

Dsc1 Cas9-KO Strategy

Designer: Xueting Zhang

Reviewer: Yanhua Shen

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Project Overview

Project Name

Dsc1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Dsc1* gene. The schematic diagram is as follows:



- The *Dsc1* gene has 4 transcripts. According to the structure of *Dsc1* gene, exon2-exon6 of *Dsc1-201* (ENSMUST00000038710.5) transcript is recommended as the knockout region. The region contains 709bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Dsc1* gene. The brief process is as follows: CRISPR/Cas9 system v

- According to the existing MGI data, Mutants with targeted disruptions of this gene have fragile epidermis, flaky skin, and defects in the epidermal barrier, leading to chronic dermatitis and display abnormal epidermal differentiation as indicated by hyperproliferation and overexpression of keratin 6 and 16.
- The *Dsc1* 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)

Dsc1 desmocollin 1 [*Mus musculus* (house mouse)]

Gene ID: 13505, updated on 24-Oct-2019

Summary

- Official Symbol** Dsc1 provided by MGI
- Official Full Name** desmocollin 1 provided by MGI
- Primary source** MGI:MGI:109173
- See related** Ensembl:ENSMUSG00000044322
- 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** AI507491; 1110020A10Rik
- Summary** This gene encodes a member of the cadherin family of proteins that mediates adhesion in desmosomes. The encoded preproprotein undergoes proteolytic processing to generate the mature, functional protein. Mice lacking the encoded protein exhibit epidermal fragility together with defects of epidermal barrier and differentiation. The neonatal mice lacking the encoded protein exhibit epidermal lesions and older mice develop chronic dermatitis. This gene is located in a cluster of desmosomal cadherin genes on chromosome 18. Alternate splicing of this gene results in multiple transcript variants encoding different isoforms that may undergo similar proteolytic processing. [provided by RefSeq, Jan 2016]
- Expression** Biased expression in stomach adult (RPKM 1.7), lung adult (RPKM 1.0) and 2 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 18; 18 A2 See Dsc1 in [Genome Data Viewer](#)

Exon count: 17

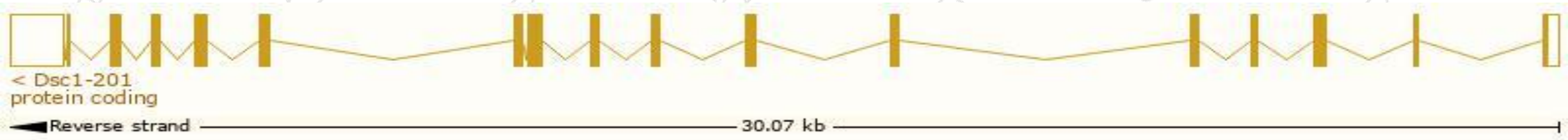
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	18	NC_000084.6 (20083471..20114773, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	18	NC_000084.5 (20243204..20273274, complement)

Transcript information (Ensembl)

