



Supplementary Figure 2. Amplification bias reproducibility. 10 ng NT2 cDNA was pre-amplified for 10 PCR cycles, the sample was then used to quantify target gene expression by qPCR. Target gene expression in the original cDNA samples was also determined using 10 ng cDNA per target. The experiment was performed three times and the average values are reported. (A) PreAmp amplification bias is plotted against target gene expression for a cDNA sample derived from control NT2 cells. (B) PreAmp bias standard deviation (SD) is plotted against target gene expression for a cDNA sample derived from control NT2 cells. (C) PreAmp bias from six NT2 samples, representing a time course of RA treatment, was calculated. The average bias of the six samples is plotted against average target gene expression. Only gene targets where all time points have a Cq<30 are assessed. (D) PreAmp bias standard deviation for the six NT2 samples is plotted against average target gene expression.