

Fancg Cas9-KO Strategy

Designer:

Huimin Su

Reviewer:

Ruirui Zhang

Design Date:

2019/10/16

Project Overview

Project Name

Fancg

Project type

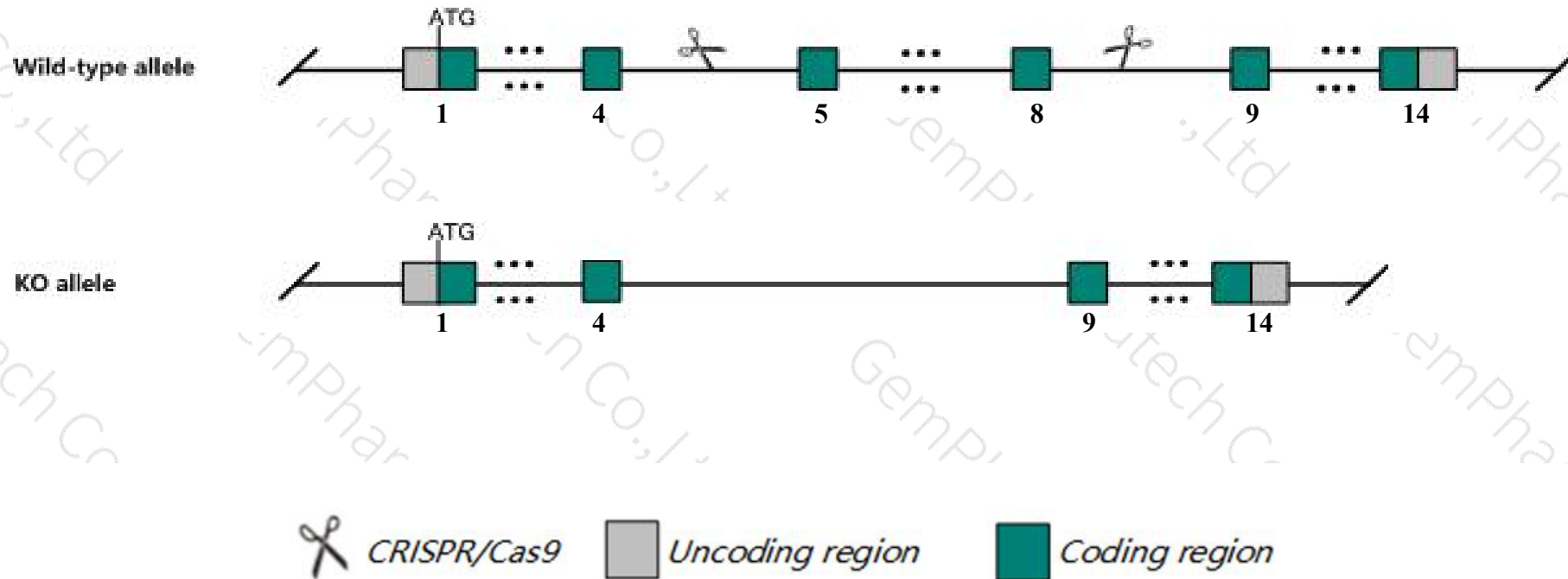
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Fancg* gene has 10 transcripts. According to the structure of *Fancg* gene, exon5-exon8 of *Fancg-201* (ENSMUST00000030165.4) transcript is recommended as the knockout region. The region contains 566bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fancg* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Females and males homozygous for targeted null mutations exhibit hypogonadism and reduced fertility. Cytogeneic analysis showed somatic chromosome aberrations occur at a higher spontaneous rate and are easier to induce than in normal cells. Cells are also more sensitive to mitomycin C.
- The *Fancg* gene is located on the Chr4. 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)

Fancg Fanconi anemia, complementation group G [*Mus musculus* (house mouse)]

Gene ID: 60534, updated on 12-Aug-2019

Summary

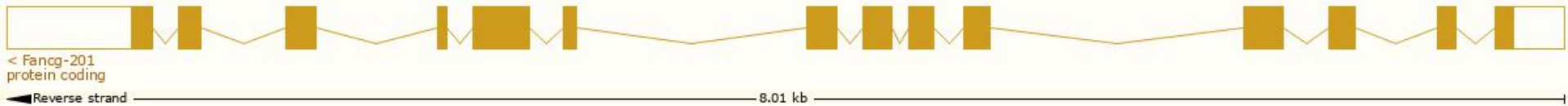
Official Symbol	Fancg provided by MGI
Official Full Name	Fanconi anemia, complementation group G provided by MGI
Primary source	MGI:MGI:1926471
See related	Ensembl:ENSMUSG00000028453
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Xrcc9; AU041407
Expression	Ubiquitous expression in testis adult (RPKM 21.5), CNS E18 (RPKM 8.9) and 26 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

