Akap13 Cas9-CKO Strategy

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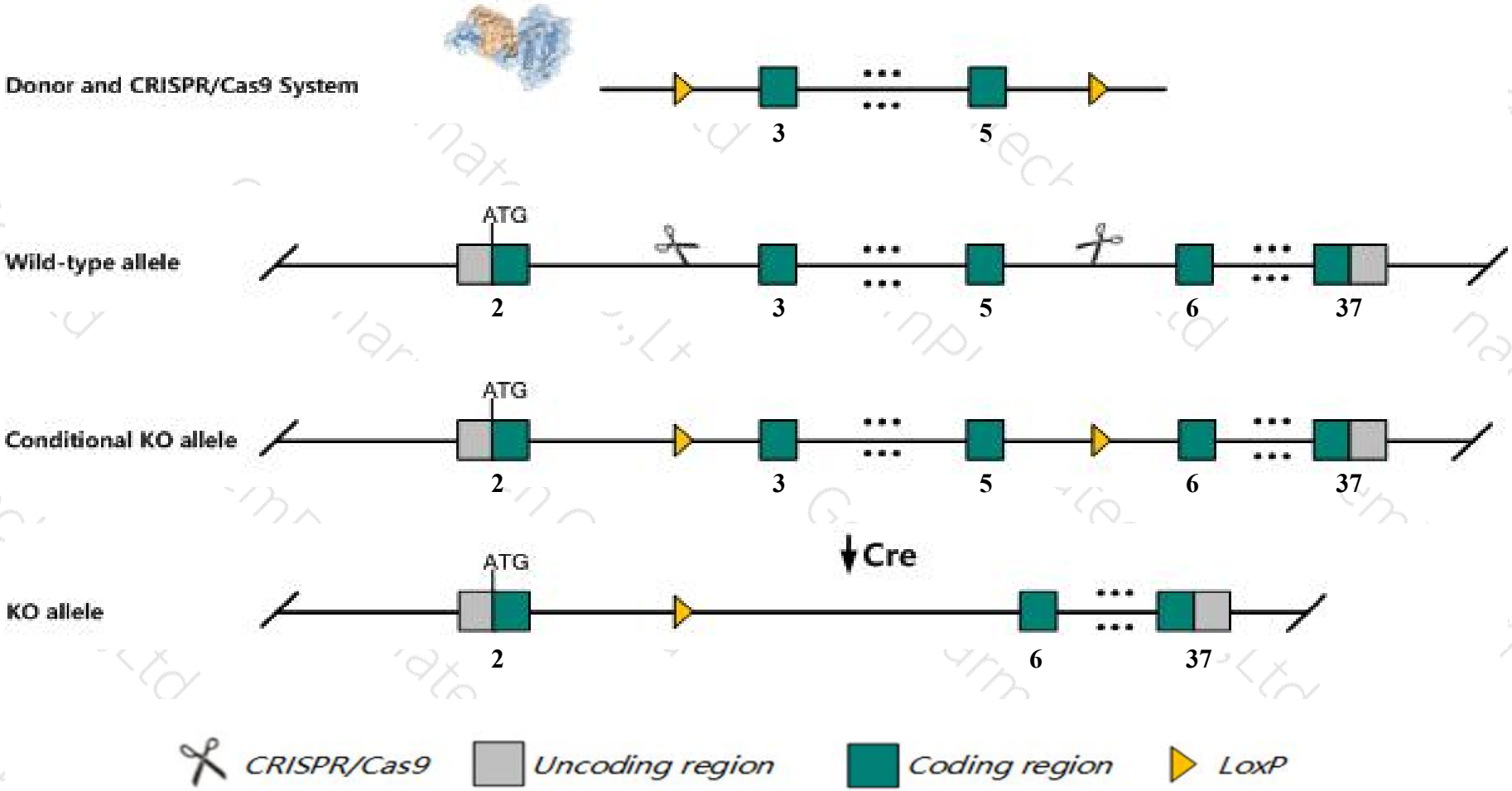
Project Overview

Project Name	***Akap13***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Akap13* gene. The schematic diagram is as follows:



Technical routes

- The *Akap13* gene has 16 transcripts. According to the structure of *Akap13* gene, exon3-exon5 of *Akap13-201* (ENSMUST00000166315.6) transcript is recommended as the knockout region.The region contains 629bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Akap13* gene. The brief process is as follows:CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt 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/6JGpt mice.

- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice

- According to the existing MGI data,Mice homozygous for a null allele exhibit embryonic lethality during organogenesis, arrested heart development, and forebrain hypoplasia. Heterozygous mice exhibit small spleen, impaired lymphocyte response to osmotic stress, decreased response to glucocorticoid, osteoporosis and impared osteogenesis.
- Transcript *Akap13*-202&203&204&209&210&211&213&214&216 may not be affected .And the effect on transcript-207&2018&215 is unknown.
- The *Akap13* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Akap13 A kinase (PRKA) anchor protein 13 [Mus musculus (house mouse)]

Gene ID: 75547, updated on 19-Mar-2019

Summary

Official Symbol	Akap13 provided by MGI
Official Full Name	A kinase (PRKA) anchor protein 13 provided by MGI
Primary source	MGI:MGI:2676556
See related	Ensembl:ENSMUSG00000066406
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	1700026G02Rik, 5730522G15Rik, 5830460E08Rik, AKAP-13, AKAP-Lbc, BRX, Ht31, LBC, PROTO-LB, PROTO-LBC
Expression	Ubiquitous expression in spleen adult (RPKM 15.7), lung adult (RPKM 14.2) and 28 other tissues See more
Orthologs	human all

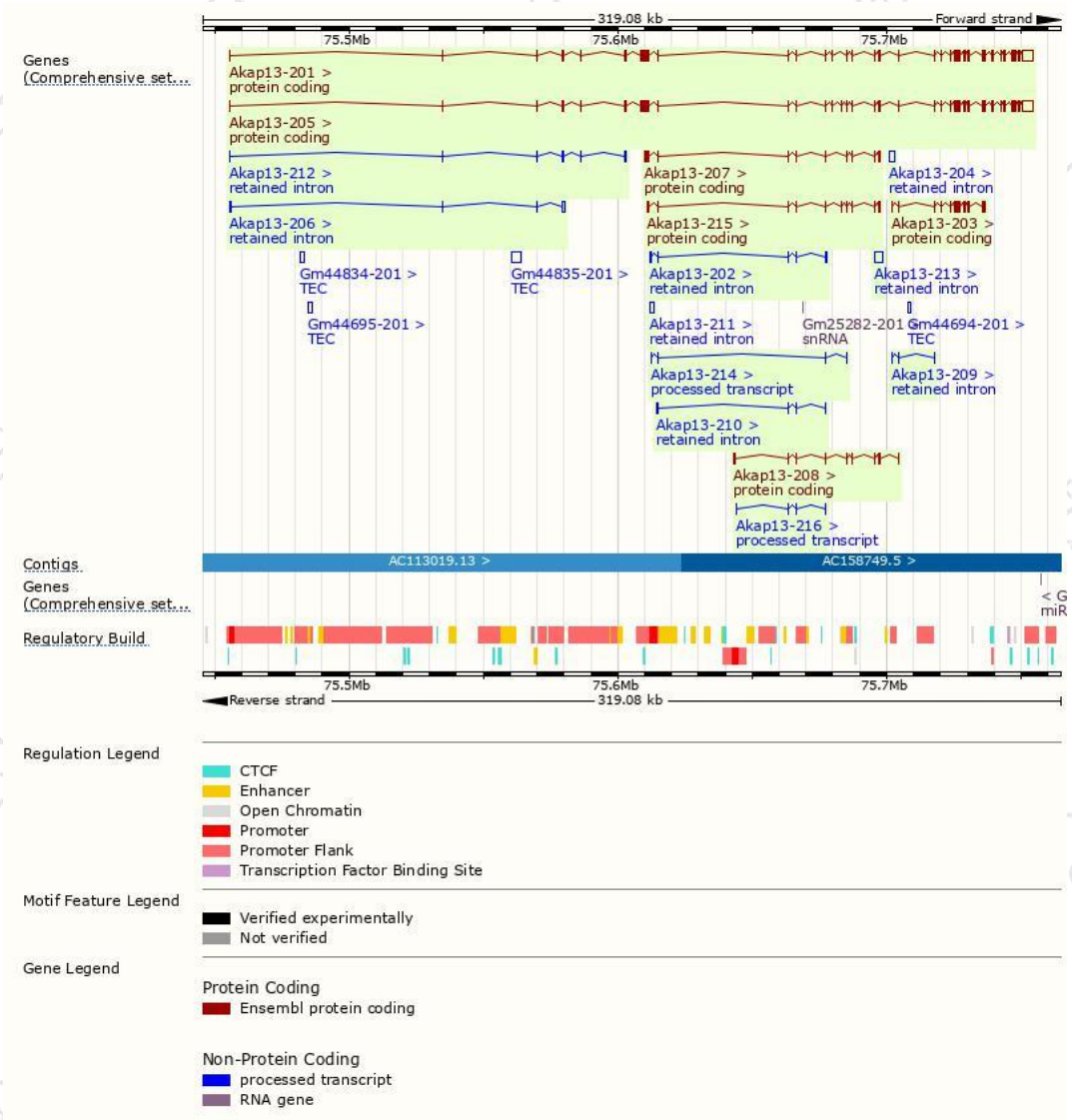
Transcript information（Ensembl）

The gene has 16 transcripts,all transcripts are shown below:

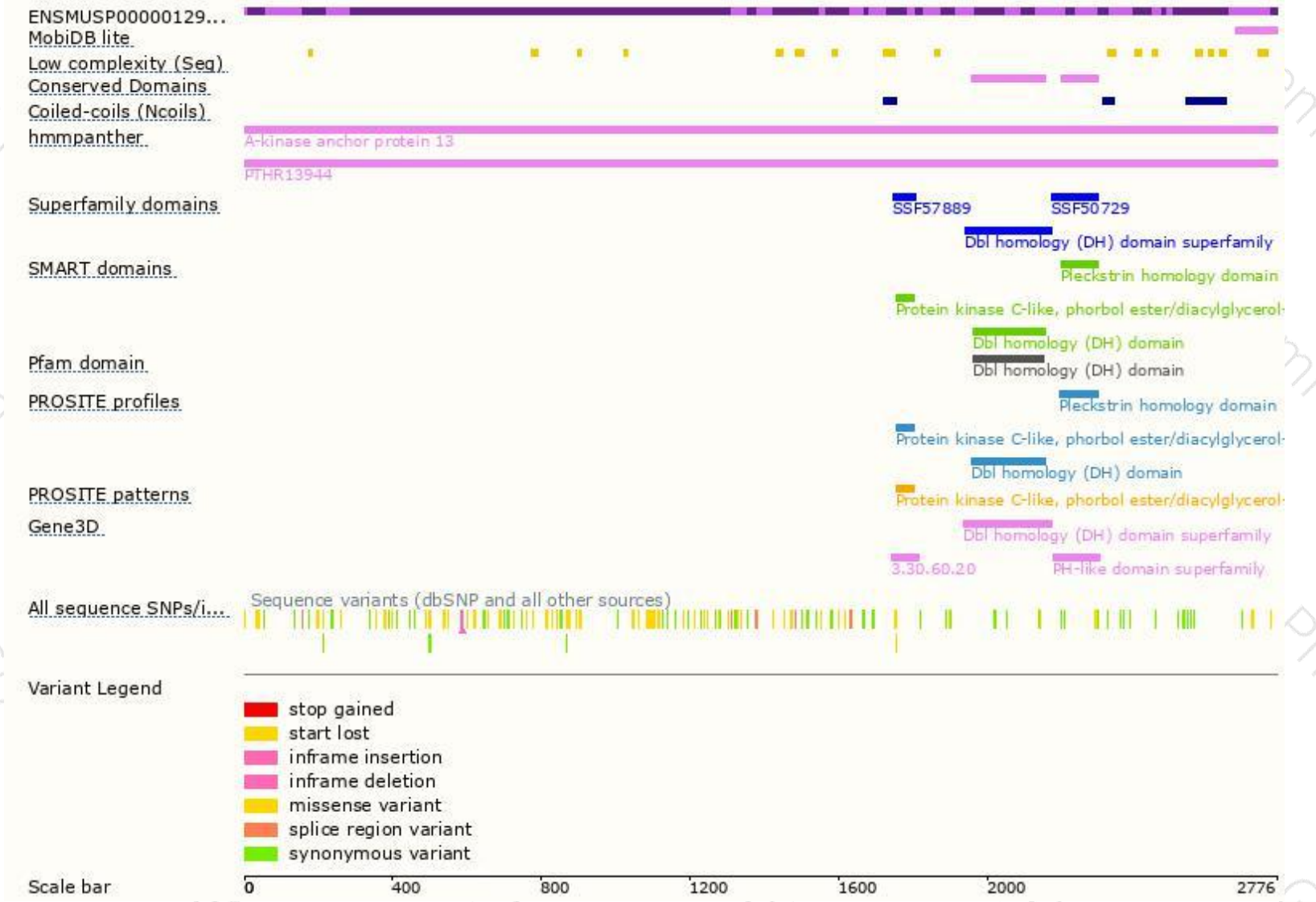
