Wellcome Trust Sanger Institute
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Barhl1 (EUDS; CEPD0033_1_D02)

Allele: *Barhl1*$^{tm1(EGFP\_CreERT2)Wtsi}$

Embryonic stem cell targeted: JM8.N4
Embryonic stem cell origin: C57BL/6N
Background used for Germ Line Transmission: C57BL/6N
Subsequent backcross background: C57BL/6N and inter cross from within Colony
Genetic background: C57BL/6N

Coat Colour Information:

Black

Breeding Performance and Lifespan:

- Generally heterozygous mice from this colony conform to normal expectations of the background strain.
  For maintenance of our colonies we pay particular attention to the age of the mating pairs and the resulting litters. In our experience the C57BL/6N substrain used to establish and progress this colony has shown some characteristics such as poor breeding, high pre-weaning mortality rates and failure to breed beyond three litters. We believe disturbance of litters has a detrimental effect on the mating pair. For our core and mutant colonies we have actively reduced our intervention with the mice. Daily observations, health checks, cleaning and cage movement is minimised in litters under 14 days of age.
- Viability at Weaning – Currently Undetermined

Bedding:

Aspen Chip derived from a Baltic supply – Supplier B&K Universal

Diet:

Autoclavable Mouse Breeder Diet 5021 – A controlled constant-nutrient diet formulated to compensate for nutrient losses that occur during steam sterilization. Supplier Lab Diet www.labdiet.com

Husbandry:

Cleaning frequency is based against cage occupancy and technician assessed level of soiling. Base changing is performed in a HEPA filtered change station which remains positive to the room environment. Gloved hands are disinfected between each cage. Diet is fed ad-libitum.

Housing System:

Individual Ventilated Cages maintained at positive pressure to the room with an average of 60 HEPA filtered air changes per hour.

Further Information

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Whilst all reasonable effort is made to verify the mouse line and verify the individual mouse genotype at shipment, we recommend this is confirmed by the recipient.

The Cre expression pattern is expected to mirror that of the host gene, but this may not be fully described and/or may be modified in the targeted allele. Although characterisation of the Cre expression pattern is an objective of EUCOMMTools this is an ongoing process which may be incomplete. It is therefore recommended that the recipient verifies the Cre expression pattern. For the tm1(EGFP_CreERT2) allele, the promoter-driven selection cassette is flanked with Rox sites and may be removed using Dre recombinase.

General Information

Sanger MGP mutant mouse lines are mouse lines in development; information about breeding and phenotyping characteristics may be incomplete.

As the mutant mouse strains progress through the Sanger MGP primary phenotypic characterisation, the information gathered may be viewed through the Sanger Mouse Portal (www.sanger.ac.uk/mouseportal) and the International Mouse Phenotyping Consortium (IMPC; www.mousephenotype.org).

Information supplied here is current as of the date indicated below.
Please consult the Sanger MGP Mouse Resource Portal and IMPC for progressive updates on colony information such as Viability at weaning, Fertility, General Observations.
Contact MGPEnquiries@sanger.ac.uk

Early notification on phenotyping data may be received by subscribing to the MGP-Early-Phenotyping-Alert (www.sanger.ac.uk/mouseportal).

Phenotype enquiries may be made through the contact MGPEnquiries@sanger.ac.uk .

Details of the colony quality control tests performed for a specific mouse line may be observed through the International Mouse Phenotyping Consortium (IMPC; www.mousephenotype.org), searching for your gene and follow the link from ‘Product Details’ for the mouse strain of interest.

General Descriptions of the mouse strain quality control (QC) assays.
www.i-dcc.org/kb/25

General information about structure of IMPC alleles and their derivatives
www.mousephenotype.org/martsearch_ikmc_project/about/targeting-strategies

Guidelines for converting alleles
www.i-dcc.org/kb/entry/105

International Mouse Phenotyping Consortium (IMPC) Mouse Resources
www.mousephenotype.org

IKMC Knowledgebase
www.i-dcc.org/kb

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Publications

Bradley A, Anastassiadis K, Ayadi A, Battey JF, Bell C, Birling M-C, Bottomley J, Brown SD, Bürger A, Bult CJ, Bushell W, Collins FS, Desaintes C, Doe B, Economides A, Eppig JT, Finnell RH, Fletcher C, Fray M, Frendewey D, *et al.* (2012) The mammalian gene function resource: the international knockout mouse consortium. *Mamm. Genome*, **23**, 580-586.

Liang,Q., Conte,N., Skarnes,W. C. and Bradley, A. (2008). Extensive genomic copy number variation in embryonic stem cells. *Proc. Nat. Acad. Sci*., **105** (11), 17453-17456.

Pettitt SJ, Liang Q, Rairdan XY, Moran JL, Prosser HM, Beier DR, Lloyd KC, Bradley A & Skarnes WC (2009) Agouti C57BL/6N embryonic stem cells for mouse genetic resources. *Nature methods,* **6,** 493-495.

Ryder, E., Doe, B., Gleeson, D., Houghton, R., Dalvi, P., Grau, E., … Ramirez-Solis, R. (2013). Rapid conversion of EUCOMM/KOMP-CSD alleles in mouse embryos using a cell-permeable Cre recombinase. *Transgenic research*. 23(1), 177–185.

Ryder E, Gleeson D, Sethi D, Vyas S, Miklejewska E, Dalvi P, Habib B, Cook R, Hardy M, Jhaveri K, Bottomley J, Wardle-Jones H, Bussell JN, Houghton R, Salisbury J, Skarnes WC; Sanger Mouse Genetics Project, Ramirez-Solis R. (2013). Molecular characterization of mutant mouse strains generated from the EUCOMM/KOMP-CSD ES cell resource. *Mamm. Genome,* **24**, 286–294.

Skarnes, W.C., Rosen, B., West, A.P., Koutsourakis, M., Bushell, W., Iyer, V., Mujica, A.O., Thomas, M., Harrow, J., Cox, T. *et al.* (2011) A conditional knockout resource for the genome-wide study of mouse gene function. *Nature*, **474**, 337-342.

White, J. K., Gerdin, A.-K., Karp, N. A., Ryder, E., Buljan, M., Bussell, J. N., Salisbury, J., *et al*. (2013). Genome-wide Generation and Systematic Phenotyping of Knockout Mice Reveals New Roles for Many Genes. *Cell*, **154**(2), 452–464.

Additional Useful Publications

Birling M.C., Gofflot F. and Warot X. (2009). Site-specific recombinases for manipulation of the mouse genome. *Methods Mol. Biol*., **561**, 245-263. Review.

Farley FW, Soriano P, Steffen LS, Dymecki SM. (2000). Widespread recombinase expression using FLPeR (flipper) mice. *Genesis*, **28** (3-4), 106-110.

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