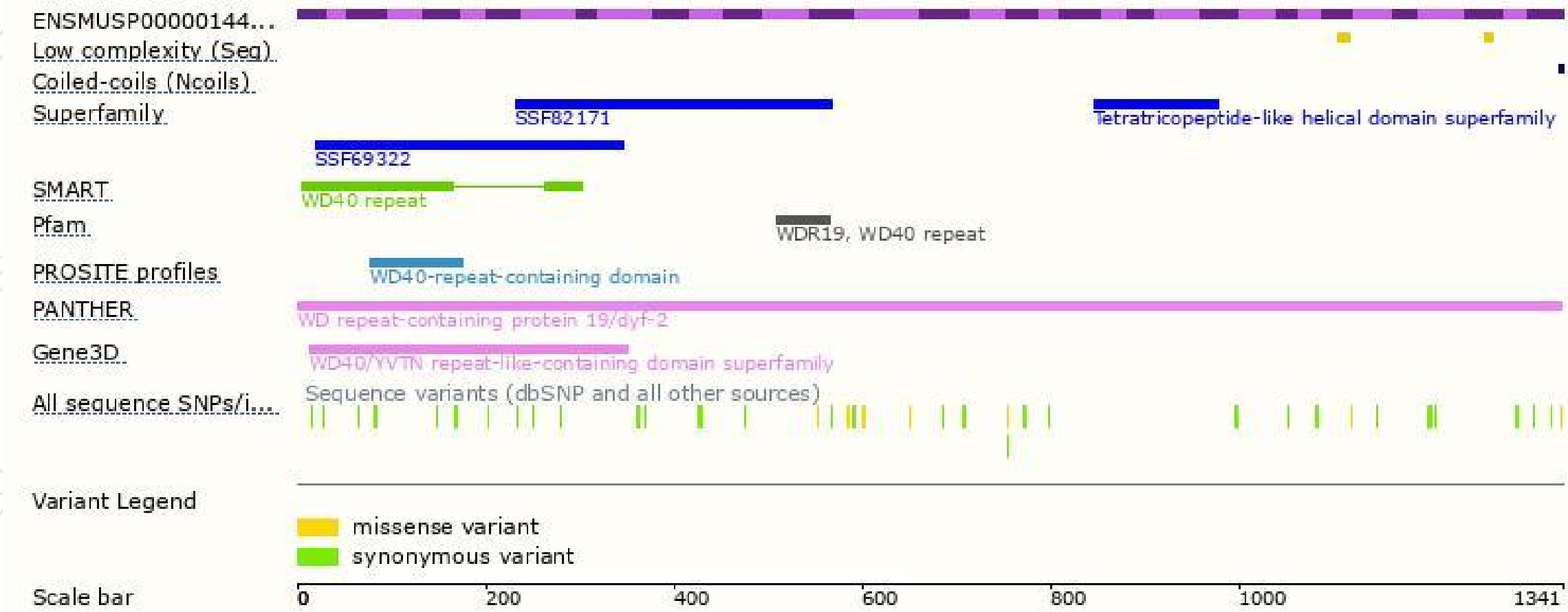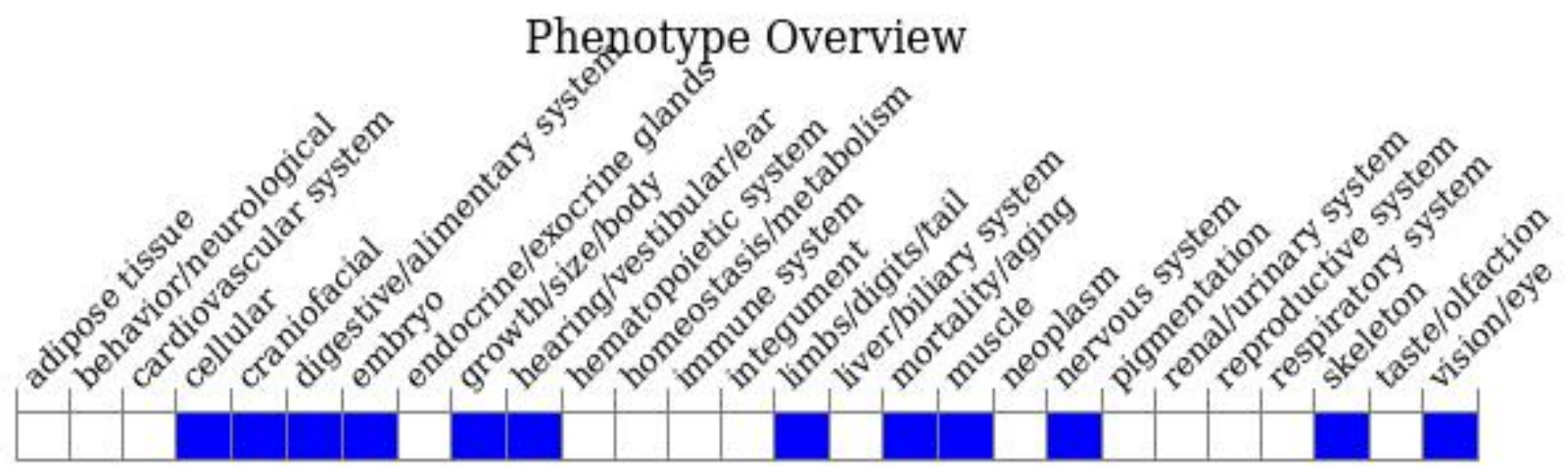
Genomic location distribution

Protein domain

ENSMUSP00000144...	
Low complexity (Seg)	
Coiled-coils (Ncoils)	
Superfamily	SSF82171 — Tetratricopeptide-like helical domain superfamily
	SSF69322
SMART	WD40 repeat
Pfam	WDR19, WD40 repeat
PROSITE profiles	WD40-repeat-containing domain
PANTHER	WD repeat-containing protein 19/dyf-2
Gene3D	WD40/YVTN repeat-like-containing domain superfamily
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)

Variant Legend

- missense variant
- synonymous variant

Scale bar: 0   200   400   600   800   1000   1341

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/).

According to the existing MGI data,mice homozygous for a transgenic gene disruption exhibit embryonic lethality at E10.