Epb41l3 Cas9-CKO Strategy

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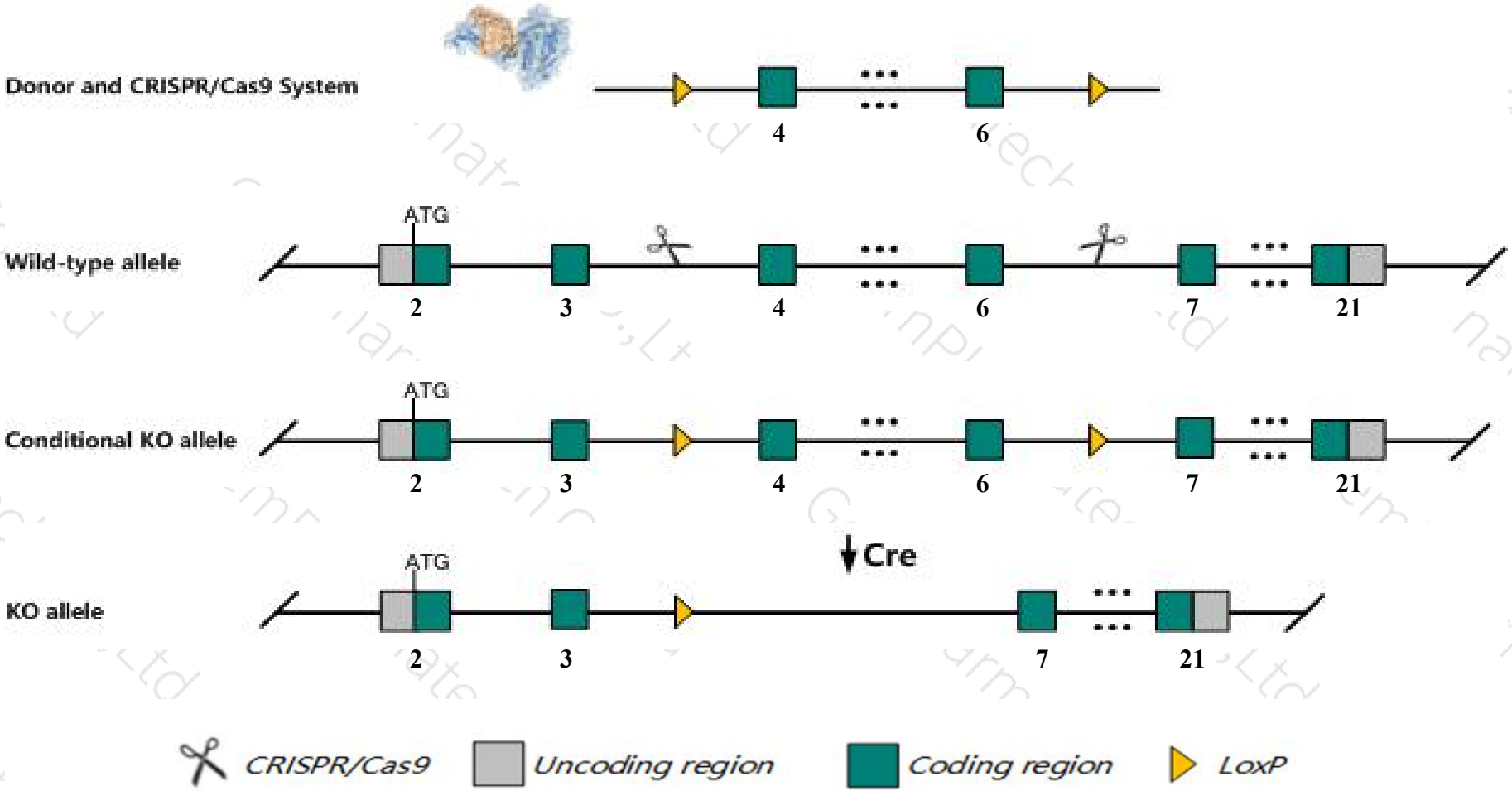
Project Overview

Project Name	***Epb41l3***
Project type	**Cas9-CKO**
Strain background	**C57BL/6JGpt**

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Epb41l3* gene. The schematic diagram is as follows:



Technical routes

- The *Epb41l3* gene has 18 transcripts. According to the structure of *Epb41l3* gene, exon4-exon6 of *Epb41l3-201* (ENSMUST00000080208.6) transcript is recommended as the knockout region.The region contains 224bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Epb41l3* gene. The brief process is as follows:CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice.Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.

- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

Notice

➢ According to the existing MGI data,Mice homozygous for one knock-out allele display a normal phenotype. Mice homozygous for a different knock-out allele exhibit ataxia, gait abnormalities, clasping, hypermyelination, abnormal axon morphology, and decreased internode length.

➢ The *Epb41l3* gene is located on the Chr17. 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 loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information （NCBI）

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Epb41l3 erythrocyte membrane protein band 4.1 like 3 [*Mus musculus* (house mouse)]

Gene ID: 13823, updated on 14-Aug-2019

Summary

Official Symbol	Epb41l3 provided by MGI
Official Full Name	erythrocyte membrane protein band 4.1 like 3 provided by MGI
Primary source	MGI:MGI:103008
See related	Ensembl:ENSMUSG00000024044
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	4.1B; Dal1; NBL3; DAL1P; Epb4.1l3
Expression	Broad expression in cerebellum adult (RPKM 14.3), frontal lobe adult (RPKM 11.1) and 15 other tissues See more
Orthologs	human all

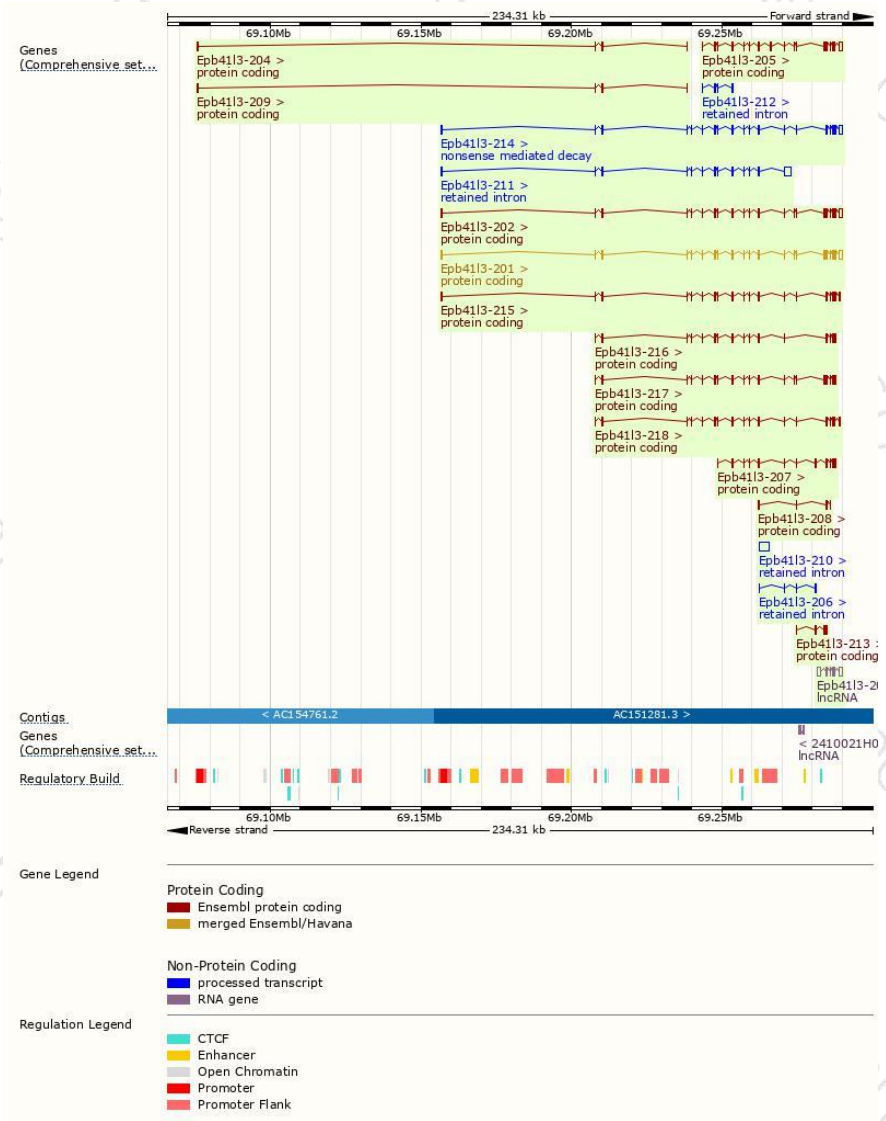
Transcript information（Ensembl）

The gene has 18 transcripts,all transcripts are shown below:

