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Ptger1 Cas9-KO Strategy

Designer: Xingkai Xiao

Reviewer: Yanhua Shen

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Overview

Target Gene Name

- *Ptger1*

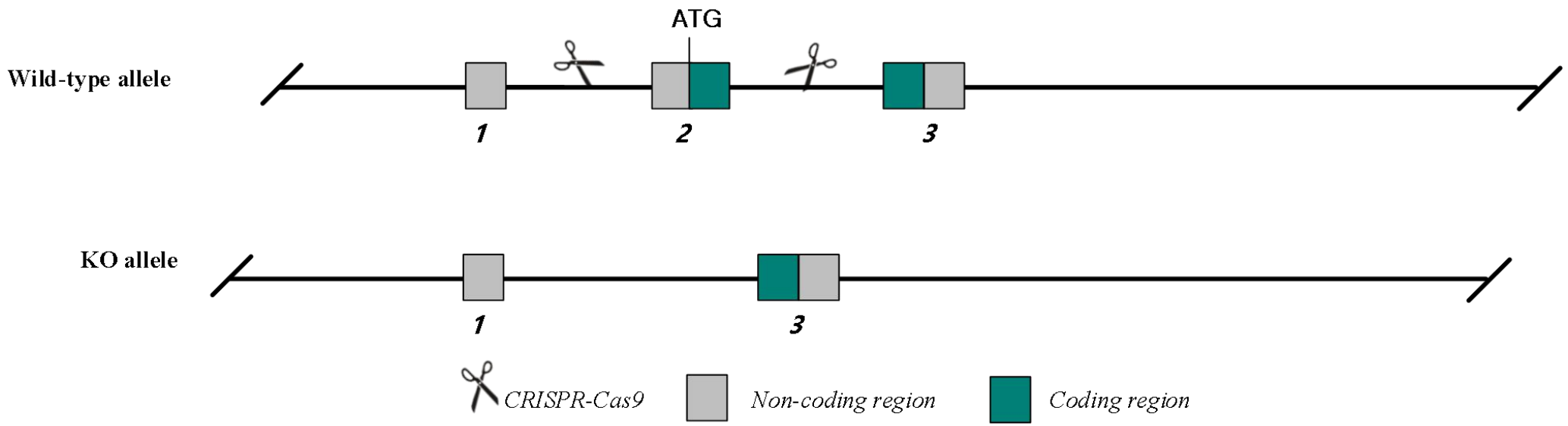
Project Type

- Cas9-KO

Genetic Background

- C57BL/6JGpt

Strain Strategy



Schematic representation of CRISPR-Cas9 engineering used to edit the *Ptger1* gene.

Technical Information

- The *Ptger1* gene has 3 transcripts. According to the structure of *Ptger1* gene, exon2 of *Ptger1*-201 (ENSMUST00000019608.7) transcript is recommended as the knockout region. The region contains 951 bp of coding sequences. Knocking out the region will result in deletion start codon and the most coding region of *Ptger1*, which may disrupt the function of *Ptger1*.
- In this project we use CRISPR-Cas9 technology to modify *Ptger1* gene. The brief process is as follows: Cas9 and gRNAs 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 on-target amplicon sequencing. A stable F1-generation mouse strain was obtained by mating positive F0-generation mice with C57BL/6JGpt mice and confirmation of the desired mutant allele was carried out by PCR and on-target amplicon sequencing.

Gene Information

Ptger1 prostaglandin E receptor 1 (subtype EP1) [*Mus musculus* (house mouse)]

Download Datasets

Gene ID: 19216, updated on 27-Jun-2023

Summary

Official Symbol	Ptger1 provided by MGI
Official Full Name	prostaglandin E receptor 1 (subtype EP1) provided by MGI
Primary source	MGI:MGI:97793
See related	Ensembl:ENSMUSG00000019464 AllianceGenome:MGI:97793
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	EP1; Ptgerep1
Summary	Enables D1 dopamine receptor binding activity. Involved in adenylate cyclase-activating dopamine receptor signaling pathway. Acts upstream of or within response to lipopolysaccharide. Predicted to be located in membrane. Predicted to be integral component of membrane. Predicted to be active in plasma membrane. Is expressed in several structures, including adipose tissue; alimentary system; brain; genitourinary system; and immune system. Orthologous to human PTGER1 (prostaglandin E receptor 1). [provided by Alliance of Genome Resources, Apr 2022]
Expression	Ubiquitous expression in thymus adult (RPKM 44.9), spleen adult (RPKM 41.4) and 28 other tissues See more
Orthologs	human all

