# *Tcirg1* Cas9-KO Strategy

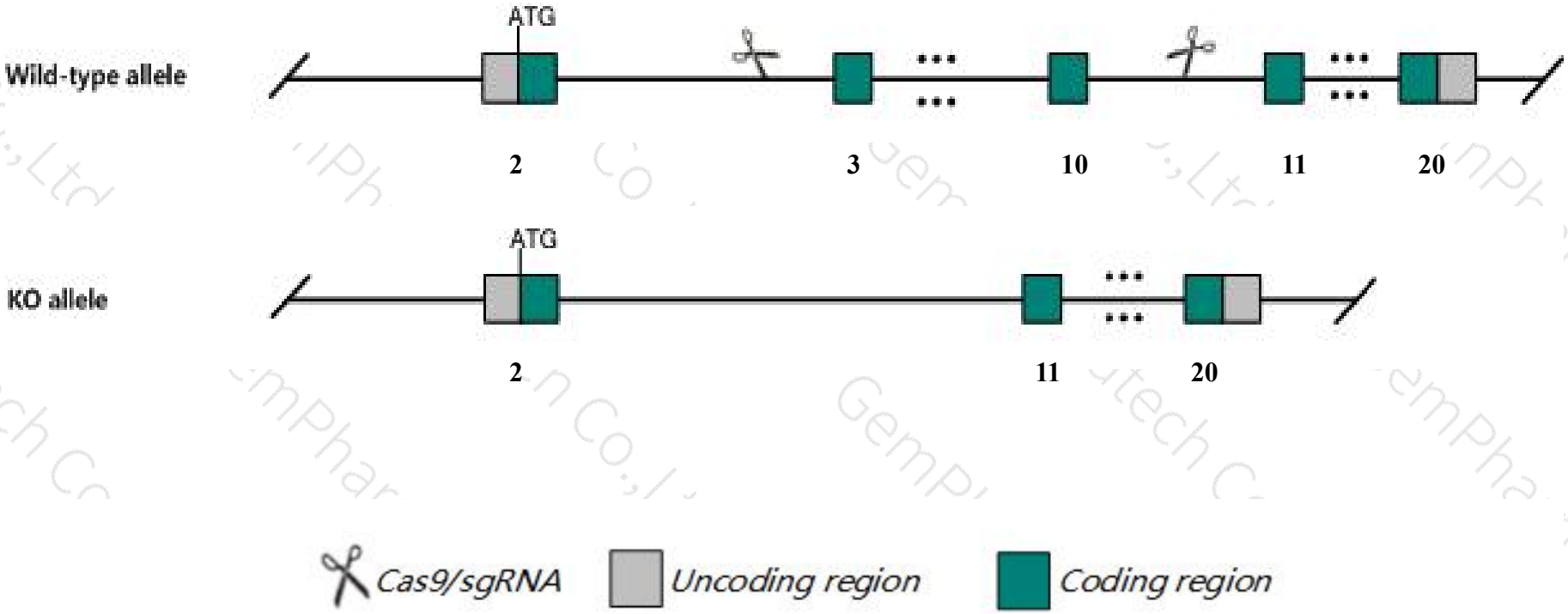
Designer:

# Project Overview

| | |
|---|---|
| **Project Name** | ***Tcirg1*** |
| **Project type** | **Cas9-KO** |
| **Strain background** | **C57BL/6J** |

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Tcirg1* gene. The schematic diagram is as follows:



# Technical routes

➢ The *Tcirg1* gene has 14 transcripts. According to the structure of *Tcirg1* gene, exon3-exon10 of *Tcirg1-204* (ENSMUST00000126070.8) transcript is recommended as the knockout region.The region contains 1051bp coding sequence. Knock out the region will result in disruption of protein function.

➢ In this project we use CRISPR/Cas9 technology to modify *Tcirg1* gene. The brief process is as follows: sgRNA was transcribed in vitro.Cas9 and sgRNA were microinjected into the fertilized eggs of C57BL/6J 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/6J mice.

# Notice

- According to the existing MGI data,Homozygotes for mutant alleles exhibit severe osteopetrosis with increased bone density due to failure of secondary bone resorption. Mutants lack teeth and die around 30-40 days of age.

- The *Tcirg1* gene is located on the Chr19. 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 gene transcription and translation processes, all risks cannot be predicted under existing information.

