# *Ankrd27* Cas9-KO Strategy

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# Project Overview

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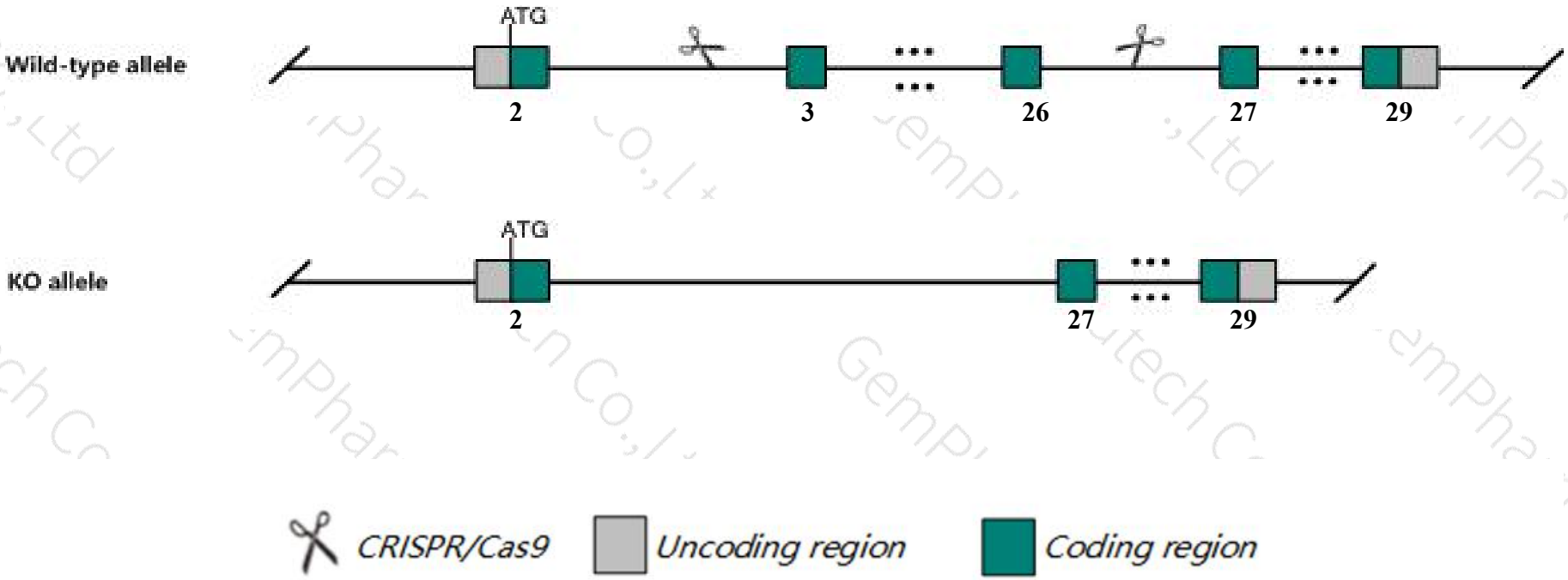
|---|---|
| **Project Name** | ***Ankrd27*** |
| **Project type** | **Cas9-KO** |
| **Strain background** | **C57BL/6JGpt** |

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ankrd27* gene. The schematic diagram is as follows:



# Technical routes

➢ The *Ankrd27* gene has 10 transcripts. According to the structure of *Ankrd27* gene, exon3-exon26 of *Ankrd27-201* (ENSMUST00000040844.15) transcript is recommended as the knockout region.The region contains 2662bp coding sequenc Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Ankrd27* gene. The brief process is as follows: CRISPR/Cas9 syste

# Notice

➢ The *Ankrd27* gene is located on the Chr7. 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）

