Supporting Information

Text S1. Supplemental Results

Identification and analyses of bZIP domain sequences from fungal genomes

We carried out HMMER search (1) using the PFAM profile bZIP_1 (PF00170) and identified 123 putative bZIP domain protein sequences from *Candida* clade genomes *C. albicans, C. dubliniensis, C. tropicalis, C. parapsilosis, C. lusitaniae, Lodderomyces elongisporus, C. guilliermondii, Debaryomyces hansenii*, and the *Saccharomyces cerevisiae* and *C. glabrata* genomes. The amino acid sequences of these 123 bZIP domains and that of *S. pombe* Yap1-like protein Pap1 (2) were aligned and a multiple sequence alignment (MSA) was constructed of a minimal region of 38 amino acids that exhibited maximum sequence identity in all bZIP domain sequences. The trimmed sequence began five amino acids amino-terminus to the conserved Asn (N) in the basic region and either continued till the carboxyl-terminus of the protein or until the *d* position of the second heptad of the leucine zipper region (3,4). The MSA revealed that each bZIP domain has the invariant (Asn)-X_2-(Ala)-X_4-(Arg)- X_9-(Leu/Met)- X_6-(Leu/Val)-X_6-(Leu) motif (Fig. S1). The MSA was used to construct a neighbor-joining phylogenetic tree using the MEGA version 4.0 software (5).

Because a total of 52 of the 124 sequences were Yap proteins, a high bit score was obtained for the Yap-specific Gln residue indicated at position 10 in the logo. Furthermore the logo also revealed that the conservation of the Leu residue in the leucine zipper is largely restricted to the first and the second heptads (3,4). The phylogenetic analysis also led to the grouping of the *Candida* clade Yap/bZIP domains into distinct sub-clusters containing one or more *S. cerevisiae* Yap/bZIP domains. The eight *S. cerevisiae* Yaps were grouped into five sub-clusters Yap3, Yap1-Yap2, Yap4-Yap6, Yap8 and Yap5-Yap7 respectively. This clustering is consistent with Yap1-Yap2, Yap4-Yap6 and Yap5-Yap7 domains being paralogous pairs as noted previously (6,7). We also noted that each of the Yap sub-cluster contained two Yap proteins from *C. glabrata* and *S. cerevisiae*, except for the Yap8 branch that had no *C. glabrata* protein. For two of the *Saccharomyces* Yap sub-clusters, Yap8 and Yap5-Yap7, no bZIP domain was identified from the *Candida* clade genomes. For the *Saccharomyces* Yap1-Yap2 and Yap4-Yap6 sub-clusters, one *Candida* clade bZIP domain each was identified, represented by the *C. albicans* orf19.1623 and orf19.861 respectively. Conversely, two *Candida* clade Yap/bZIP domains, represented by the *C. albicans* orf19.681 and orf19.3193 were found in the *Saccharomyces* Yap3 sub-cluster. The *Candida* Yap proteins were named Cap1 (orf19.1623), Cap2 (orf19.681), Cap3 (orf19. 3193) and Cap4 (orf19.861) by retaining the names for Cap1 and Cap3 proteins as they were part of the Yap1 and Yap3 sub-cluster respectively. We assigned Cap4 as a potential Yap4/Yap6-like bZIP domain protein, and the remaining *Candida* Yap protein, orf19.681, was named Cap2.

Identification of the HAP4-like domain bearing bZIP proteins in fungal genomes

To comprehensively identify fungal genomes encoding proteins that contained both a bZIP domain and a HAP4-like domain, we carried out extensive bioinformatics search as follows. We extracted the HAP4-like domain sequences from *S. cerevisiae*, *N. crassa*, *C. neoformans*, *U. maydis*, *K. lactis*, *A. nidulans*, *A. oryzae*, *A. clavatus*, *A. fumigatus*, *Y. lipolytica*, *D. hansenii* and *C. albicans* genomes. An MSA was constructed of the 25 amino acid region, and an HMM profile was generated and was used to search amino acid sequences of all proteins from 62 fungal genomes. The HMMER search identified 131 protein sequences bearing a HAP4L domain with an E-value ≤ 10.0 in 56 of the 62 genomes examined. The bipartite HAP4L-bZIP domain sequences were retrieved from each of the 131 sequences and aligned using MUSCLE. The alignment was visually inspected for sequence conservation and thereafter two core sequences were identified spanning the 15 amino acid HAP4L and the 33 amino acid bZIP domains. The gaps in the alignment between the two domains were purged and a 60 amino acid region that extended from the HAP4L domain up to the 2nd heptad of the bZIP domain was retained for further analyses. Sixty six sequences from 48 genomes had highly conserved residues in the HAP4L domain. It was previously reported that a substitution of the Leu residue in the HAP4L domain led to loss of function of the Hap4 in *Hansenula polymorpha* (8); therefore, we retained only those sequences that had a Leu or Ile residue (none had a Val residue at this position) in the HAP4L domain. Finally, we obtained 47 sequences and constructed a multiple alignment and a phylogenetic tree using the MEGA 4.0 software (5).

SUPPLEMENTARY FIGURE LEGEND

Fig. S1. Multiple Sequence Alignment (MSA) of the bZIP domains from *Candida* clade organisms. (Top) A multiple sequence alignment of the identified bZIP domains from *Candida* clade organisms, *S. cerevisiae* bZIP domains and *S. pombe Pap1* bZIP domain was created using MUSCLE 3.0 software. is included in the MSA for reference. The sequences begin five amino acids to the N-terminus of the conserved asparagine (N) in the basic region and continue until the *'d'* position of the second heptad of the leucine zipper region. (Bottom) A sequence logo (constructed at http://weblogo.berkeley.edu/logo.cgi) generated from multiple sequence alignment of 124 bZIP domains showed the conservation of various residues. The consensus bZIP domain sequence identified from the logo is N-X_2-A-X_4-R-X_9-L/M-X_6-L/V-X_6-L and the highly conserved amino acid residues are indicated by '*' below the alignment.

Table S1. List of plasmids used in this study

Plasmid	Description	Source/Reference
pSN40	*C.m.LEU2*	(9)
pSN52	*C.d.HIS1*	(9)
pSN69	*C.d. ARG4*	(9)
CIp10	*C.a.URA3 RPS1*	(10)
pSFS2A	*caSAT1* Flipper cassette	(11)
pFA-HIS1	*C.a.HIS1*	(12)
pFA-CdHIS1	*C.d.HIS1*	(13)
pFA-CmLEU2	*C.m.LEU2*	(13)
pGEX-5X3	P_{tac} promoter with N-terminal GST	Amersham Biosciences
pET28b+	$T7_{lac}$ promoter with N- and C-terminal 6xHis	Novagen
CIp10-C.d.ARG4	CIp10 with *C.d.ARG4* in place of *C.a.URA3*	This work
pRC1	CIp10 with *C.m.LEU2* in place of *C.a.URA3*	This work
pRC10	*CAP2*-Upflank in pSFS2A	This work
pRC11	*CAP2*-Upflank and Downflank in pSFS2A	This work
pRC20	*CAP2* in CIp10-*C.d.ARG4*	This work
pRC45	*cap2-2* in CIp10-*C.d.ARG4* vector	This work
pRC53	*cap2-2* in CIp10-*C.d.ARG4* vector	This work
pRC60	*cap2-1* in CIp10-*C.d.ARG4* vector	This work
pRC62	*cap2-1* in CIp10-*C.d.ARG4* vector	This work
Ip6	*CAP2ΔC* in pGEX-5X-3	This work
Ip9	*CAP2ΔC* in pET28b+	This work
pSL301	Cloning vector Amp^R	Invitrogen
pNIM1	*ACT1t*	(14)
pPK335	TAP	(15)
Ip18	*C.m.LEU2*	This work
Ip19	*C.d.HIS1*	This work
Ip20	*ACT1t*	This work
Ip21	*C.m.LEU2* TAP *ACT1t*	This work
Ip22	*C.d.HIS1* TAP *ACT1t*	This work
pLITMUS28	Cloning vector Amp^R	New England Biolabs
Ip27	*caSAT1*	This work
pNA7	*caSAT1 CAP2 RPS1*	This work
pNA13	*caSAT1 cap2-2 RPS1*	This work
pNA17	*caSAT1 cap2-1 RPS1*	This work
pSH26-5	*caSAT1-FLIP 6xHIS-2xGly-3xFLAG-ACT1t*	This work

C.a./ca, Candida albicans; *C.d., Candida dubliniensis*; *C.m., Candida maltose.*

CaSAT1-FLIP denotes CaSAT1 Flipper cassette: FRT-MAL2p-CaFLP-ACT1t-CaSAT1-FRT

Table S2. *C. albicans* strains used in this study

Strain	**Relevant Genotype**	**Phenotype**	**Source/Reference**
SN152	*arg4Δ/arg4Δ leu2Δ/leu2Δ his1Δ/his1Δ URA3/ura3Δ::imm*^{434} *IRO1/iro1Δ::imm*^{434}	Arg$^-$ Leu$^-$ His$^-$	(9)
RPC51	SN152 *CAP2/cap2Δ::C.d.HIS1*	Arg$^-$ Leu$^-$	This work
RPC75	SN152 *cap2Δ::C.m.LEU2/cap2Δ::C.d.HIS1*	Arg$^-$	This work
RPC132	SN152 *his1Δ/his1Δ::*<pFA-*HIS1*> *RPS1/rps1::*<pRC1 *C.m.LEU2*>	Arg$^-$	This work
RPC192	RPC75 *RPS1/rps1::*<pRC20 *C.d.ARG4-CAP2*>	Prototroph	This work
RPC206	SN152 *his1Δ/his1Δ::*<pFA-*HIS1*> *RPS1/rps1::*<CIp10-*C.d.ARG4*>	Leu$^-$	This work
RPC278	RPC75 *RPS1/rps1::*<CIp10-*C.d.ARG4*>	Prototroph	This work
RPC286	RPC75 *RPS1/rps1::<pRC53 C.d.ARG4-cap2-2>*	Prototroph	This work
RPC309	RPC75 *RPS1/rps1::<pRC62 C.d.ARG4-cap2-1>*	Prototroph	This work
RPC326	RPC75 *RPS1/rps1::<pRC62 C.d.ARG4-cap2-1>*	Prototroph	This work
RPC391	SN152 *SFU1::SFU1-TAP-C.m.LEU2/ SFU1::SFU1-TAP-C.d.HIS1*	Arg$^-$	This work
RPC422	RPC391 *cap2Δ::FRT /cap2Δ::FRT*	Nou^S Arg$^-$	This work
RPC431	SN152 *hap32::FRT/ hap32::FRT*	Nou^S Arg$^-$ Leu$^-$ His$^-$	This work
RPC434	SN152 *sfu1::C.m.LEU2/ sfu1::C.d.HIS1*	Arg$^-$	This work
RPC445	SN152 *hap31::C.m.LEU2/ hap32::C.d.HIS1*	Arg$^-$	This work
RPC449	RPC445 *hap32::FRT/ hap32::FRT*	Nou^S Arg$^-$	This work
RPC453	SN152 *HAP5::HAP5-TAP-C.m.LEU2/ HAP5::HAP5-TAP-C.d.HIS1*	Arg$^-$	This work
RPC474	RPC434 *cap2Δ::FRT /cap2Δ::FRT*	Nou^S Arg$^-$	This work
RPC506	RPC286 *RPS1/rps1::*<pRC53 *C.d.ARG4-cap2-2* <pNA7 *caSAT1-CAP2*>>	Prototroph, Nou^R	This work
RPC510	RPC278 *RPS1/rps1::*<CIp10-*C.d.ARG4*< pNA7 *caSAT1-CAP2*>>	Prototroph, Nou^R	This work
RPC511	RPC326 *RPS1/rps1::<pRC62 C.d.ARG4-cap2-1* < pNA7 *caSAT1-CAP2*>>	Prototroph, Nou^R	This work
RPC517	RPC286 *RPS1/rps1::*<pRC53 *C.d.ARG4-cap2-2* < pNA17 *caSAT1-cap2-1*>>	Prototroph, Nou^R	This work
RPC521	RPC326 *RPS1/rps1::<pRC62 C.d.ARG4-cap2-1*< pNA13 *caSAT1-cap2-2*>>	Prototroph, Nou^R	This work
RPC552	SN152 *HAP5::HAP5-His*$_6$*-FLAG*$_3$*-caSAT1-FLIP/ HAP5*	Nou^R Arg$^-$ Leu$^-$ His$^-$	This work
RPC562	RPC431 *HAP5::HAP5-TAP-C.m.LEU2/ HAP5::HAP5-TAP-C.d.HIS1*	Nou^R Arg$^-$	This work
087	SN152 *hap2Δ::C.m.LEU2/hap2Δ::C.d.HIS1*	Arg$^-$	(16)
093	SN152 *hap5Δ::C.m.LEU2/hap5Δ::C.d.HIS1*	Arg$^-$	(16)

