

Dapp1 Cas9-KO Strategy

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Project Overview

Project Name

Dapp1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Dapp1* gene. The schematic diagram is as follows:



- The *Dapp1* gene has 7 transcripts. According to the structure of *Dapp1* gene, exon2-exon3 of *Dapp1-201* (ENSMUST00000029806.12) transcript is recommended as the knockout region. The region contains 257bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Dapp1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Inactivation of this gene invokes immune defects stemming from impaired B cell receptor crosslinking.
- The *Dappl* gene is located on the Chr3. 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)

Dapp1 dual adaptor for phosphotyrosine and 3-phosphoinositides 1 [Mus musculus (house mouse)]

Gene ID: 26377, updated on 31-Jan-2019

Summary



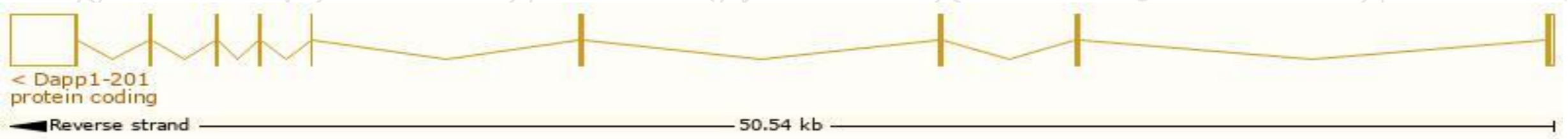
Official Symbol	Dapp1 provided by MGI
Official Full Name	dual adaptor for phosphotyrosine and 3-phosphoinositides 1 provided by MGI
Primary source	MGI:MGI:1347063
See related	Ensembl:ENSMUSG00000028159
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Bam32
Expression	Ubiquitous expression in bladder adult (RPKM 5.5), liver E14 (RPKM 5.3) and 26 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

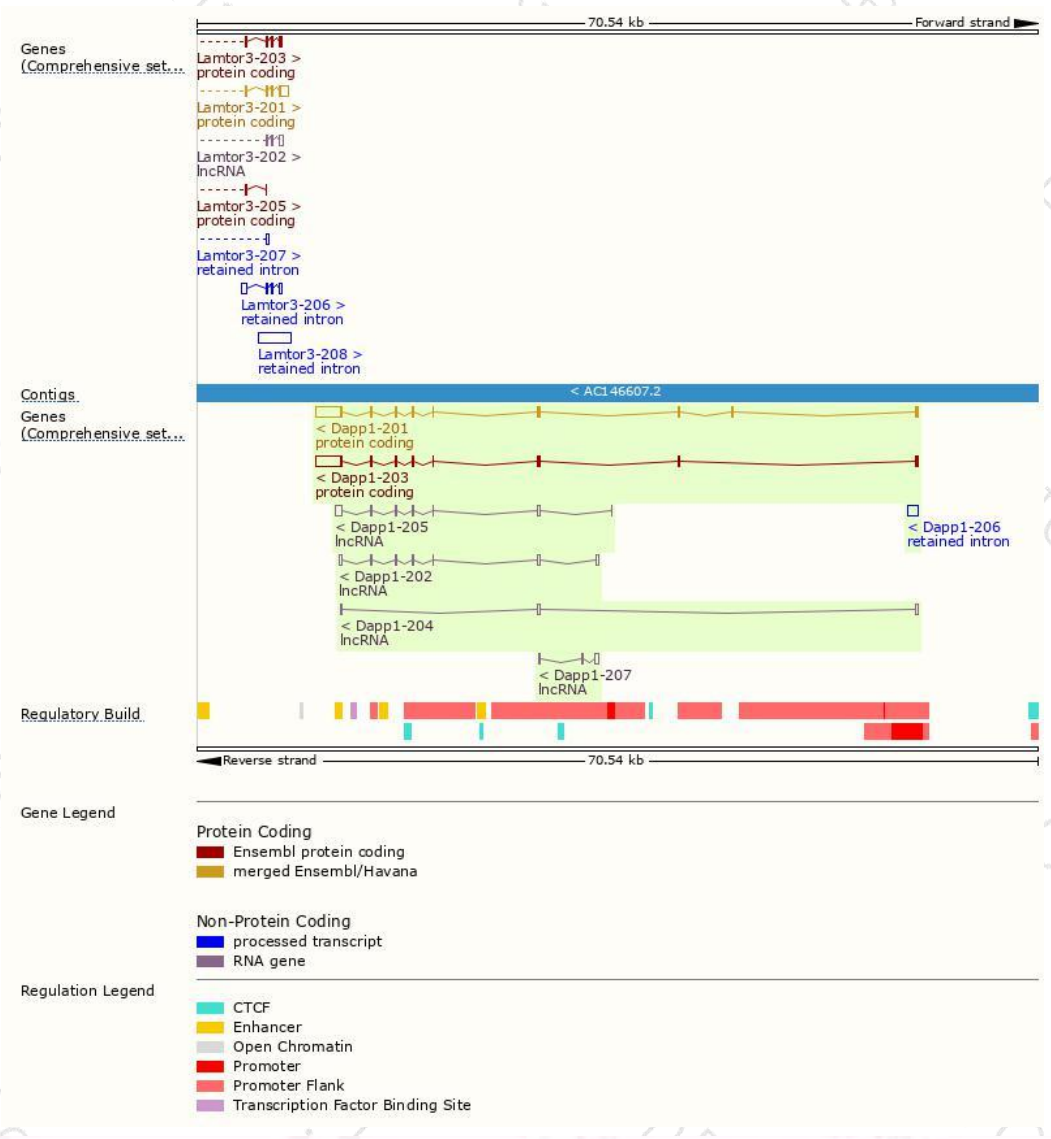
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dapp1-201	ENSMUST00000029806.12	3083	280aa	Protein coding	CCDS17864	Q3UK44 Q9QXT1	TSL:1 GENCODE basic APPRIS P1
Dapp1-203	ENSMUST00000136613.3	2950	239aa	Protein coding	CCDS80029	Q3TEK6	TSL:1 GENCODE basic
Dapp1-206	ENSMUST00000199541.1	832	No protein	Retained intron	-	-	TSL:NA
Dapp1-205	ENSMUST00000184222.5	962	No protein	lncRNA	-	-	TSL:1
Dapp1-202	ENSMUST00000124827.7	782	No protein	lncRNA	-	-	TSL:3
Dapp1-207	ENSMUST00000200596.1	439	No protein	lncRNA	-	-	TSL:5
Dapp1-204	ENSMUST00000154716.1	429	No protein	lncRNA	-	-	TSL:2

