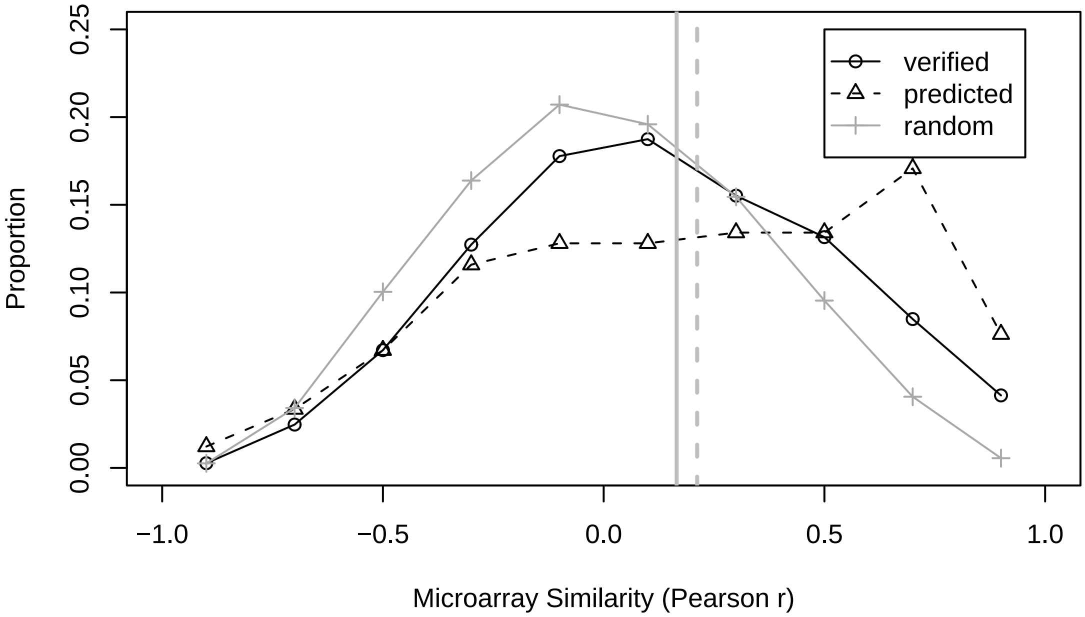

Supplementary Figure 2: In B. subtilis, predicted regulatory sites from phylogenetic footprinting are as predictive of expression patterns as experimentally verified sites. We show the distribution of microarray similarity for random pairs of genes, for pairs of genes with predicted sites from the same cluster of phylogenetic footprints (Terai *et al.* 2001), and from pairs of genes that are experimentally verified to bind the same TF (Makita *et al.* 2004), with sigma factors excluded. Microarray similarities were computed with Pearson correlation coefficients of normalized log-ratios across 78 *B. subtilis* microarray experiments that compared mRNA levels (Gollub *et al.* 2003). The vertical solid line shows the median over all TFs of the mean similarity of the pairs that are verified to bind that TF. This median is right-shifted from the overall distribution for pairs sharing a verified site because some of the less predictive TFs have many binding sites. The corresponding median for the predicted clusters of sites is also shown as the vertical dashed line. This median is to the right of the median for verified sites, which confirms that the relationship between predicted sites and expression patterns is very strong.