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Akap13-201	ENSMUST00000166315.6	12543	2776aa	Protein coding	CCDS52276	E9Q394	TSL:5 GENCODE basic APPRIS P2
Akap13-205	ENSMUST00000207750.1	12597	2794aa	Protein coding	-	A0A140LJJ5	TSL:5 GENCODE basic APPRIS ALT2
Akap13-207	ENSMUST00000207923.1	2612	870aa	Protein coding	-	A0A140LIX0	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:1
Akap13-203	ENSMUST00000207239.1	1908	607aa	Protein coding	-	A0A140LHG3	CDS 3' incomplete TSL:1
Akap13-215	ENSMUST00000208708.1	1705	569aa	Protein coding	-	A0A140LID7	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Akap13-208	ENSMUST00000207998.1	1269	423aa	Protein coding	-	A0A140LHQ3	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:1
Akap13-214	ENSMUST00000208456.1	716	No protein	Processed transcript	-	-	TSL:1
Akap13-216	ENSMUST00000209040.1	470	No protein	Processed transcript	-	-	TSL:2
Akap13-213	ENSMUST00000208248.1	3133	No protein	Retained intron	-	-	TSL:NA
Akap13-204	ENSMUST00000207511.1	2061	No protein	Retained intron	-	-	TSL:NA
Akap13-211	ENSMUST00000208182.1	1455	No protein	Retained intron	-	-	TSL:NA
Akap13-202	ENSMUST00000207079.1	1406	No protein	Retained intron	-	-	TSL:1
Akap13-212	ENSMUST00000208187.1	1381	No protein	Retained intron	-	-	TSL:2
Akap13-206	ENSMUST00000207751.1	1295	No protein	Retained intron	-	-	TSL:1
Akap13-210	ENSMUST00000208053.1	615	No protein	Retained intron	-	-	TSL:3
Akap13-209	ENSMUST00000208009.1	601	No protein	Retained intron	-	-	TSL:1

