Pdcd10 Cas9-KO Strategy

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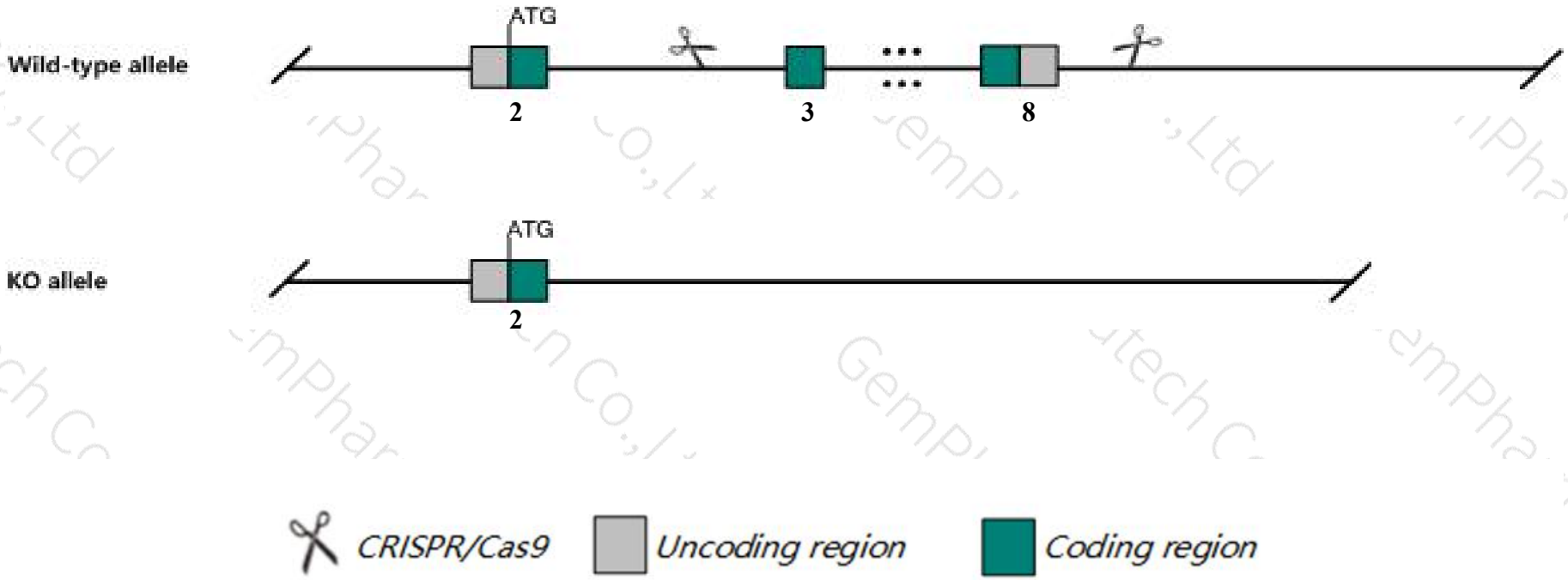
Design Date: 2019-7-18

Project Overview

Project Name	***Pdcd10***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pdcd10* gene. The schematic diagram is as follows:



Technical routes

➢ The *Pdcd10* gene has 6 transcripts. According to the structure of *Pdcd10* gene, exon3-exon8 of *Pdcd10-205* (ENSMUST00000161137.7) transcript is recommended as the knockout region.The region contains most 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 *Pdcd10* gene. The brief process is as follows: CRISPR/Cas9 syster

Notice

- According to the existing MGI data,Homozygous knockout is embryonic lethal due to impaired hematopoeisis, vasculogenesis, and abnormal heart morphology. Conditional knockout in myeloids increases degranulation of, and exocytosis by, neutrophils.

- The *Pdcd10* 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）

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Pdcd10 programmed cell death 10 [Mus musculus (house mouse)]

Gene ID: 56426, updated on 31-Jan-2019

Summary

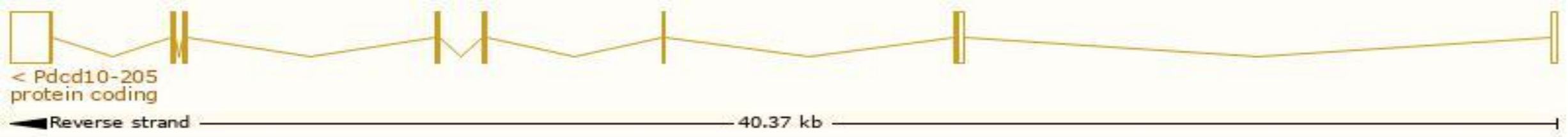
Official Symbol	Pdcd10 provided by MGI
Official Full Name	programmed cell death 10 provided by MGI
Primary source	MGI:MGI:1928396
See related	Ensembl:ENSMUSG00000027835
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2410003B13Rik, Ccm3, Tfa15, Tfar15
Expression	Broad expression in placenta adult (RPKM 13.4), bladder adult (RPKM 12.3) and 20 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

