Vil1 Cas9-KO Strategy

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Reviewer:Shilei Zhu

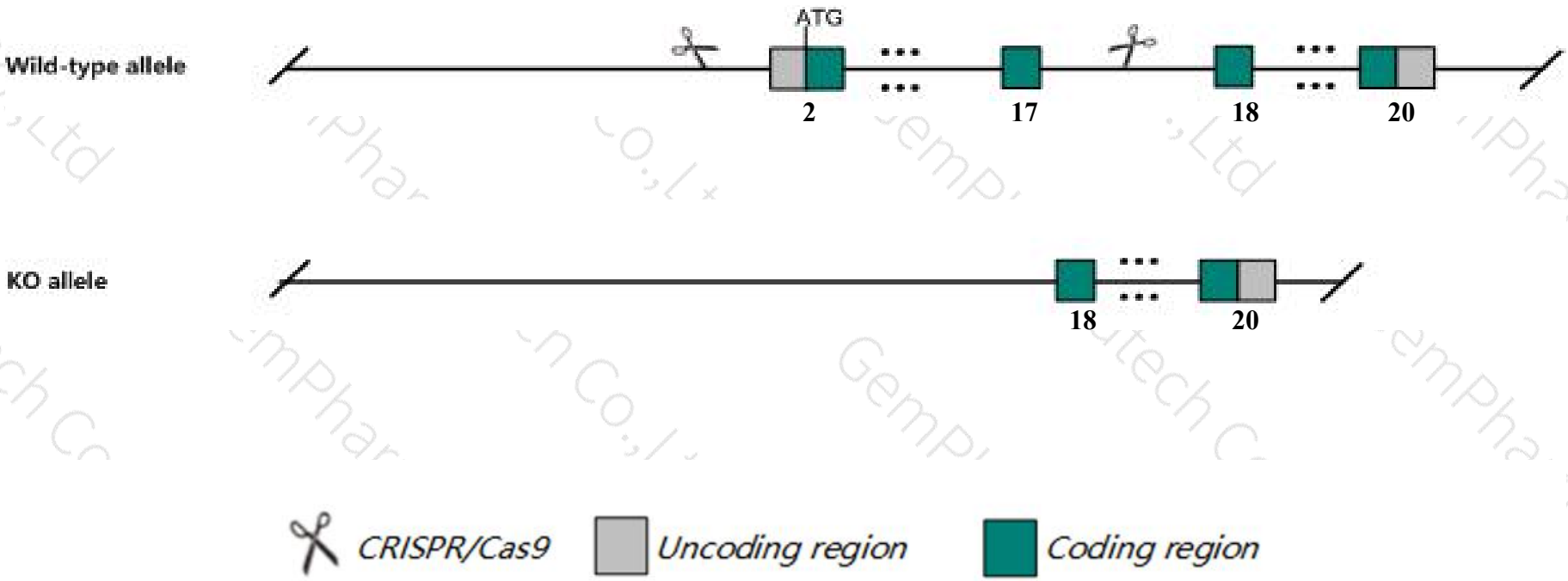
Design Date:2020-2-27

Project Overview

Project Name	***Vil1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Vil1* gene. The schematic diagram is as follows:



Technical routes

➢ The *Vil1* gene has 4 transcripts. According to the structure of *Vil1* gene, exon2-exon17 of *Vil1-201* (ENSMUST00000027366.12) 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 *Vil1* gene. The brief process is as follows: CRISPR/Cas9 system w

Notice

- According to the existing MGI data,Homozygous null mutants do not exhibit gross abnormalities or apparent defects of microvilli morphogenesis, however in one line, an increased sensitivity to colitis induced by dextran sulfate was observed.

- The *Vil1* 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 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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Vil1 villin 1 [Mus musculus (house mouse)]

Gene ID: 22349, updated on 31-Jan-2019

Summary

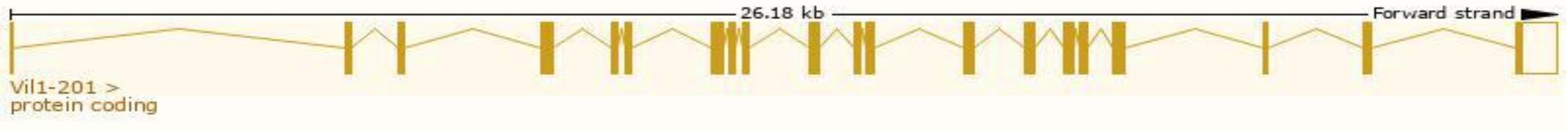
Official Symbol	Vil1 provided by MGI
Official Full Name	villin 1 provided by MGI
Primary source	MGI:MGI:98930
See related	Ensembl:ENSMUSG00000026175
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Vil
Expression	Biased expression in large intestine adult (RPKM 318.1), small intestine adult (RPKM 235.7) and 4 other tissues See more
Orthologs	human all