The strategy is based on the design of *Akap13-201* transcript,The transcription is shown below

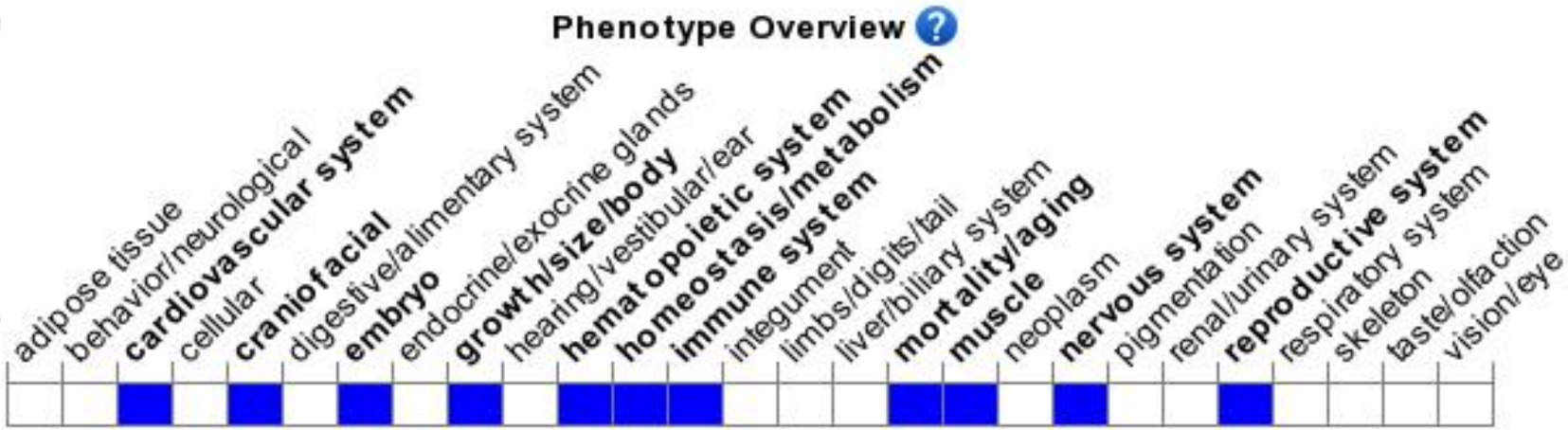
Genomic location distribution



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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