Matk Cas9-CKO Strategy

Designer: Huan Fan
Reviewer: Huan Wang

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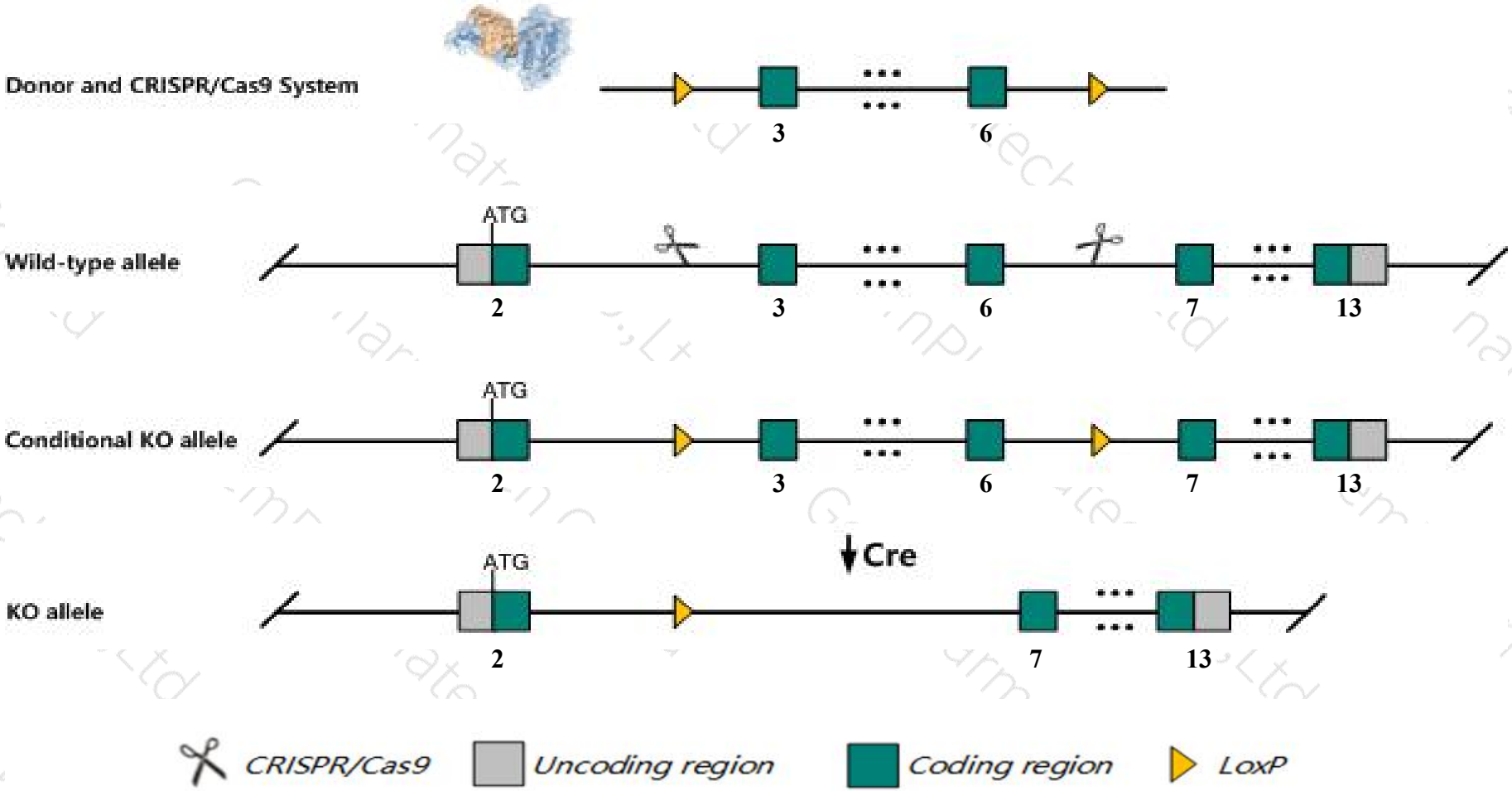
Project Overview

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

Conditional Knockout strategy

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



Technical routes

- The *Matk* gene has 11 transcripts. According to the structure of *Matk* gene, exon3-exon6 of *Matk-201* (ENSMUST00000105328.9) transcript is recommended as the knockout region.The region contains 541bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Matk* 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,Homozygous mice are viable and fertile and appear normal. Unchallenged mutant mice exhibit no hematopoietic defects. SPKLS cell numbers are elevated. IL-7 induced BM cell proliferation and pre-B cell colony formation are enhanced. Antigen induced IFN-gamma secretion is reduced.

