Dnpep Cas9-CKO Strategy

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Design Date: **2020-5-12**

Project Overview

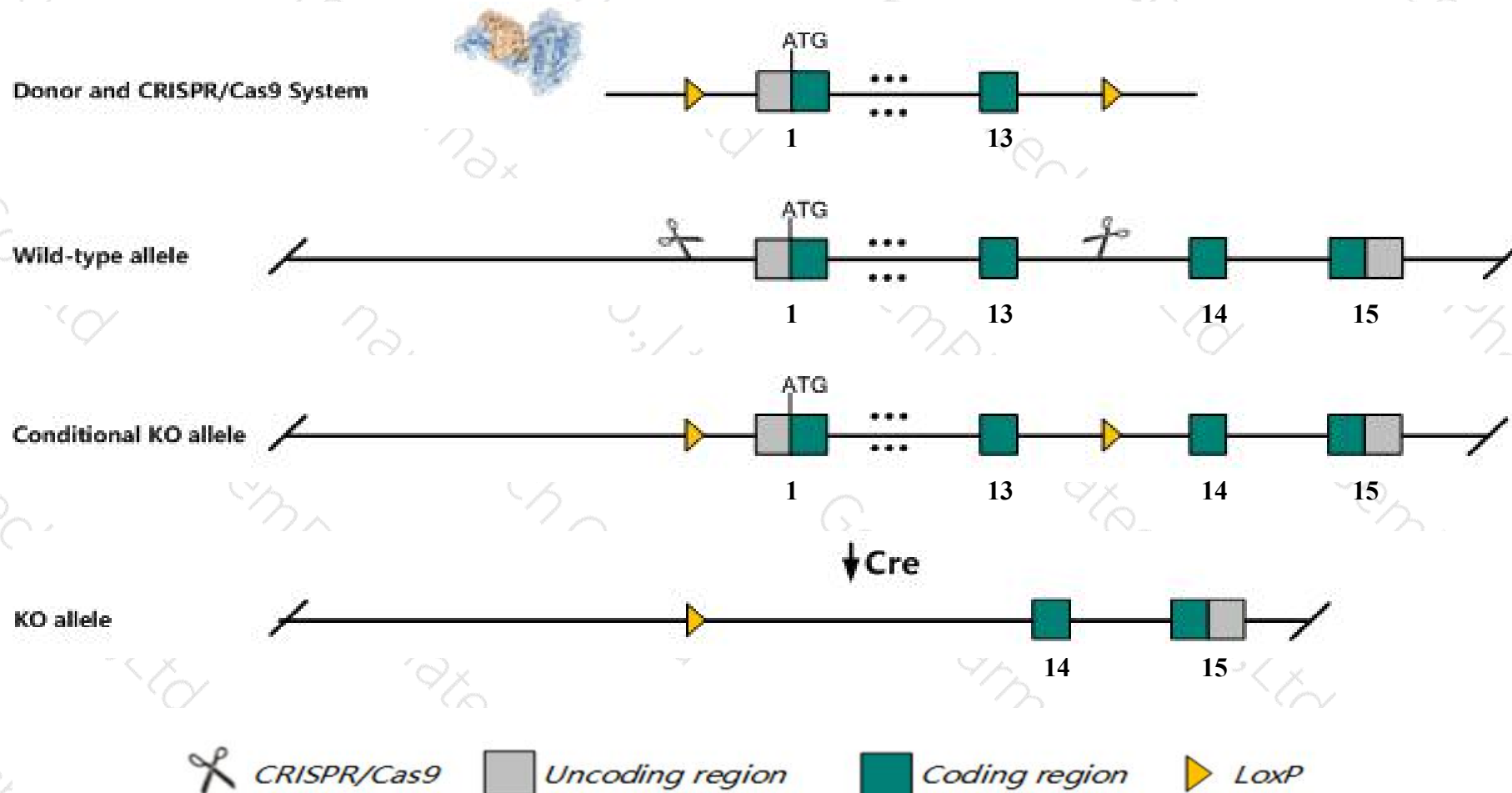| Project Name	*Dnpep*
Project type	Cas9-CKO
Strain background	C57BL/6JGpt

Conditional Knockout strategy

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

Technical routes

➤ The *Dnpep* gene has 14 transcripts. According to the structure of *Dnpep* gene, exon1-exon13 of *Dnpep-204* (ENSMUST0000185797.6) transcript is recommended as the knockout region.The region contains start codon ATG. Knock out the region will result in disruption of protein function.

