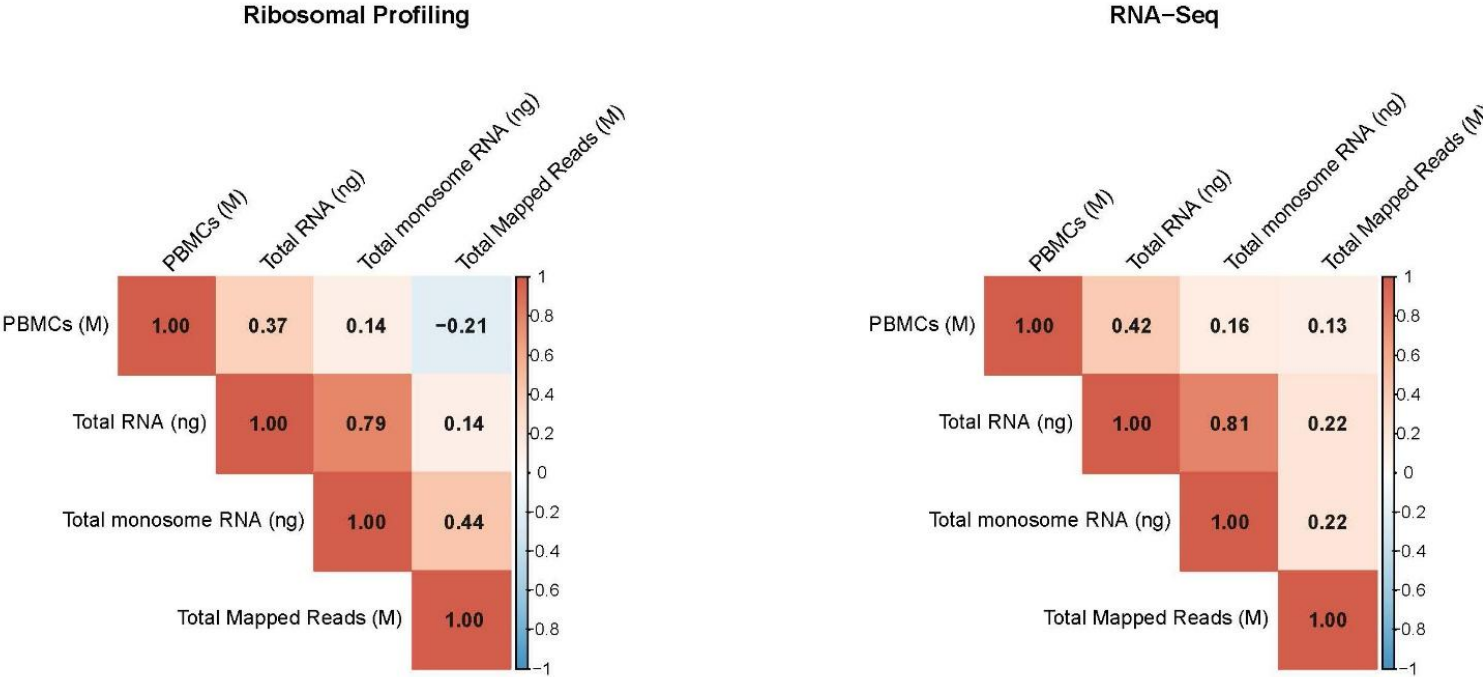


Supplementary Figure 1: Correlation analysis of early metrics of quality. Spearman correlation performed using the entire dataset (PS + MS), except for missing data points which were omitted from the calculation, to compare metrics of quality generated during wet lab processing (total PBMCs, total RNA and monosomes) and both RP and RNA-Seq sequencing library quality (as measured by the total number of reads mapped to the human genome).



Supplementary Data 1: Quality metrics used to assess wet-lab workflows and bioinformatics processing for RP (orange columns) and RNA-Seq (green columns) in both the pilot study (PS) and main study (MS). Cells are color-coded using a heat-map, where desirable counts are shown in blue, and less desirable counts are shown in red. Samples that failed quantification or sequencing are shaded grey. For quick comparison purposes, we also show average values for PS (light green row) and MS (dark green row) samples.

Supplementary Data 2: Genes differentially transcribed at Day 2 compared to Day 1 (RNA-Seq, DTP). Sorted by descending absolute $\log_2$ fold change (Day 2 vs. Day 1). Gene model summaries and annotations are based on Ensembl Version 100 (April 2020).

Supplementary Data 3: Genes differentially transcribed at Day 2 compared to Day 1 (RNA-Seq, DTaP). Sorted by descending absolute $\log_2$ fold change (Day 2 vs. Day 1). Gene model summaries and annotations are based on Ensembl Version 100 (April 2020).

Supplementary Data 4: Genes differentially transcribed at Day 8 compared to Day 1 (RNA-Seq, DTaP). Sorted by descending absolute $\log_2$ fold change (Day 8 vs. Day 1). Gene model summaries and annotations are based on Ensembl Version 100 (April 2020).

Supplementary Data 5: Genes differentially translated at Day 2 compared to Day 1 (RP, DTP). Sorted by descending absolute $\log_2$ fold change (Day 2 vs. Day 1). Gene model summaries and annotations are based on Ensembl Version 100 (April 2020).

Supplementary Data 6: Genes differentially translated at Day 2 compared to Day 1 (RP, DTaP). Sorted by descending absolute $\log_2$ fold change (Day 2 vs. Day 1). Gene model summaries and annotations are based on Ensembl Version 100 (April 2020).

Supplementary Data 7: Genes differentially translated at Day 8 compared to Day 1 (RP, DTP). Sorted by descending absolute $\log_2$ fold change (Day 8 vs. Day 1). Gene model summaries and annotations are based on Ensembl Version 100 (April 2020).

Supplementary Data 8: Genes differentially translated at Day 8 compared to Day 1 (RP, DTaP).

Sorted by descending absolute $\log_2$ fold change (Day 8 vs. Day 1). Gene model summaries and annotations are based on Ensembl Version 100 (April 2020).