# Gene information（NCBI）

集萃药康 GemPharmatech

## Tcirg1 T cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein A3 [Mus musculus (house mouse)]

Gene ID: 27060, updated on 3-Feb-2019

### Summary

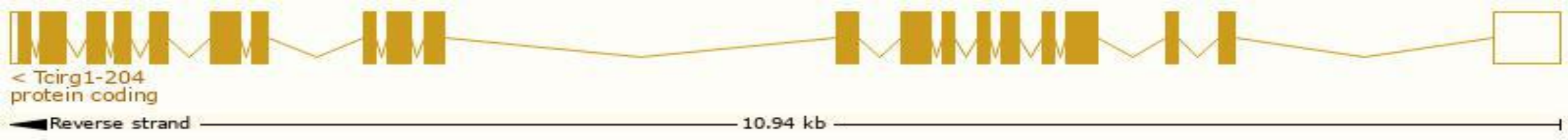
| | |
|---|---|
| **Official Symbol** | Tcirg1 provided by MGI |
| **Official Full Name** | T cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein A3 provided by MGI |
| **Primary source** | MGI:MGI:1350931 |
| **See related** | Ensembl:ENSMUSG00000001750 |
| **Gene type** | protein 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** | ATP6N1C, ATP6a3, Atp6i, OC-116, OPTB1, Stv1, TIRC7, Vph1, oc |
| **Expression** | Ubiquitous expression in spleen adult (RPKM 61.8), adrenal adult (RPKM 46.6) and 27 other tissues See more |
| **Orthologs** | human all |

# Transcript information（Ensembl）

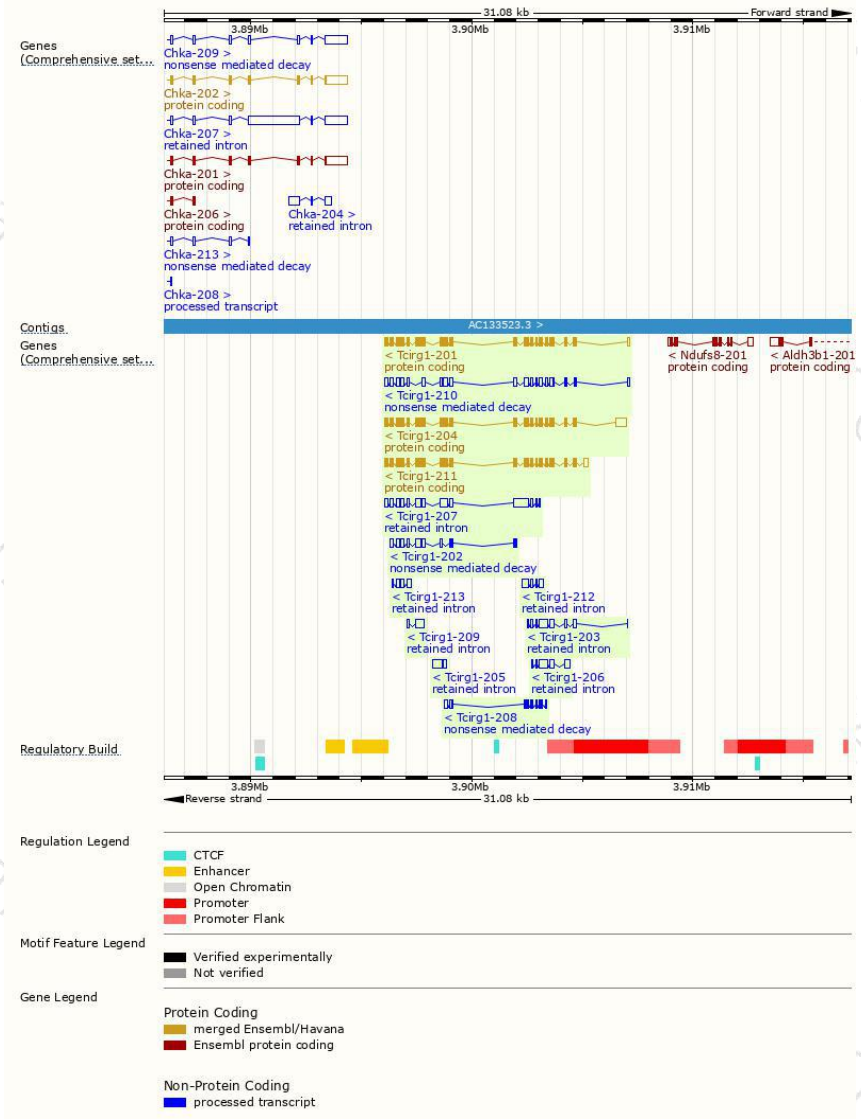
The gene has 14 transcripts,all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|---|---|---|---|---|---|---|---|
| Tcirg1-204 | ENSMUST00000126070.8 | 3041 | 834aa | Protein coding | CCDS29401 | Q9JHF5 | TSL:1 GENCODE basic APPRIS P1 |
| Tcirg1-211 | ENSMUST00000145791.7 | 2729 | 834aa | Protein coding | CCDS29401 | Q9JHF5 | TSL:1 GENCODE basic APPRIS P1 |
| Tcirg1-201 | ENSMUST00000001801.10 | 2688 | 834aa | Protein coding | CCDS29401 | Q9JHF5 | TSL:1 GENCODE basic APPRIS P1 |
| Tcirg1-214 | ENSMUST00000236590.1 | 333 | 65aa | Protein coding | - | - | CDS 3' incomplete |
| Tcirg1-210 | ENSMUST00000135070.7 | 2424 | 72aa | Nonsense mediated decay | - | D6RFN1 | TSL:5 |
| Tcirg1-202 | ENSMUST00000122885.7 | 1233 | 91aa | Nonsense mediated decay | - | F6ZFB8 | CDS 5' incomplete TSL:5 |
| Tcirg1-208 | ENSMUST00000132164.1 | 813 | 191aa | Nonsense mediated decay | - | F6XRE6 | CDS 5' incomplete TSL:5 |
| Tcirg1-207 | ENSMUST00000131327.7 | 2350 | No protein | Retained intron | - | - | TSL:2 |
| Tcirg1-203 | ENSMUST00000125792.8 | 1066 | No protein | Retained intron | - | - | TSL:5 |
| Tcirg1-206 | ENSMUST00000127308.1 | 923 | No protein | Retained intron | - | - | TSL:5 |
| Tcirg1-212 | ENSMUST00000159824.7 | 692 | No protein | Retained intron | - | - | TSL:2 |
| Tcirg1-205 | ENSMUST00000126643.2 | 568 | No protein | Retained intron | - | - | TSL:2 |
| Tcirg1-213 | ENSMUST00000162688.1 | 467 | No protein | Retained intron | - | - | TSL:1 |
| Tcirg1-209 | ENSMUST00000134698.1 | 463 | No protein | Retained intron | - | - | TSL:3 |

