

***Epb42* Cas9-KO Strategy**

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Date: 2020-02-05

Project Overview

Project Name

Epb42

Project type

Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Epb42* gene. The schematic diagram is as follows:



- The *Epb42* gene has 7 transcripts. According to the structure of *Epb42* gene, exon2-exon12 of *Epb42-202* (ENSMUST00000102490.9) transcript is recommended as the knockout region. The region contains 1903bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Epb42* gene. The brief process is as follows: CRISPR/Cas9 system

- According to the existing MGI data, Homozygotes for a targeted null mutation exhibit erythrocytic abnormalities including mild spherocytosis, altered ion transport, and dehydration.
- The *Epb42* 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)

Epb42 erythrocyte membrane protein band 4.2 [*Mus musculus* (house mouse)]

Gene ID: 13828, updated on 12-Aug-2019

Summary

- Official Symbol** Epb42 provided by MGI
- Official Full Name** erythrocyte membrane protein band 4.2 provided by MGI
- Primary source** MGI:MGI:95402
- See related** Ensembl:ENSMUSG00000023216
- Gene type** protein coding
- RefSeq status** REVIEWED
- Organism** *Mus musculus*
- Lineage** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
- Also known as** Epb4.2
- Summary** The protein encoded by this gene is the key component of a macromolecular complex involved in the structure of erythrocytes. [provided by RefSeq, Aug 2015]
- Expression** Biased expression in liver E14.5 (RPKM 57.9), liver E14 (RPKM 55.2) and 3 other tissues [See more](#)
- Orthologs** [human](#) [all](#)

Genomic context

Location: 2 E5; 2 60.37 cM See Epb42 in [Genome Data Viewer](#)

Exon count: 14

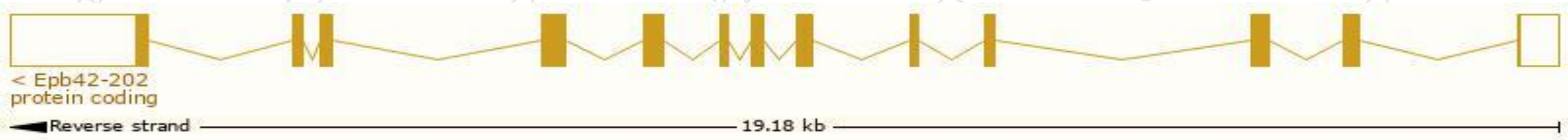
Annotation release	Status	Assembly	Chr	Location
108	current	GRCm38.p6 (GCF_000001635.26)	2	NC_000068.7 (121017891..121036877, complement)
Build 37.2	previous assembly	MGSCv37 (GCF_000001635.18)	2	NC_000068.6 (120843953..120862491, complement)

Transcript information (Ensembl)

