Akt1 Cas9-KO Strategy

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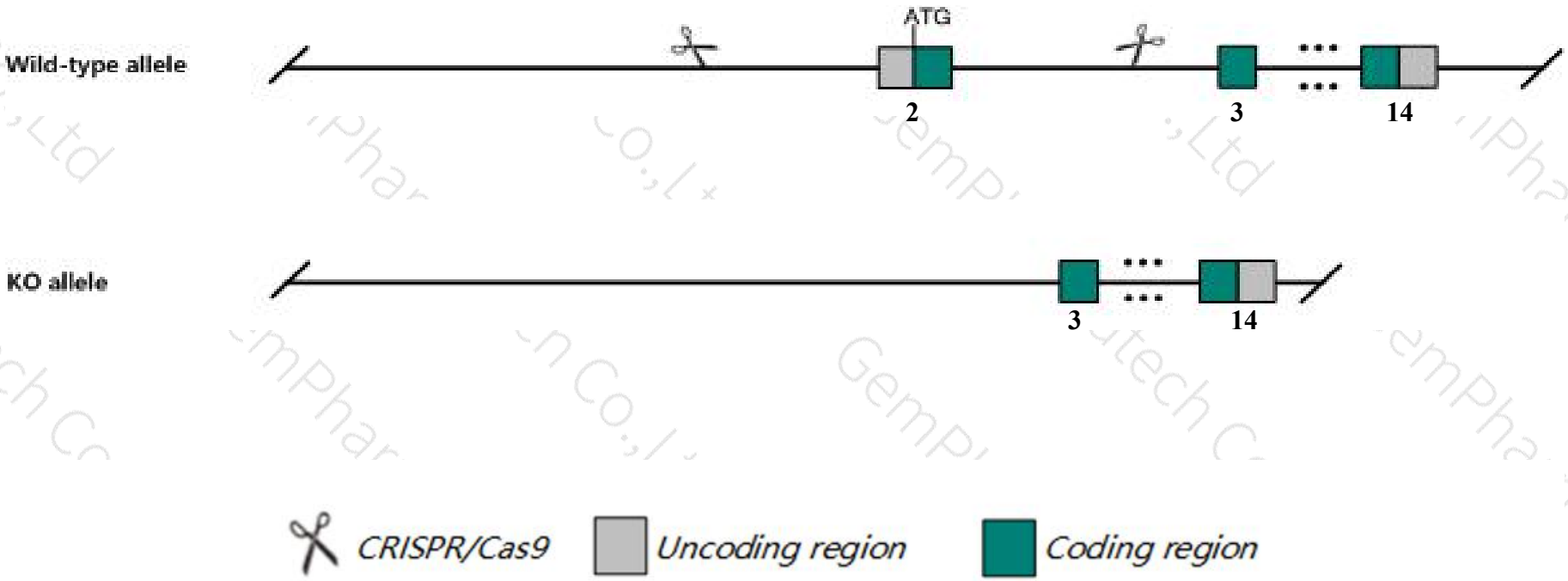
Project Overview

Project Name	***Akt1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Akt1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Akt1* gene has 9 transcripts. According to the structure of *Akt1* gene, exon2 of *Akt1-201* (ENSMUST00000001780.9) transcript is recommended as the knockout region.The region contains start codon ATG. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Akt1* gene. The brief process is as follows: CRISPR/Cas9 system w

Notice

- According to the existing MGI data,Mutant homozygotes are smaller than sibs due to retarded prenatal and postnatal growth and exhibit increased apoptosis and decreased lifespan with genotoxic stress. Mice are fertile, but males have attenuated spermatogenesis and abnormal testes.

- The *Akt1* gene is located on the Chr12. 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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Akt1 thymoma viral proto-oncogene 1 [Mus musculus (house mouse)]

