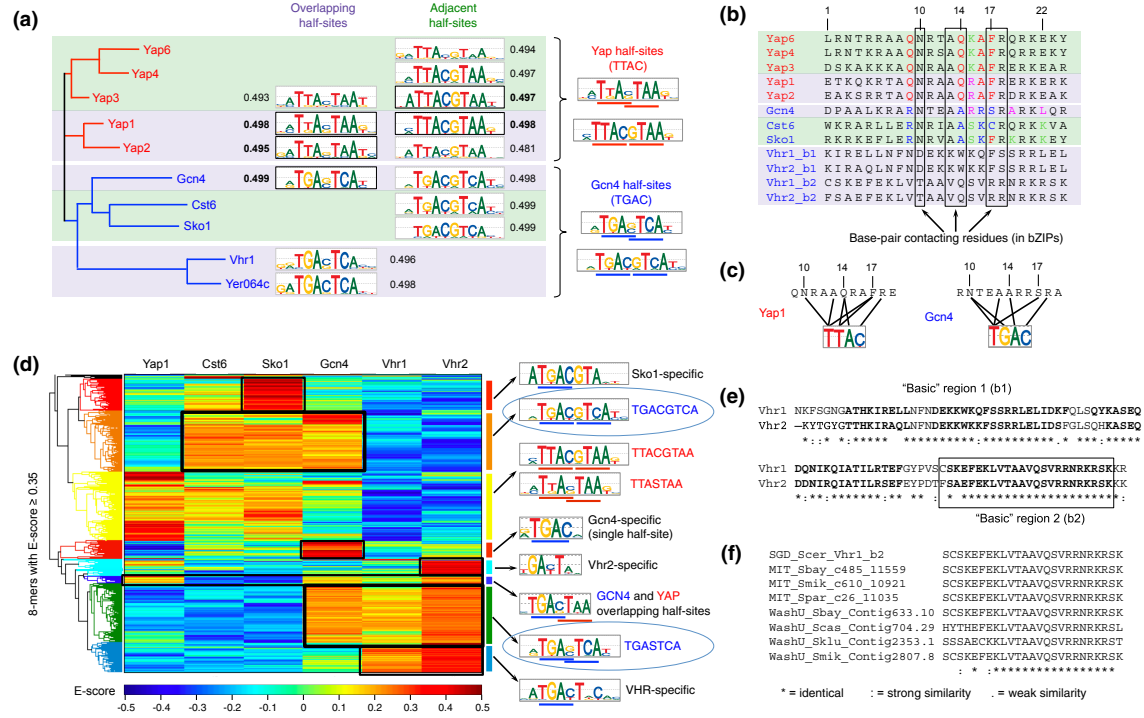

(a)
Overlapping half-sites
Adjacent half-sites
Yap6
Yap4
Yap3
Yap1
Yap2
Gcn4
Cst6
Sko1
Vhr1
Yer064c
0.493
0.498
0.495
0.499
0.496
0.498
0.494
0.497
0.497
0.498
0.481
0.498
0.499
0.499
Yap half-sites (TTAC)
Gcn4 half-sites (TGAC)
(b)
1
10
14
17
22
Yap6 LRNTRRAAQNRTAQKAFRQRKEKY
Yap4 LRNTKRAAQNRSAQKAFRQRREKY
Yap3 DSKAKKKAQNRAAQKAFRERKEAR
Yap1 ETKQKRTAQNRAAQRAFRERKERK
Yap2 EAKSRRTAQNRAAQRAFRDRKEAK
Gcn4 DPAALKRARNTEAAARRSRARKLQR
Cst6 WKRARLLERNRIAASKCRQRKKVA
Sko1 RKRKEFLERNRVAAAKFRKRKKEY
Vhr1_b1 KIRELLNFNDEKKWKQFSSRRLEL
Vhr2_b1 KIRAQLNFNDEKKWKKFSSRRLEL
Vhr1_b2 CSKEFEKLVTAAVQSVRRNRKRSK
Vhr2_b2 FSAEFEKLVTAAVQSVRRNRKRSK
Base-pair contacting residues (in bZIPs)
(c)
10
14
17
QNRAAQRAFRE
Yap1
RNTEAARRSRA
Gcn4
(d)
Yap1
Cst6
Sko1
Gcn4
Vhr1
Vhr2
8-mers with E-score ≥ 0.35
E-score
-0.5
-0.4
-0.3
-0.2
-0.1
0
0.1
0.2
0.3
0.4
0.5
Sko1-specific
TGACGTCA
TTACGTAA
TTASTAA
Gcn4-specific (single half-site)
Vhr2-specific
GCN4 and YAP overlapping half-sites
TGASTCA
VHR-specific
(e)
"Basic" region 1 (b1)
Vhr1 NKPSGNGATHKIRELLNFNDEKKWKQFSSRRLELIDKFQLSQYKASEQ
Vhr2 -KYTGYGTTHKIRAQLNFNDEKKWKKFSSRRLELIDSFGLSQHKASEQ
Vhr1 DQNIKQIATILRTEFGYPVSCSKEFEKLVTAAVQSVRRNRKRSKKR
Vhr2 DDNIRQIATILRSEFEYPDTFSAEFEKLVTAAVQSVRRNRKRSKKK
"Basic" region 2 (b2)
(f)
SGD_Scer_Vhr1_b2 SCSKEFEKLVTAAVQSVRRNRKRSK
MIT_Sbay_c485_11559 SCSKEFEKLVTAAVQSVRRNRKRSK
MIT_Smik_c610_10921 SCSKEFEKLVTAAVQSVRRNRKRSK
MIT_Spar_c26_11035 SCSKEFEKLVTAAVQSVRRNRKRSK
WashU_Sbay_Contig633.10 SCSKEFEKLVTAAVQSVRRNRKRSK
WashU_Scas_Contig704.29 HYTHEFEKLVTAAVQSVRRNRKRSL
WashU_Sklu_Contig2353.1 SSSAECKKLVTAAVQSVRRNRKRST
WashU_Smik_Contig2807.8 SCSKEFEKLVTAAVQSVRRNRKRSK
* = identical
: = strong similarity
. = weak similarity