Table 6. The ability of the proposed scoring scheme to distinguish the correct motifs from incorrect ones.

TF	top-1 score	top-2 score	Comments
ABF1	**8.02**	0.93	
ACE2	**0.70**	0.30	
BAS1	**4.83**	1.50	
CBF1	**16.83**	5.00	
CIN5_H2O2Lo	**1.23**	0.28	
DIG1	**3.34**	0.64	
FHL1	**2.66**	1.62	
FKH1	**2.45**	0.68	
FKH2	**2.82**	0.79	
GAL4_GAL	**6.17**	2.85	
HAP1	**2.85**	0.99	
HAP4	**2.51**	1.60	
HIR1	**3.10**	2.80	
HIR2	**8.65**	8.38	The top-1 motif is correct, but its score is only slightly better than the top-2 score.
MAC1_H2O2Hi	**2.90**	2.55	
MBP1	**3.81**	1.59	
MCM1	**4.39**	2.16	
MET31	**4.11**	3.26	
MET32	2.58	2.10	The top-3 motif is correct, whose score is **1.97**. The top-1 motif is actually the binding site of CBF1, and top-2 motif is similar to the top-1.
MET4	**11.19**	8.15	
MIG1	Failed		
MIG2	**4.54**	4.23	The top-1 motif is correct, but its score is only slightly better than the top-2 score.
MSN4_H2O2Hi	0.99	0.77	The top-3 motif is correct, whose score is **0.72**.
RAP1	**2.20**	**1.85**	Top-1: , Top-2: . Both are correct.
REB1	**9.98**	3.87	
RLM1	**0.51**	0.49	The top-1 motif is correct, but its score is only slightly better than the top-2 score.
SMP1	**0.51**	0.50	The top-1 motif is correct, but its score is only slightly better than the top-2 score.
STB1	**4.61**	4.51	The top-1 motif is correct, but its score is only slightly better than the top-2 score.
STE12	**4.50**	0.41	
SWI4	**3.21**	2.29	
SWI5	**0.71**	0.29	
TEC1	1.35	**0.77**	The top-2 motif is correct.