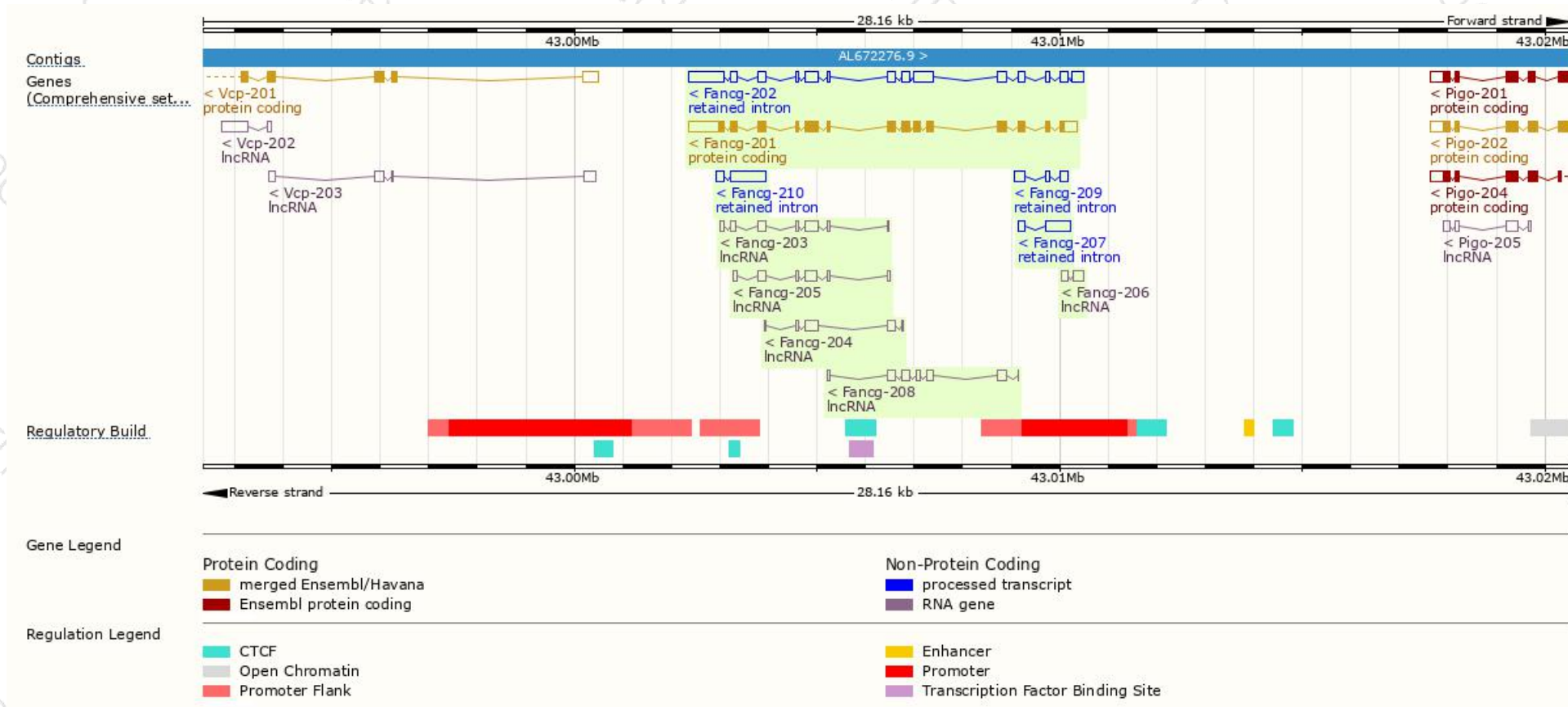
The gene has 10 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fancg-201	ENSMUST00000030165.4	2771	623aa	Protein coding	CCDS18087	Q9EQR6	TSL:1 GENCODE basic APPRIS P1
Fancg-202	ENSMUST00000123332.7	2974	No protein	Retained intron	-	-	TSL:2
Fancg-210	ENSMUST00000148018.1	877	No protein	Retained intron	-	-	TSL:2
Fancg-207	ENSMUST00000133915.1	638	No protein	Retained intron	-	-	TSL:2
Fancg-209	ENSMUST00000135362.1	476	No protein	Retained intron	-	-	TSL:2
Fancg-208	ENSMUST00000134083.1	767	No protein	lncRNA	-	-	TSL:5
Fancg-203	ENSMUST00000124645.7	727	No protein	lncRNA	-	-	TSL:5
Fancg-205	ENSMUST00000127067.7	664	No protein	lncRNA	-	-	TSL:5
Fancg-204	ENSMUST00000125570.7	539	No protein	lncRNA	-	-	TSL:5
Fancg-206	ENSMUST00000132273.1	357	No protein	lncRNA	-	-	TSL:2

