

Dpp4 Cas9-KO Strategy

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Project Overview



Project Name

Dpp4

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Dpp4* gene. The schematic diagram is as follows:



- The *Dpp4* gene has 6 transcripts. According to the structure of *Dpp4* gene, exon3-exon5 of *Dpp4-201* (ENSMUST00000047812.7) 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 *Dpp4* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygous mutants show hypoglycemia, hyperinsulinemia, and increased plasma glucagon-like peptide 1 in glucose tolerance tests.
- The knockout region is in the intron of *Gm13561*, Knockout the region may affect *Gm13561* gene.
- The *Dpp4* gene is located on the Chr2. 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)

Dpp4 dipeptidylpeptidase 4 [Mus musculus (house mouse)]

Gene ID: 13482, updated on 9-Apr-2019

Summary



Official Symbol	Dpp4 provided by MGI
Official Full Name	dipeptidylpeptidase 4 provided by MGI
Primary source	MGI:MGI:94919
See related	Ensembl:ENSMUSG00000035000
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	Cd26, Dpp-4, THAM
Expression	Biased expression in large intestine adult (RPKM 30.2), small intestine adult (RPKM 11.7) and 11 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

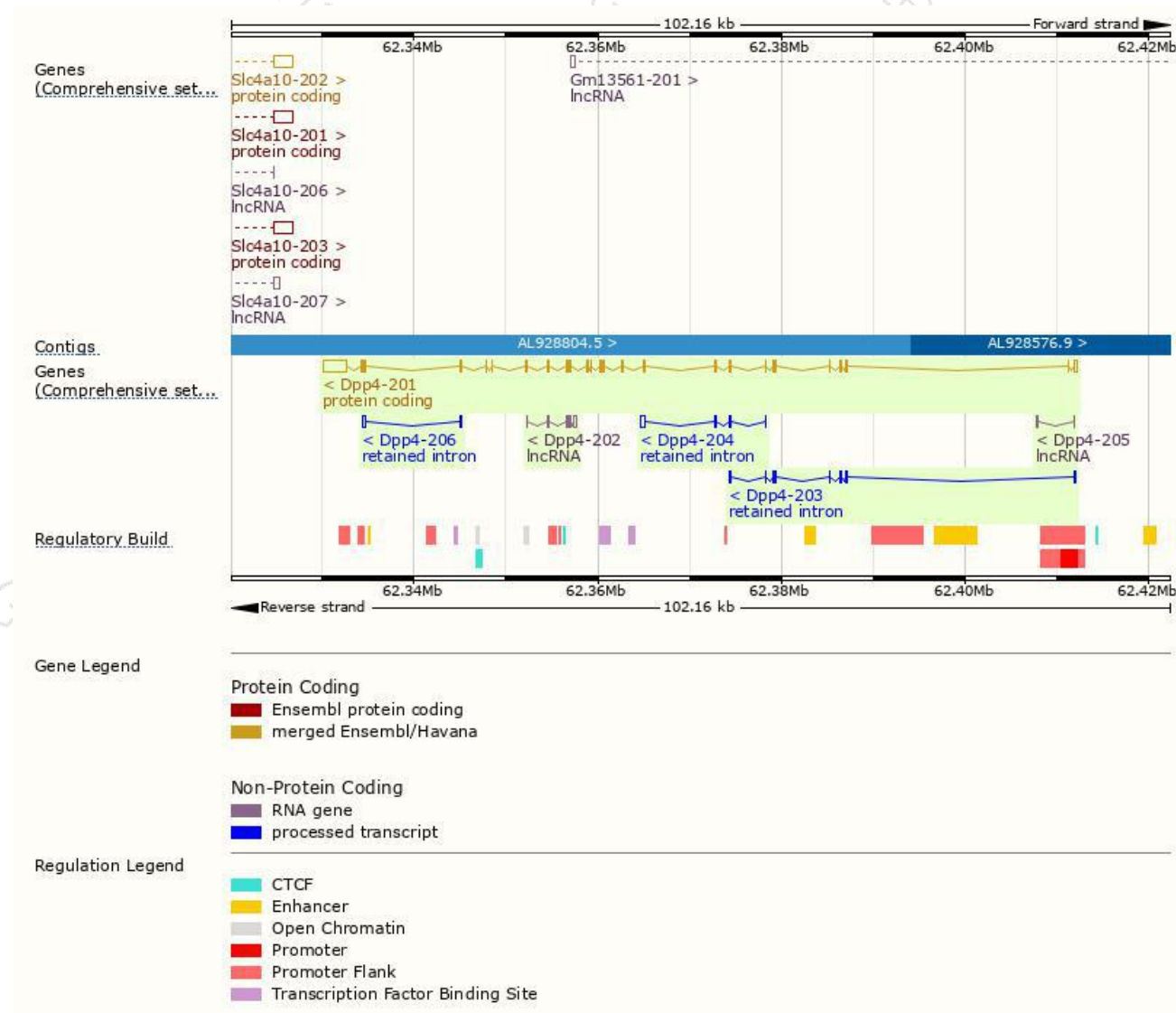
The gene has 6 transcripts, all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dpp4-201	ENSMUST00000047812.7	5268	760aa	Protein coding	CCDS16065	P28843	TSL:1 GENCODE basic APPRIS P1
Dpp4-203	ENSMUST00000149306.1	1012	No protein	Retained intron	-	-	TSL:1
Dpp4-204	ENSMUST00000150979.1	666	No protein	Retained intron	-	-	TSL:3
Dpp4-206	ENSMUST00000156871.1	288	No protein	Retained intron	-	-	TSL:5
Dpp4-202	ENSMUST00000129738.1	617	No protein	lncRNA	-	-	TSL:3
Dpp4-205	ENSMUST00000151818.1	315	No protein	lncRNA	-	-	TSL:1

