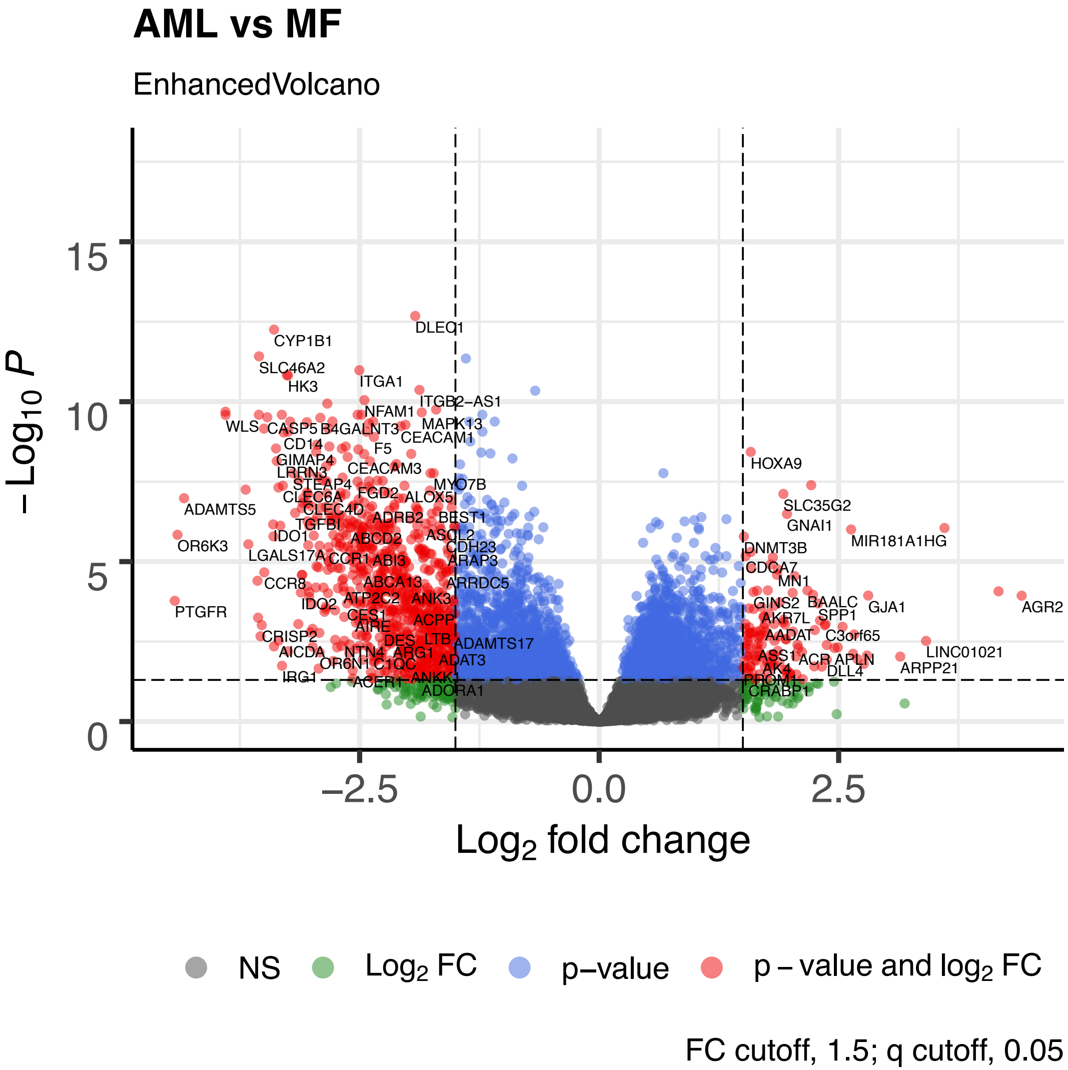

Figure S1. *Volcano plot of RNA-seq analysis of MF samples pre and post transformation to AML.* This plot shows the result of DESeq2 based RNA-seq analysis comparing transformed MPN cases ('AML') to samples gathered from the same patients prior to transformation. The analysis utilized a model statement incorporating both disease stage and sample identity to adjust for sample specific features. Log fold change of gene expression is plotted against adjusted significance. Genes are colored according to whether the log fold change is above 1.5 (green), q value is less than 0.05 (blue), or both (red). Selected genes with logFC above threshold and a significant q value are printed.

