

Vdr Cas9-KO Strategy

Designer:

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Project Overview

Project Name

Vdr

Project type

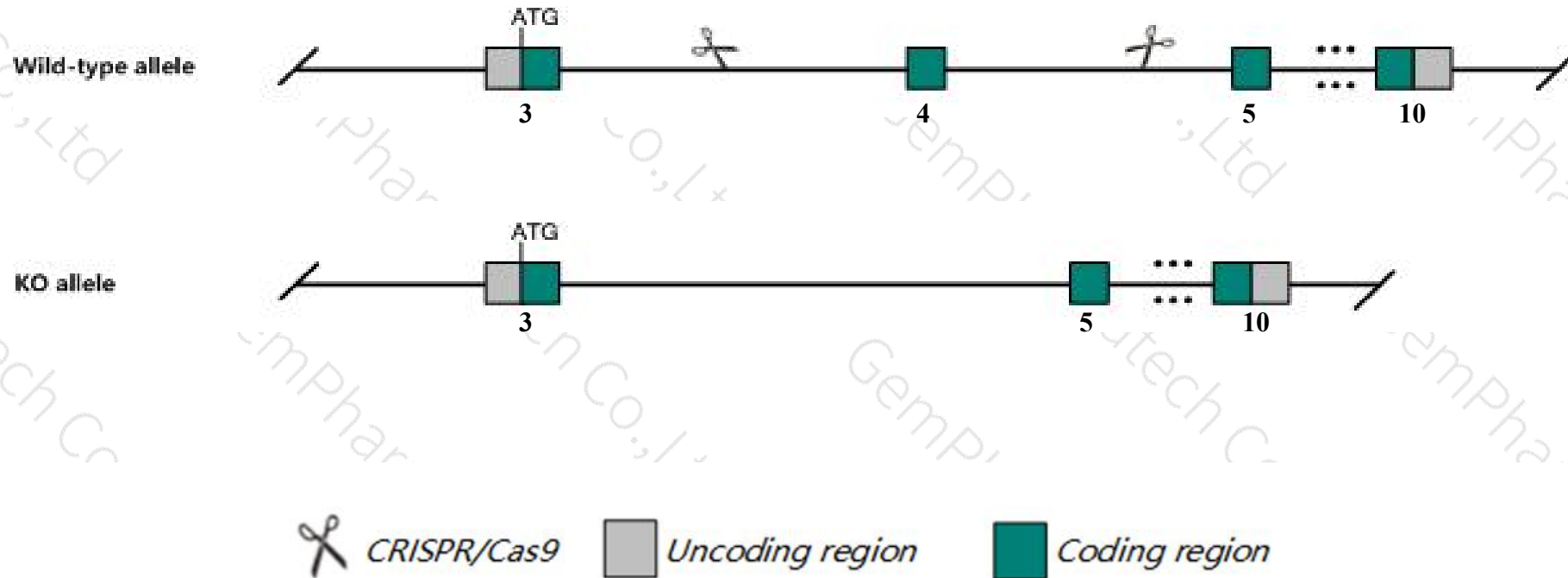
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Vdr* gene has 6 transcripts. According to the structure of *Vdr* gene, exon4 of *Vdr-201* (ENSMUST00000023119.14) transcript is recommended as the knockout region. The region contains 131bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Vdr* gene. The brief process is as follows: CRISPR/Cas9 system w

- According to the existing MGI data, Homozygous null mutants fail to thrive after weaning and may exhibit excess mortality. Postweaning mutant mice develop alopecia, hypocalcemia, infertility, and rickets. Mutant females exhibit uterine hypoplasia with impaired follicular development.
- The *Vdr* gene is located on the Chr15. 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)

Vdr vitamin D (1,25-dihydroxyvitamin D3) receptor [Mus musculus (house mouse)]

