

# *Keap1* Cas9-KO Strategy

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**Reviewer:**

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# Project Overview

**Project Name**

***Keap1***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Keap1* gene. The schematic diagram is as follows:



- The *Keap1* gene has 6 transcripts. According to the structure of *Keap1* gene, exon2 of *Keap1*-202 (ENSMUST00000164812.7) transcript is recommended as the knockout region. The region contains 686bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Keap1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous null mice exhibit scaly skin, hyperkeratosis of the esophagus and stomach mucosa, and die around 3 weeks of age, putatively due to malnutrition resulting from the abnormal alimentary epithelium.
- The *Keap1* gene is located on the Chr9. 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)

## Keap1 kelch-like ECH-associated protein 1 [Mus musculus (house mouse)]

Gene ID: 50868, updated on 9-Apr-2019

### Summary



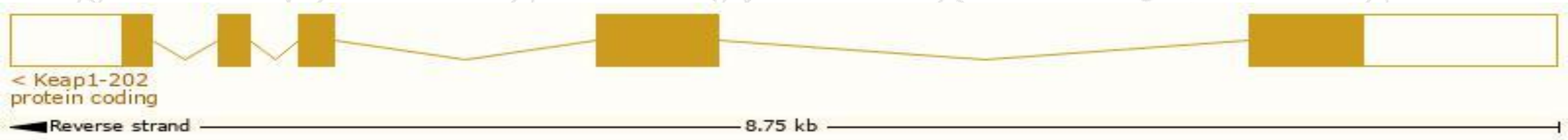
|                           |   |
|---------------------------|---|
| <b>Official Symbol</b>    | Keap1 provided by <a href="#">MGI</a>   |
| <b>Official Full Name</b> | kelch-like ECH-associated protein 1 provided by <a href="#">MGI</a>   |
| <b>Primary source</b>     | <a href="#">MGI:MGI:1858732</a>   |
| <b>See related</b>        | <a href="#">Ensembl:ENSMUSG00000003308</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>      | INRF2, mKIAA0132  |
| <b>Expression</b>         | Ubiquitous expression in ovary adult (RPKM 41.2), adrenal adult (RPKM 36.0) and 28 other tissues <a href="#">See more</a>   |
| <b>Orthologs</b>          | <a href="#">human</a> <a href="#">all</a>   |

