



Supplementary Figure: Results shown are for a two group simulation with $n=3$ samples per group where one sample was simulated to be more variable than the others.
 Top row: Average number of genes with false discovery rate (FDR)<0.05 for each method versus sample variability for different true positive FCs (2-fold in panel A, 4-fold in panel B).
 Bottom row: Averaged empirical FDR at a FDR cut-off of 0.05 for each method versus sample variability of the 6th sample for different true positive FCs (2-fold in panel C, 4-fold in panel D).