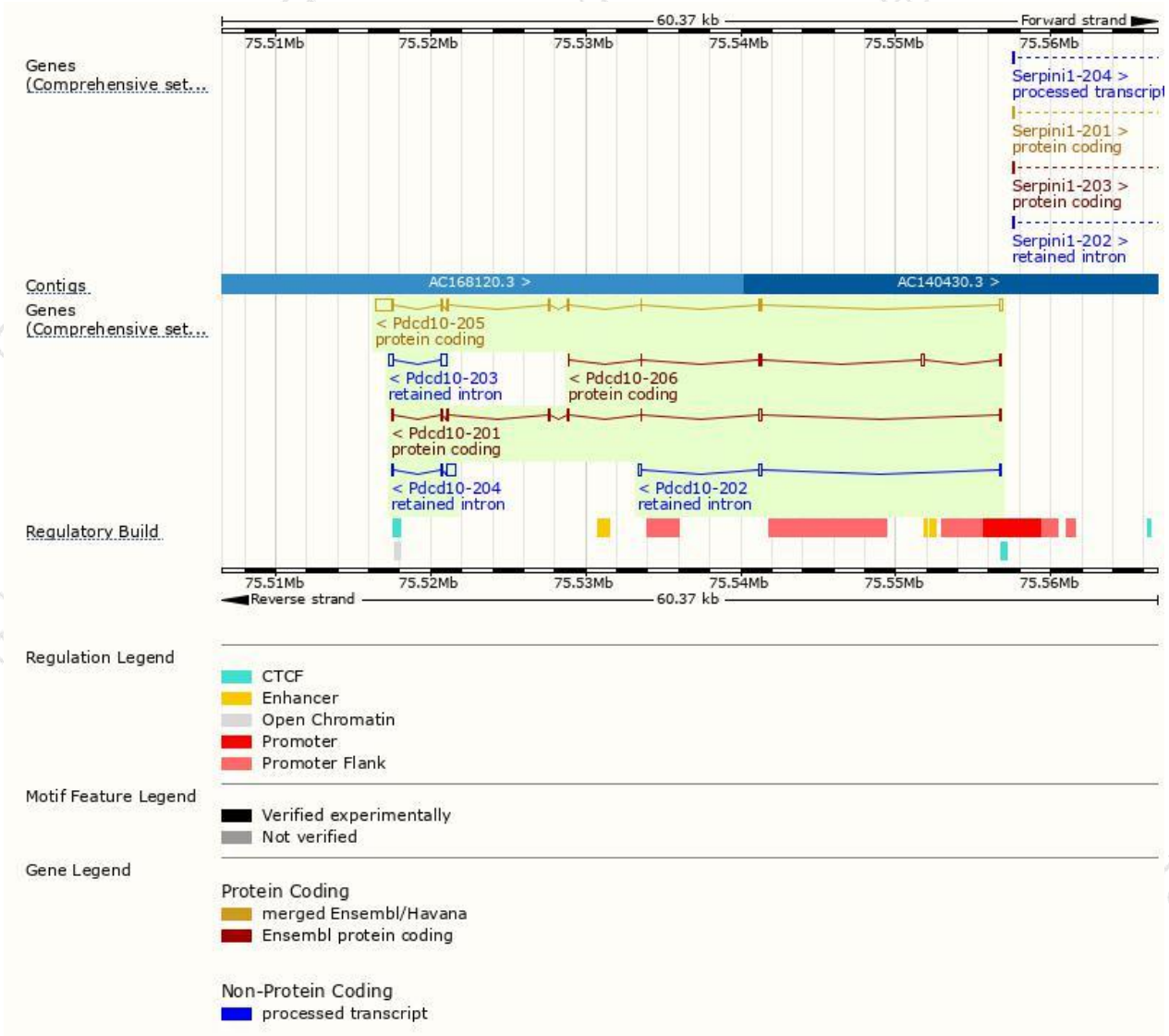
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pdcd10-205	ENSMUST00000161137.7	1927	212aa	Protein coding	CCDS17414	Q8VE70	TSL:1 GENCODE basic APPRIS P1
Pdcd10-201	ENSMUST00000029424.11	907	149aa	Protein coding	-	F8WI55	TSL:5 GENCODE basic
Pdcd10-206	ENSMUST00000162138.1	509	66aa	Protein coding	-	E0CY82	CDS 3' incomplete TSL:3
Pdcd10-204	ENSMUST00000160196.1	697	No protein	Retained intron	-	-	TSL:2
Pdcd10-203	ENSMUST00000159519.1	655	No protein	Retained intron	-	-	TSL:2
Pdcd10-202	ENSMUST00000159217.1	545	No protein	Retained intron	-	-	TSL:2