集萃药康 GemPharmatech

## Ankrd27 ankyrin repeat domain 27 (VPS9 domain) [Mus musculus (house mouse)]

Gene ID: 245886, updated on 19-Mar-2019

### Summary

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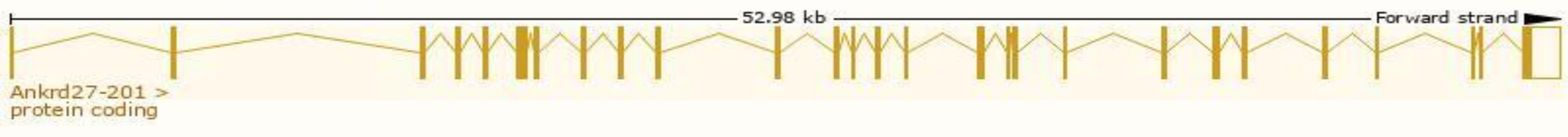
|---|---|
| **Official Symbol** | Ankrd27 provided by MGI |
| **Official Full Name** | ankyrin repeat domain 27 (VPS9 domain) provided by MGI |
| **Primary source** | MGI:MGI:2444103 |
| **See related** | Ensembl:ENSMUSG00000034867 |
| **Gene type** | protein coding |
| **RefSeq status** | VALIDATED |
| **Organism** | Mus musculus |
| **Lineage** | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| **Also known as** | AA408090, BC016493, D330003H11Rik, Varp |
| **Expression** | Ubiquitous expression in limb E14.5 (RPKM 10.8), bladder adult (RPKM 7.7) and 28 other tissues See more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

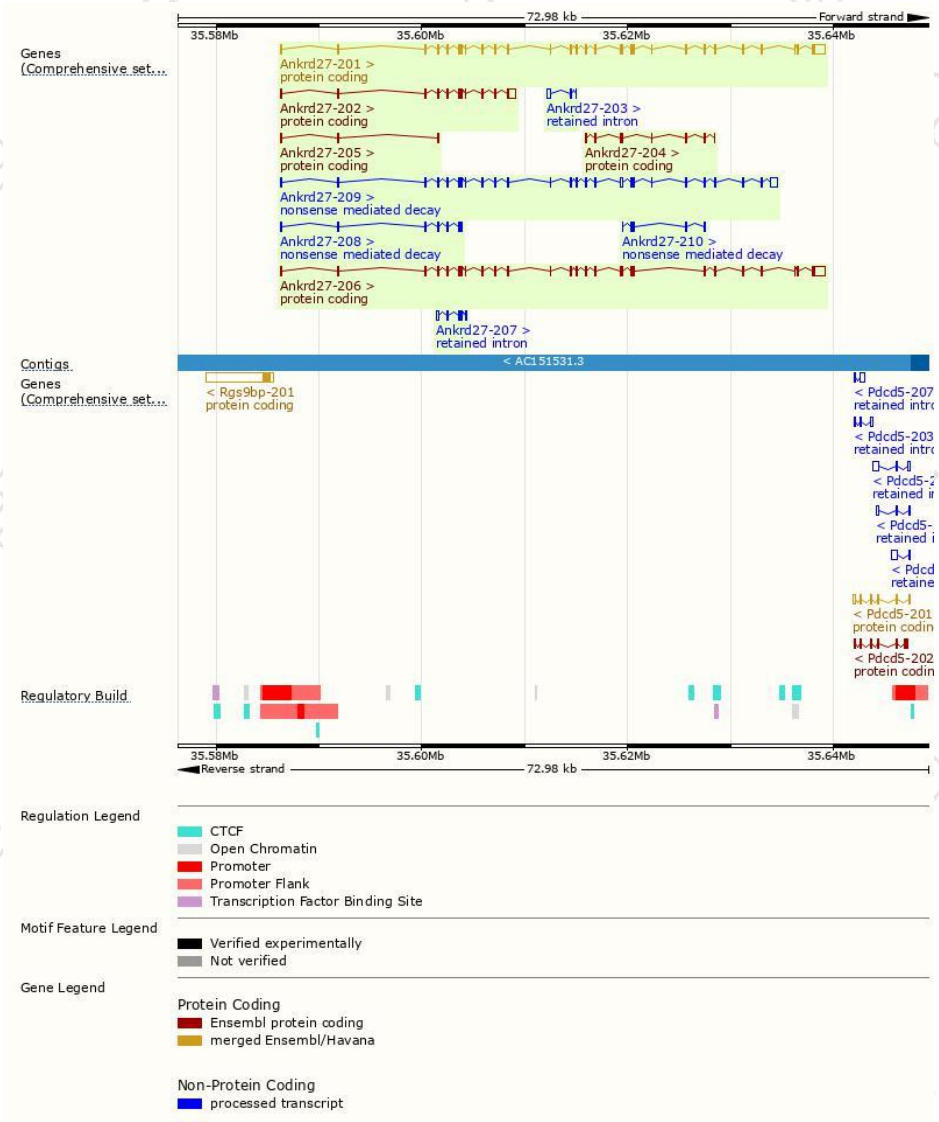
The gene has 10 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Ankrd27-201 | ENSMUST00000040844.15 | 4284 | 1048aa | Protein coding | CCDS21154 | Q3UMR0 | TSL:1 GENCODE basic APPRIS P2 |
| Ankrd27-202 | ENSMUST00000186245.6 | 1926 | 377aa | Protein coding | CCDS80706 | A0A0R4J2C4 | TSL:1 GENCODE basic |
| Ankrd27-206 | ENSMUST00000190503.6 | 4086 | 993aa | Protein coding | - | Q3UMR0 | TSL:1 GENCODE basic APPRIS ALT2 |
| Ankrd27-204 | ENSMUST00000187807.1 | 693 | 231aa | Protein coding | - | A0A087WS06 | 5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5 |
| Ankrd27-205 | ENSMUST00000188906.6 | 405 | 85aa | Protein coding | - | A0A087WPF2 | CDS 3' incomplete TSL:3 |
| Ankrd27-209 | ENSMUST00000206472.1 | 3583 | 388aa | Nonsense mediated decay | - | A0A0U1RPT7 | TSL:5 |
| Ankrd27-208 | ENSMUST00000206157.1 | 797 | 76aa | Nonsense mediated decay | - | A0A0U1RPG1 | TSL:5 |
| Ankrd27-210 | ENSMUST00000206632.1 | 475 | 23aa | Nonsense mediated decay | - | A0A0U1RP40 | CDS 5' incomplete TSL:3 |
| Ankrd27-207 | ENSMUST00000205801.1 | 699 | No protein | Retained intron | - | - | TSL:2 |
| Ankrd27-203 | ENSMUST00000187567.1 | 551 | No protein | Retained intron | - | - | TSL:3 |

