Nek10 Cas9-KO Strategy

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Project Overview

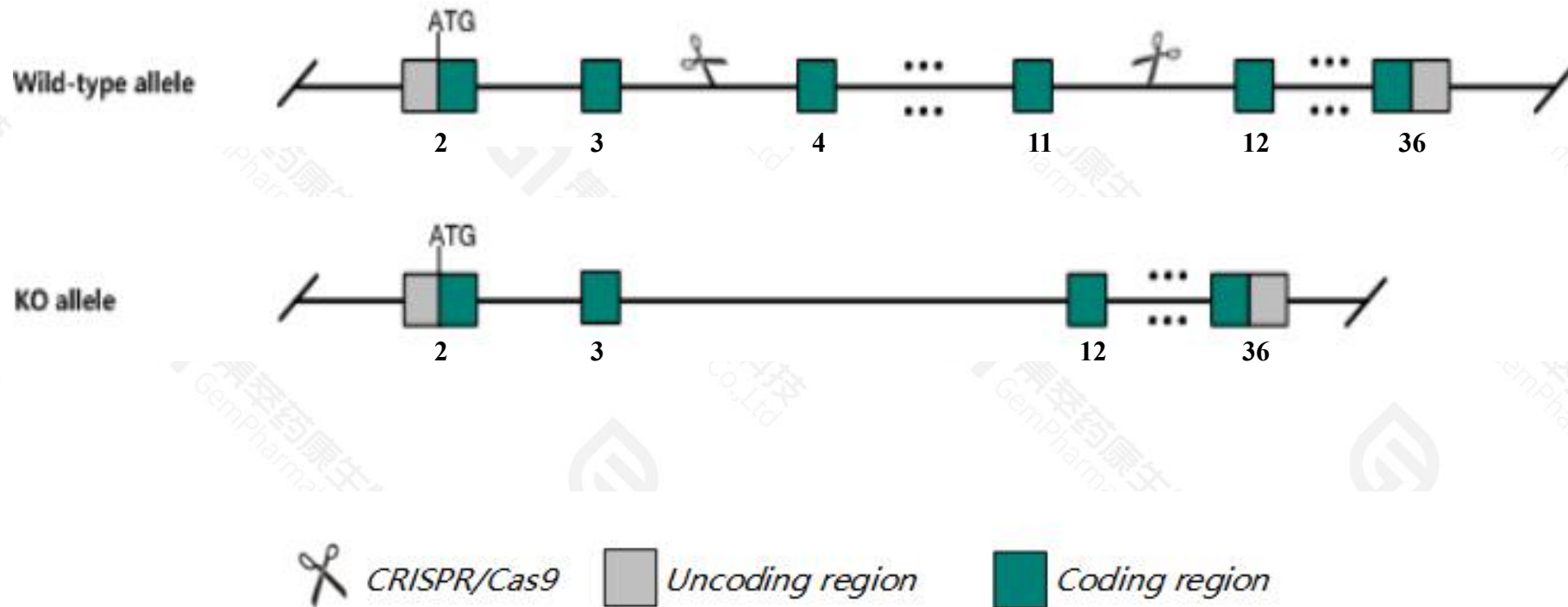|	
Project Name	*Nek10*
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

This model will use CRISPR/Cas9 technology to edit the *Nek10* gene. The schematic diagram is as follows:

➤ The *Nek10* gene has 6 transcripts. According to the structure of *Nek10* gene, exon4-exon11 of *Nek10-206*(ENSMUST00000224491.2) transcript is recommended as the knockout region.The region contains 671bp coding sequence. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Nek10* gene. The brief process is as follows: CRISPR/Cas9 system 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 *Nek10* gene is located on the Chr14. 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）

Nek10 NIMA (never in mitosis gene a)- related kinase 10 [Mus musculus (house mouse)]

Gene ID: 674895, updated on 17-Dec-2020

▲Summary

Official Symbol	Nek10 provided by MGI
Official Full Name	NIMA (never in mitosis gene a)- related kinase 10 provided by MGI
Primary source	MGI:MGI:2685128
See related	Ensembl:ENSMUSG00000042567
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	Gm282
Expression	Low expression observed in reference datasetSee more
Orthologs	human all

Transcript information（Ensembl）

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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Nek10-206	ENSMUST00000224491.2	9567	1115aa	Protein coding	CCDS56937		GENCODE basic , APPRIS P2 ,
Nek10-202	ENSMUST00000112630.9	3348	1115aa	Protein coding	CCDS56937		TSL:5 , GENCODE basic , APPRIS P2 ,
Nek10-203	ENSMUST00000112631.9	3386	1111aa	Protein coding	-		TSL:5 , GENCODE basic , APPRIS ALT2 ,
Nek10-205	ENSMUST00000136826.3	1446	279aa	Nonsense mediated decay	-		CDS 5' incomplete , TSL:5 ,
Nek10-201	ENSMUST00000063220.14	1566	No protein	Processed transcript	-		TSL:5 ,
Nek10-204	ENSMUST00000134866.2	3312	No protein	Retained intron	-		TSL:2 ,

The strategy is based on the design of *Nek10-206* transcript,the transcription is shown below:

