Pbrm1 Cas9-KO Strategy

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Project Overview

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Project Name	***Pbrm1***
Project type	**Cas9-KO**
Strain background	**C57BL/6JGpt**

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pbrm1* gene. The schematic diagram is as follows:

Technical routes

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- The *Pbrm1* gene has 17 transcripts. According to the structure of *Pbrm1* gene, exon4 of *Pbrm1-208* (ENSMUST00000112098.10) transcript is recommended as the knockout region.The region contains 98bp coding sequence. Knock out the region will result in disruption of protein function.

- In this project we use CRISPR/Cas9 technology to modify *Pbrm1* gene. The brief process is as follows: CRISPR/Cas9 system

Notice

- According to the existing MGI data,Homozygous null mice display embryonic lethality with hypoplastic cardiac ventricular chambers and malformation of the placenta.
- Transcript *Pbrm1*-216 may not be affected.
- The knockout region is near to the N-terminal of *Gnl3* gene,this strategy may influence the regulatory function of the N-terminal of *Gnl3* gene.
- The *Pbrm1* gene is located on the Chr14. 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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Pbrm1 polybromo 1 [Mus musculus (house mouse)]

Gene ID: 66923, updated on 31-Jan-2019

Summary

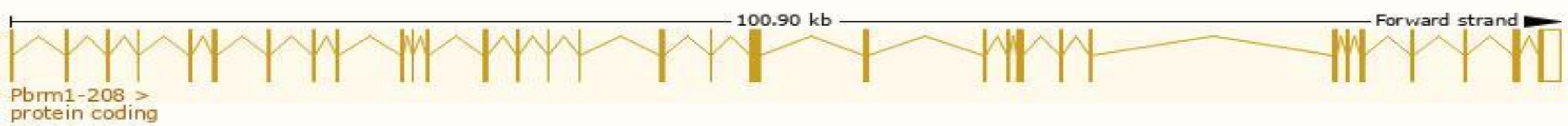
Official Symbol	Pbrm1 provided by MGI
Official Full Name	polybromo 1 provided by MGI
Primary source	MGI:MGI:1923998
See related	Ensembl:ENSMUSG00000042323
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	2610016F04Rik, AI507524, BAF180, Pb1
Expression	Ubiquitous expression in CNS E11.5 (RPKM 12.5), CNS E14 (RPKM 10.0) and 28 other tissuesSee more
Orthologs	human all

Transcript information（Ensembl）

The gene has 17 transcripts,all transcripts are shown below:

