

# ***Mknk2*** Cas9-CKO Strategy

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**Reviewer:**

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**Design Date:**

**2019-11-1**

# Project Overview

**Project Name**

***Mknk2***

**Project type**

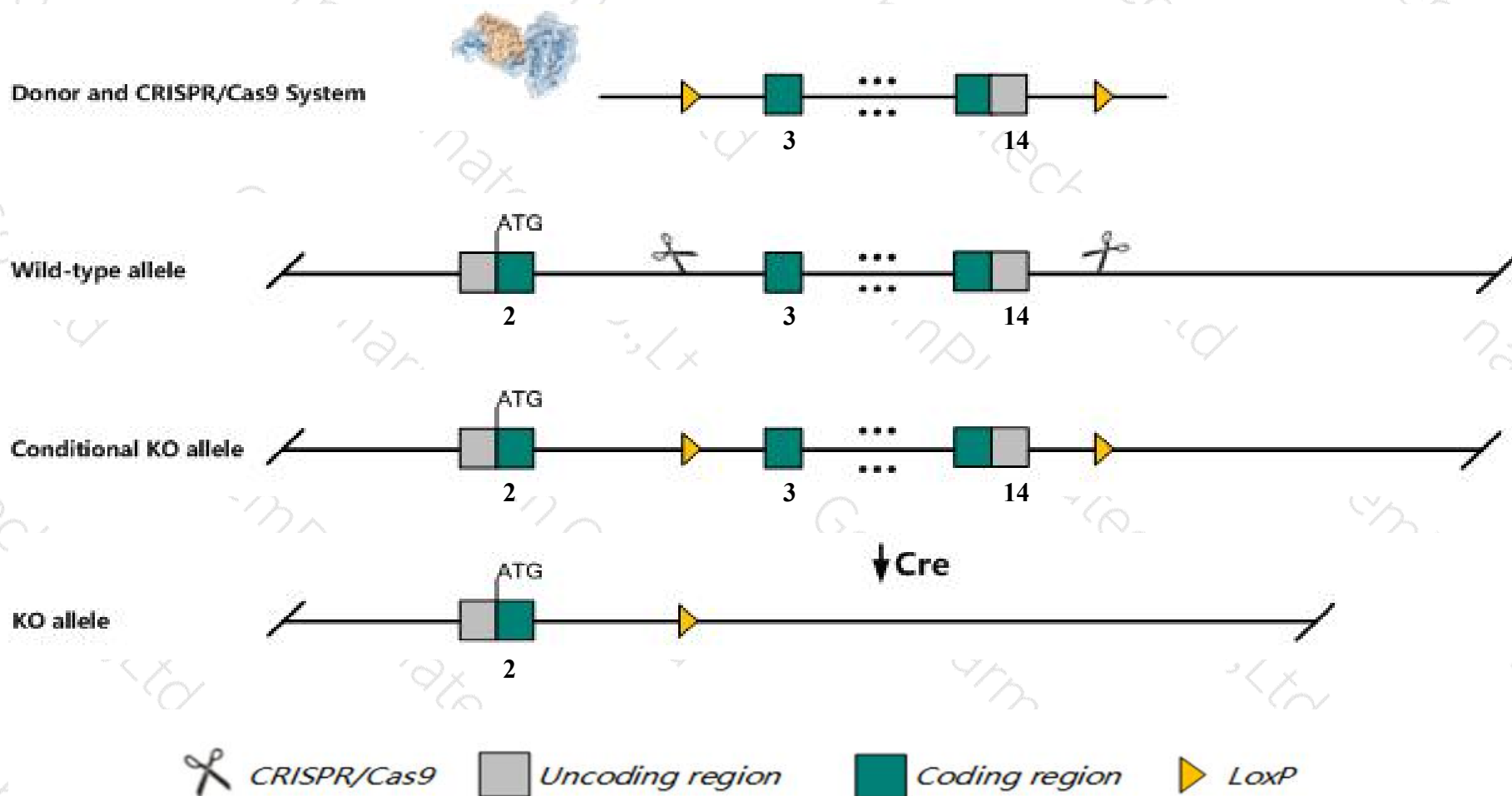
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Mknk2* gene. The schematic diagram is as follows:



- The *Mknk2* gene has 5 transcripts. According to the structure of *Mknk2* gene, exon3-exon14 of *Mknk2*-205 (ENSMUST00000200082.4) transcript is recommended as the knockout region. The region contains most of the coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Mknk2* 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.

