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GemPharmatech

Abcf1 Cas9-KO Strategy

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Design Date: **2020-4-7**

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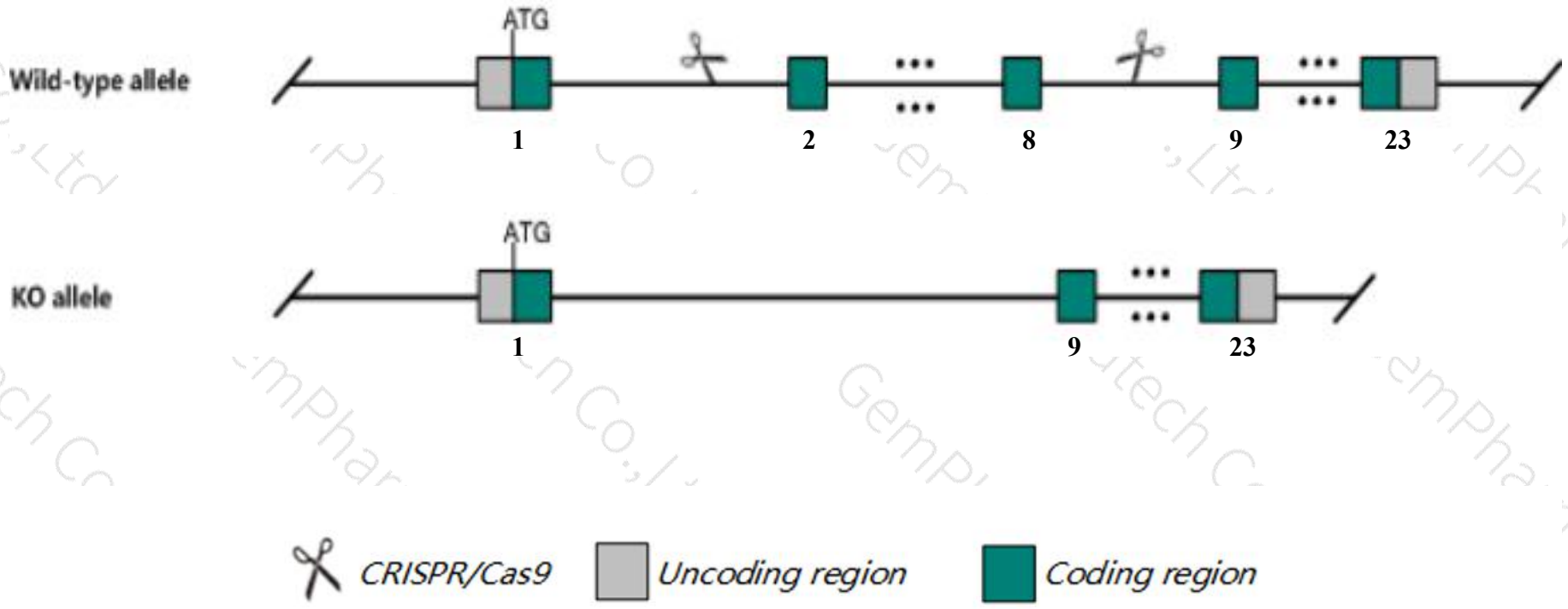
Project Overview

Project Name	***Abcf1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Abcf1* gene. The schematic diagram is as follows:



Technical routes

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- The *Abcf1* gene has 8 transcripts. According to the structure of *Abcf1* gene, exon2-exon8 of *Abcf1-201* (ENSMUST00000043757.14) transcript is recommended as the knockout region.The region contains 596bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Abcf1* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Mice homozygous for a null allele display lethality shortly after implantation.

- The KO region contains functional region of the *Abcf1* gene.Knockout the region may affect the function of *Mir877* gene.

