Appl1 Cas9-KO Strategy

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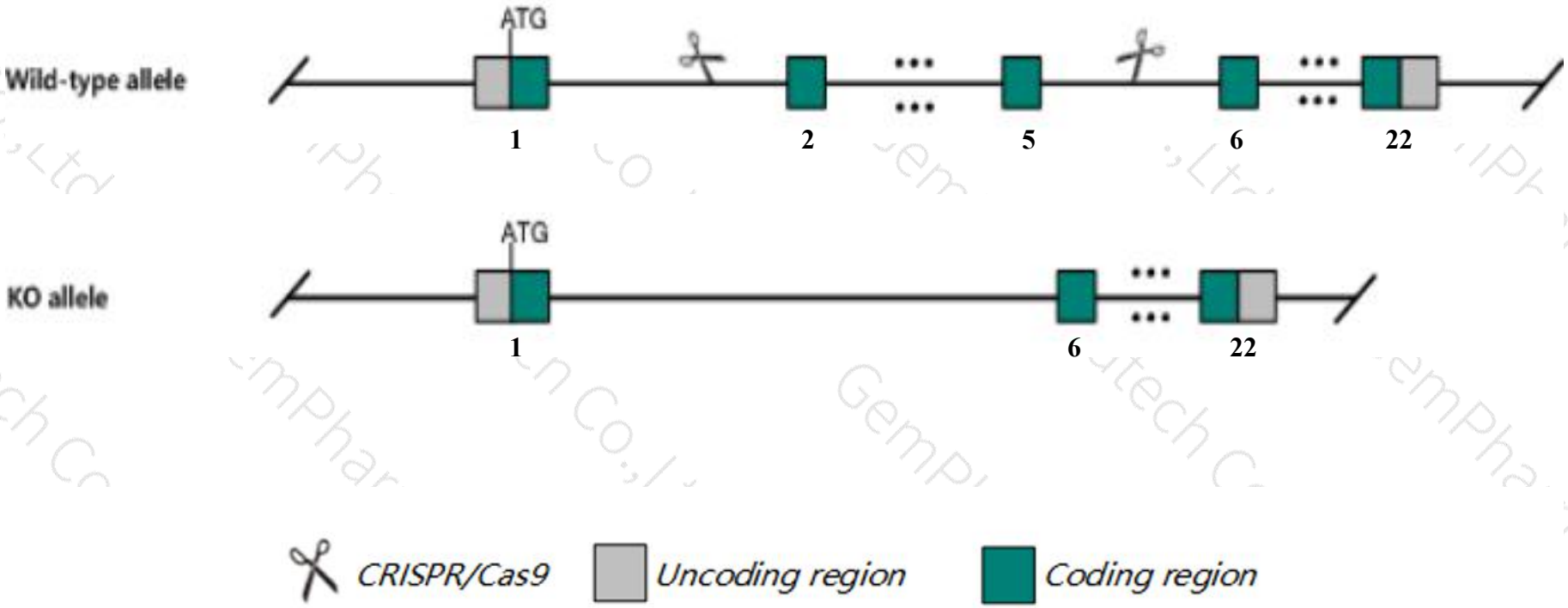
Design Date:2018-12-7

Project Overview

Project Name	***Appl1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Appl1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Appl1* gene has 5 transcripts. According to the structure of *Appl1* gene, exon2-exon5 of *Appl1-201* (ENSMUST00000036570.4) transcript is recommended as the knockout region.The region contains 319bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Appl1* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,mice homozygous for a null allele exhibit decreased insulin-induced relaxation and increased insulin-induced et-1-dependent vasoconstriction when fed a high fat diet. homozygotes for a second null allele show increased hematocrit and t cell proliferation, and decreased fibroblast cell migration. homozygotes for a third null allele show hyperactivity, increased body core temperature, and insulin resistance.
- The *Appl1* gene is located on the Chr14. 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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Appl1 adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 1 [Mus musculus (house mouse)]

