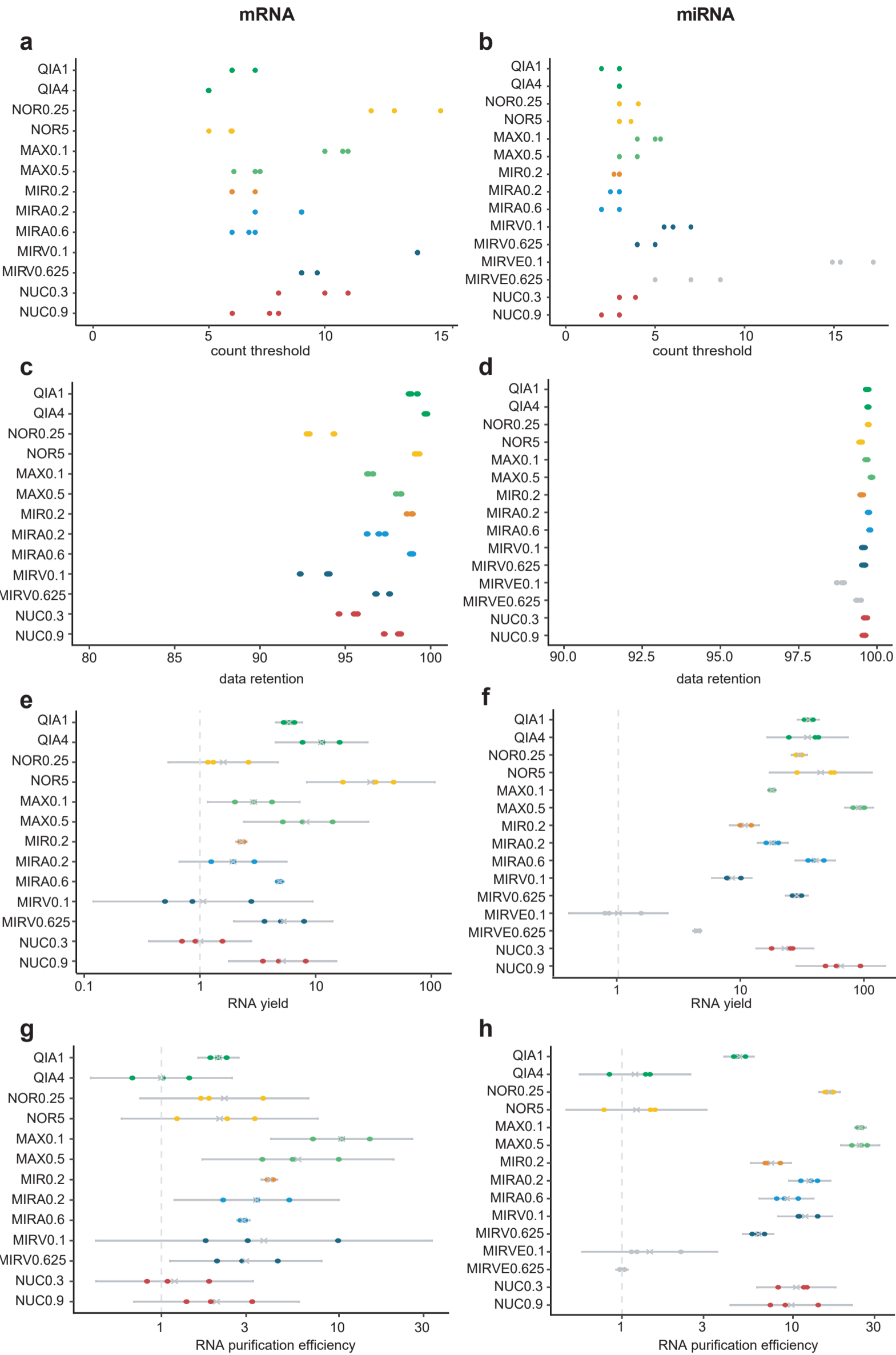


Supplementary Fig. S4.



Supplementary Fig. S4: Performance of RNA purification methods on count threshold, data retention, RNA yield, and RNA purification efficiency at mRNA and miRNA level. For each of the unique RNA purification method-plasma input volume combinations, 3 technical replicates are analyzed (n=39 for mRNA capture sequencing, n=45 for miRNA sequencing). Count threshold required to eliminate at least 95% of single positive genes (a) or miRNAs (b) between technical replicates. Low count thresholds indicate a good performance. Percentage of total counts that are kept after applying the count threshold for mRNA capture (c) and miRNA (d) sequencing. High data retention percentages indicate good performance. Relative mRNA (e) and miRNA (f) yield, obtained by correcting the RNA concentration for eluate volume, values are log rescaled to the lowest mean of all methods and transformed back to linear space, mean and 95% confidence interval are shown. High RNA yields indicate good performance. mRNA (g) and miRNA (h) purification efficiency, obtained by correcting the RNA yield for input volume, values are log rescaled to the lowest mean of all methods and transformed back to linear space, mean and 95% confidence interval are shown. High RNA purification efficiencies indicate good performance. The number in the y-axis labels is the plasma input volume (in ml).