

Recql5 Cas9-KO Strategy

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Project Overview

Project Name

Recql5

Project type

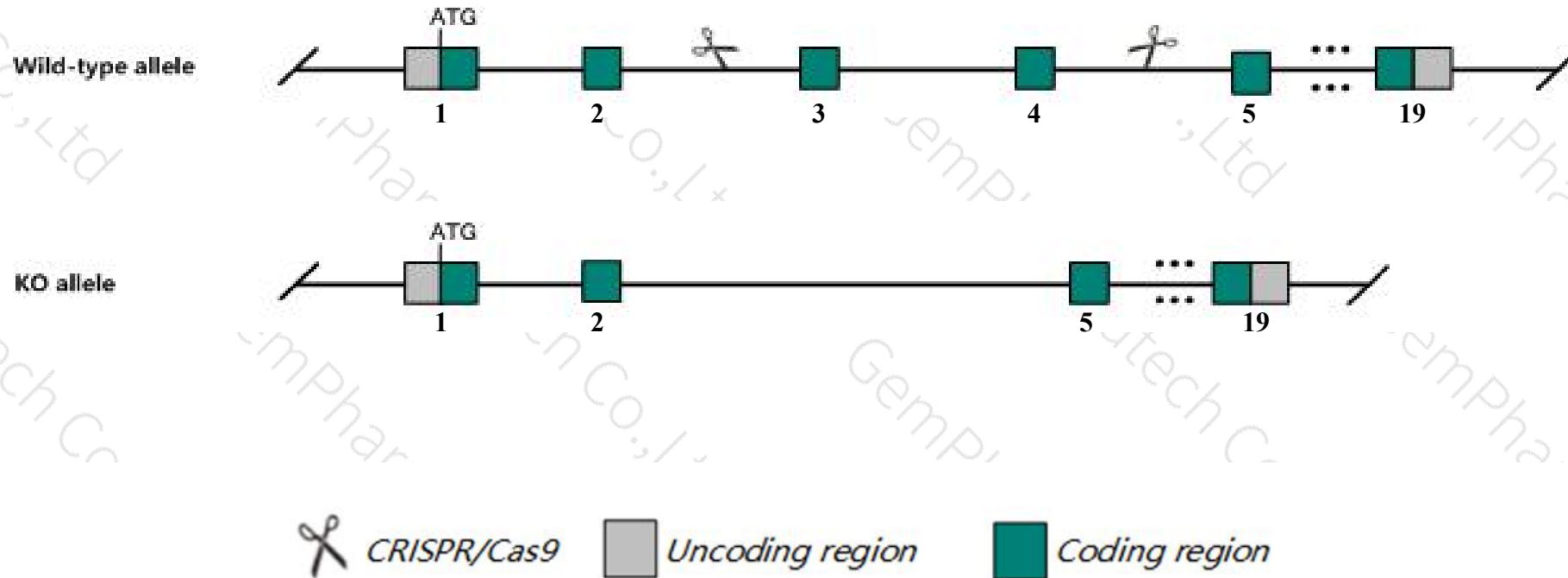
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Recql5* gene. The schematic diagram is as follows:



- The *Recql5* gene has 8 transcripts. According to the structure of *Recql5* gene, exon3-exon4 of *Recql5-201* (ENSMUST00000021097.9) transcript is recommended as the knockout region. The region contains 625bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Recql5* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, mice homozygous for disruptions in this gene express elevated levels of sister chromatid exchange due to a failure to suppress crossovers.
- The *Recql5* gene is located on the Chr11. 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)

Recql5 RecQ protein-like 5 [*Mus musculus* (house mouse)]

Gene ID: 170472, updated on 10-Oct-2019

Summary

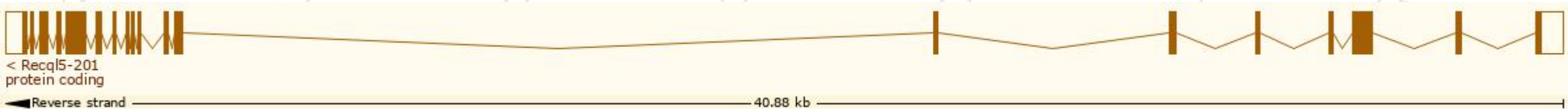
Official Symbol	Recql5 provided by MGI
Official Full Name	RecQ protein-like 5 provided by MGI
Primary source	MGI:MGI:2156841
See related	Ensembl:ENSMUSG00000020752
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	RecQ5; Recq5b; Recql5b
Expression	Ubiquitous expression in testis adult (RPKM 8.0), large intestine adult (RPKM 8.0) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

