



Figure S1 RT-PCR analysis shows an expression profile of all G-protein subunits in each of the labellum and the whole body. MWM: Molecular weight marker was ϕ X174 digested by HaeIII. Primer sequences were designed to synthesize cDNA sized to 472 bp for CG17760 (forward, ATGGACTGCTGCCTATCGGA; reverse, CGAACATGAAGAATGTCCTG), 532 bp for CG2812 (forward, ATGAATCCGGAATCGAGGGA; reverse, CTGTAGGCCTGGAAGGGAGT), 522 bp for CG3004 (forward, GGATGGGGGACCAACAGCAG; reverse, ATGGCAACATCCTGAATGGA), 622 bp for *cta* (forward, GCGATGTCTGGCATTACATT; reverse, GCATCATAAGCATCCTGTTC), 536 bp for CG17766 (forward, ATGGTGAGTACCAATCTGGTG; reverse, GGCCAACACTACGTCATCCTT), 214 bp for *G α 49B* (forward, CTAGTTAGCATGGAGTGCTG; reverse, TGTTGTGGGCACACGAACTC), 532 bp for CG30054 (forward, TGACAAACAGTTGCGCCTTG; reverse, AGCACGCAGAATGTCCTGAT), 518 bp for *G α 73B* (forward, CGGCCACAATTGGTACAACA; reverse, CAGGGGAAACTCATTTGAGC), 572 bp for *G- $\iota\alpha$ 65A* (forward, GAAGATGGGTTGTGCCGTGA; reverse, GTGTCTCGATGATGCCAGTG), 560 bp for *G- $\omicron\alpha$ 47A* (forward, AATACGCACCATGGGCTGCG; reverse, CAGTGGTCTTGACGCGAGTG), 534 bp for *G- $\sigma\alpha$ 60A* (forward, TGGGCTGCGATGGGTTGCTT; reverse, TTGATTGTGCTCACTCGGTC), 484 bp for *G β 13F* (forward, TAGACAGTCTCAGGCAGGAA; reverse, ATATCACCGGAGCTGGTCAC), 546 bp for *G β 5* (forward, CATCTCAGAGCAACCATGTC; reverse, CGTGAGGATTTGCTGATCGG), 549 bp for *G β 76C* (forward, ATGCCGAAAATTGACCCAGA; reverse, TTGACACCCTTCTCCAGATC), 216 bp for *G γ 1* (forward: ATGGACGTAATGTCATCATC; reverse, TCCTTAGAGAACGGTGCAGG), and 840 bp for *G γ 30A* (forward, AGTCGCCATCCTGCGAAGC; reverse, AGCCTAGATCGAACTCATAAC).