

Evl Cas9-KO Strategy

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Project Overview

Project Name

Evl

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

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



- The *Evl* gene has 7 transcripts. According to the structure of *Evl* gene, exon2-exon3 of *Evl-201* (ENSMUST00000021689.13) transcript is recommended as the knockout region. The region contains 347bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Evl* gene. The brief process is as follows: CRISPR/Cas9 system will

- According to the existing MGI data, Mice homozygous for a knock-out allele are viable with no apparent defects in gross morphology or histology. Mice homozygous for a different knock-out allele are viable and fertile but display defects in monocyte migration.
- The *Evl* gene is located on the Chr12. 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)

Evl Ena-vasodilator stimulated phosphoprotein [Mus musculus (house mouse)]

Gene ID: 14026, updated on 5-Mar-2019

Summary



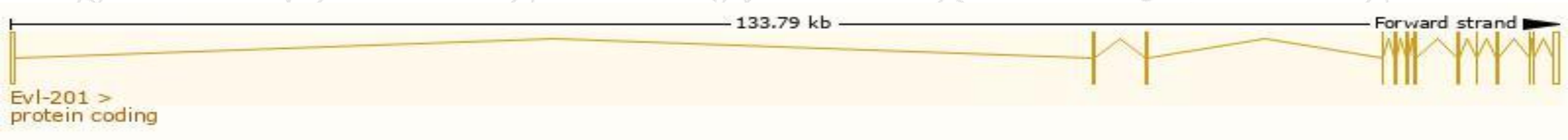
Official Symbol	Evl provided by MGI
Official Full Name	Ena-vasodilator stimulated phosphoprotein provided by MGI
Primary source	MGI:MGI:1194884
See related	Ensembl:ENSMUSG000000021262
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AI528774, b2b2600Clo
Expression	Broad expression in whole brain E14.5 (RPKM 64.8), CNS E14 (RPKM 64.7) and 27 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

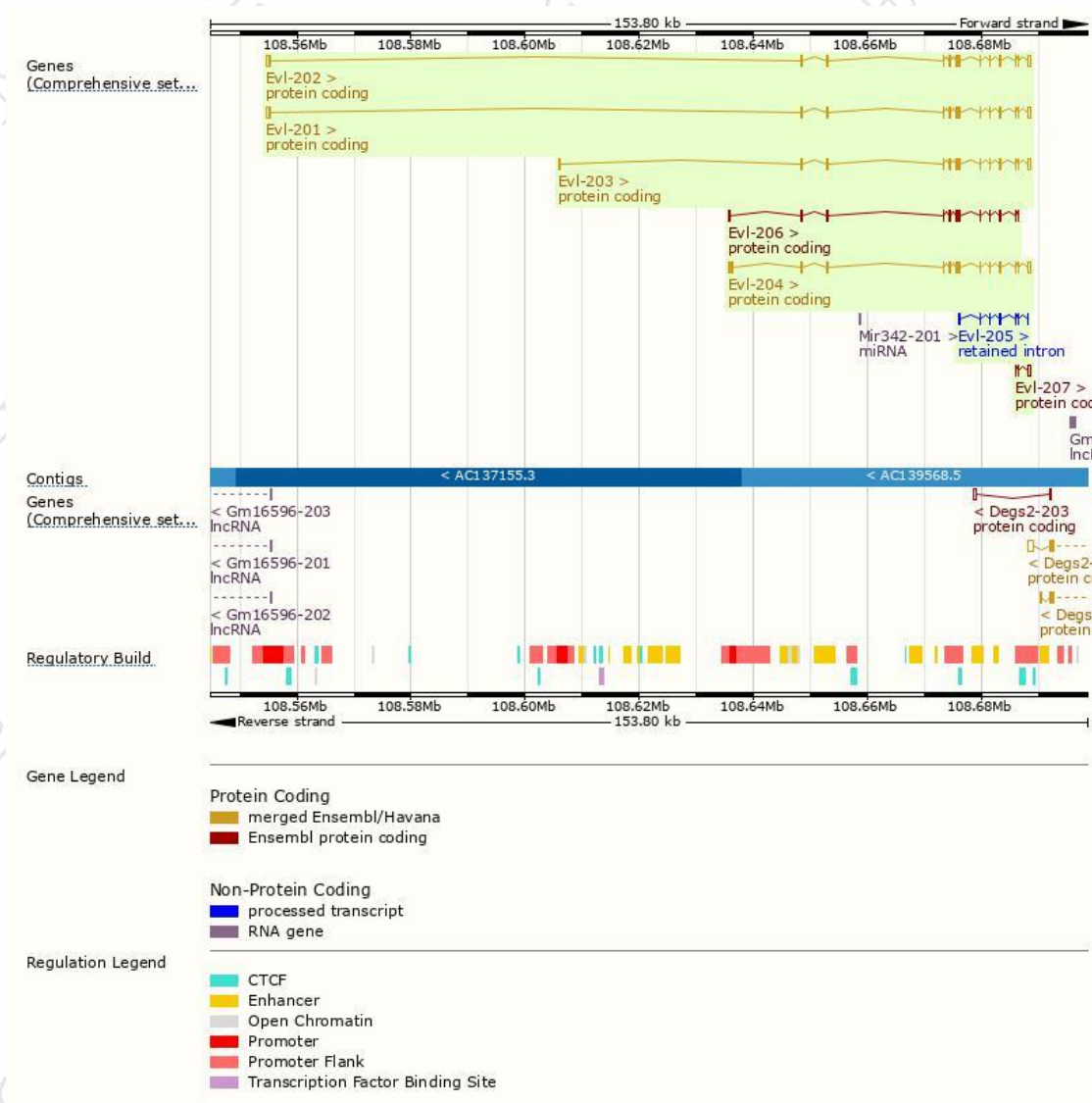
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Evl-201	ENSMUST00000021689.13	2180	414aa	Protein coding	CCDS49167	P70429	TSL:1 GENCODE basic APPRIS P4
Evl-202	ENSMUST00000077735.12	2121	393aa	Protein coding	CCDS26161	P70429	TSL:1 GENCODE basic
Evl-204	ENSMUST00000172409.1	1955	401aa	Protein coding	CCDS49169	E9PVP4	TSL:1 GENCODE basic
Evl-203	ENSMUST00000109854.8	1870	399aa	Protein coding	CCDS49168	F8WJB9	TSL:1 GENCODE basic APPRIS ALT1
Evl-206	ENSMUST00000223109.1	1487	426aa	Protein coding	-	A0A1Y7VJA2	CDS 3' incomplete TSL:1
Evl-207	ENSMUST00000223548.1	569	39aa	Protein coding	-	A0A1Y7VNI5	CDS 5' incomplete TSL:3
Evl-205	ENSMUST00000222048.1	765	No protein	Retained intron	-	-	TSL:5