The strategy is based on the design of *Dapp1-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain



集萃药康
GemPharmatech

ENSMUSP00000029...

Superfamily

SH2 domain superfamily

SSF50729

SMART

SH2 domain

Pleckstrin homology domain

Prints

PR00678

SH2 domain

SH2 domain

Pleckstrin homology domain

Pfam

PROSITE profiles

SH2 domain

Pleckstrin homology domain

PANTHER

PTHR14336

PTHR14336:SF7

Gene3D

SH2 domain superfamily

PH-like domain superfamily

CDD

DAPP1, SH2 domain

cd10573

All sequence SNPs/i...

Sequence variants (dbSNP and all other sources)

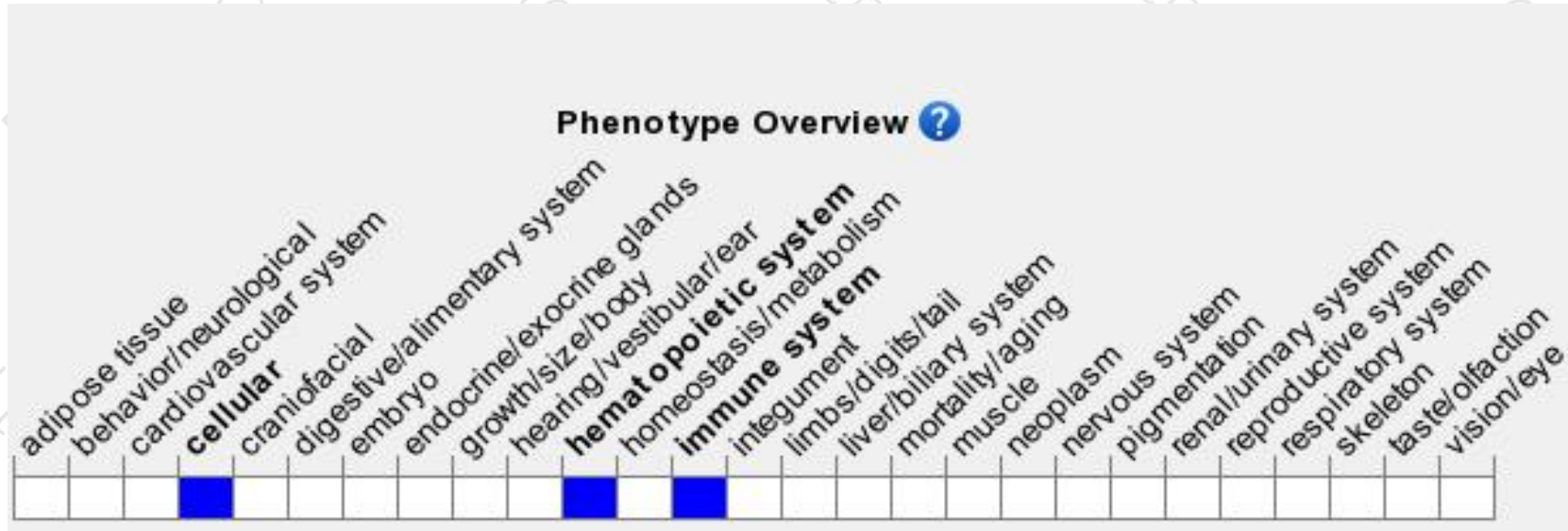
Variant Legend

synonymous variant

Scale bar

0 40 80 120 160 200 240 280

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, Inactivation of this gene invokes immune defects stemming from impaired B cell receptor crosslinking.

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

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