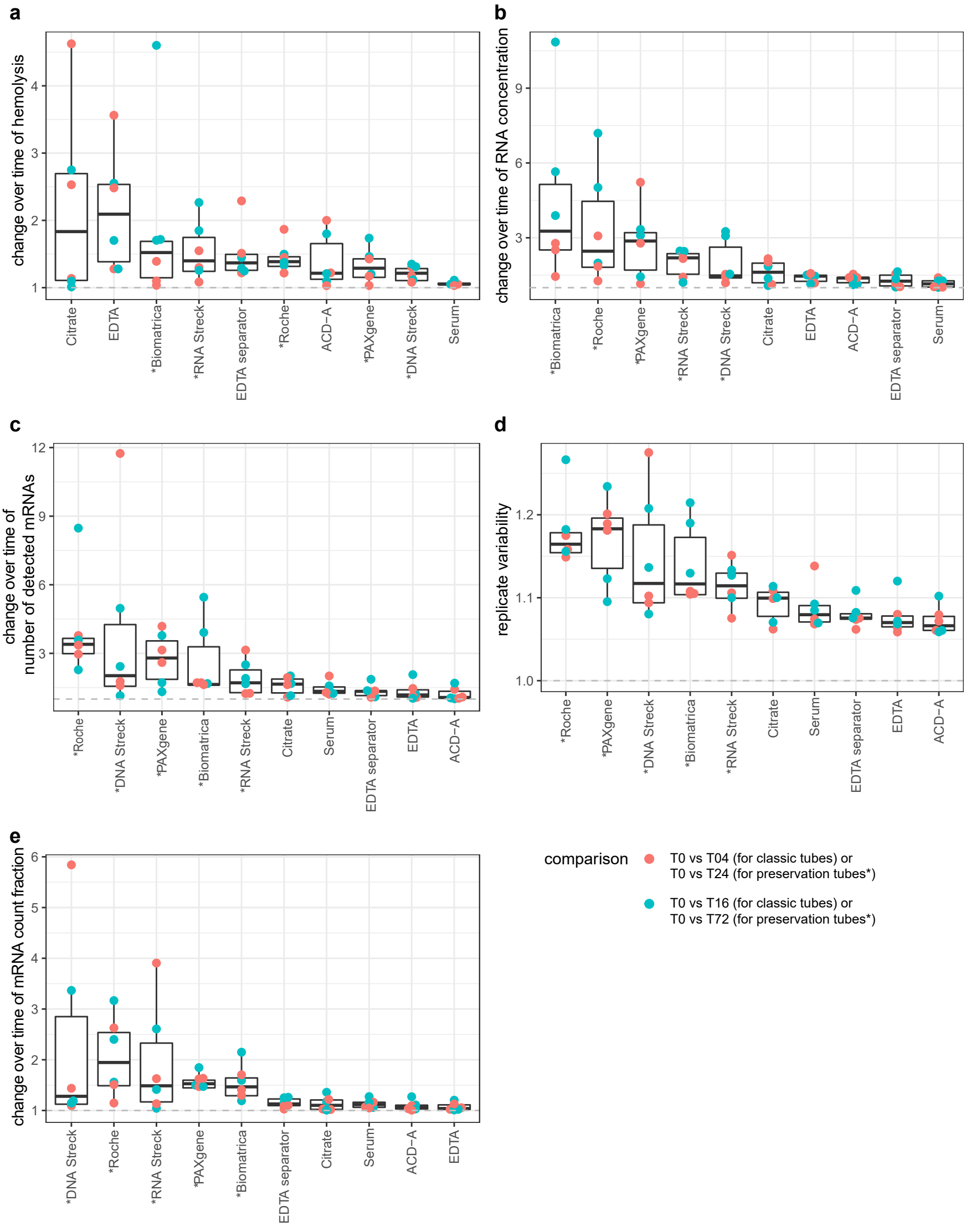
Supplementary Fig. S9.



Supplementary Fig. S9: Changes over time of each blood collection tube performance metric at mRNA level. Boxplot of the fold-change within each donor across time intervals, per tube, for hemolysis (a) as measured by absorbance at 414 nm with Nanodrop. Boxplot of fold-change of plasma RNA concentration (b), based on the ratio of endogenous vs Sequin spike-in RNA read counts. Boxplot of the fold-change of the number of detected genes (c) after filtering out genes with counts fewer than 6 reads. Replicate variability (d), i.e., area left of the curve, transformed from log2 to linear scale. Boxplot of the fold-change of the fraction of the counts mapping to mRNA versus all counts (e). In the boxplots, the lower and upper hinge of the boxes represents the 25th and 75th percentile, respectively. The whiskers extend to the lowest and highest value that is within 1.5 times the interquartile range. Data beyond the end of the whiskers are outliers. Individual data points are shown as colored dots. Tubes are ordered by mean fold-changes. Small changes indicate good performance. *Preservation tubes* are indicated with an asterisk. T0=plasma prepared immediately after blood draw. T04, T16, T24, T72=plasma prepared 4, 16, 24 and 72 hours after blood draw, respectively. Note that different donors were sampled and that tubes were processed at different time intervals for *preservation* and classic tubes.