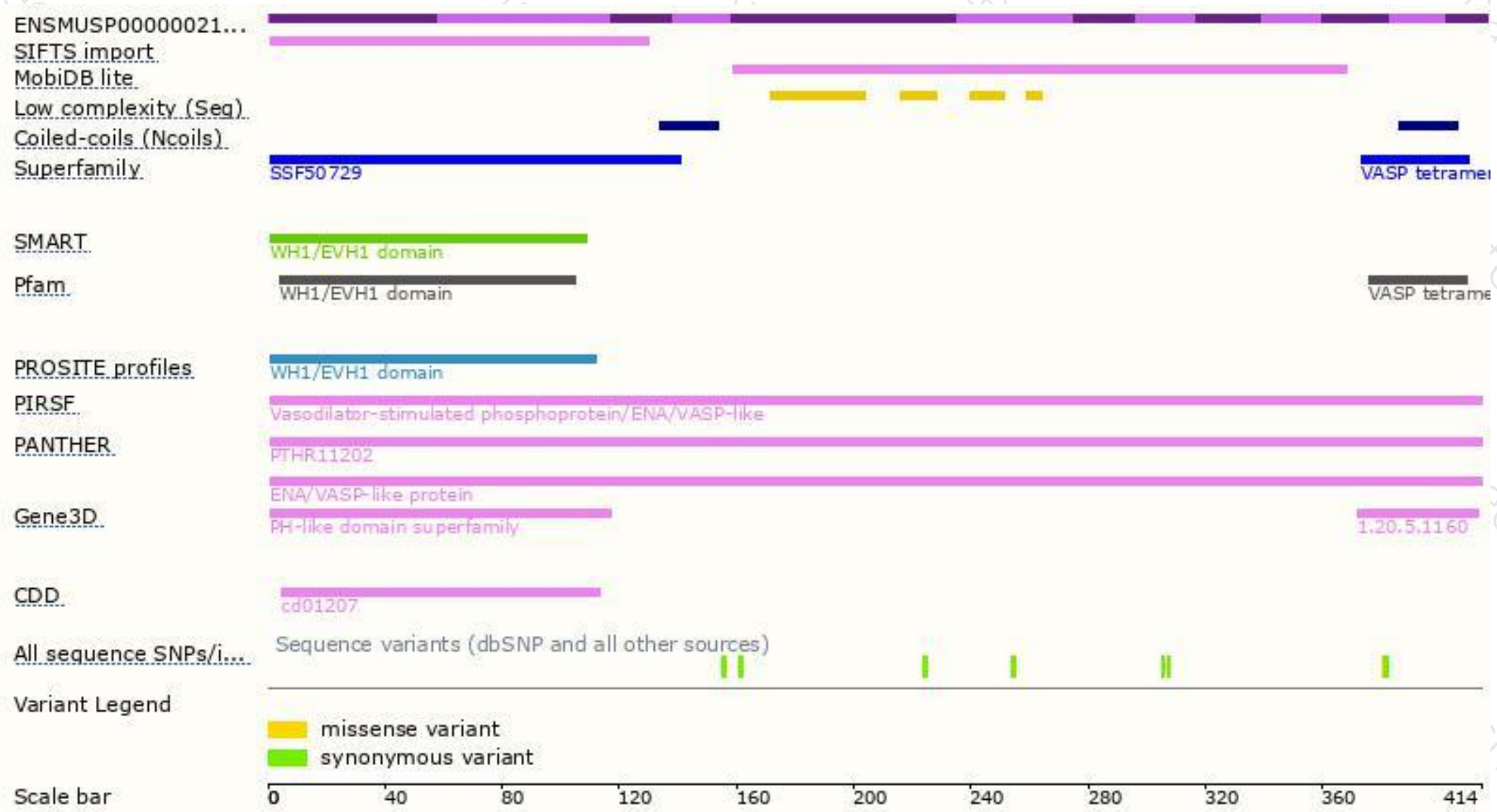
The strategy is based on the design of *Evl-201* transcript,The transcription is shown below



