Tbl2 Cas9-KO Strategy

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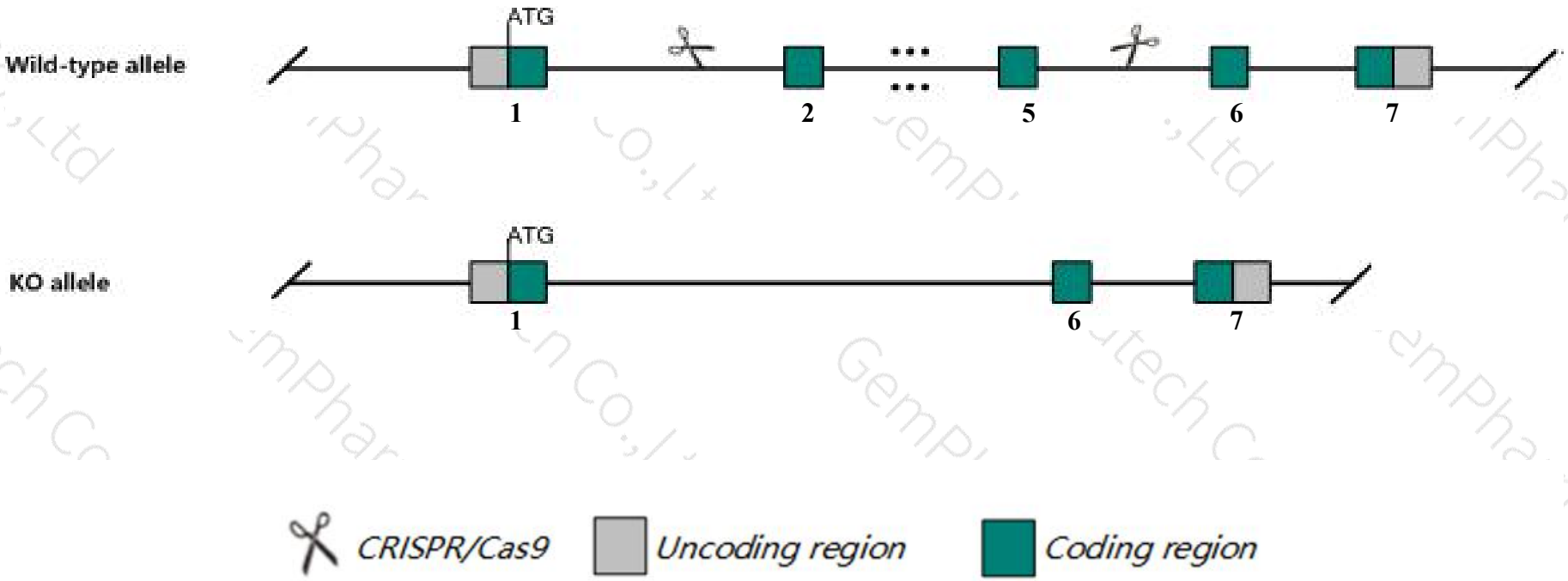
Design Date: 2019-11-13

Project Overview

Project Name	***Tbl2***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tbl2* gene. The schematic diagram is as follows:



Technical routes

➢ The *Tbl2* gene has 5 transcripts. According to the structure of *Tbl2* gene, exon2-exon5 of *Tbl2-204* (ENSMUST00000153183.7) transcript is recommended as the knockout region.The region contains 586bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Tbl2* gene. The brief process is as follows: CRISPR/Cas9 system w

Notice

➢ The *Tbl2* 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）

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Tbl2 transducin (beta)-like 2 [Mus musculus (house mouse)]

Gene ID: 27368, updated on 31-Jan-2019

Summary

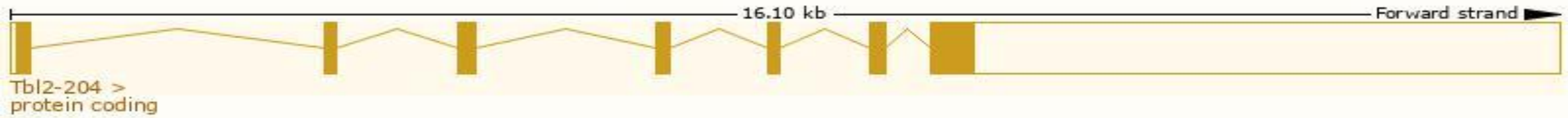
Official Symbol	Tbl2 provided by MGI
Official Full Name	transducin (beta)-like 2 provided byMGI
Primary source	MGI:MGI:1351652
See related	Ensembl:ENSMUSG00000005374
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	C76179, WS-bTRP
Expression	Ubiquitous expression in testis adult (RPKM 13.5), limb E14.5 (RPKM 7.2) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

