Several published gene signatures describing lymphocyte infiltration in breast cancer were obtained from HTG EdgeSeq data of the GeparNuevo samples. Results are compared by scatter plots and Pearson correlations presented. The following signatures were used: (*1*) The pre-specified 10 gene "GeparSixto immune signature" applied throughout all current analyses [13], (*2*) a 4 gene core of the GeparSixto immune signature, (*3*) the 2 gene "CYT" metric [14], (*4*) an 18 gene T-cell cluster from unsupervised clustering of the GeparNuevo HTG EdgeSeq data, (*5*) the "T-cell inflamed GEP" from Ayers et al. [15], as well as those genes available from the *HTG EdgeSeq Oncology Biomarker Panel* of the T cell clusters from studies of (*6*) FFPE-RNA-Seq of GeparQuinto [16], (*7*) RNA-Seq from TNBC of TCGA [9], and (*8*) Affymetrix microarrays of TNBC [17] .