Neu4 Cas9-CKO Strategy

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Project Overview
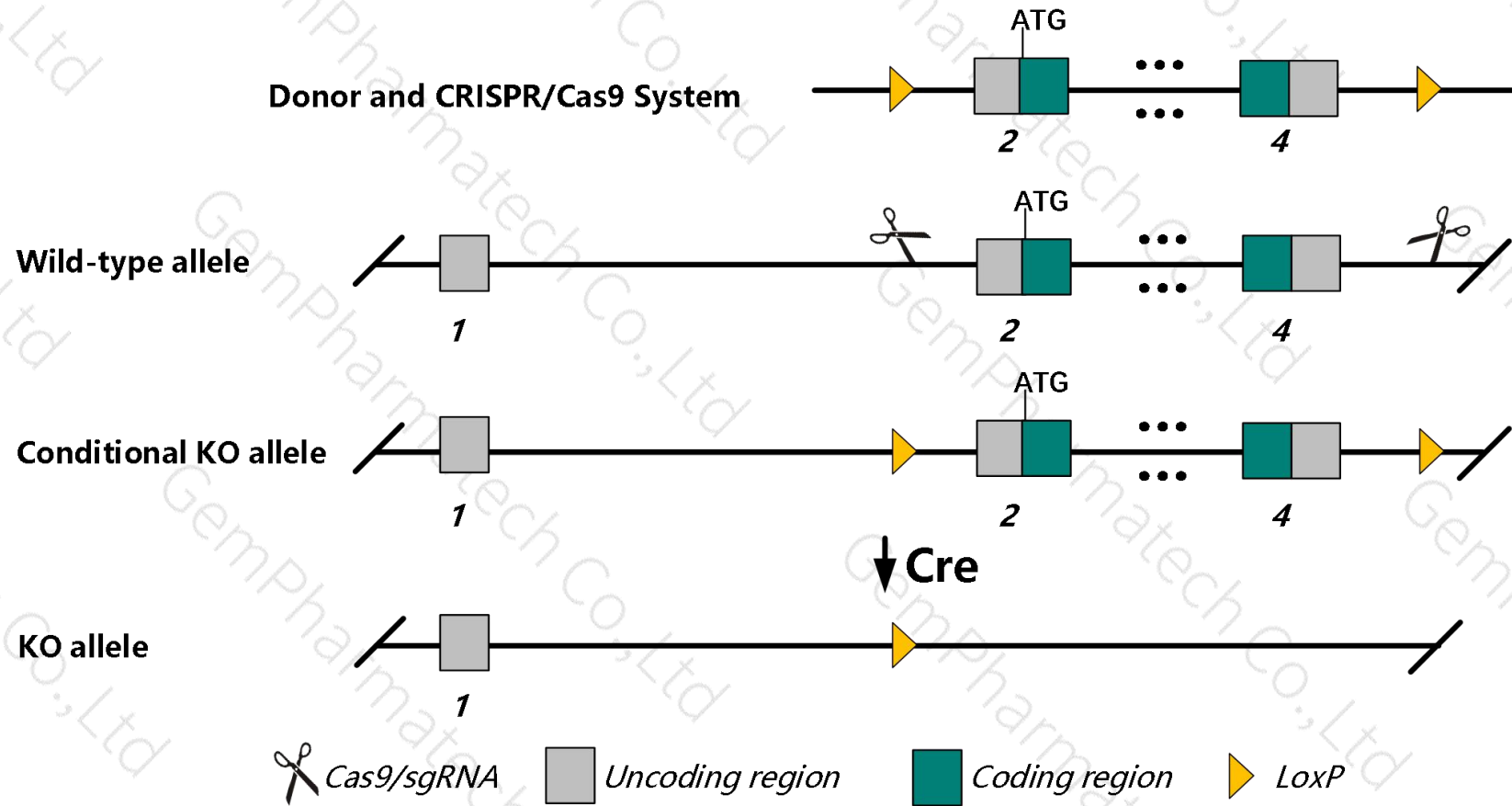

Project Name	*Neu4*
Project type	Cas9-CKO
Strain background	C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Neu4* gene. The schematic diagram is as follows:

Technical routes

➤ The *Neu4* gene has 2 transcripts. According to the structure of *Neu4* gene, exon2-exon4 of *Neu4-201* (ENSMUST00000050890.7) transcript is recommended as the knockout region.The region contains all of the coding sequence.Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Neu4* gene. The brief process is as follows:CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt 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/6JGpt mice.

