

Pcbp2 Cas9-CKO Strategy

Designer:

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Design Date:

2019-7-25

Project Overview

Project Name

Pcbp2

Project type

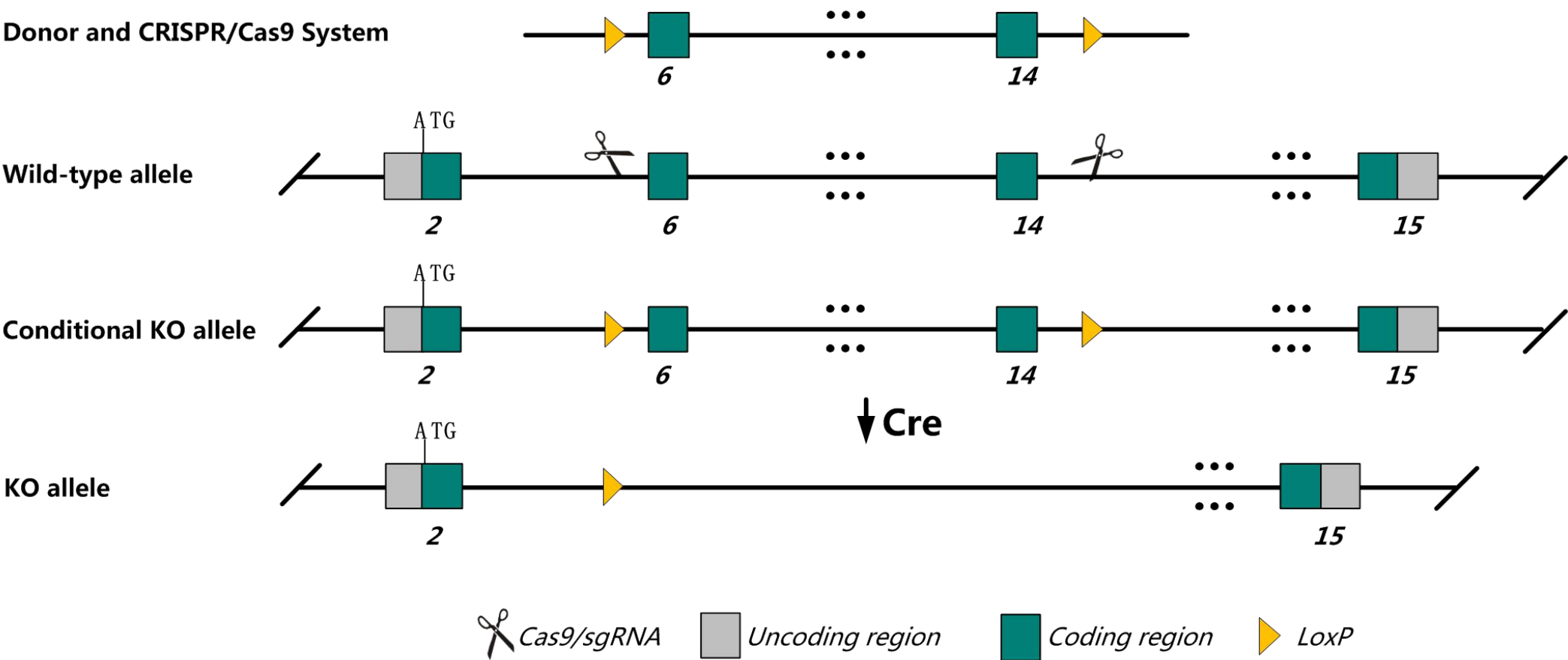
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Pcbp2* gene. The schematic diagram is as follows:



Technical routes

- The *Pcbp2* gene has 31 transcripts. According to the structure of *Pcbp2* gene, exon6-14 of *Pcbp2-201* (ENSMUST00000077037.12) transcript is recommended as the knockout region. The region contains 809bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Pcbp2* 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.

