

Abcc5 Cas9-KO Strategy

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Reviewer:

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Design Date:

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Project Overview

Project Name

Abcc5

Project type

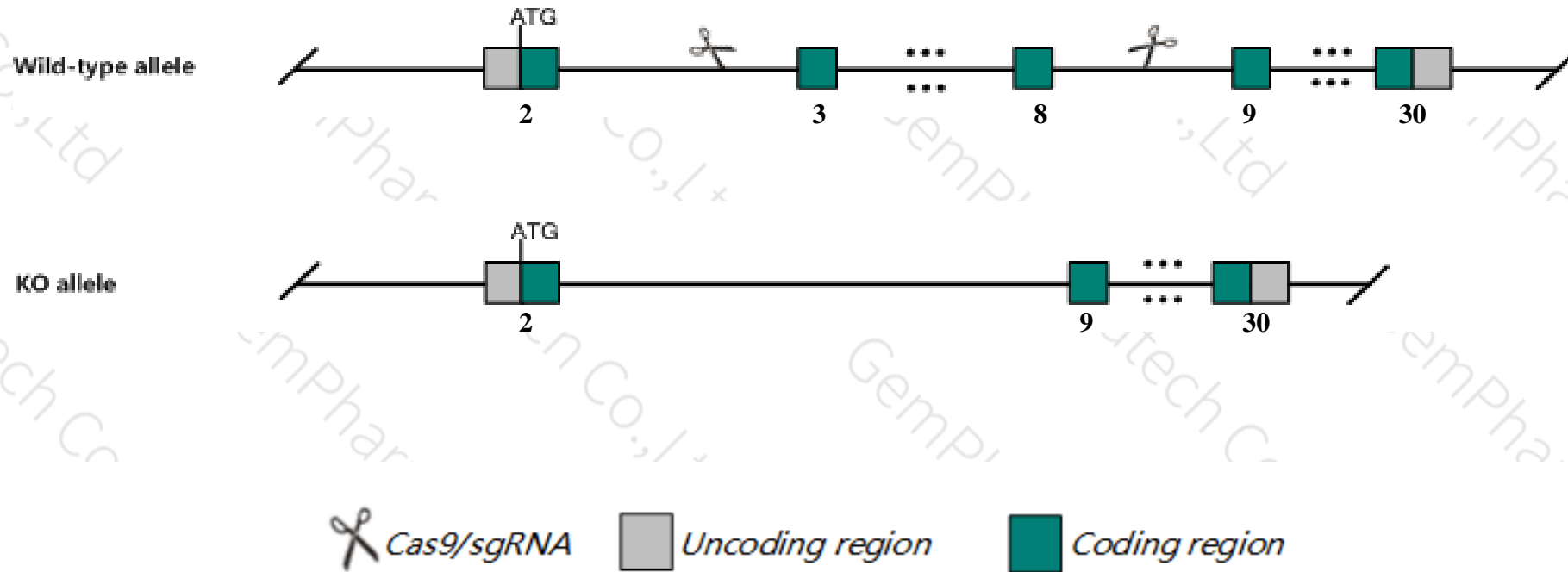
Cas9-KO

Strain background

C57BL/6JGpt

Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Abcc5* gene. The schematic diagram is as follows:



- The *Abcc5* gene has 13 transcripts. According to the structure of *Abcc5* gene, exon3-exon8 of *Abcc5*-202 (ENSMUST00000079158.12) transcript is recommended as the knockout region. The region contains 1018bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Abcc5* gene. The brief process is as follows: sgRNA was transcribed in vitro. Cas9 and sgRNA 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.

- According to the existing MGI data, Mice homozygous for a knock-out allele display normal cGMP transport into erythrocyte membrane vesicles.
- The *Abcc5* gene is located on the Chr16. 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)

Abcc5 ATP-binding cassette, sub-family C (CFTR/MRP), member 5 [Mus musculus (house mouse)]

Gene ID: 27416, updated on 31-Jan-2019

Summary

Official Symbol Abcc5 provided by [MGI](#)

Official Full Name ATP-binding cassette, sub-family C (CFTR/MRP), member 5 provided by [MGI](#)

Primary source [MGI:MGI:1351644](#)

See related [Ensembl:ENSMUSG00000022822](#)

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 2900011L11Rik, AI132311, Abcc5a, Abcc5b, Mrp5

