Table 5. Consistency of EMCMODULE **over different runs and prior settings**

Prior	% Common sites	Sens (sd)	Spec (sd)
5	100	0.23 (0.000)	0.20 (0.000)
10	91	0.23 (0.011)	0.20 (0.009)
50	92	0.22 (0.014)	0.19 (0.012)
100	100	0.23 (0.012)	0.20 (0.009)

The algorithmic consistency was tested using the skeletal muscle regulatory sequence data (*Human and Mouse Skeletal Muscle Regulatory Sequences*) and a starting set of motifs from BIOPROSPECTOR of 50 nonredundant motifs. Five runs with different starting seeds were made over four prior settings for the geometric distribution for intersite distances that correspond to prior mean distances of 5, 10, 50, and 100, respectively. EMCMODULE was run for 20,000 iterations in each case. The final motifs selected by EMCMODULE (posterior mode) corresponded to the same set over all runs, though individual instances of motif sites varied slightly. The sensitivity (Sens) and specificity (Spec) of predictions were almost unchanged in all the runs with different settings, showing the robustness of the algorithm. % Common sites, percentage of sites that are common to all five motif runs, rounded to nearest integer. Sensitivity (Sens) and specificity (Spec) are defined as follows: Sens= (# true sites found)/154. Spec= (# true sites found)/(# motif sites found). The numbers in parentheses refer to the standard deviation over the five runs.