

Adrb2 Cas9-KO Strategy

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Reviewer:

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Project Overview

Project Name

Adrb2

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Adrb2* gene. The schematic diagram is as follows:



- The *Adrb2* gene has 1 transcript. According to the structure of *Adrb2* gene, exon1 of *Adrb2-201* (ENSMUST00000053640.4) 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 *Adrb2* gene. The brief process is as follows: gRNA was transcribed in vitro. Cas9 and gRNA 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.

- According to the existing MGI data, Mice homozygous for targeted mutations that inactivate the gene exhibit increased bone mass. The primary physiological consequences are seen during exercise stress and result from alterations in vascular tone and energy metabolism.
- The KO region contains functional region of the *Gm9949* gene. Knockout the region may affect the function of *Gm9949* gene.
- The *Adrb2* gene is located on the Chr18. 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)

Adrb2 adrenergic receptor, beta 2 [Mus musculus (house mouse)]

Gene ID: 11555, updated on 23-Feb-2019

Summary



Official Symbol Adrb2 provided by [MGI](#)

Official Full Name adrenergic receptor, beta 2 provided by [MGI](#)

Primary source [MGI:MGI:87938](#)

See related [Ensembl:ENSMUSG00000045730](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as Adrb-2, Badm, Gpcr7

Summary This intronless gene belongs to the G-protein-coupled receptor superfamily, which includes transmembrane proteins that play a role in signal transduction across biological membranes resulting in a variety of physiological responses. The encoded protein is a beta-2 adrenergic receptor which is activated by catecholamine ligands such as adrenaline and epinephrine. The protein participates in the classical signaling pathway involving G protein, adenylyl cyclase, cAMP (3'-5'-cyclic adenosine monophosphate) and protein kinase A (PKA). In humans, this gene is implicated in susceptibility to nocturnal asthma, obesity and type 2 diabetes. [provided by RefSeq, Apr 2013]

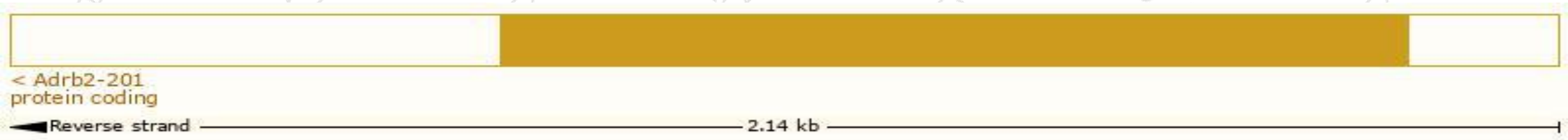
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