CaSAT1-FLIP denotes CaSAT1 Flipper cassette: FRT-MAL2p-CaFLP-ACT1t-CaSAT1-FRT

Table S3. Oligonucleotides used in this study

Primer Name	Sequence (5’-3’)	Description
ONC2	TAGAGGCACTCATGCTCACGGTT GTTCAAATTGAAATTCTAA	Rev Primer for amplifying upflank of *CAP2*
ONC3	TCATAGCCAACACAGGGCGATGA CTTACAGTATGAAGTATTTCC	Fwd Primer for amplifying upflank of *CAP2*
ONC4	TGTTGTCAAGATTGTCTTGC	Rev Primer for amplifying upflank of *CAP2*
ONC5	CGTGAGCATGAGTGCCTCTAACCAGTGTGATGGATATCTGC	Fwd Primer for amplifying Selectable markers from pSN40/pSN52
ONC6	TCGCCCTGTGTTGGCTATGA AGCTCGGATCCACTAGTAACG	Rev Primer for amplifying Selectable markers from pSN40/pSN52
ONC7	CATCAGCAAATGAAGTTGTG	Fwd Primer for diagnostic PCR; bind to *CAP2* 5’ UTR
ONC8	AAACAAGCACTTACTCGATG	Rev Primer for for diagnostic PCR; bind to *CAP2* 3’ UTR
ONC9	CGGAATTCCATGCCCGCAAAAGGTCCT	Fwd Primer for *CAP2*; bears EcoRI site
ONC10	GCCGCTCGAGGCAGAAGCTGTAGAAGCT	Rev Primer for *CAP2*; bears XhoI site
ONC19	AAAGAAACAATTTCCTTTTG	Fwd Primer for amplifying upflank of *CAP2*
ONC30	ATTTCTTCCATGGTTAACAG	Rev Primer for *C.d.HIS1*
ONC33	GATATCATTTCCGATGAAGC	Rev Primer for *C.m.LEU2*
ONC40	TGTTGTCTAGATTGTCTTGC	Rev Primer for CAP2 locus
ONC56	AATTAAAGGTGGAGAACC	Fwd Primer for *CAP2*
ONC57	AGACAAAACAGAAAACGC	Fwd Primer for *CAP2*
ONC58	AACTTTTTATGACGAGAC	Rev Primer for *CAP2*
ONC59	ATGGGCCCAATAAATTACACAAAG C	Fwd Primer for amplifying 5’ *CAP2*; bears ApaI site
ONC60	TTCTCGAGTAGAGGCACTCATGCTCACGTATAATATTAGGACCTTTTGC	Rev Primer for amplifying 5’ *CAP2*; bears XhoI site
ONC61	TTACCGCGGTCATAGCCAACACAGGGCGAAATTAGATAGAAGAGCAT	Fwd Primer for amplifying 3’ *CAP2*; bears SacII site
ONC62	ATG AGC TCT TGT CAA GAT TGT CTT GC	Rev Primer for amplifying 3’ *CAP2*; bears SacI site
ONC66	AACCTTTCCACAAACTGA CG	Rev primer for diagnostic PCR; binds to *caFLP* region in *SAT1* flipper cassette
ONC81	ATTCTTTGAATAACCCTC	Fwd Primer for *CAP2*
ONC91	GAAGTTCCTATTCTCTAGAAAGTATA	Rev primer for diagnostic PCR; binds to FRT region in *SAT1* flipper cassette
ONC101	TCTCACAAACAATTAGTCTCC GA	Fwd Primer for *CAP2* locus
ONC140	TCT TGG TGA GAA CAG CGA CCG AAA	Rev Primer for amplifying up-split fragment of *HAP32* disruption cassette
ONC141	GGA GCG ATA AGC GTG CTT CTG CCG	Fwd Primer for amplifying down-split fragment of *HAP32* disruption cassette
ONC145	CGTATTCACTTAATCCCACAC	Rev Primer for the *RPS1*; binds in 3’-UTR of *RPS1* locus
ONC214	CGTCAAGTGATGTCGATCCCAAGTGTTGATACTCCA	Fwd SDM-HAP4 primer for *CAP2* (sense)
ONC215	TGGAGTATCAACACTTGGGATCGACATCACTTGACG	Rev SDM-HAP4 primer for *CAP2* (anti-sense)
ONC223	ATGTCGATCCCAAGTGTT	Fwd Diagnostic Primer for SDM-HAP4
ONC230	AGCGTCGAAAAGAAAAGCTCAAGAAAGAGCTGCAGGGAGAGCCTCTGAAGAGAGAAGAGCAACCAGAG	Fwd SDM-bZIP primer for *CAP2* (sense)
ONC231	CTCTGGTTGCTCTTCTCTCTTCAGAGGCTCTCCCTGCAGCTCTTTCTTGAGCTTTTCTTTTCGACGCT	Rev SDM-bZIP primer for *CAP2* (antisense)
ONC243	TTTCAACAAAGTCAACCACCGTTTATGAATTTAACGCTATAACAATCATTTAATATATTAGAAGCTTCGTACGCTGCAGGTC	Fwd Primer for *SFU1* disruption
ONC247	ATT TGC AGC TGG TTC AAC	Rev diagnostic primer for *SFU1* disruption
ONC248	CGG TAC CGA CGT GAT CAC CTG GTA	Rev diagnostic primer for *CmLEU2*
ONC249	TCT AAA CTG TAT ATC GGC ACC GC	Rev diagnostic primer for *CdHIS1*
ONC257	AGATGAAAACAAGCCAATCAAGCAAGAAGAACATCGGAGTGCACTTTCTATTGGGAAGTTGTTAAATGGAGGATCCATGGAAAAGAGA	Fwd Primer for TAP tagging of *SFU1*
ONC258	TTCCGATTTTCAATTTTGTTACACAAACATAAATCATGCTCATTAAATGCAAGAAAGGGGATTGTTTTGCGTGTGATGGATATCTGCA	Rev Primer for TAP tagging of *SFU1*
ONC263	AAACAGCTATGACCATGA	Fwd Primer binding to CIp10 vector
ONC264	ATTACCGATGATGCTCCTGGAGAATATGATGACGATGATTGCATTGGTGAATGAGAGAGCTCTGATATCATCGATGAATTCGAG	Rev Primer for *SFU1* disruption
ONC267	GGCGGAAAATGCAAATGGTCATAATGATGAAGCTACGTATGAAAATTTTAACGGTTACCAAAACAATATGGATCCATGGAAAAGAGA	Fwd Primer for TAP tagging of *HAP5*
ONC268	CTAATATCCGAGTGCTTCCGATGAAACAAACCCACCGAAATATCAACTATGTAATCAAGTGAGGAACTGAGTGTGATGGATATCTGCA	Rev Primer for TAP tagging of *HAP5*
ONC269	TACTTGCTCTTGTGGCTCAAAG	Rev diagnostic primer for *HAP5-TAP* tagging
ONC286	TTTTATAATTATTAATAATTTCAAATGAAACCATACAACTAACCCTAATATAGCCATTCAATTAAAAAACGAAGTTCCTATACTTTCTAG	Fwd Primer for *HAP32* disruption

Primer Name	**Sequence (5’-3’)**	**Description**
ONC287	ATACACAGAACTATTTCCTCATTGTACTTTATAACAAATATCACCAAGTTTGGCAAAAAAAAAAACCACAGAAGTTCCTATTCTCTAGAA	Rev Primer for *HAP32* disruption
ONC290	TATTTGCTCACATTCTAATTCACAC	Fwd diagnostic primer for *SFU1* disruption
ONC298	ACC ATA TAT AAC AGA AAT GTG ATA TTT TG	Fwd diagnostic primer for *HAP32* disruption
ONC299	TGG TGT TGA AAC TAT TGA ACT G	Rev diagnostic primer for *HAP32* disruption
ONC307	GCAACGAAAGCTAAGCACCATTAGAAGTAACTACATAATCCAGGTTAAAATAAGAATATTGAAGCTTCGTACGCTGCAGGTC	Fwd Primer for *HAP31* disruption
ONC308	AATAAATAATAACGTTTGCATTGGCCTATATCAAATTATATCTAAATATGGAAAATATGATCTGATATCATCGATGAATTCGAG	Rev Primer for *HAP31* disruption
ONC309	TTGTGTTAATGACAATTCCCTCG	Fwd Diagnostic primer for *HAP31* disruption
ONC310	AAC CTA GGC TTT GAG GGA C	Rev Diagnostic primer for *HAP31* disruption
ONC315	TCT CTC TCT AAA GGC TCT CTG	Rev Diagnostic Primer for SDM-bZIP with wild type sequence
ONC316	TCT CTT CAG AGG CTC TCC C	Rev Diagnostic Primer for SDM-bZIP with mutant sequence
ONC460	GCAAATGGTCATAATGATGAAGCTACGTATGAAAATTTTAACGGTTACCAAAACAATTATCATCATCACCATCATCATGGT	Fwd Primer for His$_6$-FLAG$_3$ tagging of *HAP5*
ONC461	ACCGAAATATCAACTATGTAATCAAGTGAGGAACTGAGAACTGATCTTACAAATAAGAGCGCTGGAGCTCCACCGCGGTG	Rev Primer for His$_6$-FLAG$_3$ tagging of *HAP5*
ONC174	CAATAAAACTGGTGGCTCCAATG	Fwd RT-PCR primer for *CAP2*
ONC175	GCATCTGCACATGGAATGAAA	Rev RT-PCR primer for *CAP2*
ONC176	TGCTCGTGTACCTGCTGTTTG	Fwd RT-PCR primer for *SCR1*
ONC177	ACACTGATTACTCTAGCGTTCAGAATTC	Rev RT-PCR primer for *SCR1*
ONC198	AAGAAATGGTTTGACGGAAGAAC	Fwd RT-PCR primer for *HMX1*
ONC199	GAAATATGTCCAAGTACCCGAAAG	Rev RT-PCR primer for *HMX1*
ONC200	TGTGAAAAAGTCGGTGTGTCATG	Fwd RT-PCR primer for *FET3*
ONC201	AATACCTCTAGCAGTGAAACCAGTTG	Rev RT-PCR primer for *FET3*
ONC202	GCCATTCACCAAGAATTTGACTT	Fwd RT-PCR primer for *FTR1*
ONC203	ACAATTCATCCTTTTCAGCTTTGTT	Rev RT-PCR primer for *FTR1*
ONC206	CAGTCGATGGCAGTTACTTCATG	Fwd RT-PCR primer for *FRP1*
ONC207	CACCCTTCTAGCACTTTGACAATG	Rev RT-PCR primer for *FRP1*
ONC208	TGCACTTTTCATGAGAGACCACA	Fwd RT-PCR primer for *ARN1*
ONC209	TTTCTTCTTGAAATTGCCGAAGA	Fwd RT-PCR primer for *ARN1*
ONC210	GCCATTAATCGACTTCCTCCAA	Fwd RT-PCR primer for *SFU1*
ONC211	GAATATGATGACGATGATTGCATTG	Rev RT-PCR primer for *SFU1*
ONC213	CTATTGCAATGGGAGACGGTGC	Rev Primer for *CAP2* promoter amplification
ONC270	TCCACCGATACCAGAAACAGAA	Fwd RT-PCR primer for *HAP5*
ONC271	CATCCTGATGTGAATGCTTGACA	Rev RT-PCR primer for *HAP5*
ONC272	AACAAAATGAACAATCGAATCAAGAG	Fwd RT-PCR primer for *HAP2*
ONC273	TTCATTATTGTCATCAACATGCTGG	Rev RT-PCR primer for *HAP2*
ONC274	CGTTCATAACAAGTGAAGCAAGTGA	Fwd RT-PCR primer for *HAP31*
ONC275	TTTTTAAAACTTCGGCGTAATTCTC	Rev RT-PCR primer for *HAP31*
ONC276	CAATTCAGTGATATTAACCCAACTACAGA	Fwd RT-PCR primer for *HAP32*
ONC277	ATTGTCTAGGTTGGGGATTCGTT	Rev RT-PCR primer for *HAP32*
ONC280	TTGCTAGTCCTCCACCAATTACTATG	Fwd RT-PCR primer for *COX5*
ONC281	GAATAACCAGTGAATGGATTAGCATTC	Rev RT-PCR primer for *COX5*
ONC282	TTGAGAGTTCATCCAAAGGAAGGT	Fwd RT-PCR primer for *ACO1*
ONC283	AAGTTCAAAGCAGAACCGTGTTT	Rev RT-PCR primer for *ACO1*
ONC317	TGTAACCGATGGTTCTGTGTCAAC	Fwd RT-PCR primer for *HAP41*
ONC318	GTATTACGAGAAACACCACCATTGAC	Rev RT-PCR primer for *HAP41*
ONC319	CCTAATAACTTGAATGGTGATGATCTTG	Fwd RT-PCR primer for *HAP42*
ONC320	TCACATTACTGGAGCCACTCATG	Rev RT-PCR primer for *HAP42*
ONC348	AGAGGAGGAATTGTTGAGACAGC	Fwd RT-PCR primer for *HAP33*
ONC349	ATTGGTTTTGCAAACGAGCTC	Rev RT-PCR primer for *HAP33*
ONC240	ACCCGAAAGAAAAGTGGTCTTG	Fwd ChIP RT-PCR primer for *FRP1*
ONC241	GCATTCAATAAACCTTATTATCATCAGAC	Rev ChIP RT-PCR primer for *FRP1*
ONC482	ACCCTTATATAACGTTAAACCCGAAA	Fwd ChIP RT-PCR primer for *FRP1*
ONC483	TTGCGATCCGAGACTAATCTGAT	Rev ChIP RT-PCR primer for *FRP1*
ONC484	CTTACACTTTTGAGCAACACATTGAC	Fwd ChIP RT-PCR primer for *FRP1*
ONC485	TTGTCCATATTGGGATACAGGATG	Rev ChIP RT-PCR primer for *FRP1*
ONC500	TTTTTTGCTTGCAAAGAGAGAAAA	Fwd ChIP RT-PCR primer for *ACO1*
ONC501	ATCGGATCCATAAAATGGACAAG	Rev ChIP RT-PCR primer for *ACO1*
ONC502	ACCAATCAGCGCCCTCTTAA	Fwd ChIP RT-PCR primer for *ACO1*
ONC503	GTTCTCCAGATTTCAACACAATGC	Rev ChIP RT-PCR primer for *ACO1*

