Supplementary Materials:

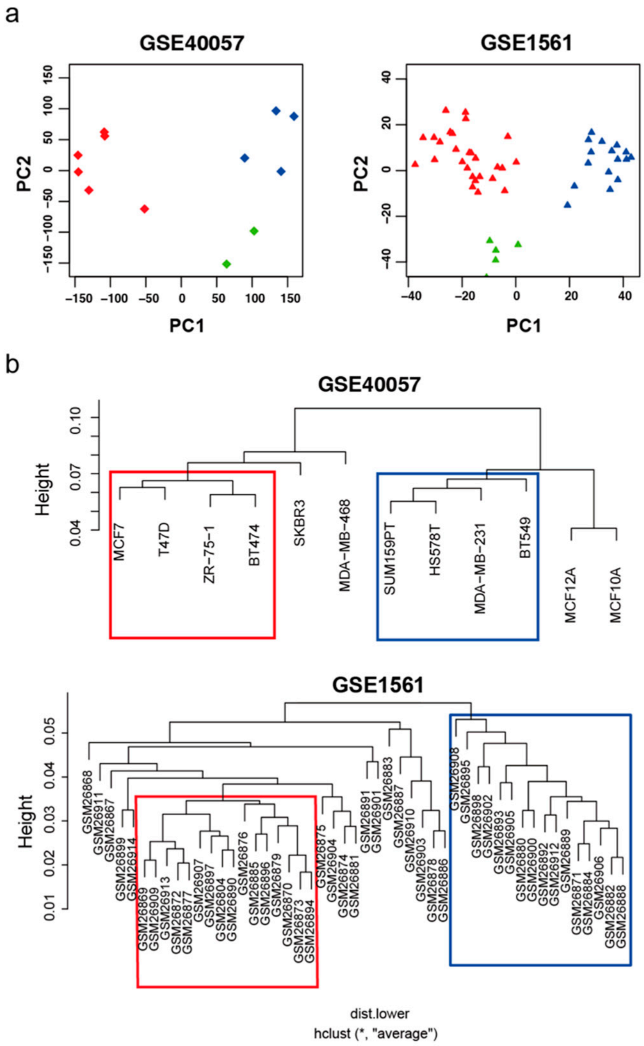

Figure S1 Unsupervised analysis. (a) Principal components of all genes. The first two PCA are plotted. The three major groups were colored in blue, red and green. (b) Hierarchical clustering of all samples. 8 cell lines from GSE40057 and 32 tissue samples from GSE1561, representing basal-like (blue) and luminal-like (red) groups were chosen for subsequent analysis