Gene ID: 11651, updated on 9-Apr-2019

Summary

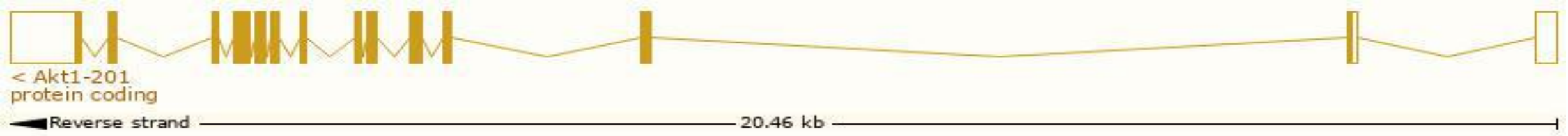
Official Symbol	Akt1 provided by MGI
Official Full Name	thymoma viral proto-oncogene 1 provided by MGI
Primary source	MGI:MGI:87986
See related	Ensembl:ENSMUSG00000001729
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Akt, LTR-akt, PKB, PKB/Akt, PKBalpha, Rac
Summary	This gene encodes the founding member of the Akt serine-threonine protein kinase gene family that also includes Akt2 and Akt3. This kinase is a major downstream effector of the phosphatidylinositol 3-kinase (PI3K) pathway that mediates the effects of various growth factors such as platelet-derived growth factor (PDGF), epidermal growth factor (EGF), insulin and insulin-like growth factor I (IGF-I). It is activated through recruitment to cellular membranes by PI3K lipid products and by phosphorylation by 3-phosphoinositide dependent kinase-1. It then further phosphorylates different downstream proteins in response to various extracellular signals and thus plays a pivotal role in mediating a variety of cellular processes, such as glucose metabolism, glycogen biosynthesis, protein synthesis and turn over, inflammatory response, cell survival (anti-apoptosis) and development. Alternatively spliced transcript variants encoding different isoforms have been found for this gene. [provided by RefSeq, Sep 2009]
Expression	Ubiquitous expression in adrenal adult (RPKM 140.9), limb E14.5 (RPKM 84.5) and 28 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

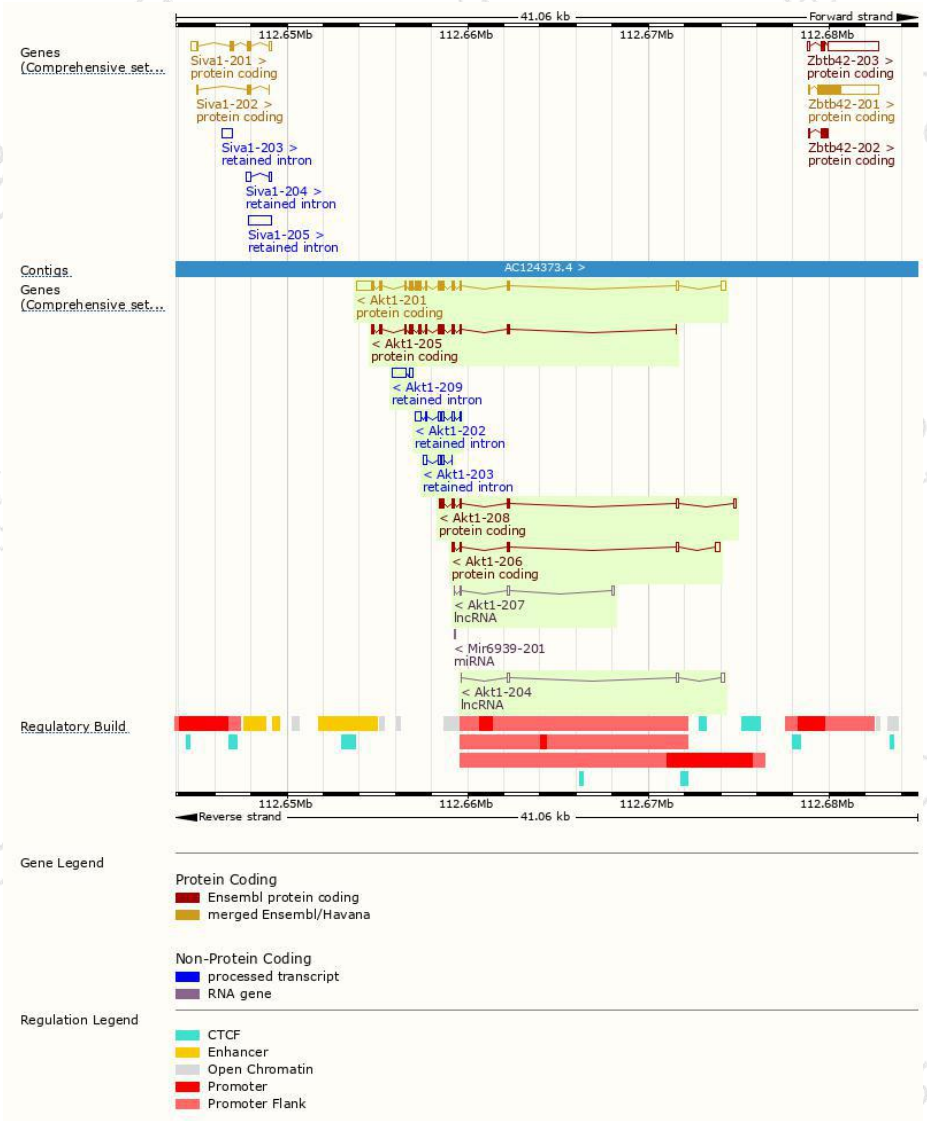
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Akt1-201	ENSMUST00000001780.9	2690	480aa	Protein coding	CCDS26194	P31750	TSL:1 GENCODE basic APPRIS P1
Akt1-205	ENSMUST00000128300.8	1342	437aa	Protein coding	-	D3Z783	TSL:5 GENCODE basic
Akt1-208	ENSMUST00000144550.8	862	202aa	Protein coding	-	D3YXX3	CDS 3' incomplete TSL:5
Akt1-206	ENSMUST00000130342.1	736	134aa	Protein coding	-	D3YYP9	CDS 3' incomplete TSL:3
Akt1-204	ENSMUST00000127902.1	526	No protein	Processed transcript	-	-	TSL:3
Akt1-207	ENSMUST00000139388.2	397	No protein	Processed transcript	-	-	TSL:3
Akt1-209	ENSMUST00000159815.1	944	No protein	Retained intron	-	-	TSL:2
Akt1-202	ENSMUST00000123563.8	803	No protein	Retained intron	-	-	TSL:2
Akt1-203	ENSMUST00000127588.2	386	No protein	Retained intron	-	-	TSL:2

