

Wdr13 Cas9-CKO Strategy

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Reviewer:

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Design Date:

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Project Overview

Project Name

Wdr13

Project type

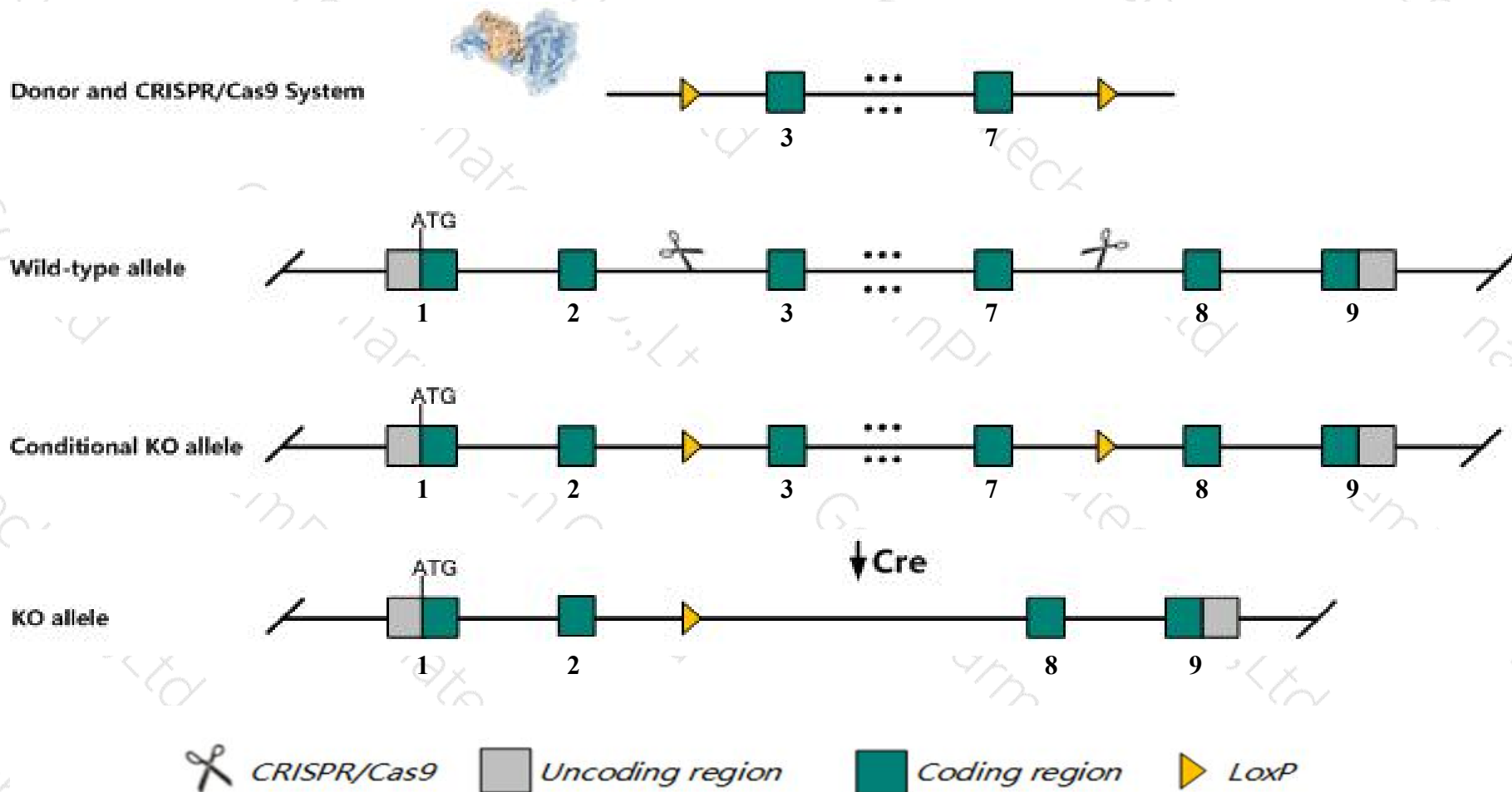
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional 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 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 will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

