



Supplementary Figure 1: Comparison of *C. fleckeri* transcripts to *H. magnipapillata* and *N. vectensis*. Bit scores from searches of the assembled transcripts against databases containing *H. magnipapillata* and *N. vectensis* proteins using blastx. Solid line is the best simple linear regression model which suggests that generally *C. fleckeri* protein products possess more sequence homology to *H. magnipapillata* than *N. vectensis*. $Y = X$ is shown as a dotted line.