

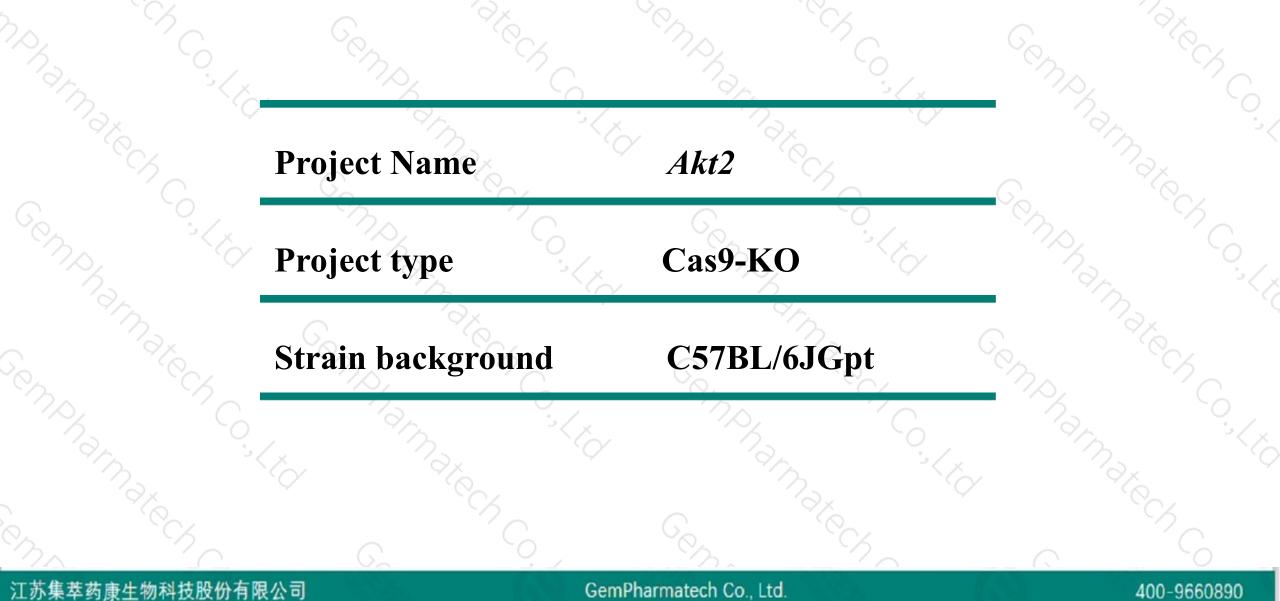
Akt2 Cas9-KO Strategy

Designer: Design Date:

Huan Fan 2019-7-25

Project Overview

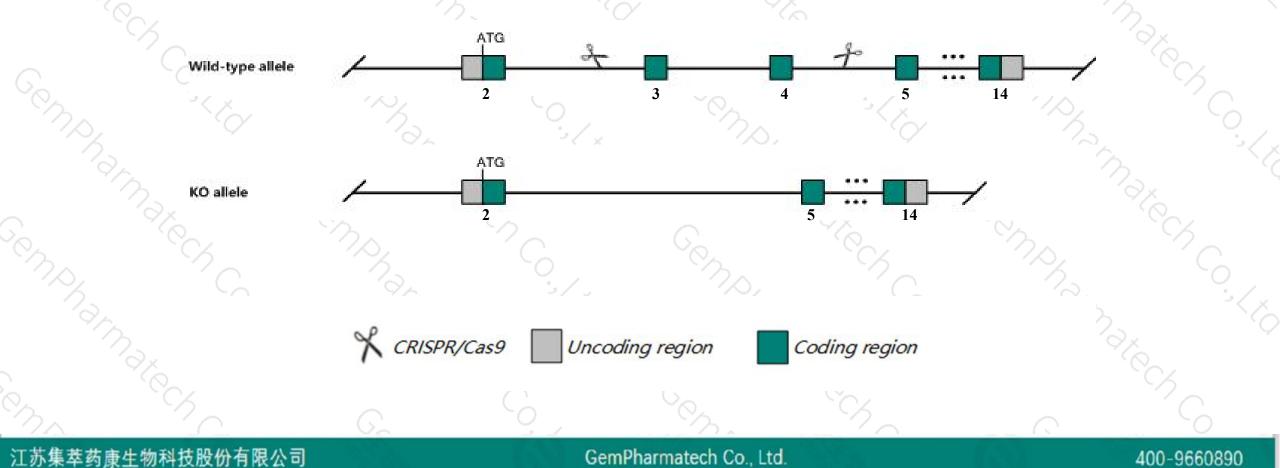




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Akt2* gene. The schematic diagram is as follows:





