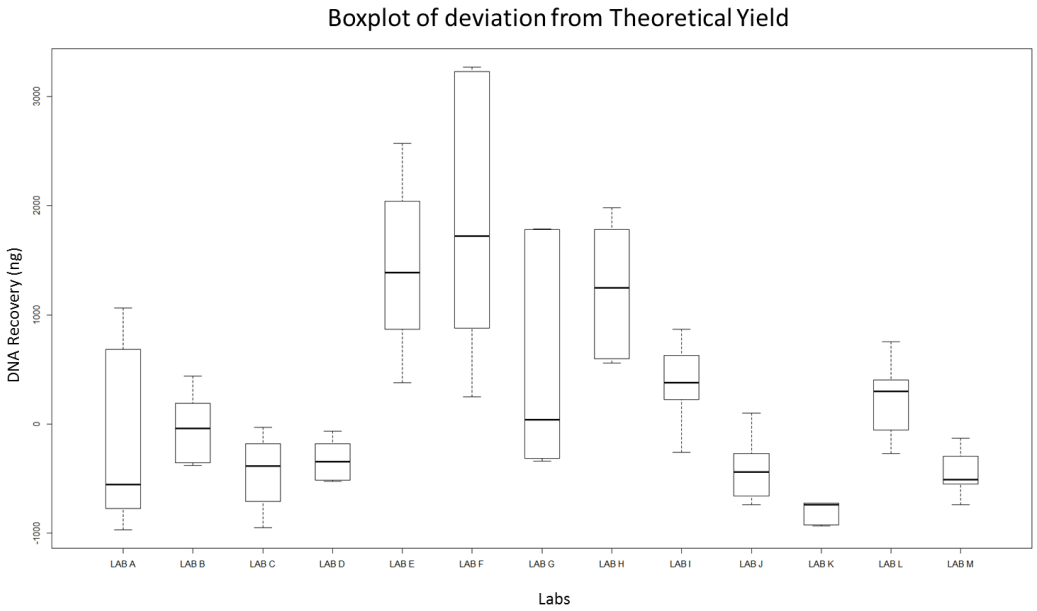
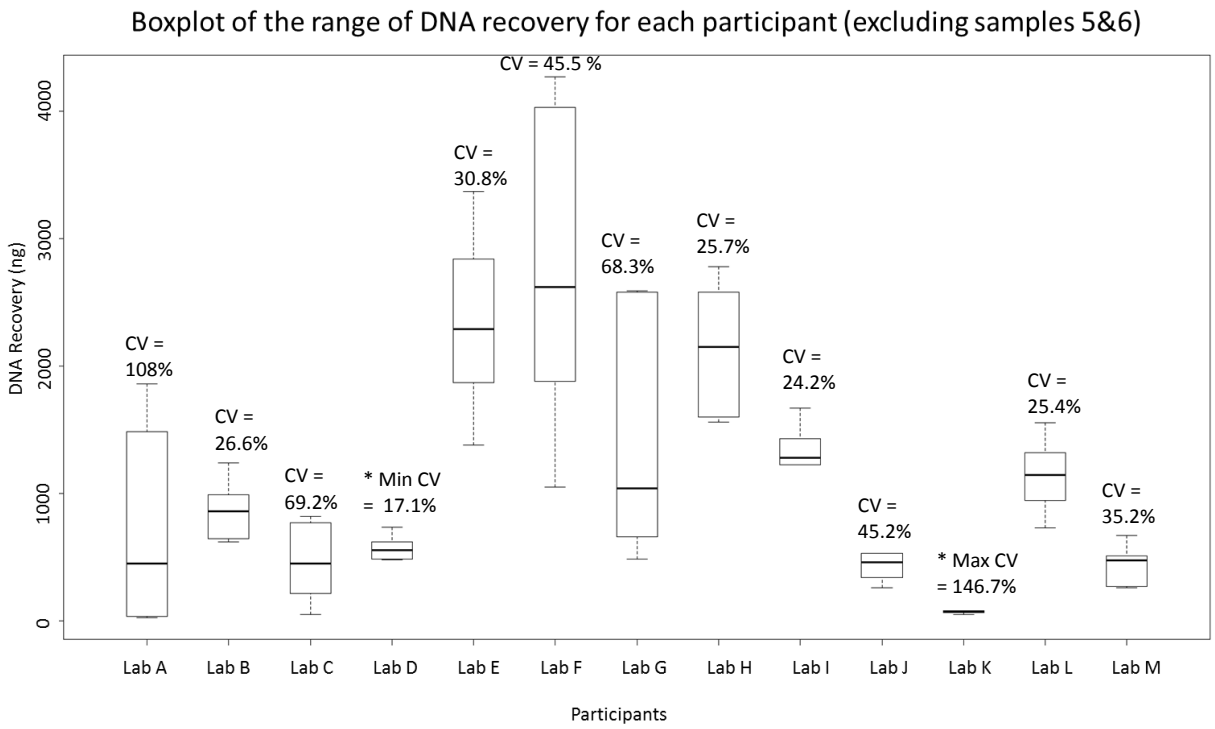
Supplemental Tables and Graphs to the Ring Trial Manuscript – For Publication

Allele	Primer Sequence
BRAF_V600E-For	GAAGACCTCACAGTAAAAATAGGTG
BRAF_V600E-Rev	TCCACAAAATGGATCCAGAC
EGFR_G719X-For	TGGAGCCTCTTACACCCAGT
EGFR_G719X-Rev	CCTTATACACCGTGCCGAAC
EGFR_L858R-For	AGCCAGGAACGTACTGGTGA
EGFR_L858R-Rev	TGCCTCCTTCTGCATGGTAT

