

Dek Cas9-KO Strategy

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Project Overview

Project Name

Dek

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- 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 w

- 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

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

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

Summary



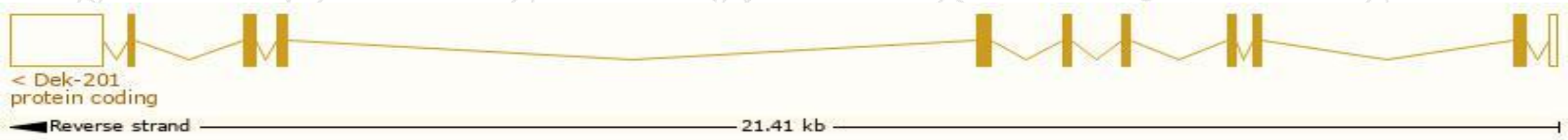
Official Symbol	Dek provided by MGI
Official Full Name	DEK oncogene (DNA binding) provided by MGI
Primary source	MGI:MGI:1926209
See related	Ensembl:ENSMUSG000000021377
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	1810019E15Rik, D13H6S231E
Expression	Biased expression in liver E14 (RPKM 94.0), liver E14.5 (RPKM 74.8) and 12 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

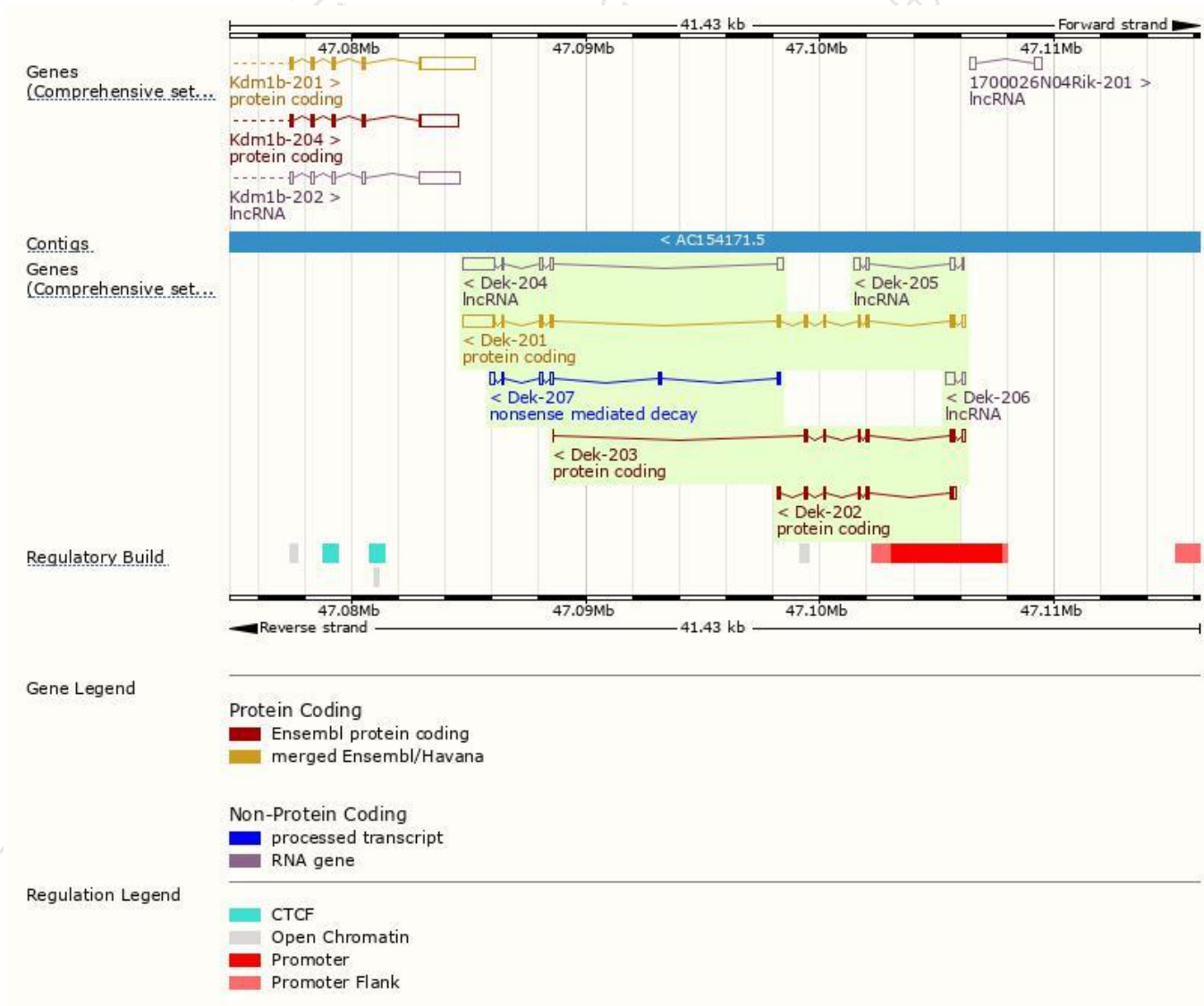
The gene has 7 transcripts,all transcripts are shown below:

