

# *Map3k20* Cas9-KO Strategy

<b>Designer:</b>	<b>Huan Wang</b>
<b>Reviewer:</b>	<b>Huan Fan</b>
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# Project Overview

**Project Name**

*Map3k20*

**Project type**

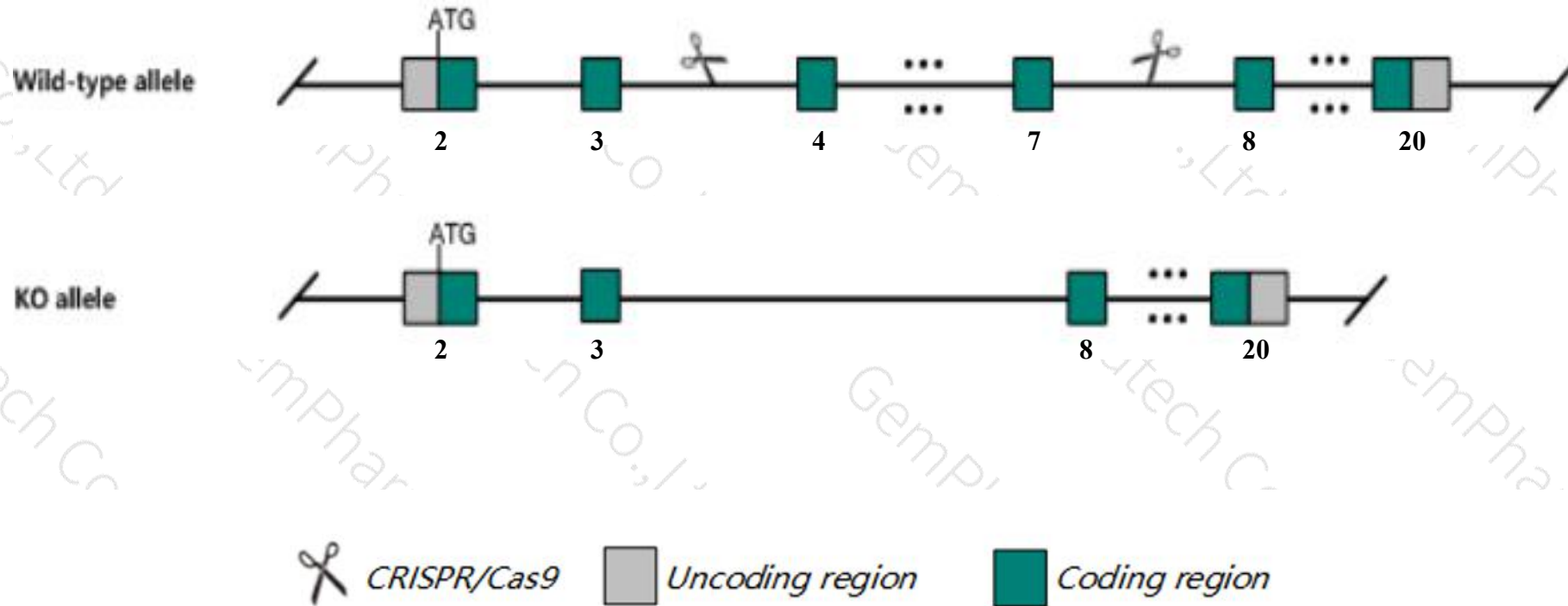
**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Map3k20* gene. The schematic diagram is as follows:



- The *Map3k20* gene has 6 transcripts. According to the structure of *Map3k20* gene, exon4-exon7 of *Map3k20-201* (ENSMUST00000090824.11) transcript is recommended as the knockout region. The region contains 335bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Map3k20* gene. The brief process is as follows: CRISPR/Cas9 syst

- According to the existing MGI data, mice homozygous for a knock-out allele exhibit complete lethality at e9.5 with growth retardation. mice homozygous for an allele lacking the sam domain exhibit low penetrant unilateral complex hindlimb duplication phenotype.
- The *Map3k20* gene is located on the Chr2. 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)