- According to the existing MGI data, Mice heterozygous for a knock-out allele exhibit decreased body weight, impaired erythroblast maturation and lowered mean platelet counts. Mice homozygous for this allele die between E12.5 and E15.5 with hemorrhage and edema.
- Transcript *Pcbp2-209* may not be affected.
- The KO region contains functional region of the *Gm26518*, *Gm27406* gene. Knockout the region may affect the function of *Gm26518*, *Gm27406* gene.
- The *Pcbp2* gene is located on the Chr15. 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)

Pcbp2 poly(rC) binding protein 2 [Mus musculus (house mouse)]

Gene ID: 18521, updated on 7-Apr-2019

Summary



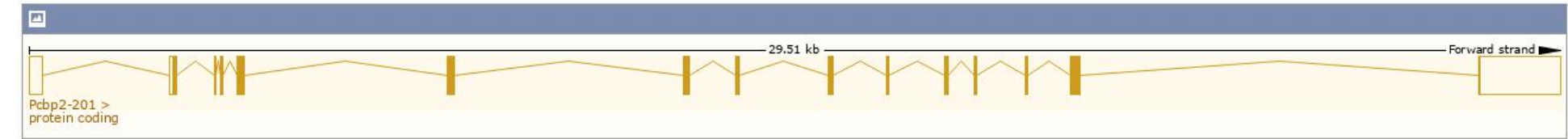
Official Symbol	Pcbp2 provided by MGI
Official Full Name	poly(rC) binding protein 2 provided by MGI
Primary source	MGI:MGI:108202
See related	Ensembl:ENSMUSG00000056851
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	AW412548, Hnrpx, alphaCP-2
Expression	Ubiquitous expression in testis adult (RPKM 95.3), limb E14.5 (RPKM 65.4) and 28 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

