Table S1. Binding site PWM models used in our study. Values are the length (8.7±2.6 bp, mean±s.d.), GC content (0.53±0.19) and mean information content (I) per position (1.33±0.29) of each PWM (after processing as described in Protocol S1). The value of I can vary between 0 and 2, and is a measure of the energy contribution of a position to TF binding. Each PWM is summarized by its canonical sequence: "." indicates a position with $I = 0$; "[/]" indicates bases with the same weight at a given position. Letters in parentheses after TF names indicate the study from which we took the PWM data: B, Badis *et al.* (2008); H, Harbison *et al.* (2004); M, MacIsaac *et al.* (2006); Zhu *et al.* (2009).

TF (Study)	Length	GC content	Information	Canonical sequence
ABF1 (B)	14	0.4965	0.810	TCGTATAAAGTGAT
ABF1 (H)	12	0.4035	0.745	TCACTATATACG
ABF1 (M)	13	0.4878	1.016	ATCACTATGCACG
ABF2 (B)	6	0.3571	1.772	TCTAGA
ACE2 (B)	7	0.7096	1.362	ACCAGCA
ACE2 (M)	8	0.6029	0.876	AACCAGCA
ADR1 (H)	5	0.7856	1.366	GG[A/G]G[G/T]
AFT1 (Z)	9	0.5536	1.295	ATTGCACCC
AFT2 (B)	8	0.7140	1.437	CACACCCC
AFT2 (H)	6	0.7342	1.085	GGGTGC
AFT2 (M)	7	0.7480	1.217	GGCACCC
ARG80 (M)	6	0.5650	1.518	AGACGC
ARG81 (M)	8	0.4725	1.370	GTGACTCA
ARO80 (M)	22	0.6293	1.417	CGAGGGTAGCCGCGAGTTGCCG
ARO80 (Z)	8	0.5990	1.202	CTCGGCAA
ARR1 (H)	7	0.1601	1.719	TTACTAA
ARR1 (M)	8	0.2780	1.015	ACTTGAAT
ASG1 (B)	6	0.6713	1.479	CCGGAA
ASG1 (Z)	15	0.7371	0.851	CCGGCCGAGTTCCGG
ASH1 (H)	6	0.4206	1.573	[C/T]TGACT
ASH1 (M)	10	0.6674	1.025	CCGGATCGGG
AZF1 (B)	7	0.2411	1.520	AAAAGAA
AZF1 (H)	15	0.2743	0.969	TTTTTCTTTTTCTGT
AZF1 (M)	18	0.4340	0.810	TTTTTCTTTTCCTGTGTC
BAS1 (H)	6	0.4970	1.741	TGACTC
BAS1 (M)	7	0.5390	1.375	TGACTCG

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TF (Study)	Length	GC content	Information	Canonical sequence
BAS1 (Z)	9	0.6012	1.394	CCAGAGTCA
CAD1 (H)	9	0.2965	1.328	TTAGTAAGC
CAD1 (M)	10	0.3259	1.161	GCTTACTAAT
CAT8 (B)	5	0.8647	1.706	CCGGA
CBF1 (B)	8	0.5972	1.565	GCACGTGA
CBF1 (M)	8	0.6239	1.627	GTCACGTG
CBF1 (Z)	10	0.6033	1.112	GTCACGTGAC
CEP3 (B)	7	0.5263	1.652	CTCGGAA
CEP3 (Z)	8	0.4902	1.207	TTCGGAAA
CHA4 (B)	8	0.7500	1.399	GGCGGAGA
CHA4 (M)	8	0.5897	1.201	GCGATGAG
CHA4 (Z)	9	0.6319	1.199	ATCTCCGCC
CIN5 (H)	8	0.2178	1.152	TTACGTAA
CIN5 (M)	9	0.3193	0.978	CTTACGTAA
CRZ1 (B)	9	0.6821	0.917	CTAAGCCAC
CRZ1 (M)	7	0.7066	1.611	GAGGCTG
CST6 (B)	8	0.4605	1.419	ATGACGTA
CST6 (M)	6	0.3405	1.488	GCATTT
CUP9 (B)	8	0.3974	1.292	TGACACAT
DAL80 (B)	7	0.3849	1.567	CGATAAG
DAL81 (H)	19	0.6253	1.721	AAAAGCCGCGGGCGGGATT
DAL82 (B)	9	0.5643	1.043	AATGTGCGC
DAL82 (H)	7	0.3427	1.445	GATAAGA
DAL82 (M)	9	0.4414	0.984	AAAGATGCG
DIG1 (M)	12	0.3952	0.663	AAATATGAAACA
DOT6 (B)	5	0.5050	1.619	CGATG
ECM22 (B)	7	0.6429	1.331	CTCCGGA
ECM22 (M)	7	0.2973	1.740	GTATAAG
ECM22 (Z)	12	0.7252	1.033	CGGGTGGCCGGA
ECM23 (B)	6	0.3913	1.236	AGATCT
FHL1 (Z)	8	0.5438	1.326	GACGCAAA
FKH2 (B)	7	0.2679	1.922	GTAAACA
FKH2 (H)	11	0.2606	0.986	AAAAGTAAACA
FKH2 (Z)	8	0.2242	1.591	GTAAACAA