- According to the existing MGI data, Homozygous null mice are viable and fertile with no gross abnormalities.
- The *Mknk2* 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)

## Mknk2 MAP kinase-interacting serine/threonine kinase 2 [ *Mus musculus* (house mouse) ]

Gene ID: 17347, updated on 12-Aug-2019

### Summary

<b>Official Symbol</b>	Mknk2 provided by MGI
<b>Official Full Name</b>	MAP kinase-interacting serine/threonine kinase 2 provided by MGI
<b>Primary source</b>	MGI:MGI:894279
<b>See related</b>	Ensembl:ENSMUSG00000020190
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	REVIEWED
<b>Organism</b>	<i>Mus musculus</i>
<b>Lineage</b>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
<b>Also known as</b>	Mnk2; Gprk7; 2010016G11Rik
<b>Summary</b>	The protein encoded by this gene is a serine/threonine-protein kinase, which is targeted by both the extracellular signal-regulated kinase and p38 mitogen-activated protein kinase pathways. This enzyme targets several substrates including eukaryotic translation initiation factor 4E and mammalian target of rapamycin, which are negatively regulated by its phosphorylation. Null mutant mice do not exhibit developmental or reproductive defects. However, mice null for both this protein and mitogen-activated protein kinase-interacting serine/threonine protein kinase 1 have delayed tumor development in phosphatase and tensin homolog mutant mice, indicating an oncogenic function for this gene in tumor development. [provided by RefSeq, Oct 2014]
<b>Expression</b>	Broad expression in mammary gland adult (RPKM 326.2), subcutaneous fat pad adult (RPKM 252.6) and 25 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>



# Transcript information (Ensembl)

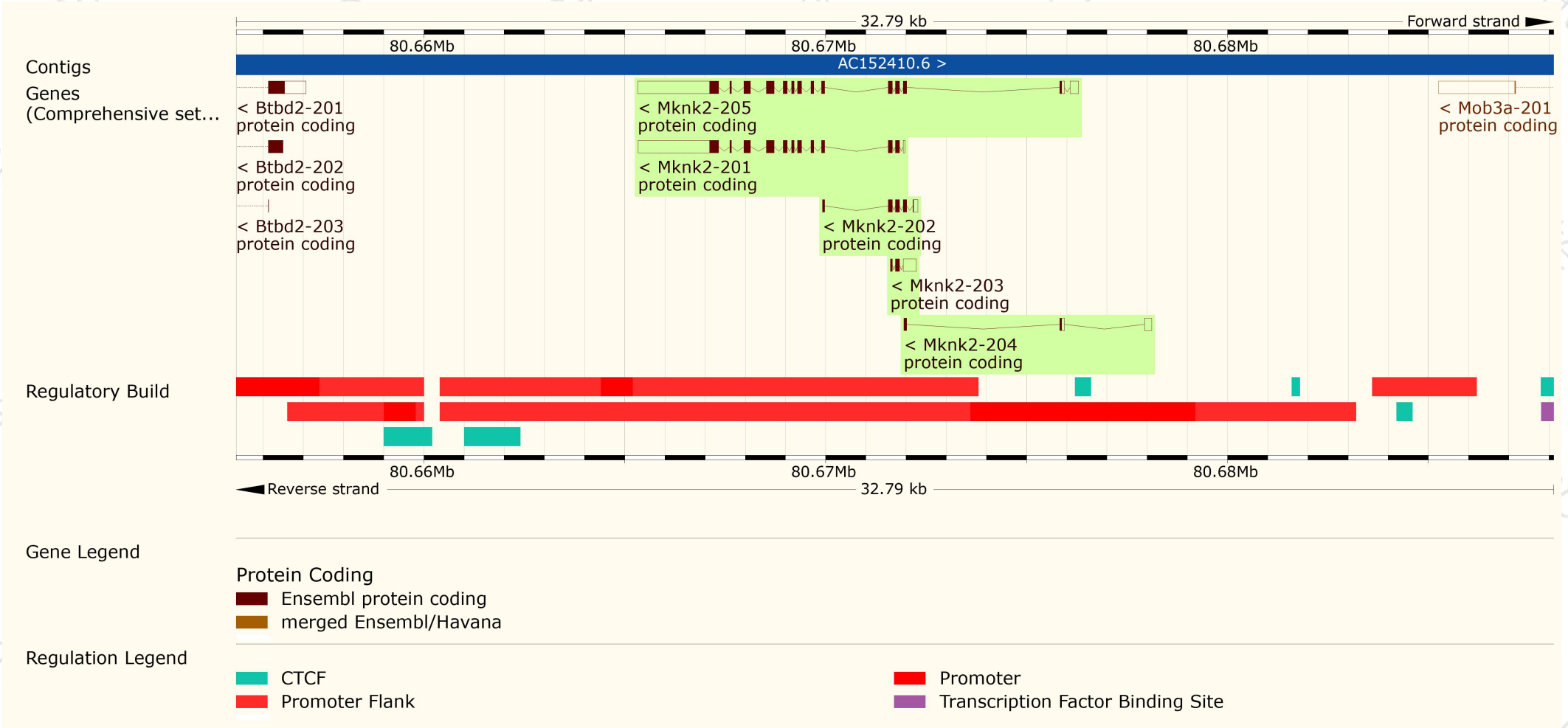
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Translation ID	Biotype	CCDS	UniProt	Flags
Mknk2-205	<a href="#">ENSMUST00000200082.4</a>	3439	<a href="#">459aa</a>	<a href="#">ENSMUSP00000143508.1</a>	Protein coding	<a href="#">CCDS24030</a>	<a href="#">Q8CDB0</a>	TSL:1 GENCODE basic APPRIS P2
Mknk2-201	<a href="#">ENSMUST00000003433.10</a>	3065	<a href="#">412aa</a>	<a href="#">ENSMUSP00000003433.6</a>	Protein coding	-	<a href="#">A0A0R4IZX7</a>	TSL:1 GENCODE basic APPRIS ALT2
Mknk2-203	<a href="#">ENSMUST00000198819.1</a>	473	<a href="#">49aa</a>	<a href="#">ENSMUSP00000142388.1</a>	Protein coding	-	<a href="#">A0A0G2JDJ0</a>	CDS 3' incomplete TSL:5
Mknk2-202	<a href="#">ENSMUST00000197276.1</a>	463	<a href="#">118aa</a>	<a href="#">ENSMUSP00000143679.1</a>	Protein coding	-	<a href="#">A0A0G2JGS6</a>	CDS 3' incomplete TSL:3
Mknk2-204	<a href="#">ENSMUST00000199949.1</a>	364	<a href="#">40aa</a>	<a href="#">ENSMUSP00000143655.1</a>	Protein coding	-	<a href="#">A0A0G2JGQ2</a>	CDS 3' incomplete TSL:3

