

Rnase10 Cas9-CKO Strategy

Designer:

Daohua Xu

Reviewer :

Huimin Su

Design Date:

2019-9-28

Project Overview



Project Name

Rnase10

Project type

Cas9-CKO

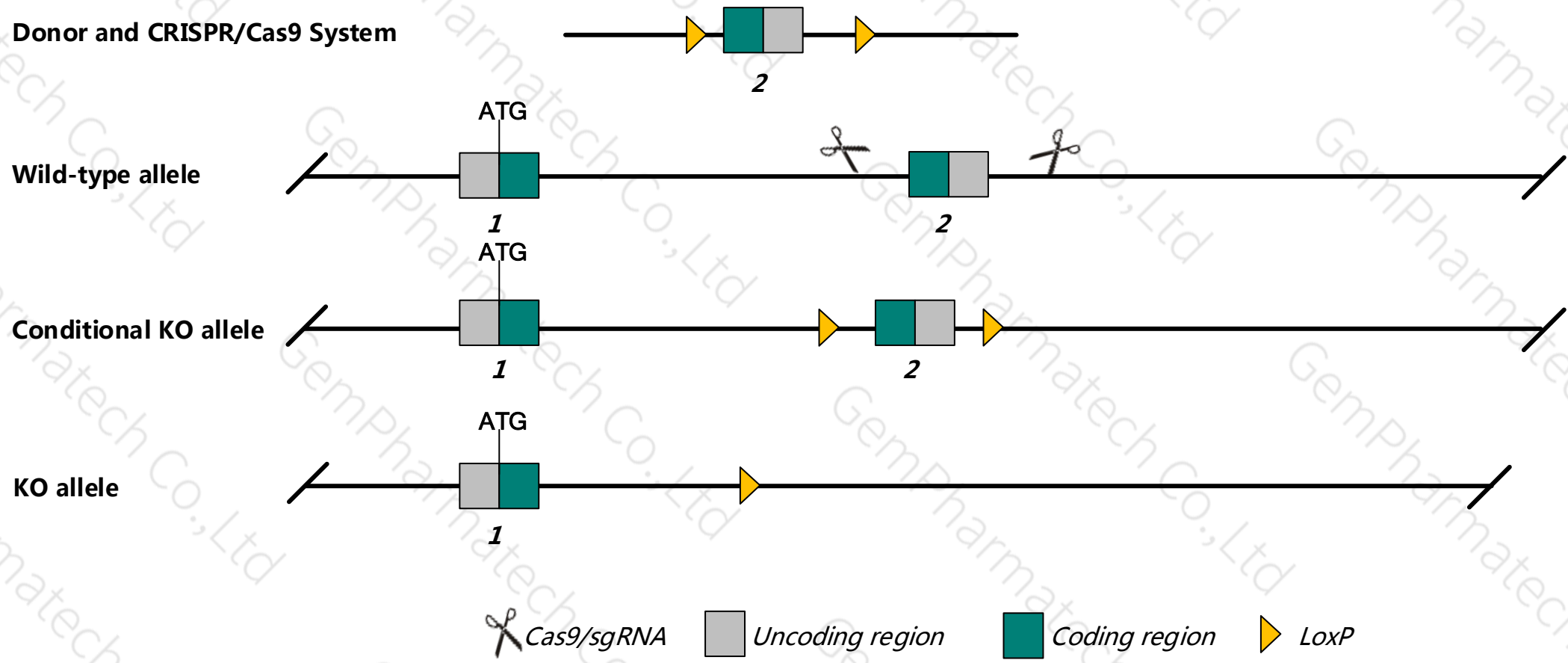
Animal background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Rnase10* gene. The schematic diagram is as follows:

Donor and CRISPR/Cas9 System



Technical routes

- The *Rnase10* gene has 2 transcripts, According to the structure of *Rnase10* gene, exon2 of *Rnase10-201* transcript is recommended as the knockout region. The region contains the most of coding sequence. Knock out the region, result in destruction of protein.
- This project uses CRISPR/Cas9 technology to modify *Rnase10* gene. The brief process is as follows: sgRNA was transcribed in vitro, donor vector was constructed, Cas9, sgRNA and donor were microinjected into fertilized eggs of C57BL/6JGpt mice and homologous recombination was carried out to obtain F0 mice. A stable and hereditary F1 generation mouse model was obtained by mating F0 generation mice with C57BL/6JGpt mice which were confirmed positive by PCR-sequencing.
- The flox mice was knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data , Homozygous disruption of this gene leads to decreased bone mineral density, alterations in B cell, T cell and NK cell number, and abnormal circulating glucose, creatinine, chloride and serum albumin levels.
- The *Rnase10* gene is located in the Chr14. If the knockout mice are mixed with other mice, two target genes are avoided on the same chromosome as possible, otherwise the offspring of mice with double gene positive and homozygous gene knockout can not be obtained.
- 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)