- The *Abcf1* gene is located on the Chr17. 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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Abcf1 ATP-binding cassette, sub-family F (GCN20), member 1 [Mus musculus (house mouse)]

Gene ID: 224742, updated on 13-Mar-2020

Summary

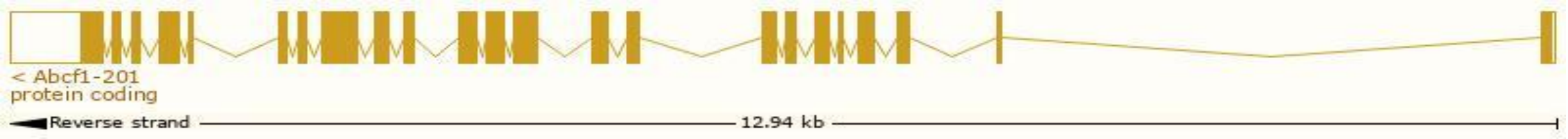
Official Symbol	Abcf1 provided by MGI
Official Full Name	ATP-binding cassette, sub-family F (GCN20), member 1 provided byMGI
Primary source	MGI:MGI:1351658
See related	Ensembl:ENSMUSG00000038762
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AU041969, Abc50, D17Wsu166e, GCN20
Expression	Ubiquitous expression in testis adult (RPKM 41.9), CNS E11.5 (RPKM 33.3) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

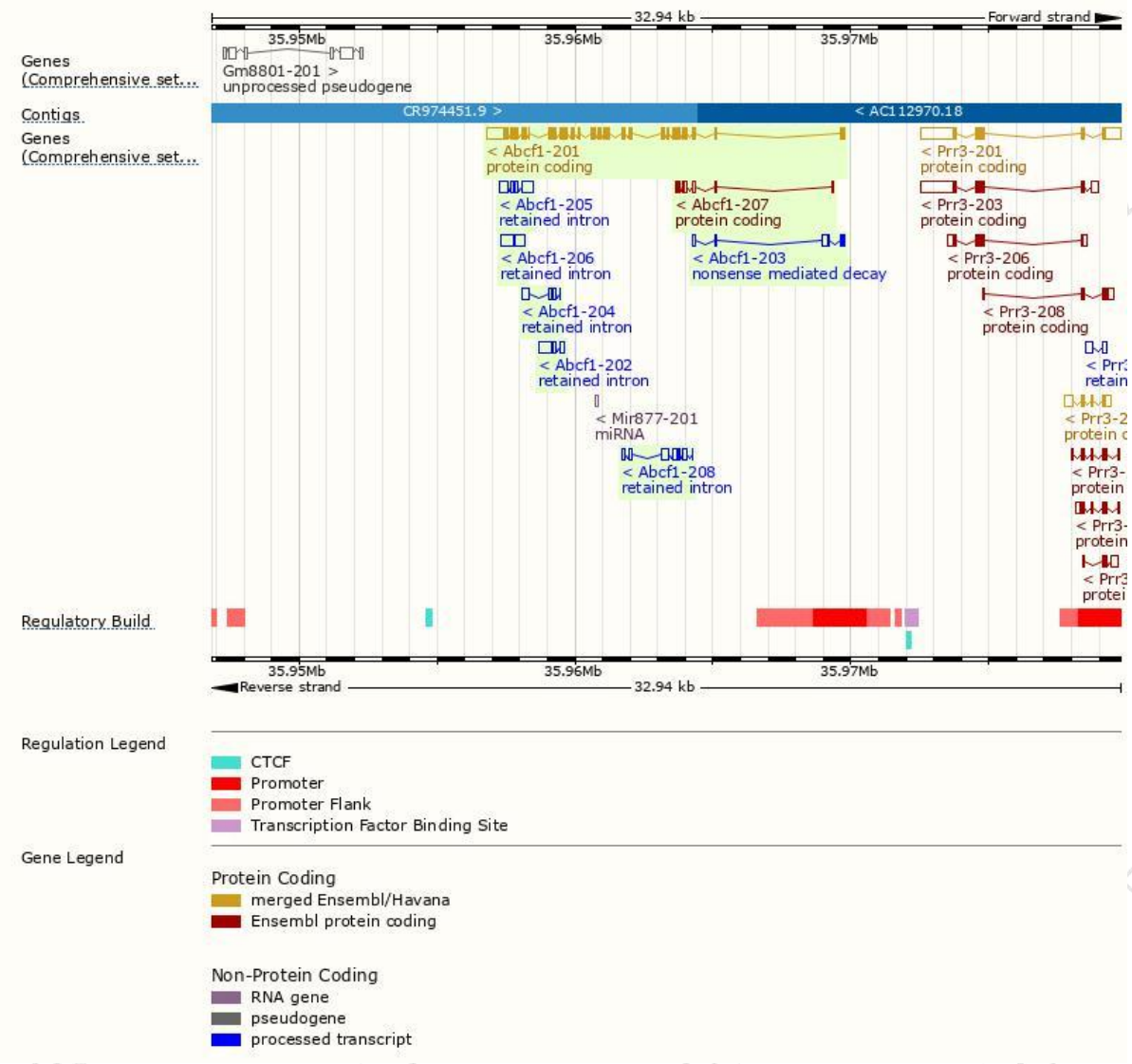
The gene has 8 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Abcf1-201	ENSMUST00000043757.14	3161	837aa	Protein coding	CCDS28713	Q6P542	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 P1
Abcf1-207	ENSMUST00000174128.7	376	43aa	Protein coding	-	G3V012	CDS 3' incomplete TSL:5
Abcf1-203	ENSMUST00000172661.1	516	48aa	Nonsense mediated decay	-	G3UYI0	TSL:5
Abcf1-205	ENSMUST00000173111.1	855	No protein	Retained intron	-	-	TSL:1
Abcf1-206	ENSMUST00000173125.1	798	No protein	Retained intron	-	-	TSL:3
Abcf1-208	ENSMUST00000174834.1	787	No protein	Retained intron	-	-	TSL:3
Abcf1-202	ENSMUST00000087205.6	724	No protein	Retained intron	-	-	TSL:2
Abcf1-204	ENSMUST00000173090.7	464	No protein	Retained intron	-	-	TSL:2