# Transcript information (Ensembl)

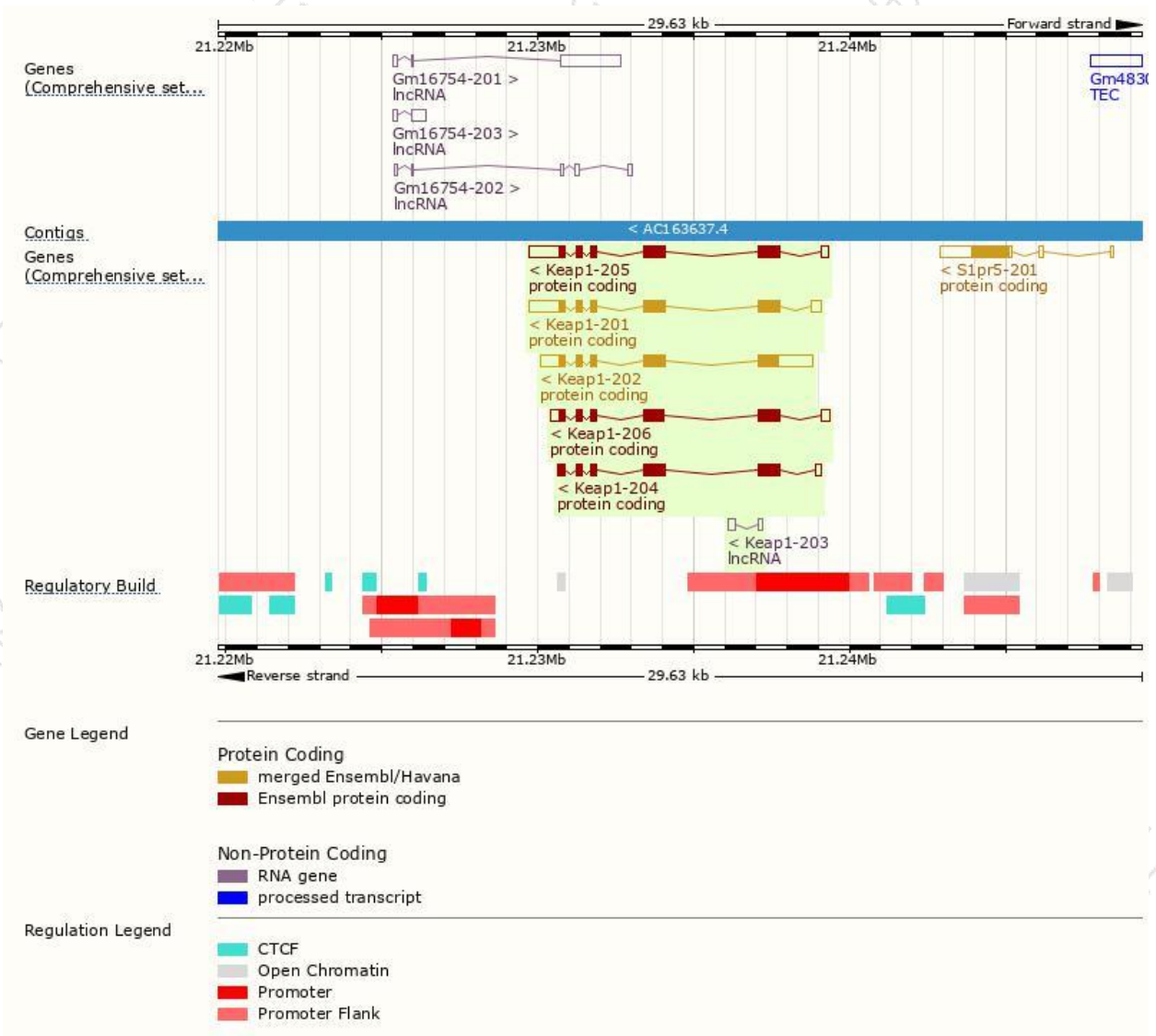
The gene has 6 transcripts,all transcripts are shown below:

| Name      | Transcript ID                        | bp   | Protein               | Biotype        | CCDS                      | UniProt                    | Flags                           |
|-----------|--------------------------------------|------|-----------------------|----------------|---------------------------|----------------------------|---------------------------------|
| Keap1-202 | <a href="#">ENSMUST00000164812.7</a> | 3614 | <a href="#">624aa</a> | Protein coding | <a href="#">CCDS22897</a> | <a href="#">Q9Z2X8</a>     | TSL:1 GENCODE basic APPRIS P2   |
| Keap1-201 | <a href="#">ENSMUST00000049567.9</a> | 3172 | <a href="#">624aa</a> | Protein coding | <a href="#">CCDS22897</a> | <a href="#">Q9Z2X8</a>     | TSL:1 GENCODE basic APPRIS P2   |
| Keap1-205 | <a href="#">ENSMUST00000194542.5</a> | 3151 | <a href="#">624aa</a> | Protein coding | <a href="#">CCDS22897</a> | <a href="#">Q9Z2X8</a>     | TSL:1 GENCODE basic APPRIS P2   |
| Keap1-204 | <a href="#">ENSMUST00000193982.1</a> | 2163 | <a href="#">624aa</a> | Protein coding | <a href="#">CCDS22897</a> | <a href="#">Q9Z2X8</a>     | TSL:1 GENCODE basic APPRIS P2   |
| Keap1-206 | <a href="#">ENSMUST00000216436.1</a> | 2498 | <a href="#">620aa</a> | Protein coding | -                         | <a href="#">A0A1L1SS10</a> | TSL:5 GENCODE basic APPRIS ALT2 |
| Keap1-203 | <a href="#">ENSMUST00000193247.1</a> | 317  | No protein            | lncRNA         | -                         | -                          | TSL:5                           |

The strategy is based on the design of *Keap1-202* transcript,The transcription is shown below

