

Twist2 Cas9-KO Strategy

Designer:

Daohua Xu

Reviewer:

Huimin Su

Design Date:

2019-9-28

Project Overview

Project Name

Twist2

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Twist2* gene. The schematic diagram is as follows:



- The *Twist2* gene has 2 transcripts. According to the structure of *Twist2* gene, exon1 of *Twist2-202* (ENSMUST00000186075.1) 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 *Twist2* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Deletion of this gene results in high postnatal lethality. Progressive growth retardation is observed with adipose tissue deficiency, skin, hair and muscle abnormalities, as well as hematopoietic and lymphoid organ defects including the spleen, thymus, and liver.
- The *Twist2* 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 the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)

Twist2 twist basic helix-loop-helix transcription factor 2 [Mus musculus (house mouse)]

Gene ID: 13345, updated on 9-Apr-2019

Summary



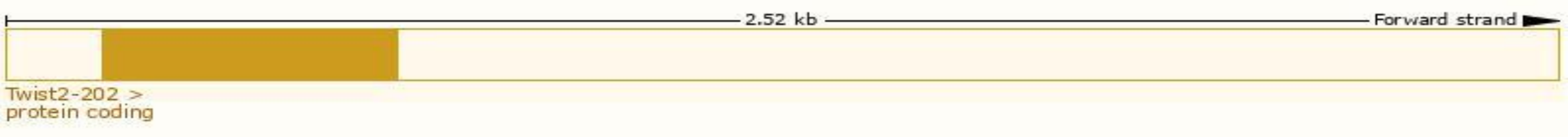
Official Symbol	Twist2 provided by MGI
Official Full Name	twist basic helix-loop-helix transcription factor 2 provided by MGI
Primary source	MGI:MGI:104685
See related	Ensembl:ENSMUSG000000007805
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Dermo1, bHLHa39
Expression	Biased expression in limb E14.5 (RPKM 83.6), subcutaneous fat pad adult (RPKM 39.3) and 9 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

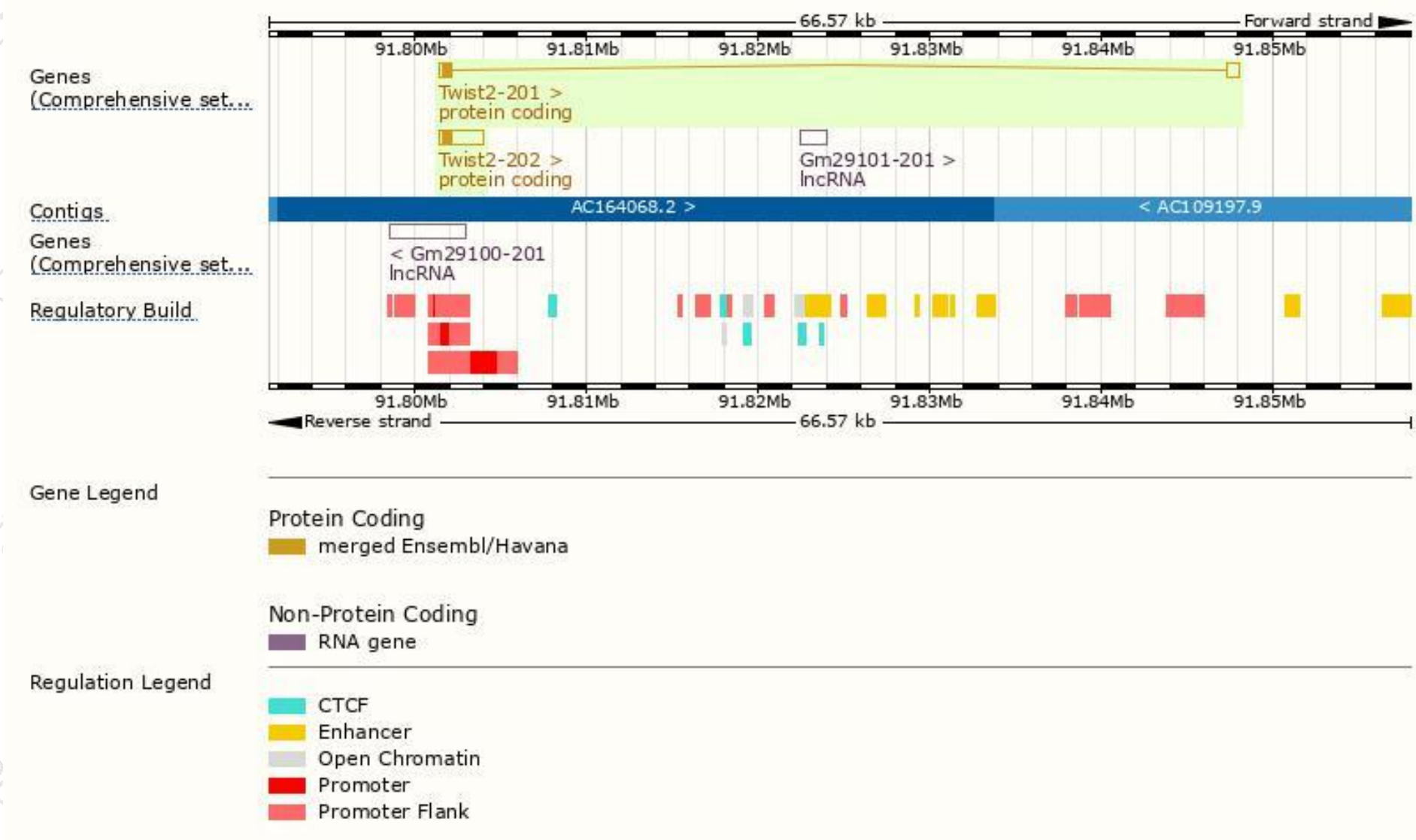
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Twist2-202	ENSMUST00000186075.1	2525	160aa	Protein coding	CCDS15166	A5D6P6	TSL:NA GENCODE basic APPRIS P1
Twist2-201	ENSMUST00000007949.3	1329	160aa	Protein coding	CCDS15166	A5D6P6	TSL:1 GENCODE basic APPRIS P1

