***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** |
| CCTCGATCGGTTTACATTCG  CCATAAACCCAAACGAGCTG | X:4,607,333..4,607,433 | ATTTGGACTGGGGCAGTTTC  CTGAAACACGGAAGTTGAGTCC | 3L:18,062,106..18,062,230 |
| CACATGGTGTCCTTGCATTC  GCCTAAACCAGCGATTCAAC | X:4,643,535..4,643,626 | AAAACACAAGCACATAGGCAAC  AGTTTCTGGCGTTGTATCCG | 3L:18,087,066..18,087,175 |
| GGGATGTGCTGCCTTTTATG  AGTTGCCACGACCAAAACTC | X:4,673,491..4,673,595 | GTGCACGGACGCGTATAATC  AAGTTAGCTCACGTGAGATGATG | 3L:18,164,427..18,164,499 |
| TGAAGGCCCTGGATGATAAG  TGGCATAGATATCGGTGTGC | X:4,706,888..4,706,995 | ACTATTATTTCTGGCTGGCTACG  GCCGGCTGCTACTTATGGC | 3L:18,188,845..18,188,948 |
| GGCTTGATTTTCGACTGCTC  AAAGGAAACAGCTCCGTGTG | X:4,742,052..4,742,153 | ATACAGATACAGCTCGCACTGG  AGTGGTGCCGATGGAAAAAC | 3L:18,214,103..18,214,210 |
| TTGCAGTGCCTCAAAGTCAG  ACCGACCAAAATCGAGACTG | X:4,774,644..4,774,740 | ACCACGCCCCTAAGCAAATAG  ATCTCGCCAGCTAAAGATCTCG | 3L:18,238,935..18,239,021 |
| CCTATCACCTGCCCATTTTG  TTACGTCCCTGGTTTCTTGC | X:4,826,332..4,826,430 | TGGGGCATTTTTGACGGTAG  GCTTTTAGCCTCGAGAAACCG | 3L:18,263,954..18,264,043 |
| AGCCATCCTGTTGCATCTTC  GCGCCAACAAATTCTCTCAG | X:4,856,456..4,856,547 | CTTGGCTCAGGTTTCCCTTC  AAAGGACGCCACAACAATGC | 3L:18,313,914..18,314,025 |
| ACCTCGCCAACATTACCAAC  AAACAACACGACGGCTCTTC | X:4,873,801..4,873,880 | ATCTCTCTGGGGCATCCAAG  CGCCAGCGCAGTTAAAAGTAAC | 3L:18,338,911..18,339,046 |
| AACTGCCCAAAGTGAAGGTG  GTTCAAGTGCAGCCAATGTG | X:4,893,272..4,893,370 | TGCACCAAGCTACACAATGG  CACAGGACTCCAAATTCTGCAC | 3L:18,364,090..18,364,232 |
| CGGCAAACACGACTACAATG  CAGTCGGATGCTGGTAGATATG | X:4,920,840..4,920,943 | AGTGATAGCGGAGTAACAGTGG  GTGGCGTGGATCCAACTTTATG | 3L:18,414,106..18,414,187 |
| AGCATGGACCCATCGATTAC  TTTCCCTGGGTAGCATTCAC | X:4,951,780..4,951,879 | TGCGCTAGTTCTCACCAACG  ACCAACTTAAGCACCAACTAAGG | 3L:18,439,417..18,439,489 |
| GAGATGCAAGATGCCACAAG  CCTTAGAGCGCTTCAATTCG | X:4,982,299..4,982,391 | ACGGGTGCCCTTAATGTTTAC  GGTCGTTGCCCATGTCTTTG | 3L:18,464,296..18,464,376 |
| AGGCAACCTGCAACTGAAAC  ACAATTGCGTACGTGAGCTG | X:5,009,757..5,009,859 | CAACCCTATCCATCCATCCATG  CAATCGGCCTAATTCACCCATG | 3L:18,491,978..18,492,057 |
| GTCTTGGAGTTGCCGTTTTG  TGCGCTGATCTCGTTAGATG | X:5,033,854..5,033,945 | ACATATTCGCCGACCAAGTG  ACACTAACACGTGCCCCTAAC | 3L:18,520,543..18,520,680 |
| CTAACCATCGCCAAATCCTC  CGTCCACAATTAGCTTGCAG | X:5,064,863..5,064,959 |  | |
| **Cytological location 86D9** | |
| TCCCTGCGACAACCTTTAAC  CTCCGTGACATGCTTGATTC | X:5,097,851..5,097,941 | **Sequence** | **Genomic coordinates** |
| TGGCGCCGCTTTCTTATTAG  AGAACAGGTTTGTGCGCTTG | 3R:11,261,333..11,261,450 |
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