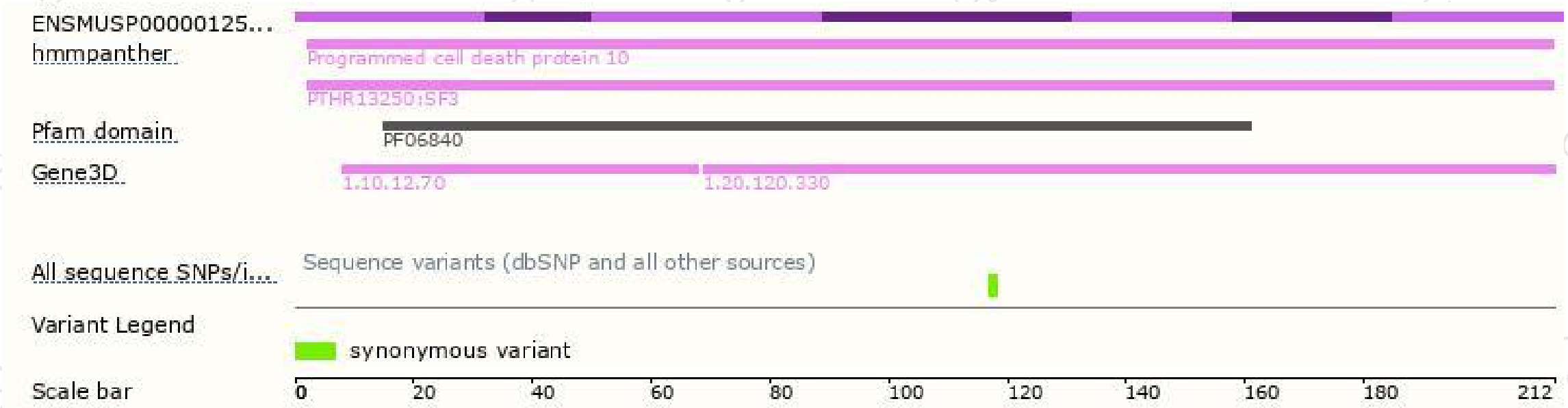
The strategy is based on the design of *Pdcd10-205* transcript,The transcription is shown below



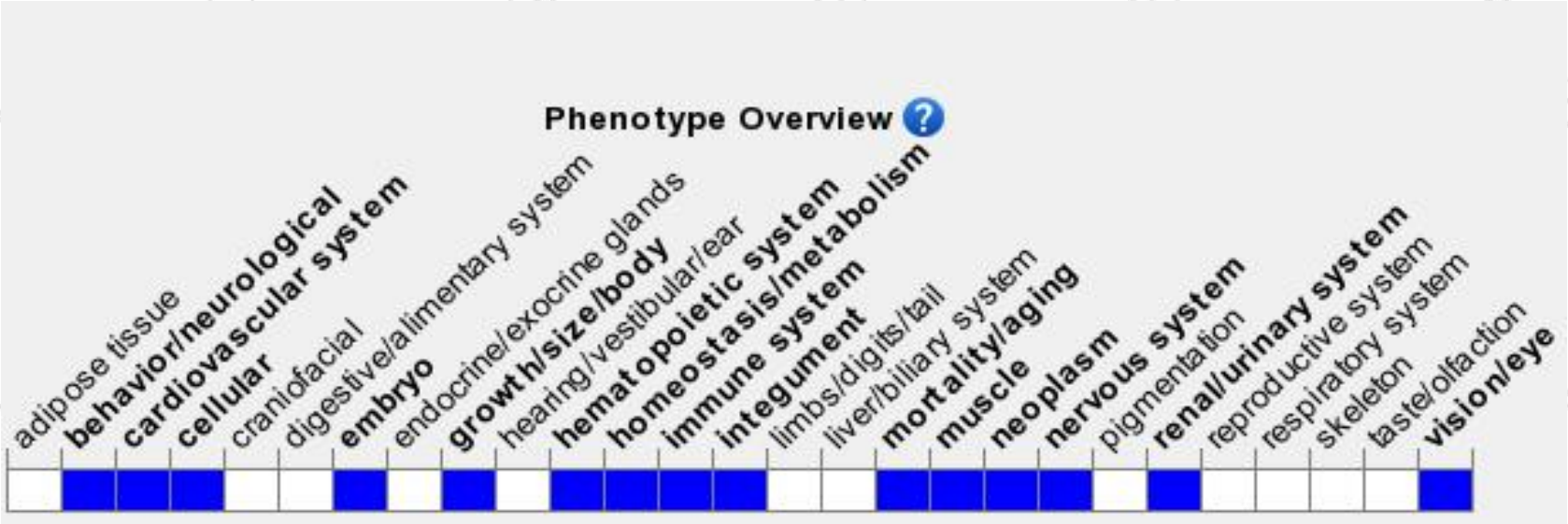
Genomic location distribution



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/).

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

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