NEW **Try the new Gene table**

Try the new Transcript table

Source: https://www.ncbi.nlm.nih.gov/

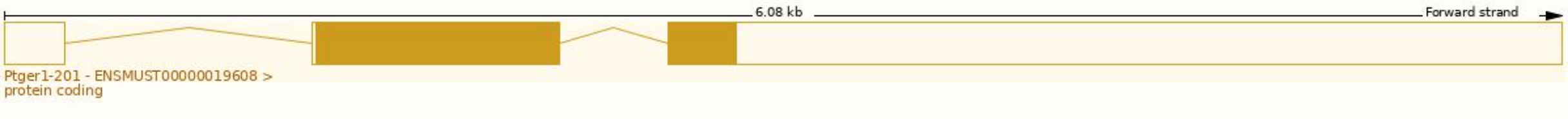
Transcript Information

The gene has 3 transcripts, all transcripts are shown below:

Show/hide columns (1 hidden) Filter

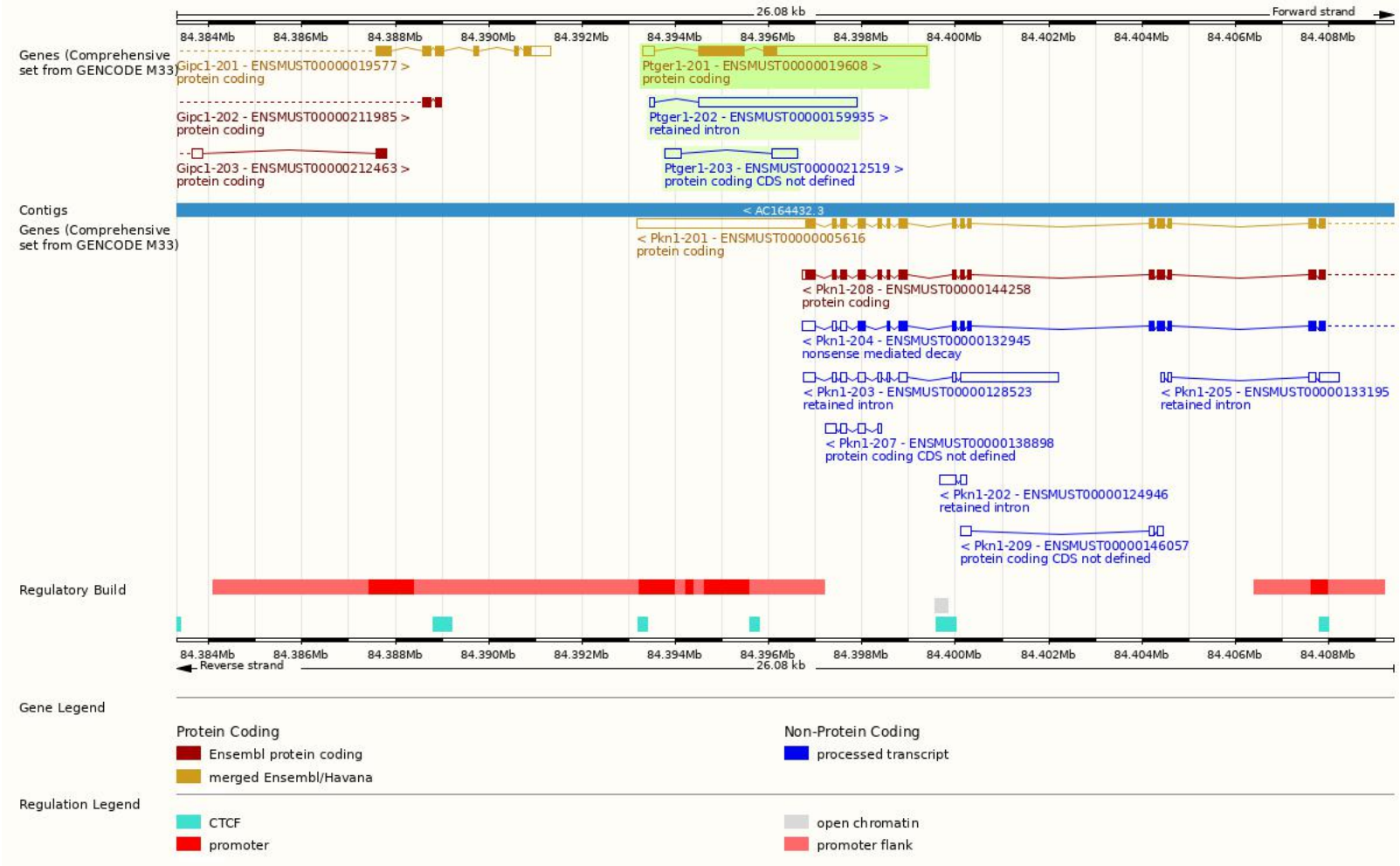
Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	Flags
ENSMUST00000019608.7	Ptger1-201	4694	405aa	Protein coding	CCDS22458	B2RS62 P35375	Ensembl Canonical GENCODE basic APPRIS P1 TSL:1
ENSMUST00000212519.2	Ptger1-203	884	No protein	Protein coding CDS not defined		-	TSL:3
ENSMUST00000159935.2	Ptger1-202	3474	No protein	Retained intron		-	TSL:1

