Model score (-p*log10(pval)): 14.39

Wilcoxon p-value (pval): 3.74e-33

Penalty (p): 0.444

Average yes-set score: 6.25

Average no-set score: 5.07

AUC: 0.74

Middle-point: 5.50

False-positive: 33.10%

False-negative: 28.06%

The AUC of the model achieves value significantly higher than expected for a random set of regulatory regions

Z-score = 4.44

Figure 2. Composite model of transcription factors potentially regulating the target genes of our interest. It consists of 15 position weight matrices (PWMs) of transcription factors. Results of CMA analysis of up-regulated genes in short-term survivors. **A)** Combination of 15 Position weight matrices (PWMs) with their optimized cut-offs and max_number_of_site (N) identified by genetic algorithm. **B)** The discriminative parameters of the composition of the Composite Score (p-value of the Wilcoxon test, AUC, rates of false positives and false negatives) and two histograms of the distributions of the Composite Score values in Yes (720 genes of our interest) and No (random set of 300 housekeeping genes) promoters.