Rnase10 ribonuclease, RNase A family, 10 (non-active) [*Mus musculus* (house mouse)]

Gene ID: 75019, updated on 23-Oct-2018

Summary

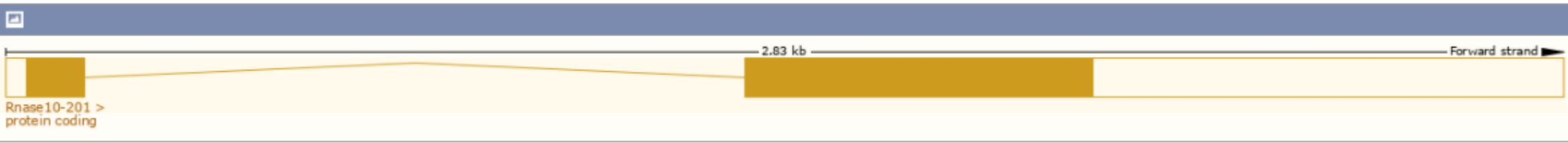
| | |
|--------------------|---|
| Official Symbol | Rnase10 provided by MGI |
| Official Full Name | ribonuclease, RNase A family, 10 (non-active) provided by MGI |
| Primary source | MGI:MGI:1922269 |
| See related | Ensembl:ENSMUSG000000021872 |
| Gene type | protein coding |
| RefSeq status | VALIDATED |
| Organism | Mus musculus |
| Lineage | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| Also known as | Rah1; 4930474F22Rik |
| Expression | Restricted expression toward genital fat pad adult (RPKM 393.6) See more |
| Orthologs | human all |

Transcript information (Ensembl)

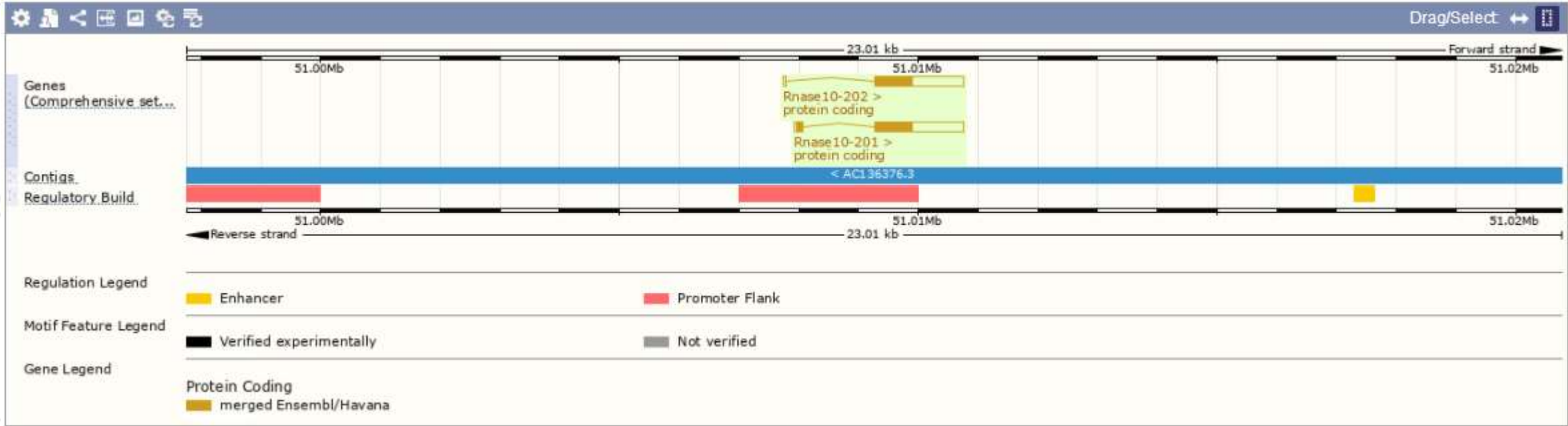
The gene has 2 transcripts, and all transcripts are shown below :

| Show/hide columns (1 hidden) | | | | | | | | Filter | |
|------------------------------|--------------------------------------|------|-----------------------|----------------|---------------------------|------------------------|--|--------|---------------------------|
| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | RefSeq | Flags | |
| Rnase10-201 | ENSMUST00000022424.7 | 1629 | 245aa | Protein coding | CCDS27030 | E9QPU5 | NM_029145 NP_083421 | TSL:1 | GENCODE basic APPRIS P3 |
| Rnase10-202 | ENSMUST00000164632.1 | 1521 | 208aa | Protein coding | CCDS49480 | G3UWD1 | NM_001162863 NP_001156335 | TSL:1 | GENCODE basic APPRIS ALT2 |