Transcript information（Ensembl）

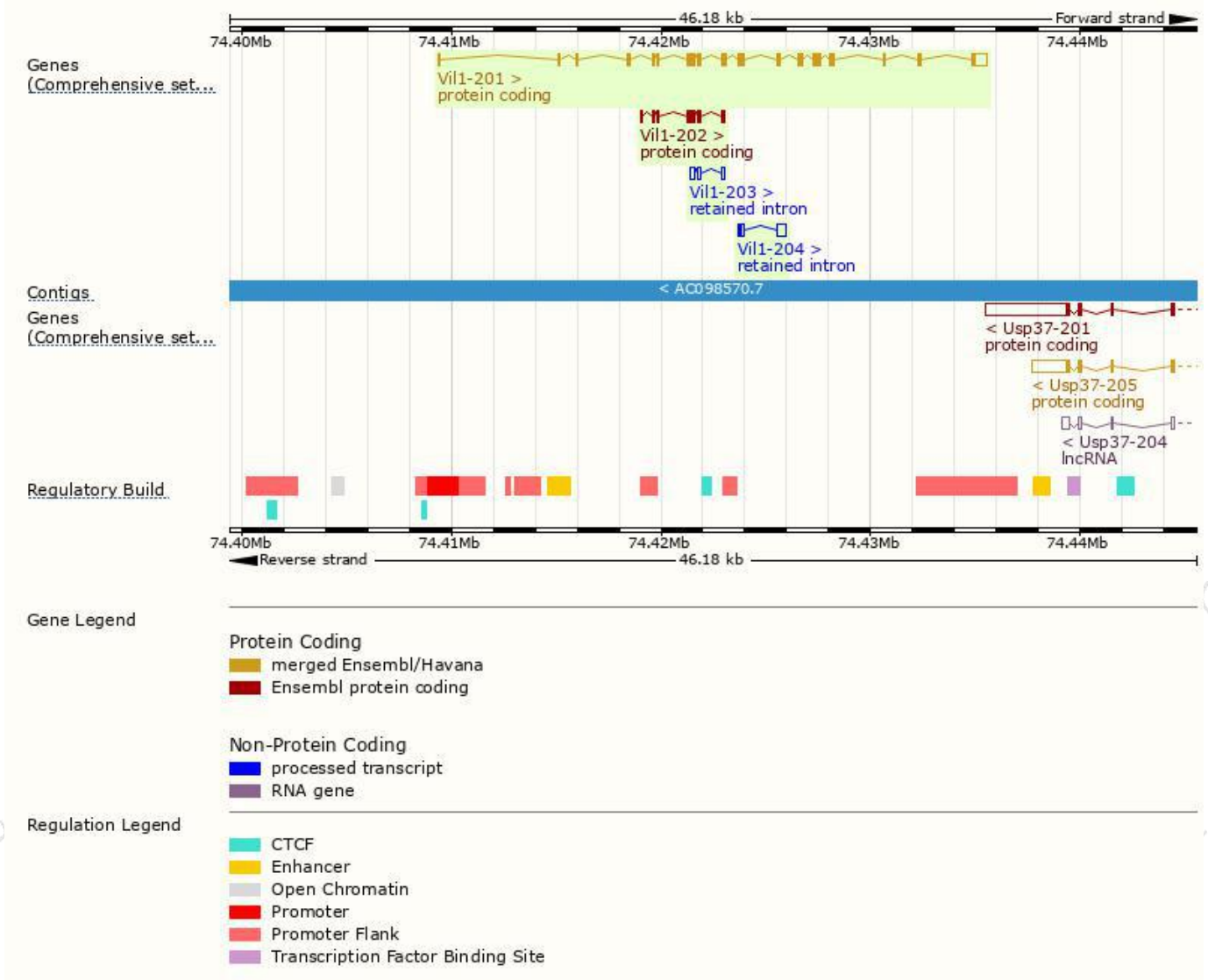
The gene has 4 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Vil1-201	ENSMUST00000027366.12	3124	827aa	Protein coding	CCDS15049	Q62468	TSL:1 GENCODE basic APPRIS P1
Vil1-202	ENSMUST00000159749.1	744	248aa	Protein coding	-	F6V2H5	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:5
Vil1-204	ENSMUST00000163018.1	658	No protein	Retained intron	-	-	TSL:3
Vil1-203	ENSMUST00000161087.1	408	No protein	Retained intron	-	-	TSL:2

