

Supplemental Figure 2: Comparative analysis of gene expression fold-changes by microarray and qPCR. The X-axis represents fold-change on the Agilent platform and the Y-axis represents fold-change on the qPCR platform (both scales expressed as \log_2 ratio of obese vs. lean). The dashed lines represent the positions for invariant gene expression (\log_2 ratio = 0). Genes showing agreement in the direction of fold-change between microarray and qPCR are indicated by open diamonds whereas genes discordant for directionality are indicated by crosses. The degree of correlation between the magnitudes of fold-changes between the two platforms is indicated by the line of best fit and its accompanying p-value.

