Cfap100 Cas9-KO Strategy

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Project Overview

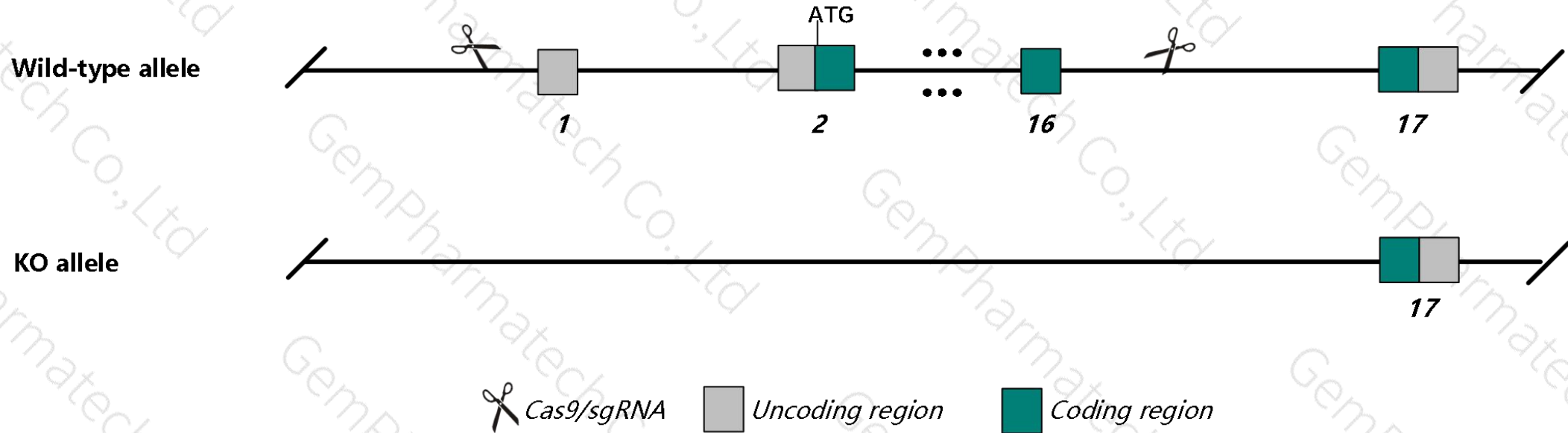|	
Project Name	***Cfap100***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Cfap100* gene. The schematic diagram is as follows:

Technical routes

➢ The *Cfap100* gene has 7 transcripts. According to the structure of *Cfap100* gene, exon1-exon16 of *Cfap100-207* (ENSMUST00000165673.4) 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 *Cfap100* gene. The brief process is as follows: CRISPR/Cas9 syste

Notice

➢ The *Cfap100* gene is located on the Chr6. 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）

Cfap100 cilia and flagella associated protein 100 [Mus musculus (house mouse)]
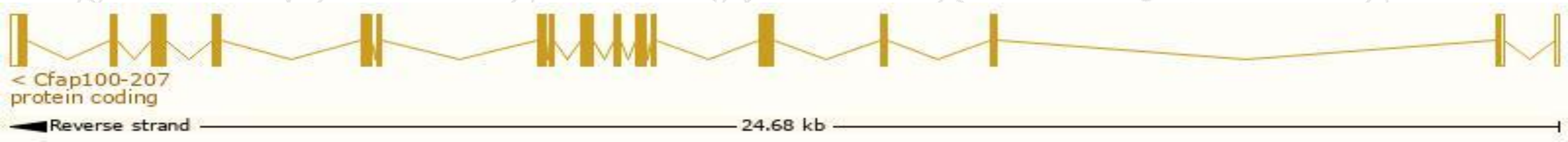
Gene ID: 243538, updated on 13-Mar-2020