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Supporting information

Table S4A. List of bZIPdomain proteins in Fig. 1A

S. No.	Unique ID in	Systematic name	Organism
1	CAAL_1032	orf19.1032	*C.albicans SC5314*
2	CAAL_1358	orf19.1358	*C.albicans SC5314*
3	CAAL_1623	orf19.1623	*C.albicans SC5314*
4	CAAL_2432	orf19.2432	*C.albicans SC5314*
5	CAAL_3193	orf19.3193	*C.albicans SC5314*
6	CAAL_5312	orf19.5312	*C.albicans SC5314*
7	CAAL_6102	orf19.6102	*C.albicans SC5314*
8	CAAL_681	orf19.681	*C.albicans SC5314*
9	CAAL_7046	orf19.7046	*C.albicans SC5314*
10	CAAL_861	orf19.861	*C.albicans SC5314*
11	CAALW_1	CAWG_00314	*C.albicans WO-1*
12	CAALW_2	CAWG_00794	*C.albicans WO-1*
13	CAALW_3	CAWG_01014	*C.albicans WO-1*
14	CAALW_4	CAWG_01358	*C.albicans WO-1*
15	CAALW_5	CAWG_02548	*C.albicans WO-1*
16	CAALW_6	CAWG_03389	*C.albicans WO-1*
17	CAALW_7	CAWG_04124	*C.albicans WO-1*
18	CAALW_8	CAWG_04566	*C.albicans WO-1*
19	CAALW_9	CAWG_05429	*C.albicans WO-1*
20	CAALW_10	CAWG_06066	*C.albicans WO-1*
21	CADU_3	cdub_11-snap.296	*C.dubliniensis*
22	CADU_4	cdub_13-snap.343	*C.dubliniensis*
23	CADU_5	cdub_13-snap.946	*C.dubliniensis*
24	CADU_1	cdub_1-snap.15	*C.dubliniensis*
25	CADU_2	cdub_1-snap.363	*C.dubliniensis*
26	CADU_6	cdub_2-snap.158	*C.dubliniensis*
27	CADU_7	cdub_588-snap.186	*C.dubliniensis*
28	CADU_8	cdub_599.2-snap.229	*C.dubliniensis*
29	CADU_9	cdub_730-snap.193	*C.dubliniensis*
30	CADU_10	cdub_730-snap.668	*C.dubliniensis*
31	CAGL_1	XP_446029	*C.glabrata*
32	CAGL_4	XP_446103	*C.glabrata*
33	CAGL_2	XP_446996	*C.glabrata*
34	CAGL_3	XP_447154	*C.glabrata*
35	CAGL_5	XP_447475	*C.glabrata*
36	CAGL_6	XP_447975	*C.glabrata*
37	CAGL_7	XP_448338	*C.glabrata*
38	CAGL_8	XP_448598	*C.glabrata*
39	CAGL_9	XP_448602	*C.glabrata*
40	CAGL_10	XP_448761	*C.glabrata*
41	CAGL_11	XP_448878	*C.glabrata*
42	CAGL_12	XP_449728	*C.glabrata*
43	CAGL_13	XP_449785	*C.glabrata*
44	CAGL_14	XP_446651	*C.glabrata*
45	CAGU_1	PGUG_00021.1	*C.guilliermondii*
46	CAGU_2	PGUG_00023.1	*C.guilliermondii*
47	CAGU_3	PGUG_00397.1	*C.guilliermondii*
48	CAGU_4	PGUG_00664.1	*C.guilliermondii*
49	CAGU_5	PGUG_01090.1	*C.guilliermondii*
50	CAGU_6	PGUG_01812.1	*C.guilliermondii*
51	CAGU_7	PGUG_02316.1	*C.guilliermondii*
52	CAGU_8	PGUG_02606.1	*C.guilliermondii*
53	CAGU_9	PGUG_03388.1	*C.guilliermondii*
54	CAGU_10	PGUG_03756.1	*C.guilliermondii*
55	CAGU_11	PGUG_04717.1	*C.guilliermondii*
56	CAGU_12	PGUG_05046.1	*C.guilliermondii*
57	CAGU_13	PGUG_DH11	*C.guilliermondii*
58	CALU_1	CLUG_02366.1	*C.lusitaniae*
59	CALU_2	CLUG_02541.1	*C.lusitaniae*
60	CALU_3	CLUG_02670.1	*C.lusitaniae*
61	CALU_4	CLUG_02715.1	*C.lusitaniae*

S. No.	Unique ID in	Systematic name	Organism
62	CALU_5	CLUG_03450.1	*C.lusitaniae*
63	CALU_6	CLUG_03727.1	*C.lusitaniae*
64	CALU_7	CLUG_04433.1	*C.lusitaniae*
65	CALU_8	CLUG_04484.1	*C.lusitaniae*
66	CALU_9	CLUG_05303.1	*C.lusitaniae*
67	CALU_10	CLUG_05390.1	*C.lusitaniae*
68	CAPA_1	Contig1.g26.t1	*C.parapsilosis*
69	CAPA_2	Contig148.2.g146.t1	*C.parapsilosis*
70	CAPA_3	Contig152.1.g93.t1	*C.parapsilosis*
71	CAPA_4	Contig157.3.g38.t1	*C.parapsilosis*
72	CAPA_5	Contig160.4.g25.t1	*C.parapsilosis*
73	CAPA_6	Contig175.5.g62.t1	*C.parapsilosis*
74	CAPA_7	Contig178.1.g15.t1	*C.parapsilosis*
75	CAPA_8	Contig186.9.g177.t1	*C.parapsilosis*
76	CAPA_9	Contig187.14.g170.t1	*C.parapsilosis*
77	CAPA_10	Contig64.1.g31.t1	*C.parapsilosis*
78	CATR_1	CTRG_00304.3	*C.tropicalis*
79	CATR_2	CTRG_01197.3	*C.tropicalis*
80	CATR_3	CTRG_02060.3	*C.tropicalis*
81	CATR_4	CTRG_02398.3	*C.tropicalis*
82	CATR_5	CTRG_04121.3	*C.tropicalis*
83	CATR_6	CTRG_04276.3	*C.tropicalis*
84	CATR_7	CTRG_04281.3	*C.tropicalis*
85	CATR_8	CTRG_04352.3	*C.tropicalis*
86	CATR_9	CTRG_05070.3	*C.tropicalis*
87	CATR_10	CTRG_05304.3	*C.tropicalis*
88	DEHA_1	XP_456908.1	*D.hansenii*
89	DEHA_2	XP_457540.1	*D.hansenii*
90	DEHA_3	XP_457629.1	*D.hansenii*
91	DEHA_4	XP_457662.1	*D.hansenii*
92	DEHA_5	XP_458084.1	*D.hansenii*
93	DEHA_6	XP_458864.1	*D.hansenii*
94	DEHA_7	XP_459598.1	*D.hansenii*
95	DEHA_8	XP_459814.1	*D.hansenii*
96	DEHA_9	XP_460198.1	*D.hansenii*
97	DEHA_10	XP_461323.1	*D.hansenii*
98	DEHA_11	XP_461648.1	*D.hansenii*
99	LOEL_1	LELG_00796	*L.elongisporus*
100	LOEL_2	LELG_01280	*L.elongisporus*
101	LOEL_3	LELG_01333	*L.elongisporus*
102	LOEL_4	LELG_01449	*L.elongisporus*
103	LOEL_5	LELG_01982	*L.elongisporus*
104	LOEL_6	LELG_02543	*L.elongisporus*
105	LOEL_7	LELG_02745	*L.elongisporus*
106	LOEL_8	LELG_03758	*L.elongisporus*
107	LOEL_9	LELG_04433	*L.elongisporus*
108	LOEL_10	LELG_05058	*L.elongisporus*
109	YAP6	YDR259C	*S.cerevisiae*
110	YAP2	YDR423C	*S.cerevisiae*
111	GCN4	YEL009C	*S.cerevisiae*
112	ACA1	YER045C	*S.cerevisiae*
113	HAC1	YFL031W	*S.cerevisiae*
114	YAP3	YHL009C	*S.cerevisiae*
115	ACA2	YIL036W	*S.cerevisiae*
116	MET28	YIR017C	*S.cerevisiae*
117	YAP5	YIR018W	*S.cerevisiae*
118	YAP1	YML007W	*S.cerevisiae*
119	MET4	YNL103W	*S.cerevisiae*
120	SKO1	YNL167C	*S.cerevisiae*
121	YAP7	YOL028C	*S.cerevisiae*
122	YAP4	YOR028C	*S.cerevisiae*
123	YAP8	YPR199C	*S.cerevisiae*
124	PAP1	PAP1	*S.pombe*

Table S4B: List of HAP4L-bZIPdomain proteins in fungal genomes in Fig. 3G

Unique ID in Sequence-alignment and Tree	Systematic Name	Organism	Subphylum
CAAL 681	orf19.681	*Candida albicans* SC5314	Saccharomycotina
CAALW1	CAWG_00314	*Candida albicans* WO-1	Saccharomycotina
CADU 10	cdub_730-snap.668	*Candida dubliniensis*	Saccharomycotina
CATR 5	CTRG_04121.3	*Candida tropicalis*	Saccharomycotina
LOEL 1	LELG_00796	*Lodderomyces elongisporus*	Saccharomycotina
CAPA 8	Contig186.9.g177.t1	*Candida parapsilosis*	Saccharomycotina
CAGU 7	PGUG_02316.1	*Candida guillermondii*	Saccharomycotina
PIST 1	XP_001387398	*Pichia stipitis CBS 6054*	Saccharomycotina
CALU 4	CLUG_02715.1	*Candida lusitaniae*	Saccharomycotina
DEHA 3	XP_457629.1	*Debaryomyces hansenii CBS767*	Saccharomycotina
YALI 1	XP_500831.1	*Yarrowia lipolytica CLIB122*	Saccharomycotina
YALI 2	XP_503831.1	*Yarrowia lipolytica CLIB122*	Saccharomycotina
ASOR1	AO090102000597	*Aspergillus oryzae*	Pezizomycotina
ASFL1	AFLA_11370	*Aspergillus flavus*	Pezizomycotina
ASCL1	EAW14711.1	*Aspergillus clavatus*	Pezizomycotina
ASNI1	gi|134078498|	*Aspergillus niger*	Pezizomycotina
ASAN1	AN8251.3	*Aspergillus nidulans*	Pezizomycotina
NEFI 1	38200	*Neosartorya fischeri*	Pezizomycotina
ASFU1	XP_747952.1	*Aspergillus fumigatus*	Pezizomycotina
UNRE 1	UREG_03844.1	*Uncinocarpus reesii*	Pezizomycotina
COIM 1	CIMG_06601	*Coccidioides immitis RS*	Pezizomycotina
CHGL 1	CHGL_CHG07609.1	*Chaetomimum globsum*	Pezizomycotina
POAN 1	Pa_2_6580	*Podospora anserina*	Pezizomycotina
NECR 1	NCU08891	*Neurospora crassa OR74A*	Pezizomycotina
MAGR 1	MGG_05959.5	*Magnaporthe grisea 70-15*	Pezizomycotina
SCSC 1	SS1G_03796.1	*Sclerotinia sclerotiorum 1980*	Pezizomycotina
BOCI1	BC1G_14315.1	*Botrytis cinerea*	Pezizomycotina
TRRE 1	Trire2_77191	*Trichoderma reesei*	Pezizomycotina
FUGR 1	FGSG_05930	*Fusarium graminearum*	Pezizomycotina
NEHA 1	Necha1_192224	*Nectria haematococca*	Pezizomycotina
FUVE 1	FVEG_04503	*Fusarium verticillioides*	Pezizomycotina
FUOX 1	FOXG_07577	*Fusarium oxysporum*	Pezizomycotina
COCI 1	CC1G_06796.10	*Coprinus cinereus*	Agaricomycotina
POPL 1	Pospl1_127346	*Postia placenta*	Agaricomycotina
PHCH 1	Phchr1_6539	*Phanerochaete chrysosporium (white rot)*	Agaricomycotina
LABI 1	Lacbi1_300757	*Laccaria bicolor*	Agaricomycotina
USMA 1	UM02191.1	*Ustilago maydis 521*	Ustilaginomycotina
CRNEB 1	EAL21217.1	*Cryptococcus neoformans var. neoformans B3501*	Agaricomycotina
CRNEA 1	CNAG_01242.1	*Cryptococcus neoformans A*	Agaricomycotina
CRNEJ 1	XP_570559	*Cryptococcus neoformans var. neoformans JEC21*	Agaricomycotina
SAKU 1	skud_c2060-g5.1	*Saccharomyces kudriavzevii*	Saccharomycotina
YAP7	YOL028C	*Saccharomyces cerevisiae S288C*	Saccharomycotina
SAPA 1	spar_378-g18.1	*Saccharomyces paradoxus*	Saccharomycotina
SAMI 1	smik_66-g1.1	*Saccharomyces mikatae*	Saccharomycotina
SABA 1	sbay_c614-g15.1	*Saccharomyces bayanus*	Saccharomycotina
SAKL 1	sklu_c2248-g2.1	*Saccharomyces kluyveri*	Saccharomycotina
KLWA 1	Kwal_20824	*Kluyveromyces waltii NCYC 2644*	Saccharomycotina