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TF (Study)	Length	GC content	Information	Canonical sequence
FZF1 (B)	6	0.3333	2.000	CTATCA
GAL4 (H)	17	0.5744	0.431	CGGAAAAATATACTCCG
GAL4 (M)	17	0.7258	0.967	CGGAGGACAGTGCCCCG
GAL4 (Z)	19	0.6601	0.692	TCGGG . . . . CCGA
GAT1 (H)	7	0.3158	1.552	AGATAAG
GAT1 (Z)	8	0.4218	1.498	CCTTATCG
GAT3 (B)	7	0.4056	1.046	AGATCTA
GAT3 (M)	8	0.2771	1.371	ATAACATG
GAT4 (Z)	8	0.3227	1.478	TAGATCTA
GCN4 (M)	8	0.4194	1.337	ATGACTCA
GCN4 (Z)	7	0.4203	1.609	TGAGTCA
GCR1 (H)	9	0.6585	1.622	GGCTTCC[A/T]C
GCR1 (M)	8	0.6821	1.474	GGGCTTCC
GCR2 (M)	7	0.5798	1.369	GCTTCCA
GIS1 (B)	7	0.6151	1.403	CCCCTAA
GLN3 (B)	5	0.2543	1.562	GATAA
GLN3 (H)	9	0.3223	1.129	GATAAGATA
GLN3 (M)	8	0.4293	0.980	AGATAAGA
GLN3 (Z)	13	0.3963	1.005	TTAGGCCTTATCA
GSM1 (Z)	9	0.5997	1.274	AAACTCCGG
GTS1 (M)	6	0.3558	1.527	TACCAA
GZF3 (H)	6	0.3416	1.720	GATAAG
GZF3 (Z)	8	0.3786	1.598	CTGATAAG
HAC1 (B)	7	0.5617	1.642	GACACGT
HAC1 (H)	11	0.6729	1.639	G[A/C]CAGCGTGTC
HAC1 (M)	10	0.5089	1.541	AGGACACGTA
HAL9 (B)	5	0.6721	1.713	CGGAA
HAP1 (H)	11	0.5372	1.086	GGAAATATCGG
HAP1 (M)	10	0.5625	0.807	CGATAACGCC
HAP2 (H)	5	0.4048	1.721	CCAAT
HAP2 (M)	8	0.4946	1.143	CCAATGAG
HAP4 (H)	9	0.4485	0.873	GACCAATCA
HAP4 (M)	8	0.4460	1.380	CCAATCAG
HCM1 (B)	8	0.2595	1.112	ATAAACAA

