

# *Abcc3* Cas9-CKO Strategy

**Designer:**

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**Design Date:**

**2019-10-17**

# Project Overview

**Project Name**

*Abcc3*

**Project type**

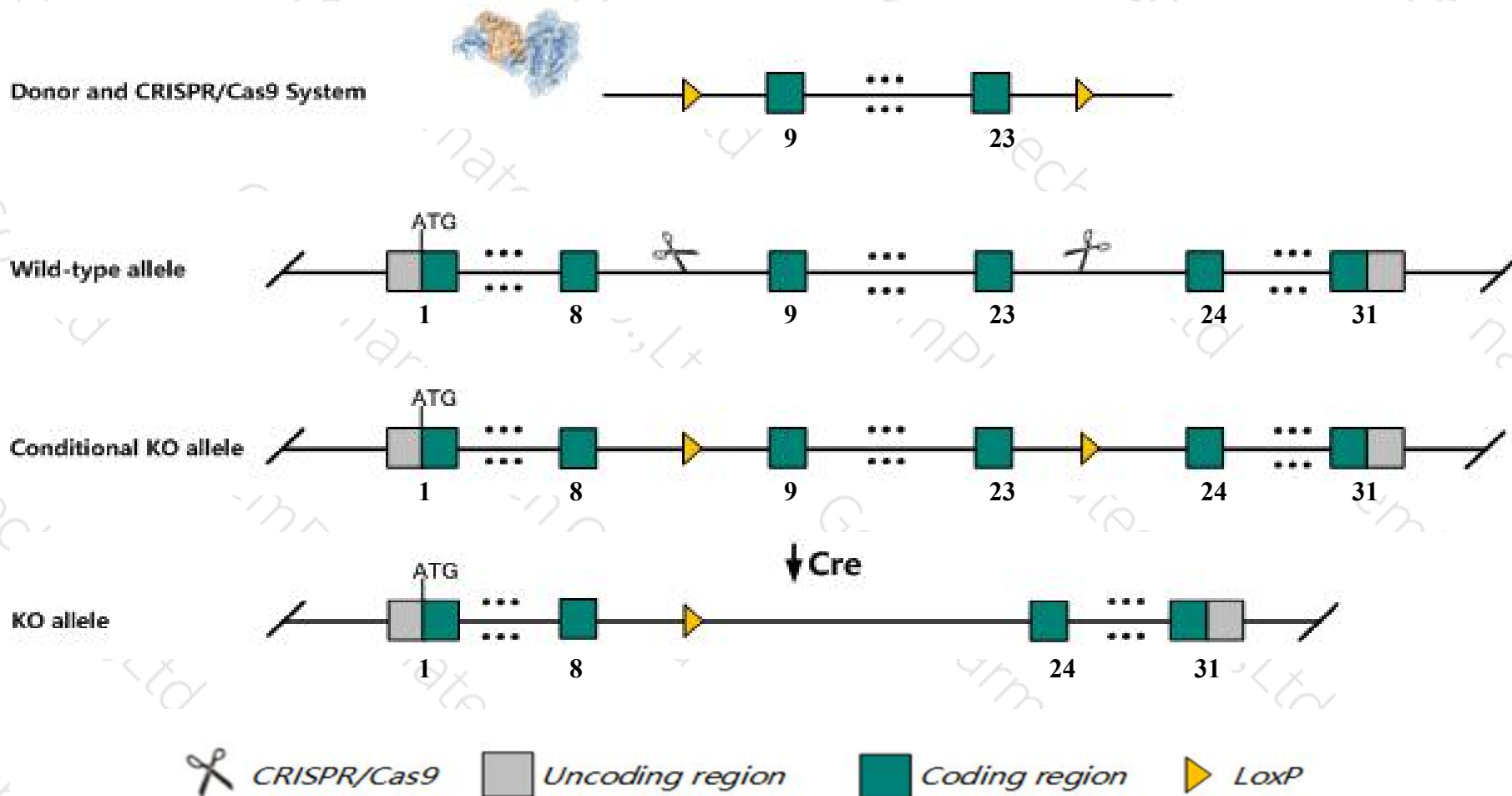
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Abcc3* gene. The schematic diagram is as follows:



- The *Abcc3* gene has 6 transcripts. According to the structure of *Abcc3* gene, exon9-exon23 of *Abcc3-201* (ENSMUST00000021231.7) transcript is recommended as the knockout region. The region contains 2368bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Abcc3* gene. The brief process is as follows: gRNA was transcribed in vitro, donor was constructed. Cas9, gRNA and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, Mice homozygous for disruptions in this gene exhibit increased liver bile acid levels after bile duct ligation
- The *Abcc3* gene is located on the Chr11. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