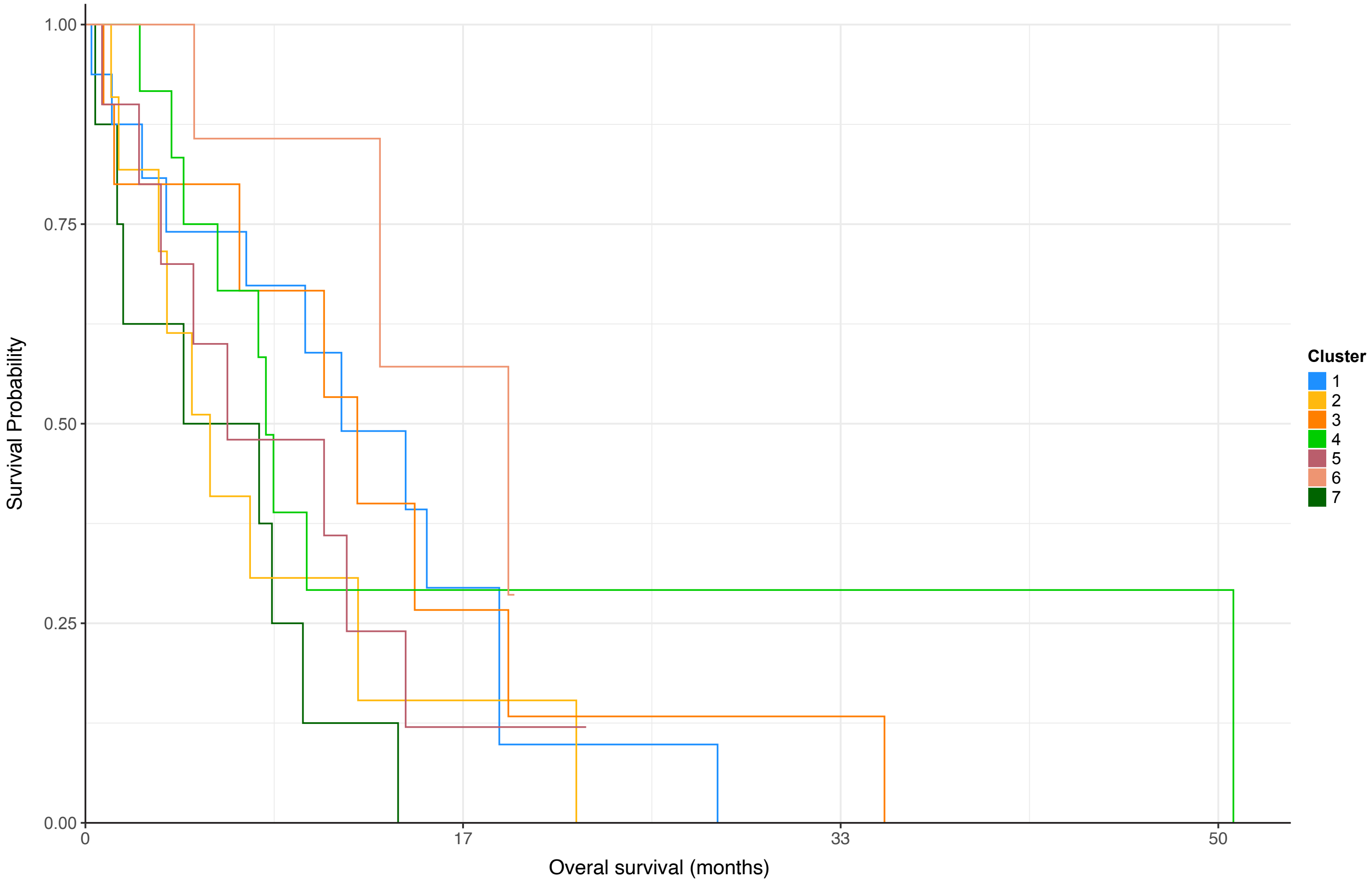

Figure S2. *Survival analysis of transformed MPN cases.* Patient groups were determined using the lineage deconvolution-based clustering shown in Figure 5A. Overall survival curves were generated starting at the time of transformation.