- The *Matk* gene is located on the Chr10. 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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Matk megakaryocyte-associated tyrosine kinase [Mus musculus (house mouse)]

Gene ID: 17179, updated on 24-Feb-2019

Summary

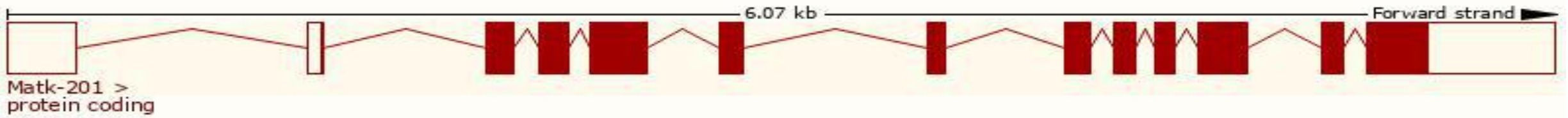
Official Symbol	Matk provided by MGI
Official Full Name	megakaryocyte-associated tyrosine kinase provided by MGI
Primary source	MGI:MGI:99259
See related	Ensembl:ENSMUSG00000004933
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	CHK, HYL, Ntk, p56ntk
Expression	Biased expression in cortex adult (RPKM 63.6), frontal lobe adult (RPKM 48.8) and 6 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

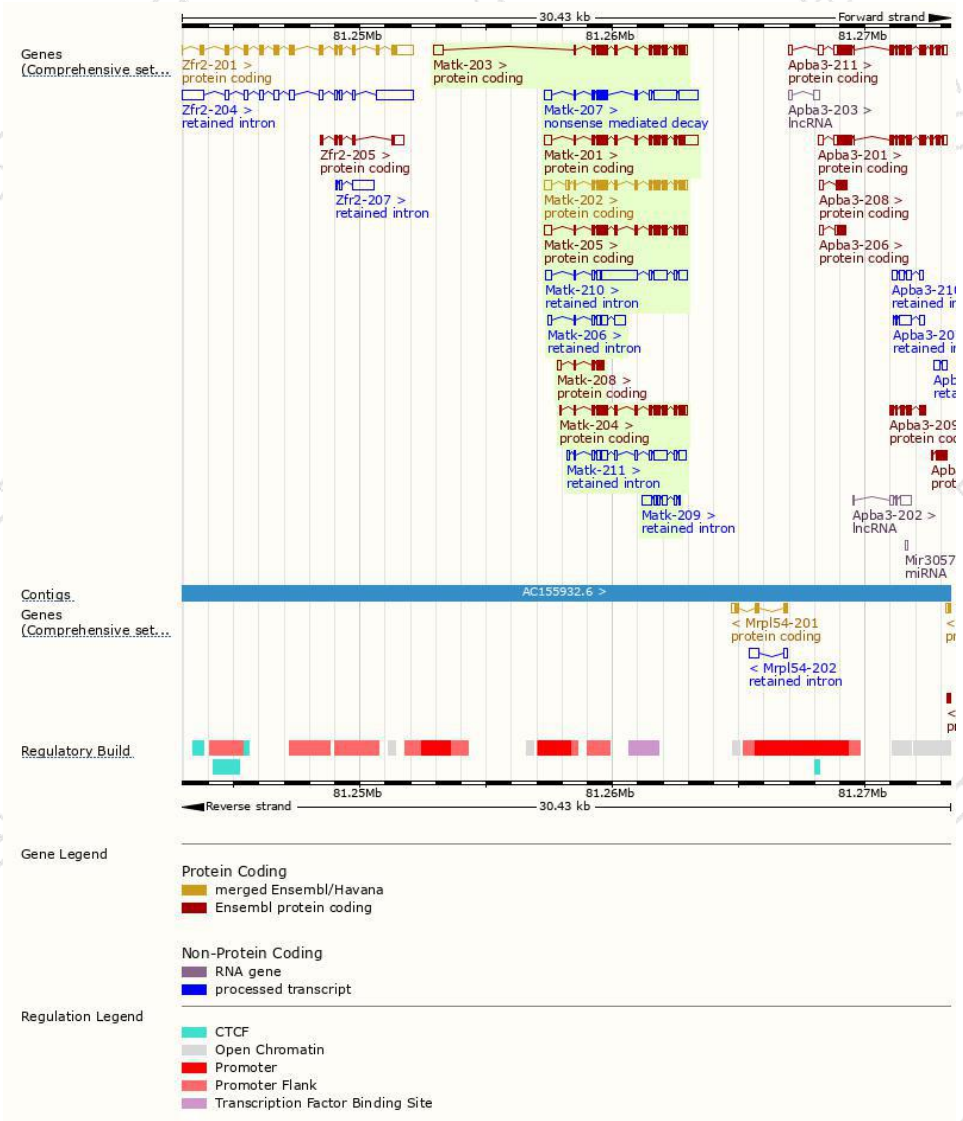
The gene has 11 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Matk-201	ENSMUST00000105328.9	2228	465aa	Protein coding	CCDS70078	A0A0R4J1P8	TSL:1 GENCODE basic APPRIS ALT1
Matk-202	ENSMUST00000117488.7	1980	505aa	Protein coding	CCDS24048	A0A0R4J1N6	TSL:1 GENCODE basic
Matk-203	ENSMUST00000119547.7	1916	465aa	Protein coding	CCDS70078	A0A0R4J1P8	TSL:1 GENCODE basic APPRIS ALT1
Matk-205	ENSMUST00000121205.7	1841	466aa	Protein coding	CCDS70077	D3Z4T5	TSL:1 GENCODE basic APPRIS P4
Matk-204	ENSMUST00000120265.1	1618	466aa	Protein coding	CCDS70077	D3Z4T5	TSL:5 GENCODE basic APPRIS P4
Matk-208	ENSMUST00000130282.7	495	101aa	Protein coding	-	D3YVQ8	CDS 3' incomplete TSL:3
Matk-207	ENSMUST00000128576.7	2599	162aa	Nonsense mediated decay	-	D6RGA0	TSL:1
Matk-210	ENSMUST00000150605.7	2983	No protein	Retained intron	-	-	TSL:1
Matk-211	ENSMUST00000151660.7	1761	No protein	Retained intron	-	-	TSL:1
Matk-206	ENSMUST00000126720.7	1075	No protein	Retained intron	-	-	TSL:1
Matk-209	ENSMUST00000148735.1	860	No protein	Retained intron	-	-	TSL:3