Summary

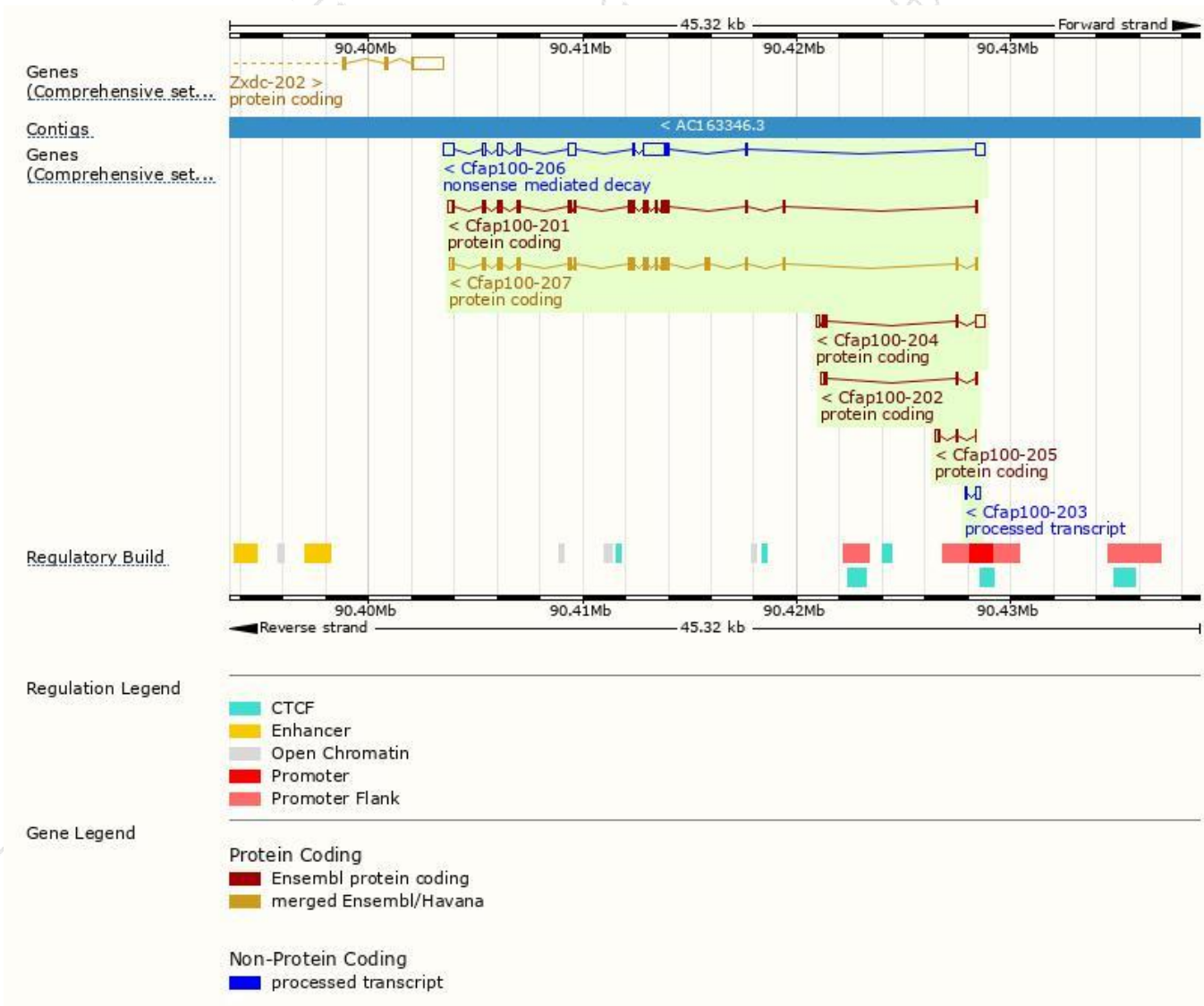|	
Official Symbol	Cfap100 provided by MGI
Official Full Name	cilia and flagella associated protein 100 provided by MGI
Primary source	MGI:MGI:2141635
See related	Ensembl:ENSMUSG00000048794
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AW048498, C030041G11Rik, C230069K22Rik, Ccdc37
Expression	Biased expression in testis adult (RPKM 13.0), CNS E18 (RPKM 2.8) and 8 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Cfap100-207	ENSMUST00000165673.4	2072	613aa	Protein coding	CCDS51849	Q80VN0	TSL:5 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P2
Cfap100-201	ENSMUST00000062750.11	1803	459aa	Protein coding	-	A0A171EBL0	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
Cfap100-204	ENSMUST00000134224.7	849	72aa	Protein coding	-	A0A0N4SVH7	TSL:1 GENCODE basic
Cfap100-202	ENSMUST00000127508.3	417	72aa	Protein coding	-	A0A0N4SVH7	TSL:2 GENCODE basic
Cfap100-205	ENSMUST00000135757.2	289	39aa	Protein coding	-	A0A0N4SUU7	TSL:5 GENCODE basic
Cfap100-206	ENSMUST00000153843.7	2992	47aa	Nonsense mediated decay	-	A0A0N4SV62	TSL:2
Cfap100-203	ENSMUST00000128124.1	253	No protein	Processed transcript	-	-	TSL:5

