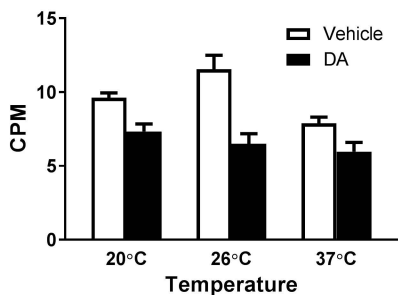
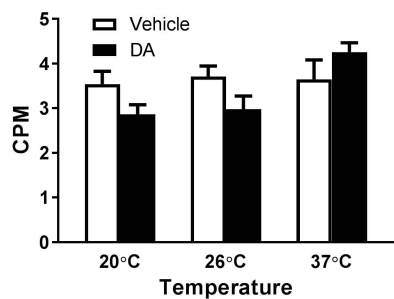
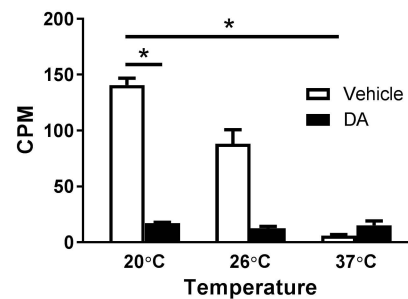
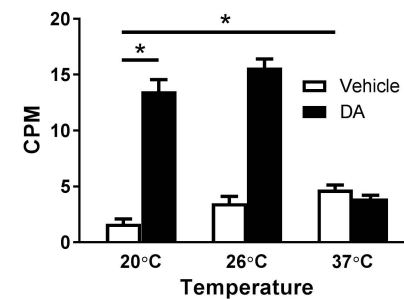
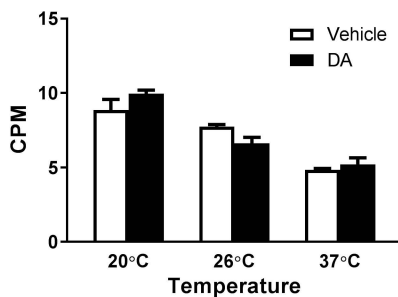
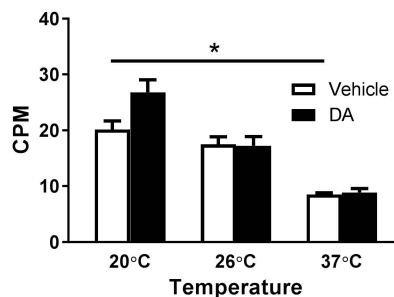
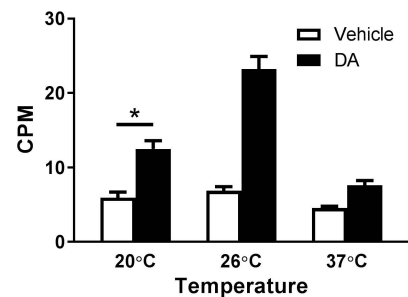
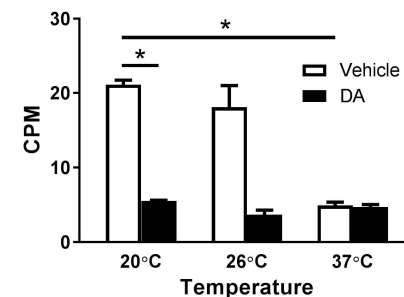
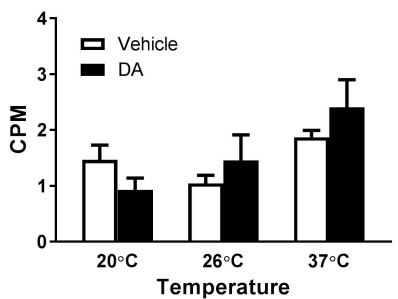