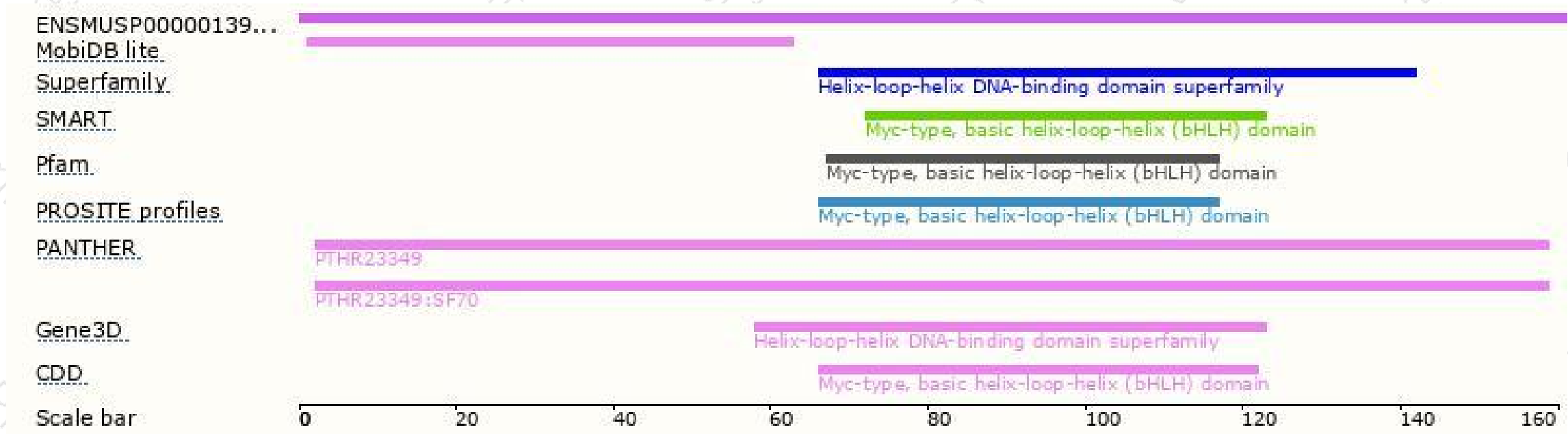
The strategy is based on the design of *Twist2-202* transcript,The transcription is shown below



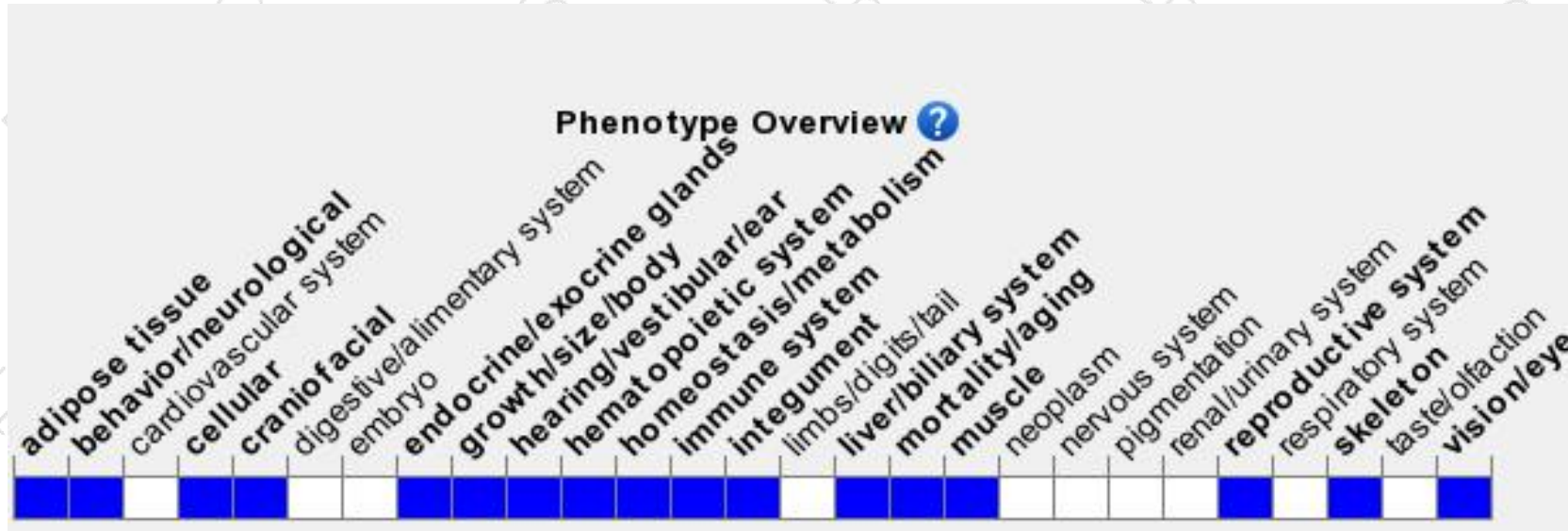
Genomic location distribution



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, Deletion of this gene results in high postnatal lethality. Progressive growth retardation is observed with adipose tissue deficiency, skin, hair and muscle abnormalities, as well as hematopoietic and lymphoid organ defects including the spleen, thymus, and liver.

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

Tel: 400-9660890