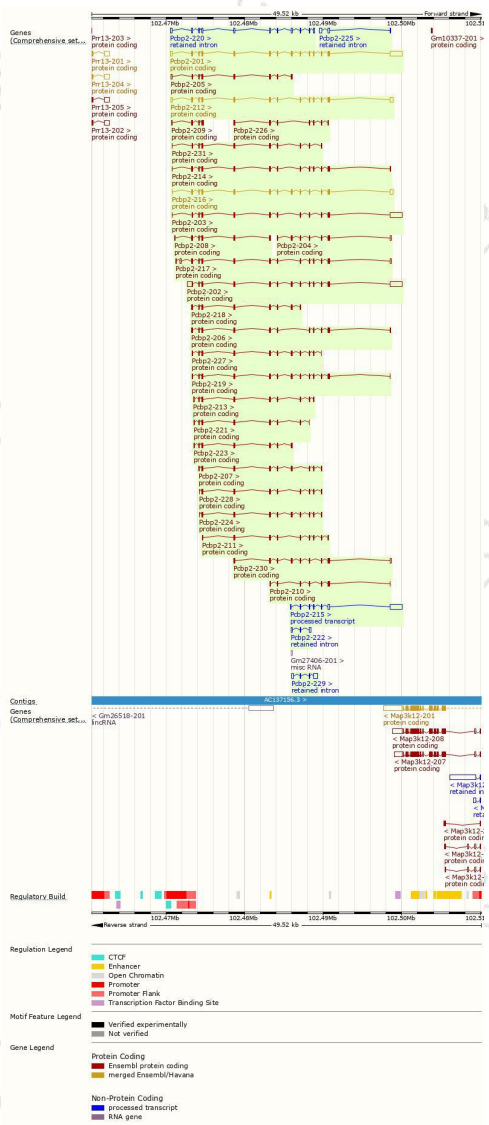
The gene has 31 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Pcbp2-202	ENSMUST00000078404.1	3222	362aa	Protein coding	CCDS49741	Q61990	TSL2 GENCODE basic APPRIS ALT1
Pcbp2-201	ENSMUST00000077037.12	2952	362aa	Protein coding	CCDS49741	Q61990	TSL1 GENCODE basic APPRIS ALT1
Pcbp2-212	ENSMUST00000229618.1	1576	331aa	Protein coding	CCDS49742	Q61990	GENCODE basic APPRIS ALT1
Pcbp2-216	ENSMUST00000229854.1	1499	349aa	Protein coding	CCDS27684	Q61990	GENCODE basic APPRIS P3
Pcbp2-203	ENSMUST00000108838.4	2571	322aa	Protein coding	-	Q31TR1	TSL2 GENCODE basic APPRIS ALT1
Pcbp2-217	ENSMUST00000229918.1	1463	335aa	Protein coding	-	A0A2RRVHP9	GENCODE basic APPRIS ALT1
Pcbp2-214	ENSMUST00000229802.1	1215	335aa	Protein coding	-	A0A2RRVHP9	GENCODE basic APPRIS ALT1
Pcbp2-206	ENSMUST00000229184.1	1090	316aa	Protein coding	-	A0A2RRVQ25	GENCODE basic
Pcbp2-219	ENSMUST00000230114.1	1086	361aa	Protein coding	-	B2M1R7	GENCODE basic APPRIS ALT1
Pcbp2-230	ENSMUST00000231085.1	915	265aa	Protein coding	-	A0A2RRW6U8	CDS 5' incomplete
Pcbp2-205	ENSMUST00000229102.1	893	224aa	Protein coding	-	A0A2RRW6L5	CDS 3' incomplete
Pcbp2-227	ENSMUST00000230728.1	873	280aa	Protein coding	-	A0A2RRV112	CDS 3' incomplete
Pcbp2-231	ENSMUST00000231089.1	843	248aa	Protein coding	-	A0A2RRVHY9	CDS 3' incomplete
Pcbp2-224	ENSMUST00000230577.1	792	264aa	Protein coding	-	A0A2RRV173	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete
Pcbp2-218	ENSMUST00000229958.1	789	241aa	Protein coding	-	A0A2RRV171	CDS 3' incomplete
Pcbp2-213	ENSMUST00000229748.1	786	205aa	Protein coding	-	A0A2RRVJY1	CDS 3' incomplete
Pcbp2-207	ENSMUST00000229219.1	759	253aa	Protein coding	-	A0A2RRVKQ0	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete
Pcbp2-221	ENSMUST00000230211.1	704	190aa	Protein coding	-	A0A2RRVKF0	CDS 3' incomplete
Pcbp2-228	ENSMUST00000230918.1	693	231aa	Protein coding	-	A0A2RRVHZ0	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete
Pcbp2-223	ENSMUST00000230539.1	690	185aa	Protein coding	-	A0A2RRVHG2	CDS 3' incomplete
Pcbp2-211	ENSMUST00000229533.1	674	225aa	Protein coding	-	A0A2RRVHL8	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete
Pcbp2-204	ENSMUST00000229061.1	669	184aa	Protein coding	-	A0A2RRW8H3	CDS 5' incomplete
Pcbp2-208	ENSMUST00000229222.1	647	169aa	Protein coding	-	A0A2RRVHN3	CDS 3' incomplete
Pcbp2-226	ENSMUST00000230682.1	575	192aa	Protein coding	-	A0A2RRV115	5' and 3' truncations in transcript evidence prevent annotation of the start and the end of the CDS. CDS 5' and 3' incomplete
Pcbp2-210	ENSMUST00000229432.1	553	191aa	Protein coding	-	A0A2RRV9B2	CDS 5' incomplete
Pcbp2-209	ENSMUST00000229275.1	516	95aa	Protein coding	-	A0A2RRVH3	GENCODE basic
Pcbp2-215	ENSMUST00000229822.1	2048	No protein	Processed transcript	-	-	
Pcbp2-220	ENSMUST00000230129.1	1230	No protein	Retained intron	-	-	
Pcbp2-229	ENSMUST00000230997.1	909	No protein	Retained intron	-	-	
Pcbp2-225	ENSMUST00000230631.1	585	No protein	Retained intron	-	-	
Pcbp2-222	ENSMUST00000230282.1	427	No protein	Retained intron	-	-	

The strategy is based on the design of *Pcbp2-201* transcript,The transcription is shown below



Genomic location distribution



Protein domain

ENSMUSP00000076...