# Gene information (NCBI)

## Abcc3 ATP-binding cassette, sub-family C (CFTR/MRP), member 3 [ *Mus musculus* (house mouse) ]

Gene ID: 76408, updated on 10-Oct-2019

### Summary



**Official Symbol** Abcc3 provided by [MGI](#)

**Official Full Name** ATP-binding cassette, sub-family C (CFTR/MRP), member 3 provided by [MGI](#)

**Primary source** [MGI:MGI:1923658](#)

**See related** [Ensembl:ENSMUSG00000020865](#)

**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** MLP2; MRP3; ABC31; MOAT-D; 1700019L09Rik

**Expression** Biased expression in liver adult (RPKM 63.1), colon adult (RPKM 54.5) and 14 other tissues [See more](#)

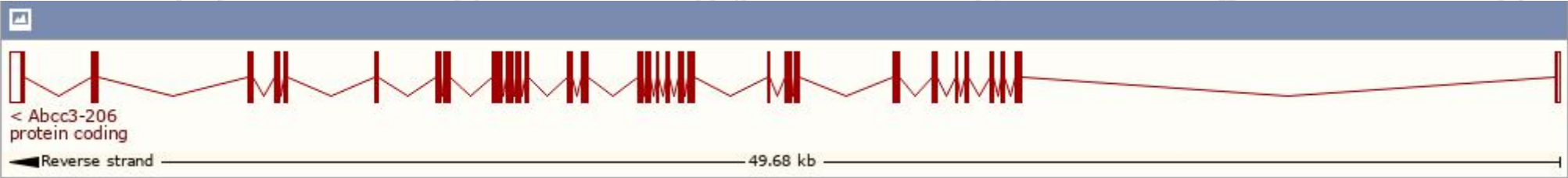
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

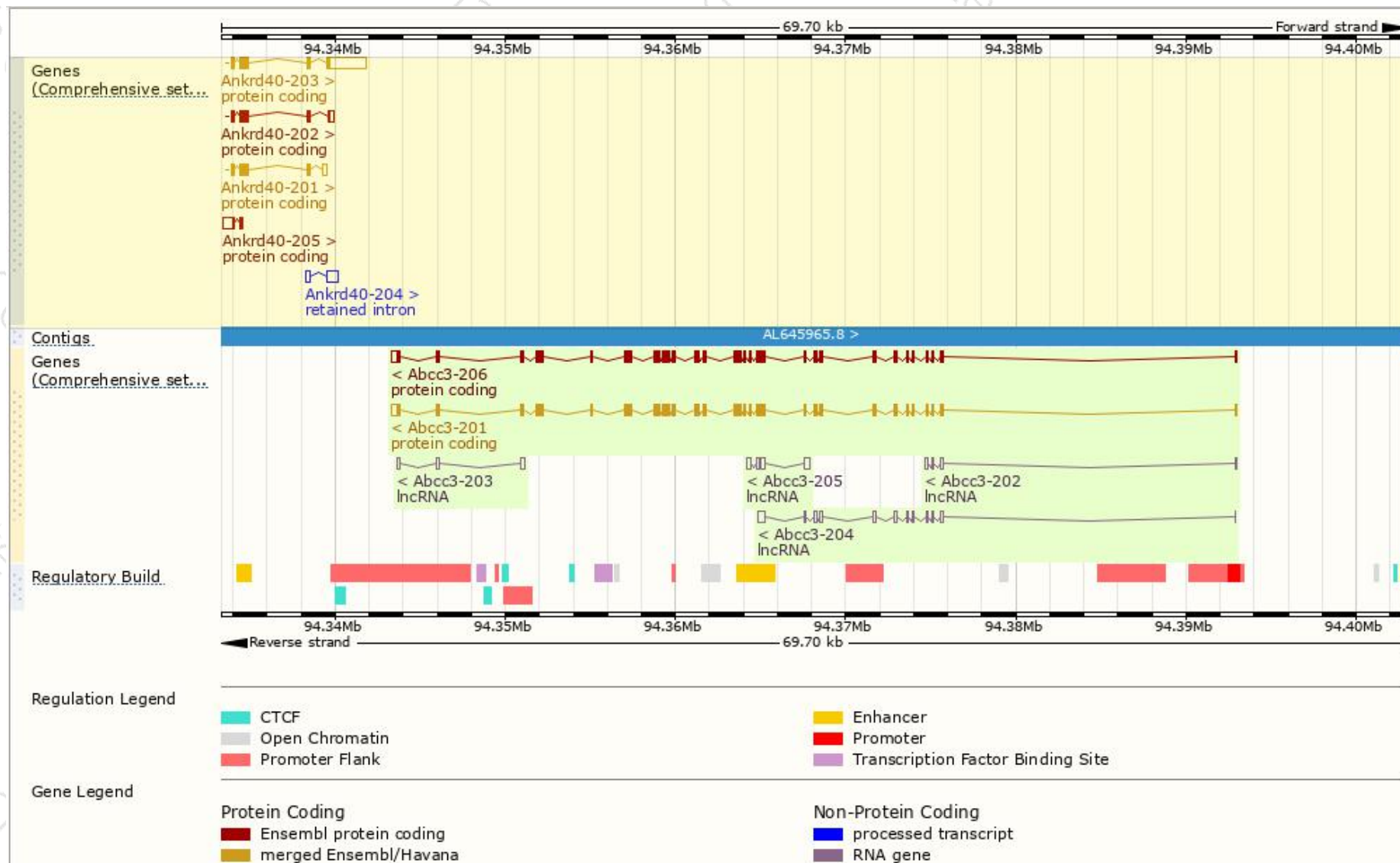
The gene has 6 transcripts,all transcripts are shown below:

