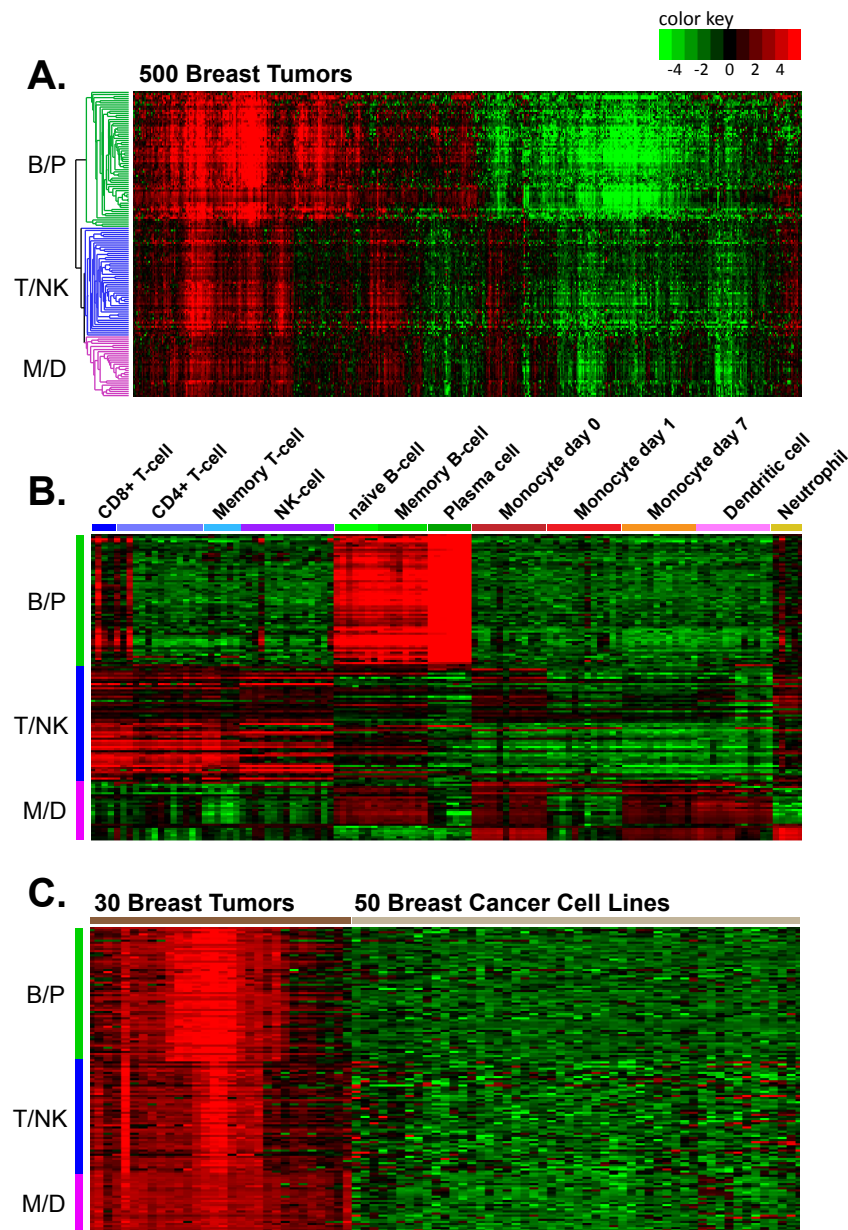


Supplementary Figure S1



Supplementary Figure S1. The B/P, T/NK and M/D immune metagenes are coordinately expressed in breast tumors and leukocytes but not in breast cancer cell lines. Heatmaps of expression microarray data are shown; red color indicates above-mean expression while green indicates below-mean expression, as depicted in the color key. **(A)** Probe sets (rows) comprising the B/P, T/NK and M/D metagenes were hierarchically clustered (Pearson correlation, average linkage) in 500 breast tumor profiles (columns) randomly selected from the MC1 meta-cohort. (Tumor dendrogram omitted for space.) **(B)** Expression levels of the immune metagenes (probe sets ordered as in **(A)**) are shown in a microarray dataset comprising 114 FACS-sorted leukocyte samples derived from human peripheral blood and bone marrow (Gene Expression Omnibus accession GSE22886; Abbas, A.R., et. al., Immune response in silico (IRIS): immune-specific genes identified from a compendium of microarray expression data. *Genes Immun.* 2005 Jun;6(4):319-31.). **(C)** Expression levels of the immune metagenes (probe sets ordered as in **(A)**) are shown in a microarray dataset comprising 51 breast cancer cell lines and 30 breast tumors (Gene Expression Omnibus accession GSE12790; Hoeflich, K.P., et. al., In vivo antitumor activity of MEK and phosphatidylinositol 3-kinase inhibitors in basal-like breast cancer models. *Clin Cancer Res.* 2009 Jul 15;15(14):4649-64.).