Supporting information

Table S5. List of 929 differentially expressed genes in the *CAP2/cap2Δ* Microarray data

Systematic Name	Standard Name	*CAP2/cap2Δ*				
		1a	*1b*	*2a*	*2b*	Ave.
orf19.7114	CSA1	7.5	6.9	5.8	6.4	6.6
orf19.5636	RBT5	6.4	6.1	4.5	5.6	5.7
orf19.5952	orf19.5952	4.7	5.1	3.8	4.2	4.4
orf19.3117	CSA2	4.5	4.3	3.4	3.9	4.0
orf19.2062	SOD4	4.1	4.2	3.1	3.7	3.8
orf19.5063	orf19.5063	4.1	3.6	3.4	3.2	3.6
orf19.5779	RNR1	3.8	3.8	2.8	3.4	3.5
orf19.5801	RNR21	4.1	3.7	2.8	2.9	3.4
orf19.681	HAP43	3.1	2.7	3.3	4.1	3.3
orf19.3548.1	WH11	5.0	3.6	2.0	1.9	3.1
orf19.6073	HMX1	3.7	2.6	2.6	2.9	2.9
orf19.2762	AHP1	4.4	3.4	2.2	1.7	2.9
orf19.4623.3	NHP6A	3.3	3.0	3.0	2.2	2.9
orf19.251	orf19.251	3.5	3.2	2.1	2.4	2.8
orf19.5964.2	RPL35	3.6	2.6	2.6	2.2	2.8
orf19.5635	PGA7	4.3	2.9	1.7	2.0	2.7
orf19.1930	CFL5	2.6	2.5	2.6	3.1	2.7
orf19.4647	HAP3	3.2	2.2	2.2	3.0	2.7
orf19.2179	SIT1	3.3	3.5	1.7	2.0	2.6
orf19.5634	FRP1	3.1	3.0	2.0	2.4	2.6
orf19.2785	ATP7	3.0	2.5	2.5	2.3	2.6
orf19.3478	NIP7	3.7	2.7	2.1	1.9	2.6
orf19.5991	orf19.5991	3.1	1.9	2.5	2.5	2.5
orf19.1853	HHT2	3.1	2.5	2.2	2.0	2.5
orf19.2468	orf19.2468	2.1	2.4	2.4	2.8	2.4
orf19.7218	RBE1	2.8	2.9	1.7	2.1	2.4
orf19.1091	orf19.1091	2.8	3.0	1.7	1.9	2.4
orf19.3690.2	orf19.3690.2	3.0	2.1	2.4	2.0	2.4
orf19.475	orf19.475	2.8	2.5	2.1	2.0	2.3
orf19.6686	ENP2	2.8	2.6	1.9	2.1	2.3
orf19.7310	orf19.7310	2.9	2.7	1.8	2.0	2.3
orf19.4125	orf19.4125	2.9	2.4	2.1	2.0	2.3
orf19.59	REI1	2.7	2.7	1.6	2.3	2.3
orf19.2990	XOG1	2.7	2.7	1.8	2.1	2.3
orf19.2717	SAS10	2.4	3.0	1.4	2.3	2.3
orf19.7021	GPH1	2.5	2.5	1.9	2.1	2.3
orf19.6648	SDA1	2.6	2.4	2.1	1.9	2.3
orf19.756	SAP7	2.6	2.1	2.1	2.2	2.2
orf19.4793	orf19.4793	2.8	2.6	1.6	1.8	2.2
orf19.7050	NOP15	2.5	2.3	2.1	1.9	2.2
orf19.5732	NOG2	2.5	2.6	1.6	2.1	2.2
orf19.1052	orf19.1052	2.8	2.4	1.6	1.9	2.2
orf19.4191	RLP24	3.0	2.2	1.8	1.6	2.2
orf19.3547	orf19.3547	2.3	2.3	1.7	2.3	2.1
orf19.2504	BMS1	2.8	2.3	1.6	1.9	2.1
orf19.2735	SEN2	2.8	2.1	1.8	1.8	2.1
orf19.3553	RPF2	3.1	2.1	1.8	1.5	2.1
orf19.7219	FTR1	2.1	1.9	1.7	2.7	2.1
orf19.6316.4	orf19.6316.4	2.8	2.5	1.7	1.4	2.1
orf19.778	PIL1	2.0	2.2	1.8	2.4	2.1
orf19.5066	orf19.5066	3.2	2.1	1.6	1.4	2.1
orf19.6814	TDH3	2.1	1.8	1.8	2.6	2.1
orf19.655	PHO84	1.4	1.5	2.6	2.7	2.1
orf19.5753	HGT10	2.6	2.0	1.8	1.9	2.1
orf19.535	RBR1	2.9	3.0	0.9	1.3	2.0
orf19.7398	orf19.7398	2.8	2.3	1.4	1.5	2.0
orf19.1105.2	PGA56	2.4	2.1	1.5	1.9	2.0
orf19.3325.3	RPS21B	2.7	2.4	1.5	1.2	2.0
orf19.76	SPB1	2.6	2.3	1.5	1.5	2.0
orf19.2314	orf19.2314	3.2	2.1	1.3	1.3	2.0
orf19.4479	orf19.4479	2.6	2.2	1.5	1.6	2.0
orf19.2688	NAN1	2.2	2.5	1.5	1.6	2.0
orf19.1902	NOC4	2.3	2.3	1.7	1.5	2.0
orf19.4689	PGA57	2.5	2.2	1.6	1.5	1.9
orf19.7306	orf19.7306	2.8	1.3	2.0	1.7	1.9
orf19.4870	DBP3	2.1	2.1	1.6	1.8	1.9
orf19.603	IMP4	2.3	2.3	1.4	1.6	1.9
orf19.2177	orf19.2177	2.1	2.2	1.2	2.1	1.9
orf19.4795	orf19.4795	2.0	1.8	2.0	1.7	1.9
orf19.2917	orf19.2917	2.3	1.8	1.7	1.7	1.9
orf19.3393	orf19.3393	2.1	1.7	2.0	1.8	1.9
orf19.107	orf19.107	2.4	1.8	1.7	1.6	1.9
orf19.1115	GUK1	2.4	2.0	1.6	1.5	1.9
orf19.5959	NOP14	2.5	1.6	1.6	1.8	1.9
orf19.3682	CWH8	2.3	2.2	1.5	1.4	1.9
orf19.4743	AFG1	1.9	2.0	1.7	1.8	1.9
orf19.1335	orf19.1335	2.2	1.7	2.0	1.5	1.9

		CAP2/cap2Δ				
Systematic Name	**Standard Name**	***1a***	***1b***	***2a***	***2b***	**Ave.**
orf19.4631	ERG251	2.0	1.9	1.6	1.9	1.9
orf19.3426	ANB1	1.9	1.8	1.9	1.8	1.9
orf19.4760	orf19.4760	2.5	1.8	1.6	1.5	1.8
orf19.813	orf19.813	2.2	2.4	1.3	1.5	1.8
orf19.1051	HTA2	2.5	1.7	1.7	1.4	1.8
orf19.4905	orf19.4905	2.3	2.3	1.2	1.5	1.8
orf19.7043.1	ACB1	2.7	1.6	1.9	1.0	1.8
orf19.563	RRP15	2.8	2.1	1.2	1.1	1.8
orf19.158	orf19.158	1.7	2.3	1.5	1.6	1.8
orf19.827.1	RPL39	2.8	1.8	1.4	1.0	1.8
orf19.6828.1	orf19.6828.1	2.4	1.7	1.7	1.3	1.8
orf19.6311	orf19.6311	3.0	1.7	1.2	1.2	1.8
orf19.979	FAS1	2.4	0.8	1.8	2.1	1.8
orf19.3777	orf19.3777	2.3	1.6	2.1	1.1	1.8
orf19.962	orf19.962	2.7	1.8	1.3	1.2	1.8
orf19.7488	orf19.7488	2.7	2.0	1.2	1.1	1.8
orf19.410.3	orf19.410.3	2.6	2.1	1.2	1.1	1.8
orf19.2090	orf19.2090	1.4	2.2	0.7	2.7	1.8
orf19.3087	UBI3	2.3	1.5	1.6	1.6	1.8
orf19.169	CHO2	1.7	1.6	1.8	1.9	1.8
orf19.2385	KTI12	2.5	1.9	1.3	1.4	1.7
orf19.2934	orf19.2934	2.3	2.2	1.4	1.1	1.7
orf19.3251	ARC19	1.8	1.6	2.5	1.1	1.7
orf19.5754	orf19.5754	2.1	1.7	1.6	1.5	1.7
orf19.809	orf19.809	2.1	1.8	1.6	1.4	1.7
orf19.7384	PRI2	1.7	1.7	1.8	1.7	1.7
orf19.2885	NOG1	1.7	1.3	1.9	2.0	1.7
orf19.4940	orf19.4940	1.9	1.9	1.6	1.4	1.7
orf19.1839	RPA190	2.1	1.6	1.7	1.6	1.7
orf19.3761	CDC54	1.6	1.6	1.8	1.8	1.7
orf19.4701	orf19.4701	2.5	1.7	1.4	1.2	1.7
orf19.172	RPC19	2.3	1.6	1.6	1.3	1.7
orf19.1609	orf19.1609	1.2	2.2	1.7	1.6	1.7
orf19.2167	orf19.2167	2.3	1.2	1.5	1.7	1.7
orf19.606	orf19.606	1.4	1.8	1.8	1.8	1.7
orf19.395	ENO1	1.4	1.3	1.9	2.2	1.7
orf19.5010	DIM1	2.1	2.0	1.0	1.7	1.7
orf19.5232	CSI2	2.4	1.0	1.8	1.5	1.7
orf19.3221	CPA2	1.5	2.0	1.5	1.7	1.7
orf19.2241	PST1	2.4	2.1	1.1	1.1	1.7
orf19.5227	orf19.5227	2.9	1.7	1.2	0.9	1.7