## Map3k20 mitogen-activated protein kinase kinase kinase 20 [Mus musculus (house mouse)]

Gene ID: 65964, updated on 20-Mar-2020

### Summary



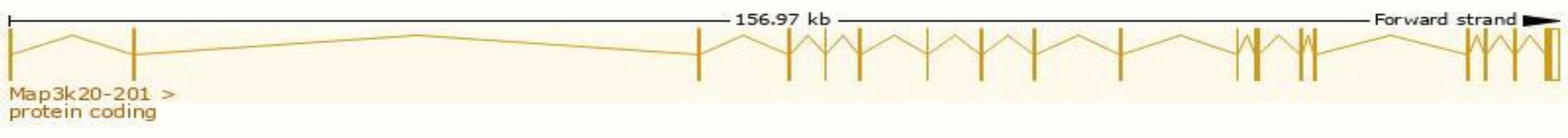
<b>Official Symbol</b>	Map3k20 provided by <a href="#">MGI</a>
<b>Official Full Name</b>	mitogen-activated protein kinase kinase kinase 20 provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:2443258</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG00000004085</a>
<b>Gene type</b>	protein coding
<b>RefSeq status</b>	VALIDATED
<b>Organism</b>	<a href="#">Mus musculus</a>
<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>	AV006891, B230120H23Rik, HCCS-4, MLTK, MLTKalpha, MLTKbeta, Zak
<b>Expression</b>	Broad expression in heart adult (RPKM 20.9), bladder adult (RPKM 15.7) and 20 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information（Ensembl）

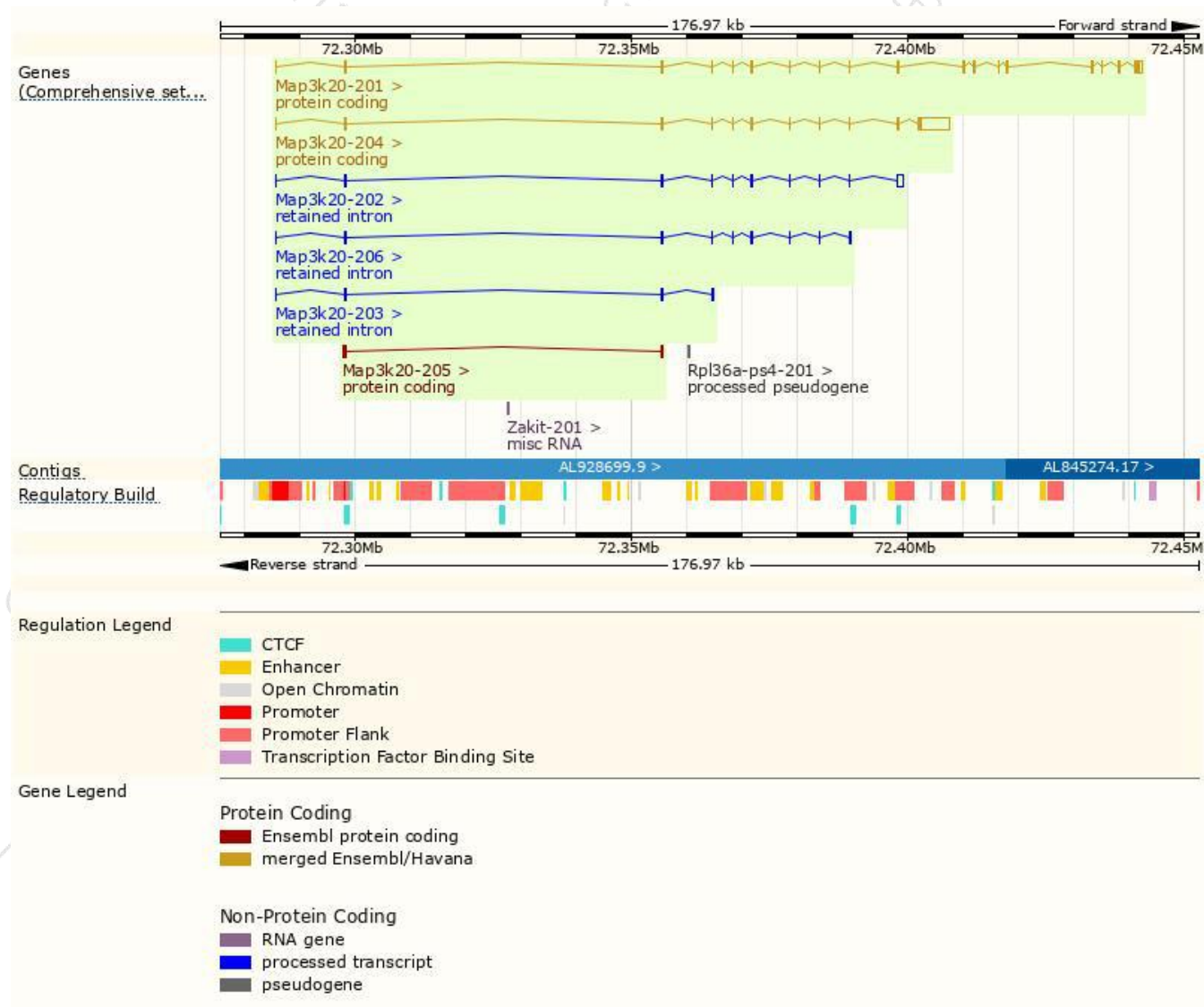
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Map3k20-204	<a href="#">ENSMUST00000135469.7</a>	6663	<a href="#">454aa</a>	Protein coding	<a href="#">CCDS50605</a>	<a href="#">Q3TRG2_Q9ESL4</a>	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT2
Map3k20-201	<a href="#">ENSMUST00000090824.11</a>	3334	<a href="#">802aa</a>	Protein coding	<a href="#">CCDS38143</a>	<a href="#">Q9ESL4</a>	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P3
Map3k20-205	<a href="#">ENSMUST00000144111.1</a>	396	<a href="#">74aa</a>	Protein coding	-	<a href="#">A2ASW6</a>	CDS 3' incomplete TSL:5
Map3k20-202	<a href="#">ENSMUST00000112073.8</a>	1925	No protein	Retained intron	-	-	TSL:2
Map3k20-206	<a href="#">ENSMUST00000150126.7</a>	1227	No protein	Retained intron	-	-	TSL:1
Map3k20-203	<a href="#">ENSMUST00000135204.1</a>	559	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Map3k20-201* transcript,the transcription is shown below

