Cdh11 Cas9-CKO Strategy

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Overview

Target Gene Name

- *Cdh11*
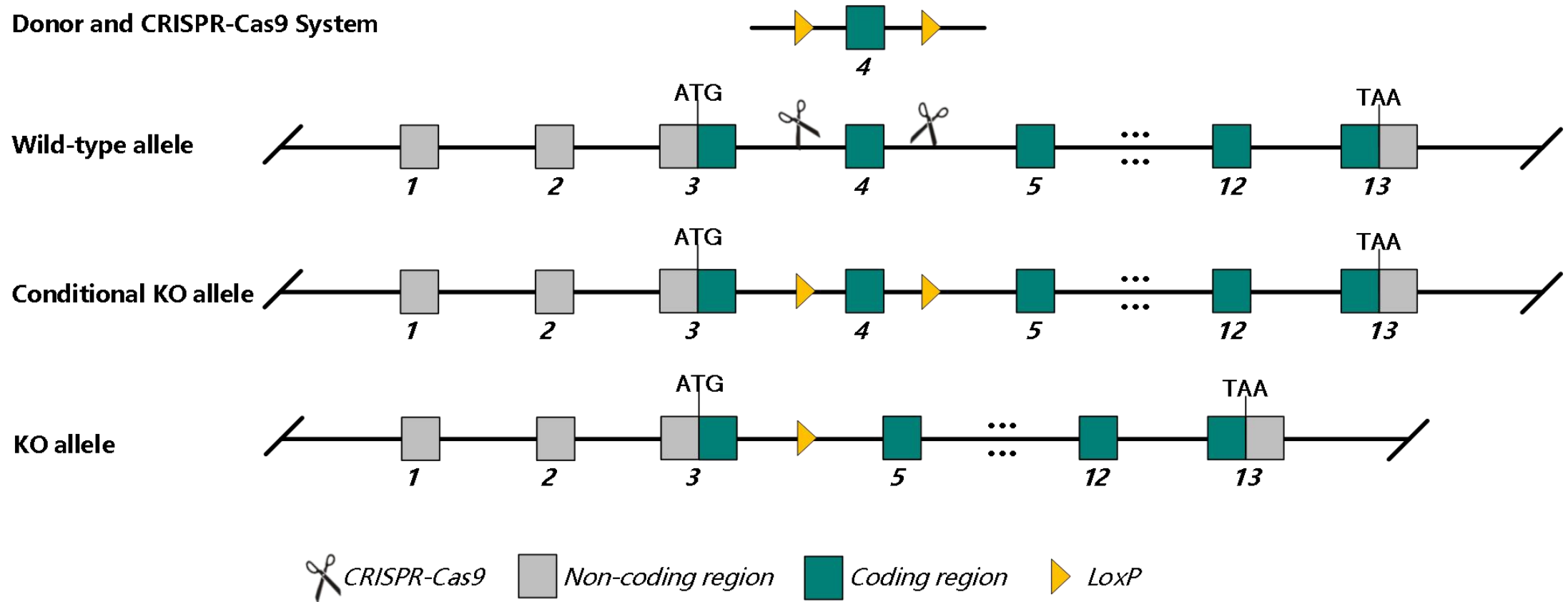
Project Type

- Cas9-CKO

Genetic Background

- C57BL/6JGpt

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Strain Strategy

Schematic representation of CRISPR-Cas9 engineering used to edit the *Cdh11* gene.

Technical Information

- The *Cdh11* gene has 3 transcripts. According to the structure of *Cdh11* gene, exon 4 of *Cdh11*-201 (ENSMUST00000075190.5) is recommended as the knockout region. The region contains 295 bp of coding sequence. Knockout the region will result in disruption of gene function.

- In this project we use CRISPR-Cas9 technology to modify *Cdh11* 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.

- 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.