The strategy is based on the design of *Ptger1*-201 transcript, the transcription is shown below:



Source: https://www.ensembl.org

Genomic Information



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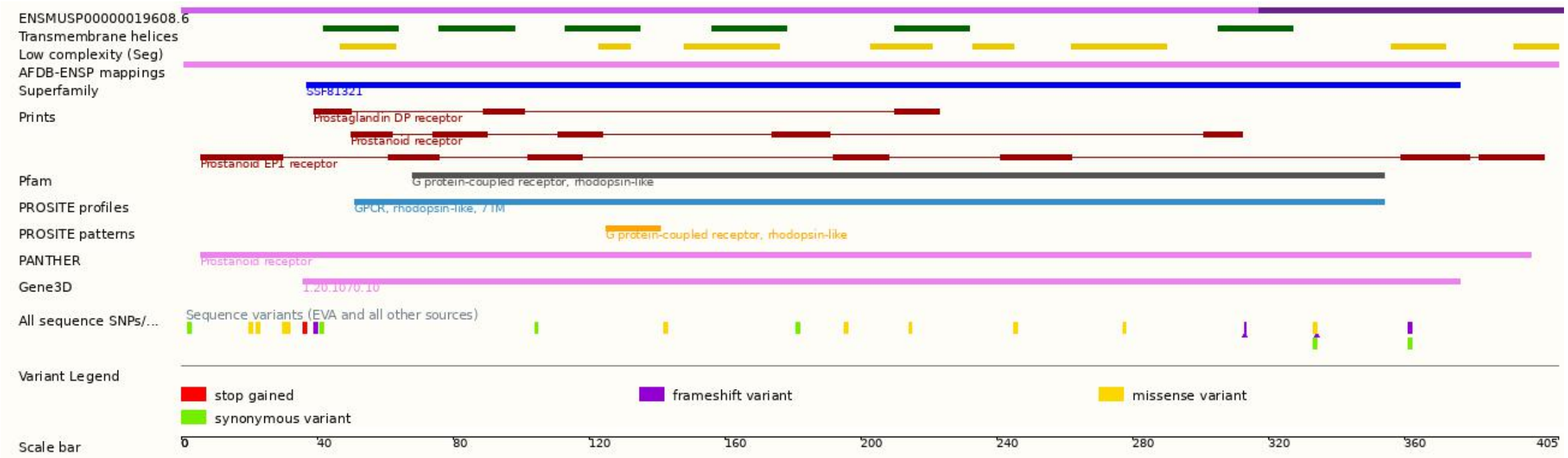
Source: : https://www.ensembl.org