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TF (Study)	Length	GC content	Information	Canonical sequence
HMRA2 (B)	8	0.2991	1.341	CATGTAAT
HSF1 (B)	8	0.3984	1.272	ATGGAACA
HSF1 (H)	13	0.3715	0.704	TTCTATAACATTC
IME1 (M)	8	0.8579	1.672	CCGCCGAG
INO2 (H)	7	0.5757	1.325	CACATGC
INO2 (M)	9	0.4971	1.354	GCATGTGAA
INO4 (H)	8	0.4133	1.319	CATGTGAA
IXR1 (M)	15	0.6214	1.380	AAGCCGGAAGCGGGG
LEU3 (B)	10	0.7536	1.224	CCGTTACCGG
LEU3 (H)	10	0.7506	1.082	CCGGTACCGG
LEU3 (Z)	9	0.6505	1.165	ACCGGCGAA
LYS14 (B)	8	0.4757	1.447	CCGGAATT
LYS14 (Z)	8	0.3886	1.706	AAATTCCG
MAC1 (H)	7	0.4320	1.721	GAGCAAA
MAC1 (M)	9	0.4837	0.886	GAGCGAAAA
MATA1 (M)	7	0.3610	1.591	[A/G]CACAAT
MATALPHA2 (Z)	8	0.2635	1.566	AACAATAG
MBP1 (B)	6	0.7109	1.191	ACGCGT
MBP1 (H)	7	0.6417	1.327	GACGCGT
MBP1 (Z)	8	0.6266	1.494	ACGCGTCA
MCM1 (H)	12	0.4435	0.691	TTCCTAATTAGG
MCM1 (Z)	12	0.4647	0.732	TCCCAATTCGGA
MET28 (M)	6	0.6621	1.708	CTGTGG
MET31 (B)	9	0.6745	1.232	[A/G]GTGTGGCG
MET31 (H)	9	0.4471	1.721	AAACTGTGG
MET31 (M)	7	0.6041	1.419	GGTGTGG
MET32 (B)	7	0.6674	1.291	CGCCACA
MET32 (M)	9	0.5688	1.641	AACTGTGGC
MET32 (Z)	9	0.6486	1.513	AGTGTGGCG
MET4 (H)	13	0.4695	1.279	AAAAAATGTGGTG
MET4 (M)	8	0.5271	1.720	AACTGTGG
MGA1 (Z)	9	0.3672	1.194	ATAGAACAC
MIG1 (B)	6	0.8992	1.511	CCCCGC
MIG1 (M)	10	0.5494	1.229	AAAAG[C/T]GGGG

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TF (Study)	Length	GC content	Information	Canonical sequence
MIG1 (Z)	8	0.7577	1.489	ATGCGGGG
MIG2 (Z)	9	0.6774	1.433	CCCCGCAAT
MOT3 (H)	6	0.4738	1.343	[A/C/T]AGG[C/T]A
MSN2 (B)	5	0.8783	1.733	AGGGG
MSN2 (H)	9	0.7076	1.297	AAGGGGCGG
MSN2 (M)	7	0.7322	1.379	AAGGGGC
MSN4 (H)	6	0.7379	1.572	[A/C]AGGGG
NDD1 (H)	13	0.4831	0.827	TTTCCCAATTGGG
NDD1 (M)	10	0.4612	1.046	AAAGGGGAAA
NDT80 (Z)	9	0.3908	1.373	GCCACAAAA
NHP10 (B)	8	0.8500	1.490	GCCGGGGA
NHP6A (Z)	10	0.1542	0.892	CTATATATAA
NHP6B (Z)	12	0.1860	0.575	TATTTATATATA
NRG1 (H)	7	0.7019	1.490	GGACCCT
NRG1 (Z)	8	0.6600	1.570	CAGGGTCC
OAF1 (B)	8	0.5982	1.263	CGGAGATA
OAF1 (Z)	9	0.4490	1.121	TAAATCCGA
OPI1 (H)	7	0.5000	1.594	TCGAA[C/T]C
OPI1 (M)	6	0.6020	1.636	GAACCG
PBF2 (Z)	8	0.5923	1.426	CTCATCGC
PDR1 (B)	8	0.7917	1.251	TCCGCGGA
PDR1 (H)	8	0.5249	1.250	GCCGAATA
PDR1 (M)	9	0.6619	1.189	CCGCCGAAA
PDR3 (H)	8	0.7378	1.720	TCCGCGGA
PDR8 (B)	8	0.5721	1.536	[A/G]CGGAGAT
PHD1 (B)	7	0.5956	1.095	CCTGCAG
PHD1 (H)	8	0.7951	0.868	GCTGCAGG
PHD1 (M)	6	0.6442	1.271	AGGCAC
PHD1 (Z)	9	0.4736	1.118	CATGCATCA
PHO2 (B)	6	0.0141	1.226	ATAATA
PHO2 (H)	11	0.7657	1.320	CGTGCGGTGCG
PHO2 (M)	6	0.1725	1.328	ATTAAG
PHO2 (Z)	8	0.0733	0.973	ATTAATTA
PHO4 (B)	7	0.7383	1.048	GCGCGTG