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Gene Information

Cdh11   cadherin 11 [*Mus musculus* (house mouse)]

 Download Datasets

Gene ID: 12552, updated on 26-Apr-2023

▲ Summary

Official Symbol	Cdh11 provided by MGI
Official Full Name	cadherin 11 provided by MGI
Primary source	MGI:MGI:99217
See related	Ensembl:ENSMUSG00000031673 AllianceGenome:MGI:99217
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	Cad11; OSF-4
Summary	This gene encodes a type II classical cadherin and preproprotein that is proteolytically processed to generate a mature protein product. This protein product is an integral membrane protein that mediates calcium-dependent cell-cell adhesion, specifically in the context of bone development. Homozygous knockout mice for this gene exhibit impaired synovium development and reduced bone density. Multiple pseudogenes of this gene have been identified in the genome. [provided by RefSeq, Aug 2015]
Expression	Biased expression in limb E14.5 (RPKM 39.5), CNS E11.5 (RPKM 18.9) and 14 other tissues See more
Orthologs	human all

NEW   Try the new **Gene table**
      Try the new **Transcript table**

▲ Genomic context

Location:	8 D1; 8 50.44 cM

See Cdh11 in Genome Data Viewer

Exon count: 15

https://www.ncbi.nlm.nih.gov/gene/12552
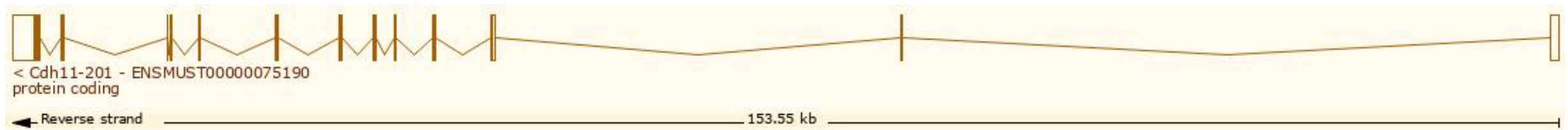
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Transcript Information

The gene has 3 transcripts, all transcripts are shown below:

Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000075190.5	Cdh11-201	5647	796aa	Protein coding	CCDS22571	P55288	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1
ENSMUST00000210425.2	Cdh11-202	5153	No protein	Retained intron		-	TSL:1
ENSMUST00000210578.2	Cdh11-203	599	No protein	Retained intron		-	TSL:2