Protein Information



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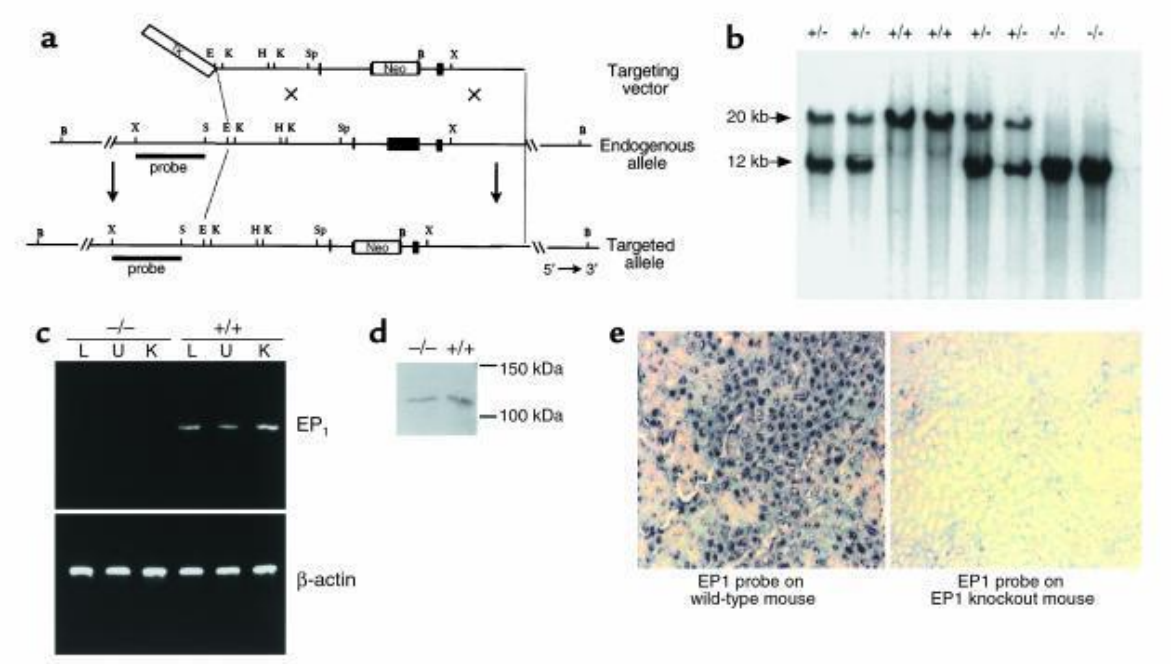
Source: : https://www.ensembl.org

Important Information

- **According to MGI, homozygous null mice may exhibit partial prenatal lethality, pain threshold abnormalities, behavioral disinhibition in response to stress, low blood pressure, defects in type IV hypersensitivity reactions, resistance to chemically induced tumors and impaired response to water deprivation.**
- **In this strategy, 89 amino acid residues are retained at the 3' of *Ptger1*, the risk is unknown.**
- **The knockout region will delete part of 3'UTR of *Pkn1*-201, which may affect the expression of *Pkn1*.**
- The knockout region is about 2.7 kb away from the 3' of *Gipc1*, which may affect the regulation of this gene.
- *Ptger1* is located on Chr8. If the knockout mice are crossed with other mouse strains to obtain double homozygous mutant offspring, please avoid the situation that the second gene is 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.

Reference

[1]



[2]

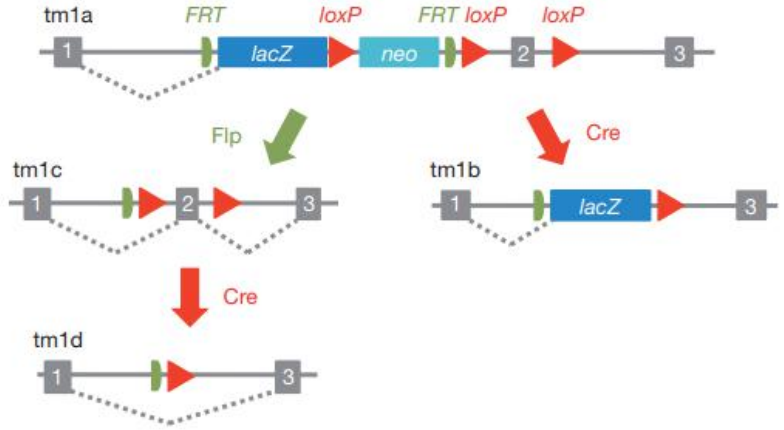


Figure 1 | Schematic of the 'knockout-first' conditional allele. The 'knockout-first' allele (tm1a) contains an IRES:*lacZ* trapping cassette and a floxed promoter-driven *neo* cassette inserted into the intron of a gene, disrupting gene function. Flp converts the 'knockout-first' allele to a conditional allele (tm1c), restoring gene activity. Cre deletes the promoter-driven selection cassette and floxed exon of the tm1a allele to generate a *lacZ*-tagged allele (tm1b) or deletes the floxed exon of the tm1c allele to generate a frameshift mutation (tm1d), triggering nonsense mediated decay of the deleted transcript.

[1] The prostaglandin E_2EP_1 receptor mediates pain perception and regulates blood pressure. J Clin Invest . 2001 Feb;107(3):325-31. DOI: 10.1172/JCI6749.

[2] Skarnes, W. C. , Rosen, B. , West, A. P. , Koutsourakis, M. , Bushell, W. , & Iyer, V. , et al. (2011). A conditional knockout resource for the genome-wide study of mouse gene function. Nature, 474(7351), 337.