Gene ID: 22337, updated on 19-Mar-2019

Summary



Official Symbol	Vdr provided by MGI
Official Full Name	vitamin D (1,25-dihydroxyvitamin D3) receptor provided by MGI
Primary source	MGI:MGI:103076
See related	Ensembl:ENSMUSG00000022479
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	Nr1i1
Expression	Biased expression in duodenum adult (RPKM 78.3), colon adult (RPKM 58.5) and 3 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

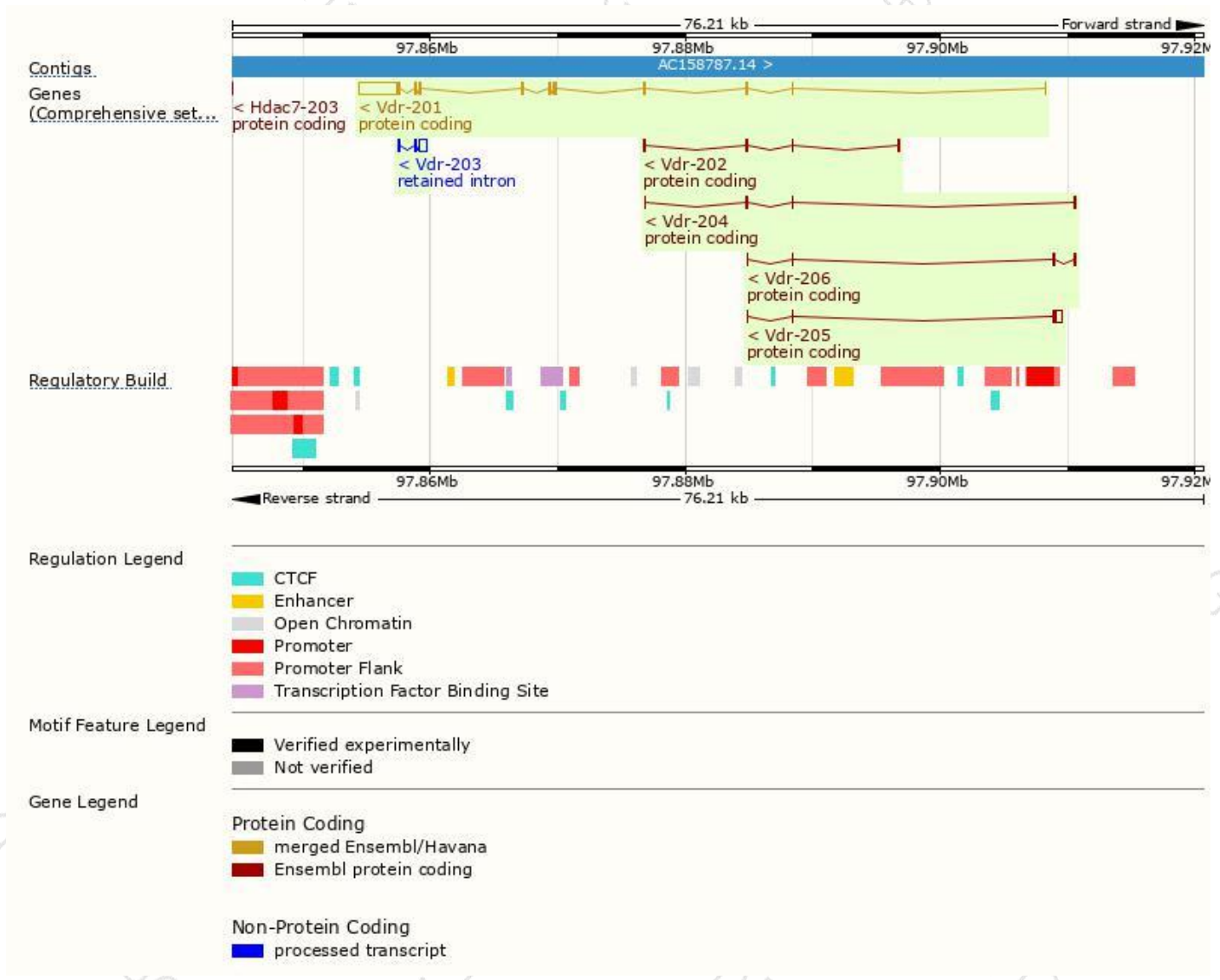
The gene has 6 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Vdr-201	ENSMUST00000023119.14	4370	422aa	Protein coding	CCDS27784	P48281	TSL:1 Gencode basic APPRIS P1
Vdr-205	ENSMUST00000173611.1	762	17aa	Protein coding	-	G3UWM9	CDS 3' incomplete TSL:5
Vdr-202	ENSMUST00000126568.7	389	75aa	Protein coding	-	D3Z3H9	CDS 3' incomplete TSL:3
Vdr-206	ENSMUST00000174633.7	376	21aa	Protein coding	-	G3UXG5	CDS 3' incomplete TSL:2
Vdr-204	ENSMUST00000173104.7	343	51aa	Protein coding	-	G3UZP9	CDS 3' incomplete TSL:2
Vdr-203	ENSMUST00000139656.1	813	No protein	Retained intron	-	-	TSL:2

