



S4 Figure: The graphs illustrate the differences between the methods when applied to differentially expressed microRNAs that show only minor censoring. Two differentially expressed microRNAs (true  $|\delta_i| = 2$ ) are tracked during the simulation study. (a) Estimates of differential expression by UCNR (green solid line), multiple  $t$ -tests with MOD normalization and LOD imputation (red dashed line), MNV+1 imputation (blue dotted line) and KNN imputation (black dotted-dashed line). Censoring an observation at some point for this particular microRNA is marked by a black circle (MNA group) or a grey square (MNSC group) on the horizontal axis. (b) Plot of  $-\log_{10} p$ -values for the hypothesis test ( $H_0 : \delta_i = 0; H_1 : \delta_i \neq 0$ ). (c) Box plot of differential expression estimates.