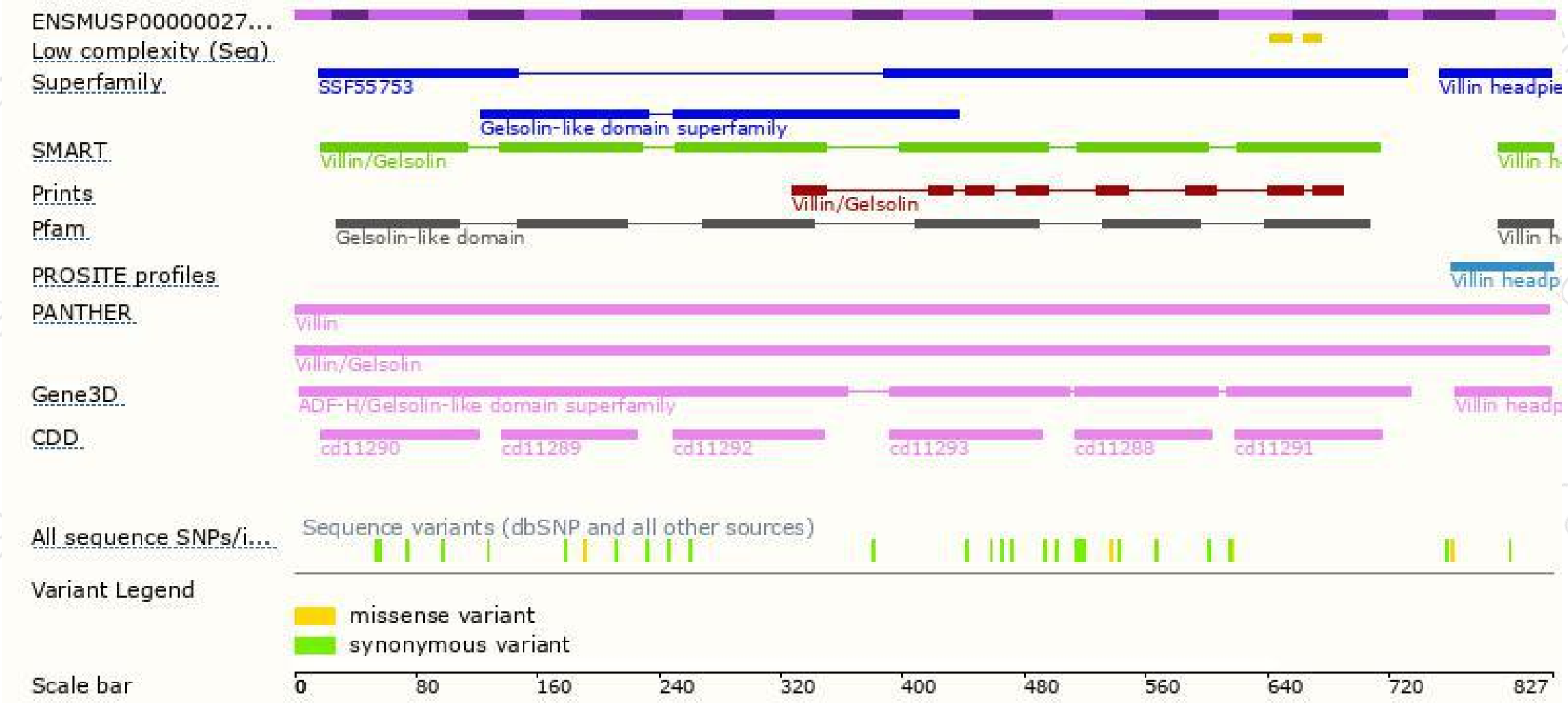
The strategy is based on the design of *Vil1-201* transcript,The transcription is shown below



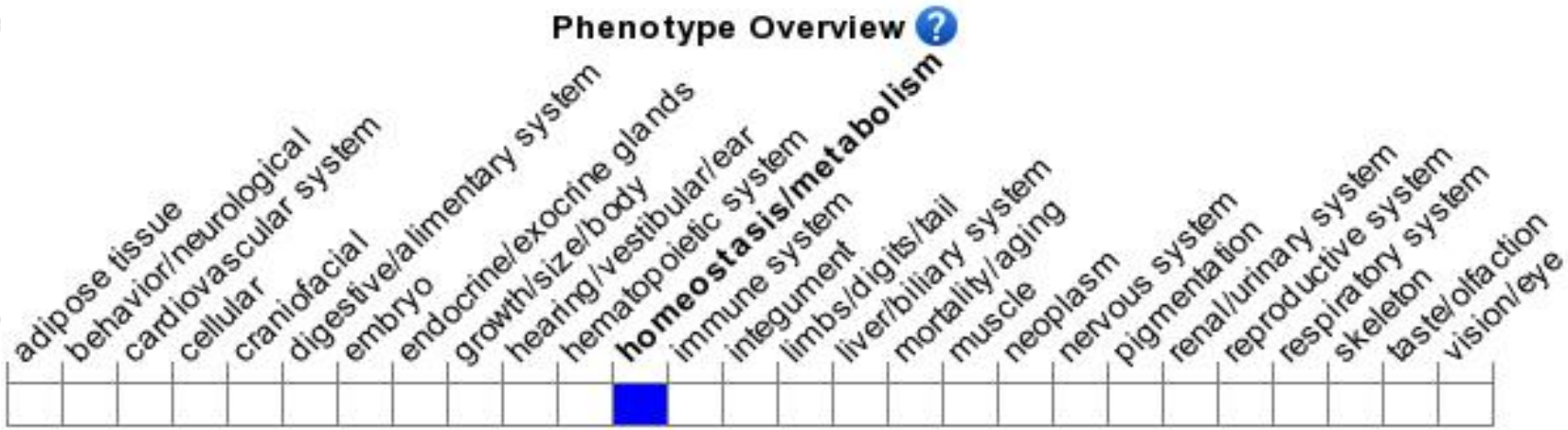
Genomic location distribution



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/).

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

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