Fancc Cas9-KO Strategy

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Design Date:	**2019/10/16**

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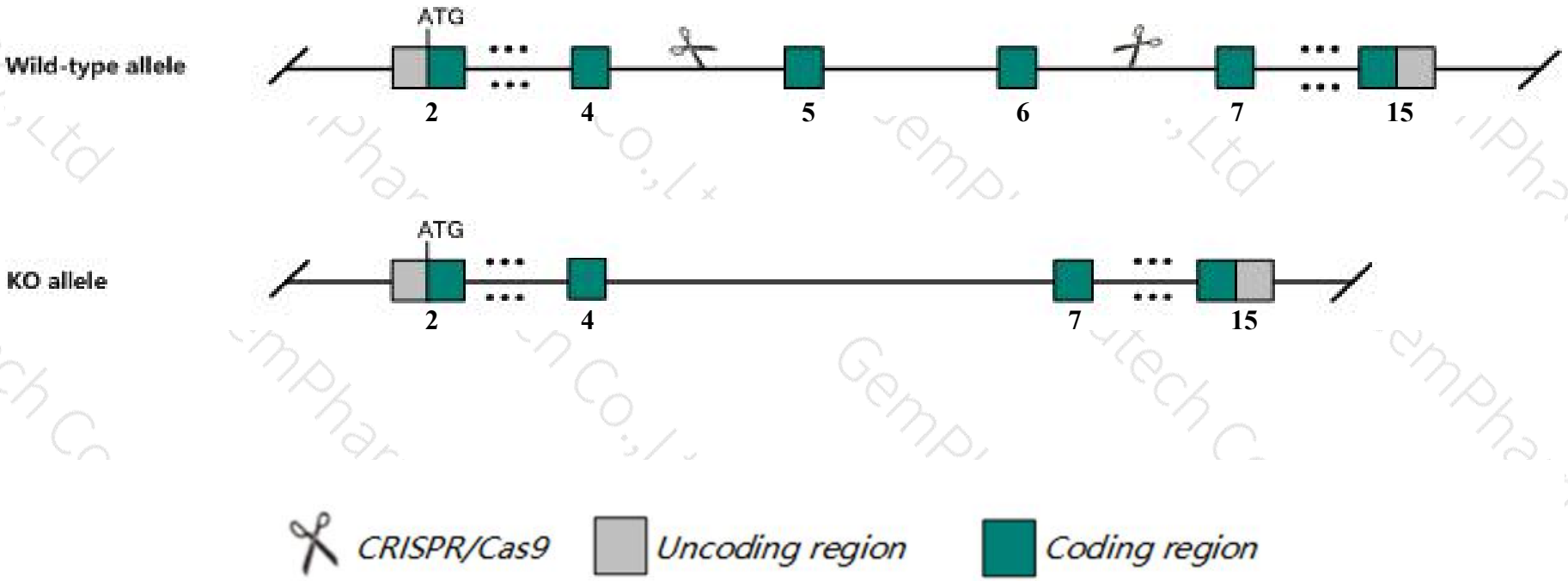
Project Overview

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

Knockout strategy

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



Technical routes

➢ The *Fancc* gene has 19 transcripts. According to the structure of *Fancc* gene, exon5-exon6 of *Fancc-201* (ENSMUST00000073029.12) transcript is recommended as the knockout region.The region contains 179bp coding sequence. Knock out the region will result in disruption of protein function.

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

Notice

- According to the existing MGI data,Homozygous null mutants are grossly normal, but chromosome aberrations and sensitivity to DNA crosslinkers are seen. Both sexes have fewer germ cell numbers and impaired fertility. Marrow progenitors show decrease in colony forming ability.
- The transcripts *Fancc-209* and *Fancc-211* are uncompleted, so the effect on them are unknown.
- The *Fancc* gene is located on the Chr13. 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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Fancc Fanconi anemia, complementation group C [*Mus musculus* (house mouse)]

Gene ID: 14088, updated on 12-Aug-2019

Summary

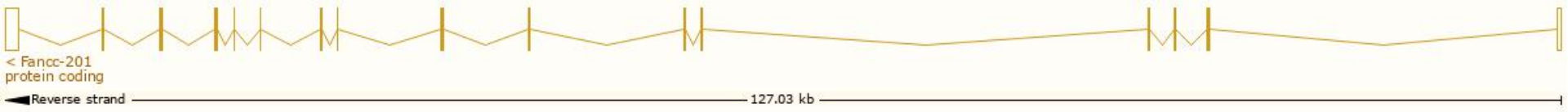
Official Symbol	Fancc provided by MGI
Official Full Name	Fanconi anemia, complementation group C provided by MGI
Primary source	MGI:MGI:95480
See related	Ensembl:ENSMUSG00000021461
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Facc
Expression	Ubiquitous expression in bladder adult (RPKM 3.8), CNS E11.5 (RPKM 3.0) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

