

# ***Dek Cas9-CKO Strategy***

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**Reviewer:**

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# Project Overview

**Project Name**

*Dek*

**Project type**

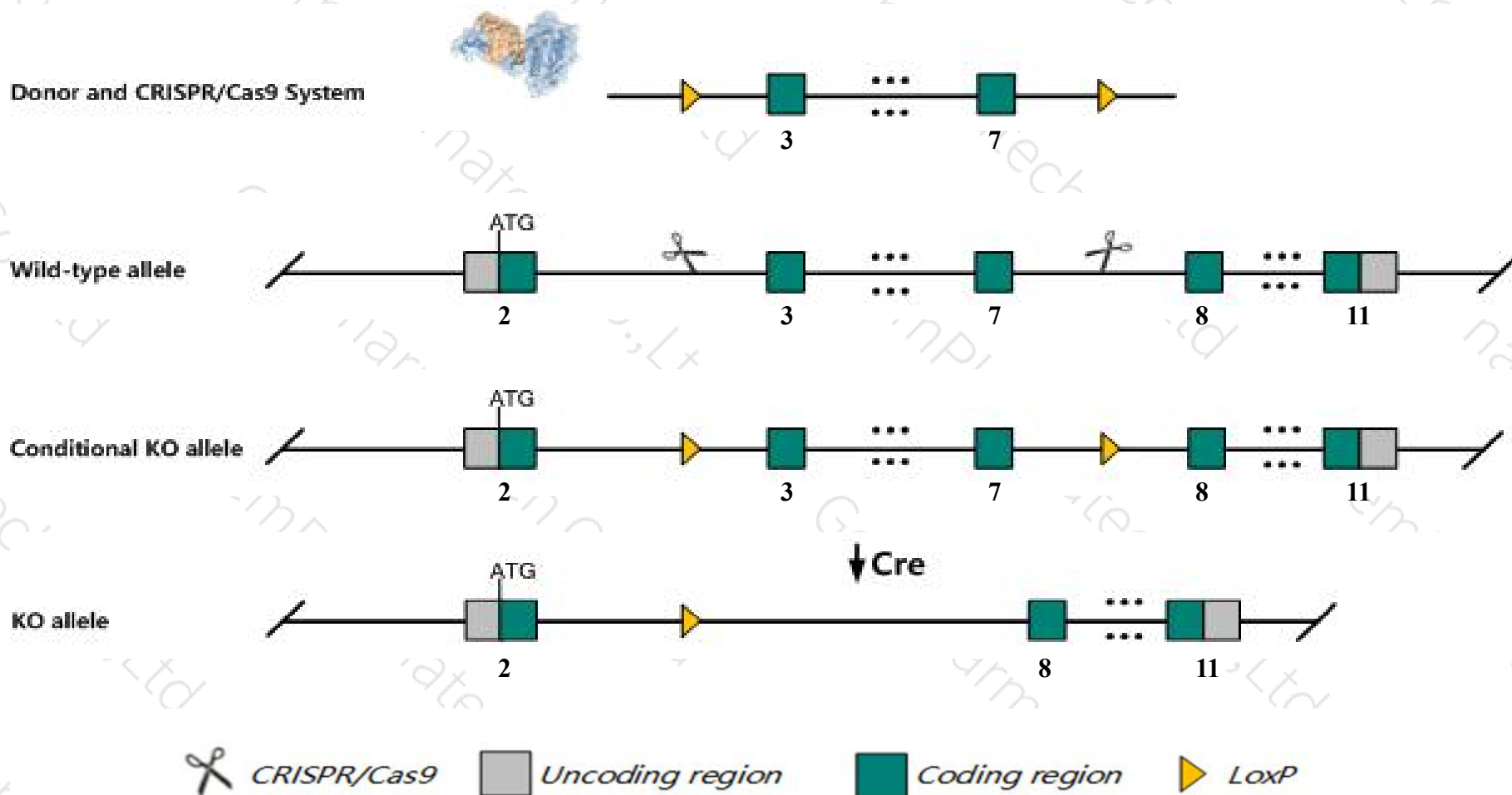
**Cas9-CKO**

**Strain background**

**C57BL/6JGpt**

# Conditional Knockout strategy

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



# Technical routes

- The *Dek* gene has 7 transcripts. According to the structure of *Dek* gene, exon3-exon7 of *Dek-201* (ENSMUST00000021807.12) transcript is recommended as the knockout region. The region contains 617bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Dek* 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, Mice homozygous for a null allele exhibit delayed development of DMBA- and TPA-induced papillomas.
- The *Dek* gene is located on the Chr13. 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)

