Supplementary_Figure 9: *First column: similarity statistic profiles giving the estimated number of variable mean-standard deviation clusters by sample group "M" and "S" in the input space of the real proteomics dataset. K-Means partitioning clustering algorithm was performed with $s = 100$ random start seedings. Red arrows indicate results of stopping rule (idem as in Figure 2). Second and Third column: distributions of means and standard deviations before and after multi-group mean-variance regularization for the real proteomics dataset.*