

Gene: *Tex261*

Colony prefix: PMER

ESC clone ID: EPD0520_4_H12

Allele: *Tex261^{tm1b(EUCOMM)Wtsi}*

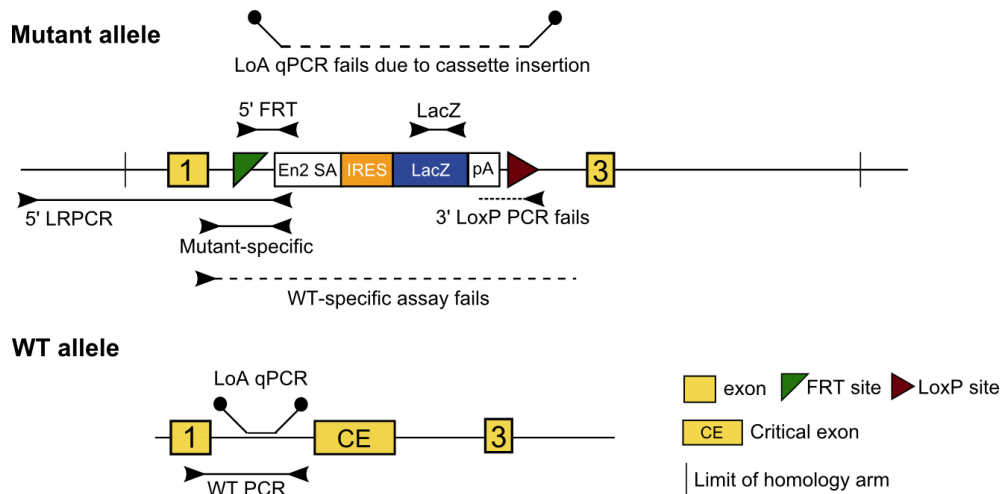
Allele type: Reporter-tagged deletion allele (post-cre)

Allele information:

Further information about the allele can be found on the 'International Mouse Phenotyping Consortium' (IMPC) web site at [http://www.mousephenotype.org/data/alleles/MGI:1096575/tm1b\(EUCOMM\)Wtsi?](http://www.mousephenotype.org/data/alleles/MGI:1096575/tm1b(EUCOMM)Wtsi?)
Details on how to determine the floxed exon can be found at <http://www.i-dcc.org/kb/entry/21/>

Mouse QC information

Promoter Driven:



| | | | | | |
|-------------------------------------|-----------------------------|--|-----------------------------|-------------------------|----|
| Southern Blot | na | TV Backbone Assay | Inferred from parent colony | 5' LR-PCR | na |
| Loss of WT Allele (LOA) qPCR | pass | Homozygous Loss of WT Allele (LOA) SR-PCR | Undetermined | Neo Count (qPCR) | na |
| LacZ SR-PCR | Inferred from parent colony | 5' Cassette Integrity | Inferred from parent colony | Neo SR-PCR | na |
| Mutant Specific SR-PCR | Inferred from parent colony | LoxP Confirmation | na | 3' LR-PCR | na |
| Genotyping Comment | | | | | |

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Southern blot confirmation:

Southern blots are not routinely performed at the Sanger Institute due to throughput constraints. A southern blot experiment design tool can be found on the IKMC web site at <http://www.mousephenotype.org/>

Links to information and frequently asked questions about the EUCOMM/KOMP alleles and MGP projects

General targeting strategies:

http://www.mousephenotype.org/martsearch_ikmc_project/about/targeting-strategies

MGP mouse phenotype data:

<http://www.sanger.ac.uk/mouseportal/>

IKMC allele types:

<http://www.i-dcc.org/kb/entry/89/>

MGP mouse quality control tests :

<http://www.i-dcc.org/kb/25/>

Allele conversion guide - genotyping tm1b, tm1c and tm1d mice:

<http://www.i-dcc.org/kb/entry/105/>

How the "critical" exon is decided:

<http://www.i-dcc.org/kb/entry/102/>

Genotyping Information

Genotyping by end-point PCR

These mice may be genotyped through a combination of separate PCR reactions that detect the cassette, the gene-specific wild type allele, and a mutant allele-specific short range PCR. Interpretation of the consolidated results produces the genotype of the mice.

For example: cassette positive, mutant positive, wild type positive = heterozygous.

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PCRs primer pairs and expected size bands

| Assay Type | Assay | Forward Primer | Reverse Primer | Expected Size Band (bp) |
|--------------|----------|----------------|----------------|-------------------------|
| Standard PCR | Wildtype | Tex261_42599_F | Tex261_42599_R | 391 |
| Standard PCR | Mutant | Tex261_42599_F | CAS_R1_Term | 294 |
| Standard PCR | Cassette | LacZ_2_small_F | LacZ_2_small_R | 108 |

Primer sequences

| Primer Name | Primer Sequence (5' > 3') |
|----------------|---------------------------|
| CAS_R1_Term | TCGTGGTATCGTTATGCGCC |
| LacZ_2_small_F | ATCACGACGCGCTGTATC |
| LacZ_2_small_R | ACATCGGGCAAATAATATCG |
| Tex261_42599_F | TGTCCAGCCCTTTCTCTTCC |
| Tex261_42599_R | GTACCCCATGTCCCATTTC |