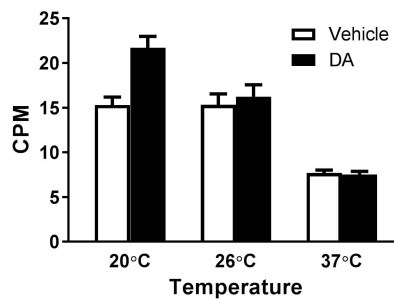
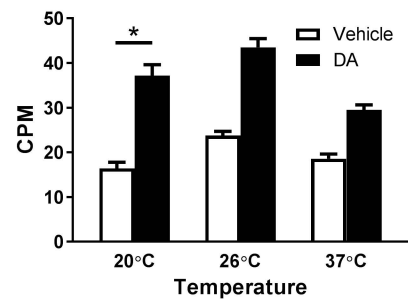
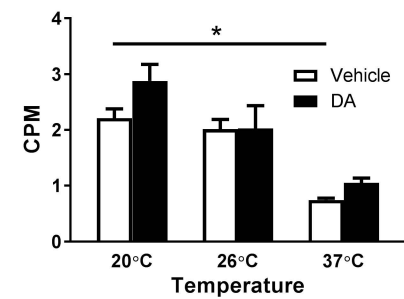
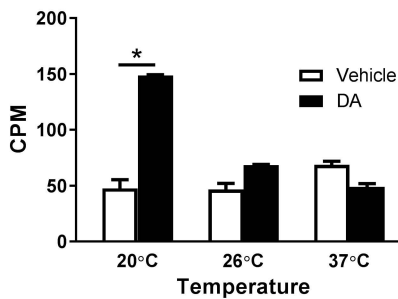
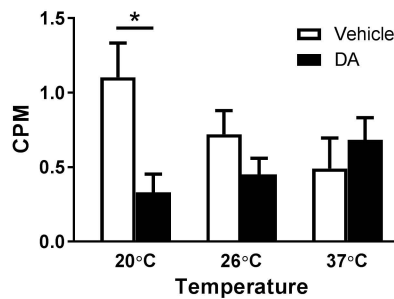
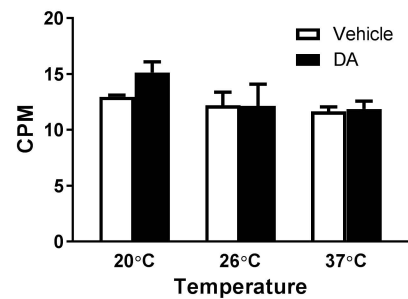
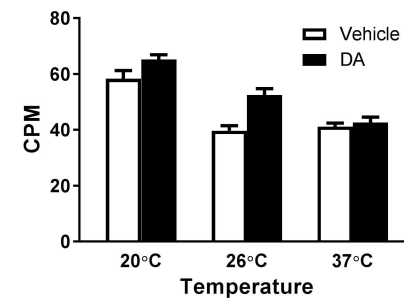
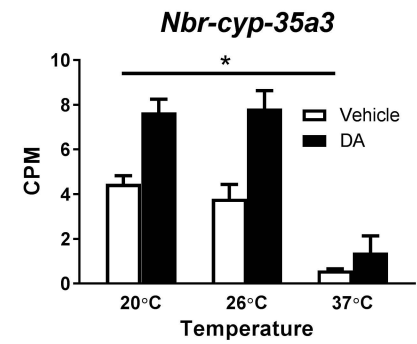
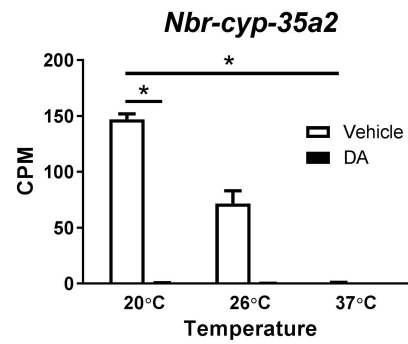
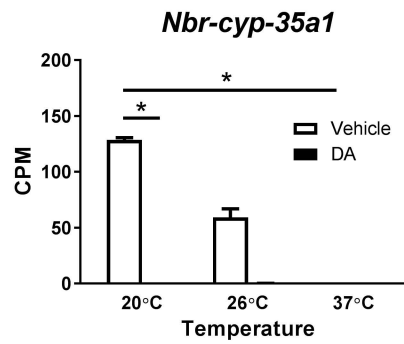
