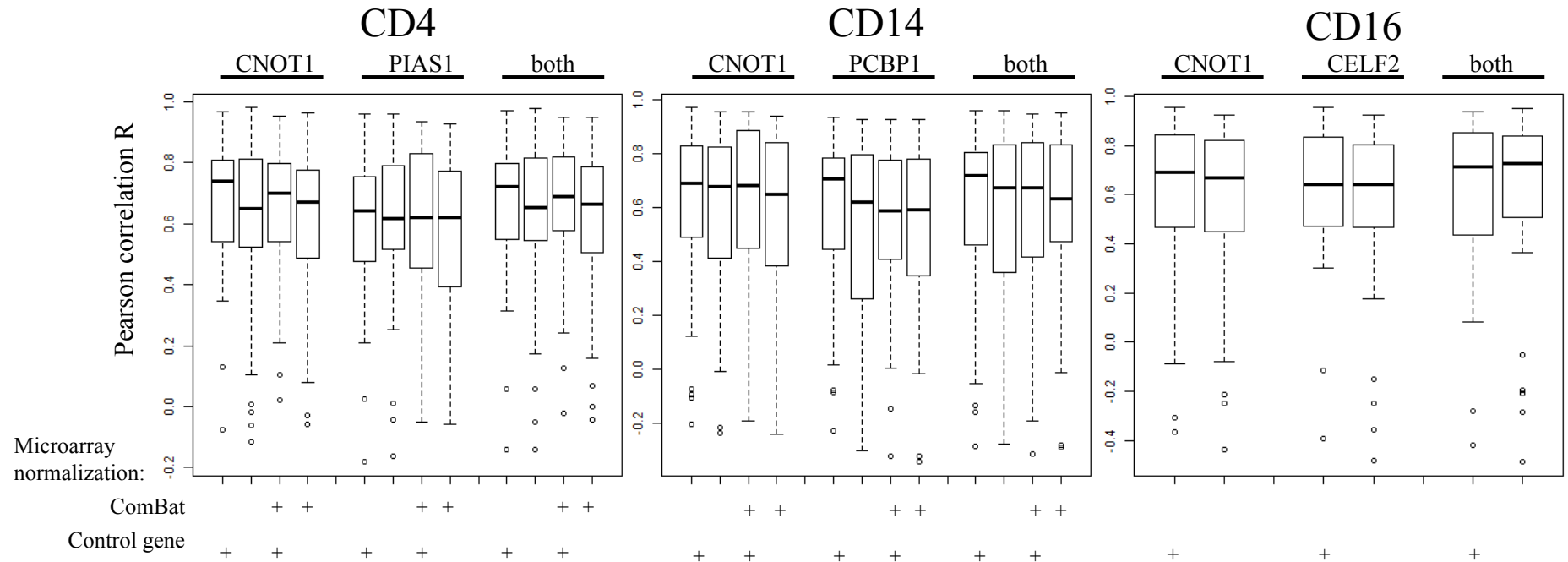


Additional File 7



Effects of microarray and nCounter processing on inter-platform correlation. Cell-type-specific nCounter datasets were normalized to the indicated control genes and log-transformed. Microarray data was preprocessed by RMA and then batch normalized through ComBat and/or normalized to control genes where indicated. Boxplots show Pearson correlation.