Supplemental Figure 4. A. Unsupervised hierarchical clustering of expressed genes in 129 MPN samples. Gene expression in ET, PV, PrePMF and MF cells or enriched CD34-positive hematopoietic stem cells was studied by RNAseq. The heatmap depicts the top 2% genes in the gene expression dataset including MF, ET, PV and PrePMF. Other than the CD34 positive cell type we did not find any clustering of samples with specific disease phenotype. B. Unsupervised hierarchical clustering of expressed genes in 65 MF samples. The heatmap depicts the top 2% genes in the gene expression dataset for MF mononuclear cell samples. There were no distinguishable gene expression cohorts that show association with disease phenotype.