Continued on next page

TF (Study)	Length	GC content	Information	Canonical sequence
PHO4 (H)	7	0.6518	1.321	CACGTGG
PHO4 (Z)	8	0.6863	1.364	GCACGTGC
PUT3 (B)	8	0.7943	1.312	CCCGGGAA
PUT3 (H)	16	0.6785	0.645	CGG . . . . CCG
PUT3 (M)	9	0.7589	1.721	CGGGAAGCC
PUT3 (Z)	8	0.7047	0.983	TCCCGGGA
RAP1 (B)	9	0.4864	1.310	ACCCATACA
RAP1 (M)	10	0.5890	1.175	ACCCATACAC
RAP1 (Z)	8	0.6003	1.296	GGGTGTAC
RDR1 (B)	8	0.6027	1.496	TGCGGAAC
RDR1 (Z)	8	0.5681	1.244	TGCGGATA
RDS1 (B)	7	0.9361	1.393	CGGCCG[A/C/G]
RDS1 (Z)	8	0.7921	1.620	TCGGCCGA
RDS2 (B)	7	0.7444	1.452	CTCGGGG
RDS2 (Z)	9	0.4640	1.225	AAAACCCGA
REB1 (B)	8	0.5250	1.668	GTTACCCG
REI1 (B)	7	0.7381	1.648	CCCCTGA
RFX1 (B)	8	0.4952	1.415	GGTTGC[C/T]A
RFX1 (H)	13	0.4651	1.195	TTGCCATGGCAAC
RGT1 (H)	7	0.5680	1.229	CGGA . . A
RGT1 (M)	8	0.3684	1.844	CGGAAAAA
RGT1 (Z)	9	0.4041	1.360	CGGAAAAAT
RIM101 (B)	7	0.6458	1.758	CGCCAAG
RIM101 (H)	7	0.5680	1.721	TGCCAAG
RLM1 (H)	10	0.2145	1.367	CTA[A/T][A/T][A/T][A/T]TAG
RLM1 (M)	9	0.2591	1.012	TATTTATAG
RLR1 (H)	11	0.2196	1.287	ATTTTCTTCTT
RLR1 (M)	13	0.3751	1.442	ACAGTACTTACAG
RME1 (M)	10	0.4143	0.960	TCCAAAGGAA
ROX1 (B)	5	0.2008	1.976	ACAAT
ROX1 (H)	9	0.3414	1.425	[C/T][C/G][C/T]ATTGTT
ROX1 (M)	9	0.6305	0.951	AAAAGCCCG
RPH1 (B)	8	0.5625	1.467	ACCCCTAA
RPH1 (H)	10	0.5952	1.721	CCCCTTAAGG

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TF (Study)	Length	GC content	Information	Canonical sequence
RPH1 (Z)	8	0.4977	1.333	ATTAGGGG
RPN4 (B)	7	0.8078	1.633	GGTGGCG
RPN4 (H)	8	0.6124	1.599	TTGCCACC
RPN4 (M)	9	0.5944	1.543	GGTGGCAAA
RPN4 (Z)	8	0.8655	1.689	CGCCACCC
RSC3 (B)	5	0.9364	1.531	CGCGC
RSC3 (Z)	12	0.7270	0.971	CGCGCGCTCTGT
RSC30 (B)	8	0.9423	1.260	CGCGCGCG
RSC30 (Z)	10	0.9026	1.115	CGCGCGCGCG
RTG3 (H)	6	0.6584	1.720	GGTCAC
RTG3 (M)	8	0.5221	1.291	ATGACGCA
RTG3 (Z)	8	0.6791	1.391	GCACGTGC
SFL1 (M)	8	0.5000	1.708	GAAGCTTC
SFL1 (Z)	9	0.3694	0.976	ATAGAAGAA
SFP1 (M)	9	0.5466	1.264	ATGTACGGG
SFP1 (Z)	9	0.0822	1.172	AAAAATTTT
SIG1 (B)	5	0.0103	1.827	ATATA
SIG1 (H)	12	0.3021	1.247	AGGAA[A/T]CAAAAA
SIP4 (B)	7	0.7016	1.241	CTCCGGA
SIP4 (H)	11	0.5428	1.119	CGGATTAATGG
SIP4 (Z)	8	0.5761	1.214	TTCCGGAA
SKN7 (B)	5	0.9012	1.557	GGCCA
SKN7 (H)	9	0.8154	0.712	GCCTGGGCC
SKN7 (M)	8	0.8377	0.955	GCCGGGCC
SKN7 (Z)	16	0.4965	0.461	AGTTATGGCCATATCT
SKO1 (H)	6	0.5000	1.721	ACGTCA
SKO1 (M)	7	0.4761	1.353	TACGTCA
SMP1 (H)	14	0.2281	1.468	ACTACTA[A/T][A/T][A/T][A/T]TAG
SMP1 (Z)	10	0.2199	0.715	CTATAATTAA
SNF1 (M)	15	0.6573	1.808	GGGGATCGAACCCGG
SNT2 (H)	9	0.6591	1.203	GGCGCTATC
SOK2 (B)	9	0.5326	0.881	ACCTGCAGG
SOK2 (H)	8	0.5737	0.817	TGCAGGAA
SOK2 (M)	8	0.5875	1.096	GCAGGCAA

