

Coro1c Cas9-KO Strategy

Designer:

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Design Date:

2019-7-25

Project Overview

Project Name

Coro1c

Project type

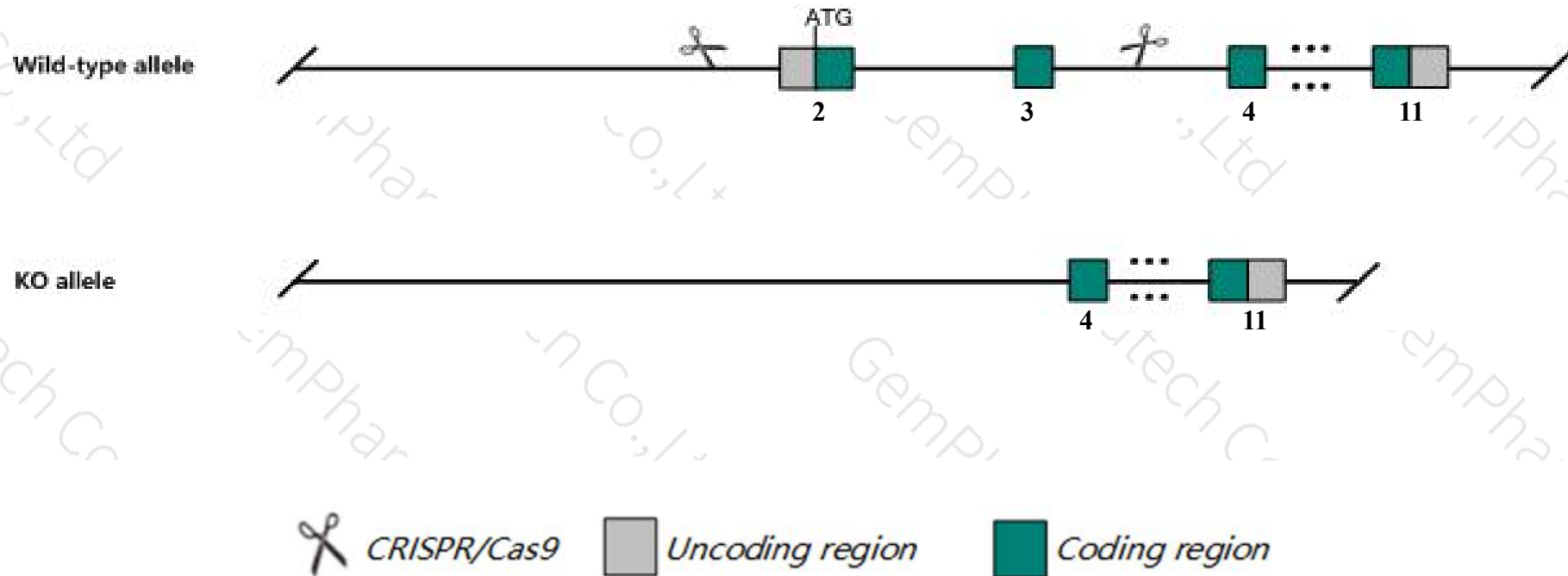
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Coro1c* gene. The schematic diagram is as follows:



- The *Coro1c* gene has 11 transcripts. According to the structure of *Coro1c* gene, exon2-exon3 of *Coro1c-201* (ENSMUST00000004646.12) transcript is recommended as the knockout region. The region contains start codon ATG. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Coro1c* gene. The brief process is as follows: CRISPR/Cas9 system

- The *Coro1c* 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)

Coro1c coronin, actin binding protein 1C [Mus musculus (house mouse)]

Gene ID: 23790, updated on 7-Apr-2019

Summary



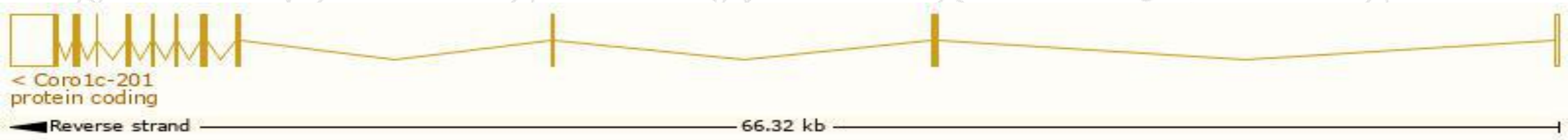
Official Symbol	Coro1c provided by MGI
Official Full Name	coronin, actin binding protein 1C provided by MGI
Primary source	MGI:MGI:1345964
See related	Ensembl:ENSMUSG000000004530
Gene type	protein coding
RefSeq status	PROVISIONAL
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AL022675, AW455561, AW548837, CRN2
Expression	Ubiquitous expression in large intestine adult (RPKM 69.2), colon adult (RPKM 57.1) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