Show/hide columns (1 hidden)							Filter	
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags	
Abcc3-201	<a href="#">ENSMUST00000021231.7</a>	4999	<a href="#">1522aa</a>	Protein coding	<a href="#">CCDS25254</a>	<a href="#">A0A0R4J015</a>	TSL:1	GENCODE basic APPRIS P2
Abcc3-206	<a href="#">ENSMUST00000178136.7</a>	5005	<a href="#">1523aa</a>	Protein coding	-	<a href="#">J3QML2</a>	TSL:1	GENCODE basic APPRIS ALT2
Abcc3-204	<a href="#">ENSMUST00000151124.7</a>	1808	No protein	lncRNA	-	-	TSL:5	
Abcc3-205	<a href="#">ENSMUST00000155253.1</a>	915	No protein	lncRNA	-	-	TSL:3	
Abcc3-202	<a href="#">ENSMUST00000126566.1</a>	667	No protein	lncRNA	-	-	TSL:3	
Abcc3-203	<a href="#">ENSMUST00000140985.1</a>	567	No protein	lncRNA	-	-	TSL:3	

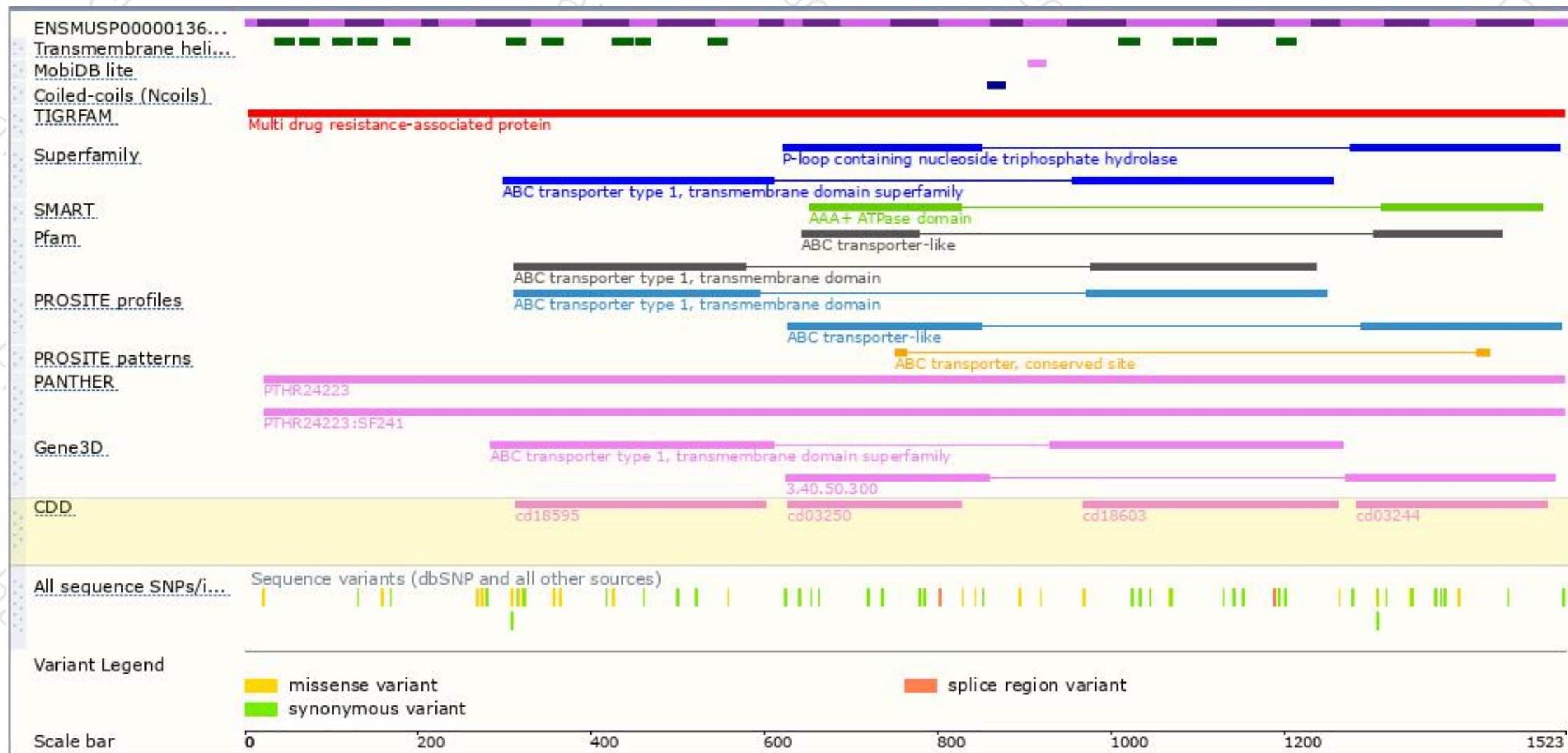
The strategy is based on the design of *Abcc3-201* transcript,The transcription is shown below



