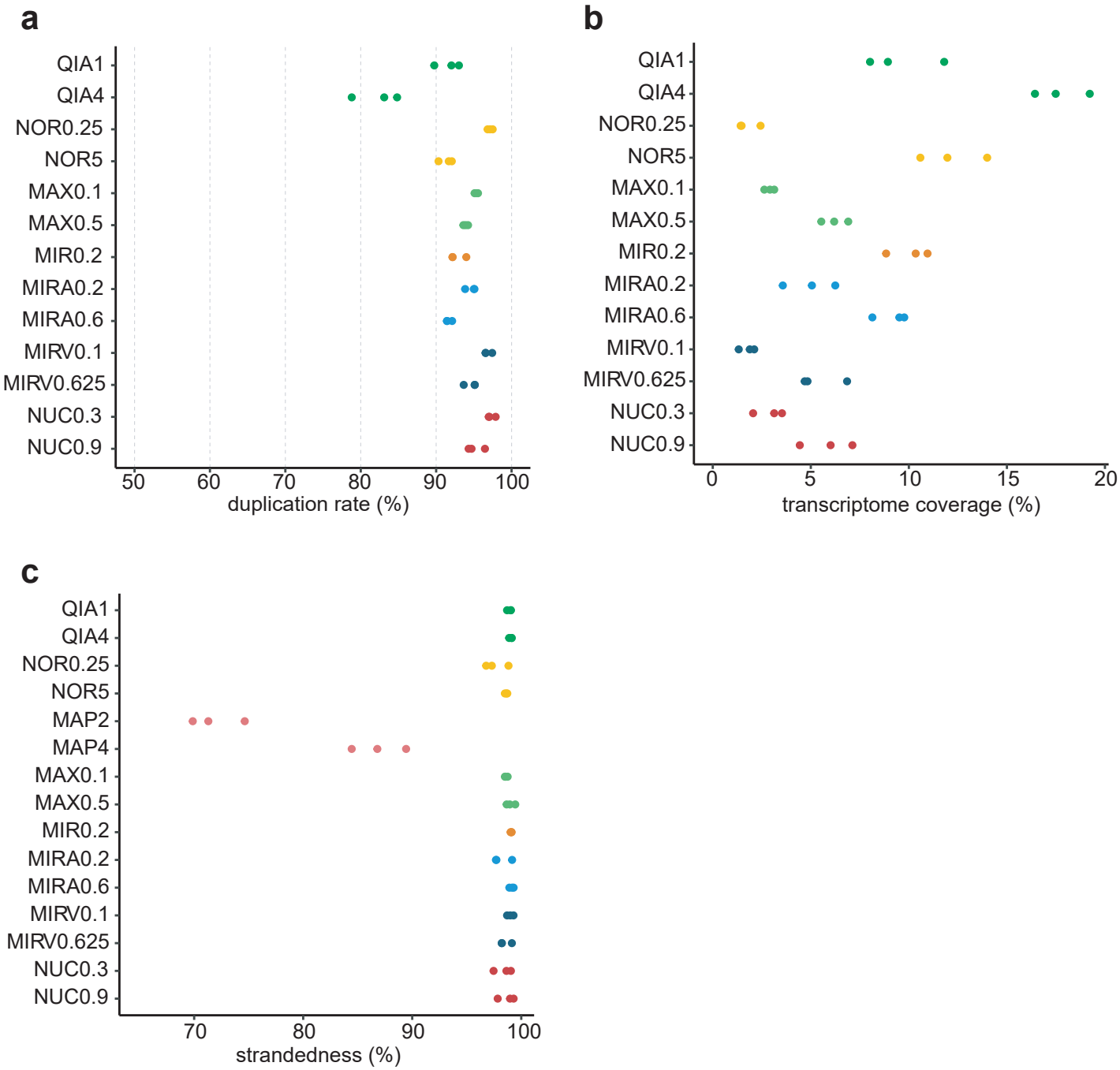
Supplementary Fig. S1.



Supplementary Fig. S1: Performance of RNA purification methods on duplication rate, transcriptome coverage and strandedness at mRNA level. For each of the unique RNA purification method-plasma input volume combinations, 3 technical replicates are analyzed. Percentage of read duplicates (a) found by Clumpify after subsampling (n=39). Low duplication rates indicate a good performance. Percentage of bases in the total transcriptome that are covered at least once ((b), n=39). High transcriptome coverages indicate a good performance. Percentage of reads on correct strand (c) according to strand-specific protocol (n=45). High percentages indicate a good performance. The number in the y-axis labels is the plasma input volume (in ml). MAP=MagNA Pure method, MAX=Maxwell method, MIR=miRNeasy method, MIRA:miRNeasy Advanced method, MIRV=mirVana method, NOR=Norgen method, NUC=NucleoSpin method, QIA=QIAamp method.