Atpif1 Cas9-KO Strategy

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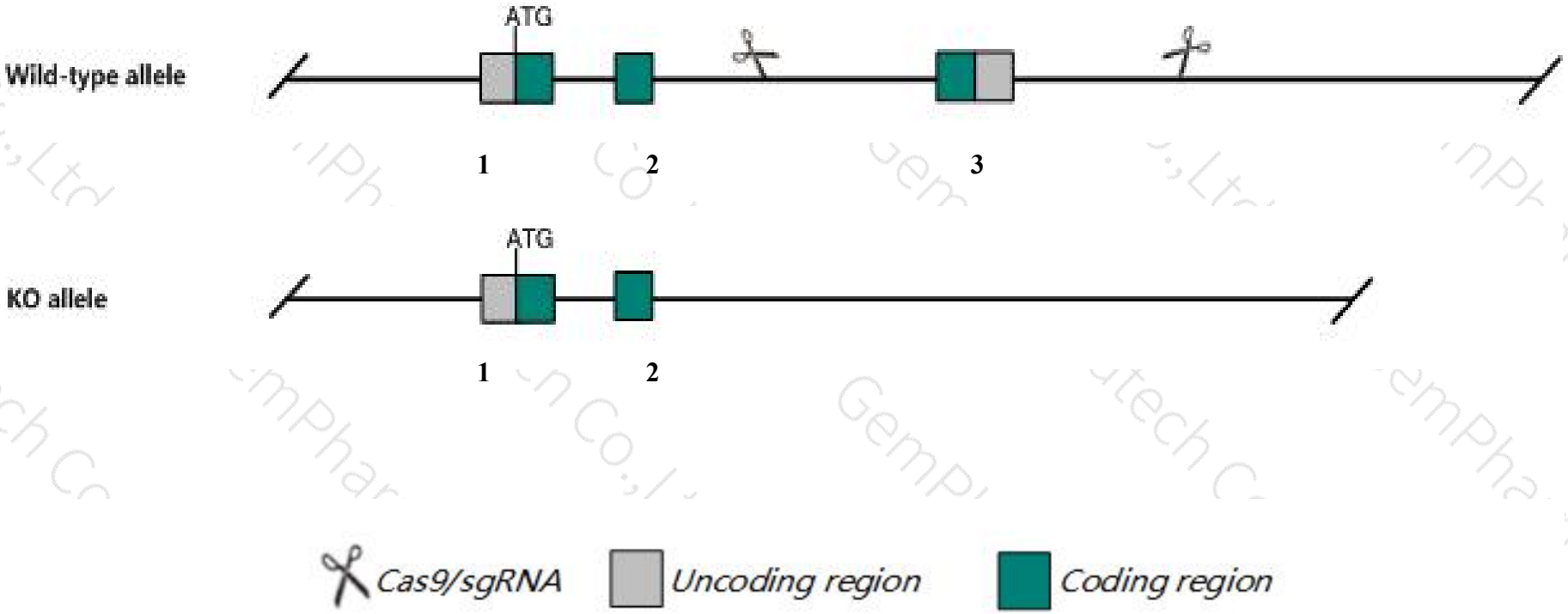
Project Overview

Project Name	***Atpif1***
Project type	**Cas9-KO**
Strain background	**C57BL/6J**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Atpif1* gene. The schematic diagram is as follows:



Technical routes

- The *Atpif1* gene has 3 transcripts. According to the structure of *Atpif1* gene, exon3 of *Atpif1-201* (ENSMUST00000067496.6) transcript is recommended as the knockout region.The region contains 142bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Atpif1* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

Notice

- The *Atpif1* 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）

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Atpif1 ATPase inhibitory factor 1 [Mus musculus (house mouse)]

Gene ID: 11983, updated on 31-Jan-2019

Summary

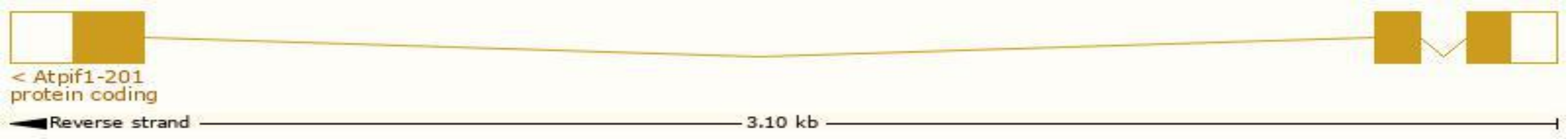
Official Symbol	Atpif1 provided by MGI
Official Full Name	ATPase inhibitory factor 1 provided byMGI
Primary source	MGI:MGI:1196457
See related	Ensembl:ENSMUSG00000054428
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	ATP5IF1, Atpi, IF(1), If1
Summary	This gene encodes a member of the ATPase inhibitor family of proteins. This protein has been shown to negatively regulate the ATP hydrolysis activity of the F1Fo-ATPase. Knockdown of this gene is associated with reduced heme synthesis in differentiating erythroid cells. Misregulation of this gene has been found to lead to increased aerobic glycolysis in mouse cancer cells, while high expression levels of this gene have been correlated with gastric and liver cancer severity in human patients. A pseudogene of this gene has been identified. [provided by RefSeq, Apr 2015]
Expression	Broad expression in liver E14 (RPKM 154.1), CNS E11.5 (RPKM 126.1) and 21 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