		CAP2/cap2Δ				
Systematic Name	**Standard Name**	***1a***	***1b***	***2a***	***2b***	**Ave.**
orf19.6415.1	orf19.6415.1	2.4	1.4	1.5	1.3	1.7
orf19.4309	GRP2	2.0	1.7	1.7	1.3	1.7
orf19.2319	orf19.2319	1.8	2.1	1.2	1.5	1.7
orf19.7011	orf19.7011	2.0	1.3	1.8	1.5	1.7
orf19.6828	orf19.6828	2.4	1.9	1.2	1.1	1.6
orf19.6766	orf19.6766	1.9	2.0	1.3	1.5	1.6
orf19.3708	SAP2	2.4	1.3	1.7	1.1	1.6
orf19.2232	RPL11	2.0	1.8	1.1	1.7	1.6
orf19.1854	HHF22	2.8	1.4	1.2	1.1	1.6
orf19.5020	orf19.5020	2.0	1.2	1.4	1.9	1.6
orf19.3676	ABP140	1.7	1.7	1.5	1.6	1.6
orf19.4632	RPL20B	2.1	1.4	1.4	1.7	1.6
orf19.5500	MAK16	2.3	1.7	1.5	1.1	1.6
orf19.5850	NOC2	1.7	1.8	1.4	1.7	1.6
orf19.7611	TRX1	2.7	1.7	1.0	1.0	1.6
orf19.2178	orf19.2178	2.0	2.1	1.3	1.1	1.6
orf19.2344	ASR1	1.8	1.9	1.2	1.5	1.6
orf19.4401	YVH1	1.5	2.2	1.2	1.6	1.6
orf19.2362	orf19.2362	2.3	1.9	1.2	1.1	1.6
orf19.3504	RPL23A	2.0	1.8	1.0	1.6	1.6
orf19.5198	NOP4	2.0	1.7	1.3	1.3	1.6
orf19.4735	orf19.4735	2.3	1.2	1.3	1.5	1.6
orf19.7546	orf19.7546	1.7	2.1	1.0	1.5	1.6
orf19.236	RPL9B	2.0	1.7	1.2	1.5	1.6
orf19.6902	DBP7	2.0	1.7	1.1	1.5	1.6
orf19.1237	ARO9	1.9	1.7	1.4	1.3	1.6
orf19.4746	JIP5	1.9	1.6	1.7	1.1	1.6
orf19.1601	RPL3	1.2	1.1	1.8	2.2	1.6
orf19.5486.1	SMD2	2.6	1.6	1.2	0.8	1.6
orf19.1791	orf19.1791	1.6	1.8	1.3	1.5	1.6
orf19.7424	NSA2	2.2	2.0	0.8	1.3	1.6
orf19.6085	RPL16A	1.7	1.4	1.2	2.0	1.6
orf19.1779	MP65	1.5	1.7	1.4	1.7	1.6
orf19.3789	RPL24A	2.0	1.4	1.5	1.4	1.6
orf19.708	orf19.708	1.6	1.4	1.8	1.5	1.6
orf19.3867	RPL7	1.8	1.0	1.7	1.7	1.6
orf19.6236	orf19.6236	2.0	2.1	1.0	1.2	1.5
orf19.1830	orf19.1830	1.9	1.1	2.0	1.2	1.5
orf19.5049	orf19.5049	1.7	2.4	1.1	1.0	1.5
orf19.2329.1	RPS17B	2.1	0.6	1.5	1.9	1.5
orf19.4490	RPL17B	1.8	0.8	1.6	2.0	1.5

		CAP2/cap2Δ				
Systematic Name	**Standard Name**	***1a***	***1b***	***2a***	***2b***	**Ave.**
orf19.411	orf19.411	2.0	1.4	1.3	1.4	1.5
orf19.1635	RPL12	1.9	1.4	1.1	1.8	1.5
orf19.6014	RRS1	2.3	1.3	1.2	1.2	1.5
orf19.1566	UTP21	1.7	1.7	1.2	1.6	1.5
orf19.6312	RPS3	1.6	1.6	1.4	1.5	1.5
orf19.6081	PHR2	1.5	1.8	0.8	1.9	1.5
orf19.1049	orf19.1049	1.4	1.7	1.6	1.4	1.5
orf19.3282	BMT3	1.7	1.7	1.3	1.3	1.5
orf19.7552	orf19.7552	1.8	1.5	1.4	1.3	1.5
orf19.687.1	RPL25	2.6	1.6	0.8	1.1	1.5
orf19.5550	MRT4	2.0	1.6	1.3	1.1	1.5
orf19.1045	orf19.1045	2.4	1.1	1.5	1.1	1.5
orf19.1258	orf19.1258	1.9	1.0	1.5	1.6	1.5
orf19.389	orf19.389	2.2	1.2	1.4	1.2	1.5
orf19.4563	orf19.4563	1.7	2.0	1.0	1.3	1.5
orf19.1332	SNG4	1.6	1.5	1.4	1.5	1.5
orf19.1618	GFA1	1.9	1.4	1.3	1.4	1.5
orf19.5905	orf19.5905	2.7	1.7	1.0	0.6	1.5
orf19.3216	orf19.3216	1.5	1.1	1.7	1.6	1.5
orf19.3756	CHR1	2.0	1.9	1.0	1.0	1.5
orf19.1059	HHF1	2.2	1.6	1.0	1.2	1.5
orf19.3370	DOT4	1.8	1.5	1.4	1.2	1.5
orf19.1578	orf19.1578	1.8	1.4	1.5	1.2	1.5
orf19.1642	orf19.1642	2.1	1.5	1.2	1.1	1.5
orf19.4634	orf19.4634	1.3	2.0	1.1	1.4	1.5
orf19.3228	orf19.3228	1.9	1.3	1.6	1.1	1.5
orf19.3477	orf19.3477	1.9	1.5	1.3	1.2	1.5
orf19.1047	ERB1	1.7	1.2	1.4	1.5	1.5
orf19.6793	orf19.6793	1.4	1.0	1.7	1.7	1.5
orf19.1535	orf19.1535	0.8	1.3	2.2	1.5	1.5
orf19.6362	SPA2	1.3	1.4	1.7	1.5	1.5
orf19.5276	orf19.5276	1.7	1.3	1.5	1.2	1.5
orf19.7202	orf19.7202	1.8	1.0	1.7	1.4	1.4
orf19.568	SPE2	1.8	1.5	1.3	1.2	1.4
orf19.7593	orf19.7593	1.4	1.5	1.5	1.4	1.4
orf19.2712	HCA4	1.6	0.9	1.5	1.7	1.4
orf19.7304	orf19.7304	1.9	1.4	1.3	1.1	1.4
orf19.2767	PGA59	1.5	1.7	1.1	1.4	1.4
orf19.903	GPM1	1.1	1.6	1.0	2.0	1.4
orf19.2527	orf19.2527	2.1	1.7	0.8	1.1	1.4
orf19.7401	ISW2	1.2	1.5	1.7	1.2	1.4
orf19.7502	orf19.7502	1.1	0.9	1.9	1.7	1.4
orf19.6234	orf19.6234	1.8	1.6	1.1	1.1	1.4
orf19.4872	orf19.4872	1.2	1.6	1.1	1.7	1.4
orf19.4145	ZCF20	2.0	1.2	0.9	1.4	1.4
orf19.1029	orf19.1029	1.8	1.8	1.1	1.0	1.4
orf19.7358	orf19.7358	1.9	0.7	1.6	1.3	1.4
orf19.6955	HBR3	1.7	1.7	1.0	1.1	1.4
orf19.7599	UTP5	1.6	1.4	1.2	1.4	1.4
orf19.6918	orf19.6918	1.4	0.9	1.8	1.6	1.4
orf19.3465	RPL10A	1.4	0.6	1.5	2.1	1.4
orf19.58	RRP6	1.4	1.8	1.2	1.2	1.4
orf19.6924	HTA1	2.2	1.7	0.7	0.9	1.4
orf19.658	GIN1	2.0	1.0	1.5	1.1	1.4
orf19.6873	RPS8A	1.5	1.3	1.0	1.7	1.4
orf19.3575	CDC19	1.0	1.0	1.6	1.9	1.4
orf19.7614	orf19.7614	1.7	1.3	0.7	1.7	1.4
orf19.4853	HCM1	1.3	1.3	1.3	1.6	1.4
orf19.2927	MNN11	1.6	1.4	1.3	1.2	1.4
orf19.2309.2	RPL2	0.9	1.6	1.0	1.9	1.4
orf19.3630	RRP8	1.9	1.7	0.9	1.1	1.4
orf19.6886		1.7	0.9	1.3	1.5	1.4
orf19.6414.3	TPM2	1.2	1.1	2.1	1.1	1.4
orf19.4805	orf19.4805	1.5	1.1	1.4	1.4	1.3
orf19.5007	ACT1	1.4	1.4	1.0	1.5	1.3
orf19.7635	YTM1	1.6	1.5	1.1	1.2	1.3
orf19.4815	DRS1	1.8	1.4	0.9	1.3	1.3
orf19.1362	SMM1	1.9	1.7	1.2	0.6	1.3
orf19.6264.4	orf19.6264.4	2.1	1.4	1.1	0.9	1.3
orf19.3554	AAT1	1.1	1.2	1.3	1.8	1.3
orf19.154	orf19.154	1.5	1.6	1.1	1.1	1.3
orf19.5166	DBF4	1.4	1.3	1.3	1.4	1.3
orf19.4963	orf19.4963	1.8	0.9	1.3	1.3	1.3
orf19.1388	orf19.1388	1.7	1.1	1.3	1.2	1.3
orf19.1228	HAP2	1.3	1.0	1.4	1.7	1.3
orf19.6813	orf19.6813	1.7	0.8	1.4	1.4	1.3
orf19.3351	orf19.3351	1.6	1.3	1.4	0.9	1.3
orf19.2830	RRP9	1.7	1.6	1.0	1.0	1.3
orf19.2631	orf19.2631	1.4	0.8	1.5	1.5	1.3
orf19.1841	orf19.1841	1.4	1.1	1.6	1.2	1.3
orf19.4093	NOP7	1.6	1.3	1.1	1.1	1.3
orf19.1849	orf19.1849	1.6	1.4	1.3	0.9	1.3

		CAP2/cap2Δ				
Systematic Name	**Standard Name**	***1a***	***1b***	***2a***	***2b***	**Ave.**
orf19.3474	IPL1	1.4	1.2	1.4	1.2	1.3
orf19.4642	orf19.4642	1.6	1.1	1.5	0.9	1.3
orf19.6975	YST1	0.9	1.3	1.1	1.8	1.3
orf19.5960	orf19.5960	1.5	1.6	0.7	1.3	1.3
orf19.5391	orf19.5391	1.2	1.5	1.4	1.1	1.3
orf19.2575	orf19.2575	1.7	0.9	1.2	1.3	1.3
orf19.2877	PDC11	0.6	1.5	1.2	1.8	1.3
orf19.3665	orf19.3665	1.7	1.6	0.8	1.0	1.3
orf19.7601	orf19.7601	1.6	1.7	0.7	1.1	1.3
orf19.1690	TOS1	1.4	1.4	0.9	1.5	1.3
orf19.2875	orf19.2875	1.5	1.1	1.4	1.2	1.3
orf19.1442	PLB4.5	1.3	1.4	1.1	1.3	1.3
orf19.1966	BUD23	1.9	1.5	0.8	0.9	1.3
orf19.3556	orf19.3556	1.2	1.4	1.2	1.3	1.3
orf19.3618	YWP1	1.5	0.8	1.1	1.6	1.3
orf19.1061	HHT21	2.0	1.4	0.7	0.9	1.3
orf19.2330	orf19.2330	1.3	1.4	1.2	1.2	1.3
orf19.715	orf19.715	1.3	1.6	1.3	0.8	1.3
orf19.2746	orf19.2746	1.4	1.0	1.4	1.3	1.3
orf19.3088	orf19.3088	1.7	1.5	1.0	0.8	1.3
orf19.1631	ERG6	1.5	1.4	1.1	1.0	1.3
orf19.6536	IQG1	1.0	1.0	1.5	1.5	1.3
orf19.2751	orf19.2751	1.8	1.1	1.0	1.0	1.3
orf19.2367	orf19.2367	1.7	1.0	1.3	1.0	1.2
orf19.1042	POR1	1.3	1.2	1.1	1.4	1.2
orf19.501	orf19.501	1.6	1.3	1.1	1.0	1.2
orf19.6691	orf19.6691	1.8	1.6	0.8	0.8	1.2
orf19.7069	orf19.7069	1.9	1.4	0.7	1.0	1.2
orf19.4273	orf19.4273	1.4	1.0	1.3	1.3	1.2
orf19.7154	UTP18	1.5	1.7	0.7	1.1	1.2
orf19.230	orf19.230	1.4	1.7	1.0	0.9	1.2
orf19.3778	orf19.3778	1.5	1.0	1.3	1.3	1.2
orf19.6346	orf19.6346	0.5	1.4	1.3	1.8	1.2
orf19.4673	BMT9	2.0	0.4	1.3	1.2	1.2
orf19.5235	orf19.5235	1.1	1.2	1.6	1.0	1.2
orf19.2185	NSA1	1.2	1.7	1.0	1.1	1.2
orf19.6589	orf19.6589	1.3	1.3	0.9	1.4	1.2
orf19.6568	SMC6	1.2	1.0	1.4	1.2	1.2
orf19.2270	SMF12	1.8	0.7	1.1	1.3	1.2
orf19.4211	FET3	1.0	0.8	1.4	1.7	1.2
orf19.2654	RMS1	1.6	0.7	1.2	1.4	1.2
orf19.6871	orf19.6871	1.2	1.1	1.4	1.3	1.2
orf19.6202	RBT4	1.2	1.3	1.0	1.4	1.2
orf19.5290	orf19.5290	1.4	1.7	0.7	1.1	1.2
orf19.1976	TRX2	1.9	1.0	1.0	0.9	1.2
orf19.6175	orf19.6175	1.3	1.5	1.1	1.0	1.2
orf19.5870	CTP1	1.4	0.7	1.2	1.6	1.2
orf19.4268	UTP13	1.5	1.0	1.2	1.2	1.2
orf19.5608	orf19.5608	1.5	1.5	0.9	0.9	1.2
orf19.4896	orf19.4896	1.9	1.2	0.9	0.9	1.2
orf19.6052	CNS1	1.6	1.4	0.8	1.0	1.2
orf19.5647	SUB2	0.7	1.3	1.1	1.7	1.2
orf19.5627	orf19.5627	1.3	1.2	1.3	1.0	1.2
orf19.6663	RPS25B	1.7	1.0	1.0	1.1	1.2
orf19.1646	orf19.1646	1.2	1.1	1.1	1.3	1.2
orf19.7332	ELF1	1.7	1.3	0.8	1.0	1.2
orf19.3098	orf19.3098	1.4	1.2	1.1	1.1	1.2
orf19.1942	SGE1	1.6	1.1	1.1	1.0	1.2
orf19.3651	PGK1	0.6	1.3	1.1	1.8	1.2
orf19.4640	PWP1	1.6	1.2	1.0	0.9	1.2
orf19.4894	orf19.4894	1.7	1.2	1.0	0.8	1.2
orf19.4660	RPS6A	1.2	1.1	1.3	1.2	1.2
orf19.6541	RPL5	0.9	1.3	1.0	1.6	1.2
orf19.4931.1	RPL14	1.0	1.3	1.3	1.2	1.2
orf19.403	PCL2	1.7	0.8	1.2	1.0	1.2
orf19.6297	orf19.6297	1.2	1.3	1.0	1.2	1.2
orf19.1665	MNT1	1.1	1.1	1.0	1.5	1.2
orf19.2795	orf19.2795	1.2	1.0	1.3	1.2	1.2
orf19.7466	ACC1	1.1	0.9	1.0	1.6	1.2
orf19.3193	FCR3	1.2	1.0	1.3	1.1	1.2
orf19.1495	orf19.1495	1.9	0.8	1.0	0.9	1.2
orf19.2170	PHM7	1.7	0.7	1.0	1.2	1.1
orf19.3100	orf19.3100	1.2	1.0	1.2	1.1	1.1
orf19.702	orf19.702	1.3	1.3	1.2	0.8	1.1
orf19.6789	orf19.6789	1.3	1.0	1.2	1.1	1.1
orf19.3541	ERF1	1.5	0.8	1.2	1.1	1.1
orf19.1721	NCE103	1.4	0.9	1.1	1.1	1.1
orf19.6577	FLU1	1.6	1.6	0.7	0.6	1.1
orf19.1687	orf19.1687	1.1	1.4	0.8	1.2	1.1
orf19.3462	SAR1	1.7	0.7	1.0	1.1	1.1
orf19.2396	IFR2	1.4	1.1	0.8	1.1	1.1
orf19.1492	PRP39	1.5	1.3	0.9	0.9	1.1