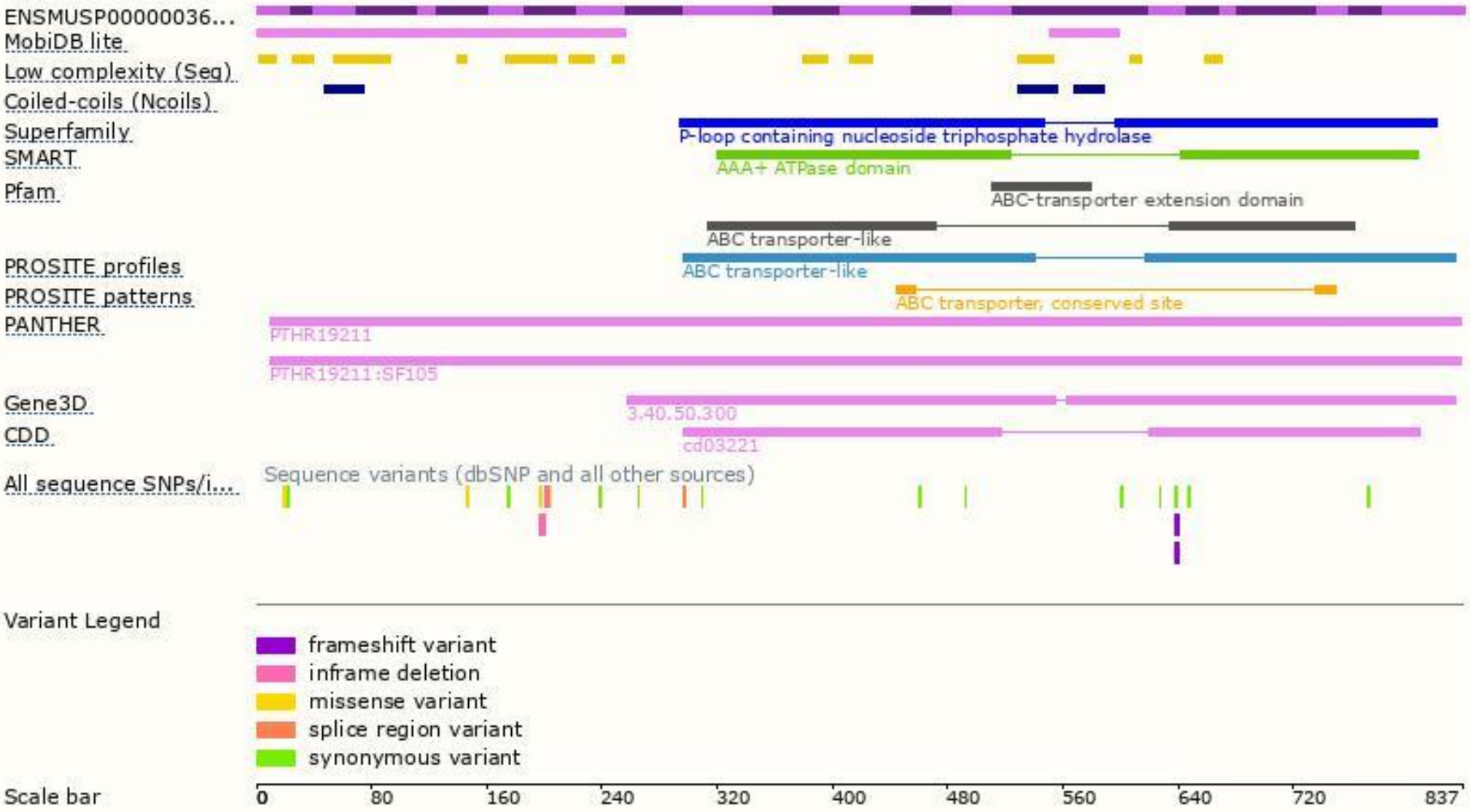
The strategy is based on the design of *Abcf1-201* transcript,The transcription is shown below