➤ In this project we use CRISPR/Cas9 technology to modify *Dnpep* gene. The brief process is as follows:CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice.Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

➤ The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice

➢ The *Dnpep* 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

Dnpep aspartyl aminopeptidase [Mus musculus (house mouse)]

Gene ID: 13437, updated on 13-Mar-2020

▲ Summary

|	
Official Symbol	Dnpep provided by MGI
Official Full Name	aspartyl aminopeptidase provided by MGI
Primary source	MGI:MGI:1278328
See related	Ensembl:ENSMUSG00000026209
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	AA407814
Expression	Ubiquitous expression in small intestine adult (RPKM 135.2), large intestine adult (RPKM 105.3) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 14 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Dnpep-204	ENSMUST00000185797.6	2510	475aa	Protein coding	CCDS78623	Q3TVK3	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS ALT1
Dnpep-201	ENSMUST00000066668.13	2488	473aa	Protein coding	CCDS15070	Q9Z2W0	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P3
Dnpep-209	ENSMUST00000187836.6	1862	473aa	Protein coding	CCDS15070	Q9Z2W0	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P3
Dnpep-202	ENSMUST00000113605.9	1571	473aa	Protein coding	CCDS15070	Q9Z2W0	TSL:1 GENCODE basic APPRIS is a system to annotate alternatively spliced transcripts based on a range of computational methods to identify the most functionally important transcript(s) of a gene. APPRIS P3
Dnpep-203	ENSMUST00000185419.6	2833	470aa	Protein coding	-	Q8BPW9	TSL:1 GENCODE basic
Dnpep-206	ENSMUST00000187000.6	944	271aa	Protein coding	-	A0A087WSE6	CDS 3' incomplete TSL:5
Dnpep-207	ENSMUST00000187075.6	898	222aa	Protein coding	-	A0A087WS31	CDS 3' incomplete TSL:3
Dnpep-212	ENSMUST00000189551.6	632	210aa	Protein coding	-	A0A087WRC1	CDS 3' incomplete TSL:5
Dnpep-211	ENSMUST00000189282.2	408	56aa	Protein coding	-	A0A087WSU0	CDS 3' incomplete TSL:2
Dnpep-210	ENSMUST00000188652.6	391	85aa	Protein coding	-	A0A087WNX3	CDS 3' incomplete TSL:3
Dnpep-214	ENSMUST00000191254.6	383	92aa	Protein coding	-	A0A087WSD3	CDS 3' incomplete TSL:5
Dnpep-208	ENSMUST00000187791.1	1268	No protein	Retained intron	-	-	TSL:5
Dnpep-205	ENSMUST00000186278.1	921	No protein	Retained intron	-	-	TSL:1
Dnpep-213	ENSMUST00000190005.1	398	No protein	Retained intron	-	-	TSL:3

The strategy is based on the design of *Dnpep-204* transcript,The transcription is shown below