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

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

Summary



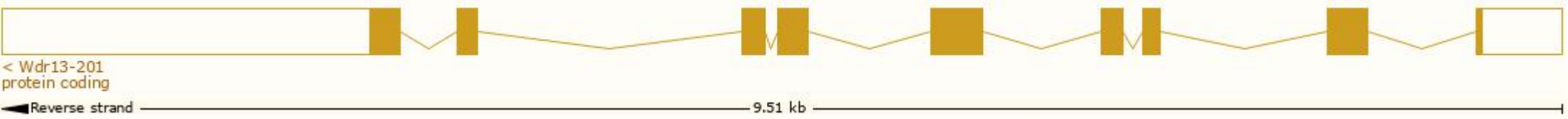
Official Symbol	Wdr13 provided by MGI
Official Full Name	WD repeat domain 13 provided by MGI
Primary source	MGI:MGI:1914661
See related	Ensembl:ENSMUSG00000031166
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1700060B08Rik, 5730411P10Rik, DXHXS7467e, W51679, mMg21
Expression	Ubiquitous expression in CNS E18 (RPKM 49.2), frontal lobe adult (RPKM 36.1) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

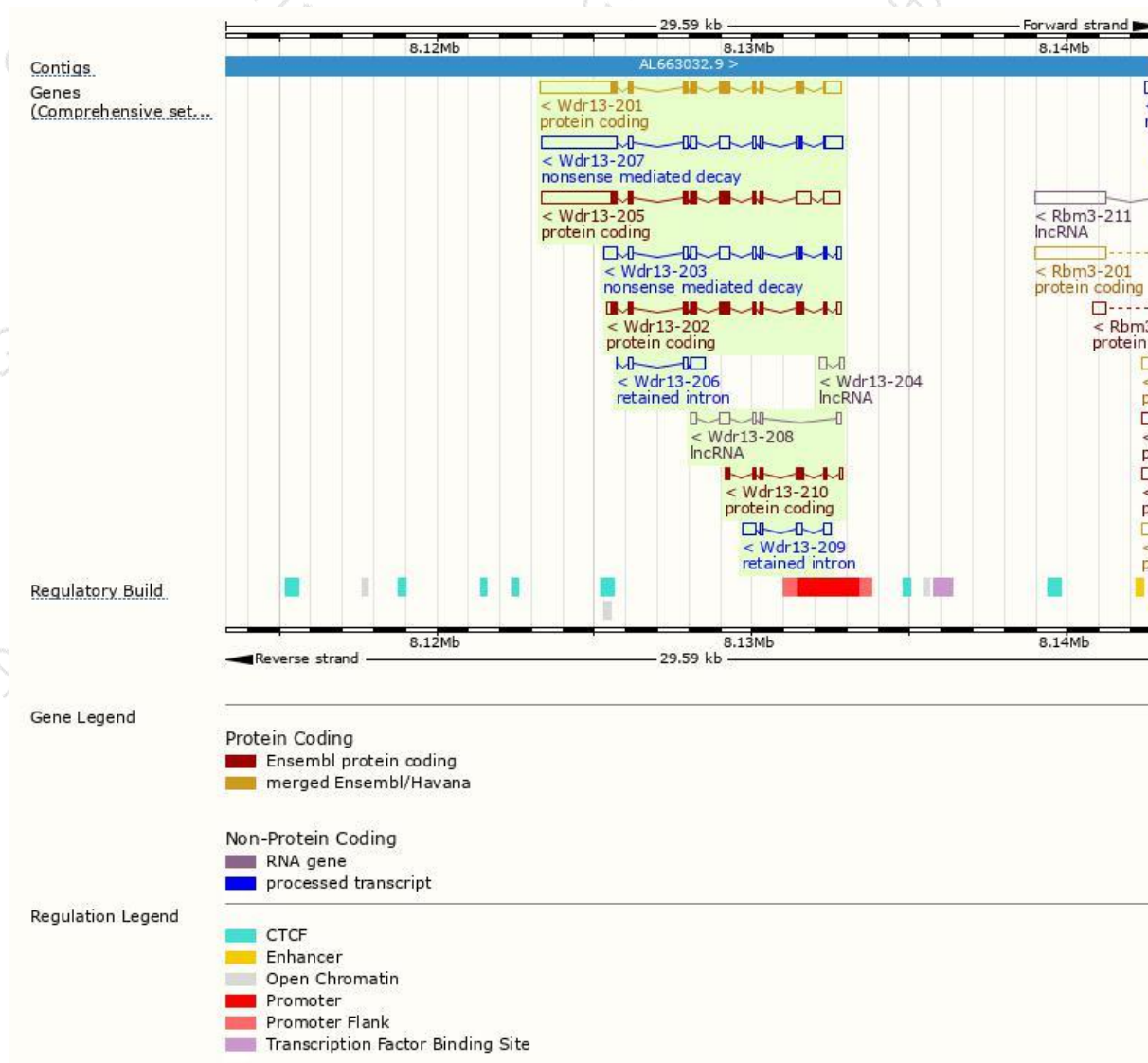
The gene has 10 transcripts,all transcripts are shown below:

