

Supplementary Tables for “Incorporating nucleosome occupancy  
information to predict transcription factors”

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Supplementary Table 1. T-test p-values and differences of predicted occupancy between functional and spurious sites predicted by OSCAR at 95% sensitivity level.

TF Name <sup>1</sup>	Lower Occupancy P-value <sup>2</sup>	Higher Occupancy P-value <sup>3</sup>	Difference in Occupancy	Evidence in Literatures <sup>4</sup>
FKH2	0.0004	0.9996	-0.08	[1], [2]
SOK2	0.0005	0.9995	-0.08	[1]
HAP2	0.0005	0.9995	-0.20	[1]
CBF1	0.0008	0.9992	-0.09	[1]
HAP5	0.0014	0.9986	-0.16	[1]
HAP3	0.0116	0.9884	-0.18	
FKH1	0.0143	0.9857	-0.03	
YAP7	0.0221	0.9779	-0.07	[1]
SUM1	0.0264	0.9736	-0.12	[1]
INO2	0.0369	0.9631	-0.15	
SUT1	0.0393	0.9607	-0.14	
STB5	0.0454	0.9546	-0.21	
INO4	0.0474	0.9526	-0.17	[1], [2]
NDD1	0.0549	0.9451	-0.09	
SKN7	0.0571	0.9429	-0.07	
SFP1	0.0743	0.9257	-0.14	
ACE2	0.0888	0.9112	-0.11	
MSN4	0.1089	0.8911	-0.04	
ROX1	0.1118	0.8882	-0.10	
HAP4	0.1234	0.8766	-0.10	
GAT1	0.1333	0.8667	-0.09	
TEC1	0.1358	0.8642	-0.04	
GAL4	0.1443	0.8557	-0.13	
REB1	0.1456	0.8544	-0.08	
AFT2	0.1557	0.8443	-0.04	
GLN3	0.1659	0.8341	-0.04	
HSF1	0.1737	0.8263	-0.03	
RCS1	0.1773	0.8227	-0.09	
HAP1	0.1932	0.8068	-0.10	
SWI4	0.2025	0.7975	-0.02	
MET32	0.2232	0.7768	-0.07	
PHO4	0.2501	0.7499	-0.06	
ABF1	0.2730	0.7270	-0.02	
CIN5	0.2740	0.7260	-0.02	

SNT2	0.2870	0.7130	-0.11
SPT23	0.2880	0.7120	-0.02
DAL82	0.2900	0.7100	-0.03
NRG1	0.2932	0.7068	-0.03
LEU3	0.2939	0.7061	-0.08
RFX1	0.3041	0.6959	-0.13
UME6	0.3047	0.6953	-0.05
SWI5	0.3277	0.6723	-0.02
PHD1	0.3546	0.6454	-0.02
DIG1	0.3556	0.6444	-0.01
GCN4	0.3582	0.6418	-0.01
STE12	0.4408	0.5592	0.00
FHL1	0.4417	0.5583	-0.01
RAP1	0.4538	0.5462	-0.01
MBP1	0.4639	0.5361	0.00
BAS1	0.4913	0.5087	0.00
RGT1	0.4980	0.5020	0.00
YAP1	0.4991	0.5009	0.00
SWI6	0.5268	0.4732	0.00
MSN2	0.5427	0.4573	0.01
CAD1	0.5723	0.4277	0.01
RPN4	0.7019	0.2981	0.05
MCM1	0.7242	0.2758	0.02
TYE7	0.7856	0.2144	0.07
MOT3	0.8452	0.1548	0.08
ADR1	0.9461	0.0539	0.12
STB1	0.9941	0.0059	0.19

<sup>1</sup> 61 transcription factors with more than 10 identified binding sites from Young's group (Harbison, *et al.* (2004) Transcriptional regulatory code of a eukaryotic genome. *Nature*, 431, 99-104).

<sup>2</sup> P-values of student t-test that functional sites show lower nucleosome occupancy are shown

<sup>3</sup> P-values of student t-test that functional sites show higher nucleosome occupancy are shown.

<sup>4</sup> Consistencies of our significant results with those in the following literatures:

[1] Segal, E., Fondufe-Mittendorf, Y., Chen, L., Thåström, A., Field, Y., Moore, I.K., Wang, J.Z. and Widorn J. (2006) A genomic code for nucleosome positioning. *Nature*, 442, 772-778.

[2] Bernstein, B. E., Liu, C. L., Humphrey, E. L., Perlstein, E. O. and Schreiber, S. L. (2004) Global nucleosome occupancy in yeast. *Genome Biology*, 5: R62.

Supplementary Table 2. T-test p-values and differences of predicted occupancy between functional and spurious sites predicted by OSCAR at 99% sensitivity level.

