



Additional File 3. Comparison of standalone motif discovery programs. Different motif discovery programs predicted motifs embedded in 125 sets of sequences belonging to the Sandve et al (2007) benchmark dataset. The benchmark software calculated the nucleotide Correlation Coefficient scores (nCC scores), a measure of the correlation between the known nucleotide positions and the predicted nucleotide positions. The nCC scores are compared for (A) BioProspector and MEME, (B) Weeder and MEME, and (C) Weeder and BioProspector. The Spearman correlation (r) between the sets of nCC scores is indicated.