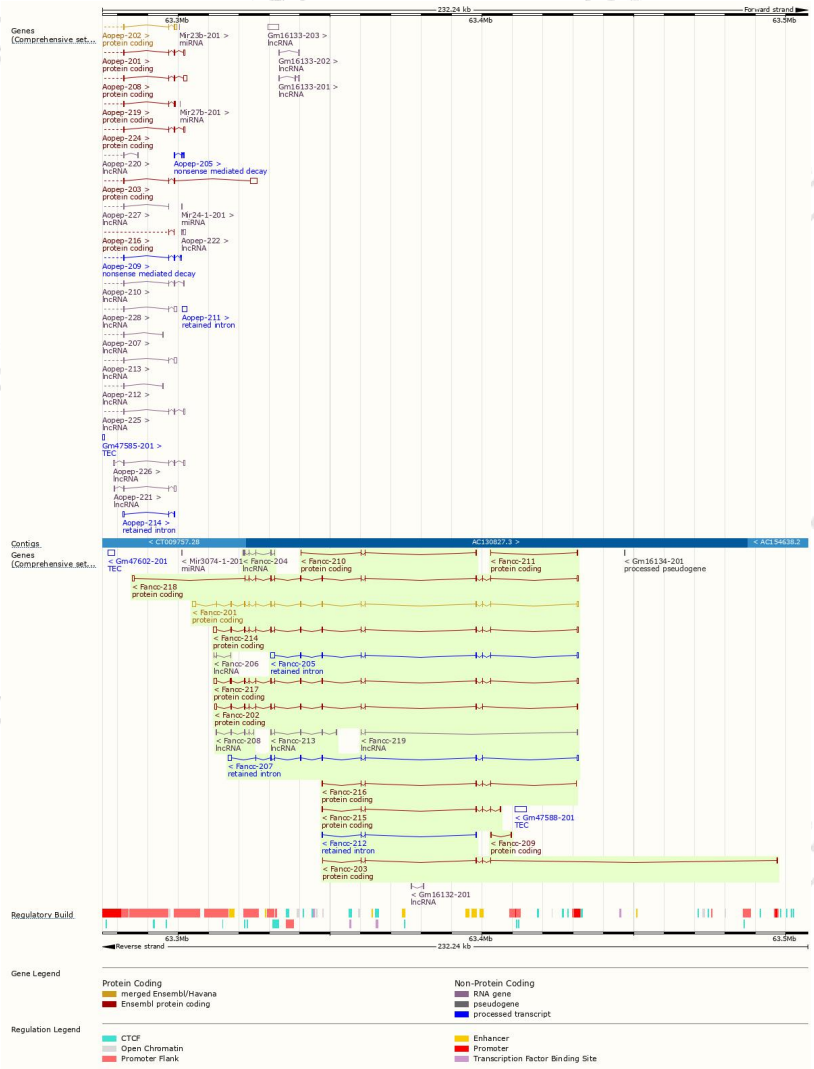
The gene has 19 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fancc-201	ENSMUST00000073029.12	3165	558aa	Protein coding	CCDS36700	Q8CBR3	TSL:1 GENCODE basic APPRIS P3
Fancc-214	ENSMUST00000161977.7	3111	558aa	Protein coding	CCDS36700	Q8CBR3	TSL:1 GENCODE basic APPRIS P3
Fancc-217	ENSMUST00000163091.7	2995	591aa	Protein coding	CCDS84029	P50652	TSL:5 GENCODE basic APPRIS ALT2
Fancc-202	ENSMUST00000099444.9	2288	461aa	Protein coding	CCDS70472	E9QAE8	TSL:5 GENCODE basic
Fancc-218	ENSMUST00000220684.1	2006	412aa	Protein coding	-	A0A1Y7VKS5	TSL:5 GENCODE basic
Fancc-216	ENSMUST00000162971.7	890	229aa	Protein coding	-	E0CYQ7	CDS 3' incomplete TSL:5
Fancc-215	ENSMUST00000162375.7	869	212aa	Protein coding	-	E0CXC4	CDS 3' incomplete TSL:5
Fancc-203	ENSMUST00000159024.1	807	216aa	Protein coding	-	E0CYC3	CDS 3' incomplete TSL:5
Fancc-211	ENSMUST00000160931.1	417	43aa	Protein coding	-	E0CYI2	CDS 3' incomplete TSL:3
Fancc-209	ENSMUST00000160617.1	375	24aa	Protein coding	-	E0CYY7	CDS 3' incomplete TSL:3
Fancc-210	ENSMUST00000160735.7	350	117aa	Protein coding	-	F7DEE2	CDS 5' and 3' incomplete TSL:3
Fancc-205	ENSMUST00000160151.7	2529	No protein	Retained intron	-	-	TSL:2
Fancc-207	ENSMUST00000160333.7	2240	No protein	Retained intron	-	-	TSL:2
Fancc-212	ENSMUST00000161507.1	494	No protein	Retained intron	-	-	TSL:3
Fancc-208	ENSMUST00000160336.7	881	No protein	lncRNA	-	-	TSL:5
Fancc-204	ENSMUST00000159056.1	824	No protein	lncRNA	-	-	TSL:5
Fancc-213	ENSMUST00000161656.1	545	No protein	lncRNA	-	-	TSL:3
Fancc-219	ENSMUST00000221054.1	363	No protein	lncRNA	-	-	TSL:5
Fancc-206	ENSMUST00000160166.1	308	No protein	lncRNA	-	-	TSL:5

