**“Normal” mice have normal telomeres**

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**Supplementary Methods**

GenBank reference sequence for RTEL1 protein from laboratory strain C57BL/6 (NP\_001001882.3) was aligned onto the genome assemblies in Table S2 using TBLASTN (blast.ncbi.nlm.nih.gov) with cutoff E-value at 1e-10. The genome sequences comprising the aligned nucleotide sequences were further verified by alignment against RTEL1 using GeneWise (ebi.ac.uk/Tools/psa/genewise) for accurate spliced alignments.

For alignment of RTEL1 protein sequences (both already deposied and newly predicted), Constraint-based Multiple Alignment Tool, COBALT (www.ncbi.nlm.nih.gov/tools/cobalt/cobalt.cgi), was used with default settings.

**Supplementary Figures and Tables**

|  |  |  |
| --- | --- | --- |
| **Species** | **Strain** | **Telomere Length** |
| *Mus musculus domesticus*\* | C57BL/6 | 30-120 kb |
| *Mus musculus domesticus*\* | 129/SvJ | 30-120 kb |
| *Mus musculus domesticus*\* | FVB/NJ | 30-120 kb |
| *Mus musculus domesticus*\* | Black Swiss (Outbred) | 30-150 kb |
| *Mus musculus domesticus*\* | Swiss Webster (Outbred) | 30-60 kb |
| *Mus musculus domesticus*\* | ICR (Outbred) | 30-120 kb |
| *Mus musculus domesticus* |   | 15-20 kb |
| *Mus musculus musculus* |   | 15-20 kb |
| *Mus musculus castaneus* | CAST/EiJ | 18-20 kb |
| *Mus musculus castaneus* |   | 15-20 kb |
| *Mus spicilegus* |   | 15-20 kb |
| *Mus macedonicus* |   | 15-20 kb |
| *Mus spretus* | SPRET/EiJ | 15-20 kb |
| *Mus caroli* |   | 15-20 kb |

**Supplementary Table 1. Telomere length in the *Mus* genus.** Data from Hemann and Greider1. Asterisks denote “classical” laboratory strains, established in the XX century from European ‘fancy’ mice (*M. m. domesticus*) bred with East Asian ‘fancy’ mice (*M. m. musculus* x *M. m. molossinus*)2.

|  |  |  |  |
| --- | --- | --- | --- |
| **Species** | **Strain** | **Type** | **Assembly accession** |
| *M. m. domesticus* | BALB/c | Classical laboratory | GenBank: GCA\_031761455.1 |
| *M. m. domesticus* | FVB/NJ | Classical laboratory | GenBank: GCA\_001624535.1 |
| *M. m. domesticus* | PGN2/Ms | Wild-derived | https://molossinus.brc.riken.jp/mogplus/ |
| *M. m. domesticus* | BFM/Ms | Wild-derived | https://molossinus.brc.riken.jp/mogplus/ |
| *M. m. domesticus* | WSB/EiJ | Wild-derived | GenBank: GCA\_029233295.1 |
| *M. m. musculus* | PWD/PhJ | Wild-derived | GenBank: GCA\_029233825.1 |
| *M. m. musculus* | PWK/PhJ | Wild-derived | GenBank: GCA\_029233695.1 |
| *M. m. musculus* | BLG/Ms | Wild-derived | https://molossinus.brc.riken.jp/mogplus/ |
| *M. m. musculus* | NJL/Ms | Wild-derived | https://molossinus.brc.riken.jp/mogplus/ |
| *M. m. musculus* | CHD/Ms | Wild-derived | https://molossinus.brc.riken.jp/mogplus/ |
| *M. m. musculus* | KJR/Ms | Wild-derived | https://molossinus.brc.riken.jp/mogplus/ |
| *M. m. musculus* | SWN/Ms | Wild-derived | https://molossinus.brc.riken.jp/mogplus/ |
| *M. m. molossinus* | JF1/MsJ | Wild-derived | GenBank: GCA\_921999095.2 |
| *M. m. molossinus* | MSM/MsJ | Wild-derived | https://molossinus.brc.riken.jp/mogplus/ |
| *M. m. castaneus* | CAST/EiJ | Wild-derived | GenBank: GCA\_029237265.1 |
| *M. m. castaneus* | HMI/Ms | Wild-derived | https://molossinus.brc.riken.jp/mogplus/ |
| *Mus spicilegus* | ZRU | Wild-derived | GenBank: GCA\_003336285.2 |
| *Mus spretus* | SPRET/EiJ | Wild-derived | GenBank: GCA\_921997135.2 |
| *Mus caroli* | CAROLI/EiJ | Wild-derived | GenBank: GCA\_900094665.2 |
| *Mus pahari* |  | Wild | GenBank: GCA\_900095145.2 |
| *Mus minutoides* |  | Wild | GenBank: GCA\_902729485.2 |

**Supplementary Table 2. Genome assemblies used in this study.**



**Supplementary Figure 1. Conservation of M492 in RTEL1.** Conserved methionine in position 492 is shown by arrow. Red text denotes *Mus spretus* sequences: AAS98192.1 is the sequence previously deposited in GenBank; New sequence is the one obtained in this study; MGP\_SPRETEiJ\_T0058934.1 is the sequence present in Ensembl.



**Supplementary Figure 2. Alignment of RTEL1 in the *Mus* genus.** Red bars denote amino acids different from the ones in classical laboratory strains (labels in red). Labels in green denote wild-derived inbred strains (established in the last 20-40 years).

**Supplementary References**

1. Hemann, M.T., Greider, C.W. Wild-derived inbred mouse strains have short telomeres. *Nucleic Acids Res* **28**, 4474-4478 (2000).
2. Frazer, K.A., *et al*. A sequence-based variation map of 8.27 million SNPs in inbred mouse strains. *Nature* **448**, 1050-1053 (2007).