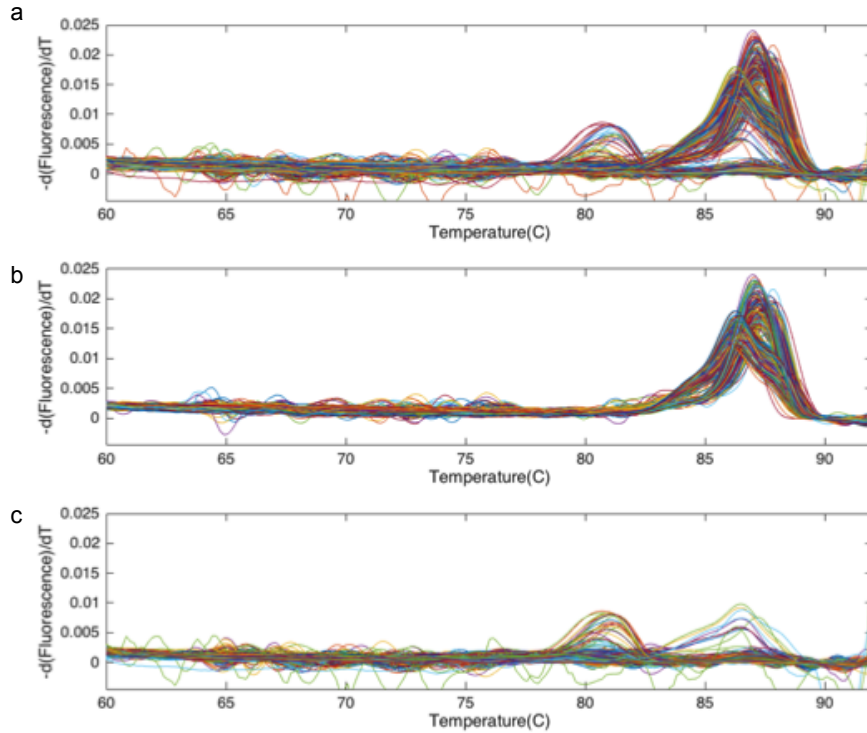


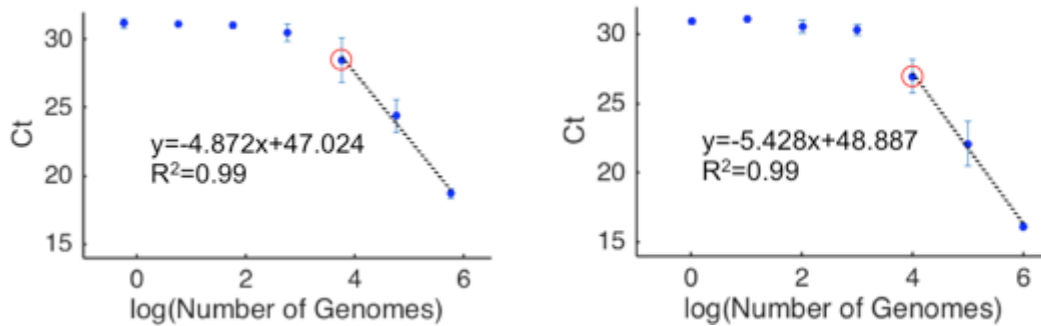
## Supplementary Figures

### **Massively parallel digital high resolution melt for rapid and absolutely quantitative sequence profiling**

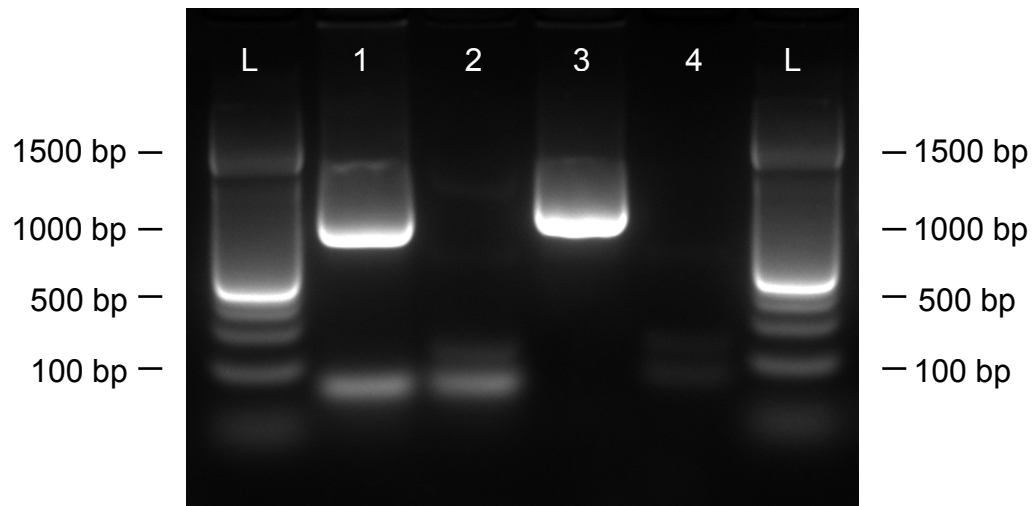
Daniel Velez Ortiz<sup>1</sup>, Hannah Mack<sup>1</sup>, Julietta Jupe<sup>1</sup>, Sinead Hawker<sup>1</sup>, Ninad Kulkarni<sup>2</sup>, Behnam Hedayatnia<sup>2</sup>, Yang Zhang<sup>1</sup>, Shelley Lawrence<sup>3</sup>, Stephanie I. Fraley<sup>1,\*</sup>



**Supplementary Figure 1. DHRM melt curves for polymicrobial mixtures.** Curves from experiment 2 in Table 2. (a) All melt curves. (b) Melt curves that were automatically identified as bacterial using our U-dHRM  $T_m$  enumeration algorithm. (c) Melt curves that were automatically identified as background/non-specific using our U-dHRM  $T_m$  enumeration algorithm.



**Supplementary Figure 2. QPCR dilution series standard curves.** (a) *S. pneumoniae* DNA (b) *L. monocytogenes* DNA. Slope of linear regime indicates primer efficiency. Red circle marks the condition used in the complimentary U-dHRM experiments.



**Supplementary Figure 3. Gel electrophoresis of qPCR amplification products corresponding to Fig. 4D.**  
**L:** DNA ladder markers. **1:** High concentration template multiplexed with calibrator sequence. 16S target amplicon appears as a band at 1000 bp. Calibrator sequence appears as a band at 60 bp. **2:** NTC with calibrator sequence, showing a faint off-target amplification band at approximately 150 bp, just above the calibrator sequences. **3:** High concentration template without calibrator sequence included. **4:** NTC without calibrator sequence, showing a faint off-target amplification band at approximately 150 bp.