

Ifngr1 Cas9-KO Strategy

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Project Overview



Project Name

Ifngr1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ifngr1* gene. The schematic diagram is as follows:



- The *Ifngr1* gene has 6 transcripts. According to the structure of *Ifngr1* gene, exon2 of *Ifngr1-201* (ENSMUST00000020188.12) transcript is recommended as the knockout region. The region contains 115bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ifngr1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a mutant allele exhibit increased susceptibility to viral infection and experimental autoimmune uveoretinitis.
- The *Ifngr1* gene is located on the Chr10. 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)

Ifngr1 interferon gamma receptor 1 [Mus musculus (house mouse)]

Gene ID: 15979, updated on 12-Mar-2019

Summary



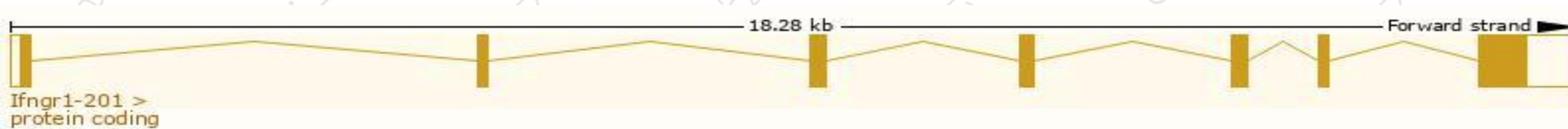
| | |
|---------------------------|---|
| Official Symbol | Ifngr1 provided by MGI |
| Official Full Name | interferon gamma receptor 1 provided by MGI |
| Primary source | MGI:MGI:107655 |
| See related | Ensembl:ENSMUSG00000020009 |
| Gene type | protein coding |
| RefSeq status | VALIDATED |
| Organism | Mus musculus |
| Lineage | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus |
| Also known as | CD119, IFN-gammaR, Ifgr, Ifngr, Nktar |
| Expression | Ubiquitous expression in thymus adult (RPKM 45.9), colon adult (RPKM 37.2) and 28 other tissues See more |
| Orthologs | human all |

Transcript information (Ensembl)

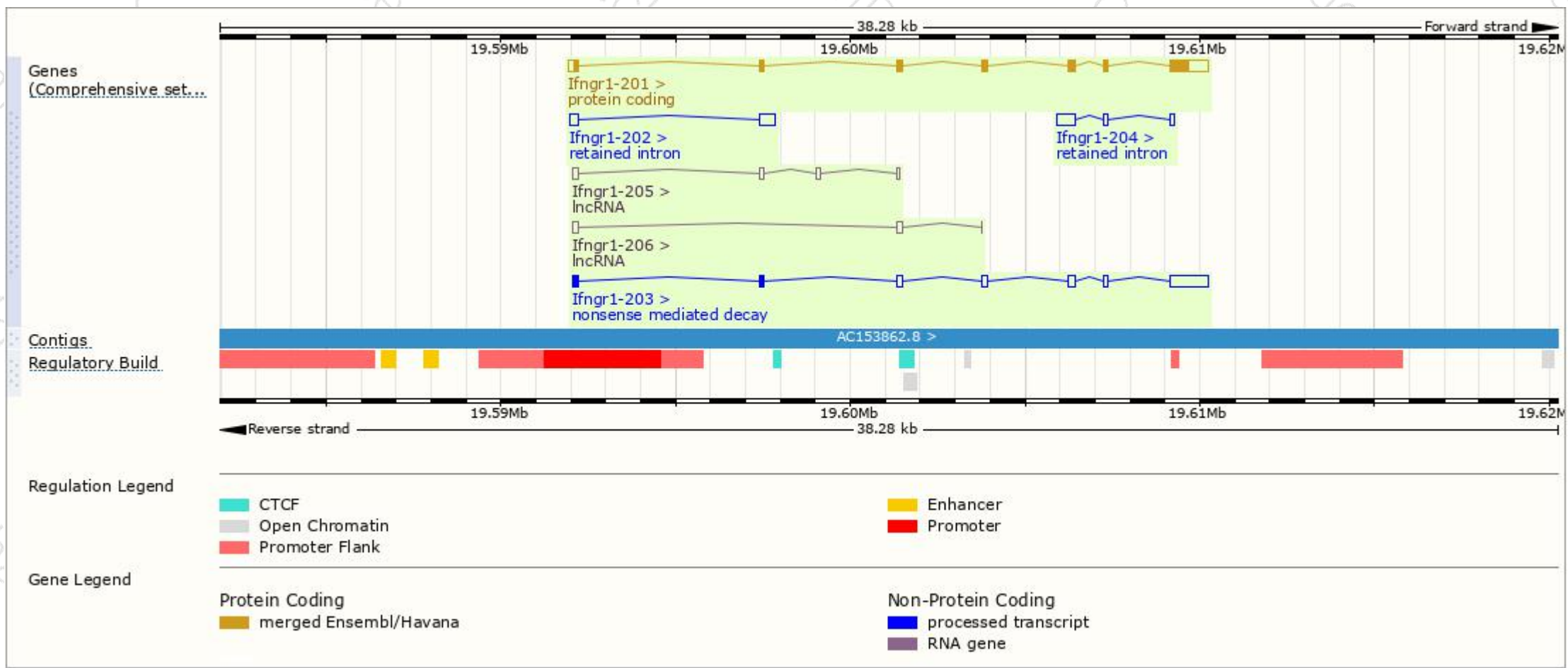
The gene has 6 transcripts, all transcripts are shown below:

| Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | Flags |
|------------|---------------------------------------|------|-----------------------|-------------------------|---------------------------|------------------------|-------------------------------|
| Ifngr1-201 | ENSMUST00000020188.12 | 2112 | 477aa | Protein coding | CCDS35856 | P15261 | TSL:1 GENCODE basic APPRIS P1 |
| Ifngr1-203 | ENSMUST00000164591.2 | 1974 | 75aa | Nonsense mediated decay | - | E9PX11 | TSL:5 |
| Ifngr1-204 | ENSMUST00000168074.1 | 747 | No protein | Retained intron | - | - | TSL:2 |
| Ifngr1-202 | ENSMUST00000110989.2 | 676 | No protein | Retained intron | - | - | TSL:2 |
| Ifngr1-205 | ENSMUST00000171772.1 | 443 | No protein | lncRNA | - | - | TSL:3 |
| Ifngr1-206 | ENSMUST00000172253.1 | 321 | No protein | lncRNA | - | - | TSL:5 |

The strategy is based on the design of *Ifngr1-201* transcript, The transcription is shown below



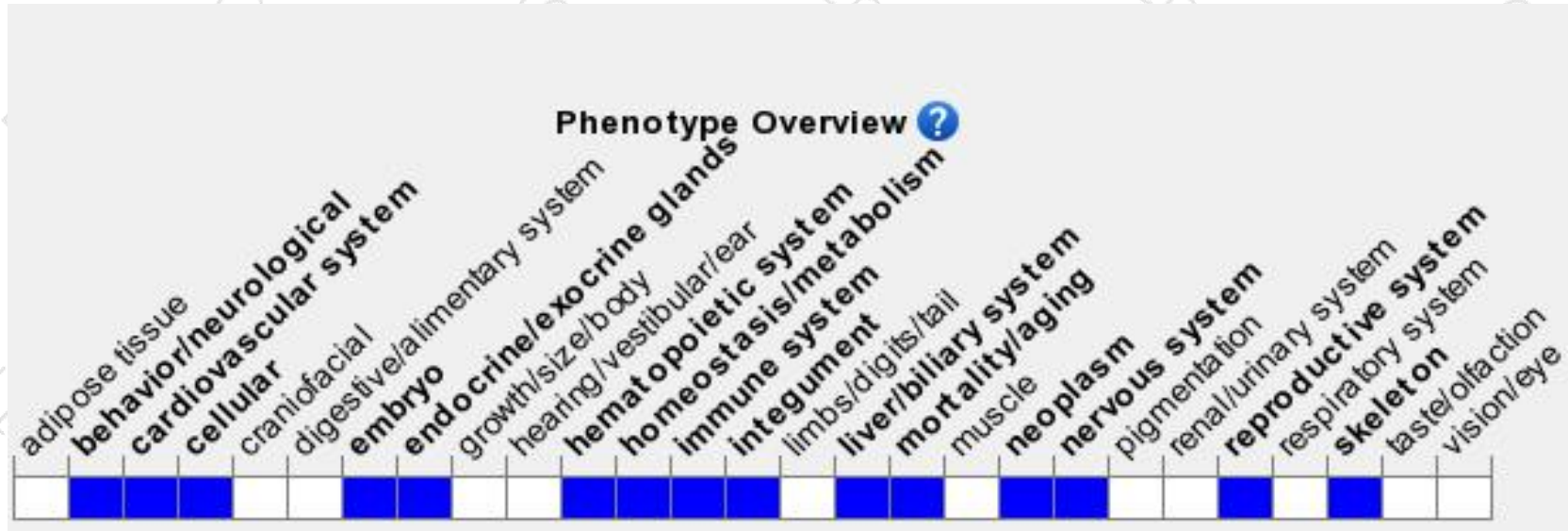
Genomic location distribution



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/>).

According to the existing MGI data, Mice homozygous for a mutant allele exhibit increased susceptibility to viral infection and experimental autoimmune uveoretinitis.

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

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