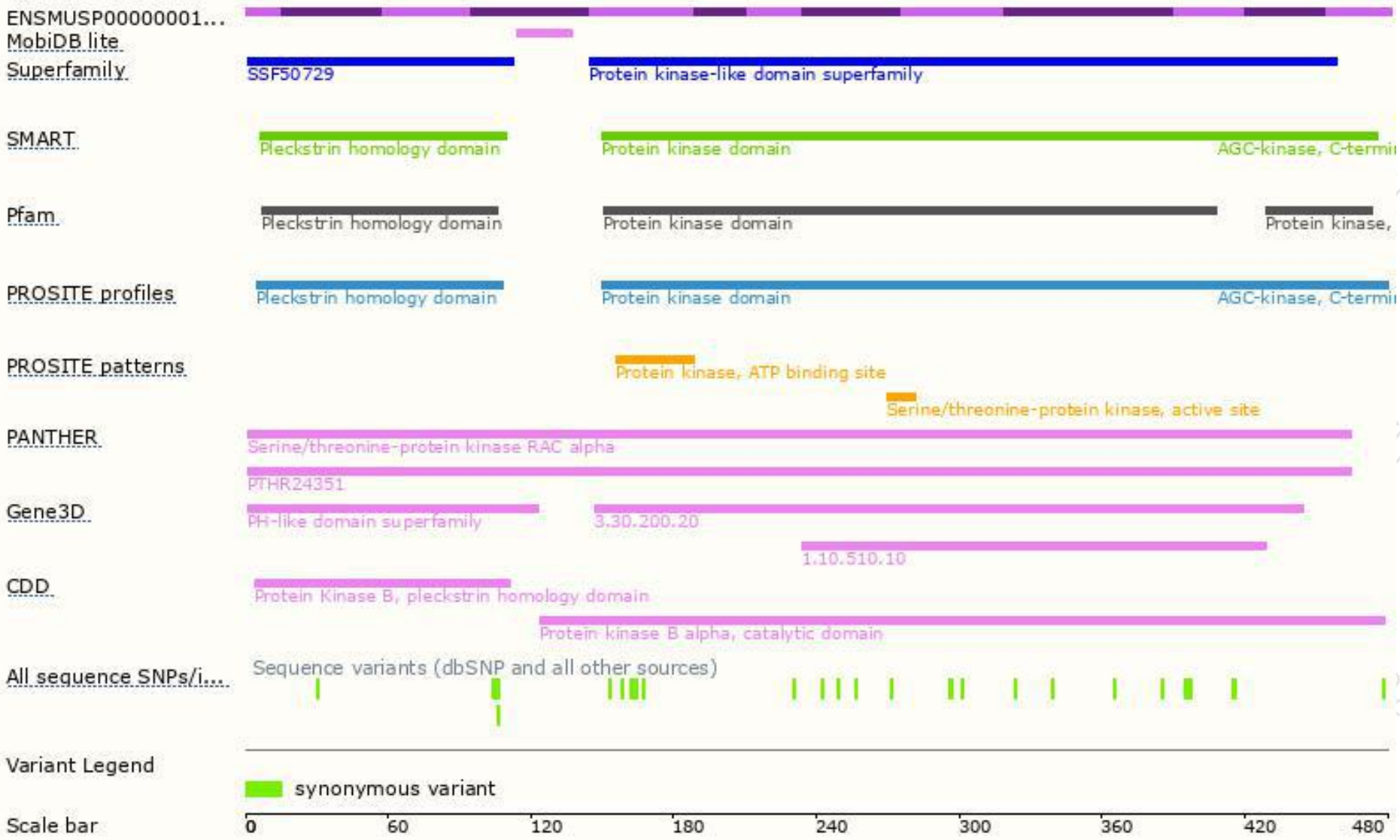
The strategy is based on the design of *Akt1-201* transcript,The transcription is shown below