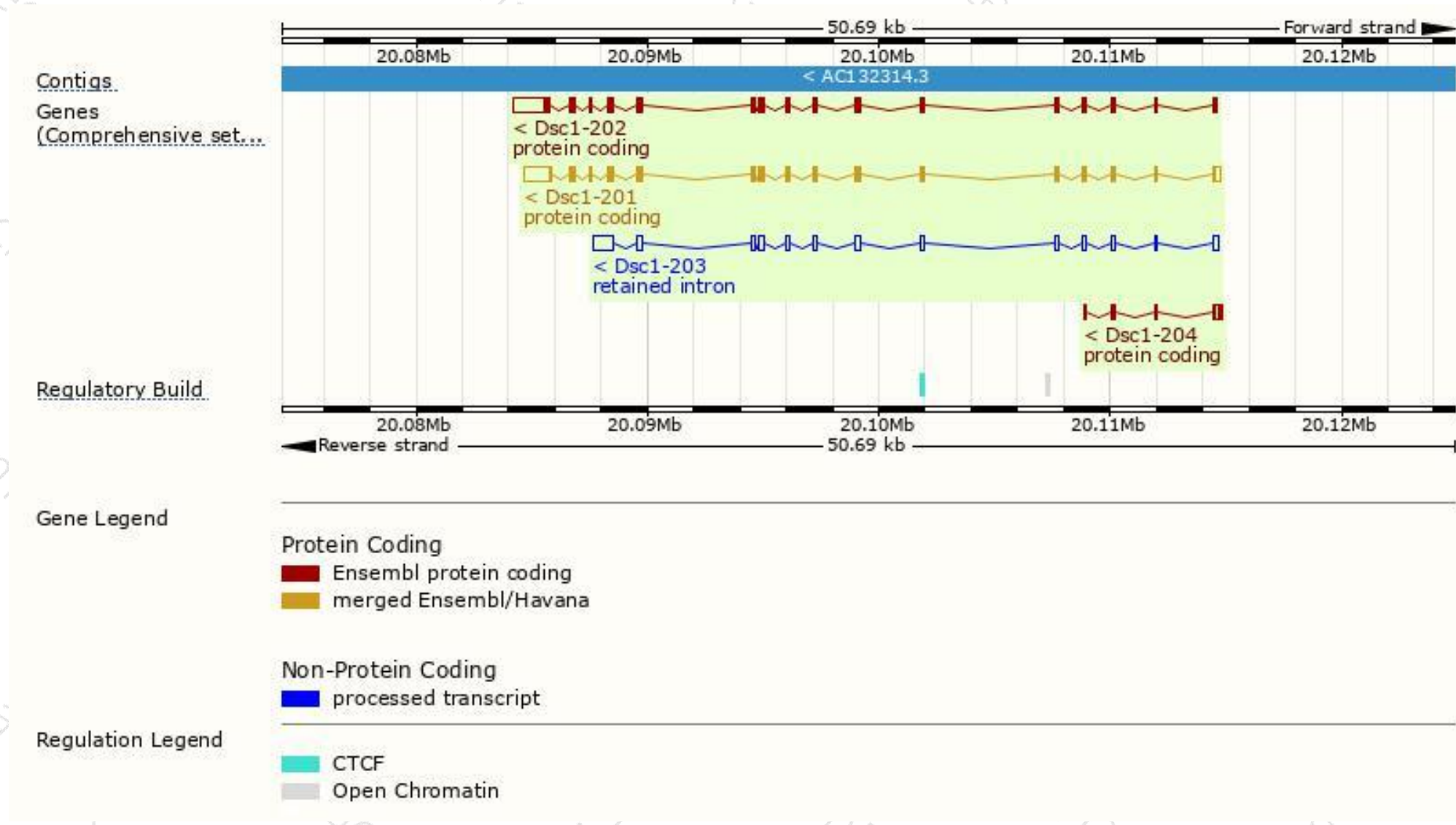
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dsc1-201	ENSMUST00000038710.5	3775	832aa	Protein coding	CCDS29078	Q32ME9	TSL:1 GENCODE basic APPRIS P2
Dsc1-202	ENSMUST00000224432.1	4085	886aa	Protein coding	-	P55849	GENCODE basic APPRIS ALT2
Dsc1-204	ENSMUST00000226115.1	663	147aa	Protein coding	-	A0A286YCT9	CDS 3' incomplete
Dsc1-203	ENSMUST00000224557.1	2872	No protein	Retained intron	-	-	

