***Figure 7⎯table supplement 1.*** Primer sequences used for qPCR. Genomic coordinates indicate full amplicons, including the length of each primer. Coordinates refer to the BDGP R6/dm3 assembly.

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| **Cytological location 4C9-E3** |  | **Cytological location 75B11-C2** |
| **Sequence** | **Genomic coordinates** | **Sequence** | **Genomic coordinates** |
| CCTCGATCGGTTTACATTCGCCATAAACCCAAACGAGCTG | X:4,607,333..4,607,433 | ATTTGGACTGGGGCAGTTTCCTGAAACACGGAAGTTGAGTCC | 3L:18,062,106..18,062,230 |
| CACATGGTGTCCTTGCATTCGCCTAAACCAGCGATTCAAC | X:4,643,535..4,643,626 | AAAACACAAGCACATAGGCAACAGTTTCTGGCGTTGTATCCG | 3L:18,087,066..18,087,175 |
| GGGATGTGCTGCCTTTTATGAGTTGCCACGACCAAAACTC | X:4,673,491..4,673,595 | GTGCACGGACGCGTATAATCAAGTTAGCTCACGTGAGATGATG | 3L:18,164,427..18,164,499 |
| TGAAGGCCCTGGATGATAAGTGGCATAGATATCGGTGTGC | X:4,706,888..4,706,995 | ACTATTATTTCTGGCTGGCTACGGCCGGCTGCTACTTATGGC | 3L:18,188,845..18,188,948 |
| GGCTTGATTTTCGACTGCTCAAAGGAAACAGCTCCGTGTG | X:4,742,052..4,742,153 | ATACAGATACAGCTCGCACTGGAGTGGTGCCGATGGAAAAAC | 3L:18,214,103..18,214,210 |
| TTGCAGTGCCTCAAAGTCAGACCGACCAAAATCGAGACTG | X:4,774,644..4,774,740 | ACCACGCCCCTAAGCAAATAGATCTCGCCAGCTAAAGATCTCG | 3L:18,238,935..18,239,021 |
| CCTATCACCTGCCCATTTTGTTACGTCCCTGGTTTCTTGC | X:4,826,332..4,826,430 | TGGGGCATTTTTGACGGTAGGCTTTTAGCCTCGAGAAACCG | 3L:18,263,954..18,264,043 |
| AGCCATCCTGTTGCATCTTCGCGCCAACAAATTCTCTCAG | X:4,856,456..4,856,547 | CTTGGCTCAGGTTTCCCTTCAAAGGACGCCACAACAATGC | 3L:18,313,914..18,314,025 |
| ACCTCGCCAACATTACCAACAAACAACACGACGGCTCTTC | X:4,873,801..4,873,880 | ATCTCTCTGGGGCATCCAAGCGCCAGCGCAGTTAAAAGTAAC | 3L:18,338,911..18,339,046 |
| AACTGCCCAAAGTGAAGGTGGTTCAAGTGCAGCCAATGTG | X:4,893,272..4,893,370 | TGCACCAAGCTACACAATGGCACAGGACTCCAAATTCTGCAC | 3L:18,364,090..18,364,232 |
| CGGCAAACACGACTACAATGCAGTCGGATGCTGGTAGATATG | X:4,920,840..4,920,943 | AGTGATAGCGGAGTAACAGTGGGTGGCGTGGATCCAACTTTATG | 3L:18,414,106..18,414,187 |
| AGCATGGACCCATCGATTACTTTCCCTGGGTAGCATTCAC | X:4,951,780..4,951,879 | TGCGCTAGTTCTCACCAACGACCAACTTAAGCACCAACTAAGG | 3L:18,439,417..18,439,489 |
| GAGATGCAAGATGCCACAAGCCTTAGAGCGCTTCAATTCG | X:4,982,299..4,982,391 | ACGGGTGCCCTTAATGTTTACGGTCGTTGCCCATGTCTTTG | 3L:18,464,296..18,464,376 |
| AGGCAACCTGCAACTGAAACACAATTGCGTACGTGAGCTG | X:5,009,757..5,009,859 | CAACCCTATCCATCCATCCATGCAATCGGCCTAATTCACCCATG | 3L:18,491,978..18,492,057 |
| GTCTTGGAGTTGCCGTTTTGTGCGCTGATCTCGTTAGATG | X:5,033,854..5,033,945 | ACATATTCGCCGACCAAGTGACACTAACACGTGCCCCTAAC | 3L:18,520,543..18,520,680 |
| CTAACCATCGCCAAATCCTCCGTCCACAATTAGCTTGCAG | X:5,064,863..5,064,959 |  |
| **Cytological location 86D9** |
| TCCCTGCGACAACCTTTAACCTCCGTGACATGCTTGATTC | X:5,097,851..5,097,941 | **Sequence** | **Genomic coordinates** |
| TGGCGCCGCTTTCTTATTAGAGAACAGGTTTGTGCGCTTG | 3R:11,261,333..11,261,450 |
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