Reaction setup

| Reagent | µl |
|---------------------------|-----------|
| DNA (~50-100 ng) | 1 |
| 10x Buffer | 2 |
| MgCl ₂ (50 mM) | 0.6 |
| Platinum Taq (Invitrogen) | 0.2 |
| dNTPs (100 mM) | 0.2 |
| Primer 1 (10 µM) | 0.4 |
| Primer 2 (10 µM) | 0.4 |
| ddH ₂ O | 15.2 |
| Total | 20 |

Amplification conditions

| Step | Conditions | Time |
|------|-----------------------|---------|
| 1 | 94°C | 5 min |
| 2 | 94°C | 30 sec |
| 3 | 58°C | 30 sec |
| 4 | 72°C | 45 sec |
| 5 | Go to '2' + 34 cycles | - |
| 6 | 72°C | 5 min |
| 7 | 12°C | forever |

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Genotyping using universal copy number qPCR assays designed to the selection cassette

The cassette qPCR assays use a hydrolysis probe assay (eg Applied Biosystems TaqMan technology) to determine genotype via the copy number of the selection cassette in a sample. Homozygotes will possess two copies, heterozygotes one copy and wild type mice will show no amplification when compared to known homozygote controls.

These FAM®-labeled assays are multiplexed with a VIC® labeled endogenous control assay (for example TaqMan® Copy Number Reference Assay, Mouse, Tfrc; Applied Biosystems part #4458366).

Please note that these assays are not gene-specific – other information should be used in conjunction with the universal cassette assays (for example the mutant-specific srPCR) when confirming the gene identity.

| Primer type | Assay Name | Forward Primer Seq. | Reverse Primer Seq. | Probe Primer Seq. |
|-------------|------------|----------------------|---------------------|-------------------------------|
| Cassette | LacZ_reg | GGAGTGCGATCTTCCTGAGG | CGCATCGTAACCGTGCATC | CGATACTGTCGTCGTCGCCCTCAAACCTG |

Reactions are performed in a 10µl volume using an Applied Biosystems 7900HT Fast Real-Time PCR System or Applied Biosystems Viiia7 with DNA prepared using the Sample-to-SNP™ kit (Applied Biosystems) from mouse ear biopsies. GTXpress™ buffer is also used (Applied Biosystems).

| Reagent | µl |
|---------------------------|-----|
| 2x GTXpress™ buffer | 5 |
| 20x target assay | 0.5 |
| ddH2O | 3 |
| Tfrc endogenous 20x assay | 0.5 |
| DNA | 1 |

Amplification conditions

| Step | Conditions | Time |
|------|-----------------------|--------|
| 1 | 95°C | 20 sec |
| 2 | 95°C | 10 sec |
| 3 | 60°C | 30 sec |
| 4 | Go to '2' + 34 cycles | - |

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Genotyping by loss of WT allele qPCR Assay (gene-specific assay)

The wild type loss of allele (LoA) qPCR assay uses a hydrolysis probe assay (for example Applied Biosystems TaqMan® technology) to determine the copy number of the wild type allele in a sample. Homozygotes will show no amplification, heterozygotes one copy and wild type mice will show two copies when compared to a wild type control.

The number of copies of the wild type allele can be detected using a FAM-labelled custom qPCR TaqMan® assay. These are multiplexed with a VIC® labelled endogenous control assay (for example TaqMan® Copy Number Reference Assay, Mouse, Tfr; Applied Biosystems part #4458366). Reference DNA controls of known genotypes should also be included to facilitate correct analysis.

Primers for LoA qPCR assay

| Gene | Forward Primer Seq. | Reverse Primer Seq. | Probe Primer Seq. | Source |
|--------|--------------------------|------------------------|---------------------|-------------------|
| Tex261 | GGACAGGAAATAGTGTGCTTCTCT | GAGGACCTTGCCAAAGAGTCAA | CCCAAACCCTCCTTCTAAC | Life Technologies |

Reaction setup

Reaction setup and amplification conditions are the same as those used for the LacZ_reg cassette qPCR assay.

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Relevant publications

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., et al. (2013). Molecular Characterization of Mutant Mouse Strains Generated from the EUCOMM/KOMP-CSD ES Cell Resource. *Mamm. Genome*, 24, 286–294.

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.

Ryder, E., Wong, K., Gleeson, D., Keane, T.M., Sethi, D., Vyas, S., Wardle-Jones, H., Bussell, J.N., Houghton, R., Salisbury, J., et al. (2013). Genomic analysis of a novel spontaneous albino C57BL/6N mouse strain. *Genesis* 51, 523–528.

Bradley, A., Anastassiadis, K., Ayadi, A., Battey, J.F., Bell, C., Birling, M.-C., Bottomley, J., Brown, S.D., Bürger, A., Bult, C.J., et al. (2012). The mammalian gene function resource: the international knockout mouse consortium. *Mamm Genome* 23, 580–586.

Birling, M.-C., Dierich, A., Jacquot, S., Héroult, Y., and Pavlovic, G. (2011). Highly-efficient, fluorescent, locus directed Cre and flpo deleter mice on a pure C57BL/6N genetic background. *Genesis*.

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.

Pettitt, S.J., Liang, Q., Rairdan, X.Y., Moran, J.L., Prosser, H.M., Beier, D.R., Lloyd, K.C., Bradley, A., and Skarnes, W.C. (2009). Agouti C57BL/6N embryonic stem cells for mouse genetic resources. *Nat Methods* 6, 493–495.

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

Farley, F.W., Soriano, P., Steffen, L.S., and Dymecki, S.M. (2000). Widespread recombinase expression using FLP_{ER} (flipper) mice. *Genesis* 28, 106–110.

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