

Supplementary material for “Visualization
methods for RNA-sequencing data analysis”

Lindsay Rutter

February 16, 2018

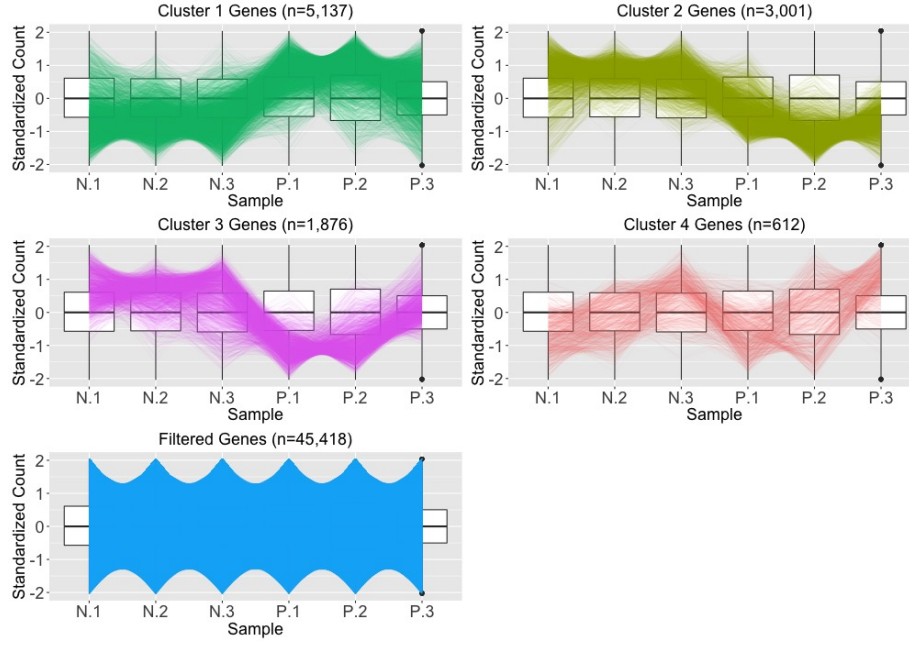


Figure 1: Example application of parallel coordinate plots using the iron-metabolism soybean dataset. We filtered genes with low means and/or variance, performed a hierarchical clustering analysis with a cluster size of four, and visualized the results using parallel coordinate lines. Most non-filtered genes were in Clusters 1 and 2, which both showed overexpression in one treatment and underexpression in the other treatment. The genes in Cluster 4 mostly showed messy patterns with low signal to noise ratios. Interestingly, Cluster looked similar to Cluster 2 (large values for group N and small values for group P), except for unexpectedly large values for the third replicate of group P.