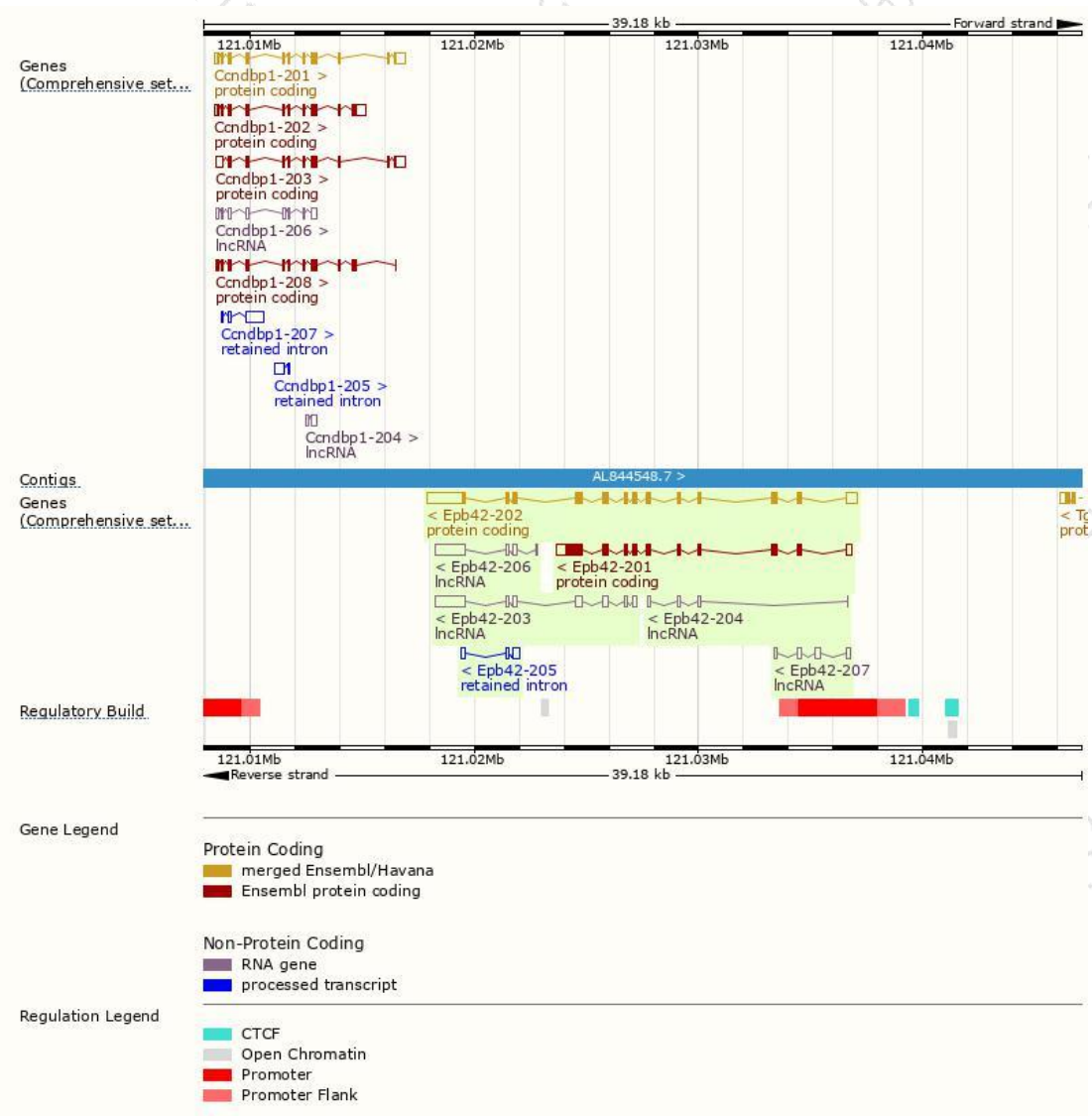
The gene has 7 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Epb42-202	ENSMUST00000102490.9	4115	691aa	Protein coding	CCDS16631	P49222	TSL:1 GENCODE basic APPRIS P1
Epb42-201	ENSMUST00000023987.5	2695	673aa	Protein coding	-	Q3UV95	TSL:1 GENCODE basic
Epb42-205	ENSMUST00000145812.1	625	No protein	Retained intron	-	-	TSL:3
Epb42-203	ENSMUST00000124703.7	2513	No protein	lncRNA	-	-	TSL:1
Epb42-206	ENSMUST00000147444.7	1752	No protein	lncRNA	-	-	TSL:1
Epb42-207	ENSMUST00000152217.1	680	No protein	lncRNA	-	-	TSL:5
Epb42-204	ENSMUST00000128360.1	366	No protein	lncRNA	-	-	TSL:5