➤ The flox mice will be 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.

Notice

➢ According to the existing MGI data,Mice homozygous for a null allele are largely normal except increased lipid content in the lung and liver and vacuolization indicative of lysosomal storage disorder.

➢ The *Neu4* gene is located on the Chr1. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Neu4 sialidase 4 [*Mus musculus* (house mouse)]

Gene ID: 241159, updated on 10-Oct-2019

▲ Summary

Official Symbol	Neu4 provided by MGI
Official Full Name	sialidase 4 provided by MGI
Primary source	MGI:MGI:2661364
See related	Ensembl:ENSMUSG00000034000
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	9330166I04
Expression	Biased expression in cortex adult (RPKM 1.5), frontal lobe adult (RPKM 1.4) and 1 other tissue See more
Orthologs	human all

▲ Genomic context

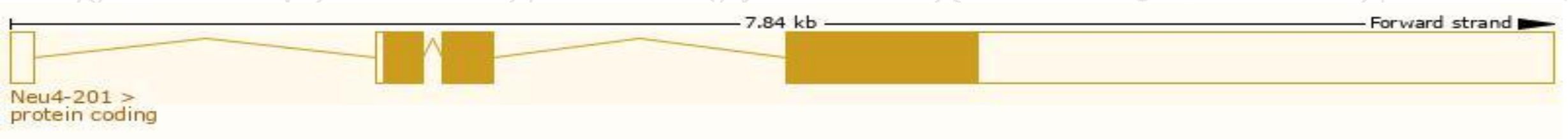**Location:** 1; 1 D

See Neu4 in Genome Data Viewer

Exon count: 5

| Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	1	NC_000067.6 (94020493..94028334)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	1	NC_000067.5 (95917070..95924911)

Transcript information（Ensembl）

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

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Neu4-201	ENSMUST00000050890.7	4511	478aa	Protein coding	CCDS15199	Q8BZL1	TSL:1 GENCODE basic APPRIS P3
Neu4-202	ENSMUST00000190212.6	1719	501aa	Protein coding	CCDS78660	C5NTX9 Q8BZL1	TSL:1 GENCODE basic APPRIS ALT2

