

Figure S1 Removal of batch effect of GSE22459 and GSE76882 datasets. (A) Venn diagrams of combined data of GSE22459 and GSE76882. The pink and blue circles indicate GSE22459 and GSE76882 dataset, respectively. 15779 genes shared by the two datasets were chosen for downstream analysis. (B) Removal of batch effect. The Sangerbox online tool (<http://sangerbox.com>) was applied to remove the batch effect of the two datasets. (C) The construction of sample clustering tree map. A sample clustering tree map was constructed to detect and eliminate outliers.

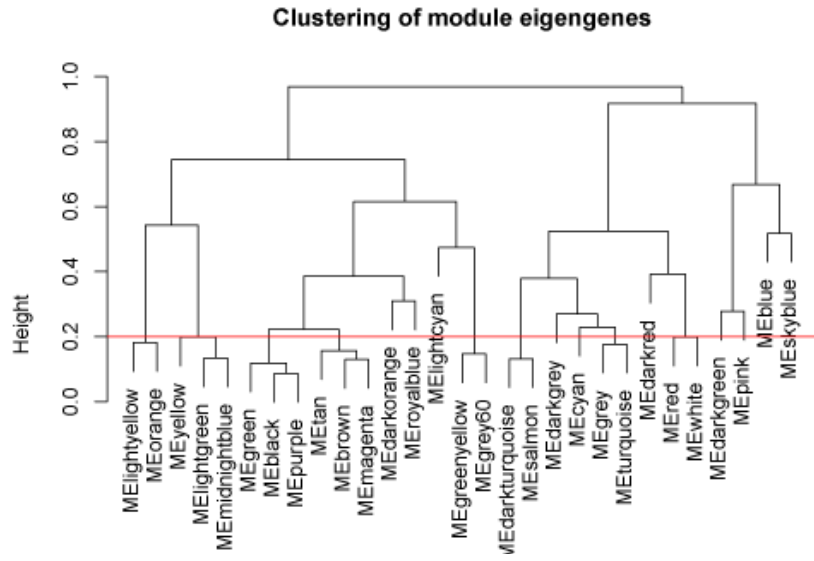


Figure S2 Clustering of module eigengenes. The 29 modules obtained from co-expression network were merged into 18 modules with 0.2 as the MEDiss Thres indicated by the red line.

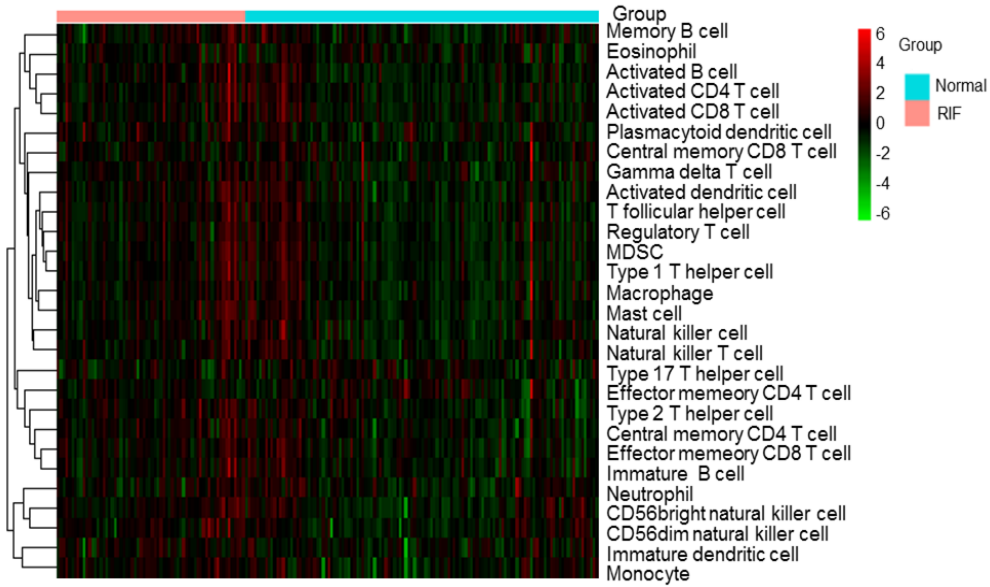


Figure S3 Heatmap of the infiltration levels of 28 immune cells in RIF and normal samples. Each row represents an immune cell and each column represents a sample. The red and green color of the tile indicates high or low expression, respectively.