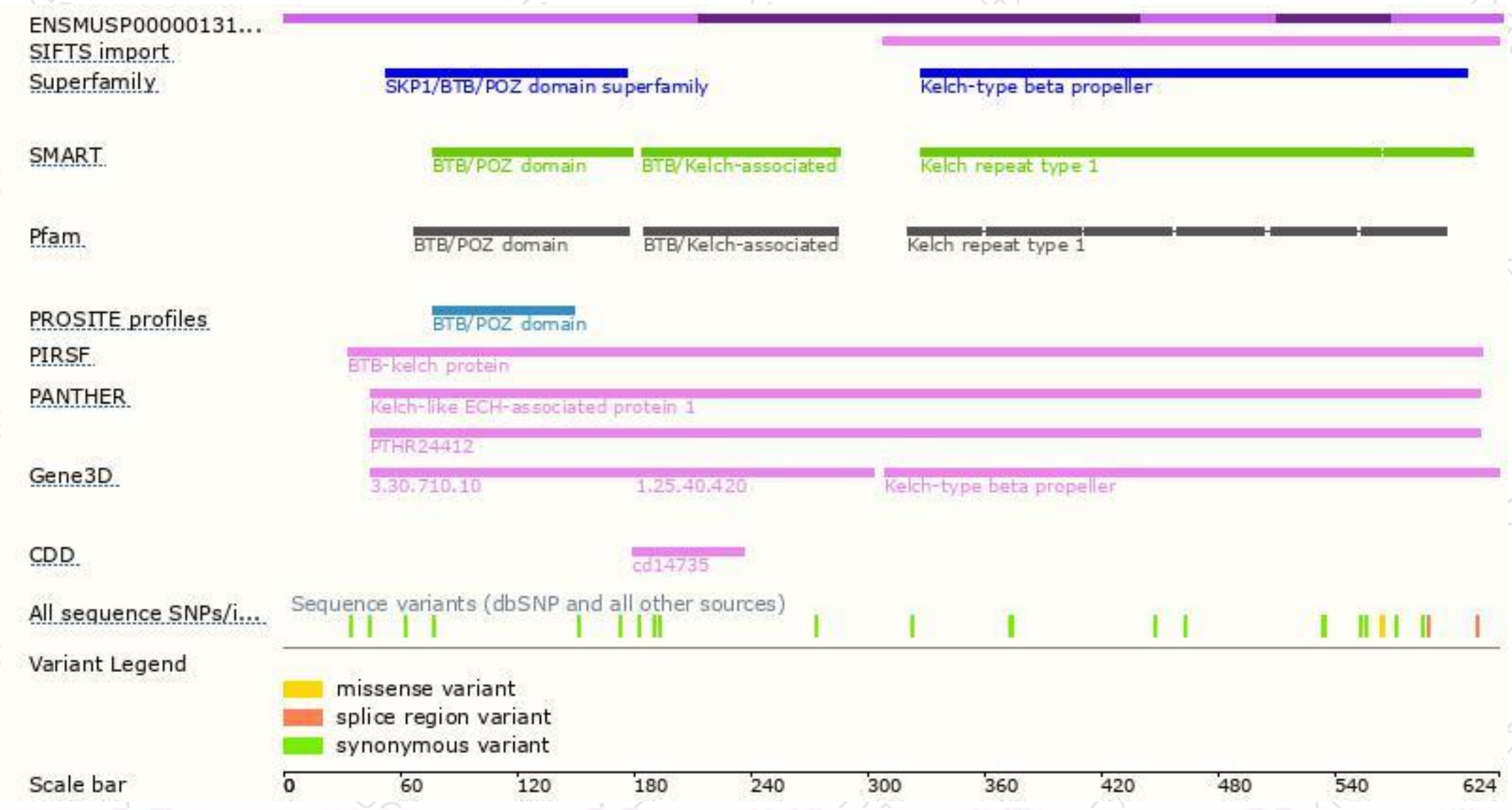


# Genomic location distribution





# 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, Homozygous null mice exhibit scaly skin, hyperkeratosis of the esophagus and stomach mucosa, and die around 3 weeks of age, putatively due to malnutrition resulting from the abnormal alimentary epithelium.

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

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