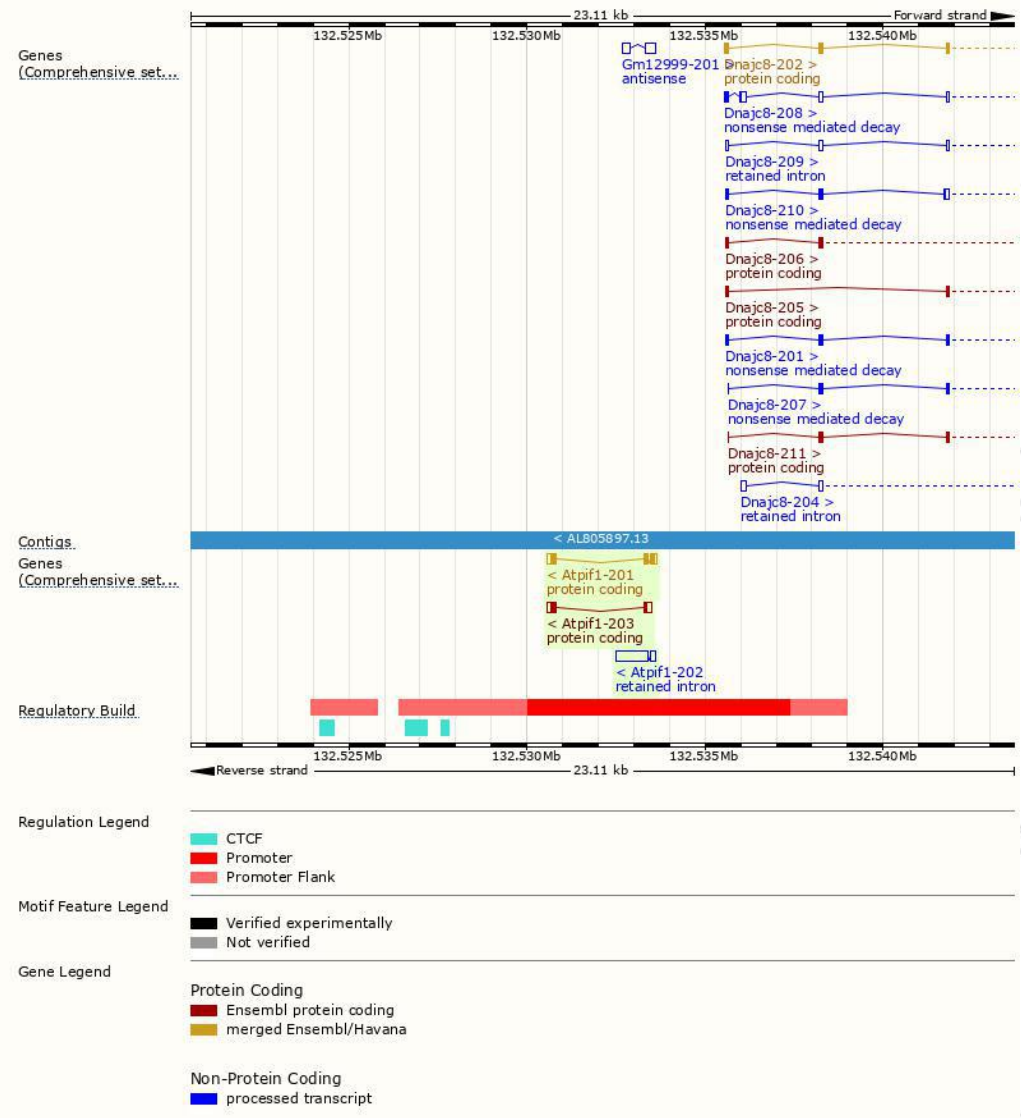
The gene has 3 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Atpif1-201	ENSMUST00000067496.6	539	106aa	Protein coding	CCDS18727	O35143	TSL:1 GENCODE basic APPRIS P1
Atpif1-203	ENSMUST00000152993.7	462	74aa	Protein coding	-	E9PV44	TSL:2 GENCODE basic
Atpif1-202	ENSMUST00000145795.1	1014	No protein	Retained intron	-	-	TSL:2