< Nek10-206
protein coding
◀— Reverse strand
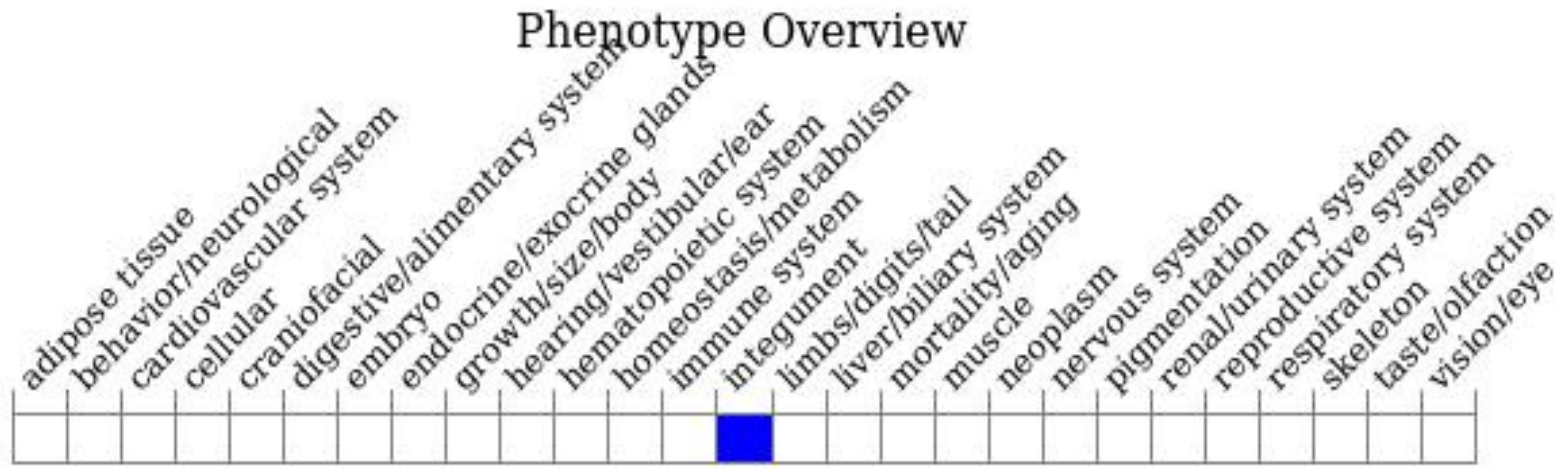|—————————————— 208.65 kb ——————————————|
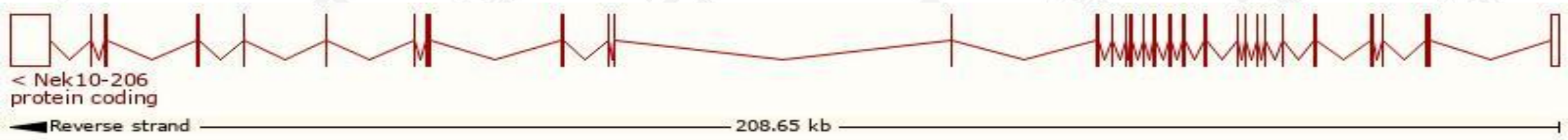
Genomic location distribution