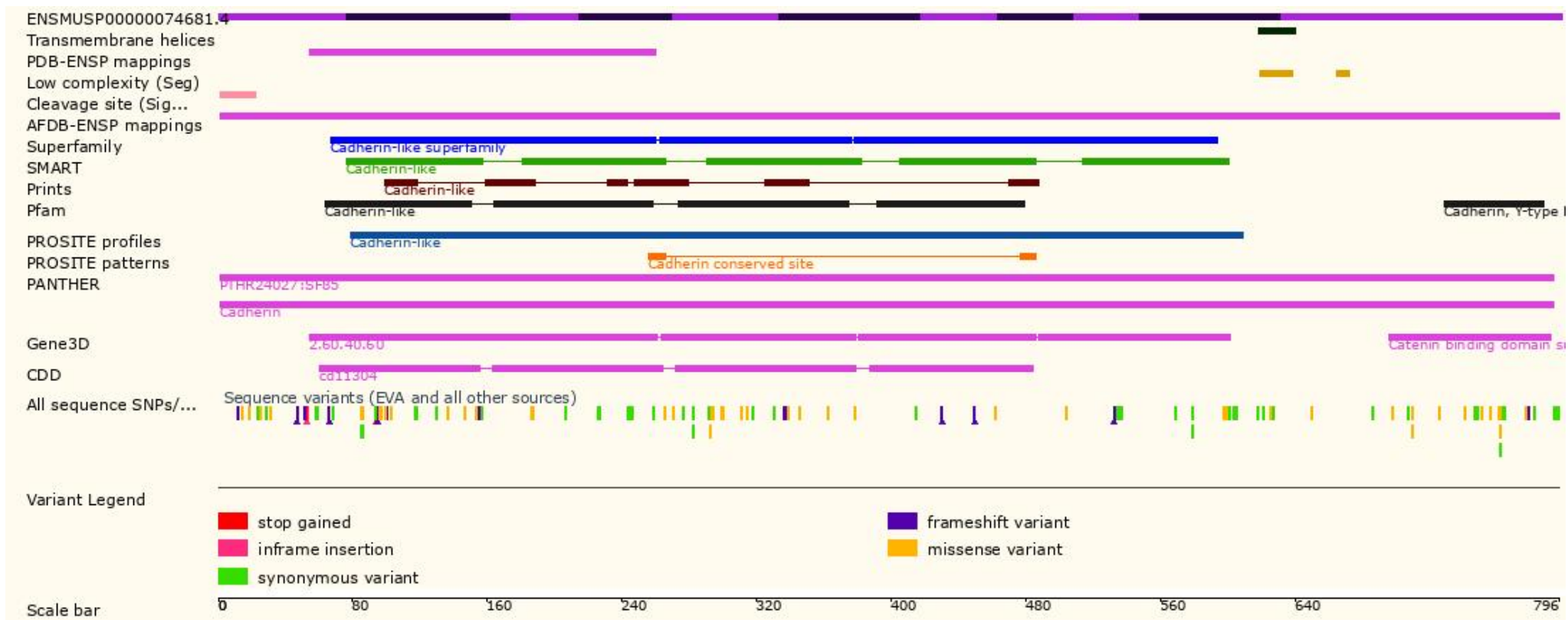The strategy is based on the design of *Cdh11*-201 transcript, the transcription is shown below:
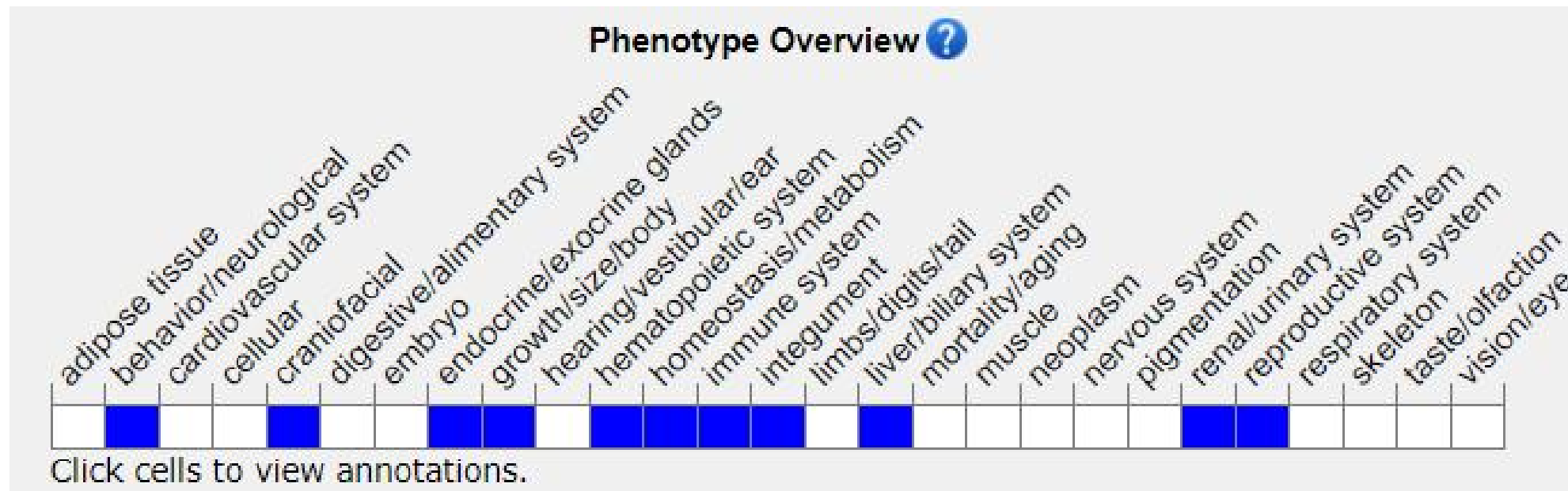

