

# *Wdr13* Cas9-KO Strategy

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**Reviewer:**

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**Design Date:**

**2020-2-19**

# Project Overview

**Project Name**

*Wdr13*

**Project type**

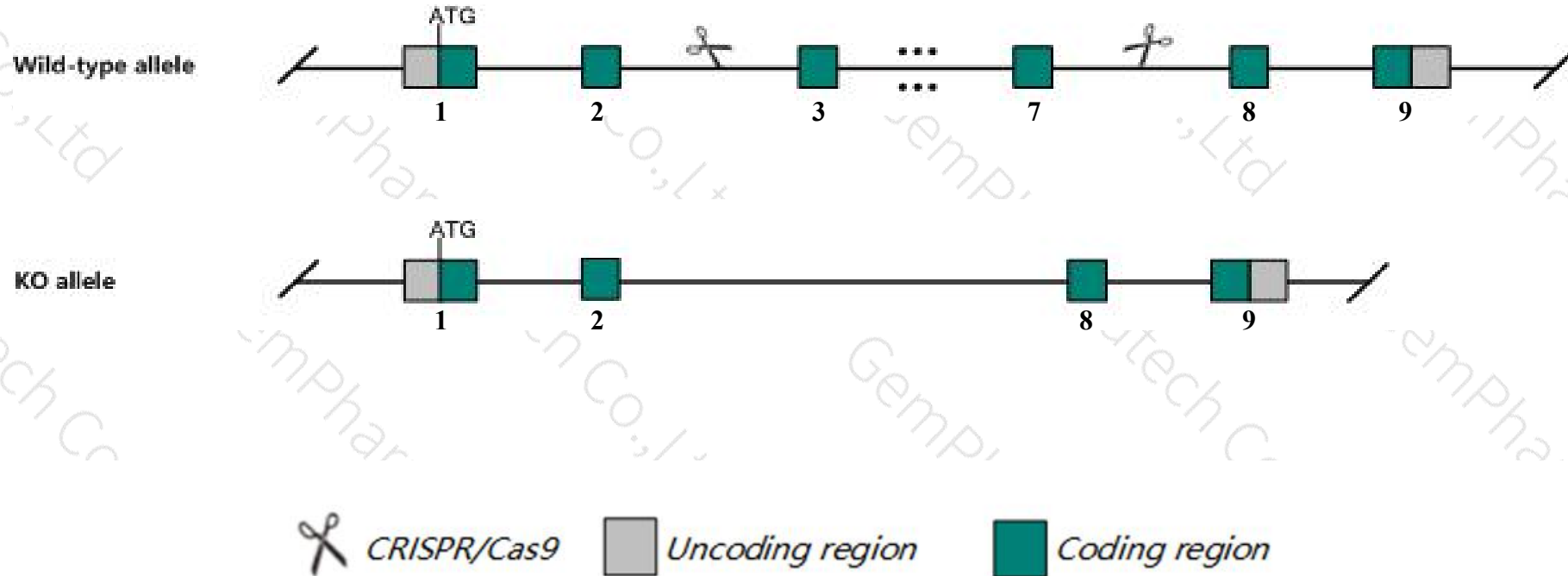
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Wdr13* gene. The schematic diagram is as follows:



- The *Wdr13* gene has 10 transcripts. According to the structure of *Wdr13* gene, exon3-exon7 of *Wdr13-201* (ENSMUST00000033506.12) transcript is recommended as the knockout region. The region contains 872bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Wdr13* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit increased pancreas beta cell proliferation, hyperinsulinemia and mild obesity.
- Some amino acids will remain at the N-terminus and some functions may be retained.
- The *Wdr13* gene is located on the ChrX. 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)

## Wdr13 WD repeat domain 13 [Mus musculus (house mouse)]

Gene ID: 73447, updated on 9-Apr-2019

### Summary



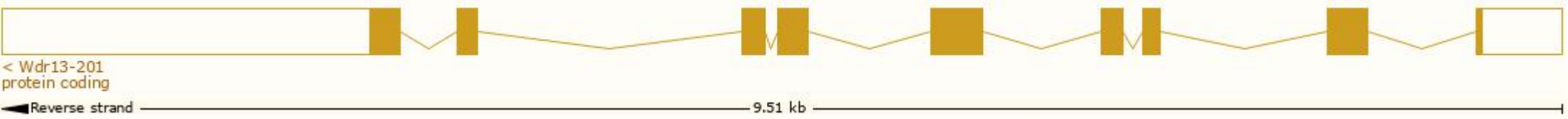
<b>Official Symbol</b>	Wdr13 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	WD repeat domain 13 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1914661</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000031166</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</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>	1700060B08Rik, 5730411P10Rik, DXHXS7467e, W51679, mMg21
<b>Expression</b>	Ubiquitous expression in CNS E18 (RPKM 49.2), frontal lobe adult (RPKM 36.1) and 28 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