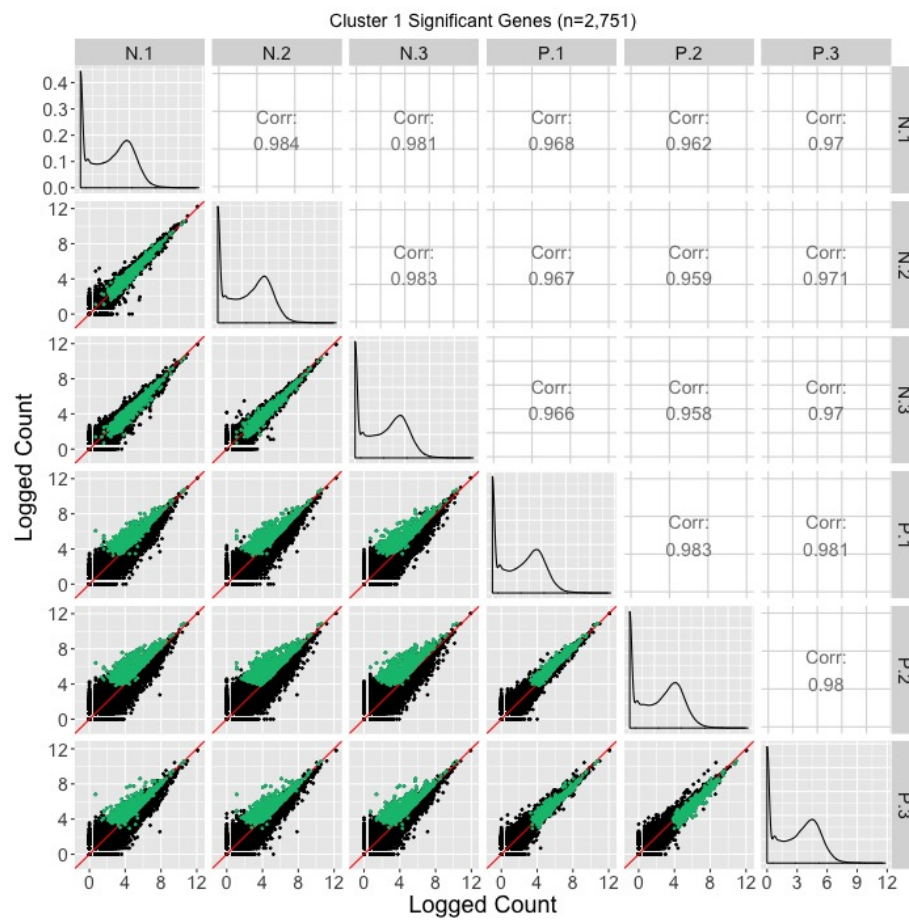


Figure 2: Caption

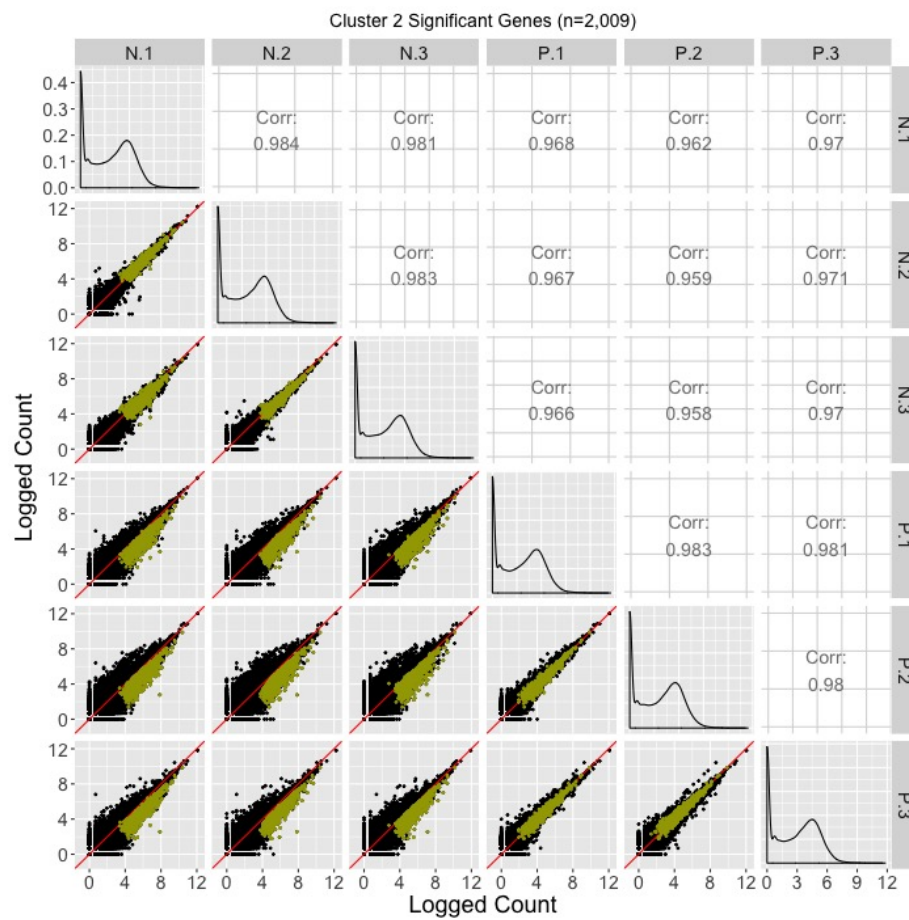