- The Akt2 gene has 14 transcripts. According to the structure of Akt2 gene, exon3-exon4 of Akt2-205 (ENSMUST00000108344.8) transcript is recommended as the knockout region. The region contains 241bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify Akt2 gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Homozygotes for targeted null mutations exhibit insulin resistance and elevated plasma triglycerides. In males, the insulin resistance may progress to overt diabetes.
- The *Akt2* gene is located on the Chr7. 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.

Notice

Gene information (NCBI)



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Akt2 thymoma viral proto-oncogene 2 [Mus musculus (house mouse)]

Gene ID: 11652, updated on 9-Apr-2019

Summary

Official SymbolAkt2 provided by MGIOfficial Full NameHymoma viral proto-oncogene 2 provided by MGIPrimary soureMGI:MGI:104874See relatedEnsembl:ENSMUSG000004056Gene typeprotein codingOrganismMus musculusLineageEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Rodentia; Myomorpha;
Muroidea; Murinae; Mus; MusAlso known as2410016A19Rik, AW554154, PKB, PKBbetaExpressionUbiquitous expression in subcutaneous fat pad adult (RPKM 40.3), mammary gland adult (RPKM 35.7) and 28 other tissues

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Transcript information (Ensembl)



Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Akt2-205	ENSMUST00000108344.8	4544	<u>481aa</u>	Protein coding	CCDS21027	Q3TY95 Q60823	TSL:1 GENCODE basic APPRIS P1
Akt2-204	ENSMUST00000108343.7	3122	<u>481aa</u>	Protein coding	CCDS21027	Q3TY95 Q60823	TSL:5 GENCODE basic APPRIS P1
Akt2-201	ENSMUST00000051356.11	2923	<u>481aa</u>	Protein coding	CCDS21027	Q3TY95 Q60823	TSL:1 GENCODE basic APPRIS P1
Akt2-214	ENSMUST00000167435.7	2865	<u>481aa</u>	Protein coding	CCDS21027	Q3TY95 Q60823	TSL:1 GENCODE basic APPRIS P1
Akt2-202	ENSMUST0000085917.4	1392	<u>438aa</u>	Protein coding	7	F8WHG5	TSL:5 GENCODE basic
Akt2-203	ENSMUST00000108342.7	1125	<u>222aa</u>	Protein coding	-	D3YXM7	CDS 3' incomplete TSL:3
Akt2-207	ENSMUST00000136962.7	940	<u>229aa</u>	Protein coding	-	D3Z3N2	CDS 3' incomplete TSL:5
Akt2-209	ENSMUST00000138459.7	712	<u>67aa</u>	Protein coding	14	D3Z0M3	CDS 3' incomplete TSL:5
Akt2-206	ENSMUST00000128540.7	453	<u>98aa</u>	Protein coding	7.0	<u>D3Z490</u>	CDS 3' incomplete TSL:5
Akt2-210	ENSMUST00000142365.7	448	<u>84aa</u>	Protein coding	-	D3YZJ5	CDS 3' incomplete TSL:3
Akt2-212	ENSMUST00000143499.7	417	<u>63aa</u>	Protein coding	-	D3Z5X2	CDS 3' incomplete TSL:3
Akt2-213	ENSMUST00000147263.1	685	No protein	Processed transcript	-	828	TSL:3
Akt2-211	ENSMUST00000143347.1	983	No protein	Retained intron	7	1.51	TSL:3
Akt2-208	ENSMUST00000136981.1	770	No protein	Retained intron	-	(7 7)	TSL:2

The gene has 14 transcripts, all transcripts are shown below:

The strategy is based on the design of *Akt2-205* transcript, The transcription is shown below