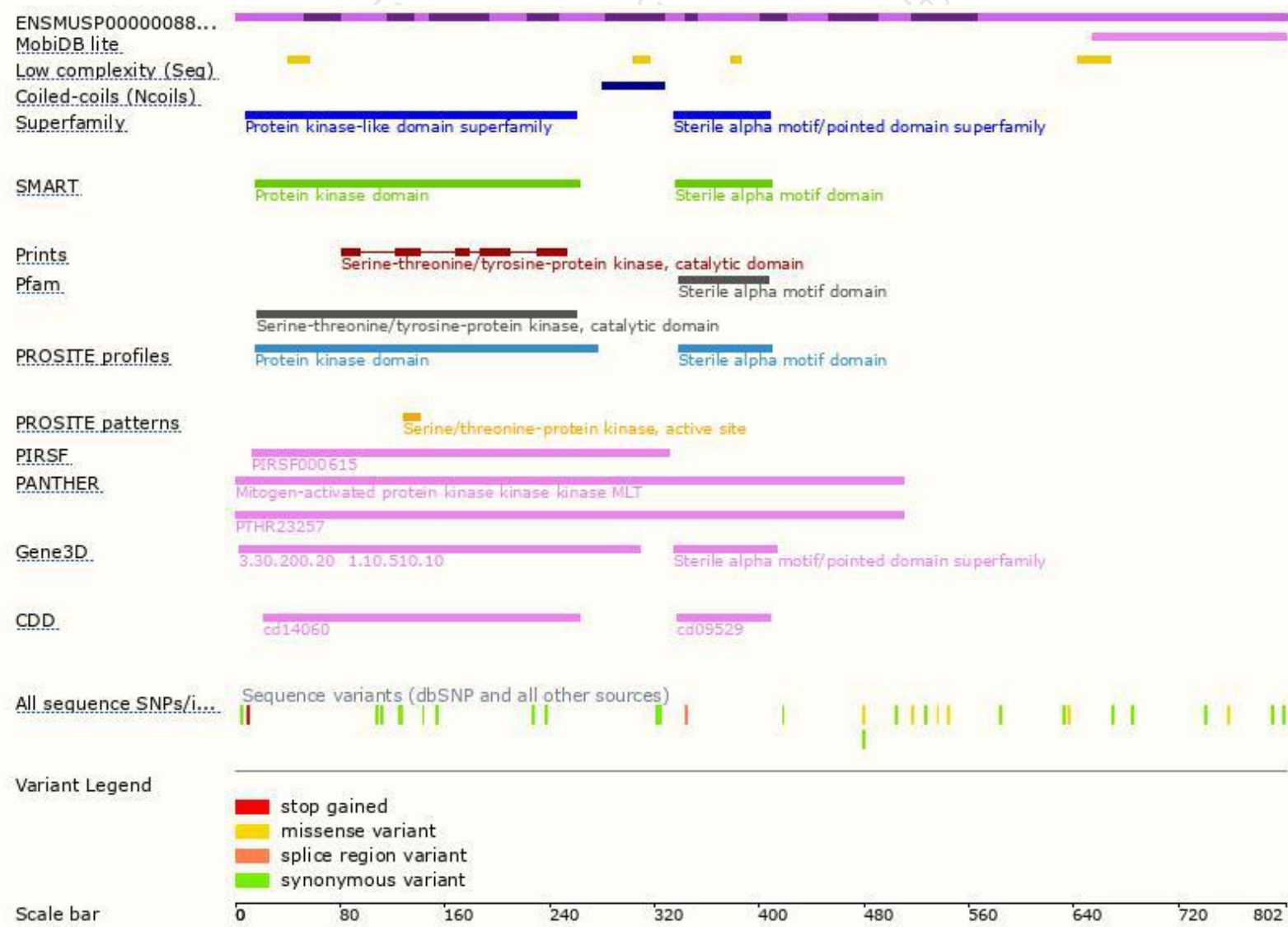


# Genomic location distribution

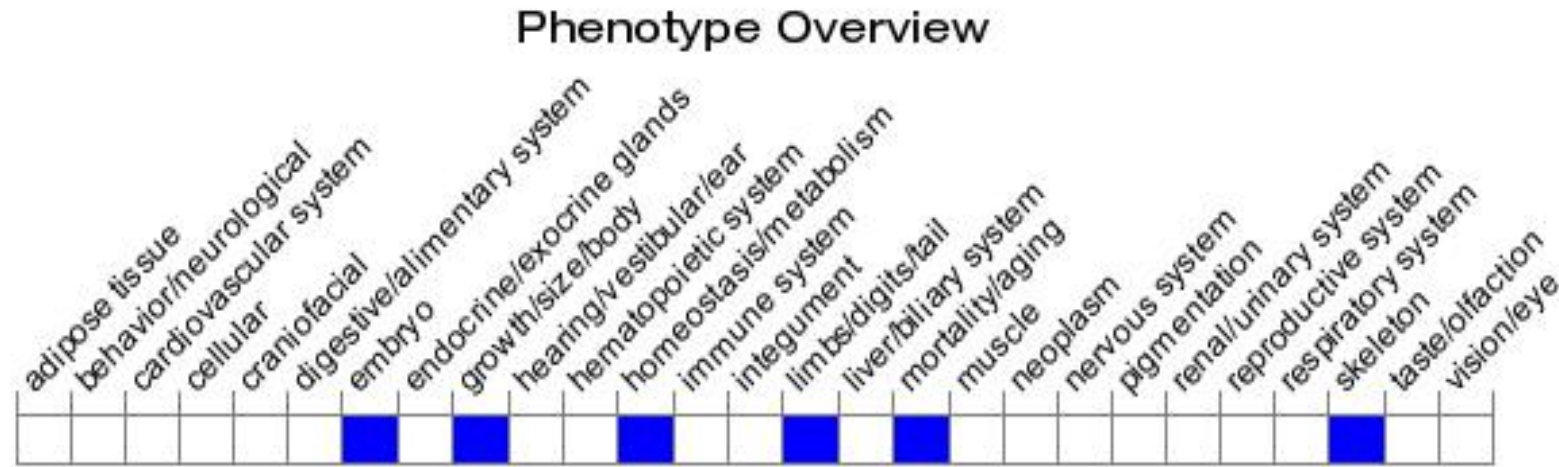




# Protein domain



# Mouse phenotype description(MGI )



*Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).*

According to the existing MGI data, mice homozygous for a knock-out allele exhibit complete lethality at E9.5 with growth retardation. Mice homozygous for an allele lacking the SAM domain exhibit low penetrant unilateral complex hindlimb duplication phenotype.

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

Tel: 400-9660890

