Figure S1. Conserved features of fruP1 core promoter region.
(Top) A close up of fruP1 genomic region, highlighting the region deleted in fruΔP1. (Bottom) Alignment of sequence surrounding the fruP1 TSS in D. melanogaster (D.mel), D. simulans (D.sim), D. suzuki (D.suz), D. elegans (D.ele), D. virilis (D.vir), D. montana (D.mon). Shown are 100 nt upstream and downstream of the D. mel TSS (in gray). CTG repeats, ‘TATA’ region, Inr and DPE regions highlighted.

Table S1. Primer and gRNA target region sequences

| Primer Name | Sequence |
|-------------|----------|
| G1_5f       | GCATTTAGAATAATTTTGGTGCACCCCTTGAACCTCGATTTGACGGAAGAGCCTGATTAGCTTCTGACCTGGC |
| G1_5r       | GAGCACTAGTAAAGATCTCCATGCATAAGGCTGATTTTGAAGAGCCTGATTAGCTTCTGACCTGGC |
| G1_3f       | GCACTACGATCGCAGGTGTGCATATGTCCGCGCCCTGTGAGTGCTAGCTTCTGACCTGGC |
| G1_3r       | GCTGAAGCAGGTGGAATTCTTGCATGCTAGCTGAGGAGTAAGACTCTAAATATATTGAAATATAATT |
| 1433e-F     | CCAGCGATATTGCCATGAA |
| 1433e-R     | TCCGGCGAGTTGAGAAATC |
| eIF1A-R     | GCCCTGGTATATCCACAC |
| eIF1A-F     | GTCTGTGAGGCAATGTG |
| Rpl32-F     | CGATCATGCTATGCTAGCTG |
| Rpl32-R     | CGACGCCACTGCTCTGAGCTG |
| Su(Tpl)-R   | GCACTCGTTGTGGAAGTAGACA |
| Su(Tpl)-F   | AAAACAAACTCACATACAACAA |
| fruM160-F   | AAGATCGAAGAGGATGTC |
| fruM160-R   | CGCTCGTGGTCTAGTGG |
| fruM161-F   | CAGTTGCGCCGGCATAG |
| fruM161-R   | GTGACGTCGATTAGCAA |
| fruP1-F1    | CGCTAACATGAGGGCAATGAG |

| gRNA Target Region | Sequence |
|--------------------|----------|
| FruS_1             | TCATTTGATGGGGCGCAATAGG |
| Fru3_3             | TGCACTGAGGCGCTGACTG |

Neville et al., 2021