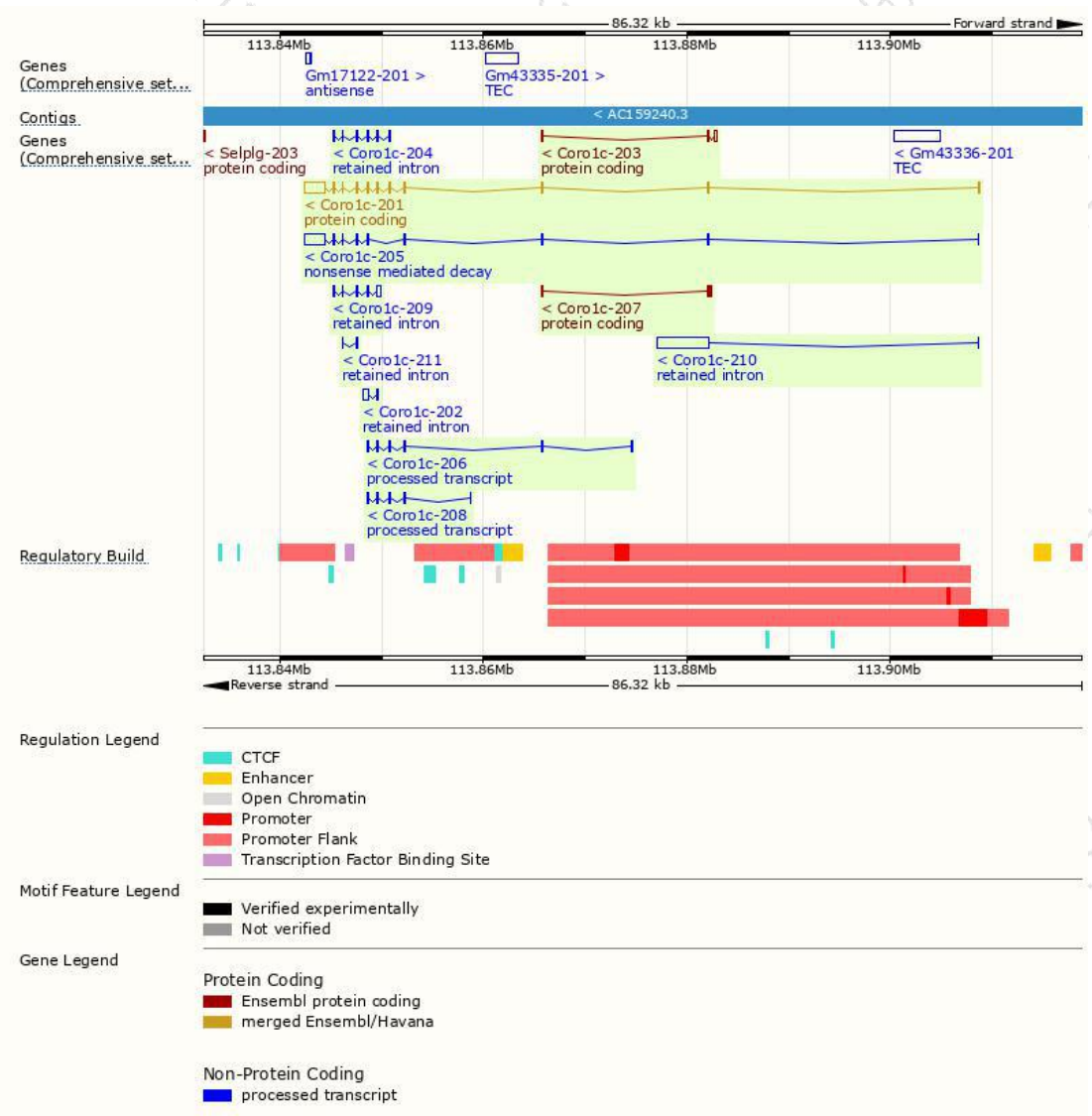
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Coro1c-201	ENSMUST00000004646.12	3491	474aa	Protein coding	CCDS19555	Q9WUM4	TSL:1 GENCODE basic APPRIS P1
Coro1c-203	ENSMUST00000163264.7	456	85aa	Protein coding	-	E9PVJ1	CDS 3' incomplete TSL:2
Coro1c-207	ENSMUST00000168399.1	393	66aa	Protein coding	-	E9PZJ0	CDS 3' incomplete TSL:5
Coro1c-205	ENSMUST00000164980.7	3136	159aa	Nonsense mediated decay	-	E9PX03	TSL:1
Coro1c-206	ENSMUST00000166647.7	748	No protein	Processed transcript	-	-	TSL:3
Coro1c-208	ENSMUST00000168493.1	524	No protein	Processed transcript	-	-	TSL:5
Coro1c-210	ENSMUST00000171630.1	5130	No protein	Retained intron	-	-	TSL:1
Coro1c-204	ENSMUST00000163995.7	805	No protein	Retained intron	-	-	TSL:2
Coro1c-209	ENSMUST00000168634.1	799	No protein	Retained intron	-	-	TSL:2
Coro1c-202	ENSMUST00000111283.2	666	No protein	Retained intron	-	-	TSL:3
Coro1c-211	ENSMUST00000172016.1	202	No protein	Retained intron	-	-	TSL:5