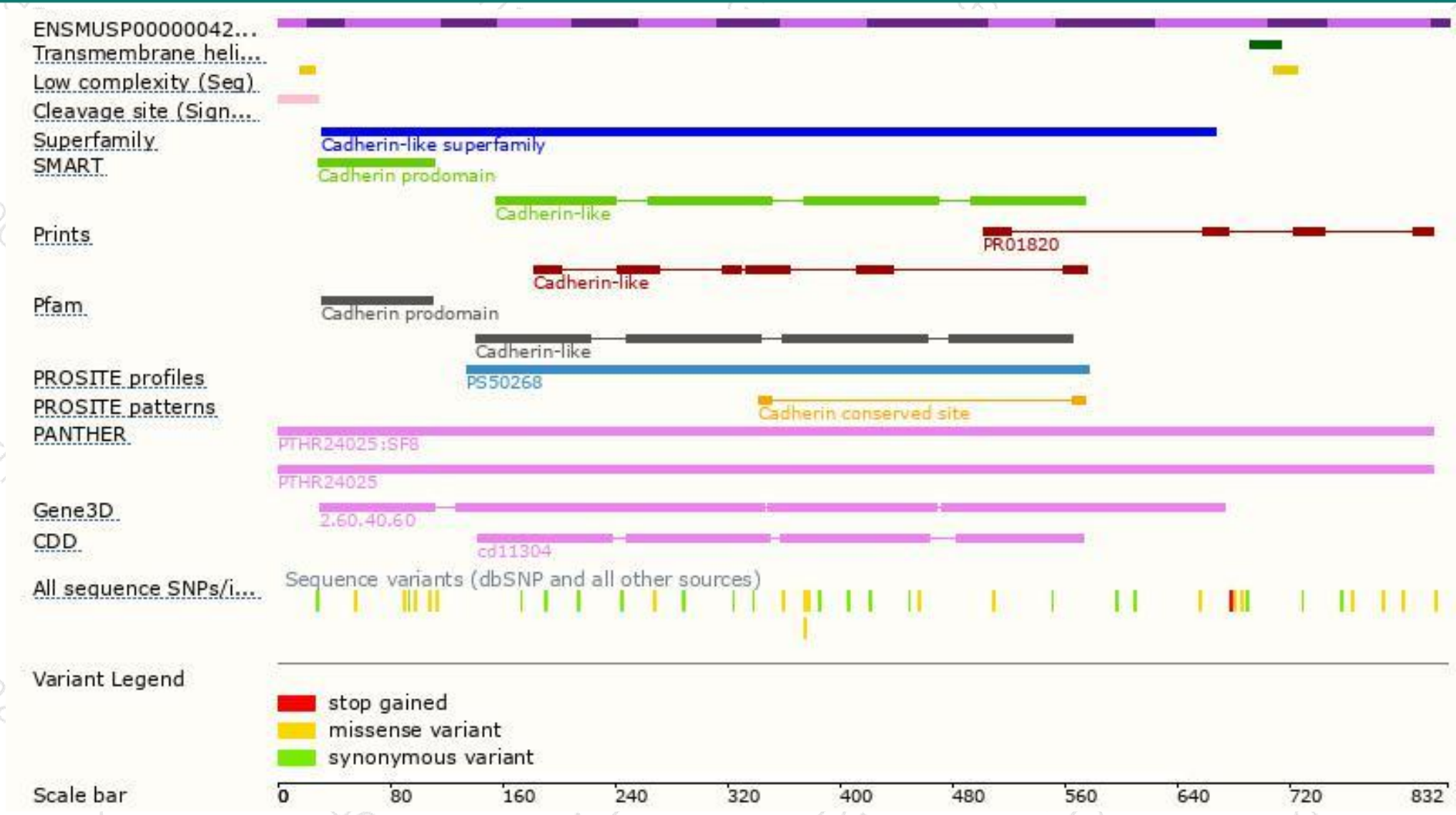
The strategy is based on the design of *Dsc1-201* transcript,The transcription is shown below



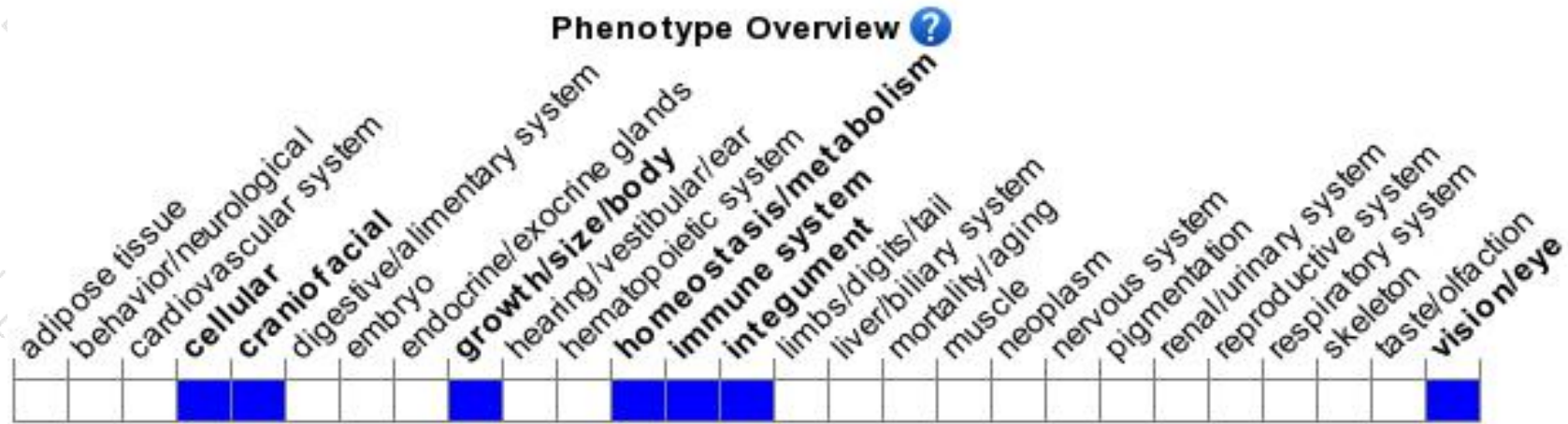
Genomic location distribution



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, Mutants with targeted disruptions of this gene have fragile epidermis, flaky skin, and defects in the epidermal barrier, leading to chronic dermatitis and display abnormal epidermal differentiation as indicated by hyperproliferation and overexpression of keratin 6 and 16.

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

Tel: 400-9660890