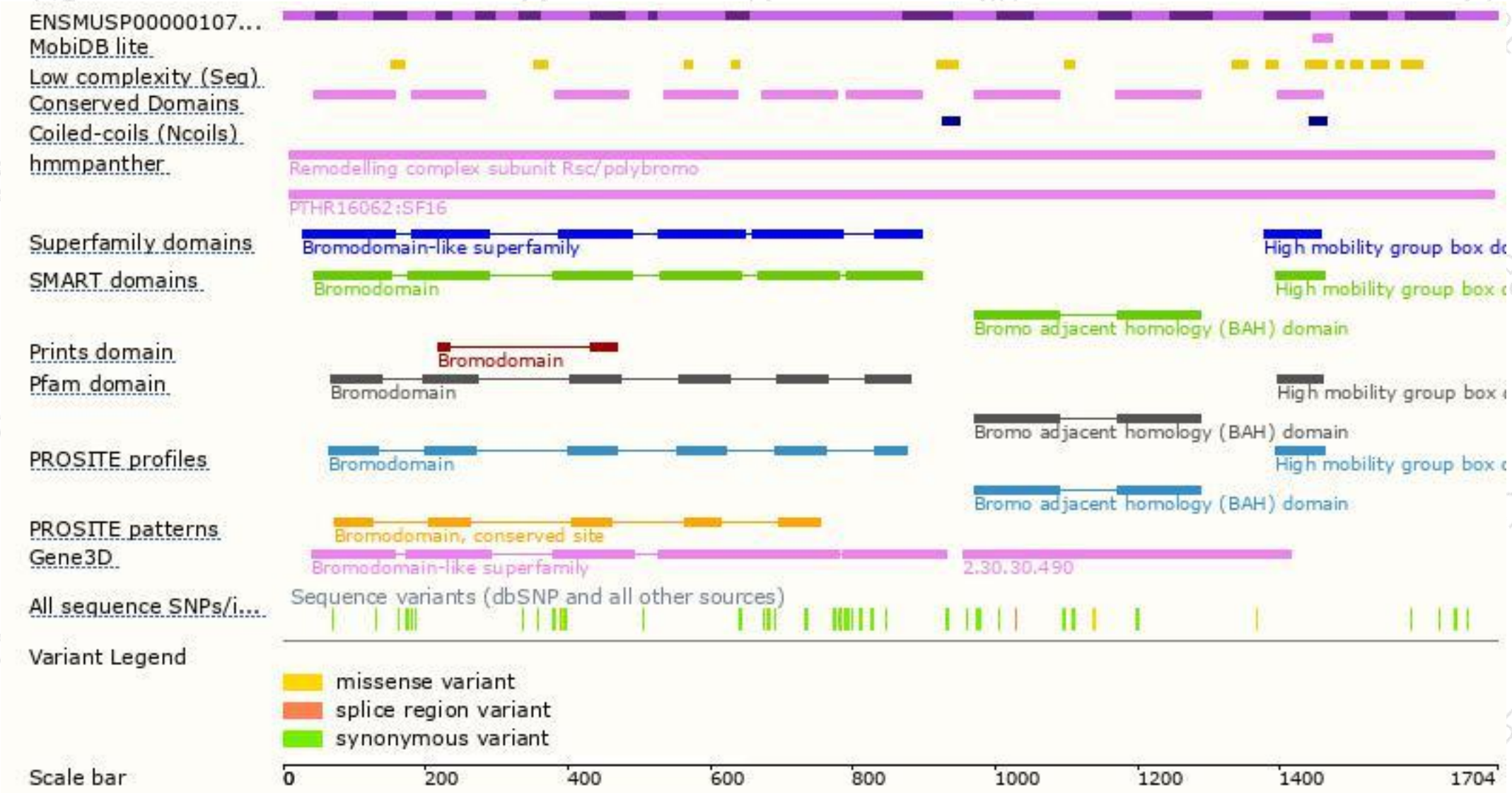
Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pbrm1-208	ENSMUST00000112098.10	6566	1704aa	Protein coding	CCDS36851	F8VQD1	TSL:5 GENCODE basic APPRIS P2
Pbrm1-207	ENSMUST00000112095.7	7907	1634aa	Protein coding	-	Q8BSQ9	TSL:5 GENCODE basic
Pbrm1-204	ENSMUST00000090214.10	6212	1689aa	Protein coding	-	E9Q4Y5	TSL:5 GENCODE basic APPRIS ALT2
Pbrm1-201	ENSMUST00000022471.11	5871	1582aa	Protein coding	-	E9Q7L3	TSL:5 GENCODE basic
Pbrm1-206	ENSMUST00000112094.7	5154	1602aa	Protein coding	-	Q8BSQ9	TSL:5 GENCODE basic
Pbrm1-203	ENSMUST00000052239.11	5065	1582aa	Protein coding	-	D3Z1W6	TSL:5 GENCODE basic
Pbrm1-205	ENSMUST00000112092.7	5009	1652aa	Protein coding	-	D3Z1N4	TSL:5 GENCODE basic
Pbrm1-202	ENSMUST00000022474.13	4843	1597aa	Protein coding	-	E9Q7L2	TSL:5 GENCODE basic
Pbrm1-217	ENSMUST00000156628.7	4388	1460aa	Protein coding	-	D3YYF2	CDS 3' incomplete TSL:5
Pbrm1-211	ENSMUST00000135704.1	3256	1085aa	Protein coding	-	F6THL5	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
Pbrm1-215	ENSMUST00000146325.7	3137	931aa	Protein coding	-	D3Z3R4	CDS 3' incomplete TSL:1
Pbrm1-209	ENSMUST00000112106.7	485	91aa	Protein coding	-	D3Z1M8	CDS 3' incomplete TSL:2
Pbrm1-213	ENSMUST00000144009.1	434	84aa	Protein coding	-	D3YYG4	CDS 3' incomplete TSL:2
Pbrm1-212	ENSMUST00000136237.7	4971	860aa	Nonsense mediated decay	-	D6RI94	TSL:5
Pbrm1-210	ENSMUST00000123678.7	4759	856aa	Nonsense mediated decay	-	D6RIL0	TSL:5
Pbrm1-214	ENSMUST00000145497.1	871	No protein	Processed transcript	-	-	TSL:3
Pbrm1-216	ENSMUST00000156407.1	817	No protein	Retained intron	-	-	TSL:5

The strategy is based on the design of *Pbrm1-208* transcript,The transcription is shown below

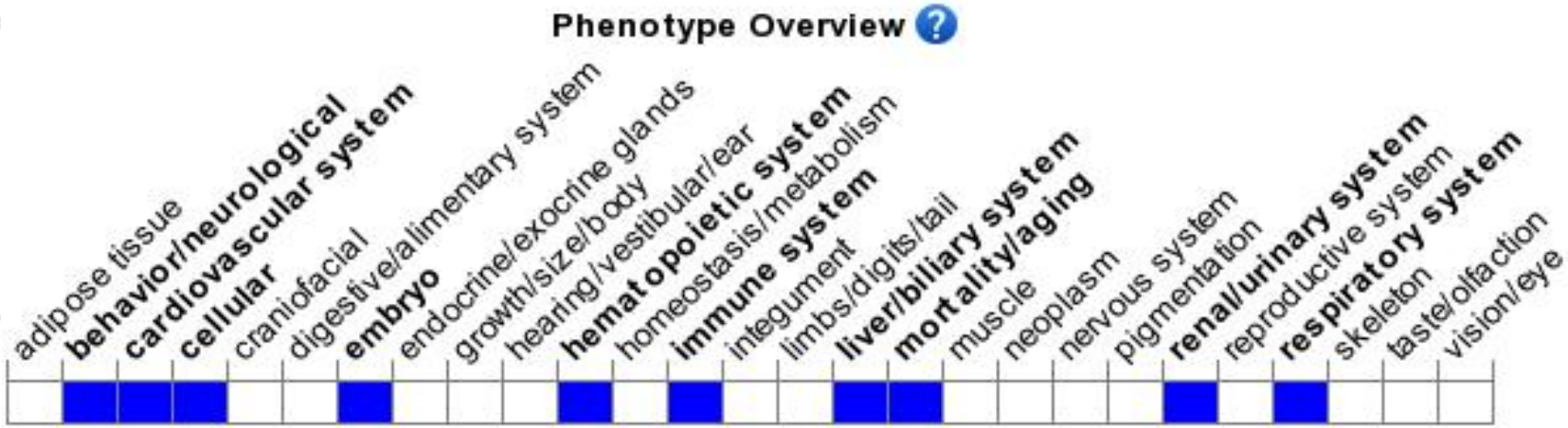


Genomic location distribution

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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