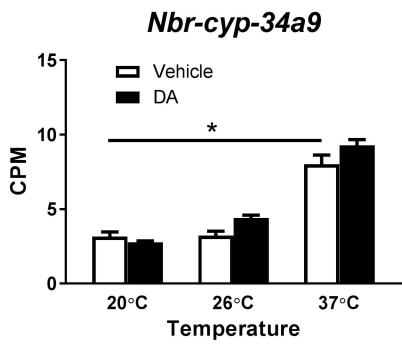
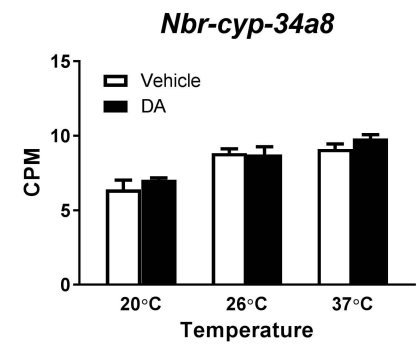
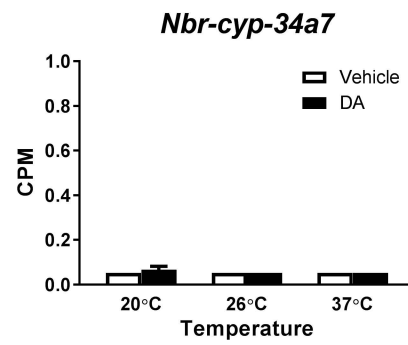
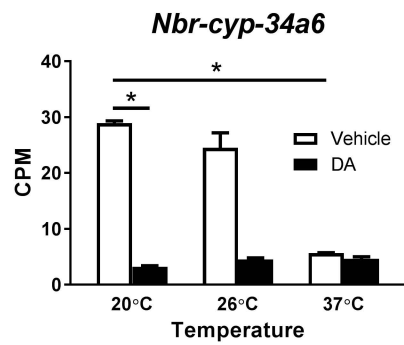
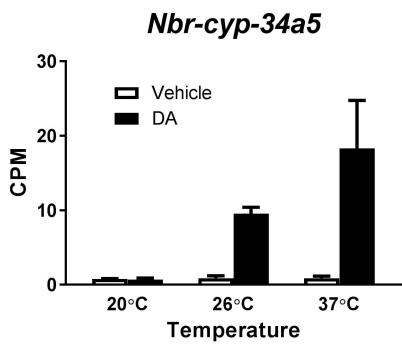
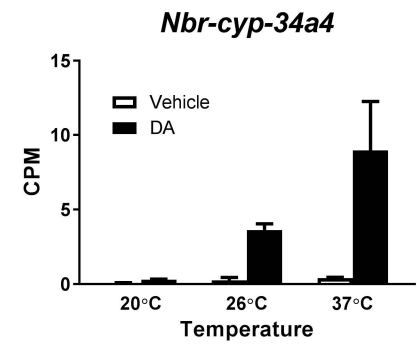
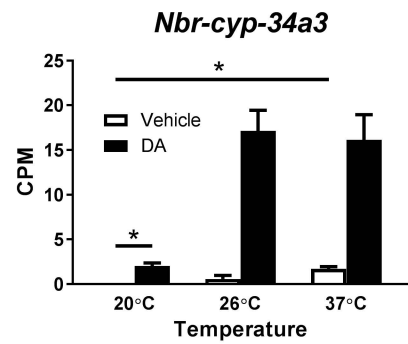
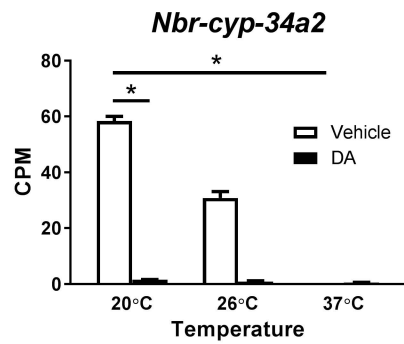
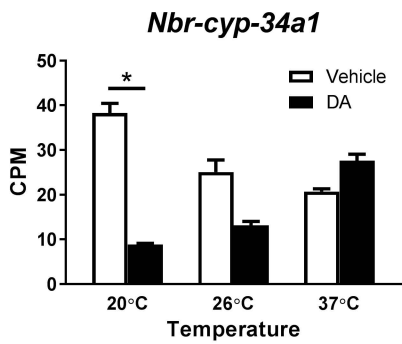
