Supplementary Figures

Figure S1

A. Raw data

B. Filtered data

Figure S1 Read Filtering. A. Distribution of log Counts Per Million (CPM) for each sample prior to filtering. Notice that genes with low expression levels are < 0. B. Distribution of log Counts Per Million (CPM) for each sample after filtering to remove lowly expressed genes (CPM < 1 in ¾ of samples).
Figure S2

A.

Boxplots of logCPMs (unnormalised)

B.

voom: Mean–variance trend

Sqrt( standard deviation )

log2( count size + 0.5 )
Figure S2 Normalization. A. Boxplots of Log2CPM values for each sample prior to normalization. B. Limma-voom trend line. C. Boxplots of Log2CPM values after TMM and limma-voom normalization.
Figure S3

A.

Diagnosis by Treatment MDS Plot
C.

Figure S3 Multi Dimensional Scaling Plots (MDS). A. MDS plot colored by diagnosis. B. MDS plot colored by sex. C. MDS plot colored by treatment.
Figure S4 KEGG Enrichments for All DEGs. Top significantly enriched KEGG pathways across lists of DEGs. See Table S4 for full lists and statistics.
Figure S5 Biological Process GO Term Enrichments for All DEGs. Top significantly enriched Biological Process Terms across lists of DEGs. See Table S4 for full lists and statistics.
Figure S6 Molecular Function GO Term Enrichments for All DEGs. Top significantly enriched Molecular Function Terms across lists of DEGs. See Table S4 for full lists and statistics.
Figure S7 Cellular Component GO Term Enrichments for All DEGs. Top significantly enriched Cellular Component Terms across lists of DEGs. See Table S4 for full lists and statistics.