



Figure S2. Regulation of transcripts encoding IIS pathway components during *N. brasiliensis* iL3 activation.

Transcript abundances were determined for the coding regions of genes predicted to compose an insulin/insulin-like growth factor 1 signaling (IIS) pathway in *N. brasiliensis*. *N. brasiliensis* iL3 were treated with either $\Delta 7$ -dafachronic acid (DA) or the vehicle control (ethanol) for 24 hours at 20 °C, 26 °C, or 37 °C. TMM-normalized transcript abundance was plotted as the mean counts per million (CPM) for each condition; error bars represent the SEM. Statistical significance was evaluated between 20 °C vehicle and 20 °C DA conditions and also between 20 °C vehicle and 37 °C vehicle conditions; * = fold-change >2.0, FDR-adjusted p-value <0.05.