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



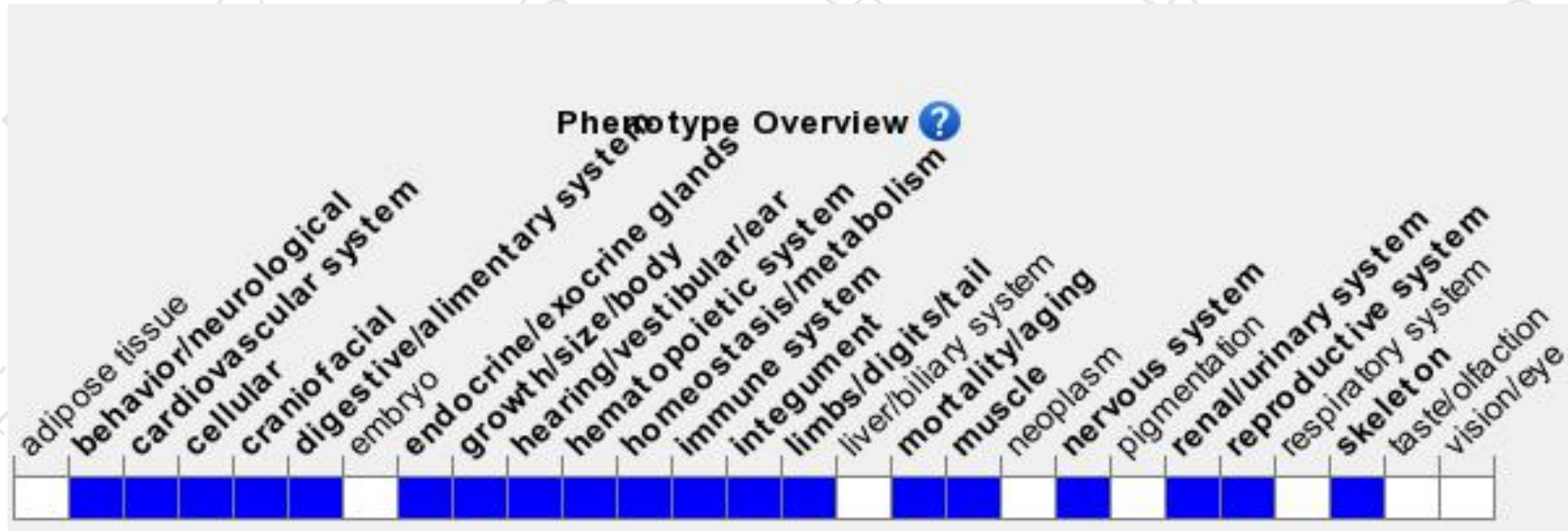
Genomic location distribution



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 null mutants fail to thrive after weaning and may exhibit excess mortality. Postweaning mutant mice develop alopecia, hypocalcemia, infertility, and rickets. Mutant females exhibit uterine hypoplasia with impaired follicular development.

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

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