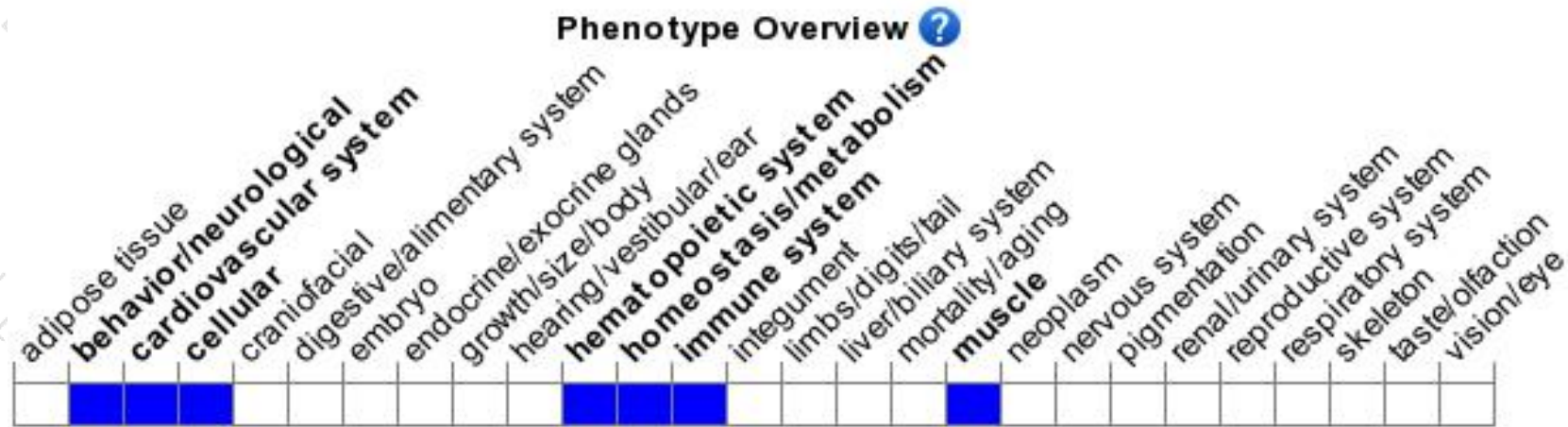
Genomic location distribution



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, Mice homozygous for a knock-out allele are viable with no apparent defects in gross morphology or histology. Mice homozygous for a different knock-out allele are viable and fertile but display defects in monocyte migration.

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

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