Figure 3: Caption

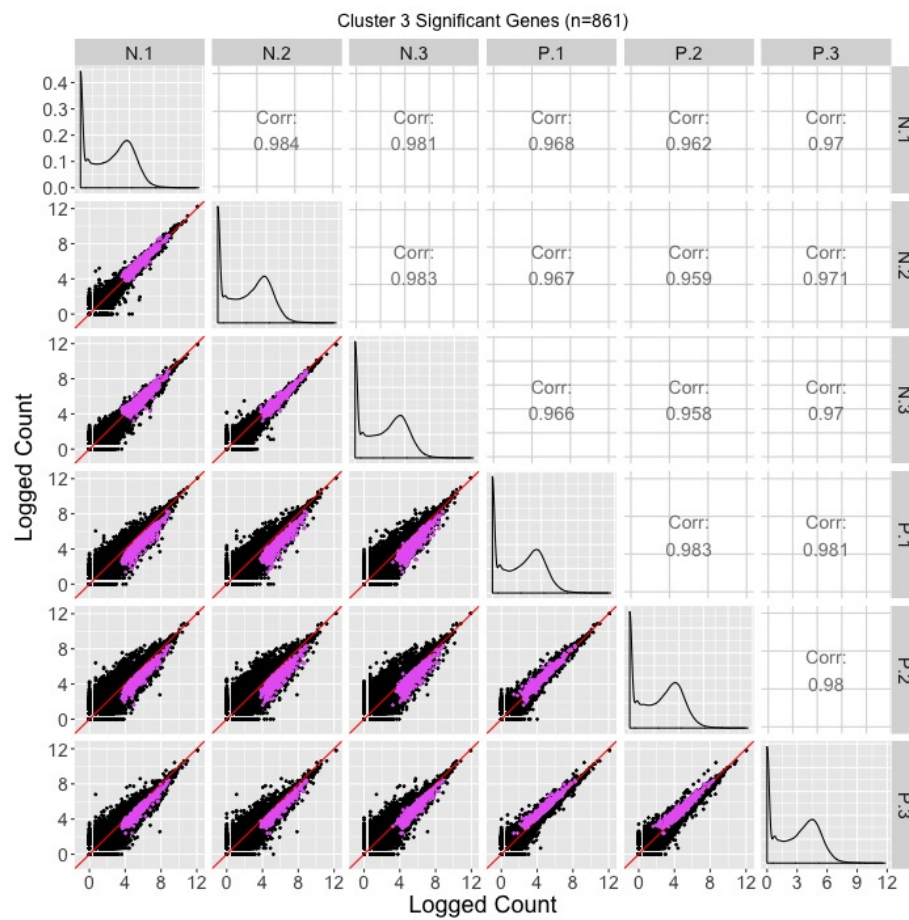


Figure 4: Caption

