

# *Fanca* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

*Fanca*

**Project type**

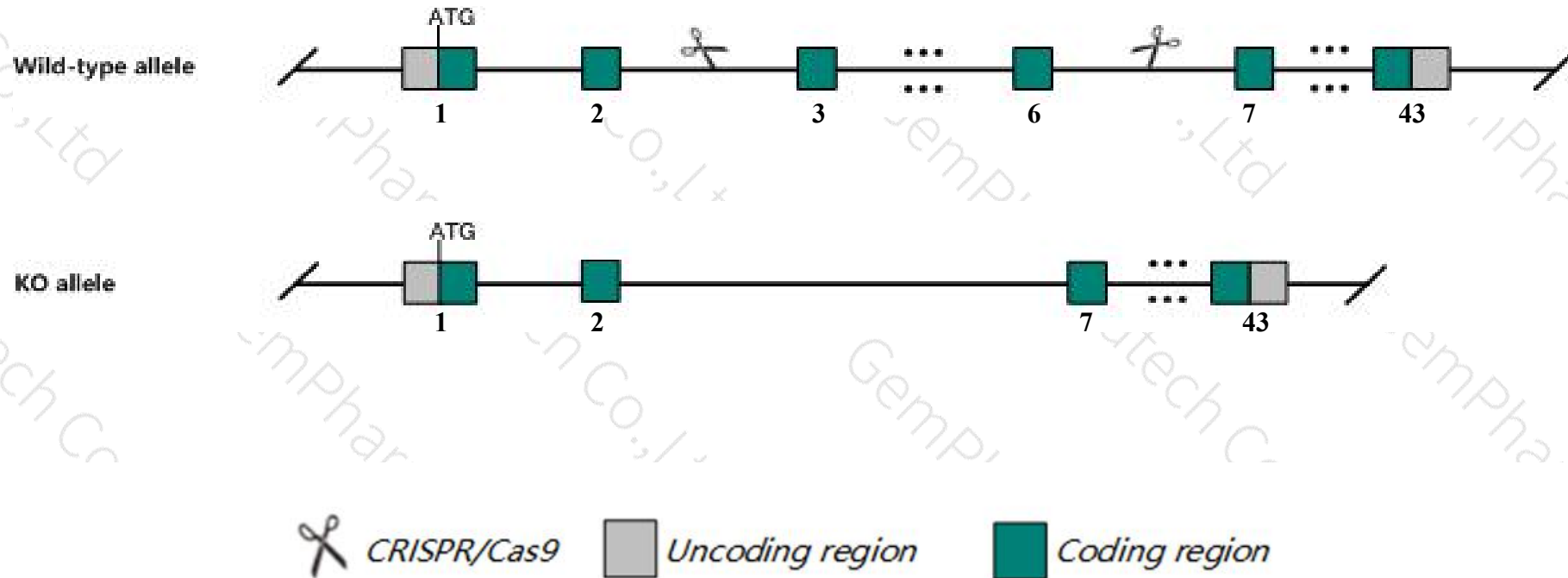
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

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



- The *Fanca* gene has 14 transcripts. According to the structure of *Fanca* gene, exon3-exon6 of *Fanca-201* (ENSMUST00000035495.14) transcript is recommended as the knockout region. The region contains 398bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Fanca* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mutants show variably: growth retardation, microphthalmia, craniofacial malformations and hematological changes, depending on allele and strain background. Both sexes show hypogonadism, including diminished primordial germ cells and impaired fertility.
- *Fanca* is located in intron of *Gm20388*, so part intorn of *Gm20388* will be deleted together.
- The *Fanca* gene is located on the Chr8. 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)