Summary The membrane-associated protein encoded by this gene is a member of the superfamily of ATP-binding cassette (ABC) transporters. ABC proteins transport various molecules across extra- and intra-cellular membranes. ABC genes are divided into seven distinct subfamilies (ABC1, MDR/TAP, MRP, ALD, OABP, GCN20, White). This protein is a member of the MRP subfamily which is involved in multi-drug resistance. The human protein functions in the cellular export of its substrate, cyclic nucleotides. This export contributes to the degradation of phosphodiesterases and possibly an elimination pathway for cyclic nucleotides. Studies show that the human protein provides resistance to thiopurine anticancer drugs, 6-mercaptopurine and thioguanine, and the anti-HIV drug 9-(2-phosphonylmethoxyethyl)adenine. Two alternatively spliced transcript variants encoding distinct isoforms have been found for this gene. [provided by RefSeq, Jul 2008]

Expression Ubiquitous expression in CNS E18 (RPKM 26.0), CNS E14 (RPKM 23.9) and 26 other tissues [See more](#)

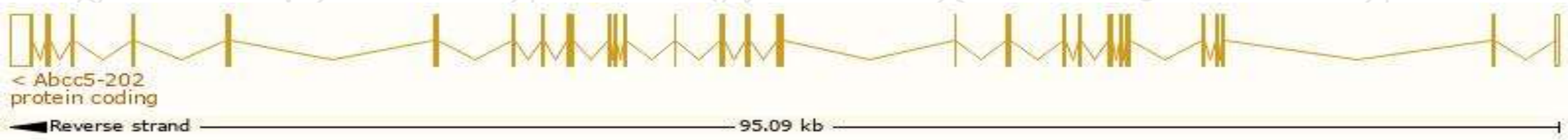
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

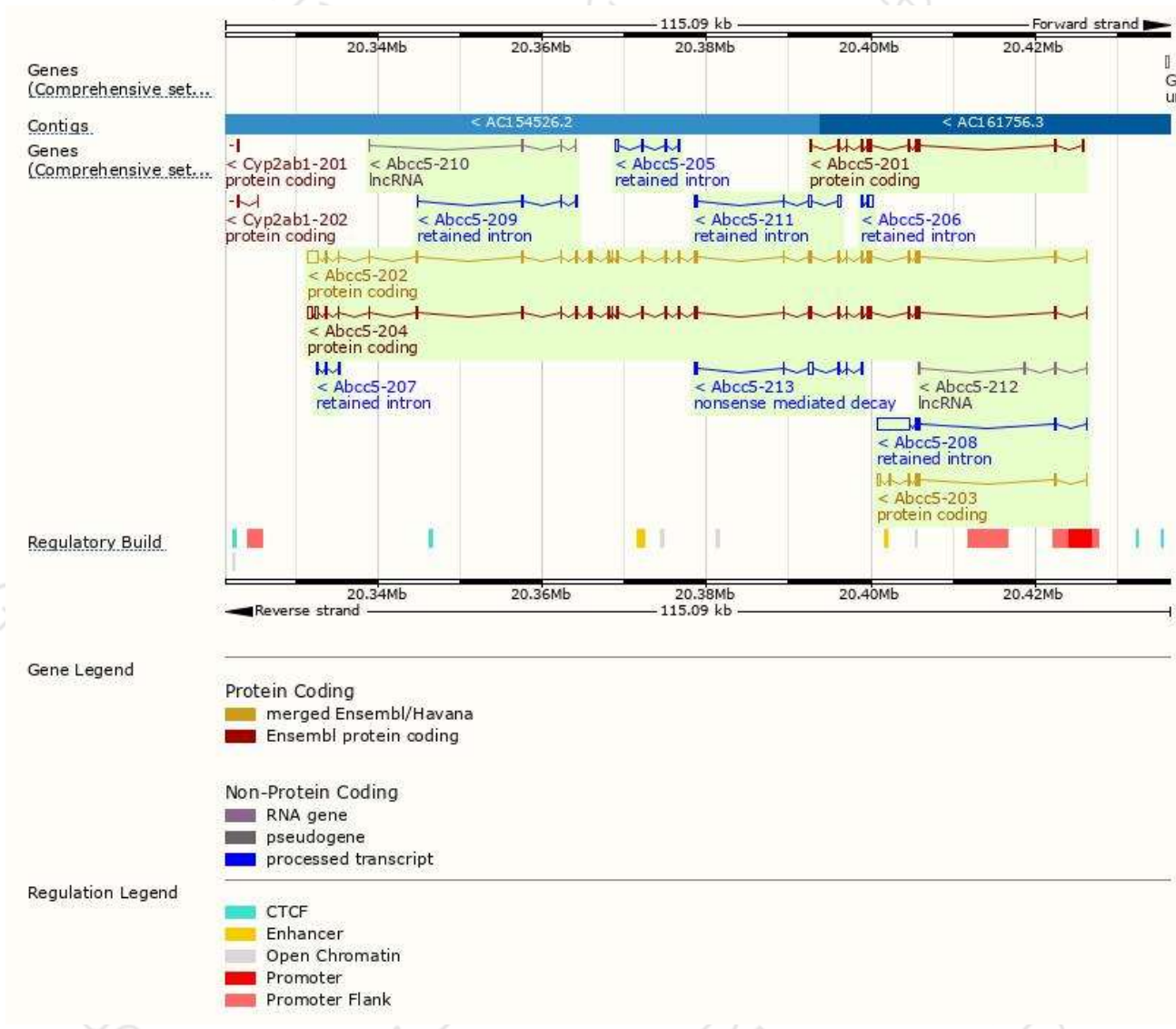
The gene has 13 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Abcc5-202	ENSMUST00000079158.12	5811	1436aa	Protein coding	CCDS28045	Q9R1X5	TSL:1 GENCODE basic APPRIS P1
Abcc5-204	ENSMUST00000115547.8	5372	1436aa	Protein coding	CCDS28045	Q9R1X5	TSL:5 GENCODE basic APPRIS P1
Abcc5-203	ENSMUST00000096199.4	1136	208aa	Protein coding	CCDS28046	Q6P8Q2	TSL:1 GENCODE basic
Abcc5-201	ENSMUST00000077867.9	1728	512aa	Protein coding	-	F8WJ10	CDS 3' incomplete TSL:1
Abcc5-213	ENSMUST00000232044.1	1094	136aa	Nonsense mediated decay	-	A0A338P7E4	CDS 5' incomplete
Abcc5-208	ENSMUST00000134962.1	4526	No protein	Retained intron	-	-	TSL:1
Abcc5-211	ENSMUST00000150340.1	979	No protein	Retained intron	-	-	TSL:2
Abcc5-206	ENSMUST00000128978.1	799	No protein	Retained intron	-	-	TSL:2
Abcc5-205	ENSMUST00000127582.1	705	No protein	Retained intron	-	-	TSL:3
Abcc5-209	ENSMUST00000137985.1	618	No protein	Retained intron	-	-	TSL:3
Abcc5-207	ENSMUST00000134413.8	523	No protein	Retained intron	-	-	TSL:5
Abcc5-212	ENSMUST00000231522.1	517	No protein	lncRNA	-	-	
Abcc5-210	ENSMUST00000148003.7	338	No protein	lncRNA	-	-	TSL:5