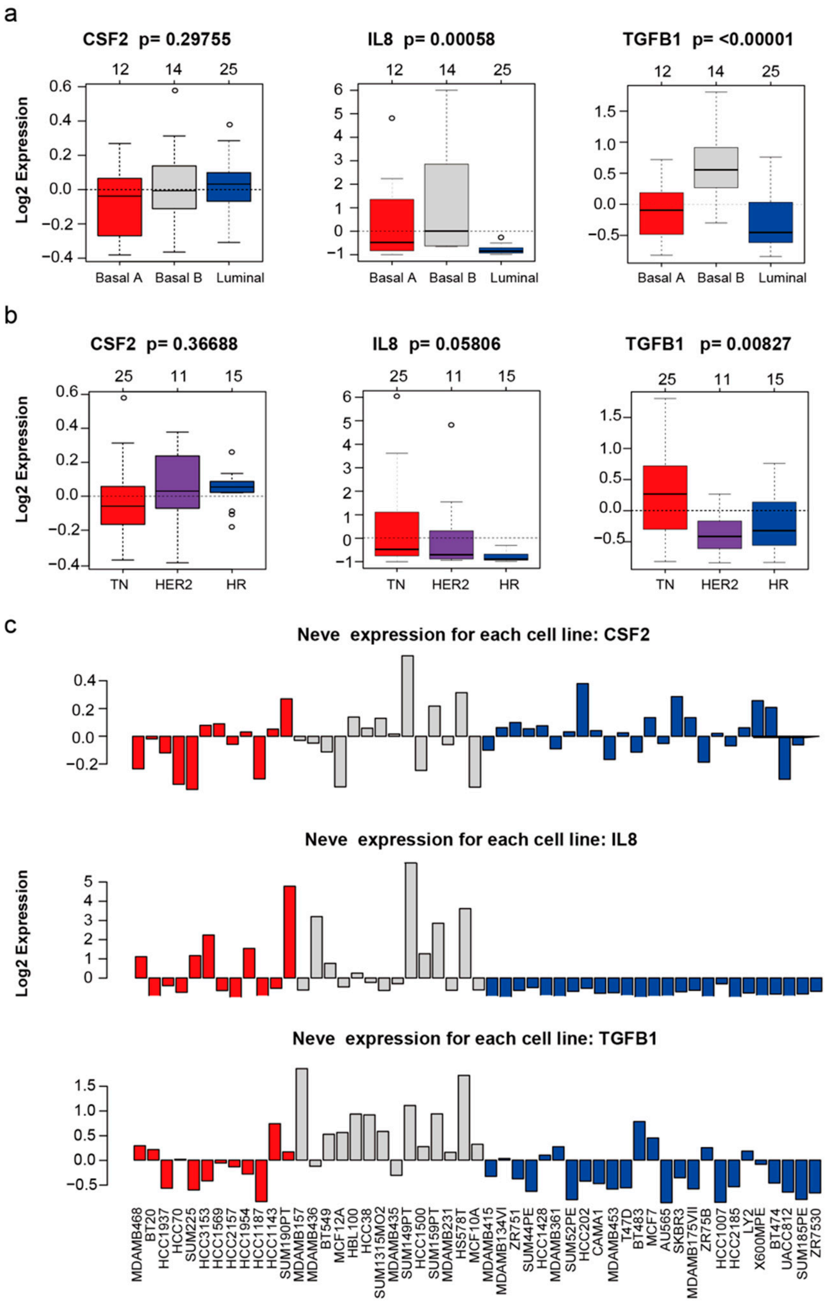

Figure S2 CSF2, IL8 and TGFβ1 expression in human breast cancer cell lines with GOBO analysis. (a) Box plots of CSF2, IL8 and TGFβ1 expression across 51 breast cancer cell lines grouped into basal A (red), basal B (grey) and luminal (blue) subgroups. (b) Box plots of CSF2, IL8 and TGFβ1 expression across 51 breast cancer cell lines grouped into triple negative (TN), HER2 positive and hormone receptor positive (HR). (c) CSF2, IL8 and TGFβ1 mRNA levels across 51 breast cancer cell lines

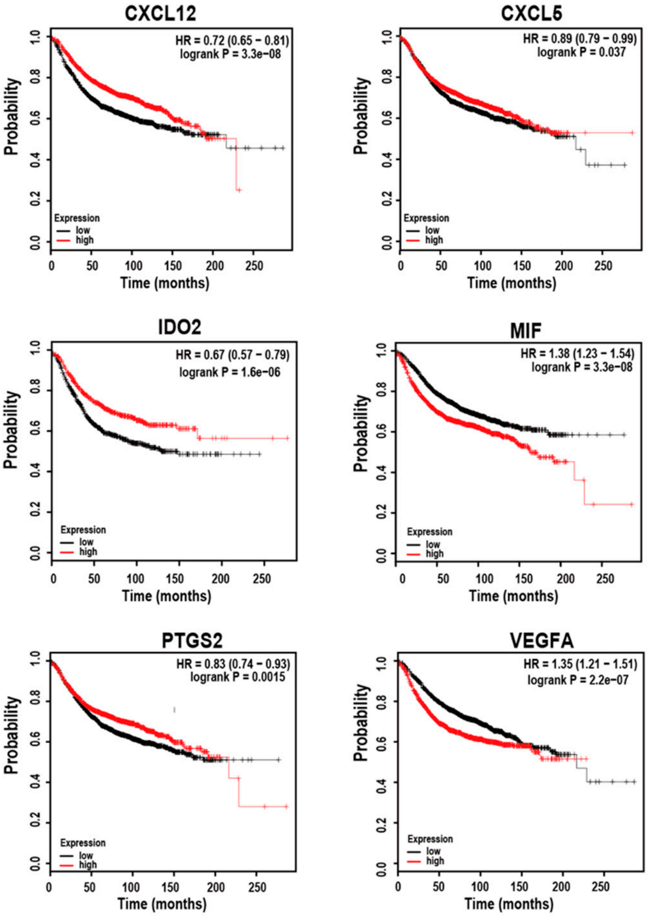

Figure S3 Kaplan-Meier Plotter determined the relationship between survival rate and mRNA expression levels of 6 immunosuppressive factors using microarray data of 4142 patients