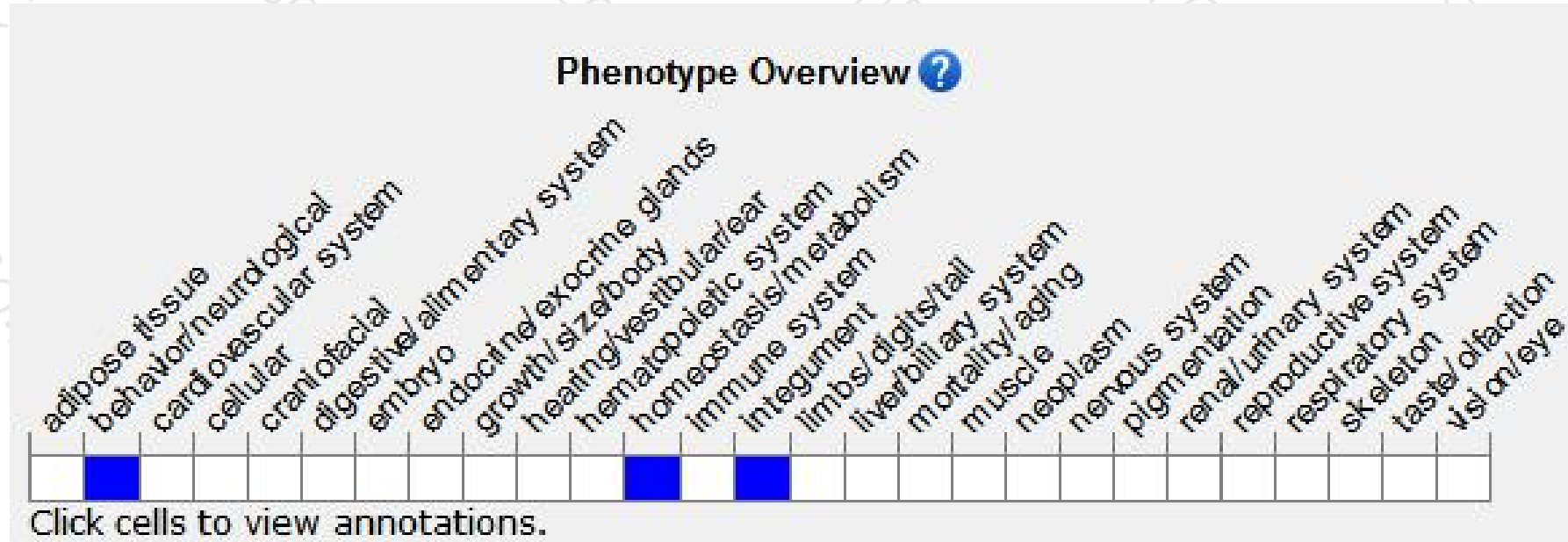
# Genomic location distribution



# 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, Mice homozygous for disruptions in this gene exhibit increased liver bile acid levels after bile duct ligation

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

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