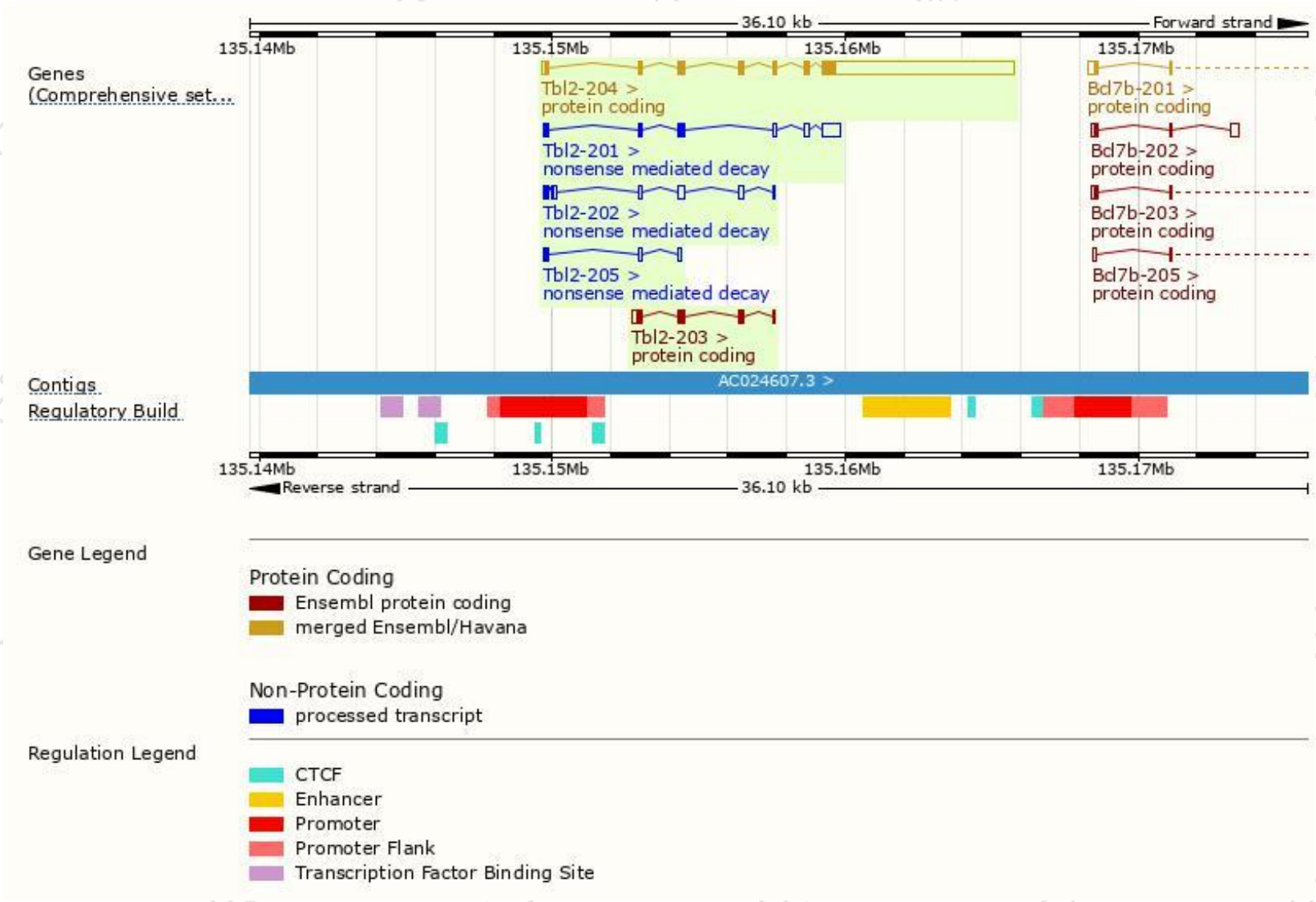
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Tbl2-204	ENSMUST00000153183.7	7488	442aa	Protein coding	CCDS19735	Q9R099	TSL:1 GENCODE basic APPRIS P1
Tbl2-203	ENSMUST00000152013.1	766	190aa	Protein coding	-	D3YZH8	CDS 3' incomplete TSL:3
Tbl2-201	ENSMUST00000005508.13	1368	153aa	Nonsense mediated decay	-	F8WI46	TSL:1
Tbl2-202	ENSMUST00000139565.7	840	66aa	Nonsense mediated decay	-	D6RI48	TSL:3
Tbl2-205	ENSMUST00000201780.1	380	42aa	Nonsense mediated decay	-	A0A0J9YUN1	TSL:3