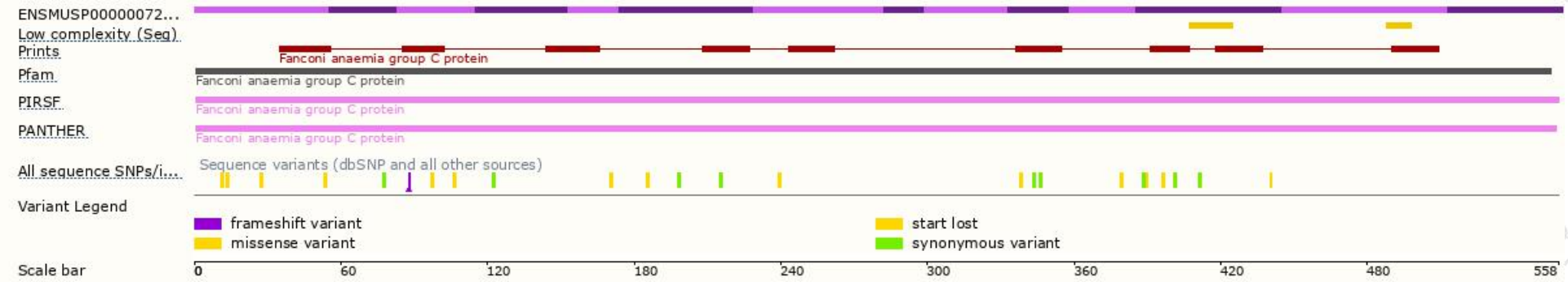
The strategy is based on the design of *Fancc-201* transcript,The transcription is shown below



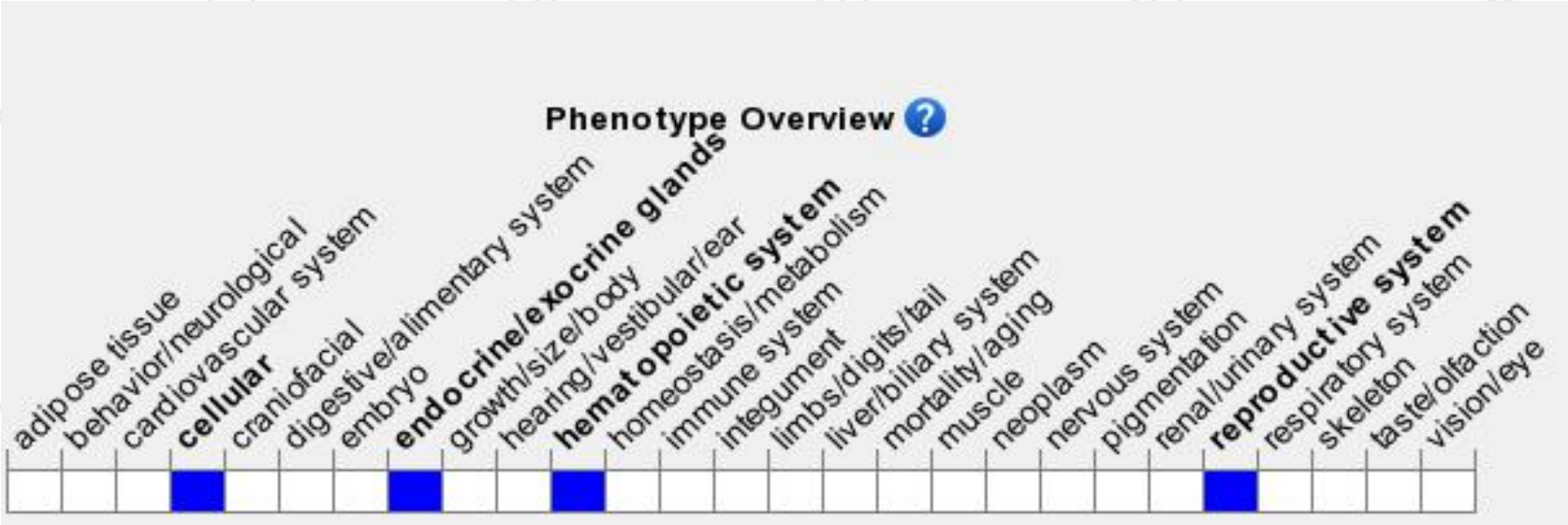
Genomic location distribution



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/).

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

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