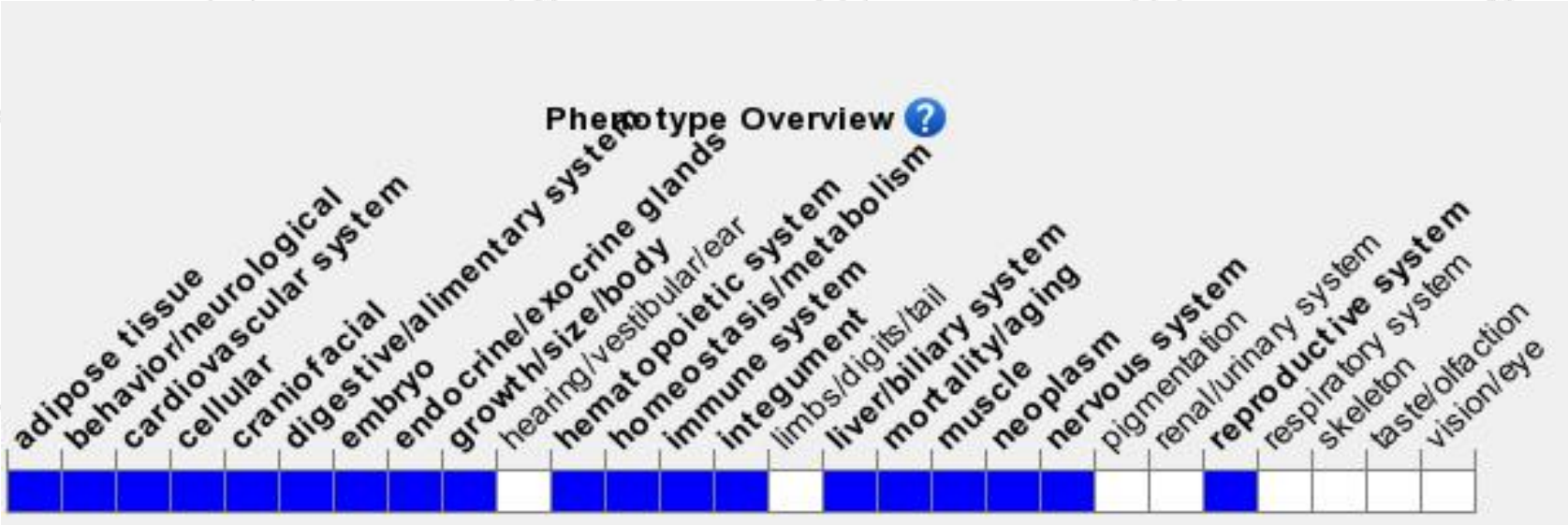
Genomic location distribution



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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