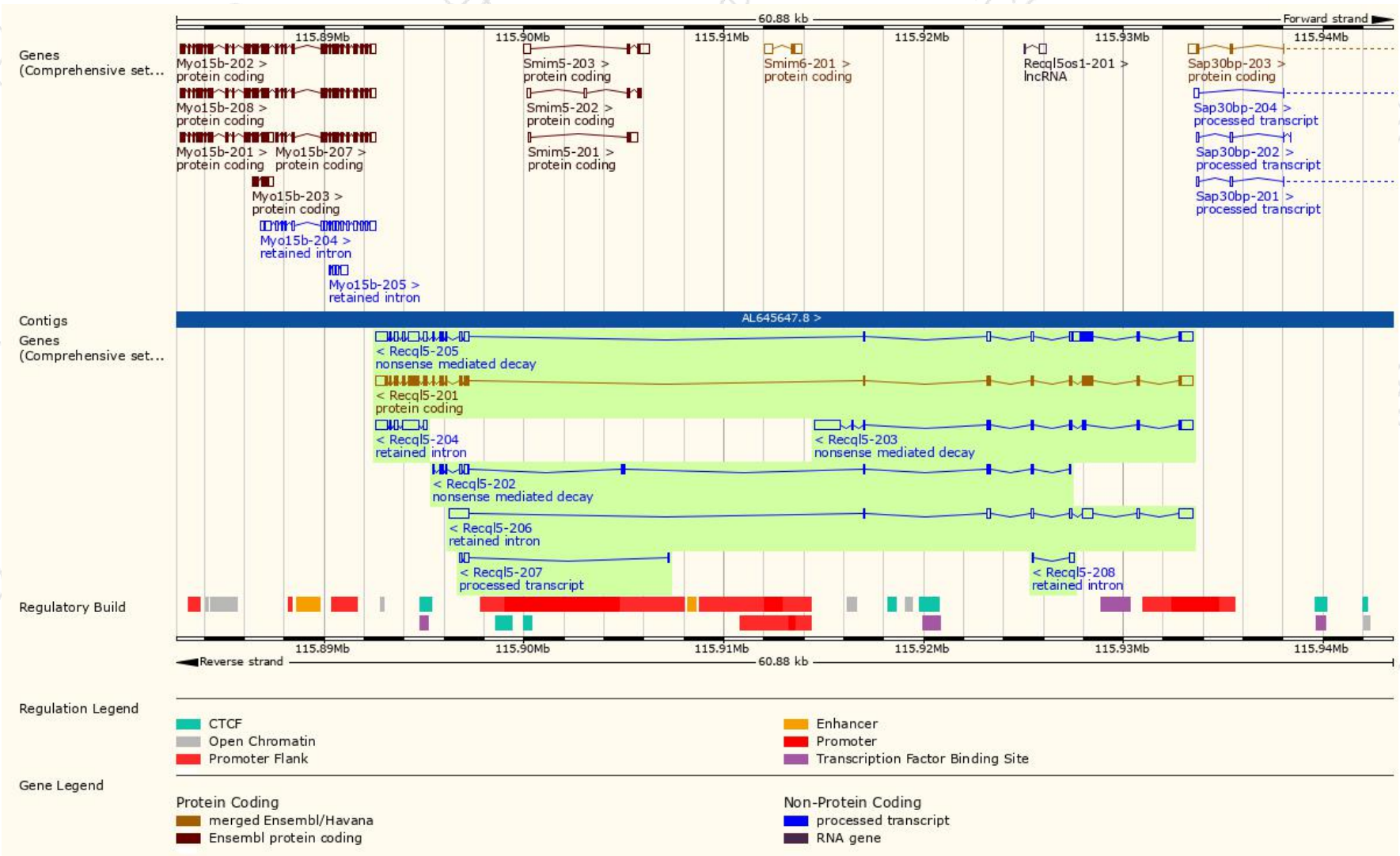
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Recql5-206	ENSMUST00000144824.1	2786	No protein	Retained intron	-	-	TSL:1
Recql5-204	ENSMUST00000136774.6	1772	No protein	Retained intron	-	-	TSL:2
Recql5-208	ENSMUST00000156776.1	302	No protein	Retained intron	-	-	TSL:3
Recql5-201	ENSMUST00000021097.9	3971	982aa	Protein coding	CCDS25650	Q8VID5	TSL:1 Gencode basic APPRIS P1
Recql5-207	ENSMUST00000147172.1	357	No protein	Processed transcript	-	-	TSL:3
Recql5-205	ENSMUST00000140174.7	4410	294aa	Nonsense mediated decay	-	J3QMY1	TSL:1
Recql5-203	ENSMUST00000134208.1	2851	305aa	Nonsense mediated decay	-	J3QP94	TSL:1
Recql5-202	ENSMUST00000131578.7	1154	220aa	Nonsense mediated decay	-	J3QM90	CDS 5' incomplete TSL:5