## Dek DEK oncogene (DNA binding) [Mus musculus (house mouse)]

Gene ID: 110052, updated on 31-Jan-2019

### Summary



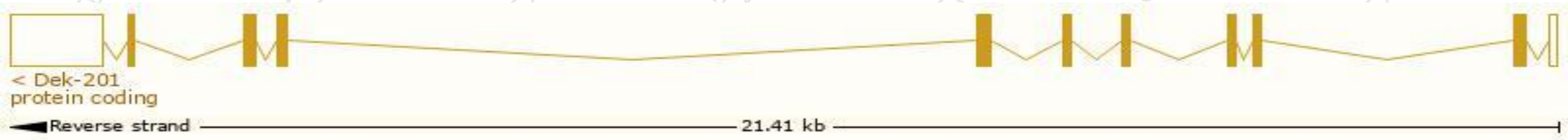
<b>Official Symbol</b>	Dek provided by <a href="#">MGI</a>
<b>Official Full Name</b>	DEK oncogene (DNA binding) provided by <a href="#">MGI</a>
<b>Primary source</b>	<a href="#">MGI:MGI:1926209</a>
<b>See related</b>	<a href="#">Ensembl:ENSMUSG000000021377</a>
<b>Gene type</b>	protein coding
<b>RefSeq 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>	1810019E15Rik, D13H6S231E
<b>Expression</b>	Biased expression in liver E14 (RPKM 94.0), liver E14.5 (RPKM 74.8) and 12 other tissues <a href="#">See more</a>
<b>Orthologs</b>	<a href="#">human</a> <a href="#">all</a>

# Transcript information (Ensembl)

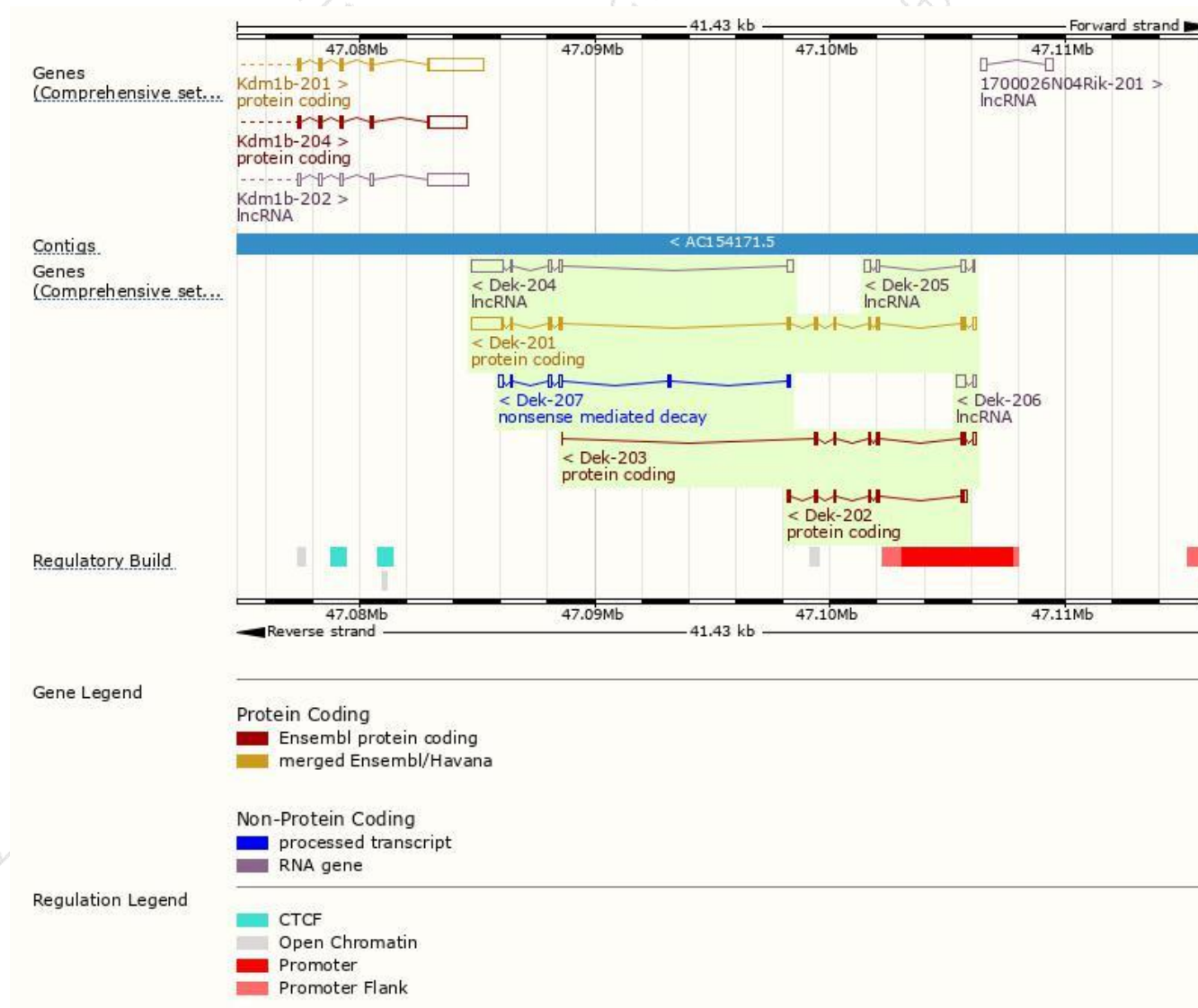
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dek-201	<a href="#">ENSMUST00000021807.12</a>	2556	<a href="#">380aa</a>	Protein coding	<a href="#">CCDS26490</a>	<a href="#">Q7TNV0</a>	TSL:1 GENCODE basic APPRIS P1
Dek-202	<a href="#">ENSMUST00000129352.2</a>	876	<a href="#">258aa</a>	Protein coding	-	<a href="#">D3YVJ6</a>	CDS 3' incomplete TSL:2
Dek-203	<a href="#">ENSMUST00000135278.7</a>	744	<a href="#">202aa</a>	Protein coding	-	<a href="#">E9Q8Y1</a>	CDS 3' incomplete TSL:1
Dek-207	<a href="#">ENSMUST00000224150.1</a>	784	<a href="#">80aa</a>	Nonsense mediated decay	-	<a href="#">A0A286YDS8</a>	CDS 5' incomplete
Dek-204	<a href="#">ENSMUST00000138401.1</a>	1946	No protein	lncRNA	-	-	TSL:1
Dek-205	<a href="#">ENSMUST00000143933.1</a>	596	No protein	lncRNA	-	-	TSL:2
Dek-206	<a href="#">ENSMUST00000150652.1</a>	468	No protein	lncRNA	-	-	TSL:1