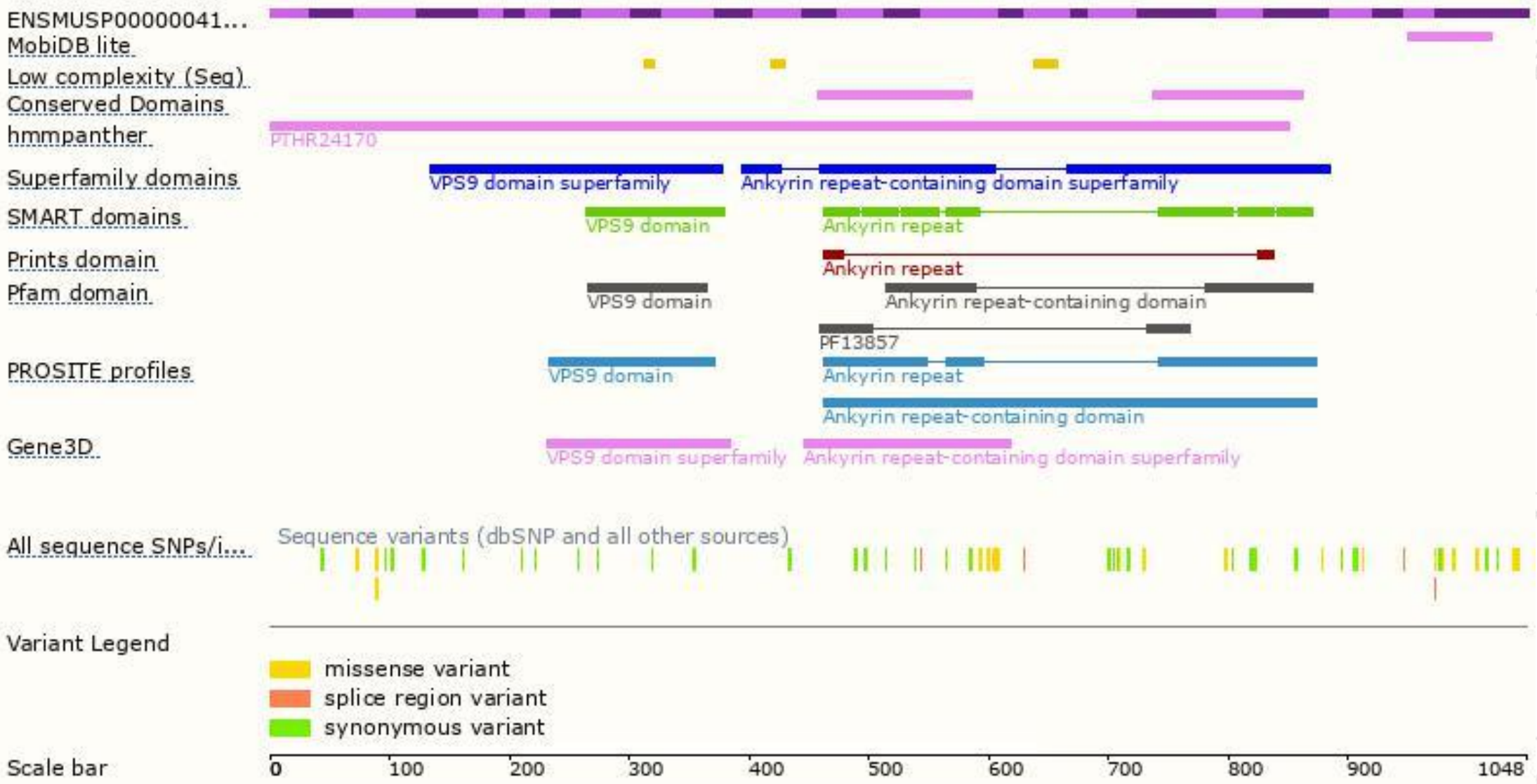
The strategy is based on the design of *Ankrd27-201* transcript,The transcription is shown below