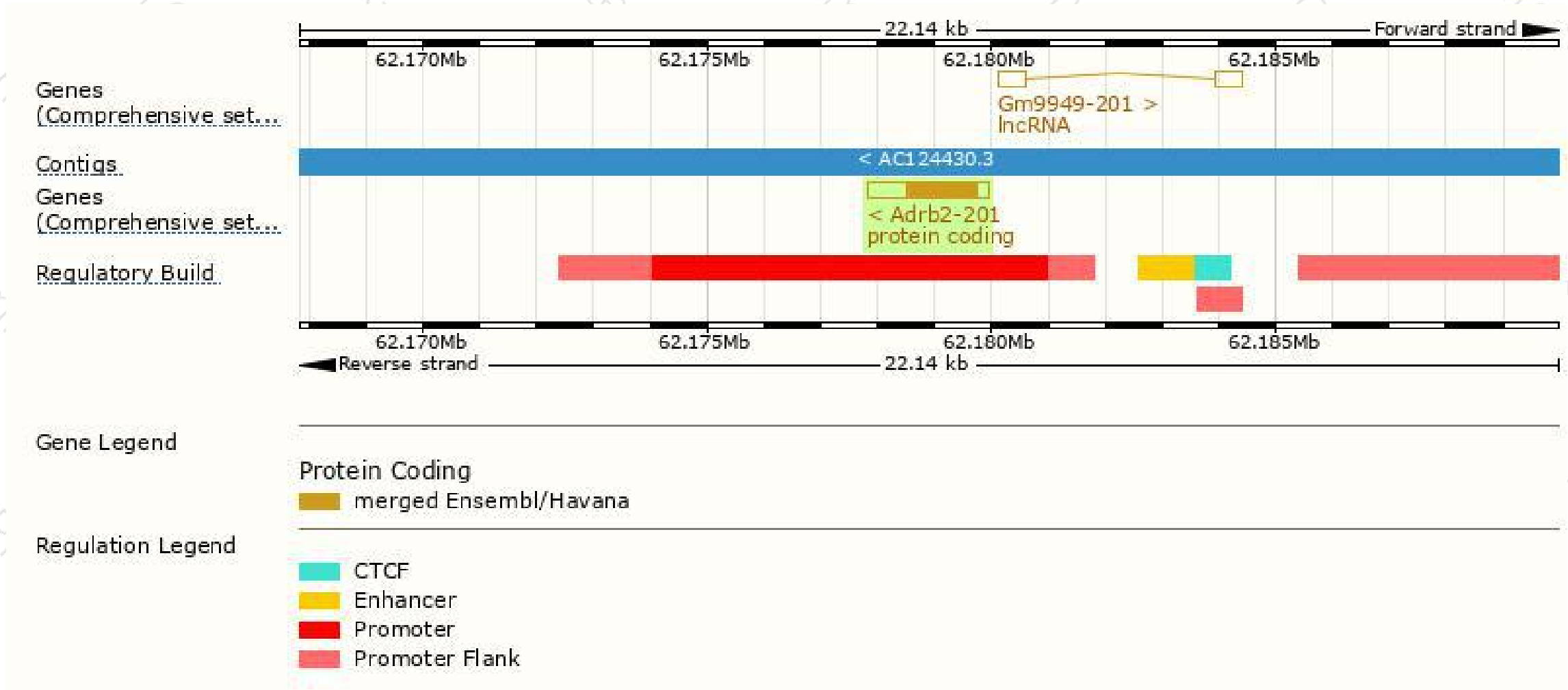
The gene has 1 transcript, and the transcript is shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Adrb2-201	ENSMUST00000053640.4	2144	418aa	Protein coding	CCDS29289	P18762	TSL:NA GENCODE basic APPRIS P1

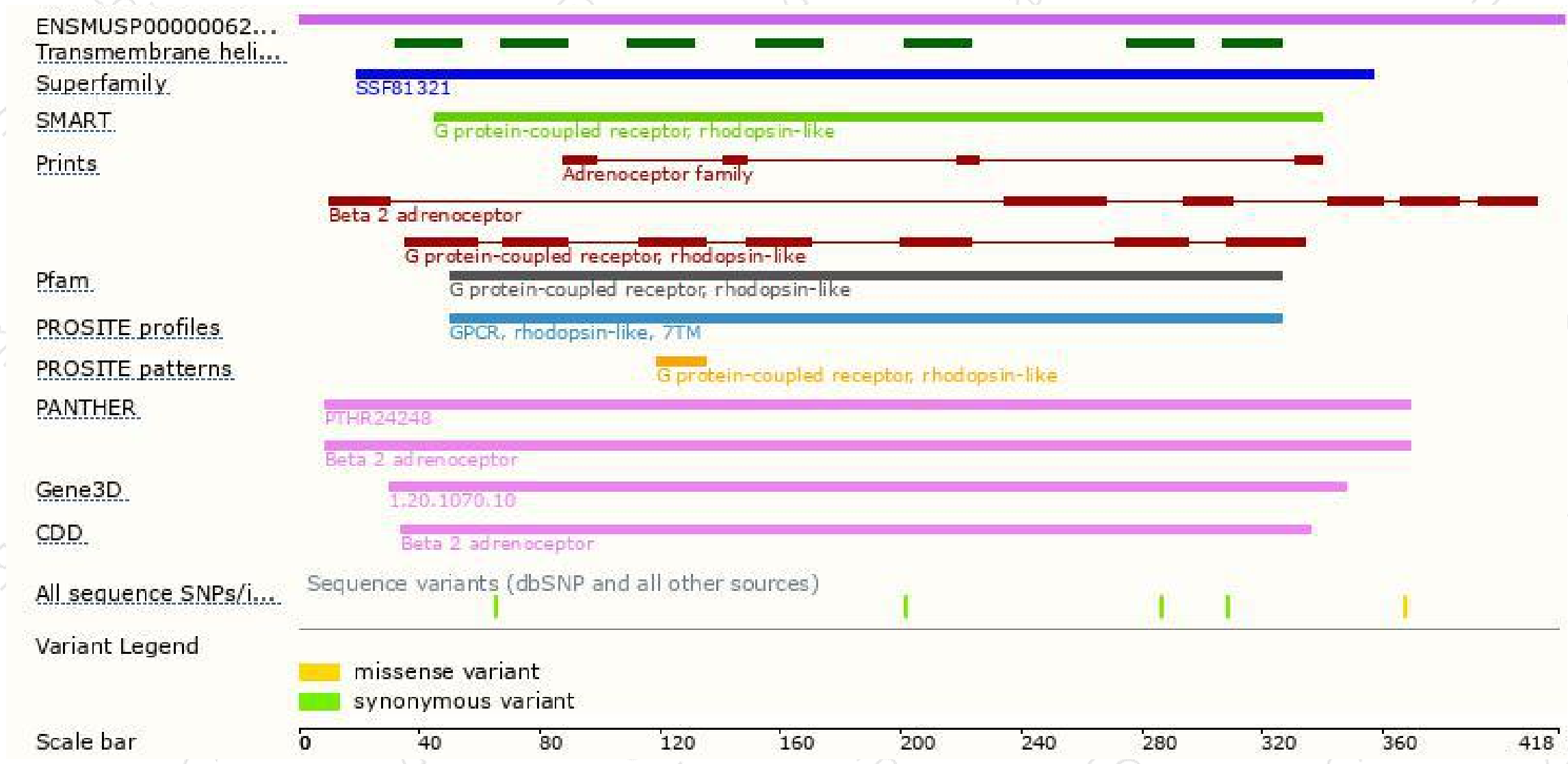
The strategy is based on the design of *Adrb2-201* transcript, The transcription is shown below



