

Epb41l1 Cas9-KO Strategy

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Project Overview

Project Name

Epb41l1

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Epb41lll* gene. The schematic diagram is as follows:



- The *Epb41l1* gene has 9 transcripts. According to the structure of *Epb41l1* gene, exon3-exon11 of *Epb41l1-201* (ENSMUST00000029155.15) transcript is recommended as the knockout region. The region contains 1123bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Epb41l1* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Mice homozygous for a null allele exhibit no obvious phenotypic abnormalities.
- Transcript *Epb4111*-207 may not be affected.
- The *Epb4111* gene is located on the Chr2. 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)

Epb41l1 erythrocyte membrane protein band 4.1 like 1 [*Mus musculus* (house mouse)]

Gene ID: 13821, updated on 24-Oct-2019

Summary

- Official Symbol** Epb41l1 provided by MGI
- Official Full Name** erythrocyte membrane protein band 4.1 like 1 provided by MGI
- Primary source** MGI:MGI:103010
- See related** Ensembl:ENSMUSG00000027624
- 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** 4.1N; NBL1; Epb4.1l1; mKIAA0338
- Expression** Broad expression in cortex adult (RPKM 33.4), cerebellum adult (RPKM 32.7) and 20 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 2 H1; 2 77.39 cM

See Epb41l1 in [Genome Data Viewer](#)

Exon count: 29

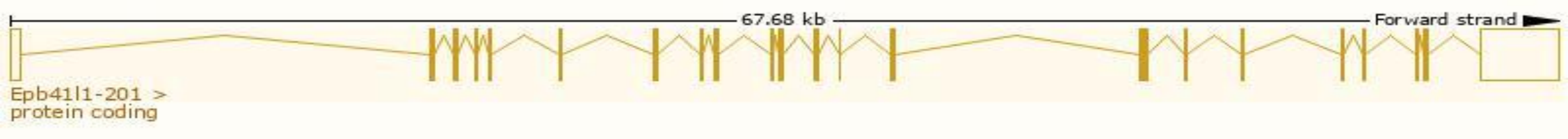
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	2	NC_000068.7 (156417595..156543214)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	2	NC_000068.6 (156246788..156368950)

Transcript information (Ensembl)

