

## Trim6 (DAFY)

**Allele:** Trim6<sup>em1(IMPC)Wtsi</sup>

**Genetic background:** C57BL/6N

**Mutation method:** Crispr/Cas9

**Breeding Strategy:** A single mosaic progeny (G1) is selected to initiate the colony by backcrossing to the C57BL/6N strain typically followed by intercross within the colony

**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 - Homozygous Subviable

### 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](http://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.

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**Last updated:** 13-12-2017

## Further Information

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 homozygous genotype for this strain has phenotypic observations noted on the following:

Homozygous viability at P14

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 International Mouse Phenotyping Consortium (IMPC; [www.mousephenotype.org](http://www.mousephenotype.org)).

Information supplied here is current as of the date indicated below.

Please consult the IMPC for progressive updates on colony information such as Viability at weaning, Fertility, General Observations.

Contact [MGPEnquiries@sanger.ac.uk](mailto:MGPEnquiries@sanger.ac.uk)

Phenotype enquiries may be made through the contact [MGPEnquiries@sanger.ac.uk](mailto: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](http://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](http://www.i-dcc.org/kb/25)

General information about structure of IMPC alleles and their derivatives

[www.mousephenotype.org/about-ikmc/targeting-strategies](http://www.mousephenotype.org/about-ikmc/targeting-strategies)

Guidelines for converting alleles

[www.infrafrontier.eu/sites/infrafrontier.eu/files/upload/public/pdf/Resources%20and%20Services/eucomm\\_komp-csd\\_allele\\_conversion\\_guide\\_v3a\\_2016.pdf](http://www.infrafrontier.eu/sites/infrafrontier.eu/files/upload/public/pdf/Resources%20and%20Services/eucomm_komp-csd_allele_conversion_guide_v3a_2016.pdf)

International Mouse Phenotyping Consortium (IMPC) Mouse Resources

[www.mousephenotype.org](http://www.mousephenotype.org)

IKMC Knowledgebase

[www.i-dcc.org/kb](http://www.i-dcc.org/kb)

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## Publications

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

Mali P, Yang L, Esvelt KM, et al (2013) RNA-guided human genome engineering via Cas9. *Science* 339:823–6. doi: 10.1126/science.1232033

Jinek M, Chylinski K, Fonfara I, et al (2012) A programmable dual-RNA-guided DNA endonuclease in adaptive bacterial immunity. *Science* 337:816–21. doi: 10.1126/science.1225829

Cong L, Ran FA, Cox D, et al (2013) Multiplex genome engineering using CRISPR/Cas systems. *Science* 339:819–23. doi: 10.1126/science.1231143

Singh P, Schimenti JC, Bolcun-Filas E (2014) A Mouse Geneticist's Practical Guide to CRISPR Applications. *Genetics* genetics.114.169771–. doi: 10.1534/genetics.114.169771

Brandl C, Ortiz O, Röttig B, et al (2015) Creation of targeted genomic deletions using TALEN or CRISPR/Cas nuclease pairs in one-cell mouse embryos. *FEBS Open Bio* 5:26–35. doi: 10.1016/j.fob.2014.11.009

Zhou J, Wang J, Shen B, et al (2014) Dual sgRNAs facilitate CRISPR/Cas9 mediated mouse genome targeting. *FEBS J*. doi: 10.1111/febs.12735

Kraft K, Geuer S, Will AJ, et al (2015) Deletions, Inversions, Duplications: Engineering of Structural Variants using CRISPR/Cas in Mice. *Cell Rep*. doi: 10.1016/j.celrep.2015.01.016

Shen B, Zhang J, Wu H, et al (2013) Generation of gene-modified mice via Cas9/RNA-mediated gene targeting. *Cell Res* 23:720–3. doi: 10.1038/cr.2013.46

Wang H, Yang H, Shivalila CS, et al (2013) One-step generation of mice carrying mutations in multiple genes by CRISPR/Cas-mediated genome engineering. *Cell* 153:910–8. doi: 10.1016/j.cell.2013.04.025

Yang H, Wang H, Shivalila CS, et al (2013) One-Step Generation of Mice Carrying Reporter and Conditional Alleles by CRISPR/Cas-Mediated Genome Engineering. *Cell* 154:1370–1379. doi: 10.1016/j.cell.2013.08.022

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