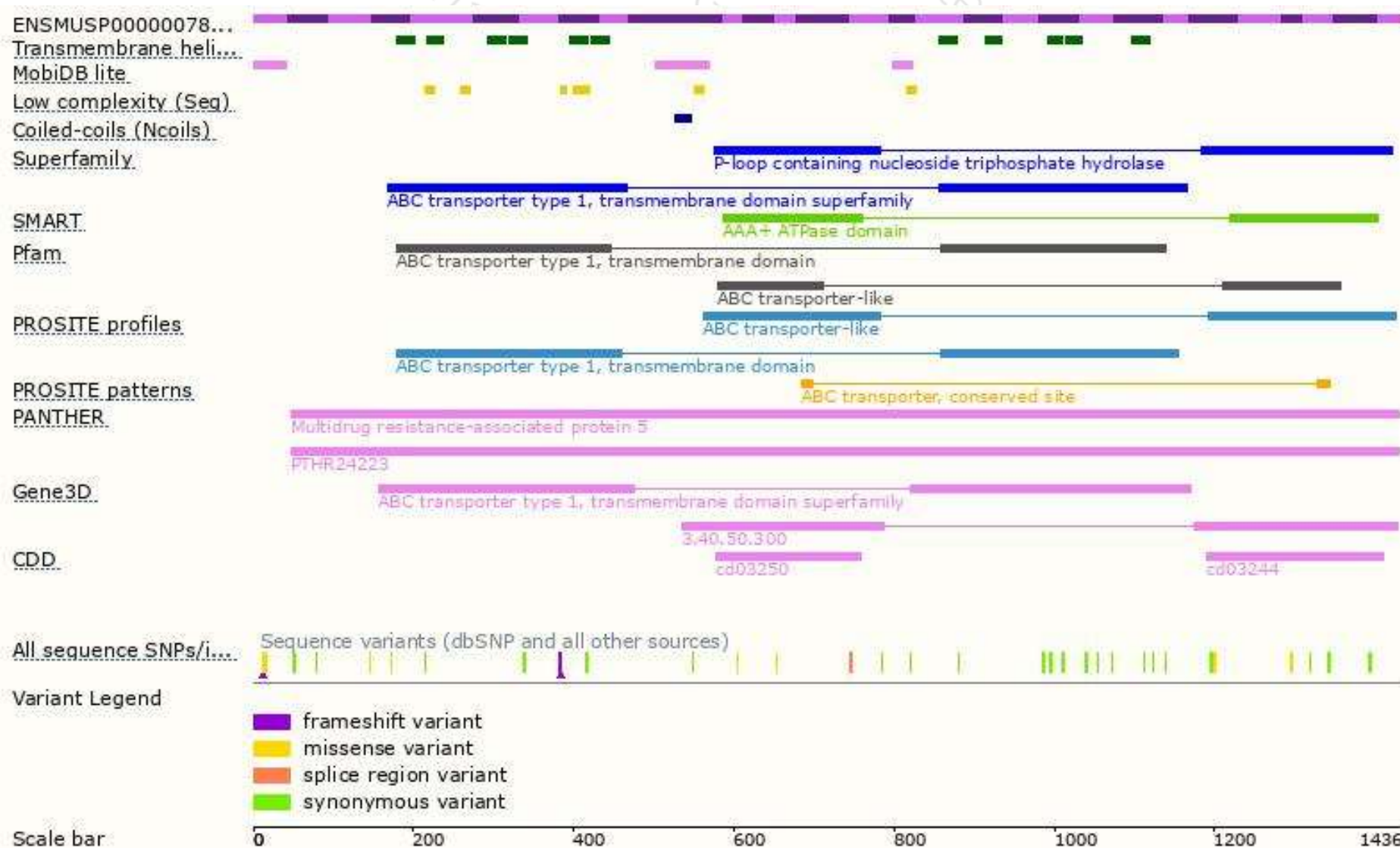
The strategy is based on the design of *Abcc5-202* transcript,The transcription is shown below