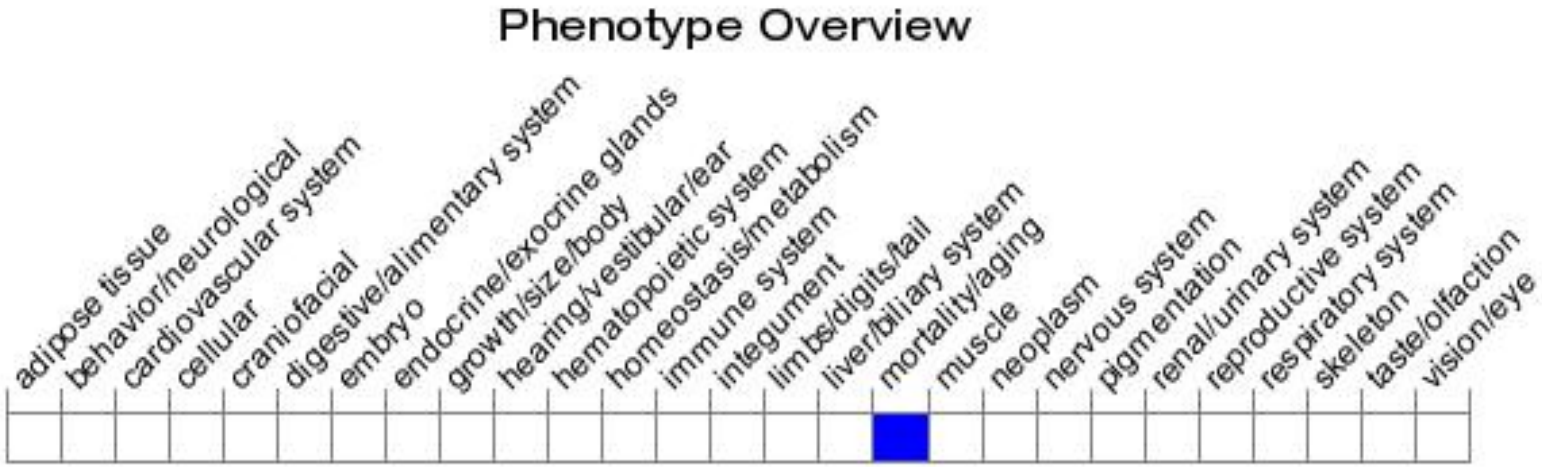
Genomic location distribution



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 a null allele display lethality shortly after implantation.

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