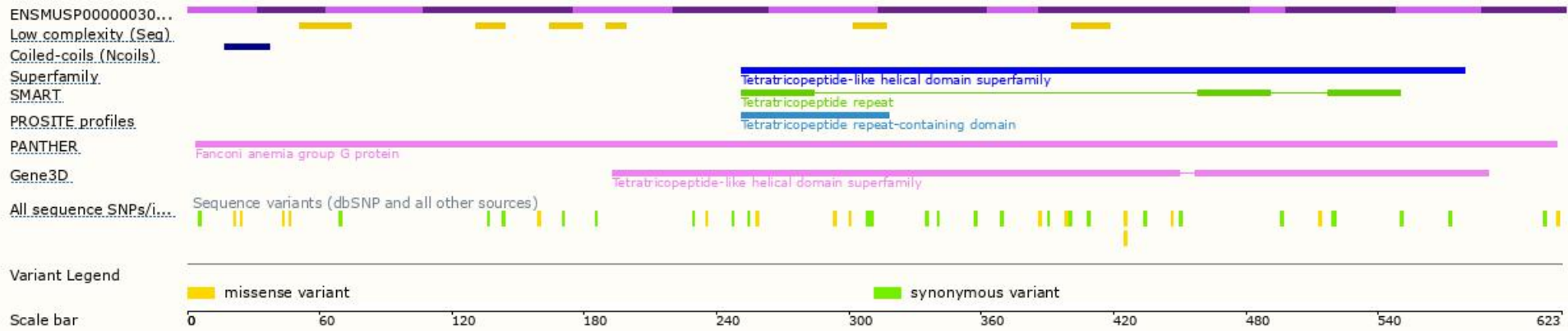
The strategy is based on the design of *Fancg-201* transcript,The transcription is shown below



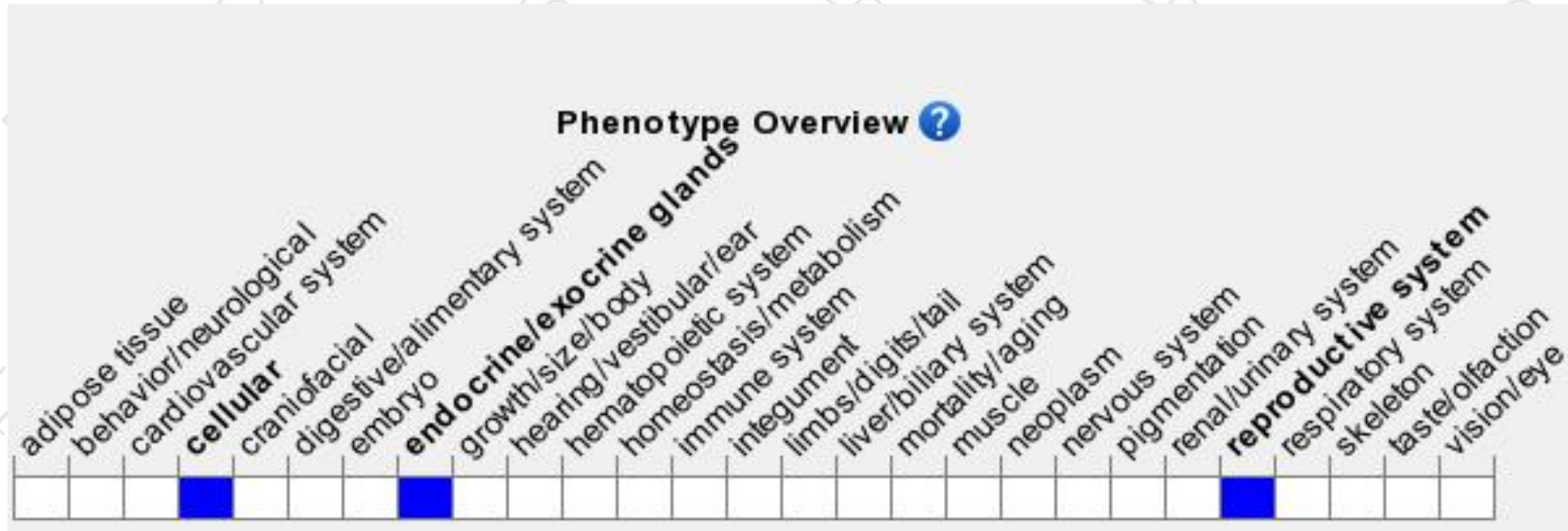
Genomic location distribution



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, Females and males homozygous for targeted null mutations exhibit hypogonadism and reduced fertility. Cytogeneic analysis showed somatic chromosome aberrations occur at a higher spontaneous rate and are easier to induce than in normal cells. Cells are also more sensitive to mitomycin C.

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

Tel: 400-9660890