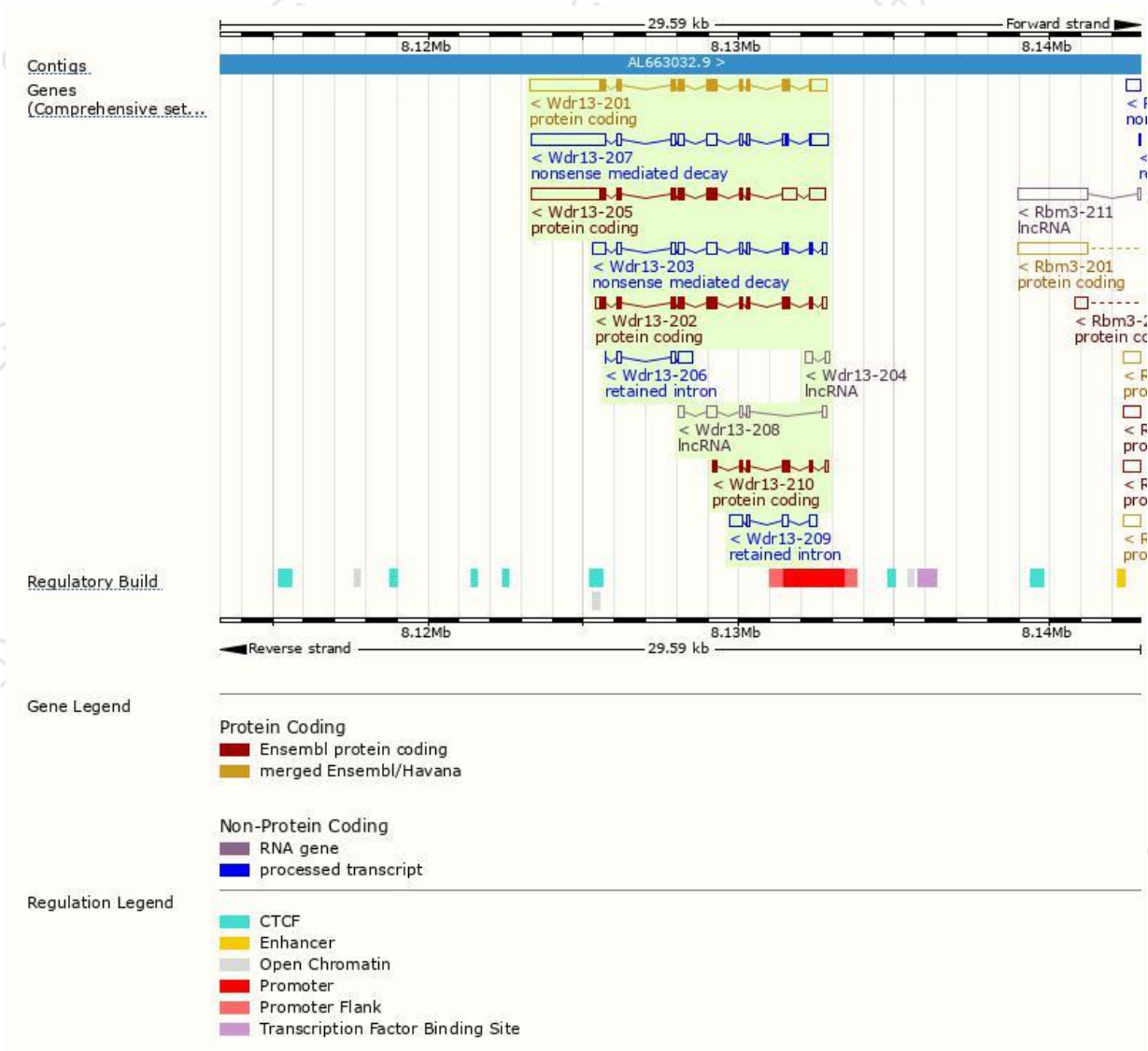
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Wdr13-205	<a href="#">ENSMUST00000130832.7</a>	4374	<a href="#">393aa</a>	Protein coding	<a href="#">CCDS72338</a>	<a href="#">S4R225</a>	TSL:5 GENCODE basic APPRIS ALT 1
Wdr13-201	<a href="#">ENSMUST00000033506.12</a>	4183	<a href="#">485aa</a>	Protein coding	<a href="#">CCDS29986</a>	<a href="#">Q32P16 Q91V09</a>	TSL:1 GENCODE basic APPRIS P3
Wdr13-202	<a href="#">ENSMUST00000115623.7</a>	1749	<a href="#">485aa</a>	Protein coding	<a href="#">CCDS29986</a>	<a href="#">Q32P16 Q91V09</a>	TSL:5 GENCODE basic APPRIS P3
Wdr13-210	<a href="#">ENSMUST00000153839.1</a>	774	<a href="#">219aa</a>	Protein coding	-	<a href="#">A2AC24</a>	CDS 3' incomplete TSL:3
Wdr13-207	<a href="#">ENSMUST00000133292.7</a>	4197	<a href="#">43aa</a>	Nonsense mediated decay	-	<a href="#">S4R258</a>	TSL:1
Wdr13-203	<a href="#">ENSMUST00000127062.8</a>	1822	<a href="#">43aa</a>	Nonsense mediated decay	-	<a href="#">S4R258</a>	TSL:5
Wdr13-209	<a href="#">ENSMUST00000149257.1</a>	958	No protein	Retained intron	-	-	TSL:2
Wdr13-206	<a href="#">ENSMUST00000131929.1</a>	774	No protein	Retained intron	-	-	TSL:2
Wdr13-208	<a href="#">ENSMUST00000148135.7</a>	844	No protein	lncRNA	-	-	TSL:5
Wdr13-204	<a href="#">ENSMUST00000130050.1</a>	373	No protein	lncRNA	-	-	TSL:3