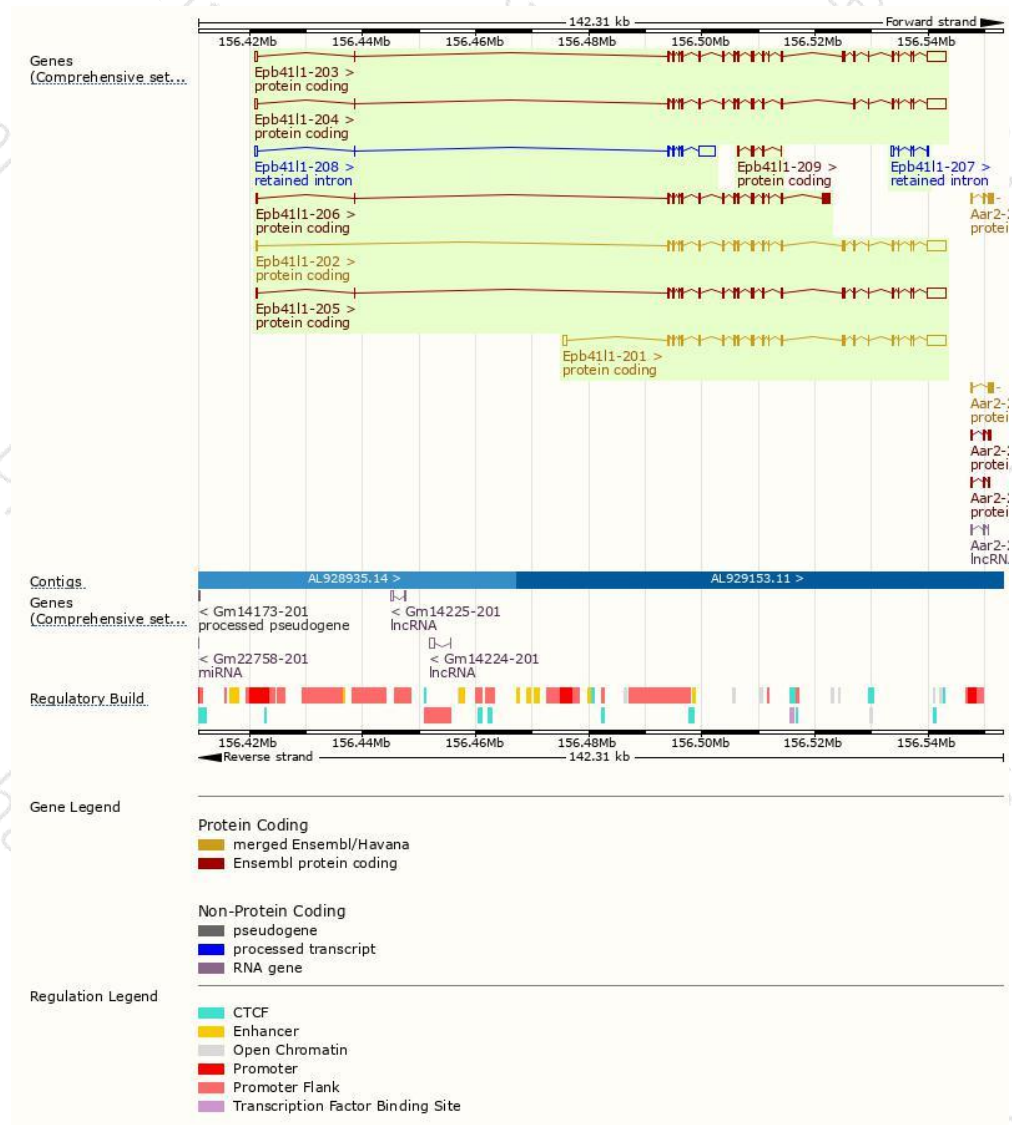
The gene has 9 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Epb41l1-201	ENSMUST00000029155.15	6521	879aa	Protein coding	CCDS16966	A2AUK5	TSL:5 GENCODE basic
Epb41l1-203	ENSMUST00000103137.9	6490	879aa	Protein coding	CCDS16966	A2AUK5	TSL:1 GENCODE basic
Epb41l1-205	ENSMUST00000109577.8	6251	867aa	Protein coding	CCDS71169	A2AUK8	TSL:5 GENCODE basic APPRIS P1
Epb41l1-202	ENSMUST00000103136.7	6249	879aa	Protein coding	CCDS16966	A2AUK5	TSL:1 GENCODE basic
Epb41l1-204	ENSMUST00000109574.7	5904	730aa	Protein coding	CCDS71170	A2AUK7	TSL:1 GENCODE basic
Epb41l1-206	ENSMUST00000125153.8	3471	1064aa	Protein coding	-	E9PV14	CDS 3' incomplete TSL:1
Epb41l1-209	ENSMUST00000144013.1	640	213aa	Protein coding	-	A0A2R8VHB6	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete TSL:3
Epb41l1-208	ENSMUST00000142048.7	3643	No protein	Retained intron	-	-	TSL:2
Epb41l1-207	ENSMUST00000137067.1	820	No protein	Retained intron	-	-	TSL:2

The strategy is based on the design of *Epb41l1-201* transcript,The transcription is shown below