Gene ID: 72993, updated on 13-Mar-2020

Summary

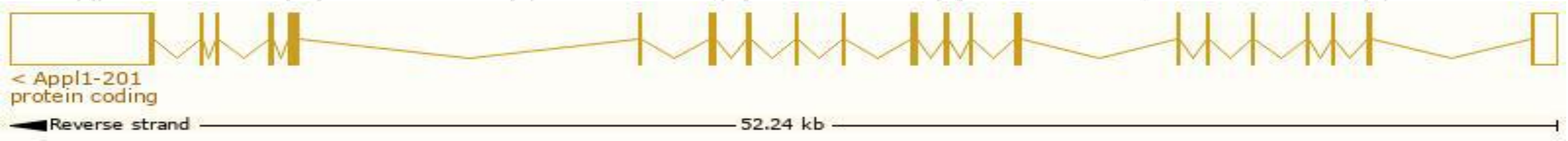
Official Symbol	Appl1 provided by MGI
Official Full Name	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 1 provided by MGI
Primary source	MGI:MGI:1920243
See related	Ensembl:ENSMUSG00000040760
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2900057D21Rik, 7330406P05Rik, AI585782, AW209077, BB022931, C88264, DIP13
Expression	Broad expression in CNS E18 (RPKM 11.1), whole brain E14.5 (RPKM 9.0) and 24 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

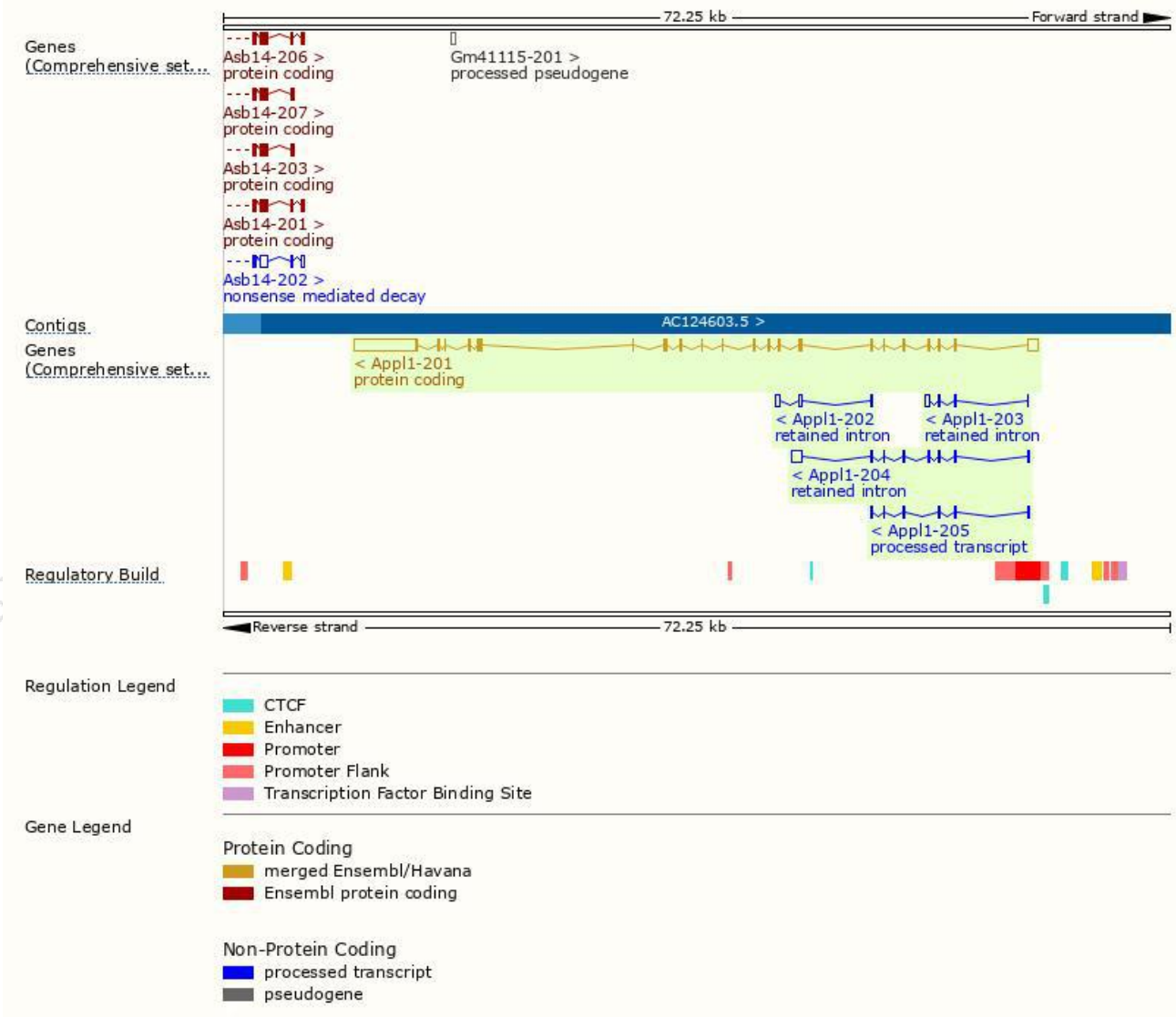
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Appl1-201	ENSMUST00000036570.4	7642	707aa	Protein coding	CCDS26883	Q8K3H0	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
Appl1-205	ENSMUST00000224406.1	427	No protein	Processed transcript	-	-	
Appl1-204	ENSMUST00000142645.7	1226	No protein	Retained intron	-	-	TSL:1
Appl1-202	ENSMUST00000141599.7	598	No protein	Retained intron	-	-	TSL:2
Appl1-203	ENSMUST00000142261.1	503	No protein	Retained intron	-	-	TSL:2