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

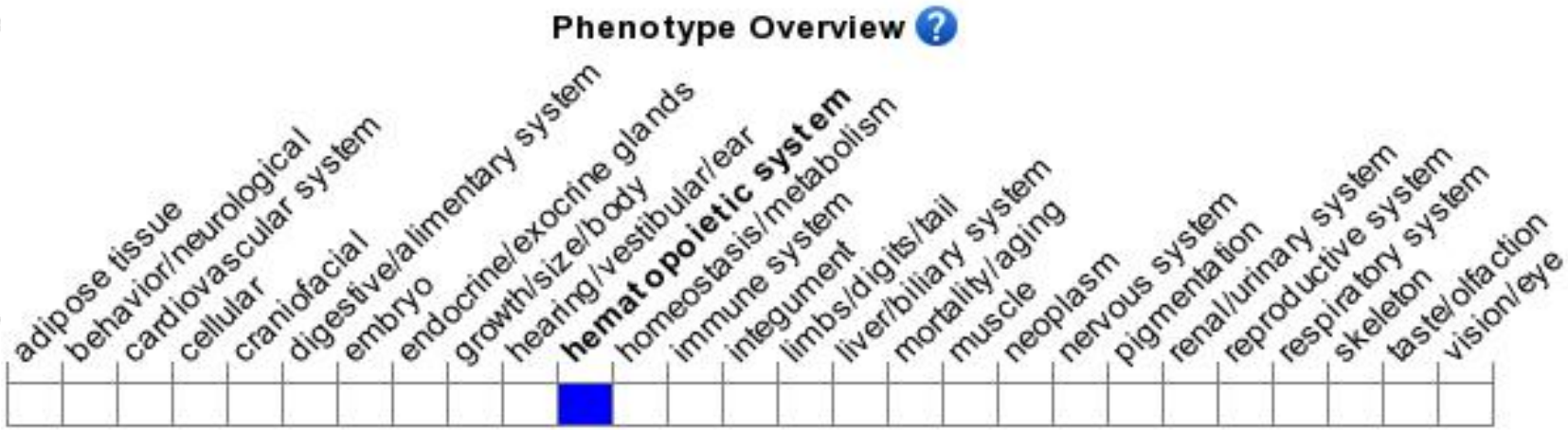


Genomic location distribution



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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GemPharmatech

If you have any questions, you are welcome to inquire.

Tel: 400-9660890

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GemPharmatech Co.,Ltd