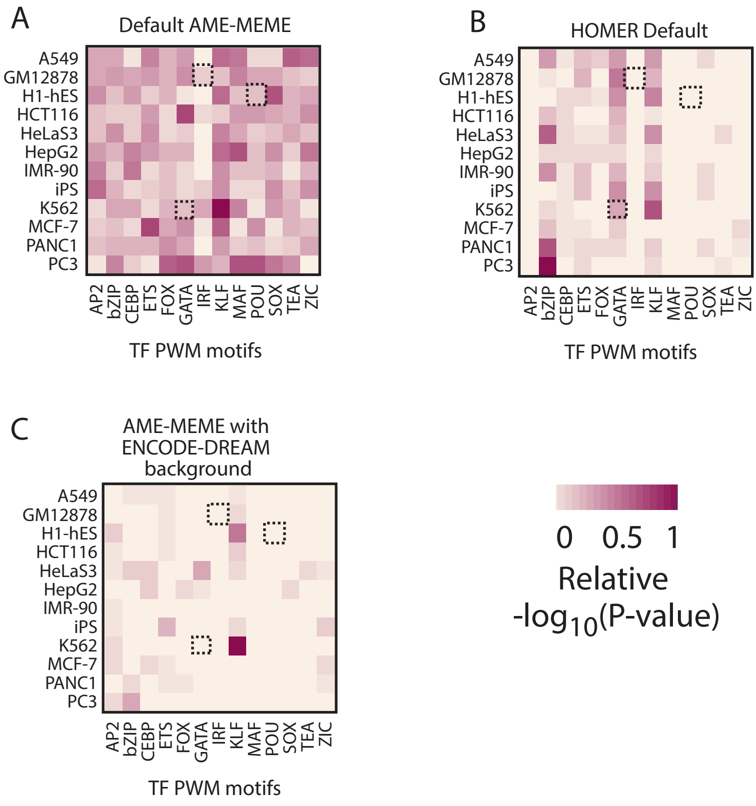

Supplemental Figure S5

Supplemental Figure S5: Motif enrichment patterns for AME and HOMER. To compare MEDEA with other state-of-the-art tools, (**A, C**) AME from the MEME suite and (**B**) findMotifsGenome.pl from the HOMER suite were used to calculate the motif enrichment of the indicated PWMs within the benchmarking ENCODE DNase-seq datasets. The upper panels use the default backgrounds of each tool (dinucleotide shuffle and GC-matching followed by autonormalization, respectively) while the bottom panel uses the ENCODE-DREAM DNase-seq datasets as a statistical background (the median value is shown) (**Methods**). Both these tools give P-values as output, which were subsequently -log10 transformed and normalized to the maximum value per plot for easier comparison between tools.