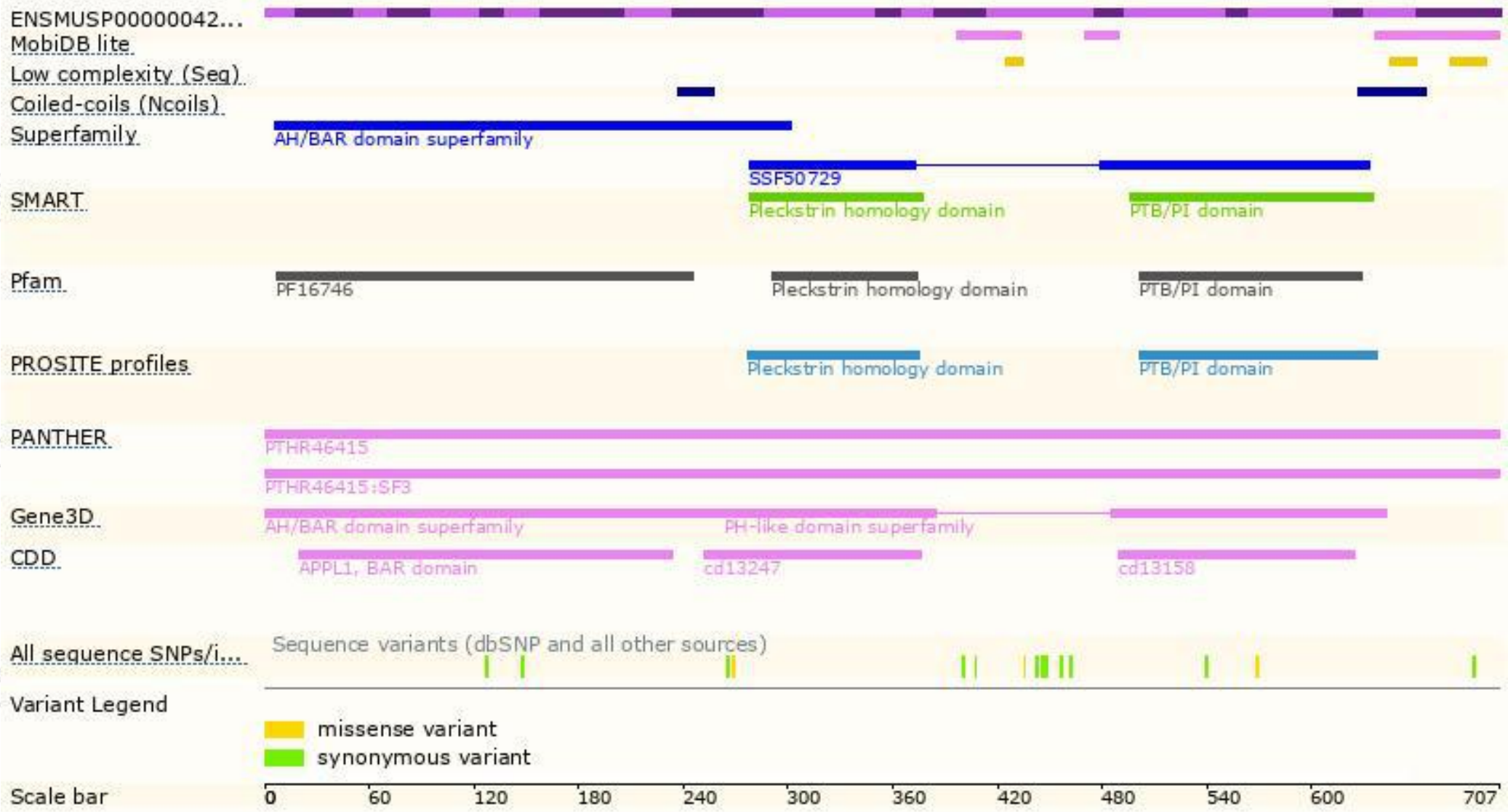
The strategy is based on the design of *Appl1-201* transcript,the transcription is shown below：



