

Supporting Information for Parallel picoliter RT-PCR assays using microfluidics

Joshua S. Marcus^{1,2}, W. French Anderson^{2,3} and Stephen R. Quake^{2,4,5}

¹Option in Biochemistry and Molecular Biophysics, ²Department of Applied Physics, California Institute of Technology, MS 128-95, Pasadena, CA 91125. ³Gene Therapy Laboratories, Keck School of Medicine, University of Southern California, Los Angeles, CA 90033

4: To whom correspondence should be addressed. Email: quake@stanford.edu

5: Current address: Bioengineering Dept., Stanford University, Clark Center, E300, Stanford, CA 94305

Table of Contents

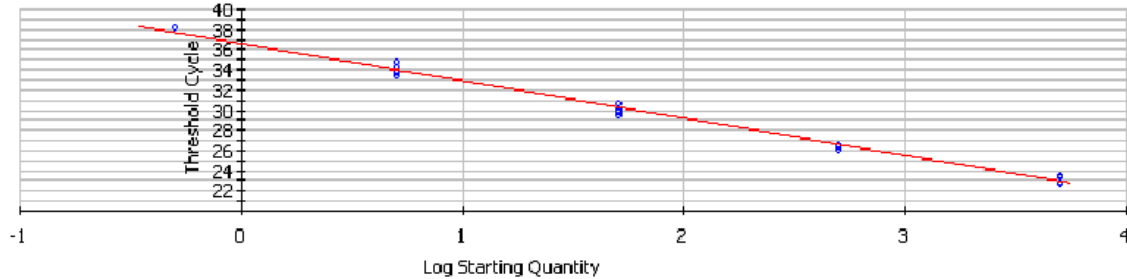
Item	Description	Page#
Figure S-1	Benchtop real time RT-PCR results	S-2
Figure S-1 legend	Legend for figure S-1	S-2

Figure S-1

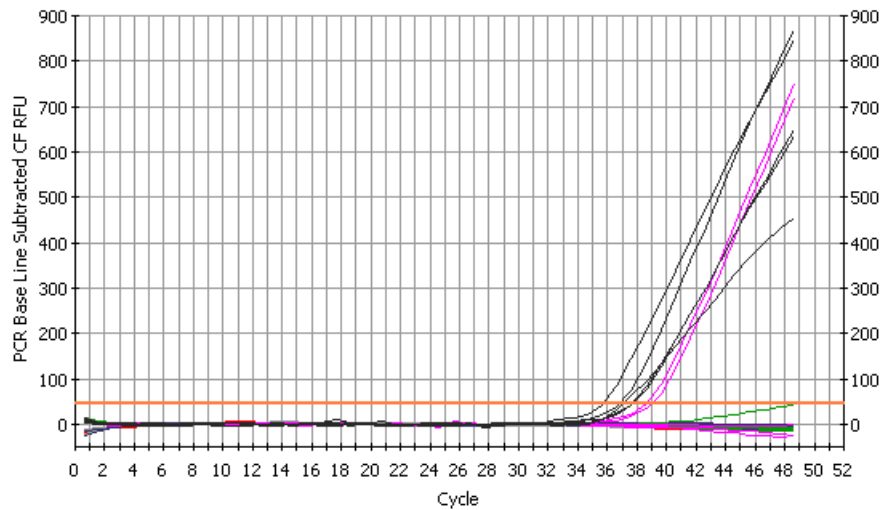
a.

Correlation Coefficient: 0.996 Slope: -3.674 Intercept: 36.599 $Y = -3.674X + 36.599$
PCR Efficiency: 87.1 %

Unknowns
Standards



b.



Supporting Figure 1: a. Benchtop qRT-PCR standard curve utilizing serially diluted human male total RNA as template. We were able to detect the 0.5 pg template in only one of five reactions. **b.** Fluorescence traces of RT-PCR control reactions. Red curves are no template reactions. All other curves are no RT reactions with serially diluted human male total RNA templates. Templates range from 0.05 pg total RNA (gray) to 500 pg total RNA (black). Only reactions with 500 pg total RNA and 50 pg total RNA (magenta) templates amplified. All other templates (5 pg total RNA, green; 0.5 pg total RNA, blue) did not amplify. We can estimate the percent of gDNA contamination by plotting the Ct values of the no RT reactions onto the off chip standard curve shown in **a**. When this is done, gDNA contamination is estimated to be 0.3% of total RNA template.