

Wdr26 Cas9-CKO Strategy

Designer:

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Project Overview

Project Name

Wdr26

Project type

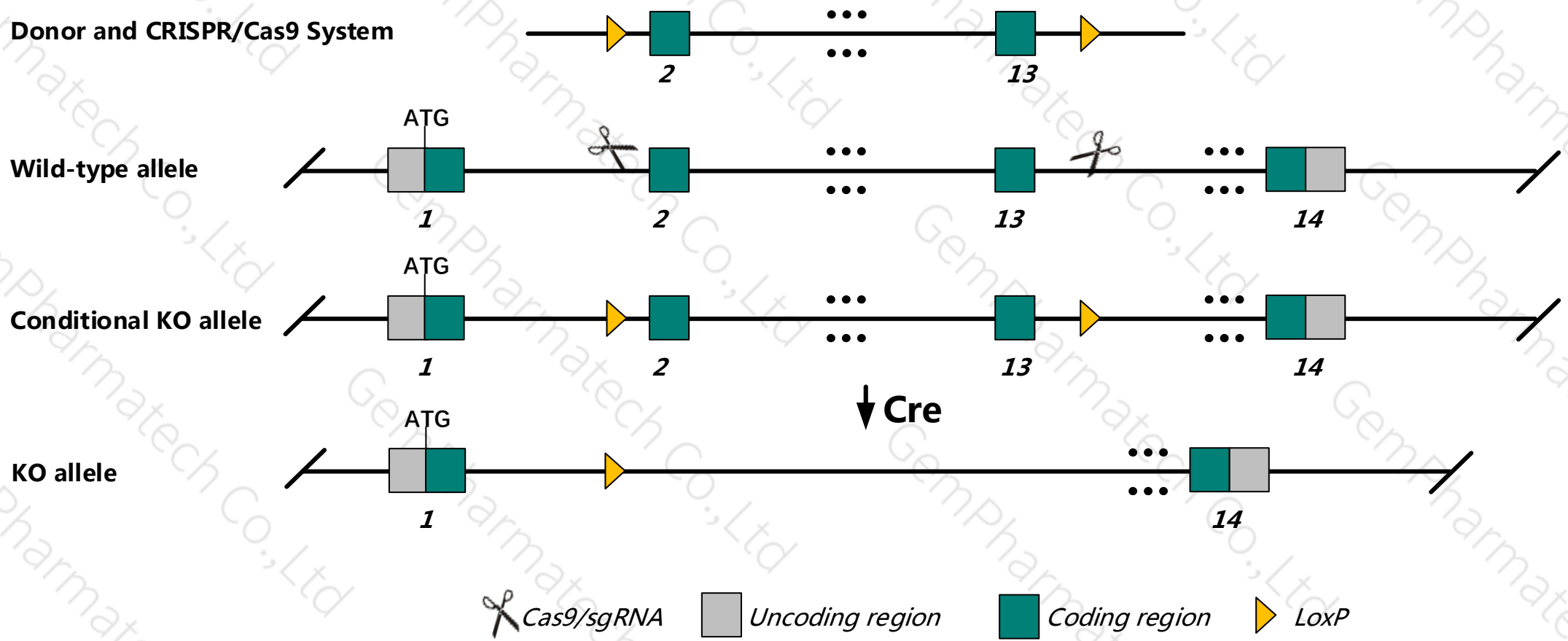
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Wdr26* gene. The schematic diagram is as follows:



- The *Wdr26* gene has 9 transcripts. According to the structure of *Wdr26* gene, exon2-exon13 of *Wdr26*-207 transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Wdr26* 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 *Wdr26* 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 gene transcription and translation processes, all risks cannot be predicted under existing information.

Gene information (NCBI)

Wdr26 WD repeat domain 26 [*Mus musculus* (house mouse)]