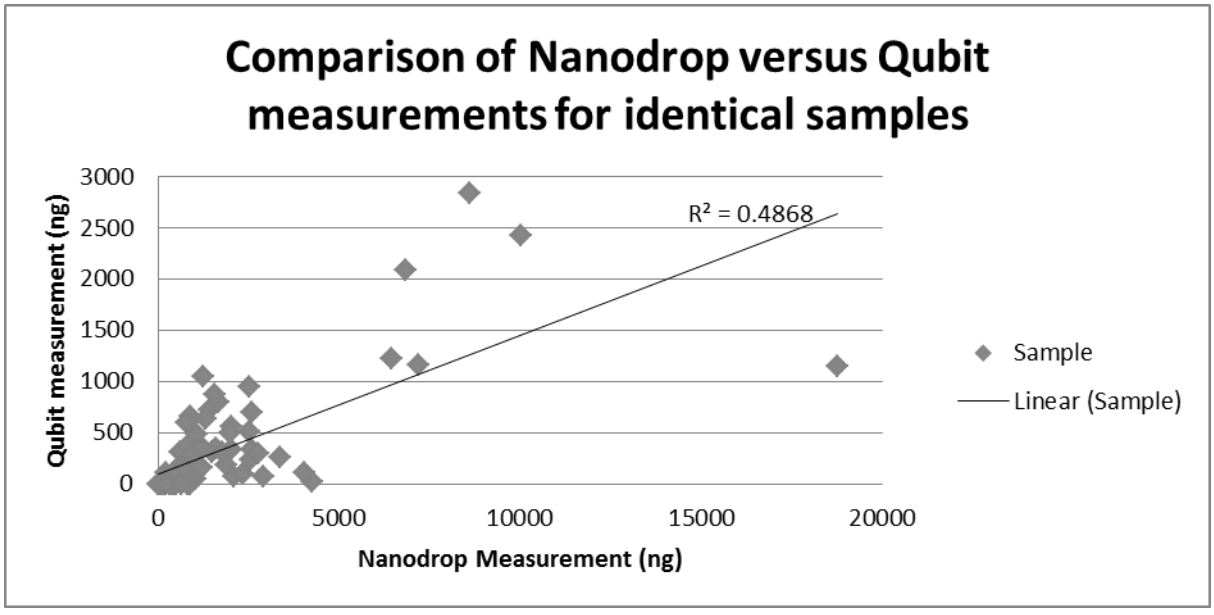
Supplemental table 1: primer sequences for confirmatory sanger sequencing performed at UCL prior to sample distribution.



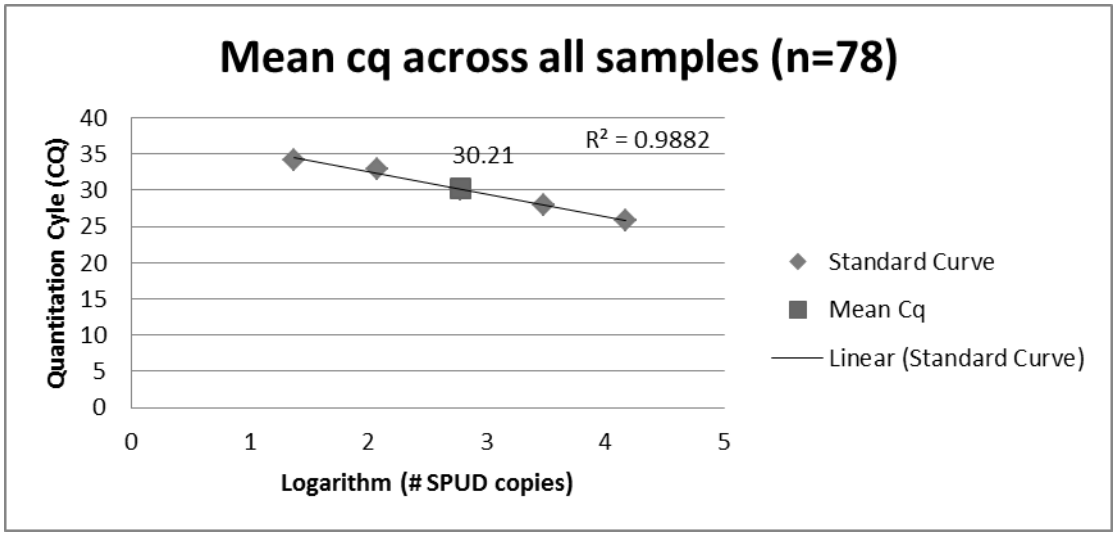
Supplemental Figure 1: Baseline (0) represents the theoretical yield of these samples. Deviation from the baseline represents the range in DNA recovery that was above or below the calculated theoretical yield. Note these deviations are based on self-reported yields. Laboratories C, D, J and M achieved the most accurate DNA measurements with respect to theoretical yields.



Supplemental Figure 2: shows the range in DNA recovery reported by participants. Yields reported for samples 5 (blank) and 6 (clinical sample) were excluded to enable unbiased comparison of each laboratory's performance. Note these results are based on original yields reported in Nanodrop.



Supplemental Figure 3: Correlation between Qubit and Nanodrop measurements for identical samples. This graph represents a total of 78 samples that were measured using both quantitation methods. R^2 value is <0.5 demonstrating poor correlation between Qubit and Nanodrop quantitation methods.



Supplemental Figure 4: SPUD qPCR assay measuring PCR inhibition. Shows the standard curve and mean Cq for all 78 samples. R^2 value is close to 1 demonstrating good correlation between the mean Cq and standard curve. Demonstrates absence of PCR inhibitors in sample preparation.