Conserved Domains

hmmpanther



Superfamily domains

K Homology domain, type 1 superfamily

SMART domains

K Homology domain

Pfam domain

K Homology domain, type 1

PROSITE profiles

PS50084

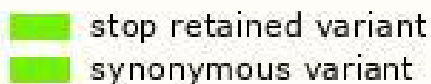
Gene3D

K Homology domain, type 1 superfamily

All sequence SNPs/i....

Sequence variants (dbSNP and all other sources)

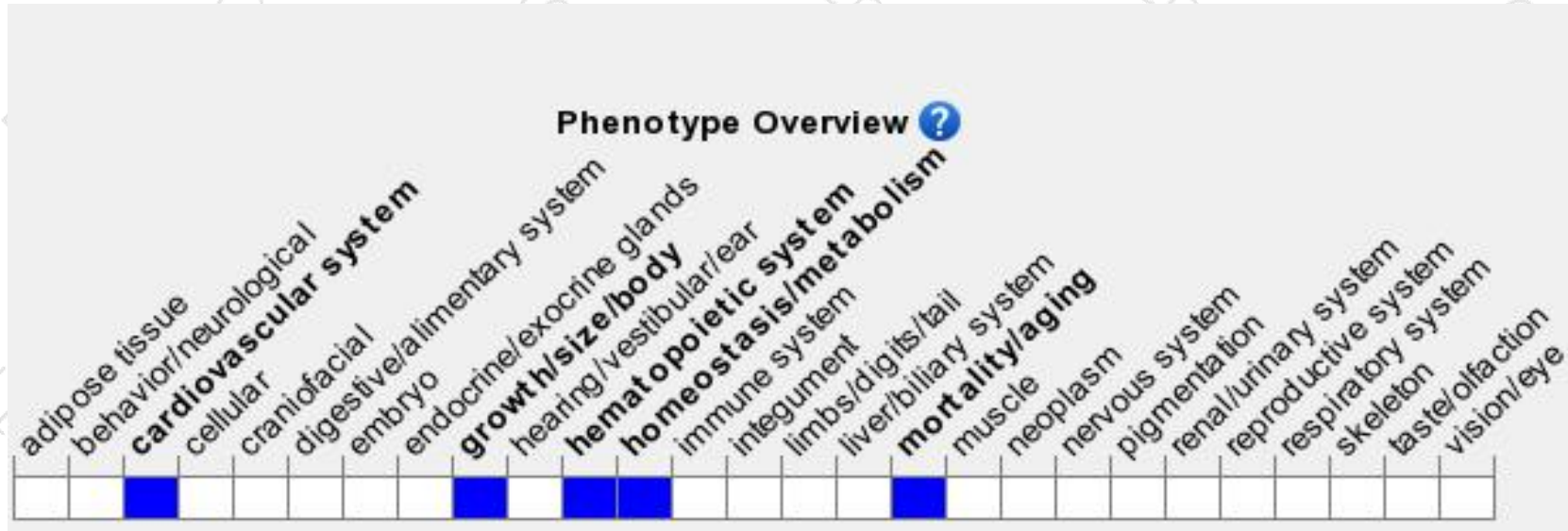
Variant Legend



Scale bar



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 heterozygous for a knock-out allele exhibit decreased body weight, impaired erythroblast maturation and lowered mean platelet counts. Mice homozygous for this allele die between E12.5 and E15.5 with hemorrhage and edema.

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

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