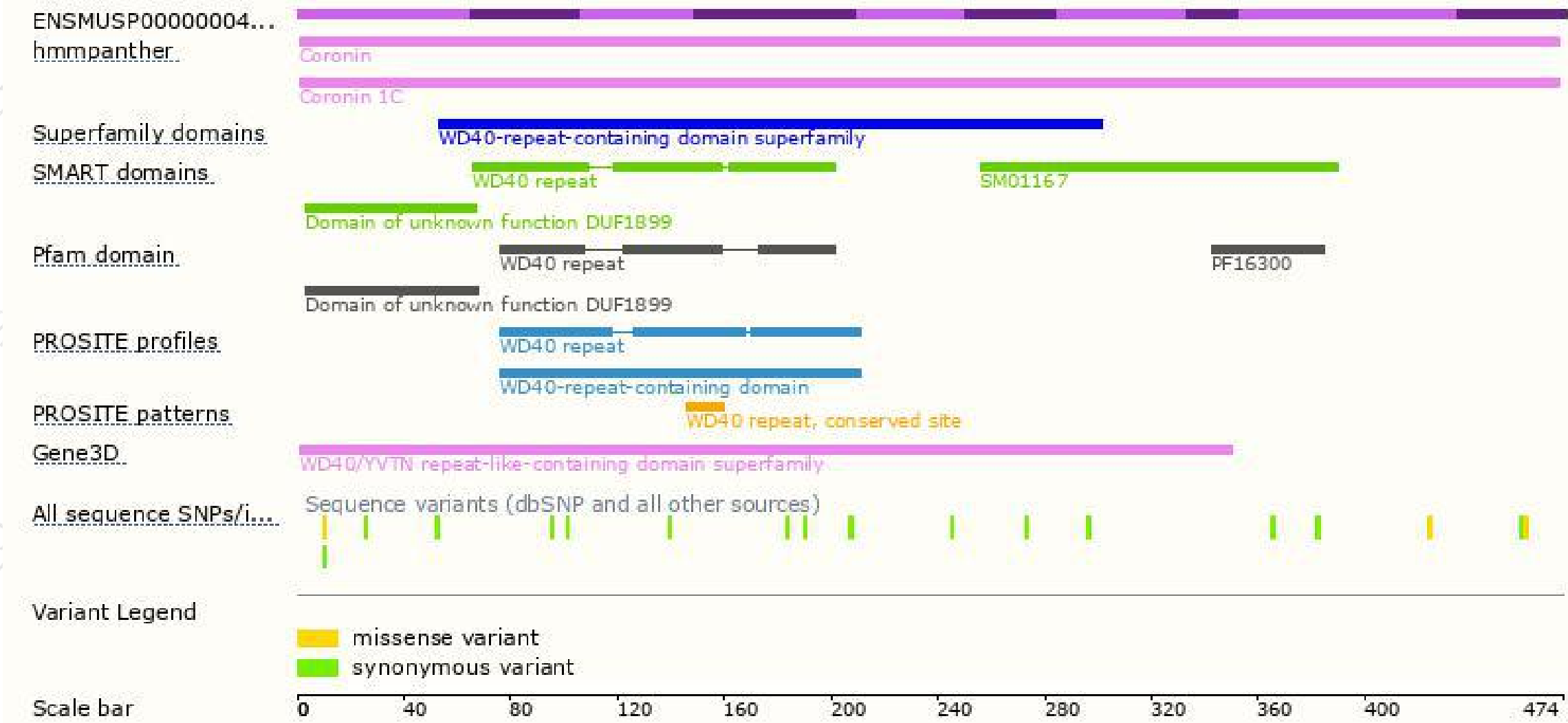
The strategy is based on the design of *Coro1c-201* transcript,The transcription is shown below



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/>).

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

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