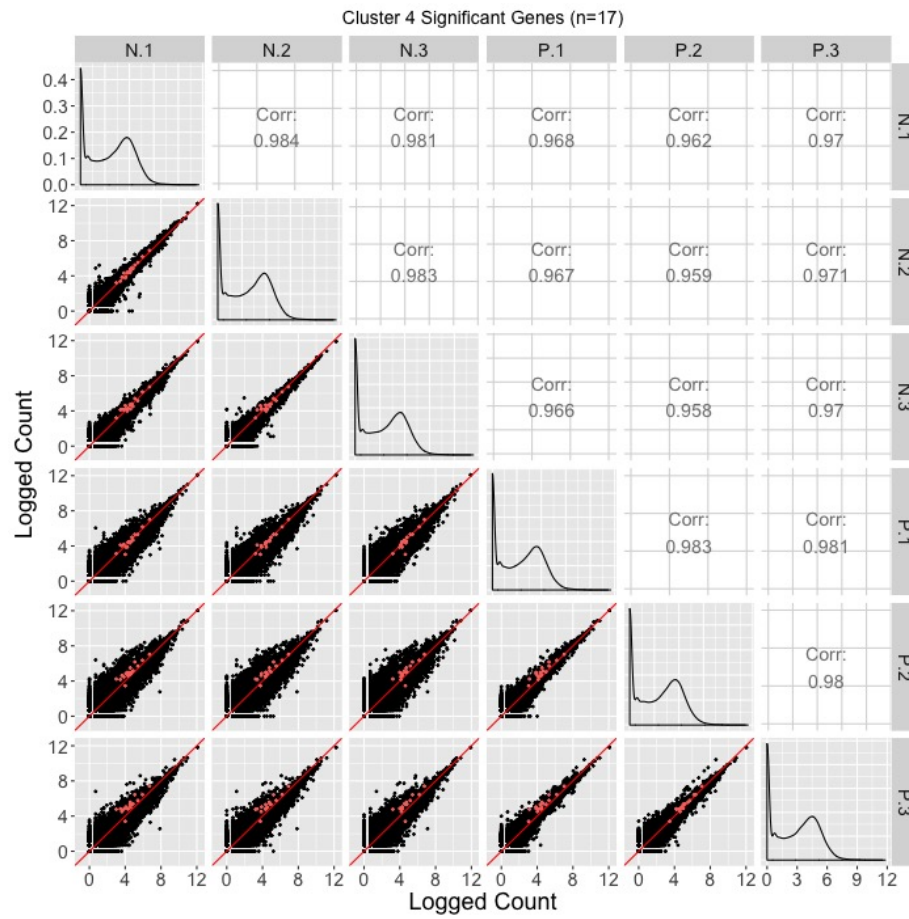


Figure 5: Caption

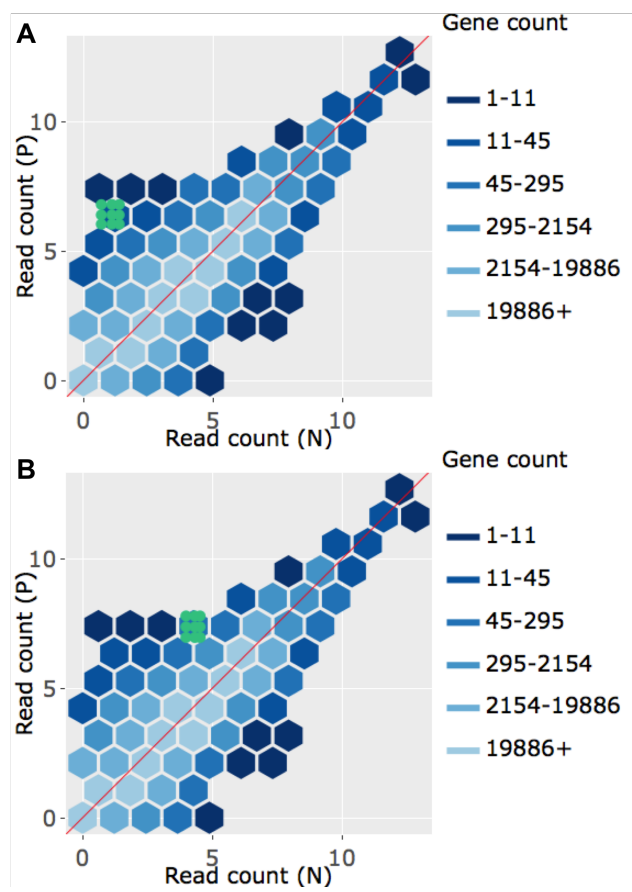


Figure 6: Caption