The strategy is based on the design of *Dpp4-201* transcript, The transcription is shown below



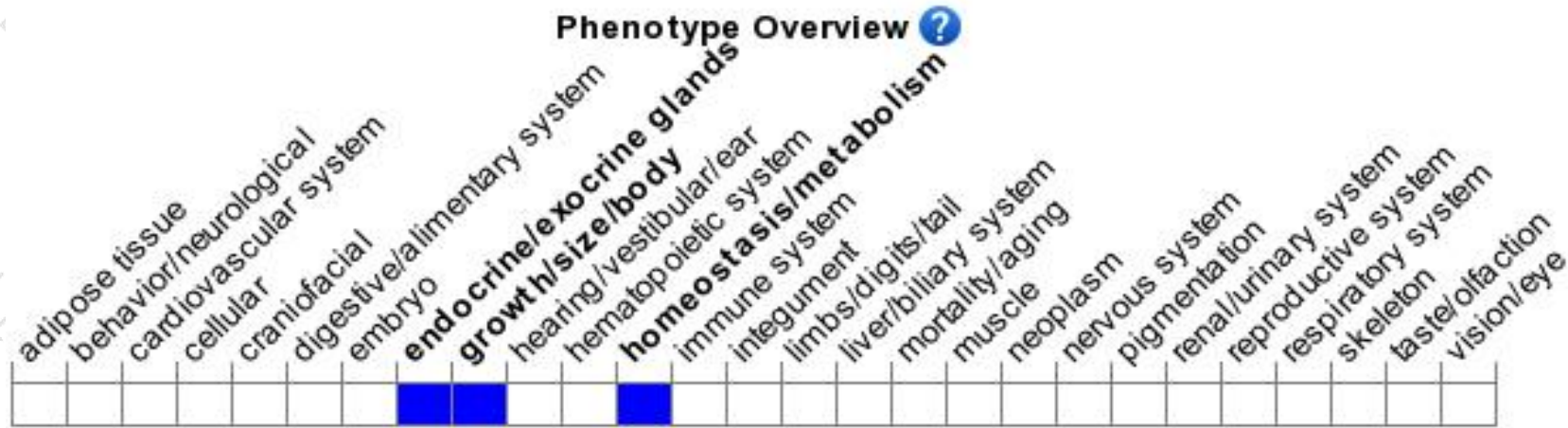
Genomic location distribution



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, Homozygous mutants show hypoglycemia, hyperinsulinemia, and increased plasma glucagon-like peptide 1 in glucose tolerance tests.

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

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