## Fanca Fanconi anemia, complementation group A [ *Mus musculus* (house mouse) ]

Gene ID: 14087, updated on 10-Oct-2019

### Summary

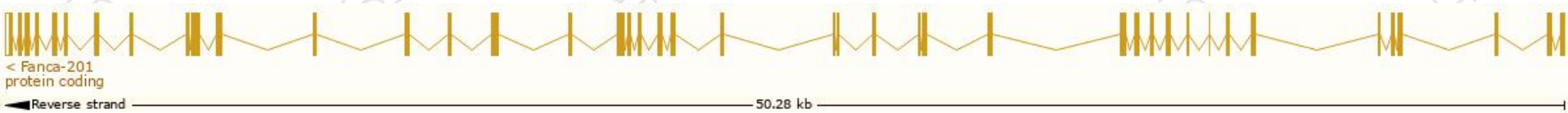
<b>Official Symbol</b>	Fanca provided by <a href="#">MGI</a>
<b>Official Full Name</b>	Fanconi anemia, complementation group A provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1341823</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG000000032815</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	FACA; AW208693
<b>Expression</b>	Ubiquitous expression in genital fat pad adult (RPKM 12.2), CNS E11.5 (RPKM 9.2) and 27 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

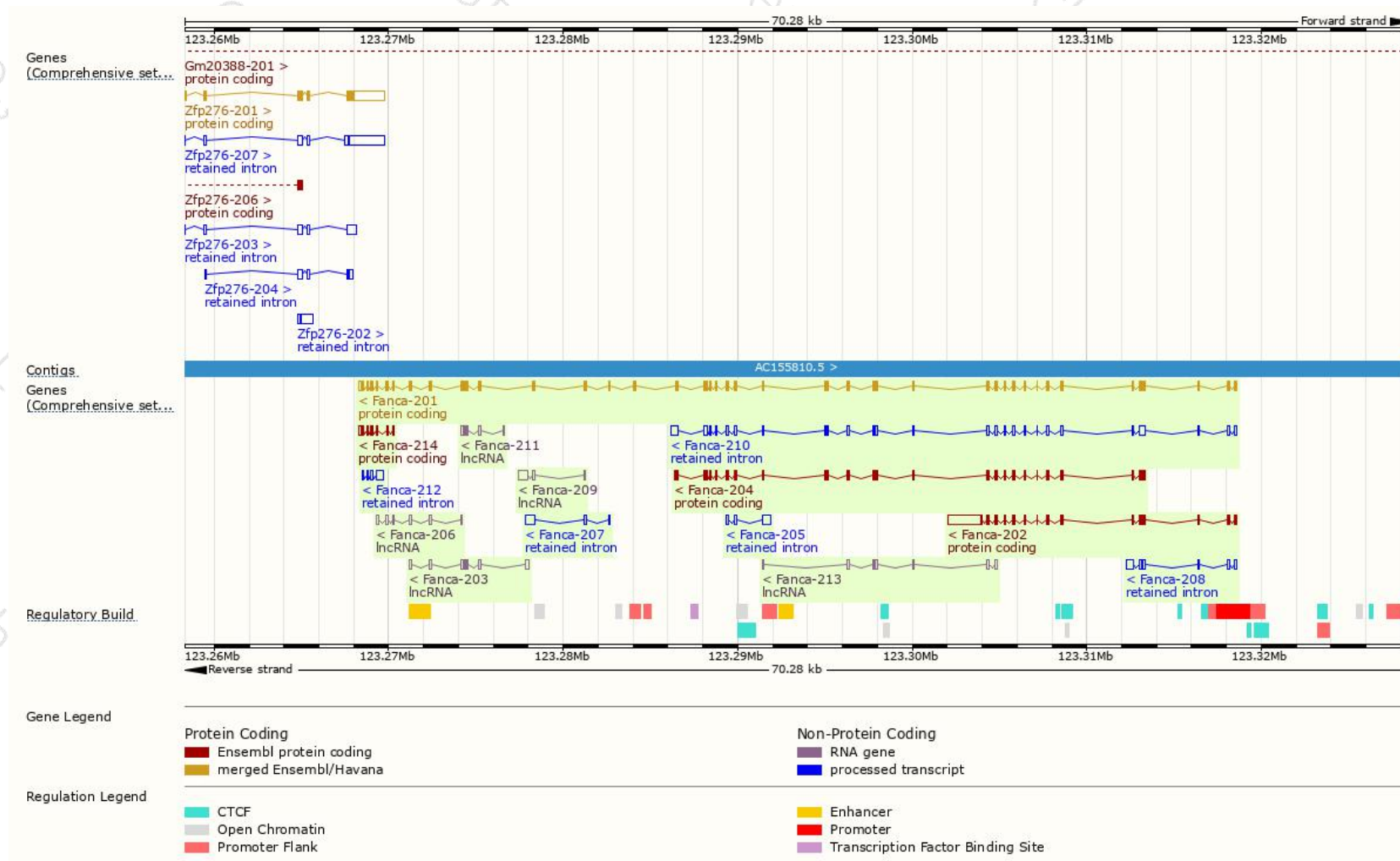
The gene has 14 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Fanca-201	<a href="#">ENSMUST00000035495.14</a>	4485	<a href="#">1439aa</a>	Protein coding	<a href="#">CCDS22753</a>	<a href="#">Q9JL70</a>	TSL:1 GENCODE basic APPRIS P1
Fanca-202	<a href="#">ENSMUST00000118395.1</a>	3274	<a href="#">481aa</a>	Protein coding	-	<a href="#">D3Z6Y5</a>	TSL:1 GENCODE basic