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

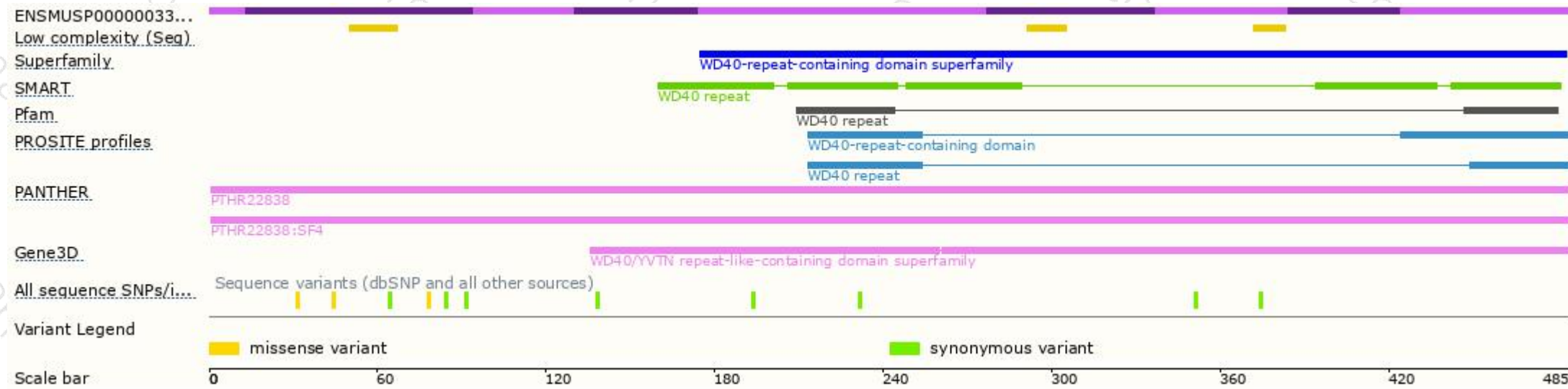
The strategy is based on the design of *Wdr13-201* transcript,The transcription is shown below



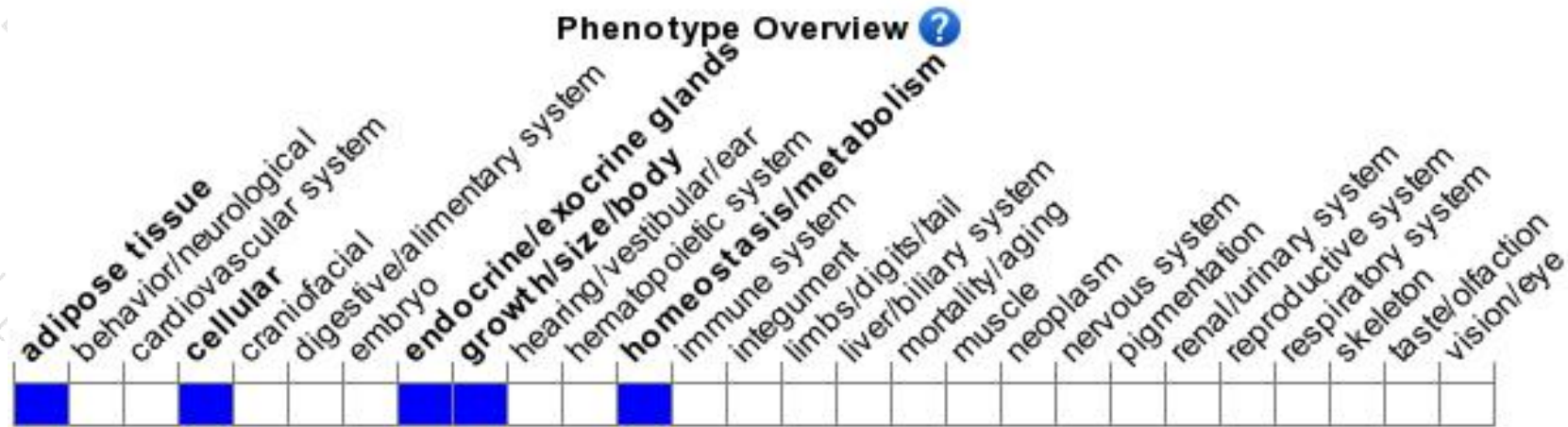
Genomic location distribution



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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