		CAP2/cap2Δ				
Systematic Name	**Standard Name**	***1a***	***1b***	***2a***	***2b***	**Ave.**
orf19.2193	PRS5	1.3	1.2	0.9	1.1	1.1
orf19.4749	orf19.4749	1.4	1.2	0.9	1.1	1.1
orf19.3042	orf19.3042	1.4	1.1	1.3	0.8	1.1
orf19.5203	orf19.5203	0.9	1.1	0.7	1.8	1.1
orf19.5032	SIM1	1.2	1.4	0.7	1.1	1.1
orf19.667.1	RPL37B	1.5	1.0	1.0	1.0	1.1
orf19.5137.1	HHO1	1.5	1.0	0.9	1.1	1.1
orf19.3097	PDA1	0.8	0.9	1.2	1.5	1.1
orf19.6771	UBI4	1.6	1.4	0.5	1.0	1.1
orf19.3276	PWP2	1.6	1.2	0.7	1.0	1.1
orf19.5271	orf19.5271	1.0	1.1	1.2	1.2	1.1
orf19.5982	RPL18	1.4	1.0	0.9	1.2	1.1
orf19.2055	NPL6	1.0	0.7	1.6	1.1	1.1
orf19.5610	ARG3	1.6	0.6	1.3	0.9	1.1
orf19.1333	SNG3	1.4	0.9	1.0	1.1	1.1
orf19.1934	orf19.1934	1.1	1.1	1.2	1.0	1.1
orf19.5106	DIP2	1.3	1.4	1.0	0.7	1.1
orf19.5100	MLT1	1.4	0.7	1.1	1.2	1.1
orf19.7018	RPS18	1.6	0.7	0.9	1.1	1.1
orf19.3727	PHO112	1.6	1.1	0.7	1.0	1.1
orf19.335	orf19.335	1.3	1.1	1.0	1.0	1.1
orf19.4626	orf19.4626	1.3	1.2	1.0	0.9	1.1
orf19.4857	orf19.4857	1.8	0.8	0.9	0.9	1.1
orf19.4517	orf19.4517	1.6	0.6	1.2	1.0	1.1
orf19.7446	OPI3	1.3	1.2	0.9	1.0	1.1
orf19.5015	MYO2	1.4	1.0	1.0	0.9	1.1
orf19.5919	MEA1	1.1	1.0	1.2	0.9	1.1
orf19.4255	ECM331	1.5	0.9	1.0	1.0	1.1
orf19.1633	UTP4	1.1	1.1	1.1	1.0	1.1
orf19.4945	MSH6	1.0	0.8	1.3	1.2	1.1
orf19.3564	RPC40	1.4	1.1	0.8	0.9	1.1
orf19.342	BMT7	1.3	0.9	1.1	1.0	1.1
orf19.7569	SIK1	1.2	1.0	0.7	1.3	1.1
orf19.4290	TRR1	1.2	1.1	0.8	1.1	1.1
orf19.3303	orf19.3303	1.4	1.2	0.8	0.9	1.1
orf19.3538	FRE9	1.1	1.0	0.9	1.1	1.1
orf19.1989	DCW1	1.2	1.6	0.6	0.9	1.1
orf19.1886	RCL1	0.7	1.2	1.0	1.3	1.1
orf19.1536	orf19.1536	1.1	1.2	1.0	0.9	1.1
orf19.1586	FGR22	0.8	1.1	1.2	1.1	1.1
orf19.2404	orf19.2404	1.4	1.2	0.8	1.0	1.1

		CAP2/cap2Δ				
Systematic Name	**Standard Name**	***1a***	***1b***	***2a***	***2b***	**Ave.**
orf19.4234	orf19.4234	1.6	1.1	0.8	0.6	1.1
orf19.6877	PNG2	1.5	1.3	0.7	0.7	1.1
orf19.2309	orf19.2309	0.9	1.3	0.9	1.0	1.0
orf19.4979	KNS1	1.3	1.3	0.8	0.8	1.0
orf19.6705	orf19.6705	0.7	1.0	1.2	1.2	1.0
orf19.2896	SOU1	1.4	1.2	0.6	1.0	1.0
orf19.4336	RPS5	1.0	1.2	0.9	1.0	1.0
orf19.348	SKN2	1.0	1.2	0.8	1.1	1.0
orf19.2992	RPP1A	1.3	1.1	0.6	1.1	1.0
orf19.4867	SWE1	1.2	0.8	1.1	1.0	1.0
orf19.1663	MNT2	1.0	1.1	1.0	1.0	1.0
orf19.7371	orf19.7371	1.2	1.1	1.0	0.8	1.0
orf19.5904	RPL19A	1.2	0.6	1.1	1.1	1.0
orf19.7372	MRR1	1.1	1.1	0.8	1.2	1.0
orf19.4456	GAP4	1.2	1.2	0.7	1.0	1.0
orf19.3833	orf19.3833	1.3	0.4	1.3	1.1	1.0
orf19.5024	GND1	0.9	1.2	0.7	1.3	1.0
orf19.5999	DYN1	1.2	0.6	1.3	1.0	1.0
orf19.3170	orf19.3170	1.0	0.8	1.2	1.0	1.0
orf19.539	LAP3	1.2	1.2	0.5	1.1	1.0
orf19.6612	orf19.6612	1.5	0.6	1.1	0.9	1.0
orf19.5510	orf19.5510	0.9	0.7	1.2	1.2	1.0
orf19.2384	orf19.2384	1.0	1.1	1.0	1.0	1.0
orf19.4739	MSS116	0.9	0.9	1.1	1.1	1.0
orf19.1946	orf19.1946	1.5	0.9	0.7	1.0	1.0
orf19.2937	PMM1	1.3	0.6	1.2	0.9	1.0
orf19.5992	WOR2	1.5	1.1	0.8	0.7	1.0
orf19.3223	ATP3	1.4	0.9	0.8	0.9	1.0
orf19.1296	orf19.1296	1.0	1.2	0.9	0.9	1.0
orf19.2651	orf19.2651	1.1	0.4	1.2	1.3	1.0
orf19.3765	RAX2	1.0	0.9	1.3	0.8	1.0
orf19.4257	INT1	0.9	0.8	1.0	1.2	1.0
orf19.2728	orf19.2728	1.0	1.2	1.0	0.7	1.0
orf19.6862	orf19.6862	1.1	0.7	1.4	0.8	1.0
orf19.530	orf19.530	0.9	1.0	1.2	0.9	1.0
orf19.832	GPI13	1.2	0.8	1.1	0.9	1.0
orf19.4188	NMD5	0.8	0.7	1.4	1.1	1.0
orf19.3138	NOP1	1.3	0.6	0.9	1.2	1.0
orf19.1299	RPN6	1.1	0.8	1.2	0.9	1.0
orf19.716	orf19.716	1.1	0.8	1.1	0.9	1.0
orf19.1484	orf19.1484	1.4	0.7	1.1	0.8	1.0

		CAP2/cap2Δ				
Systematic Name	**Standard Name**	***1a***	***1b***	***2a***	***2b***	**Ave.**
orf19.5117	OLE1	1.0	0.7	1.0	1.3	1.0
orf19.7634	MCD1	0.5	0.9	1.0	1.6	1.0
orf19.2611	MCM6	0.7	0.7	1.3	1.2	1.0
orf19.1069	RPN4	1.0	1.1	0.7	1.1	1.0
orf19.3153	MSS4	1.1	0.7	1.2	0.9	1.0
orf19.5447	HGT19	1.0	1.3	0.6	1.0	1.0
orf19.3552	orf19.3552	0.9	1.1	0.9	1.0	1.0
orf19.7516	orf19.7516	1.0	0.8	1.1	1.0	1.0
orf19.910	orf19.910	1.2	1.0	0.8	1.0	1.0
orf19.6367	SSB1	1.0	0.7	0.8	1.4	1.0
orf19.1533	orf19.1533	0.8	1.1	1.0	1.0	1.0
orf19.4748	orf19.4748	0.9	0.8	1.0	1.1	1.0
orf19.6920	orf19.6920	1.3	0.7	1.1	0.7	1.0
orf19.6966	orf19.6966	0.7	0.6	1.4	1.2	1.0
orf19.3003.1	RPL6	0.8	1.1	0.9	1.1	1.0
orf19.2398	orf19.2398	-1.0	-1.4	-0.8	-0.6	-1.0
orf19.5515	orf19.5515	-0.7	-1.4	-0.7	-1.1	-1.0
orf19.3183	orf19.3183	-0.6	-1.3	-0.9	-1.0	-1.0
orf19.2244	orf19.2244	-0.6	-1.6	-0.9	-0.8	-1.0
orf19.5323	MDH1-3	-1.1	-1.5	-0.6	-0.6	-1.0
orf19.3471	orf19.3471	-0.5	-1.5	-0.9	-0.9	-1.0
orf19.5579	orf19.5579	-0.8	-1.2	-0.9	-1.0	-1.0
orf19.5463	orf19.5463	-1.3	-1.2	-0.8	-0.5	-1.0
orf19.6255	orf19.6255	-1.1	-1.4	-0.8	-0.6	-1.0
orf19.1957	CYC3	-0.9	-1.2	-1.2	-0.6	-1.0
orf19.2640	FUR1	-0.6	-1.4	-0.9	-1.0	-1.0
orf19.4943	PSA2	-1.0	-1.4	-0.6	-0.8	-1.0
orf19.4774	AOX1	-0.7	-1.2	-0.9	-1.1	-1.0
orf19.7183	orf19.7183	-0.4	-1.4	-0.9	-1.2	-1.0
orf19.6180	orf19.6180	-0.9	-1.2	-0.9	-0.8	-1.0
orf19.3643	orf19.3643	-1.2	-1.3	-0.6	-0.7	-1.0
orf19.2985	orf19.2985	-0.4	-1.2	-1.1	-1.1	-1.0
orf19.5459	orf19.5459	-1.3	-1.2	-0.9	-0.5	-1.0
orf19.1323	orf19.1323	-1.2	-1.2	-0.8	-0.7	-1.0
orf19.6424	orf19.6424	-0.4	-1.6	-1.0	-0.9	-1.0
orf19.2113	orf19.2113	-1.1	-1.2	-0.9	-0.7	-1.0
orf19.1002	orf19.1002	-1.5	-1.1	-0.6	-0.8	-1.0
orf19.7485	orf19.7485	-0.7	-1.3	-0.9	-0.9	-1.0
orf19.3544	orf19.3544	-0.5	-1.4	-1.0	-1.0	-1.0
orf19.4187	orf19.4187	-0.9	-1.3	-0.9	-0.8	-1.0
orf19.252	orf19.252	-0.3	-1.5	-0.9	-1.2	-1.0