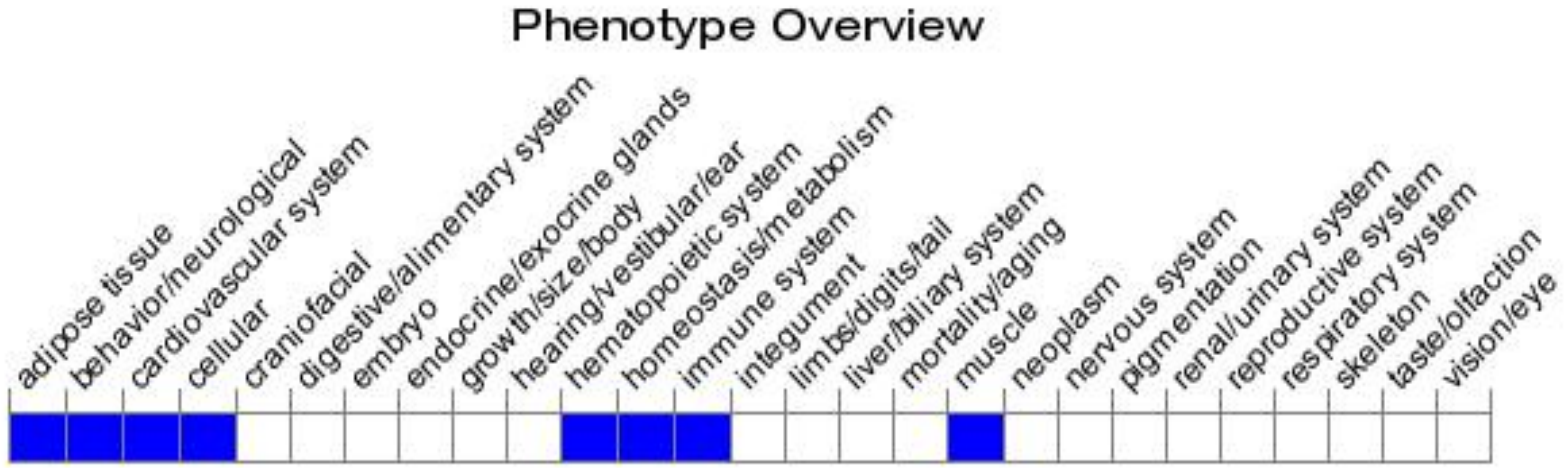
Genomic location distribution



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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