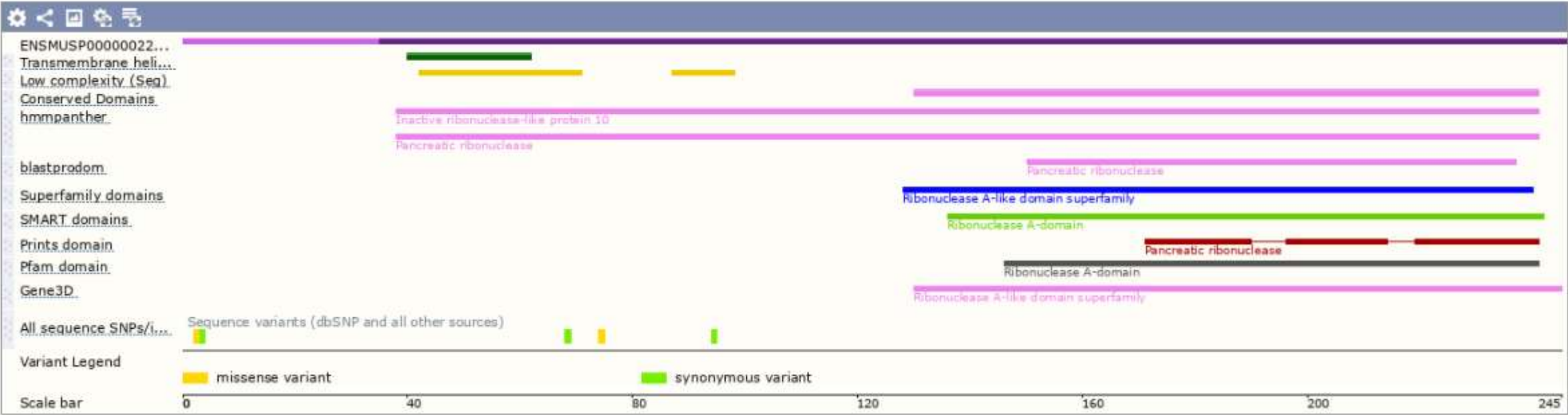
The strategy is based on the design of *Rnase10-201* transcript,The transcription is shown below :



Genomic location distribution

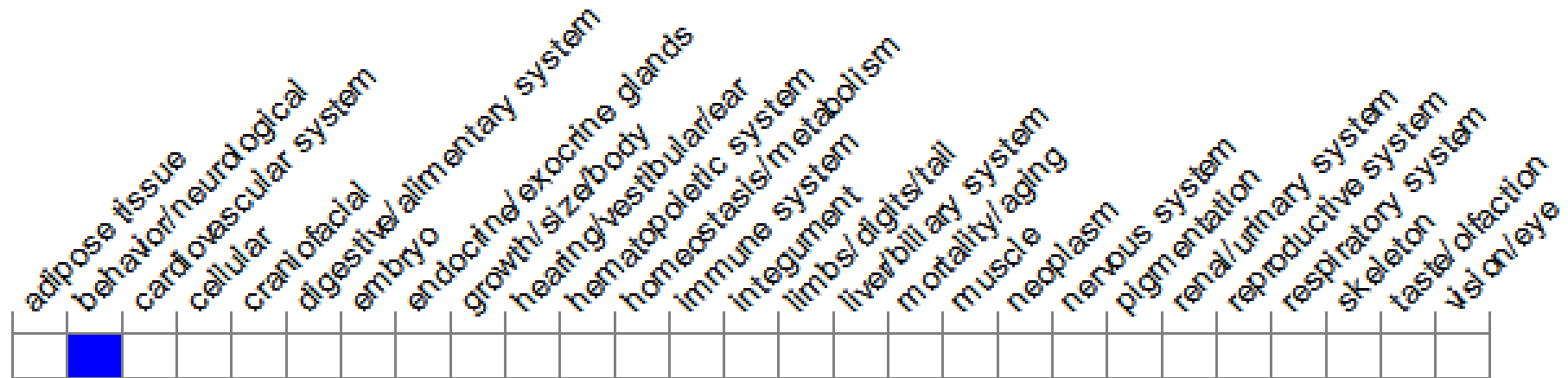


Protein domain



Mouse phenotype description(MGI)

Phenotype Overview ?



Click cells to view annotations.

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 disruption of this gene leads to decreased bone mineral density, alterations in B cell, T cell and NK cell number, and abnormal circulating glucose, creatinine, chloride and serum albumin levels.

If you have any questions, you are welcome to inquire.
Tel: 025-5864 1534