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TF (Study)	Length	GC content	Information	Canonical sequence
SPT15 (Z)	10	0.1534	1.260	GATATATATA
SPT2 (H)	10	0.3212	1.128	CCTGTATTTA
SPT2 (M)	10	0.2531	1.086	AATTAAAGAA
SPT23 (H)	8	0.1951	1.212	AAAATCAA
SRD1 (Z)	8	0.4117	1.696	AGATCTAC
STB1 (H)	9	0.5186	0.868	AAACGCGAA
STB1 (M)	8	0.5211	1.463	CGCGAAAA
STB2 (M)	8	0.6058	1.364	CGGGTAAG
STB3 (Z)	9	0.1468	1.491	AATTTTTCA
STB4 (H)	9	0.5947	1.192	TCGG[A/T][A/T]CGA
STB5 (B)	8	0.5856	1.072	CGGTGTTA
STB5 (H)	9	0.4581	1.149	CGGTGTTAT
STB5 (M)	10	0.5053	0.947	CGGTGTTATA
STE12 (B)	7	0.3095	1.867	TGAAACA
STP1 (H)	12	0.8173	1.216	CGGC . . .[A/G]CGGC
STP1 (M)	8	0.8396	1.279	TGCGGCGG
STP2 (Z)	8	0.7897	1.246	GCGCCGCA
STP3 (B)	9	0.5964	1.220	GCTAGCGCA
STP4 (M)	14	0.8355	1.457	CGCCGTGGGACGCG
STP4 (Z)	10	0.6270	1.096	GTGCGGCTGA
SUM1 (B)	8	0.0700	1.127	AAATTTTT
SUM1 (H)	9	0.4243	0.818	TGTCAGAAA
SUM1 (Z)	8	0.0154	1.079	AATTAATT
SUT1 (H)	10	0.8387	0.694	GCGGGGCCGG
SUT1 (M)	7	0.8536	1.021	CGCGGGG
SUT2 (Z)	8	0.5272	1.644	AACTCCGA
SWI4 (B)	8	0.5337	1.492	ACGCGAAA
SWI5 (B)	8	0.6202	1.423	TGCTGGTT
SWI5 (H)	6	0.6586	1.425	[G/T]GCTG[A/G]
SWI5 (M)	6	0.7152	1.050	TGCTGG
SWI6 (M)	6	0.7675	1.425	GACGCG
TBF1 (B)	7	0.5349	1.246	AACCCTA
TBF1 (Z)	8	0.4219	1.651	AACCCTAA
TBS1 (Z)	8	0.7561	1.706	CGGATCCG