The strategy is based on the design of *Mknk2-205* transcript,The transcription is shown below

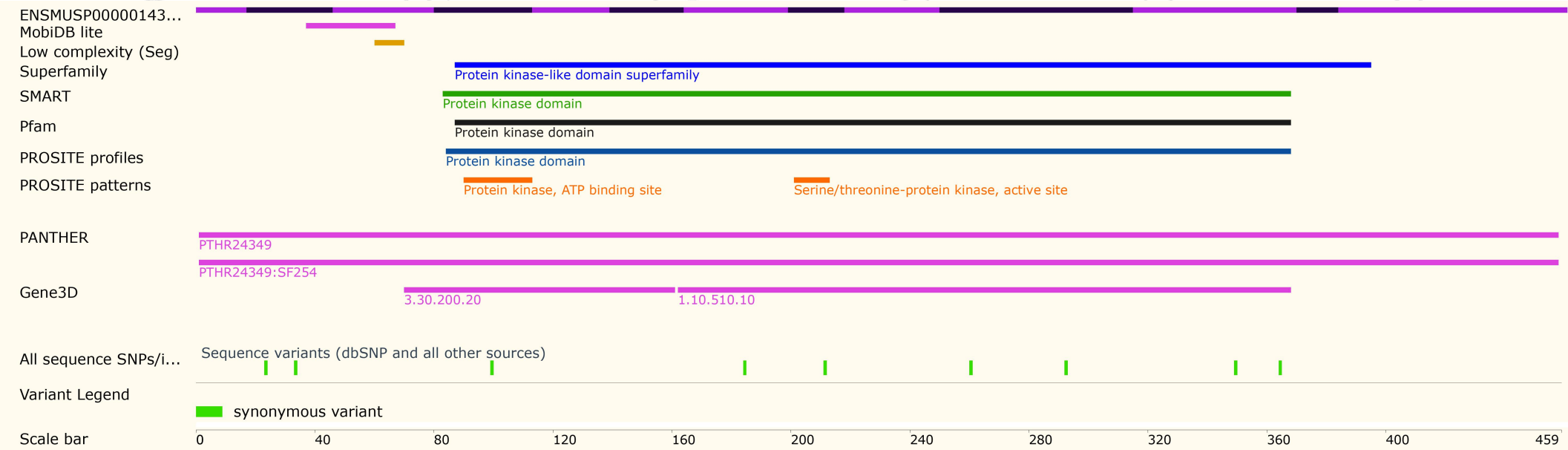


# Genomic location distribution





# Protein domain



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

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