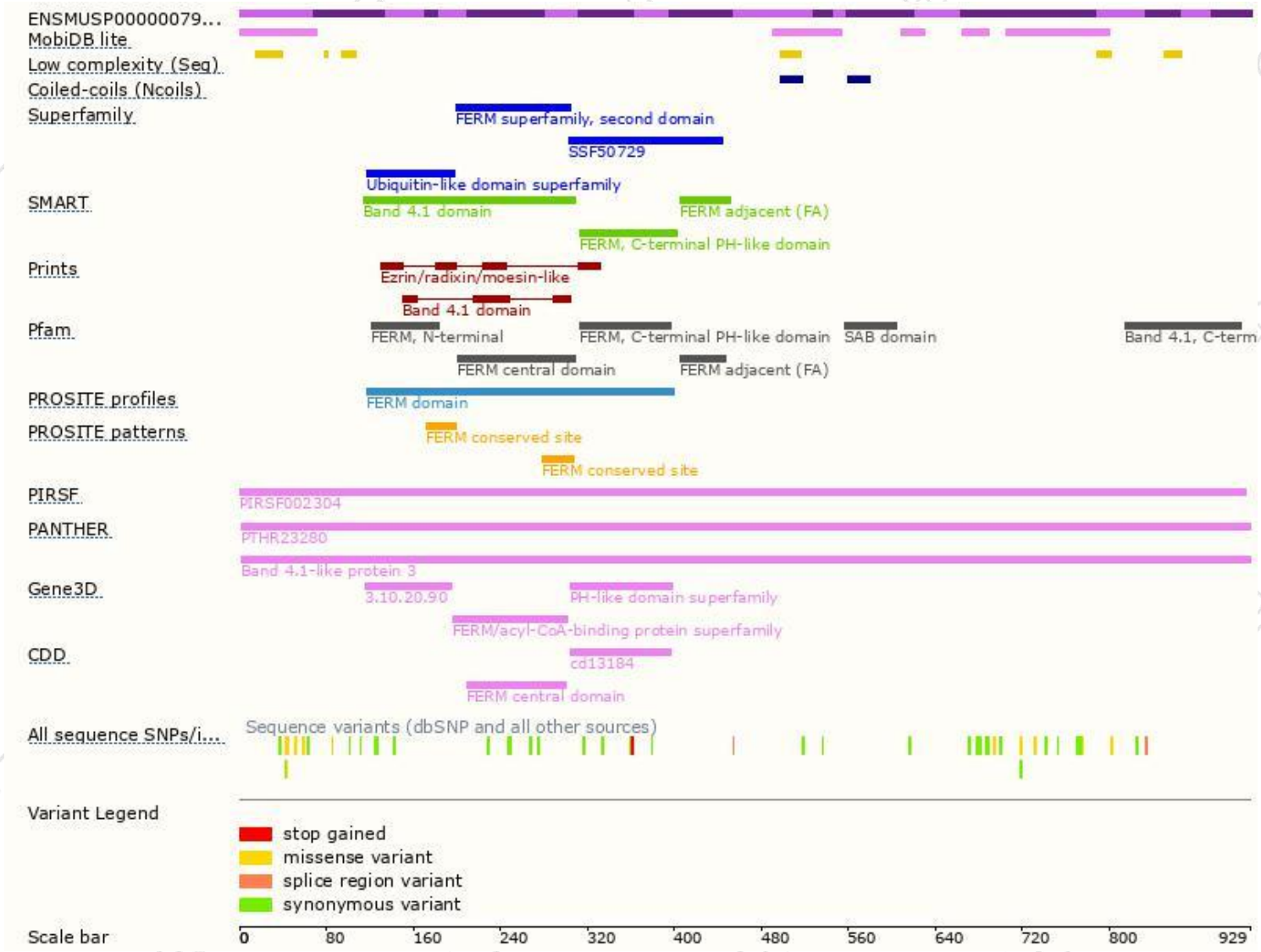
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Epb41l3-201	ENSMUST00000080208.6	4047	929aa	Protein coding	CCDS28952	Q9WV92	TSL:1 GENCODE basic APPRIS P2
Epb41l3-202	ENSMUST00000112680.7	4073	939aa	Protein coding	-	Q9WV92	TSL:5 GENCODE basic APPRIS ALT2
Epb41l3-205	ENSMUST00000223703.1	3687	852aa	Protein coding	-	A0A286YDY4	CDS 5' incomplete
Epb41l3-215	ENSMUST00000225977.1	3188	876aa	Protein coding	-	A7YY80	GENCODE basic APPRIS ALT2
Epb41l3-217	ENSMUST00000233509.1	2736	911aa	Protein coding	-	D0VYV6	GENCODE basic APPRIS ALT2
Epb41l3-218	ENSMUST00000233964.1	2703	819aa	Protein coding	-	A0A3B2WBE1	CDS 5' incomplete
Epb41l3-216	ENSMUST00000232706.1	2439	812aa	Protein coding	-	A0A3B2WD96	GENCODE basic APPRIS ALT2
Epb41l3-207	ENSMUST00000224523.1	1817	605aa	Protein coding	-	A0A286YD84	CDS 5' incomplete
Epb41l3-208	ENSMUST00000224951.1	786	262aa	Protein coding	-	A0A286YCY1	CDS 5' and 3' incomplete
Epb41l3-213	ENSMUST00000225695.1	670	223aa	Protein coding	-	A0A286YCT6	CDS 5' and 3' incomplete
Epb41l3-209	ENSMUST00000225062.1	666	29aa	Protein coding	-	A0A286YD94	CDS 3' incomplete
Epb41l3-204	ENSMUST00000223610.1	559	53aa	Protein coding	-	A0A286YDD0	CDS 3' incomplete
Epb41l3-214	ENSMUST00000225740.1	3952	287aa	Nonsense mediated decay	-	A0A286YCY8	-
Epb41l3-211	ENSMUST00000225316.1	3966	No protein	Retained intron	-	-	-
Epb41l3-210	ENSMUST00000225209.1	3219	No protein	Retained intron	-	-	-
Epb41l3-212	ENSMUST00000225604.1	647	No protein	Retained intron	-	-	-
Epb41l3-206	ENSMUST00000223816.1	471	No protein	Retained intron	-	-	-
Epb41l3-203	ENSMUST00000223565.1	3026	No protein	lncRNA	-	-	-