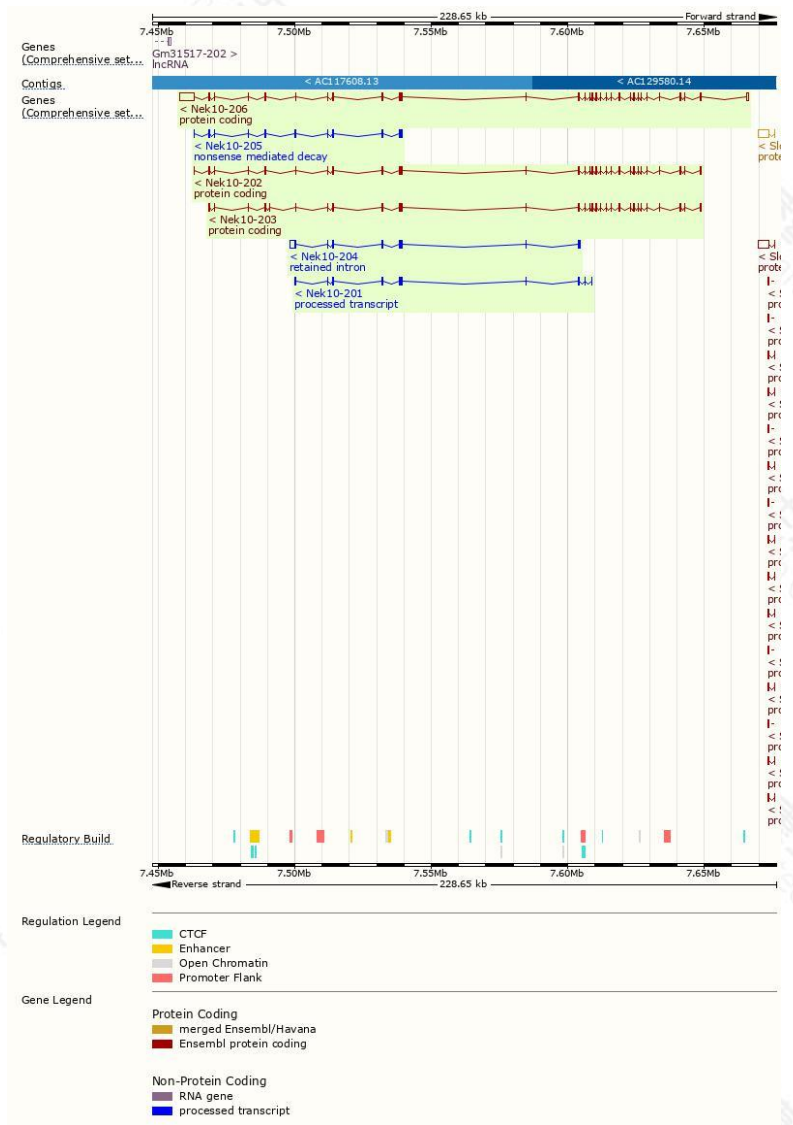
Protein domain
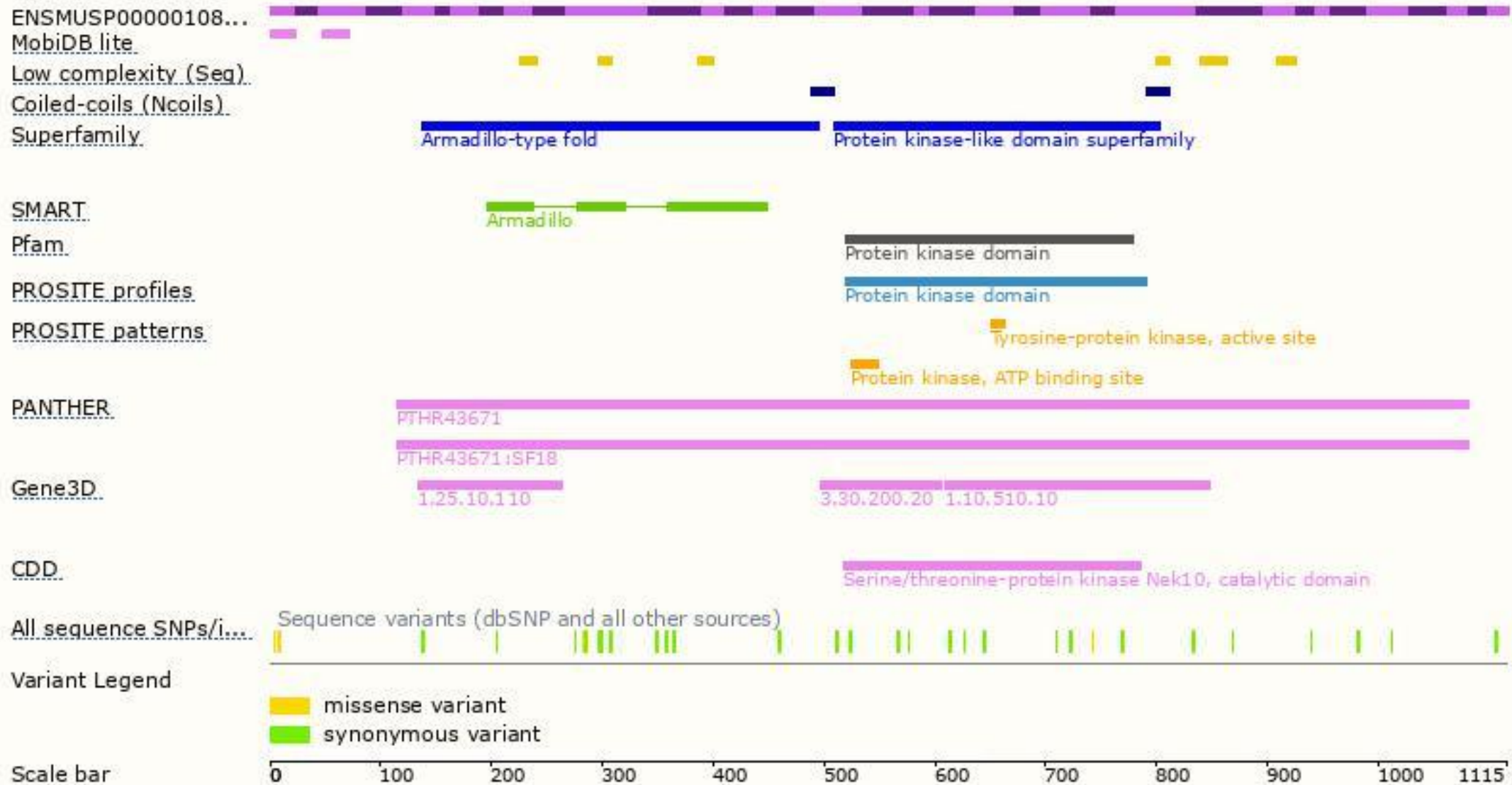
Mouse phenotype description(MGI)

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

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