< Cdh11-201 - ENSMUST00000075190
protein coding

Reverse strand   153.55 kb

Source: http://asia.ensembl.org/

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Genomic Information

Protein Information

Source: : https://www.ensembl.org
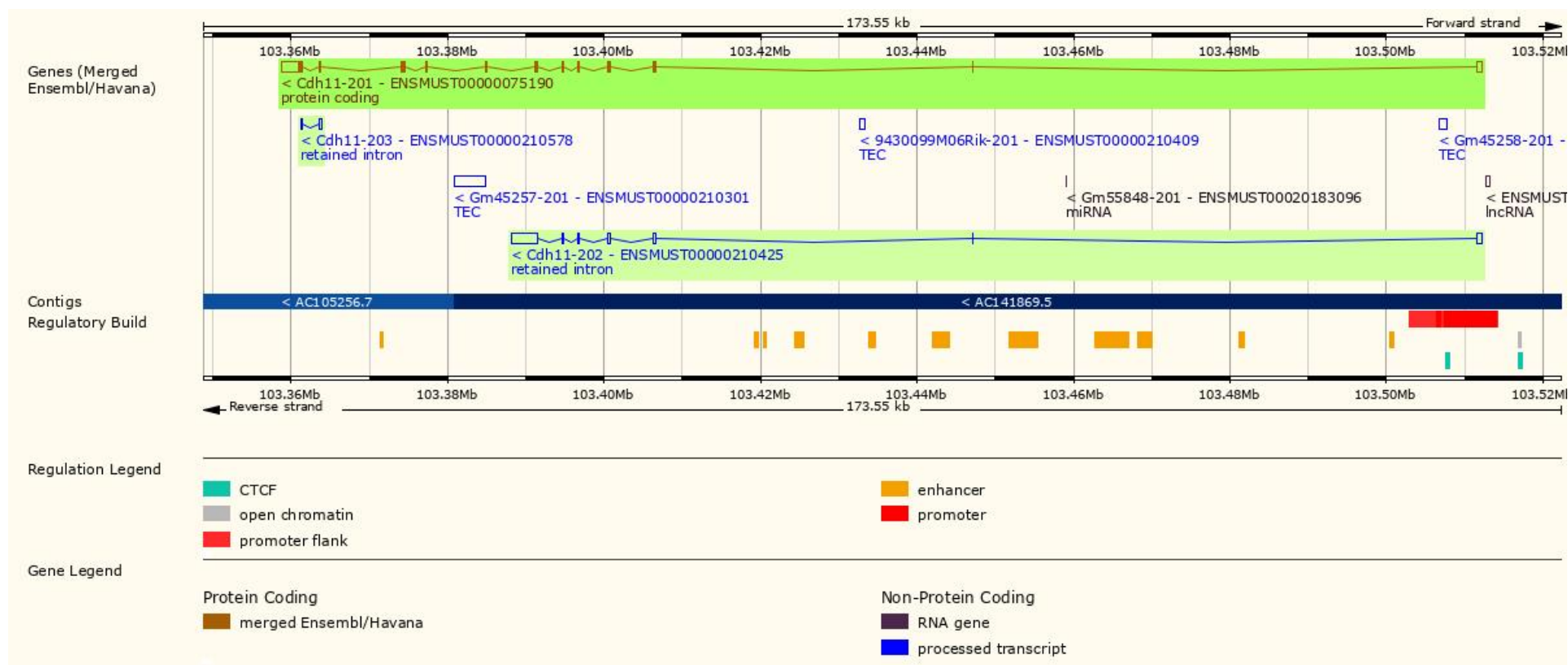
Mouse Phenotype Information (MGI)

Homozygous mutant animals appear healthy and fertile.

Source: https://www.informatics.jax.org

Important Information

- According to the existing MGI data, homozygous mutant animals appear healthy and fertile.

- This stratergy may not affect *Cdh11*-203 transcript.

- *Cdh11* is located on Chr 8. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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 the existing technology level.

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