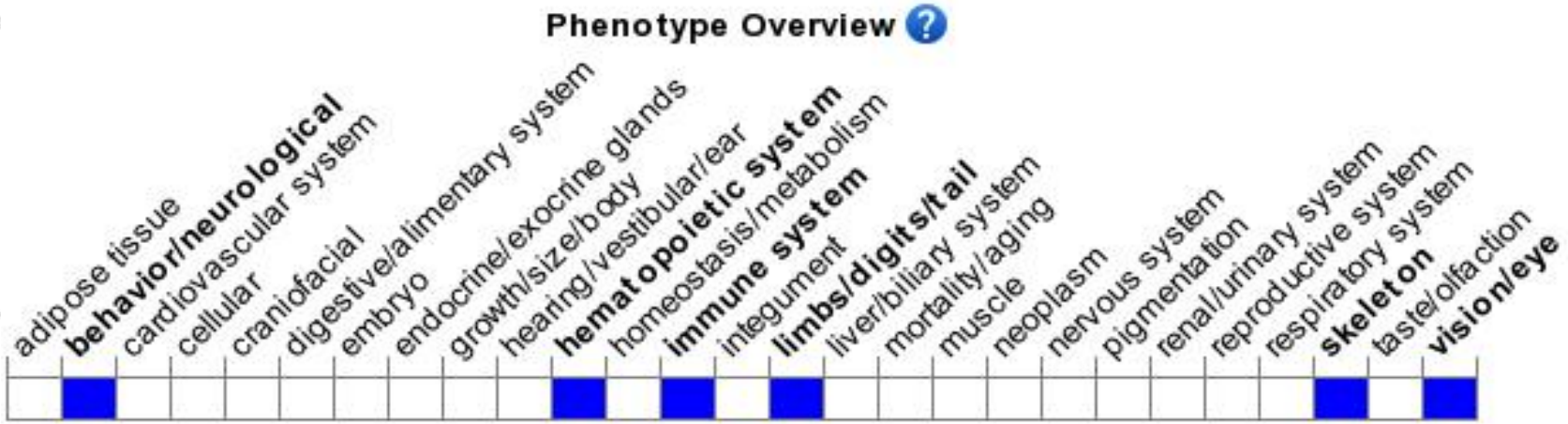
# Genomic location distribution



# 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/).*

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

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