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TF (Study)	Length	GC content	Information	Canonical sequence
TEA1 (B)	8	0.7062	1.166	GCGG[A/G]CAT
TEA1 (Z)	15	0.3749	1.239	CGGAAATTAAATACC
TEC1 (H)	7	0.3790	1.267	AAGAATG
TEC1 (M)	7	0.4341	1.400	ACATTCT
TEC1 (Z)	8	0.3856	1.451	ACATTCTT
THI2 (H)	12	0.3359	0.898	GAAACTCTAAGA
TOS8 (B)	8	0.4111	1.288	CTGTCAAA
TYE7 (B)	7	0.5857	1.700	CACGTGA
TYE7 (Z)	8	0.5265	1.361	TCACGTGA
UGA3 (B)	8	0.8281	1.371	CGGCGGGA
UGA3 (H)	10	0.7856	1.032	CCG . . . . CGG
UME1 (H)	11	0.2669	1.240	AAGGAAAAGTA
UME6 (B)	8	0.7422	1.159	CGCGGC[A/T]A
UME6 (M)	9	0.7749	1.397	AGCCGCCGA
UME6 (Z)	8	0.7109	1.439	GGCGGCTA
UPC2 (B)	6	0.4080	1.420	ATACGA
USV1 (Z)	8	0.6231	1.703	CCCCTGAA
XBP1 (B)	6	0.5248	1.482	CTCGAG
XBP1 (H)	7	0.5680	1.721	CTTCGAG
XBP1 (M)	8	0.6270	1.346	CTCGAGGA
XBP1 (Z)	8	0.5310	1.224	TCTCGAGA
YAP1 (H)	8	0.3250	1.435	TTAGTCAG
YAP1 (M)	9	0.4232	1.152	GCTGACTAA
YAP3 (B)	8	0.3317	1.552	ATTACGTA
YAP5 (M)	6	0.3216	1.344	AAGCAT
YAP6 (M)	8	0.2860	1.160	TTACATAA
YAP6 (Z)	10	0.3454	0.890	GATTACGTAA
YAP7 (H)	8	0.2395	1.099	ATTAGTAA
YBL054W (B)	8	0.6875	1.367	CGATGCCC
YBR239C (B)	8	0.5662	1.427	ACCGGAAC
YDR026C (H)	8	0.6427	1.843	TTACCCGG
YDR026C (M)	6	0.8331	1.992	ACCCGG
YDR520C (M)	9	0.8800	1.561	CTCCGGCGG
YDR520C (Z)	8	0.4968	1.758	CGGAGATA

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TF (Study)	Length	GC content	Information	Canonical sequence
YER051W (M)	6	0.3004	1.787	TTCGAA
YER130C (Z)	8	0.5021	1.646	AATAGGGG
YER184C (B)	8	0.6635	1.157	CTCCGGAA
YGR067C (Z)	8	0.7498	1.507	GCGGGGTA
YHP1 (H)	6	0.1828	1.720	TAATTG
YJL103C (B)	8	0.7300	0.958	CTCCGGAG
YKL222C (B)	8	0.5208	1.284	ACGGAAAT
YKL222C (Z)	8	0.4764	1.292	CGGAAATA
YLL054C (B)	7	0.8061	1.220	CGGCCGA
YLL054C (Z)	18	0.6200	0.554	TCCGT . . . . CGGA
YLR278C (B)	8	0.5915	1.322	CCGGAGTT
YML081W (B)	7	0.7921	1.543	CCCCGCA
YML081W (M)	9	0.4941	1.648	CCAGTCTGA
YML081W (Z)	8	0.7449	1.516	ACCCCGCA
YNR063W (Z)	8	0.5062	1.494	ATCTCCGA
YOX1 (H)	10	0.2621	1.459	A[C/G]AATA . TGA
YOX1 (M)	19	0.4060	1.441	ATTACGTTTCCTAAAAGGG
YOX1 (Z)	8	0.1038	1.378	TTAATTAA
YPR013C (B)	8	0.4492	1.332	TGTAGATC
YPR015C (Z)	8	0.3621	1.708	CGTAAATC
YPR022C (B)	6	0.7760	1.789	CCCCAC
YPR196W (Z)	9	0.4423	0.949	ATTTCTCCG
YRR1 (B)	9	0.4627	1.070	TTATCTCCG
YRR1 (M)	11	0.4248	1.379	TTTTGTTACCC
YRR1 (Z)	9	0.3695	1.515	CGGAAATAA
ZAP1 (H)	14	0.4331	1.625	ACCCT[A/C]AAGGTT[A/G]T
ZAP1 (M)	11	0.4755	1.683	ACCTTAAAGGT
ZMS1 (B)	9	0.6889	1.156	TTCCCCGCA