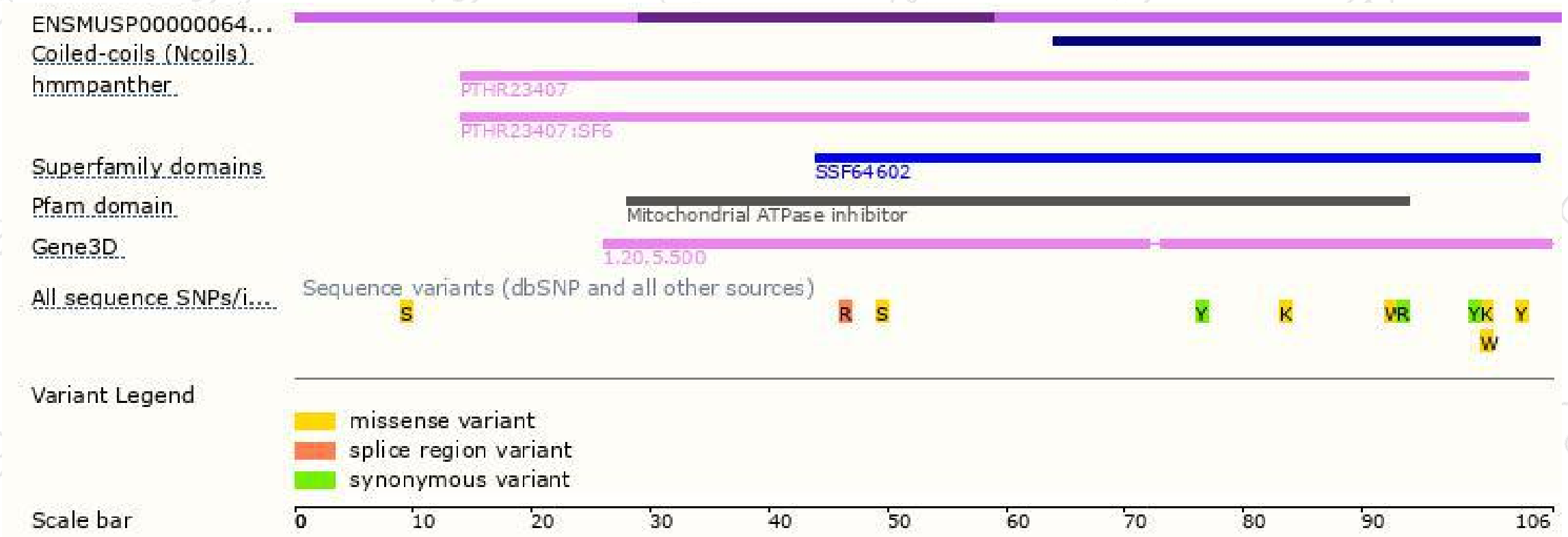
The strategy is based on the design of *Atpif1-201* transcript,The transcription is shown below



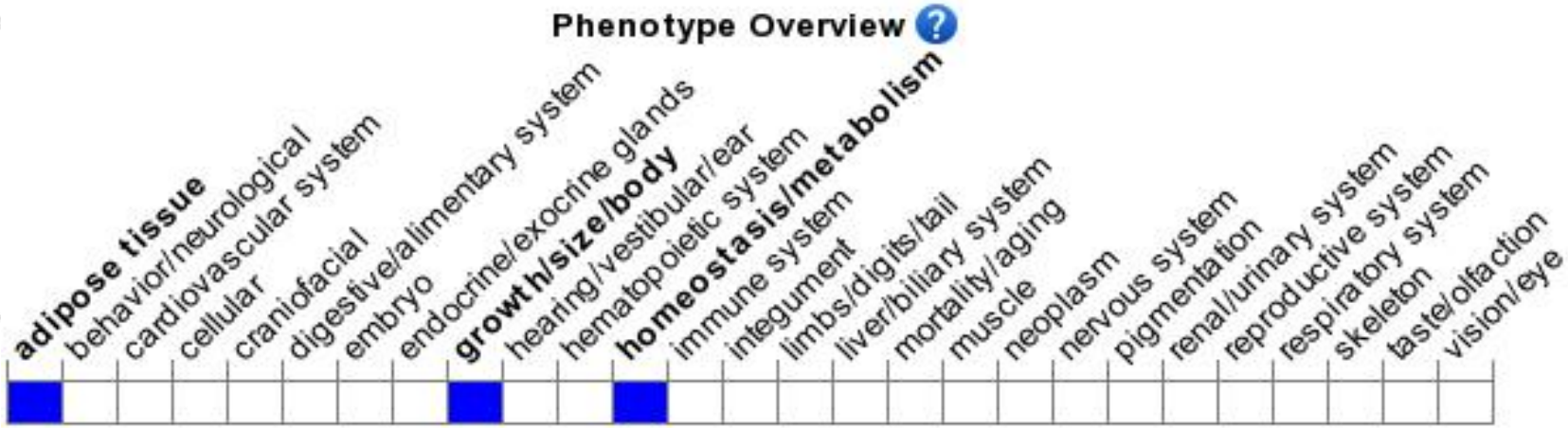
Genomic location distribution



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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