



Figure S2: SMARTseq samples show higher noise on gene level A) Scatterplot showing log2 ratio of edgeR gene level dispersion estimate for protein coding genes between SoLo and SMARTseq against average GeTMM value. Data points are colored by density on the graph. B) Scatterplot showing log2 ratio of expression normalized confidence interval size between SoLo and SMARTseq against average GeTMM value. Data points are colored by graph density. Red line marks 5 GeTMM.