		CAP2/cap2Δ				
Systematic Name	**Standard Name**	***1a***	***1b***	***2a***	***2b***	**Ave.**
orf19.2978	orf19.2978	-0.4	-1.6	-1.1	-0.9	-1.0
orf19.4373	orf19.4373	-0.6	-1.6	-0.7	-1.0	-1.0
orf19.3523	CRK1	-1.4	-1.1	-0.8	-0.7	-1.0
orf19.1414	orf19.1414	-1.1	-1.5	-0.7	-0.7	-1.0
orf19.1405	PHO13	-1.0	-1.3	-0.9	-0.8	-1.0
orf19.4470	orf19.4470	-0.9	-1.8	-0.6	-0.6	-1.0
orf19.7260	orf19.7260	-0.8	-1.5	-1.0	-0.7	-1.0
orf19.7165	orf19.7165	-1.0	-1.0	-1.1	-0.9	-1.0
orf19.376	orf19.376	-0.6	-1.0	-1.2	-1.1	-1.0
orf19.1082.1	orf19.1082.1	-0.5	-1.6	-0.9	-0.9	-1.0
orf19.6393	orf19.6393	-1.5	-1.1	-0.8	-0.6	-1.0
orf19.234	PHA2	-0.6	-1.5	-0.8	-1.0	-1.0
orf19.951	orf19.951	-0.4	-1.1	-1.2	-1.2	-1.0
orf19.2057	orf19.2057	-1.3	-1.3	-0.7	-0.7	-1.0
orf19.5248	MSO1	-0.8	-1.5	-0.8	-0.9	-1.0
orf19.6005	ECM3	-1.3	-1.4	-0.8	-0.6	-1.0
orf19.1563	HGT5	-1.0	-1.2	-0.7	-1.0	-1.0
orf19.2581	orf19.2581	-0.8	-1.6	-0.6	-1.0	-1.0
orf19.1395	orf19.1395	-0.5	-0.9	-1.3	-1.2	-1.0
orf19.7520	POT1	-1.2	-1.5	-0.7	-0.5	-1.0
orf19.6374	orf19.6374	-0.9	-1.4	-0.7	-0.9	-1.0
orf19.2005	REG1	-1.4	-1.4	-0.6	-0.6	-1.0
orf19.3781	orf19.3781	-0.9	-1.6	-0.7	-0.8	-1.0
orf19.805	orf19.805	-0.6	-1.5	-1.0	-0.9	-1.0
orf19.1656	orf19.1656	-1.2	-1.1	-0.7	-1.0	-1.0
orf19.5892	orf19.5892	-1.5	-1.2	-0.6	-0.6	-1.0
orf19.2608	ADH5	-1.3	-1.4	-0.9	-0.5	-1.0
orf19.2089	orf19.2089	-0.7	-1.3	-1.1	-1.0	-1.0
orf19.1369	CUP2	-1.2	-1.3	-0.8	-0.7	-1.0
orf19.5001	orf19.5001	-1.1	-1.2	-0.8	-1.0	-1.0
orf19.2391	orf19.2391	-1.0	-1.2	-0.9	-0.9	-1.0
orf19.3409	SEC12	-1.4	-1.3	-0.7	-0.6	-1.0
orf19.5431	orf19.5431	-0.8	-1.5	-0.8	-0.9	-1.0
orf19.2039	MSF1	-1.1	-1.1	-0.9	-1.0	-1.0
orf19.7589	orf19.7589	-0.6	-1.5	-0.8	-1.1	-1.0
orf19.439	orf19.439	-0.5	-1.4	-1.0	-1.2	-1.0
orf19.2275	orf19.2275	-0.8	-1.4	-1.2	-0.8	-1.0
orf19.3442	orf19.3442	-1.0	-1.6	-0.8	-0.7	-1.0
orf19.7046	MET28	-0.5	-1.3	-1.0	-1.2	-1.0
orf19.6640	TPS1	-1.4	-1.4	-0.6	-0.7	-1.0
orf19.2484	orf19.2484	-1.0	-1.3	-1.0	-0.8	-1.0

		CAP2/cap2Δ				
Systematic Name	**Standard Name**	***1a***	***1b***	***2a***	***2b***	**Ave.**
orf19.5054	orf19.5054	-0.8	-1.6	-0.9	-0.8	-1.0
orf19.7436.1	ECM15	-0.3	-1.6	-1.2	-1.0	-1.0
orf19.6884	orf19.6884	-1.0	-1.2	-0.9	-1.0	-1.0
orf19.3577	COQ5	-0.9	-1.2	-1.1	-0.9	-1.0
orf19.7265	orf19.7265	-1.0	-1.2	-1.0	-0.9	-1.0
orf19.150	orf19.150	-0.9	-1.2	-1.1	-0.9	-1.0
orf19.1496	orf19.1496	-1.2	-1.4	-0.6	-0.8	-1.0
orf19.5673	OPT7	-1.2	-1.5	-0.6	-0.8	-1.0
orf19.3412	ATG15	-1.3	-1.3	-0.9	-0.6	-1.0
orf19.156	FGR51	-1.2	-1.0	-0.9	-0.9	-1.0
orf19.6872	orf19.6872	-1.1	-1.6	-0.7	-0.7	-1.0
orf19.5256	orf19.5256	-1.0	-1.3	-0.8	-1.1	-1.0
orf19.7237	orf19.7237	-0.6	-1.3	-1.1	-1.1	-1.0
orf19.5046	RAM1	-1.2	-1.1	-0.8	-1.0	-1.0
orf19.2376	orf19.2376	-1.1	-1.4	-0.8	-0.8	-1.0
orf19.3249	LAG1	-1.0	-1.4	-0.8	-0.9	-1.0
orf19.3670	GAL1	-1.2	-1.1	-0.9	-0.9	-1.0
orf19.5963	orf19.5963	-1.3	-1.6	-0.6	-0.6	-1.0
orf19.6639	orf19.6639	-0.9	-1.5	-0.8	-1.0	-1.0
orf19.4245	PGA52	-1.2	-1.5	-0.8	-0.6	-1.0
orf19.1911	orf19.1911	-1.1	-1.3	-0.9	-0.8	-1.0
orf19.105	HAL22	-1.1	-1.1	-1.1	-0.8	-1.0
orf19.4084	KIS1	-1.5	-1.4	-0.6	-0.7	-1.0
orf19.2525	LYS12	-1.3	-1.7	-0.7	-0.5	-1.0
orf19.3516	orf19.3516	-0.4	-1.4	-1.1	-1.3	-1.0
orf19.3737	orf19.3737	-1.2	-1.5	-0.6	-0.8	-1.0
orf19.1963	orf19.1963	-1.2	-1.1	-0.9	-1.0	-1.0
orf19.2774	COQ4	-1.0	-1.3	-0.9	-0.9	-1.0
orf19.3008	LAB5	-0.8	-1.4	-0.9	-1.0	-1.0
orf19.5114	orf19.5114	-0.9	-1.4	-0.9	-1.0	-1.0
orf19.4878	orf19.4878	-1.6	-1.2	-0.8	-0.6	-1.0
orf19.1910	orf19.1910	-0.6	-1.5	-1.0	-1.1	-1.0
orf19.4991	MPT5	-1.3	-1.3	-0.8	-0.8	-1.1
orf19.3367	orf19.3367	-0.7	-1.6	-0.9	-1.0	-1.1
orf19.5433	orf19.5433	-0.3	-1.5	-1.2	-1.3	-1.1
orf19.1158	orf19.1158	-0.6	-1.4	-1.1	-1.2	-1.1
orf19.2383	YKU80	-1.2	-1.4	-0.9	-0.8	-1.1
orf19.7642	orf19.7642	-1.1	-1.7	-0.8	-0.7	-1.1
orf19.2046	POT1-2	-1.6	-1.4	-0.8	-0.4	-1.1
orf19.954	orf19.954	-1.0	-1.1	-1.1	-1.0	-1.1
orf19.6435	orf19.6435	-0.6	-1.5	-1.1	-1.0	-1.1

		CAP2/cap2Δ				
Systematic Name	**Standard Name**	***1a***	***1b***	***2a***	***2b***	**Ave.**
orf19.77.1	orf19.77.1	-0.7	-1.5	-0.8	-1.3	-1.1
orf19.5058	SMI1	-1.5	-1.4	-0.7	-0.7	-1.1
orf19.6408	orf19.6408	-1.4	-1.2	-0.8	-0.9	-1.1
orf19.1519	orf19.1519	-1.5	-0.9	-1.1	-0.8	-1.1
orf19.6704	orf19.6704	-1.1	-1.5	-0.8	-0.9	-1.1
orf19.5751	ORM1	-1.0	-1.3	-0.9	-1.0	-1.1
orf19.3360	orf19.3360	-1.5	-1.5	-0.5	-0.8	-1.1
orf19.6420	PGA13	-1.3	-1.3	-1.0	-0.7	-1.1
orf19.5182	POL3	-1.6	-1.3	-0.8	-0.6	-1.1
orf19.6933	orf19.6933	-0.9	-1.1	-1.3	-1.0	-1.1
orf19.7680	CTA26	-0.8	-1.1	-1.4	-1.0	-1.1
orf19.1177	orf19.1177	-1.3	-1.4	-0.9	-0.7	-1.1
orf19.3802	PMT6	-1.6	-1.4	-0.8	-0.6	-1.1
orf19.430	orf19.430	-0.7	-1.6	-0.7	-1.3	-1.1
orf19.4612	orf19.4612	-0.3	-1.4	-1.2	-1.4	-1.1
orf19.2106	orf19.2106	-1.1	-1.7	-0.8	-0.7	-1.1
orf19.5297	orf19.5297	-1.3	-1.4	-0.8	-0.9	-1.1
orf19.688	orf19.688	-0.7	-1.5	-1.0	-1.1	-1.1
orf19.3038	TPS2	-1.5	-1.2	-0.8	-0.8	-1.1
orf19.989	orf19.989	-1.2	-1.5	-1.0	-0.7	-1.1
orf19.3952	orf19.3952	-1.4	-1.3	-0.9	-0.8	-1.1
orf19.1890	orf19.1890	-0.8	-1.3	-1.1	-1.1	-1.1
orf19.5780	orf19.5780	-1.2	-1.6	-0.6	-1.0	-1.1
orf19.6129	MRPL8	-0.8	-1.5	-1.0	-1.1	-1.1
orf19.2439.1	orf19.2439.1	-0.7	-1.7	-0.8	-1.1	-1.1
orf19.6127	LPD1	-1.4	-1.6	-0.9	-0.4	-1.1
orf19.3310	orf19.3310	-0.5	-1.3	-1.3	-1.2	-1.1
orf19.347	RSN1	-1.2	-1.4	-0.8	-0.9	-1.1
orf19.3314	orf19.3314	-1.0	-1.7	-0.8	-0.9	-1.1
orf19.6809	orf19.6809	-1.0	-1.6	-0.9	-0.8	-1.1
orf19.5943	orf19.5943	-1.3	-1.3	-0.8	-0.9	-1.1
orf19.2459	orf19.2459	-1.4	-1.3	-0.8	-0.8	-1.1
orf19.309	DAL5	-0.6	-1.7	-1.0	-1.1	-1.1
orf19.6586	orf19.6586	-1.2	-1.5	-0.9	-0.7	-1.1
orf19.2644	QCR2	-1.4	-1.6	-0.9	-0.5	-1.1
orf19.4287	orf19.4287	-1.3	-1.5	-0.8	-0.9	-1.1
orf19.1667	orf19.1667	-1.0	-1.1	-0.9	-1.4	-1.1
orf19.7227	orf19.7227	-0.7	-1.4	-1.4	-0.9	-1.1
orf19.814	SSY1	-1.2	-1.2	-1.1	-1.0	-1.1
orf19.4738	orf19.4738	-1.2	-1.6	-0.8	-0.9	-1.1
orf19.6182	orf19.6182	-1.4	-1.5	-0.9	-0.7	-1.1

