

# ***Dact2*** Cas9-KO Strategy

**Designer:**

**Ruirui Zhang**

**Reviewer:**

**Huimin Su**

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# Project Overview

**Project Name**

***Dact2***

**Project type**

**Cas9-KO**

**Strain background**

**C57BL/6JGpt**

# Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Dact2* gene. The schematic diagram is as follows:



- The *Dact2* gene has 2 transcripts. According to the structure of *Dact2* gene, exon2 of *Dact2-201* (ENSMUST00000053218.6) transcript is recommended as the knockout region. The region contains 133bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Dact2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a knock-out allele develop normally but display enhanced keratinocyte migration and accelerated re-epithelialization during cutaneous wound healing.
- The *Dact2* gene is located on the Chr17. 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)

## Dact2 dishevelled-binding antagonist of beta-catenin 2 [ *Mus musculus* (house mouse) ]

Gene ID: 240025, updated on 12-Aug-2019

### Summary



**Official Symbol** Dact2 provided by [MGI](#)

**Official Full Name** dishevelled-binding antagonist of beta-catenin 2 provided by [MGI](#)

**Primary source** [MGI:MGI:1920347](#)

**See related** [Ensembl:ENSMUSG00000048826](#)

**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** Dpr2; Frd2; dapper2; A630024E20; 2900084M21Rik

**Expression** Broad expression in cortex adult (RPKM 12.9), thymus adult (RPKM 11.5) and 19 other tissues [See more](#)

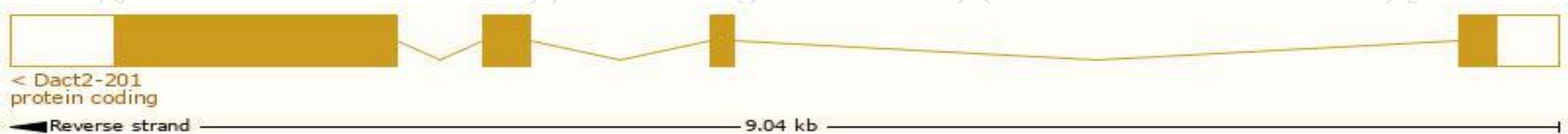
**Orthologs** [human](#) [all](#)

# Transcript information (Ensembl)

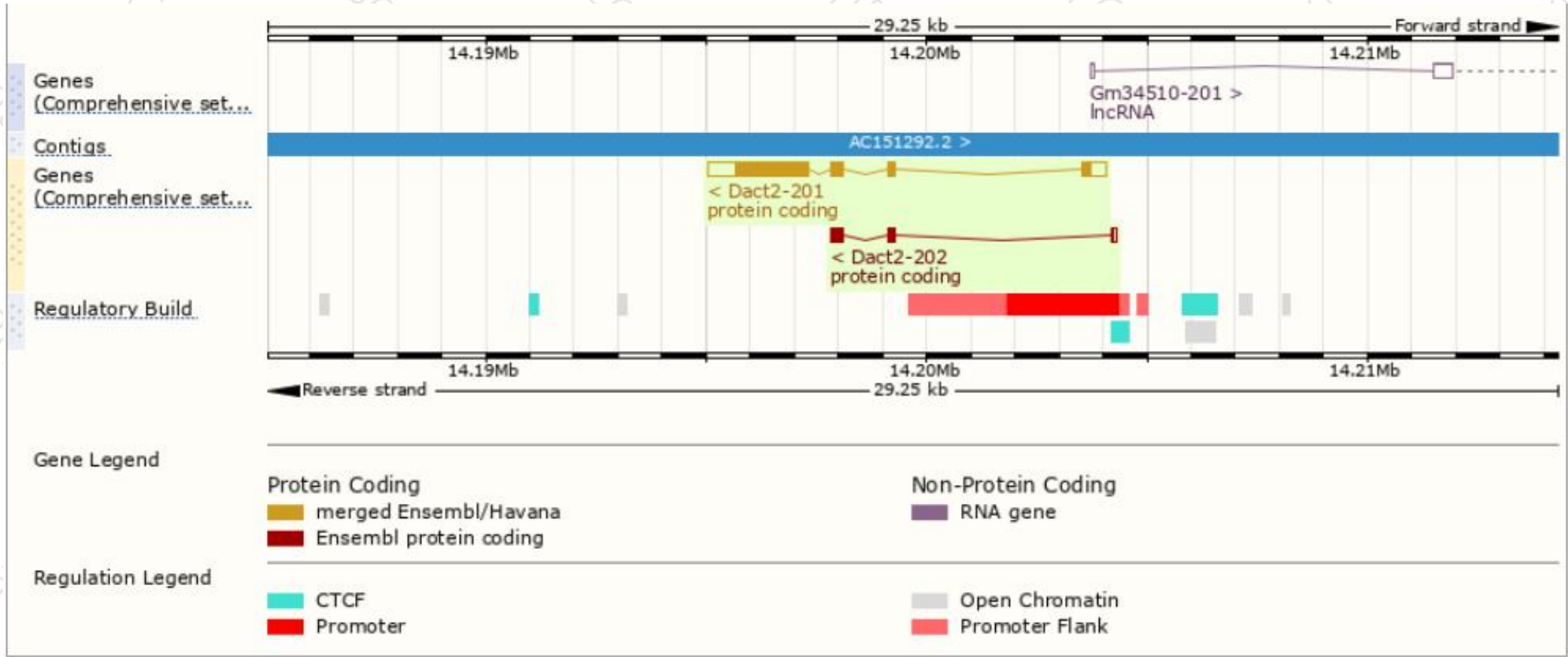
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dact2-201	<a href="#">ENSMUST00000053218.6</a>	3250	<a href="#">757aa</a>	Protein coding	<a href="#">CCDS28406</a>	<a href="#">Q7TN08</a>	TSL:1 GENCODE basic APPRIS P1
Dact2-202	<a href="#">ENSMUST00000232816.1</a>	532	<a href="#">150aa</a>	Protein coding	-	<a href="#">A0A3B2W472</a>	CDS 3' incomplete