Fanca-204	<a href="#">ENSMUST00000127904.7</a>	2355	<a href="#">771aa</a>	Protein coding	-	<a href="#">F7CK17</a>	CDS 5' incomplete TSL:1
Fanca-214	<a href="#">ENSMUST00000213090.1</a>	650	<a href="#">169aa</a>	Protein coding	-	<a href="#">A0A1D5RLC1</a>	CDS 5' incomplete TSL:5
Fanca-210	<a href="#">ENSMUST00000155488.7</a>	2994	No protein	Retained intron	-	-	TSL:1
Fanca-208	<a href="#">ENSMUST00000150318.1</a>	895	No protein	Retained intron	-	-	TSL:1
Fanca-205	<a href="#">ENSMUST00000133950.1</a>	716	No protein	Retained intron	-	-	TSL:1
Fanca-212	<a href="#">ENSMUST00000211934.1</a>	701	No protein	Retained intron	-	-	TSL:2
Fanca-207	<a href="#">ENSMUST00000146687.1</a>	668	No protein	Retained intron	-	-	TSL:3
Fanca-203	<a href="#">ENSMUST00000126834.7</a>	918	No protein	lncRNA	-	-	TSL:5
Fanca-209	<a href="#">ENSMUST00000155279.1</a>	729	No protein	lncRNA	-	-	TSL:3
Fanca-213	<a href="#">ENSMUST00000212953.1</a>	709	No protein	lncRNA	-	-	TSL:5
Fanca-206	<a href="#">ENSMUST00000135702.1</a>	667	No protein	lncRNA	-	-	TSL:5
Fanca-211	<a href="#">ENSMUST00000155510.1</a>	483	No protein	lncRNA	-	-	TSL:3

