

Motif	Consensus	Evidence
ABF1	-CGT---ARTGAT	*1
ACE2	A--RAACCAGCA	*2
AFT1	---A-CACCC---TT	*3
ARO80	CGGY-A-Y--CGG-WA	*1
AT_repeat	TATATATATA	*5
BAS1	RR-A-GAGTCA	*1
CAD1	ATTAGTAAGC	*1 (Yap2)
CBF1	RRTCACGTG-	*1
CIN5	G-TKA--TAAKC	*1 (Yap4)
CSRE	KCCGW-RT-CS-	*5
DAL81	G-G-C--K----CGGC---KS	*1
FKH1	GTAAACAACW	*3
GAL4	CGG---ASA---SKCCG	*1
GCN4	-RRTGASTCA	*1
Gcr1	-RGCTTCCTST	*3
Gis1	AWAGGGAT	*7
HAP4	GRRCCAATCA	*1
HIR2	GMGAA-----GAACR	*1 (CCA)
HSF1	GAW--TTCTAGAA	*1
INO4	CATSTGAAAA	*1
LEU3	GCCGGT-CCGG	*1
LYS14	TTCCMMYGAATTT	*5
MAC1	TGAGMAMAAA	*1
MBP1	RACGCGT-AR-	*1, 6
MCM1	TT-CC--WT--GGAAA	*1, 6
MET31	MWGTGTGGCR	*1
MET4	AMAA-TGTGG	*1
MIG1	CGCATMCCCCAC	*5
MSN24	ARGGGG	*4
ndt80	GACACAAAA	*3
NRG1	S-GGC-MRGAA	*1
OAF1	CGG-GWTAA--M-WWWWWT-CCG	*5
PAC	GCGATGAT-T	*5
PDR3	S--TCCGYGGAA	*5
PHO4	GY--TSKACGTG-G	*5
RAP1	RTGT-YGGRTG	*1
REB1	-SCGGGTAAAY	*1
RFX1	SGT-G-CA-RGCAAC	*1
RPN4	GGTGGCAAAA	*5
RRPE	TGAAAAATTT	*5
SKN7	GGGCC-SG-C	*1
STE12	A---TGAAACA--	*1
STRE	G-RGGGG-GGGG	*5
SUM1	RYGWCASWAAW	*1
SWI4	----CRCGAAAA	*1
Ume6	TCGGCGGCWA	*8
YAP1	GMTTACTAAT	*1
Zap1	ACCYT-AGGTT	*3

Sources:

1. AlignACE on ChIP data of Lee et al, Science 298:799 (2002).
2. Alignace on Fig1A ORFs from Doolin et al, Mol. Microbiol. 40:422 (2001), Ace2 and Swi5 recognize the same site.

3. <http://genetics.med.harvard.edu/~tpilpel/MotifList.html>
4. AlignACE on msn24 regulated genes from Causton et al, Mol. Biol. Cell 12:323 (2001).
5. Hughes et al, JMB 296:1205 (2000).
6. SBF=Swi4+Swi6->SCB MBF=Mbp1+Swi6->MCB MCM1->ECB
7. Gis1 consensus in Pedruzzi et al, EMBO J 19:2569 (2000).
8. Kurdistan et al, Nat. Gen. 31:248 (2002).

IUPAC CODE:

A = adenine
C = cytosine
G = guanine
T = thymine
U = uracil
R = G A (purine)
Y = T C (pyrimidine)
K = G T (keto)
M = A C (amino)
S = G C
W = A T
B = G T C
D = G A T
H = A C T
V = G C A
N = A G C T (any)