TF Name	Lower Occupancy P-value	Higher Occupancy P-value	Difference in Occupancy	Evidence in Literatures
FKH2	0.000001	0.999999	-0.11	[1], [2]
SOK2	0.000002	0.999998	-0.17	[1]
CBF1	0.0002	0.9998	-0.12	[1]
HAP2	0.0005	0.9995	-0.20	[1]
HAP5	0.0014	0.9986	-0.16	[1]
PHO4	0.0017	0.9983	-0.16	[1]
INO4	0.0018	0.9982	-0.16	[1]
STB5	0.0052	0.9948	-0.20	
SKN7	0.0062	0.9938	-0.05	
SWI6	0.0102	0.9898	-0.06	
SUM1	0.0102	0.9898	-0.07	[1]
SFP1	0.0108	0.9892	-0.11	
BAS1	0.0115	0.9885	-0.05	[1]
HAP3	0.0116	0.9884	-0.18	
YAP7	0.0133	0.9867	-0.07	[1]
GAT1	0.0181	0.9819	-0.13	
ROX1	0.0189	0.9811	-0.14	
TYE7	0.0206	0.9794	-0.10	
SUT1	0.0211	0.9789	-0.13	
HAP4	0.0280	0.9720	-0.11	[1]
ABF1	0.0304	0.9696	-0.04	
SNT2	0.0372	0.9628	-0.19	
PHD1	0.0383	0.9617	-0.08	[1], [2]
LEU3	0.0394	0.9606	-0.21	
NRG1	0.0399	0.9601	-0.07	
NDD1	0.0414	0.9586	-0.08	[1], [2]
MSN4	0.0455	0.9545	-0.08	[1], [2]
INO2	0.0491	0.9509	-0.10	
DAL82	0.0826	0.9174	-0.06	
UME6	0.0916	0.9084	-0.07	
CIN5	0.1134	0.8866	-0.04	
TEC1	0.1390	0.8610	-0.04	
ACE2	0.1581	0.8419	-0.07	
REB1	0.1727	0.8273	-0.07	
RCS1	0.1794	0.8206	-0.06	
RAP1	0.1799	0.8201	-0.03	
GLN3	0.2268	0.7732	-0.02	
GCN4	0.2303	0.7697	-0.02	
HAP1	0.2603	0.7397	-0.04	
HSF1	0.2621	0.7379	-0.02	
SWI4	0.2775	0.7225	-0.01	
SWI5	0.3064	0.6936	-0.02	

RFX1	0.3182	0.6818	-0.05
DIG1	0.3199	0.6801	-0.01
AFT2	0.3244	0.6756	-0.02
FHL1	0.3686	0.6314	-0.01
YAP1	0.4085	0.5915	-0.02
RGT1	0.4147	0.5853	-0.01
FKH1	0.4482	0.5518	0.00
SPT23	0.4520	0.5480	0.00
STE12	0.4631	0.5369	0.00
MBP1	0.6656	0.3344	0.01
MET32	0.6747	0.3253	0.03
GAL4	0.6809	0.3191	0.05
MSN2	0.7254	0.2746	0.05
CAD1	0.7856	0.2144	0.05
RPN4	0.7952	0.2048	0.04
MCM1	0.8582	0.1418	0.03
MOT3	0.8735	0.1265	0.10
ADR1	0.9311	0.0689	0.09
STB1	0.9605	0.0395	0.12

The comments of this table are the same as those of Supplementary Table 1.

Supplementary Table 3. T-test p-values and differences of predicted occupancy between functional and spurious sites predicted by Nu-OSCAR at 95% sensitivity level.

TF Name <sup>1</sup>	Lower Occupancy P-value	Higher Occupancy P-value	Difference in Occupancy
HAP2	0.0002	0.9998	-0.18
HAP5	0.0022	0.9978	-0.11
INO2	0.0414	0.9586	-0.15
SOK2	0.0536	0.9464	-0.13
NRG1	0.0663	0.9337	-0.06
SWI5	0.1055	0.8945	-0.11
HAP3	0.1516	0.8484	-0.06
UME6	0.1811	0.8189	-0.11
GCN4	0.1877	0.8124	-0.07
INO4	0.1904	0.8096	-0.12
HSF1	0.1938	0.8062	-0.04
SKN7	0.1947	0.8053	-0.07
ADR1	0.2200	0.7800	-0.01
DAL82	0.2328	0.7672	-0.08
LEU3	0.2363	0.7637	-0.09
PHD1	0.2385	0.7615	-0.06
SUT1	0.2436	0.7564	-0.08

AFT2	0.2856	0.7144	-0.05
ABF1	0.2964	0.7036	-0.07
YAP7	0.2998	0.7002	-0.03
GLN3	0.3085	0.6915	-0.04
TEC1	0.3159	0.6841	-0.03
NDD1	0.3187	0.6813	-0.07
FKH2	0.3233	0.6767	-0.03
DIG1	0.3361	0.6639	-0.02
FKH1	0.3865	0.6135	-0.01
SPT23	0.4333	0.5667	-0.01
MCM1	0.4381	0.5619	-0.02
STE12	0.4536	0.5464	-0.01
MBP1	0.5167	0.4833	0.00
RGT1	0.5521	0.4479	0.01
CBF1	0.5674	0.4326	0.02
MSN4	0.6043	0.3957	0.03
CIN5	0.7111	0.2889	0.03
MSN2	0.7767	0.2233	0.07
MOT3	0.7783	0.2217	0.06
SWI6	0.7864	0.2136	0.08
PHO4	0.7931	0.2069	0.06
SWI4	0.9088	0.0912	0.09
TYE7	0.9393	0.0607	0.09
FHL1	0.9444	0.0556	0.14
REB1	0.9510	0.0490	0.13
STB1	0.9896	0.0104	0.14

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<sup>1</sup> Results are not shown for TFs with the number of false positives smaller than one.

Other notes are the same as Supplementary Table 1.