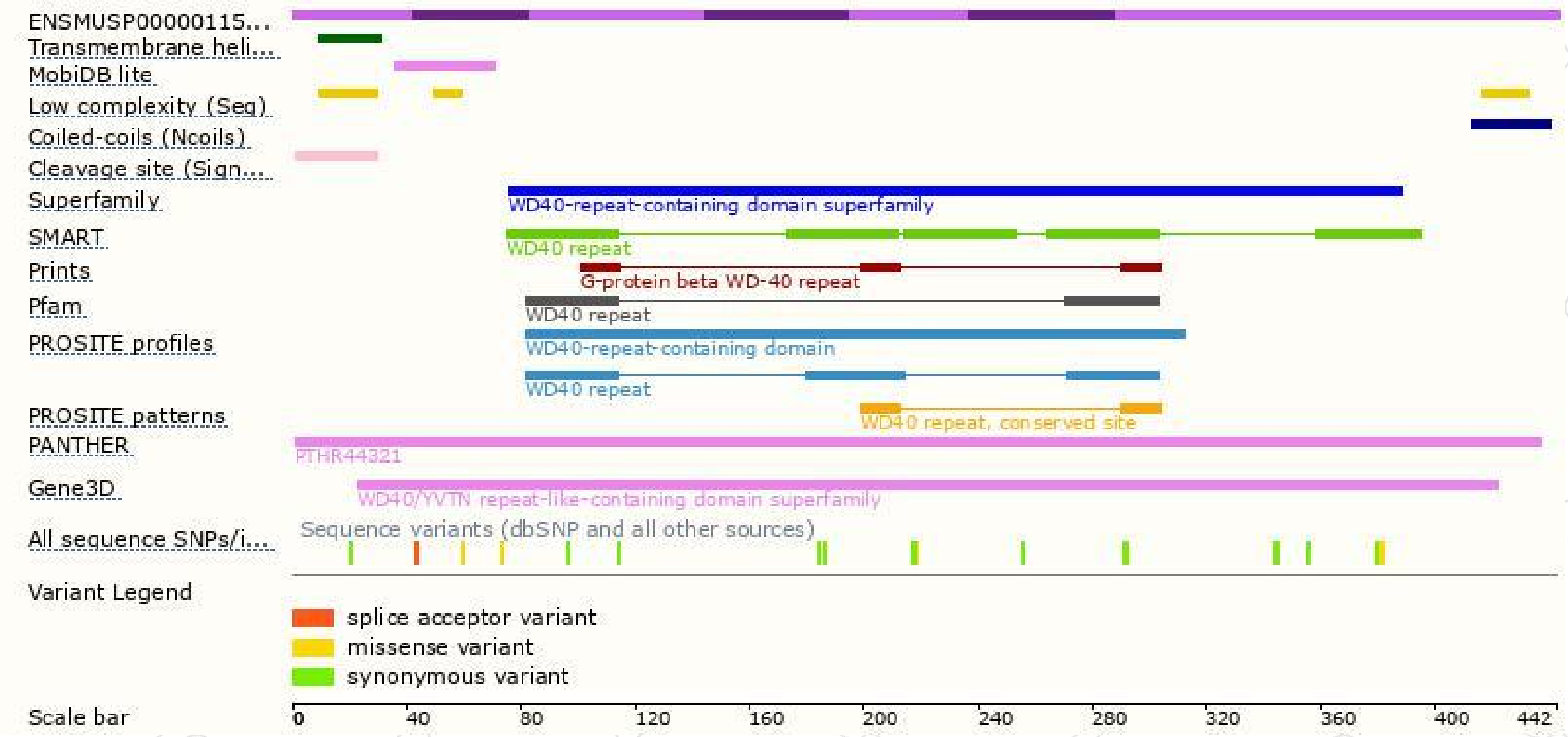
The strategy is based on the design of *Tbl2-204* transcript,The transcription is shown below



Genomic location distribution



Protein domain



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

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