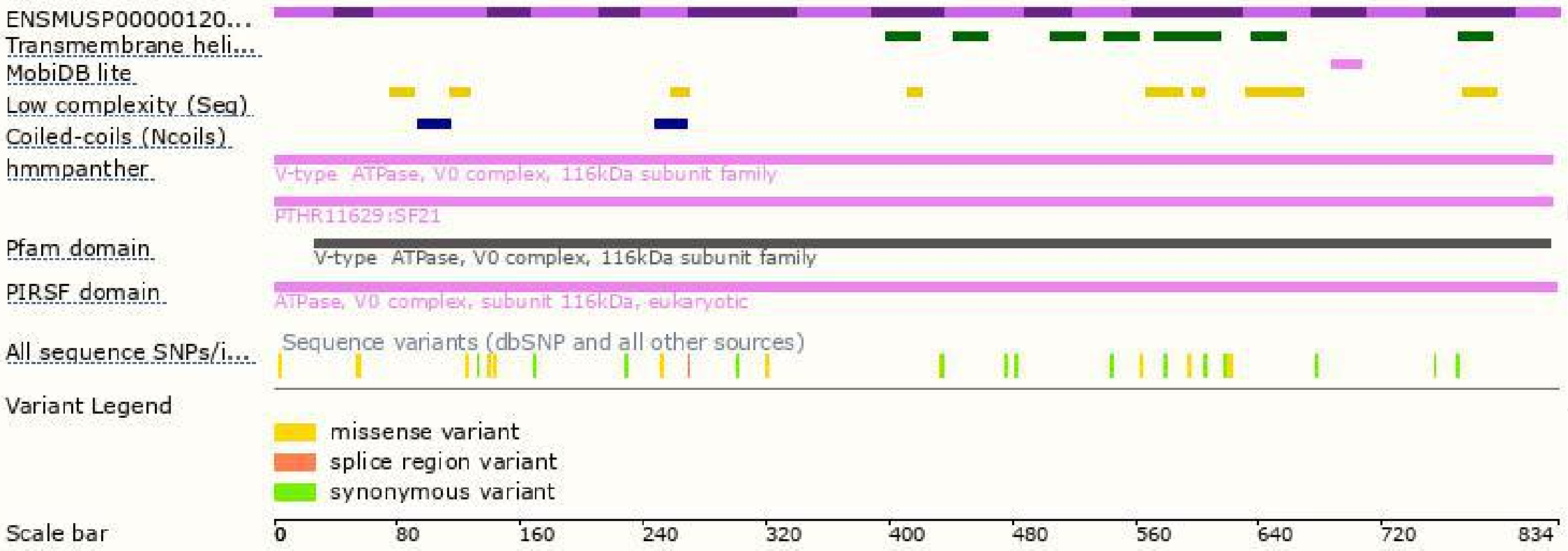
The strategy is based on the design of *Tcirg1-204* transcript,The transcription is shown below