The strategy is based on the design of *Epb41l3-201* transcript,The transcription is shown below

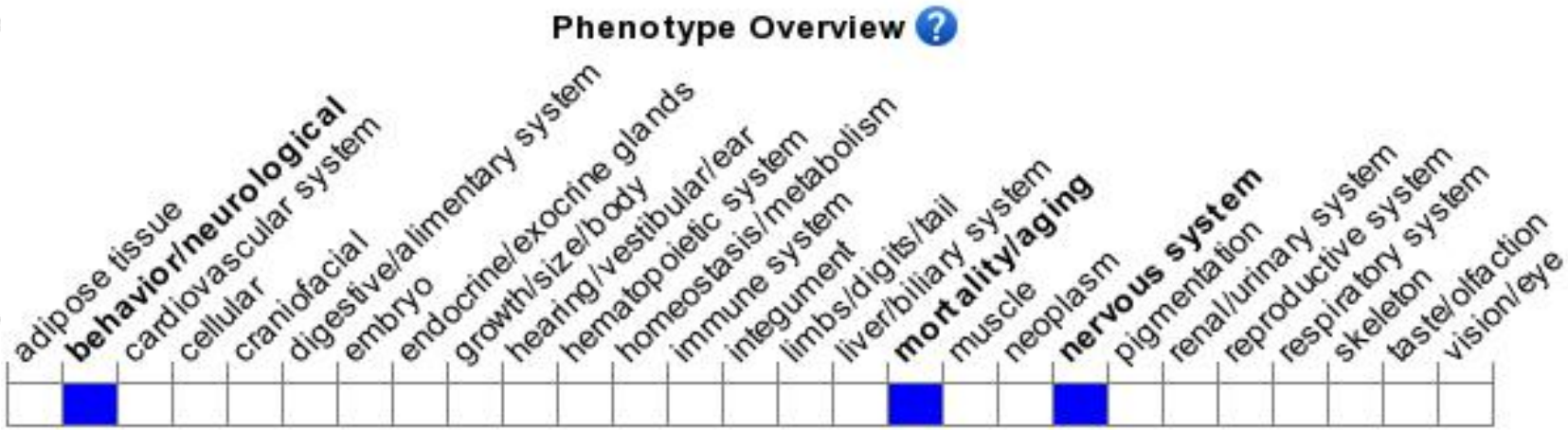
Genomic location distribution



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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