Gene ID: 226757, updated on 15-Apr-2019

Summary

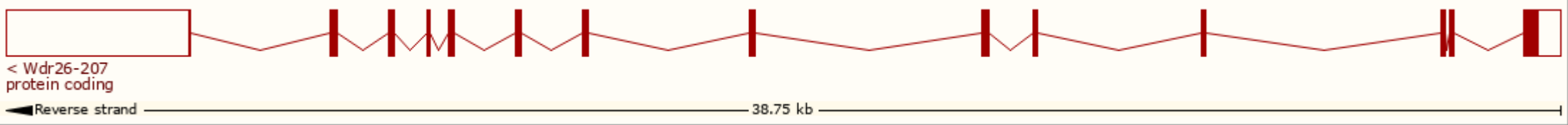
| | |
|--------------------|---|
| Official Symbol | Wdr26 provided by MGI |
| Official Full Name | WD repeat domain 26 provided by MGI |
| Primary source | MGI:MGI:1923825 |
| See related | Ensembl:ENSMUSG00000038733 |
| Gene type | protein coding |
| RefSeq status | VALIDATED |
| Organism | Mus musculus |
| Lineage | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| Also known as | Gid7; C77982; AA693241; AI447817; AU044014; 1600024A01Rik |
| Expression | Ubiquitous expression in liver E14 (RPKM 34.5), liver E14.5 (RPKM 31.1) and 28 other tissues See more |
| Orthologs | human all |

Transcript information (Ensembl)

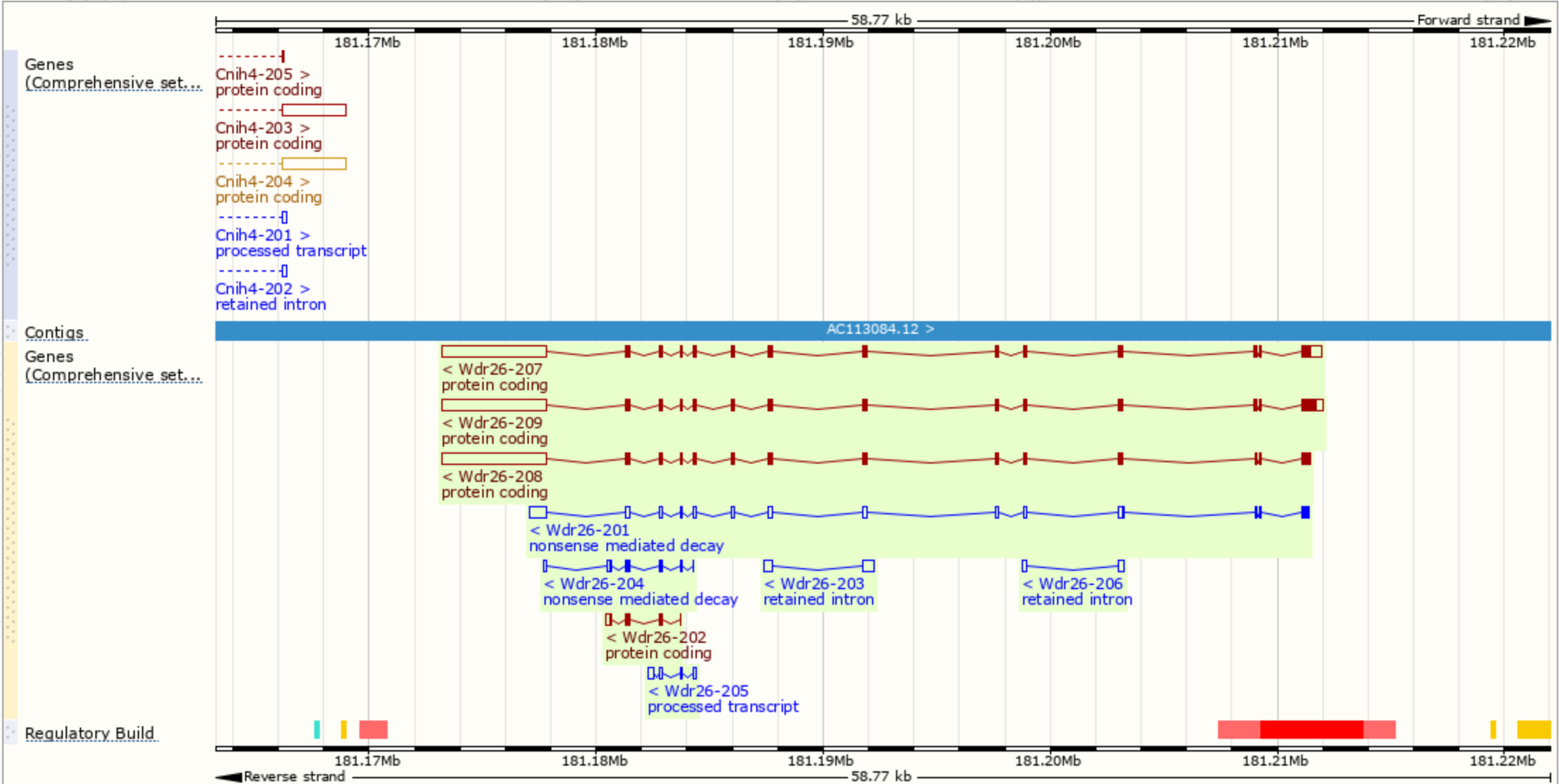
The gene has 9 transcripts, and all transcripts are shown below :