The strategy is based on the design of *Cfap100-207* transcript,the transcription is shown below:

< Cfap100-207
protein coding

◄Reverse strand

24.68 kb

Genomic location distribution

Protein domain

ENSMUSP00000126...		
Low complexity (Seg)		
Coiled-coils (Ncoils)		
Pfam	Domain of unknown function DUF4200	
PANTHER	PTHR21683:SF5	
	PTHR21683	
All sequence SNPs/i...	Sequence variants (dbSNP and all other sources)	
Variant Legend		

Variant Legend

- ▮ missense variant
- ▮ splice region variant
- ▮ synonymous variant

Scale bar   0   60   120   180   240   300   360   420   480   540   613
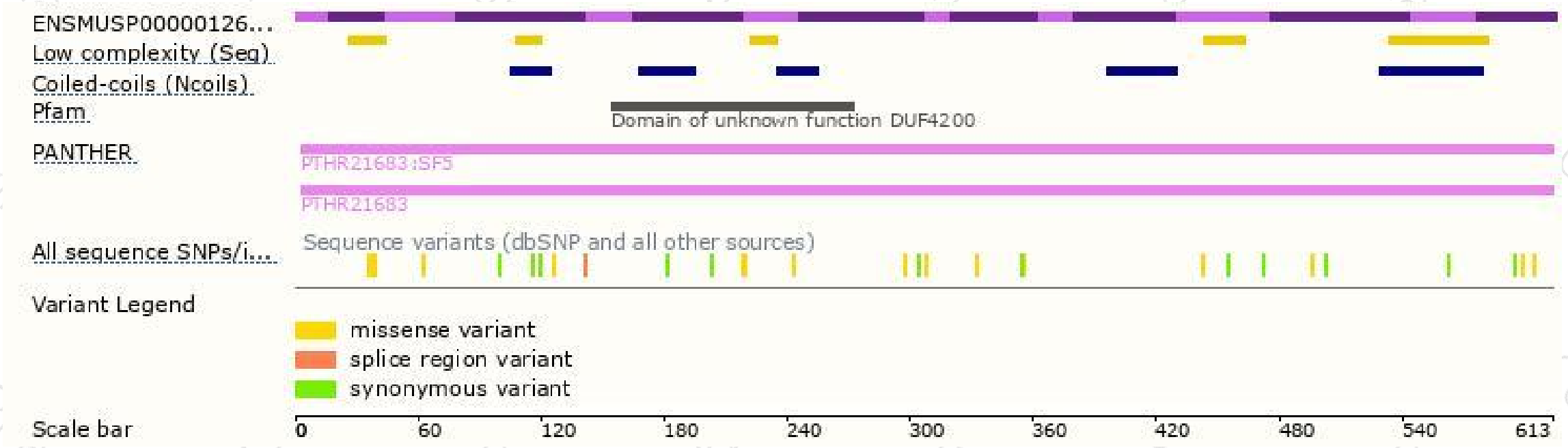
If you have any questions, you are welcome to inquire.
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