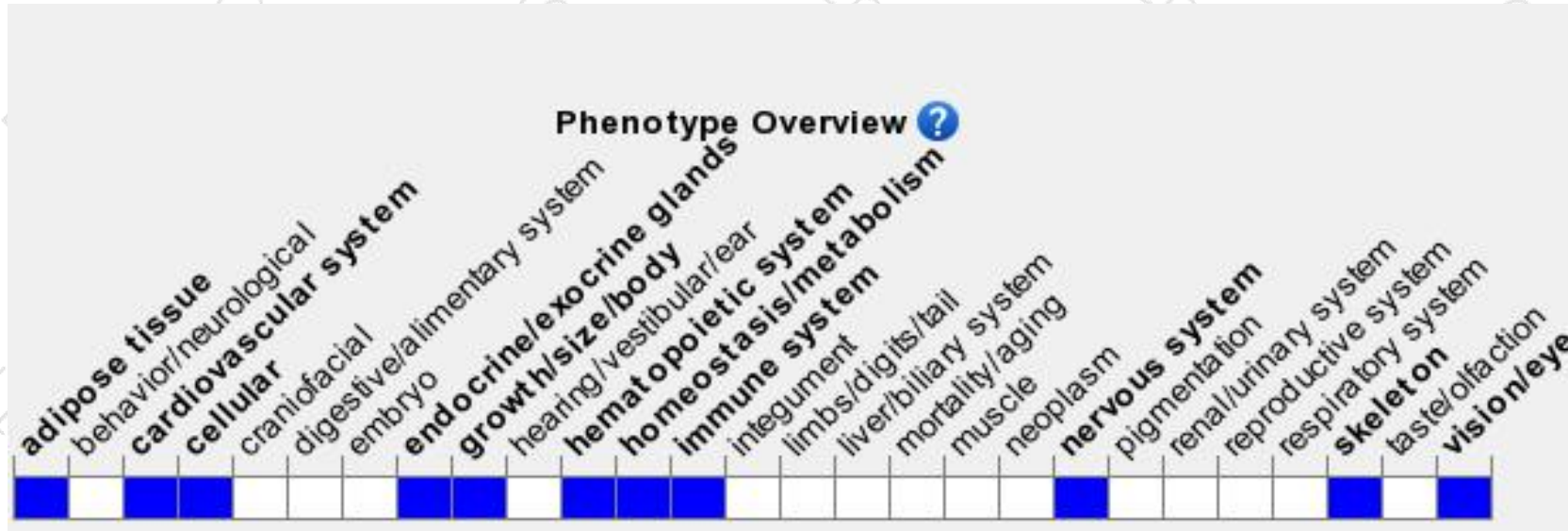
Genomic location distribution



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 targeted mutations that inactivate the gene exhibit increased bone mass. The primary physiological consequences are seen during exercise stress and result from alterations in vascular tone and energy metabolism.

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

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