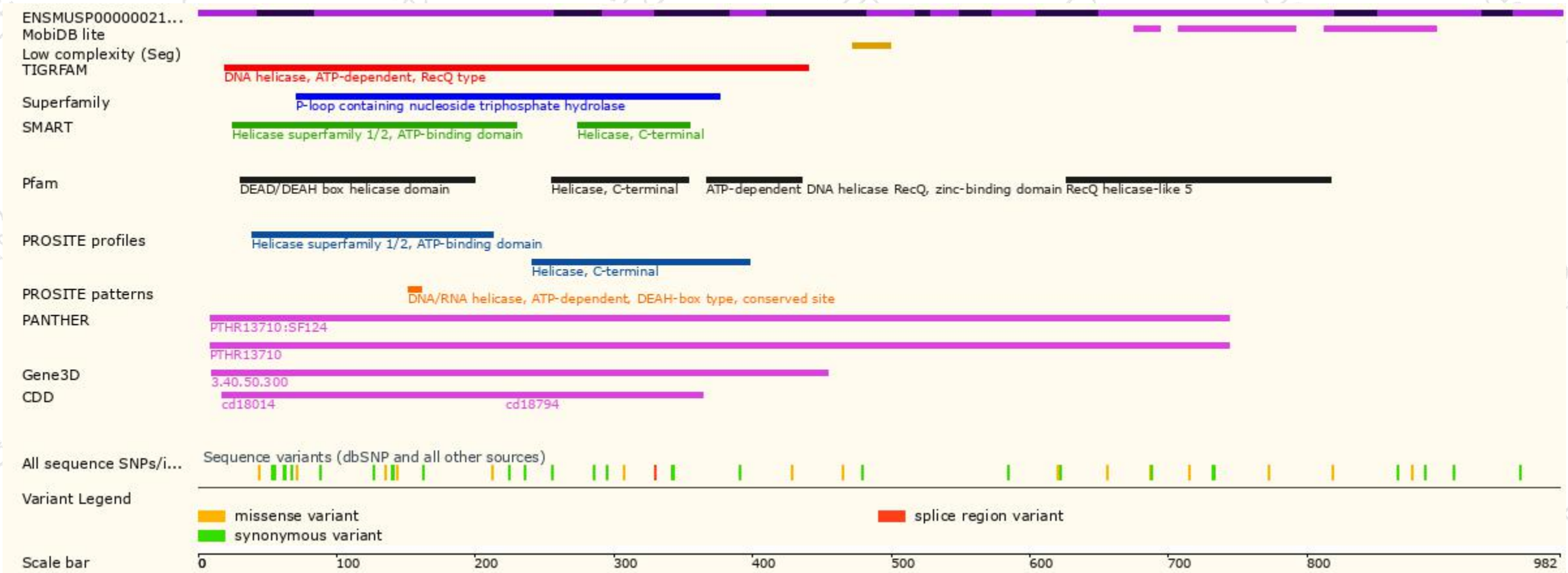
The strategy is based on the design of *Recql5-201* transcript, the transcription is shown below:



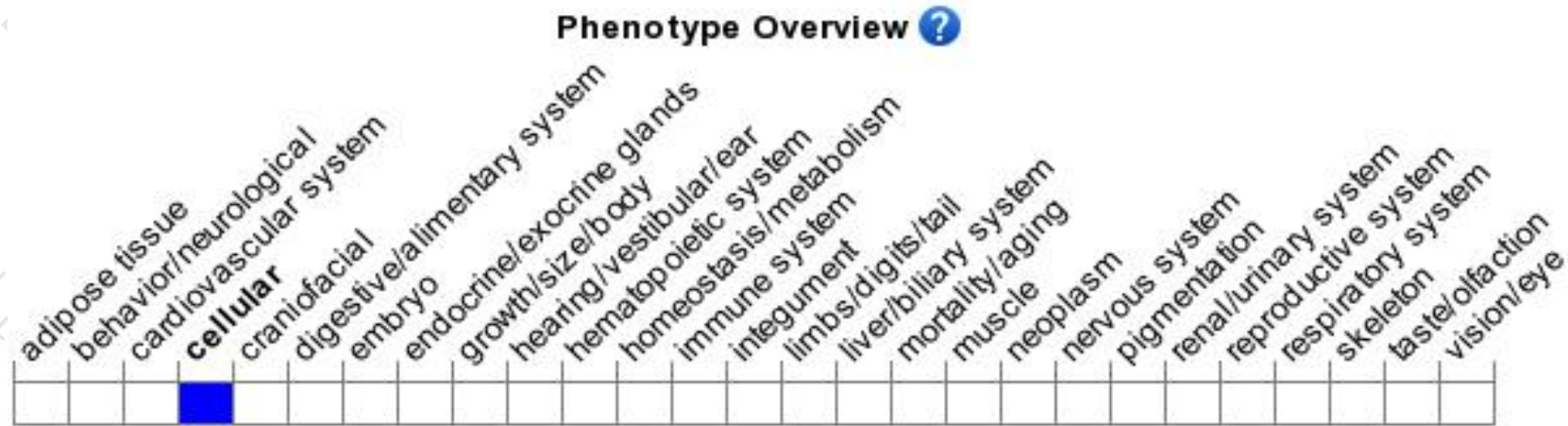
Genomic location distribution



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 disruptions in this gene express elevated levels of sister chromatid exchange due to a failure to suppress crossovers.

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

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