



**Figure S1. Regulation of transcripts encoding cGMP signaling pathway components during *N. brasiliensis* iL3 activation.**

Transcript abundances were determined for the coding regions of the following genes predicted to constitute a signaling pathway regulated by cyclic guanosine monophosphate (cGMP): *Nbr-daf-11*, which is predicted to encode a guanylyl cyclase; *Nbr-tax-2* and *Nbr-tax-4*, which are predicted to encode the subunits of a cyclic nucleotide-gated cation channel; and *Nbr-hsp90*, which is predicted to encode a homolog of *Cel-hsp90* (formerly *Cel-daf-21*). *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.