| Show/hide columns (1 hidden) | | Filter | | | | | |
|------------------------------|--------------------------------------|--------|-----------------------|-------------------------|---------------------------|------------------------|-------------------------------|
| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
| Wdr26-207 | ENSMUST00000162819.8 | 7045 | 641aa | Protein coding | CCDS15583 | Q8C6G8 | TSL:1 GENCODE basic APPRIS P1 |
| Wdr26-209 | ENSMUST00000237749.1 | 7068 | 729aa | Protein coding | - | - | GENCODE basic |
| Wdr26-208 | ENSMUST00000162963.7 | 6452 | 625aa | Protein coding | - | E0CYH4 | CDS 5' incomplete TSL:5 |
| Wdr26-202 | ENSMUST00000159290.1 | 571 | 120aa | Protein coding | - | F6UT94 | CDS 5' incomplete TSL:5 |
| Wdr26-201 | ENSMUST0000036329.11 | 2640 | 183aa | Nonsense mediated decay | - | F8WH48 | CDS 5' incomplete TSL:5 |
| Wdr26-204 | ENSMUST00000159673.7 | 751 | 147aa | Nonsense mediated decay | - | F7DFQ2 | CDS 5' incomplete TSL:5 |
| Wdr26-205 | ENSMUST00000159698.1 | 615 | No protein | Processed transcript | - | - | TSL:5 |
| Wdr26-203 | ENSMUST00000159625.1 | 811 | No protein | Retained intron | - | - | TSL:3 |
| Wdr26-206 | ENSMUST00000161531.1 | 431 | No protein | Retained intron | - | - | TSL:3 |

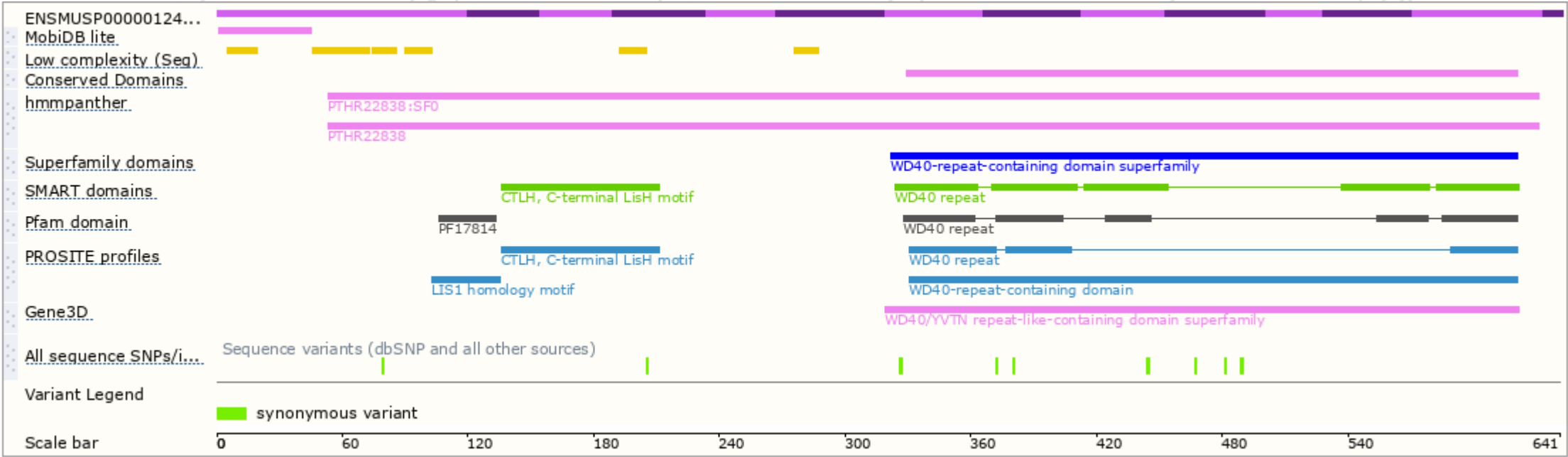
The strategy is based on the design of *Wdr26-207* transcript, The transcription is shown below



Genomic location distribution



Protein domain



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