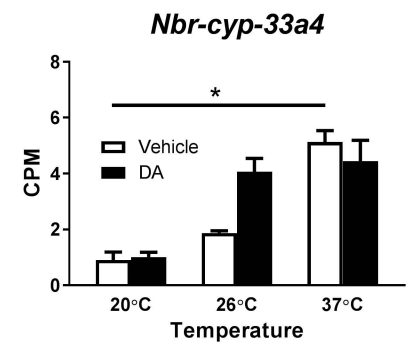
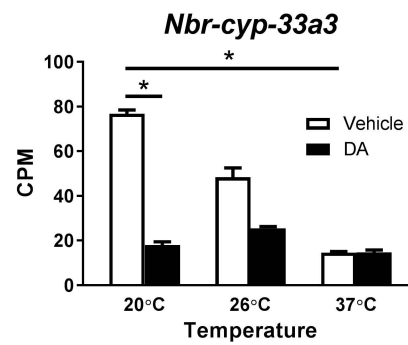
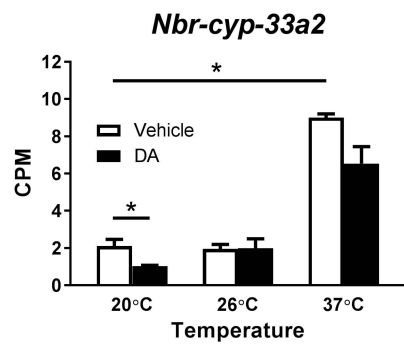
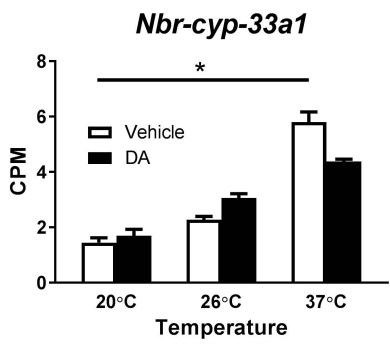
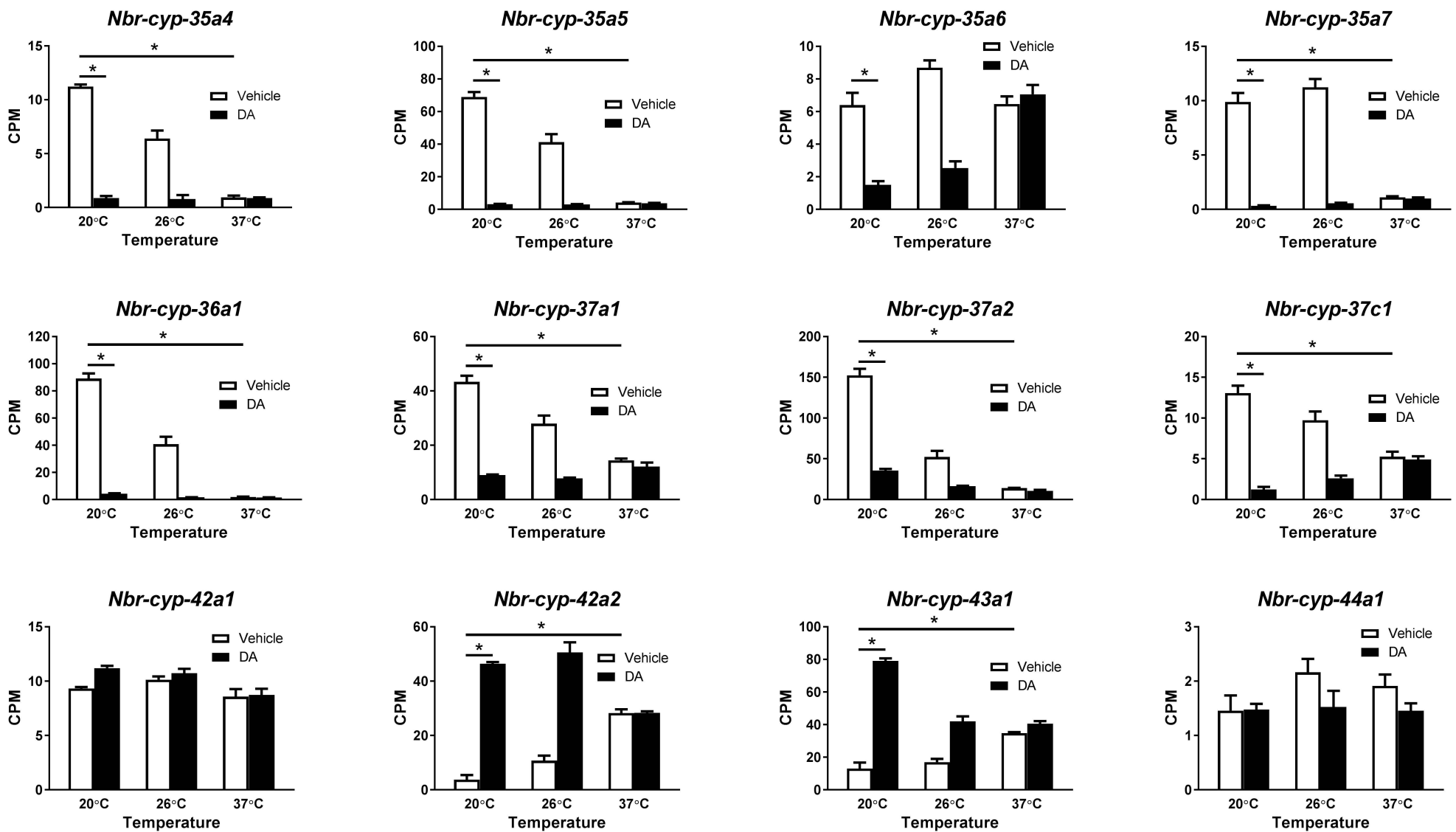


***Nbr-cyp-3a1******Nbr-cyp-13b1******Nbr-cyp-13b2******Nbr-cyp-14a1******Nbr-cyp-14a2******Nbr-cyp-14a3******Nbr-cyp-14a4******Nbr-cyp-14a5******Nbr-cyp-14a6******Nbr-cyp-14a7******Nbr-cyp-14a8******Nbr-cyp-14a9******Nbr-cyp-22a1******Nbr-cyp-23a1******Nbr-cyp-31a1******Nbr-cyp-32a1***





### Data S8 *Nippostrongylus brasiliensis* cytochrome P450-encoding transcript abundance profiles.

Transcript abundances were determined for the coding regions of genes predicted to encode cytochrome P450s 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.