The strategy is based on the design of *Wdr13-201* transcript,The transcription is shown below

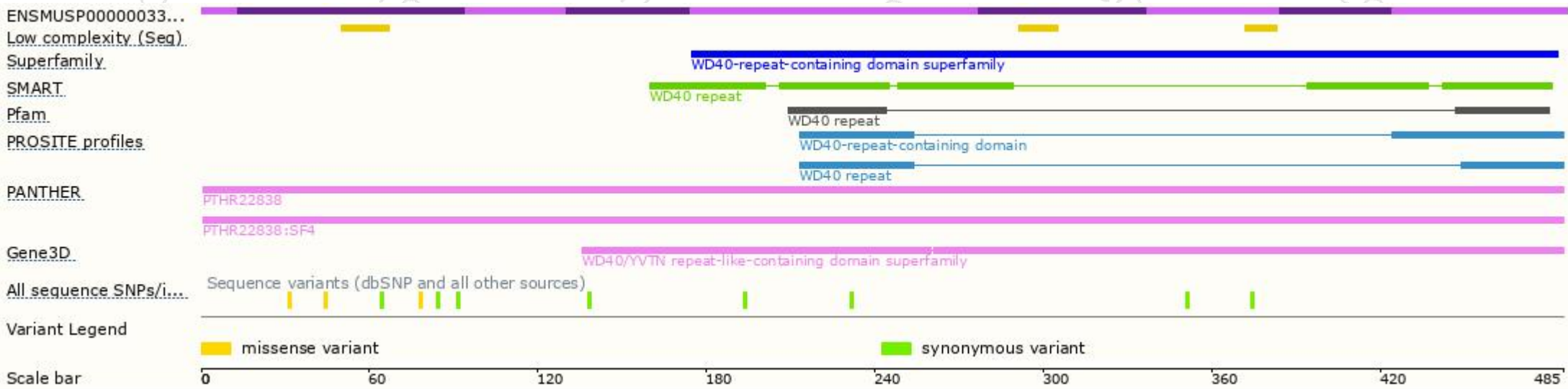


# Genomic location distribution

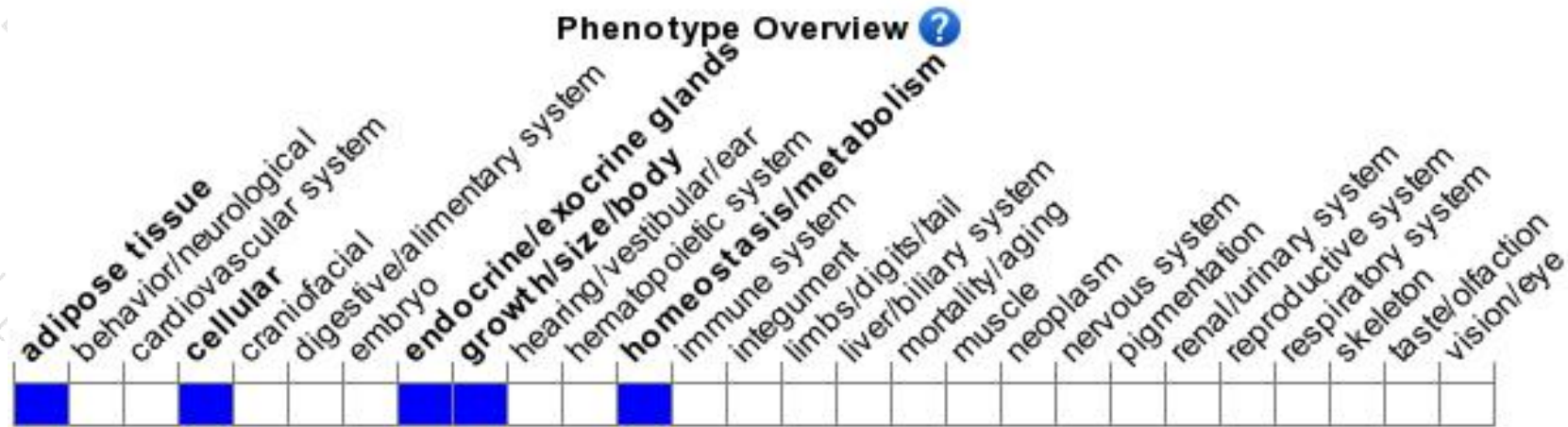




# Protein domain



# 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 a knock-out allele exhibit increased pancreas beta cell proliferation, hyperinsulinemia and mild obesity.

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

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