The strategy is based on the design of *Neu4-201* transcript,The transcription is shown below
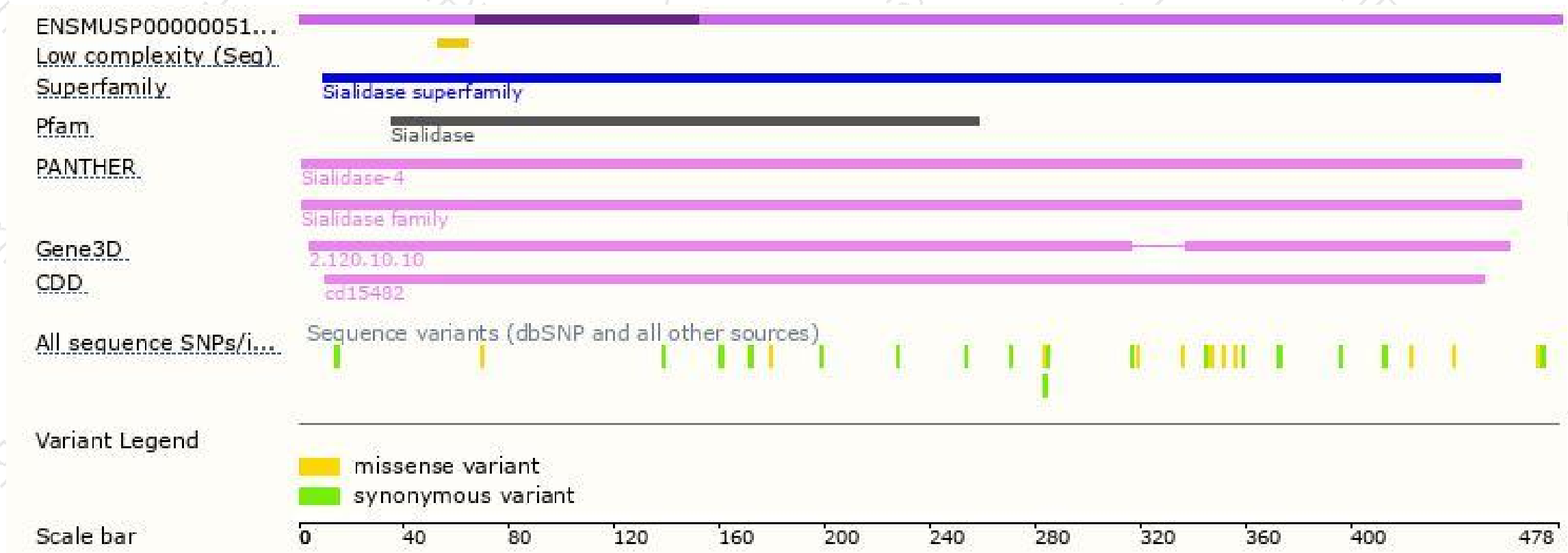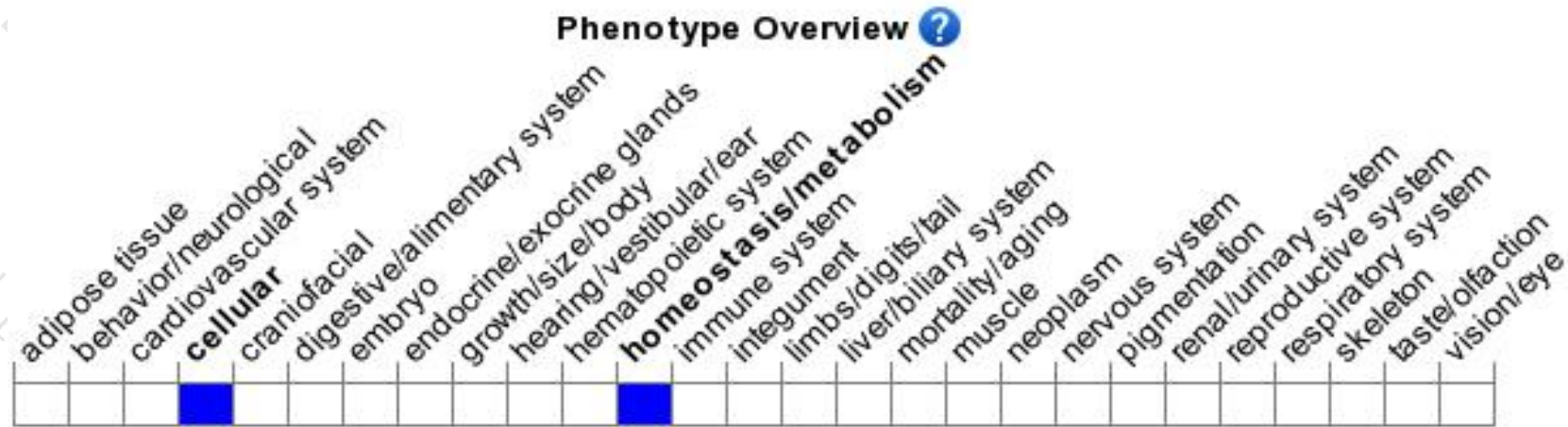
Genomic location distribution
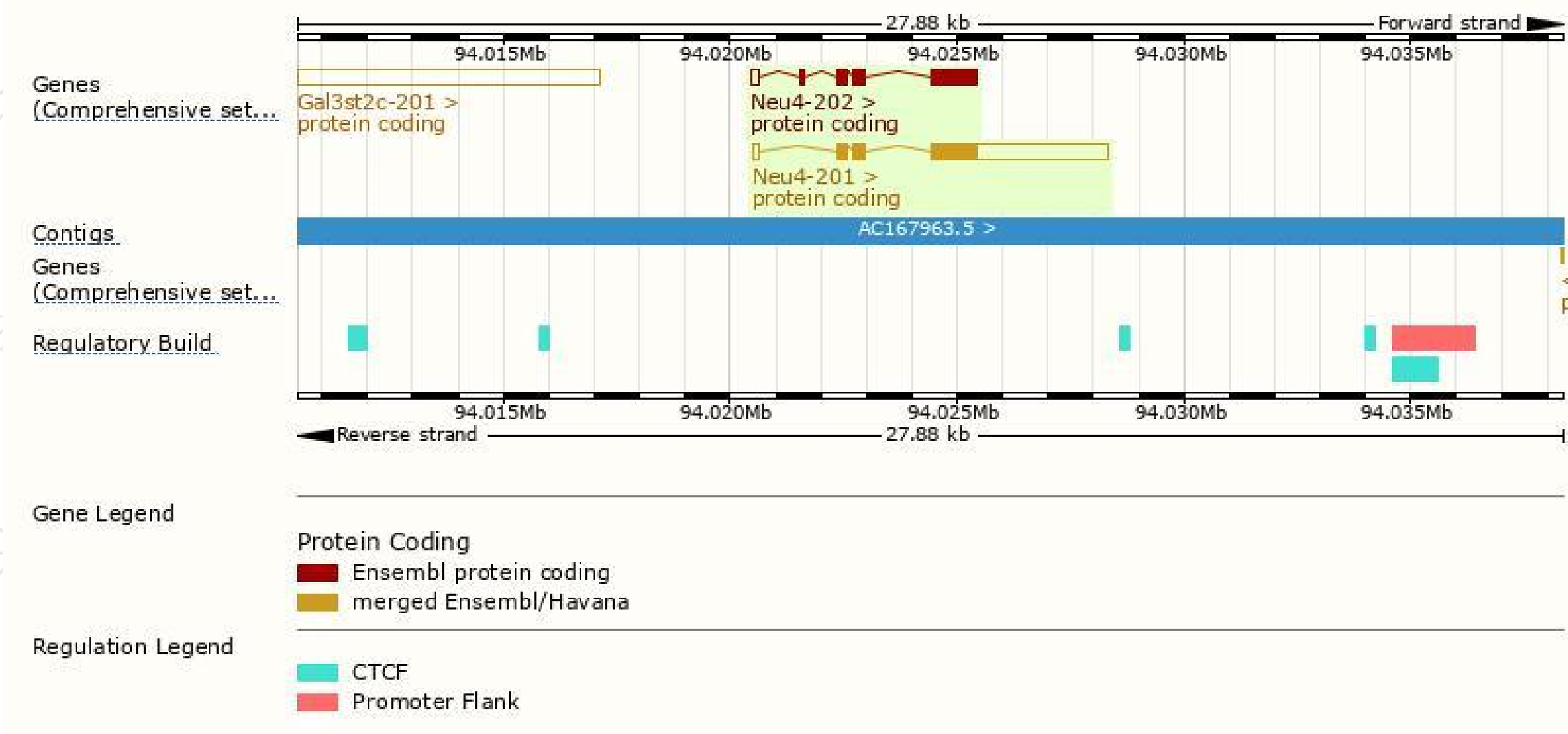
Protein domain

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 null allele are largely normal except increased lipid content in the lung and liver and vacuolization indicative of lysosomal storage disorder.

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