The strategy is based on the design of *Dact2-201* transcript,The transcription is shown below



# Genomic location distribution

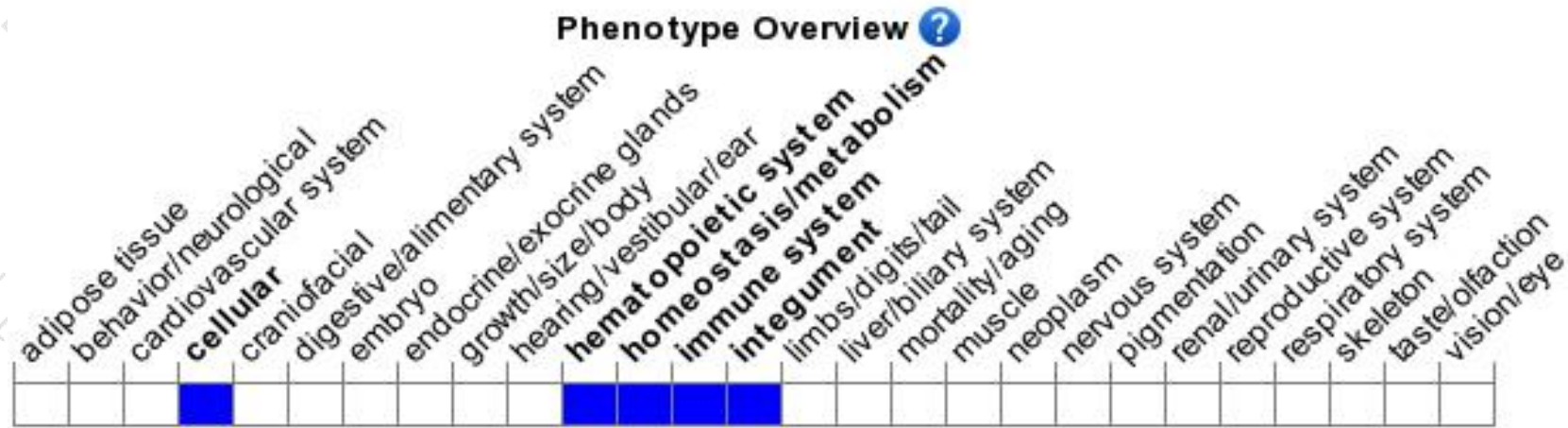




# Protein domain



# 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 knock-out allele develop normally but display enhanced keratinocyte migration and accelerated re-epithelialization during cutaneous wound healing.

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

Tel: 400-9660890