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

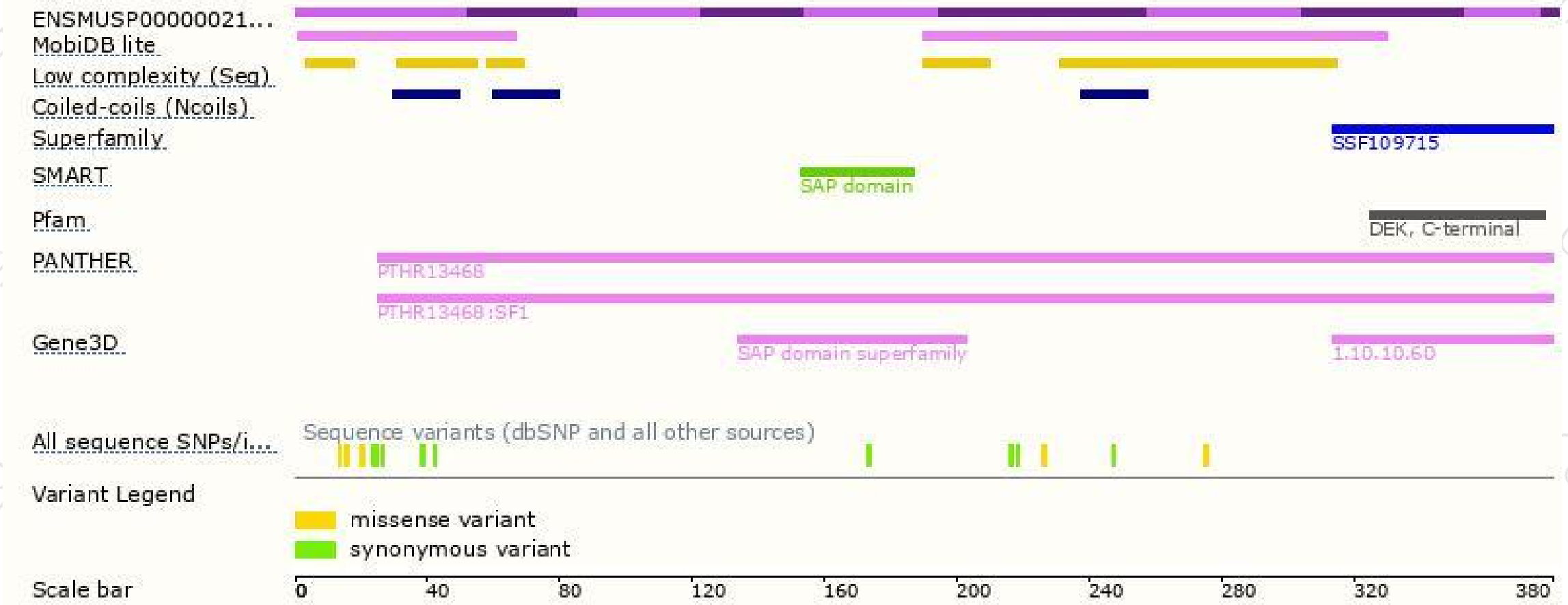
The strategy is based on the design of *Dek-201* transcript,The transcription is shown below



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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