

Additional file 6 - Cq - FPKM correlation

Linear relationship in the combined egg and ovary transcriptome between the LOG2 transformed values of transcript abundance based upon qPCR results, $(1+E)^{Cq}$, on the x-axis and the corresponding FPKM values on the Y-axis. Data used is from 19 oogenesis genes and the 3 housekeeping genes. Vitellogenin transcripts were not present in the oocyte and thus not used in the calculation. Pearson regression results (with null hypothesis that correlation is >0): $t_{41} = 2.37$, $P = 0.011$. Analyses were performed in R 2.15.2 for Mac OS X. As can be observed from the graph, the scatter around the regression line is high for the oocyte transcripts.