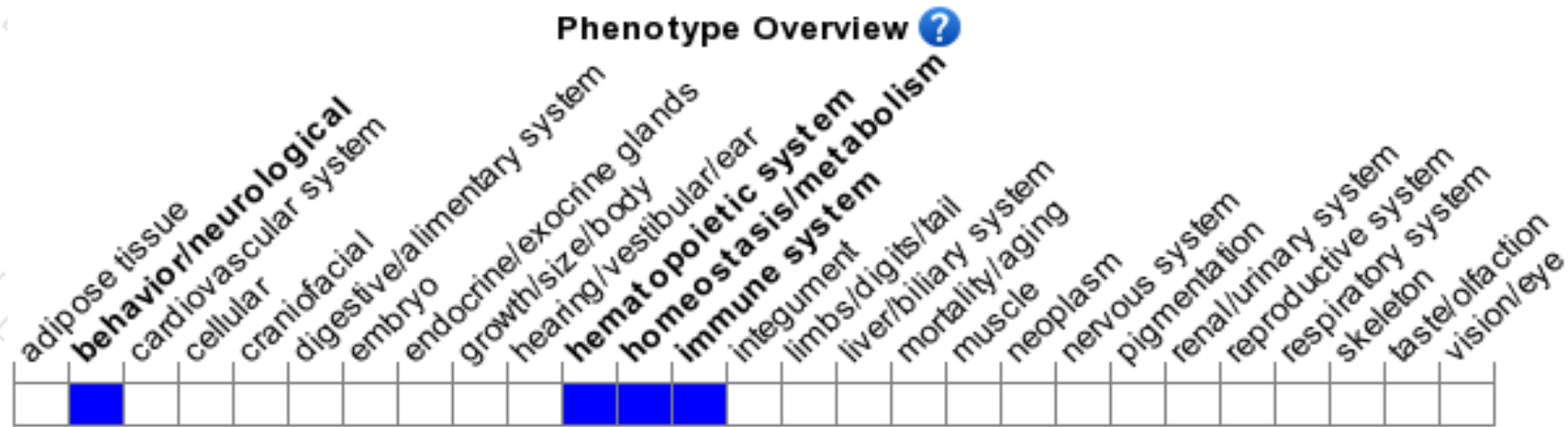
Genomic location distribution



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/>).

According to the existing MGI data, Mice homozygous for a knock-out allele display normal cGMP transport into erythrocyte membrane vesicles.

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

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