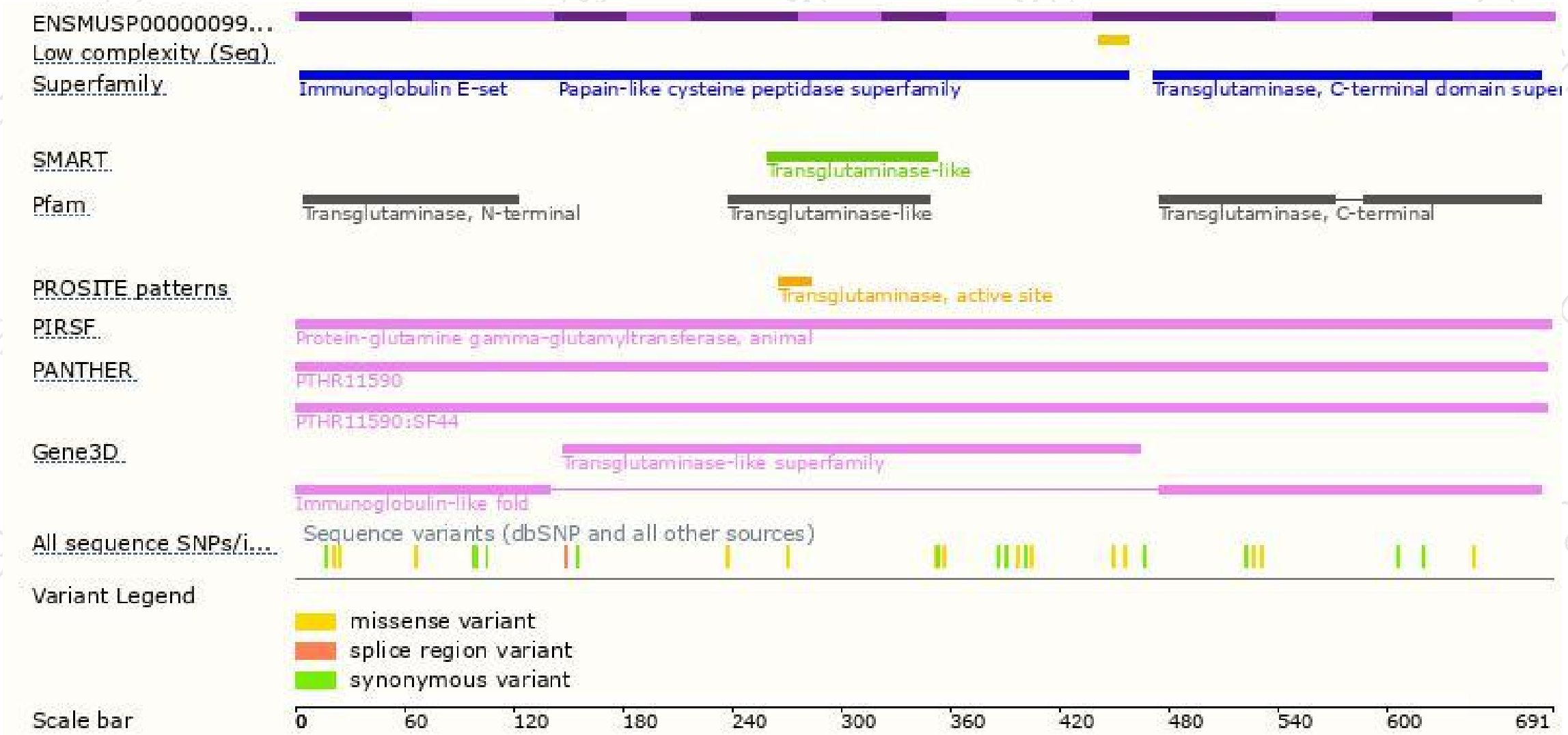
The strategy is based on the design of *Epb42-202* transcript,The transcription is shown below



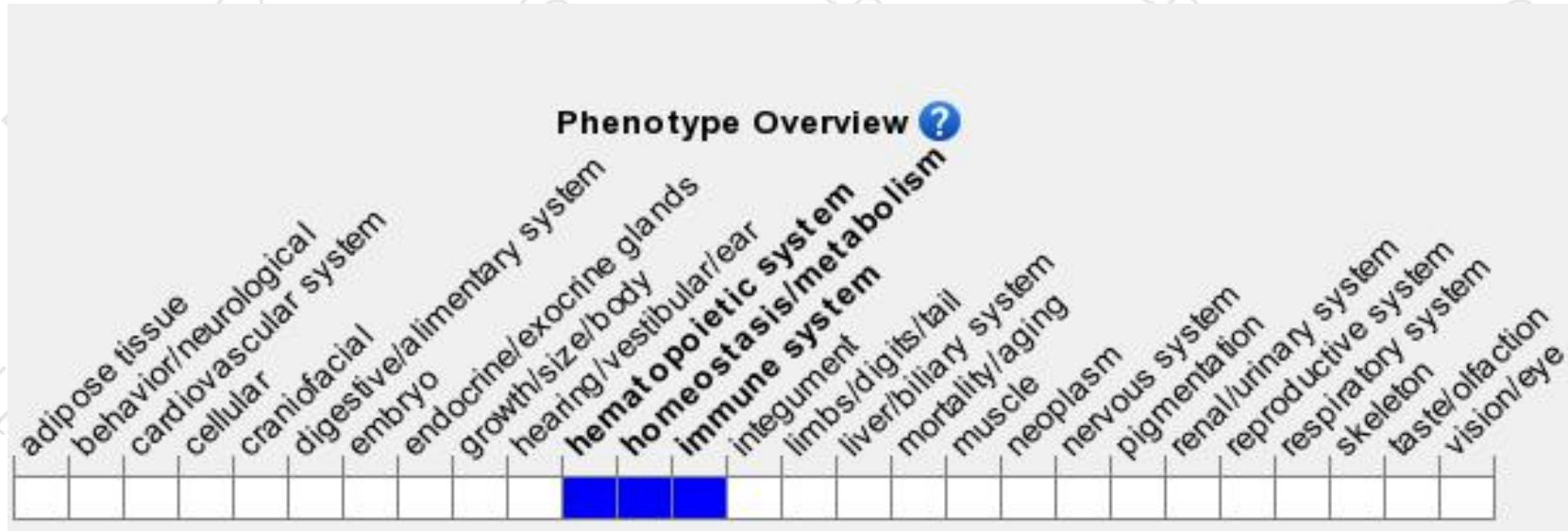
Genomic location distribution



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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