Akt2-205 > protein coding

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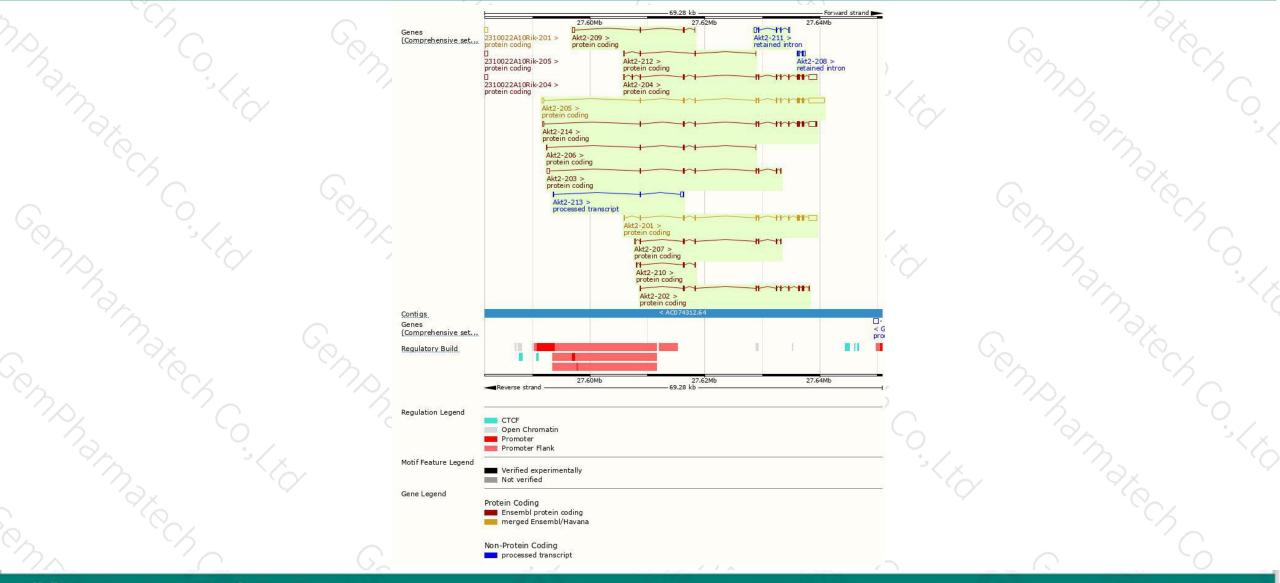
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Forward strand

Genomic location distribution





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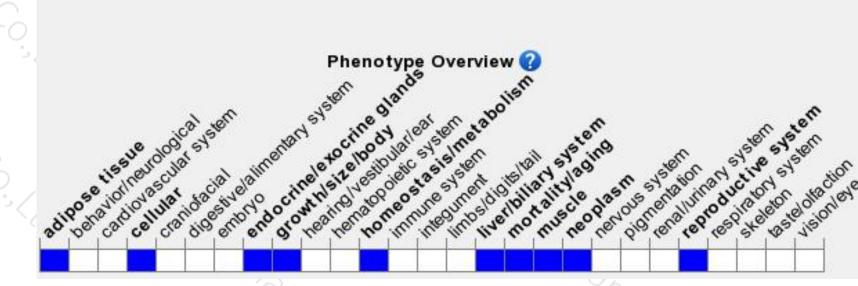
Protein domain



725	ENSMUSP00000103 Conserved Domains hmmpanther	PTHR24356		ALC CH
arma.	Superfamily domains	Serine/threonine-protein kinase RAC a	Protein kinase-like domain superfamily	í Co
- Ce	SMART domains	Pleckstrin homology domain	Protein kinase domain AGC-kinase, C-ter	-<
G	Pfam_domain_	Pleckstrin homology domain	Protein kinase domain Protein kinas	e, °°4
mp.	PROSITE profiles	Pleckstrin homology domain	Protein kinase domain AGC-kinase, C-ter	
	PROSITE patterns		Protein kinase, ATP binding site	
G.C.C.	Gene3D	PH-like domain superfamily	Serine/threonine-protein kinase, active site 1,10,510,10	· ~ ~ ~
n phan	All sequence SNPs/i	Sequence variants (dbSNP and all	3.30.200,20 other sources)	
	Variant Legend	missense variant synonymous variant		24
Sha -	Scale bar	o 60 120	180 240 300 360 420 48	
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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, Homozygotes for targeted null mutations exhibit insulin resistance and elevated plasma triglycerides. In males, the insulin resistance may progress to overt diabetes.



If you have any questions, you are welcome to inquire. Tel: 400-9660890