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

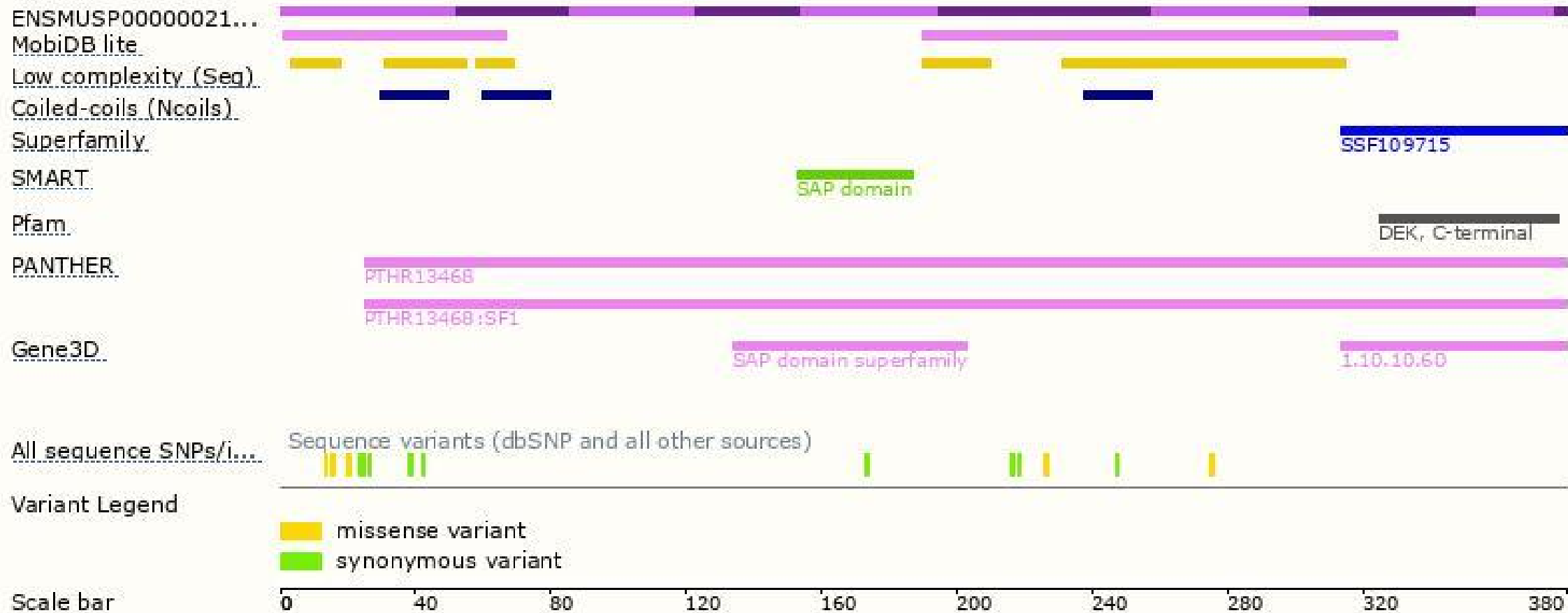


# Genomic location distribution





# 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 null allele exhibit delayed development of DMBA- and TPA-induced papillomas.

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

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