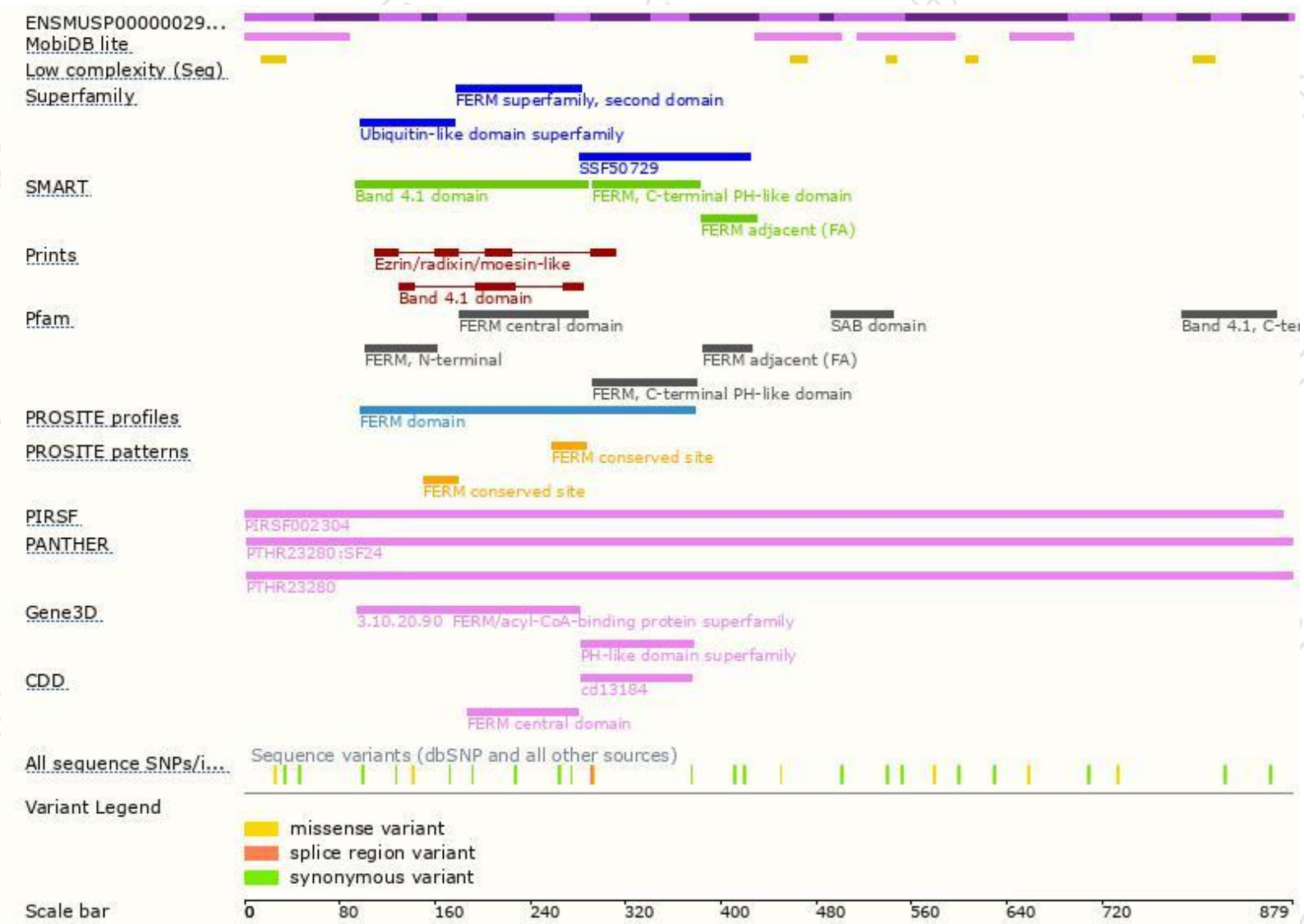
Genomic location distribution



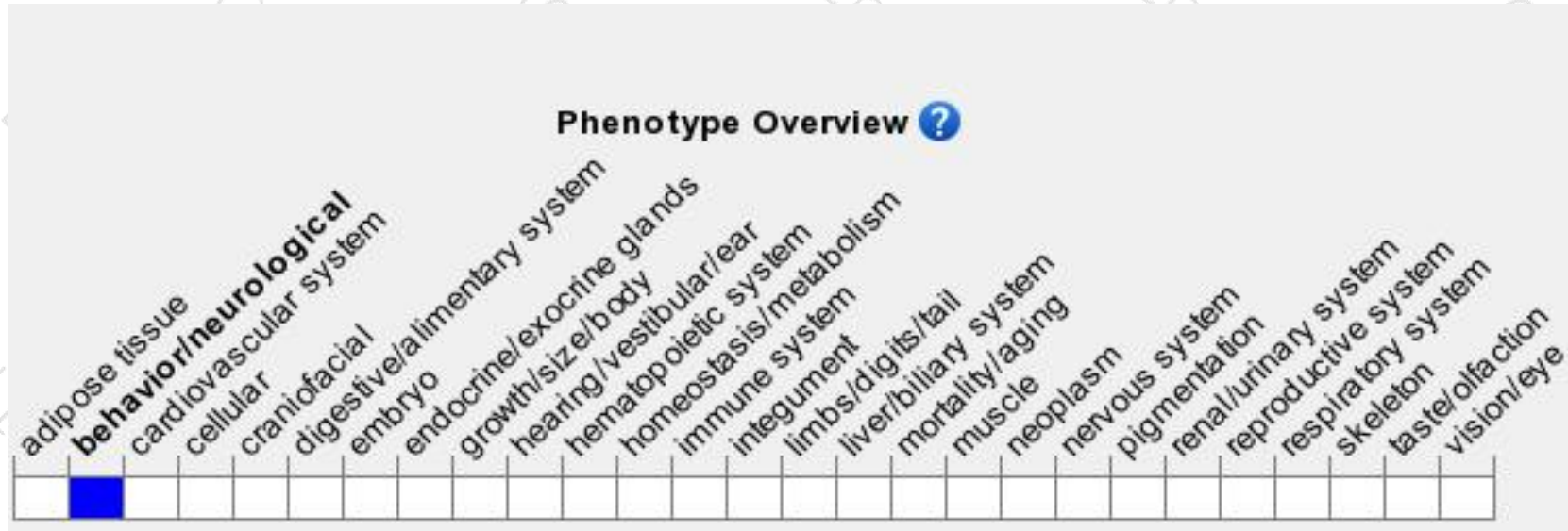
Protein domain



集萃药康
GemPharmatech



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 null allele exhibit no obvious phenotypic abnormalities.

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

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