< Dnpep-204
protein coding

◄ Reverse strand

9.76 kb
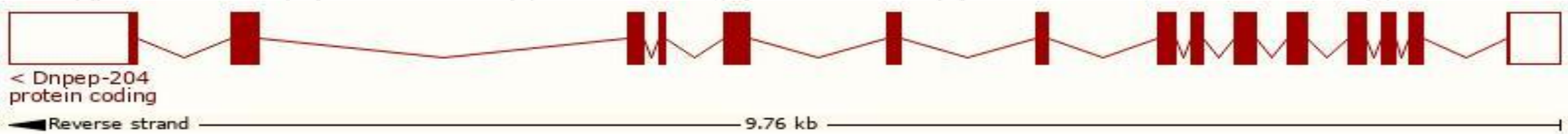
Genomic location distribution
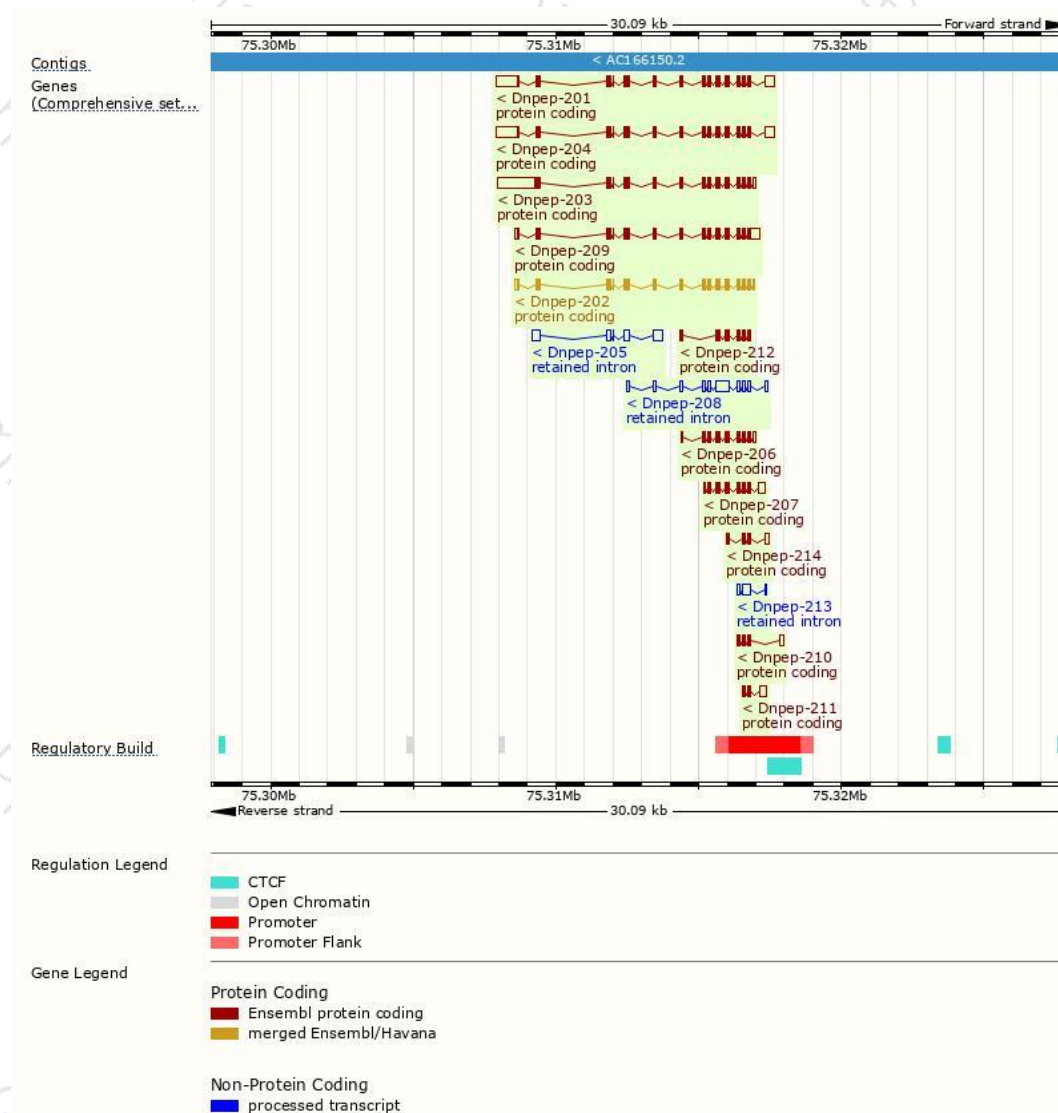
Protein domain
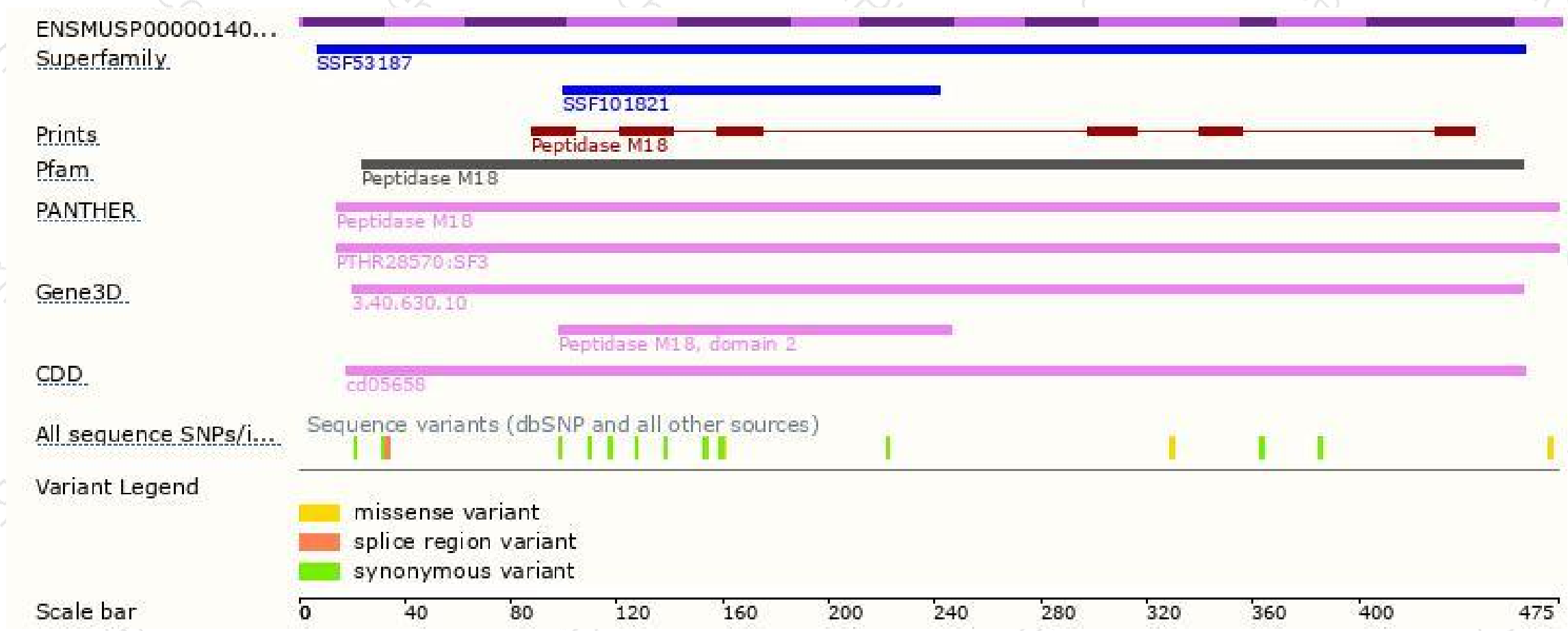
If you have any questions, you are welcome to inquire.
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