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

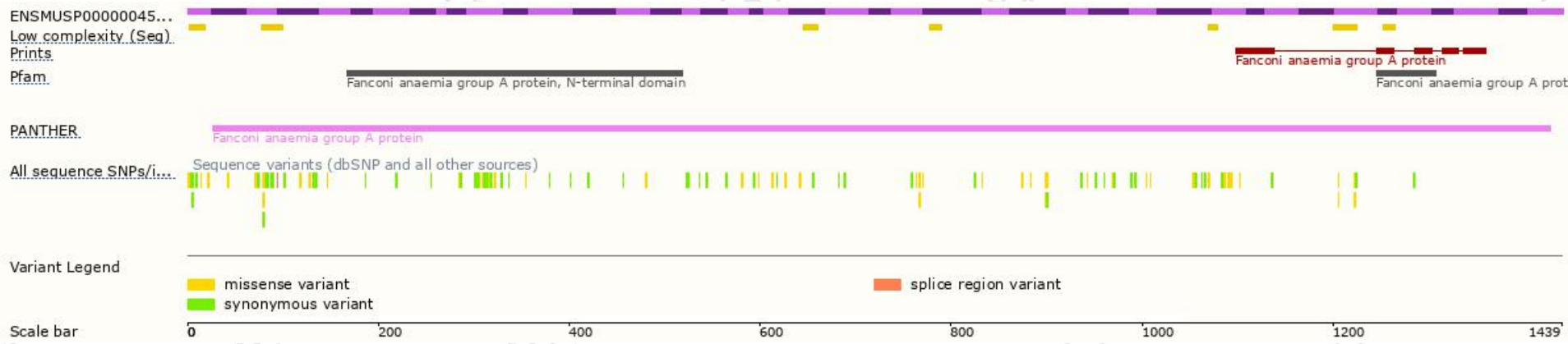


# Genomic location distribution

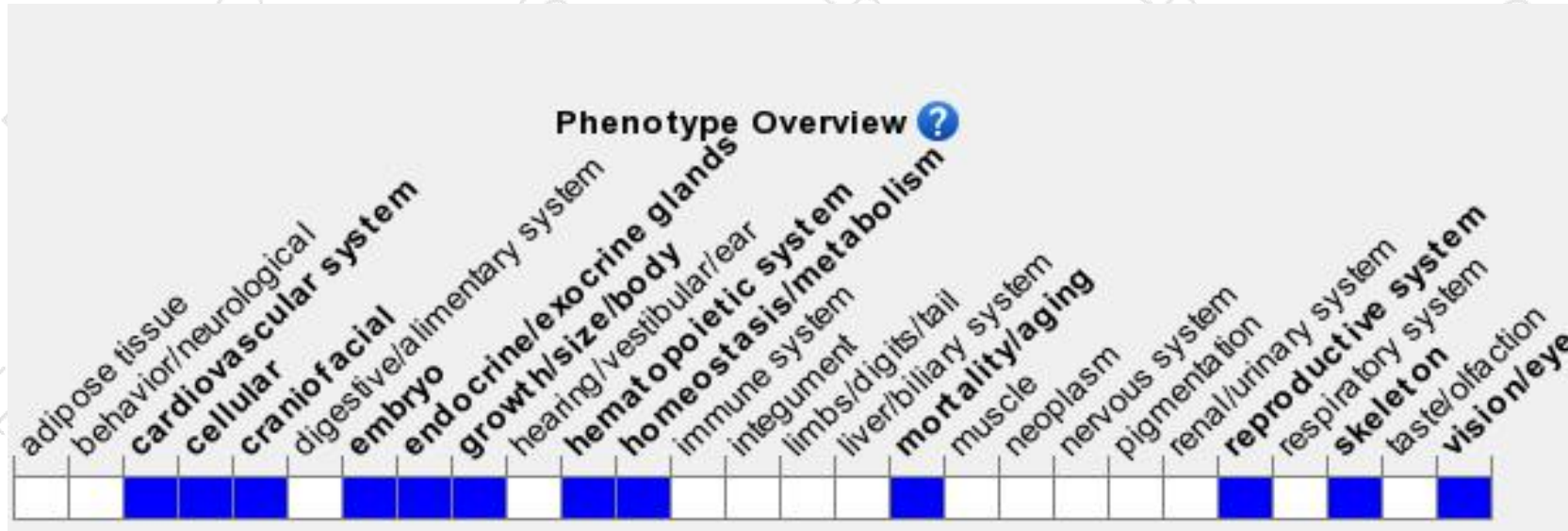




# Protein domain



# 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, Mutants show variably: growth retardation, microphthalmia, craniofacial malformations and hematological changes, depending on allele and strain background. Both sexes show hypogonadism, including diminished primordial germ cells and impaired fertility.

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

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