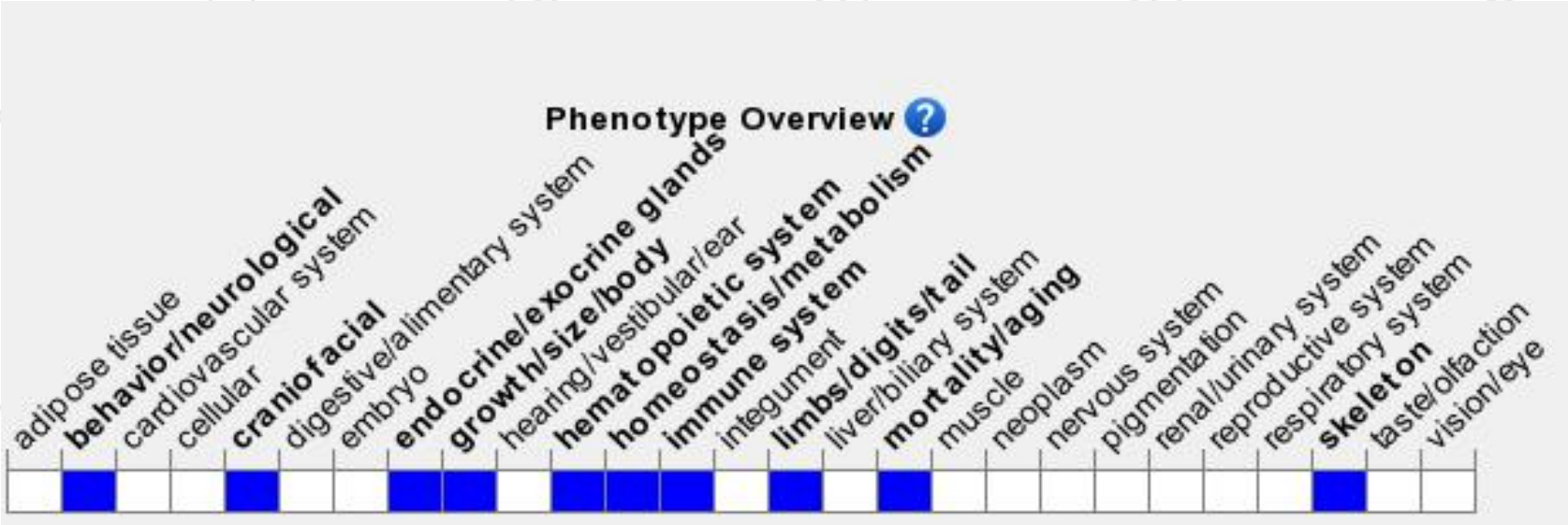
# Genomic location distribution



# 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,Homozygotes for mutant alleles exhibit severe osteopetrosis with increased bone density due to failure of secondary bone resorption. Mutants lack teeth and die around 30-40 days of age.

集萃药康
GemPharmatech

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

Tel: 025-5864 1534

集萃药康生物科技
GemPharmatech Co.,Ltd