		CAP2/cap2Δ				
Systematic Name	**Standard Name**	***1a***	***1b***	***2a***	***2b***	**Ave.**
orf19.5911	CMK1	-1.3	-1.6	-0.7	-0.9	-1.1
orf19.372	orf19.372	-0.7	-1.4	-1.3	-1.0	-1.1
orf19.3515	orf19.3515	-0.8	-1.9	-0.8	-1.0	-1.1
orf19.1401	EAP1	-1.3	-1.4	-0.9	-0.8	-1.1
orf19.4524	orf19.4524	-1.3	-1.7	-0.7	-0.8	-1.1
orf19.2670	orf19.2670	-1.1	-1.8	-0.7	-0.9	-1.1
orf19.490	orf19.490	-0.8	-1.8	-0.9	-1.1	-1.1
orf19.2069	SMF3	-1.4	-1.7	-0.8	-0.6	-1.1
orf19.1391	orf19.1391	-1.1	-1.8	-0.9	-0.8	-1.1
orf19.7522	orf19.7522	-1.2	-1.6	-0.8	-0.8	-1.1
orf19.4928	orf19.4928	-1.5	-1.4	-0.9	-0.8	-1.1
orf19.3691	orf19.3691	-1.1	-1.6	-0.8	-1.0	-1.1
orf19.6313.2	orf19.6313.2	-0.6	-1.9	-0.9	-1.2	-1.1
orf19.874	orf19.874	-1.2	-1.6	-1.1	-0.7	-1.1
orf19.3499	orf19.3499	-0.7	-1.8	-0.9	-1.1	-1.1
orf19.7159	orf19.7159	-1.3	-1.4	-0.8	-1.0	-1.1
orf19.2308	orf19.2308	-1.1	-1.5	-1.1	-1.0	-1.1
orf19.5133	orf19.5133	-1.3	-1.5	-0.9	-0.9	-1.1
orf19.357	orf19.357	-0.9	-1.3	-1.3	-1.1	-1.1
orf19.5245	orf19.5245	-1.5	-1.5	-0.4	-1.2	-1.1
orf19.5980	orf19.5980	-1.1	-1.6	-0.8	-1.1	-1.1
orf19.1403	orf19.1403	-1.2	-1.8	-0.8	-0.8	-1.1
orf19.6985	TEA1	-1.3	-1.4	-0.9	-1.0	-1.1
orf19.5443	orf19.5443	-1.6	-1.6	-0.7	-0.7	-1.2
orf19.1285	orf19.1285	-1.3	-1.5	-0.8	-0.9	-1.2
orf19.5394.1	orf19.5394.1	-0.9	-1.7	-0.8	-1.2	-1.2
orf19.1178	orf19.1178	-0.9	-1.5	-0.9	-1.2	-1.2
orf19.557	orf19.557	-1.0	-1.6	-0.9	-1.1	-1.2
orf19.449	orf19.449	-1.0	-1.5	-1.0	-1.2	-1.2
orf19.2846	orf19.2846	-0.4	-1.7	-1.1	-1.4	-1.2
orf19.354	orf19.354	-1.5	-1.6	-0.8	-0.8	-1.2
orf19.4523	orf19.4523	-1.5	-1.8	-0.7	-0.6	-1.2
orf19.2176	IFM3	-1.3	-1.4	-1.0	-0.9	-1.2
orf19.7531	orf19.7531	-0.5	-1.4	-1.3	-1.4	-1.2
orf19.3995	RIM13	-1.5	-1.4	-1.0	-0.7	-1.2
orf19.685	YHM1	-0.8	-1.6	-1.1	-1.2	-1.2
orf19.6075	orf19.6075	-0.7	-1.7	-1.1	-1.1	-1.2
orf19.5428	orf19.5428	-0.6	-1.4	-1.4	-1.3	-1.2
orf19.719	orf19.719	-1.5	-1.4	-1.0	-0.9	-1.2
orf19.5320	NCE4	-0.7	-2.0	-0.8	-1.3	-1.2
orf19.3573	orf19.3573	-1.7	-1.5	-0.8	-0.7	-1.2

		CAP2/cap2Δ				
Systematic Name	**Standard Name**	***1a***	***1b***	***2a***	***2b***	**Ave.**
orf19.7602	orf19.7602	-1.0	-1.7	-1.1	-1.1	-1.2
orf19.4318	MIG1	-1.2	-1.6	-1.0	-1.0	-1.2
orf19.458	orf19.458	-1.2	-1.7	-1.0	-0.9	-1.2
orf19.3104	YDC1	-1.0	-1.2	-1.3	-1.3	-1.2
orf19.6660	EXG2	-1.4	-1.6	-0.9	-0.9	-1.2
orf19.2952	orf19.2952	-1.0	-1.4	-1.1	-1.3	-1.2
orf19.730	orf19.730	-1.6	-1.5	-0.9	-0.8	-1.2
orf19.1742	HEM3	-1.0	-1.4	-1.1	-1.3	-1.2
orf19.6055	orf19.6055	-1.8	-1.6	-0.8	-0.6	-1.2
orf19.1168	orf19.1168	-0.4	-1.5	-1.4	-1.5	-1.2
orf19.3402	FPG1	-1.2	-1.5	-1.0	-1.1	-1.2
orf19.6944	PHB1	-1.0	-1.7	-1.3	-0.9	-1.2
orf19.2117	LEU5	-1.2	-1.9	-0.9	-0.8	-1.2
orf19.4407	orf19.4407	-1.2	-1.3	-1.1	-1.2	-1.2
orf19.4759	COX5	-1.2	-2.0	-0.8	-0.8	-1.2
orf19.1715	IRO1	-1.5	-1.5	-0.8	-1.1	-1.2
orf19.692	orf19.692	-1.0	-2.1	-0.7	-1.0	-1.2
orf19.1980	GIT4	-1.5	-1.3	-1.3	-0.7	-1.2
orf19.4299	MSW1	-1.1	-1.8	-1.0	-1.0	-1.2
orf19.1416	COX11	-1.2	-1.7	-1.1	-0.9	-1.2
orf19.5131	orf19.5131	-1.6	-1.7	-0.8	-0.8	-1.2
orf19.7111.1	SOD3	-0.6	-1.1	-1.7	-1.5	-1.2
orf19.6057	orf19.6057	-1.0	-1.4	-1.5	-1.1	-1.2
orf19.3308	orf19.3308	-1.6	-1.5	-0.9	-0.9	-1.2
orf19.362	TLO9	-0.7	-1.3	-1.5	-1.3	-1.2
orf19.2009	orf19.2009	-1.3	-1.7	-0.8	-1.1	-1.2
orf19.4549	FGR38	-1.8	-1.4	-0.8	-0.9	-1.2
orf19.7288	orf19.7288	-1.6	-1.9	-1.0	-0.5	-1.2
orf19.2127	orf19.2127	-1.1	-1.6	-1.2	-0.9	-1.2
orf19.2977	orf19.2977	-0.9	-1.6	-1.3	-1.2	-1.2
orf19.397	orf19.397	-0.4	-1.9	-1.2	-1.5	-1.2
orf19.441	RPT1	-1.3	-2.1	-0.9	-0.7	-1.2
orf19.386	SAM4	-1.6	-1.7	-1.0	-0.7	-1.2
orf19.5940	orf19.5940	-1.7	-1.8	-0.7	-0.7	-1.2
orf19.3106	MET16	-1.0	-2.0	-0.8	-1.1	-1.2
orf19.5078	orf19.5078	-0.7	-2.0	-1.0	-1.3	-1.2
orf19.4539	orf19.4539	-1.1	-1.5	-1.3	-1.1	-1.2
orf19.4107	orf19.4107	-1.1	-1.9	-1.1	-0.9	-1.2
orf19.2116	NAT2	-0.8	-1.3	-1.6	-1.3	-1.2
orf19.2098	ARO8	-1.6	-1.6	-1.1	-0.7	-1.2
orf19.6023	orf19.6023	-1.4	-1.6	-0.9	-1.1	-1.3

		CAP2/cap2Δ				
Systematic Name	**Standard Name**	***1a***	***1b***	***2a***	***2b***	**Ave.**
orf19.593	FGR32	-1.6	-1.8	-0.9	-0.8	-1.3
orf19.811	orf19.811	-1.1	-1.7	-1.0	-1.3	-1.3
orf19.1978	GIT2	-1.4	-1.7	-0.9	-1.0	-1.3
orf19.394	orf19.394	-1.4	-2.0	-0.8	-0.9	-1.3
orf19.1850	SIW14	-0.9	-1.6	-1.2	-1.2	-1.3
orf19.5640	PEX5	-1.6	-1.7	-1.0	-0.8	-1.3
orf19.409	orf19.409	-0.4	-1.6	-1.4	-1.6	-1.3
orf19.7282	PEX13	-0.7	-2.1	-1.0	-1.2	-1.3
orf19.1117	orf19.1117	-1.1	-1.9	-1.1	-1.0	-1.3
orf19.819	orf19.819	-0.6	-1.8	-1.3	-1.4	-1.3
orf19.1785	orf19.1785	-1.3	-1.9	-0.9	-0.9	-1.3
orf19.2075	DFG5	-1.5	-1.6	-1.2	-0.7	-1.3
orf19.1352	orf19.1352	-1.2	-1.6	-1.2	-1.1	-1.3
orf19.6698	orf19.6698	-1.3	-1.9	-0.8	-1.1	-1.3
orf19.2568	IFU5	-1.2	-1.5	-1.3	-1.1	-1.3
orf19.223	orf19.223	-1.5	-1.5	-1.1	-1.0	-1.3
orf19.2825	orf19.2825	-1.2	-1.4	-1.2	-1.3	-1.3
orf19.2724	orf19.2724	-1.3	-1.1	-1.5	-1.2	-1.3
orf19.1201	orf19.1201	-1.6	-1.6	-1.0	-1.0	-1.3
orf19.1381	orf19.1381	-1.5	-1.9	-0.9	-0.9	-1.3
orf19.3611	orf19.3611	-1.1	-2.1	-0.8	-1.2	-1.3
orf19.3029	orf19.3029	-1.7	-1.5	-1.2	-0.8	-1.3
orf19.5210	orf19.5210	-1.3	-2.1	-0.7	-1.2	-1.3
orf19.3419	MAE1	-2.2	-2.0	-0.6	-0.4	-1.3
orf19.2313	orf19.2313	-1.5	-1.9	-1.0	-0.8	-1.3
orf19.7479	NTH1	-1.4	-1.8	-0.9	-1.1	-1.3
orf19.6595	RTA4	-1.3	-2.0	-0.9	-1.1	-1.3
orf19.6214	ATC1	-2.1	-1.3	-1.0	-0.8	-1.3
orf19.6165	KGD1	-1.9	-1.6	-1.0	-0.8	-1.3
orf19.5630	APA2	-1.3	-1.9	-0.9	-1.1	-1.3
orf19.6678	orf19.6678	-1.3	-1.8	-0.8	-1.3	-1.3
orf19.7374	CTA4	-1.8	-1.6	-1.0	-1.0	-1.3
orf19.4174	orf19.4174	-1.3	-1.5	-1.2	-1.2	-1.3
orf19.772	LYS21	-1.6	-1.9	-1.0	-0.9	-1.3
orf19.3061	orf19.3061	-0.7	-1.8	-1.1	-1.7	-1.3
orf19.1746	orf19.1746	-1.5	-2.0	-0.8	-1.1	-1.3
orf19.5246	orf19.5246	-1.5	-1.8	-1.0	-1.0	-1.3
orf19.2821	orf19.2821	-1.5	-1.8	-0.9	-1.2	-1.3
orf19.5103	orf19.5103	-1.6	-1.6	-1.1	-0.9	-1.3
orf19.6434	orf19.6434	-1.4	-2.0	-1.0	-0.9	-1.3
orf19.5399	IFF11	-1.6	-1.5	-1.3	-1.0	-1.3

		CAP2/cap2Δ				
Systematic Name	**Standard Name**	***1a***	***1b***	***2a***	***2b***	**Ave.**
orf19.7472	IFF4	-1.7	-1.6	-1.1	-1.0	-1.3
orf19.6816	orf19.6816	-1.2	-2.2	-1.0	-1.0	-1.3
orf19.6254	ANT1	-1.5	-1.8	-1.2	-0.9	-1.3
orf19.6232	NPR1	-1.8	-1.9	-0.7	-1.0	-1.3
orf19.4072	IFF6	-1.7	-1.6	-1.3	-0.8	-1.3
orf19.7665	orf19.7665	-0.8	-1.9	-1.1	-1.5	-1.3
orf19.5770	OPT8	-1.8	-1.5	-1.2	-0.9	-1.3
orf19.3022	orf19.3022	-1.2	-1.8	-1.3	-1.1	-1.3
orf19.7229	IML2	-1.7	-1.8	-1.0	-0.9	-1.3
orf19.764	orf19.764	-1.4	-1.4	-1.3	-1.3	-1.4
orf19.1625	orf19.1625	-1.1	-2.2	-1.0	-1.1	-1.4
orf19.434	PRD1	-1.9	-1.4	-1.1	-1.0	-1.4
orf19.396	EAF6	-1.1	-1.8	-1.3	-1.3	-1.4
orf19.7212	orf19.7212	-1.9	-1.9	-0.9	-0.7	-1.4
orf19.2680	orf19.2680	-1.7	-1.9	-0.9	-1.0	-1.4
orf19.3139	orf19.3139	-1.3	-1.6	-1.4	-1.2	-1.4
orf19.5729	FGR17	-1.5	-2.1	-1.0	-0.9	-1.4
orf19.5842	orf19.5842	-1.7	-1.1	-1.3	-1.4	-1.4
orf19.4507	orf19.4507	-1.1	-1.6	-1.4	-1.4	-1.4
orf19.4522	orf19.4522	-1.1	-1.5	-1.6	-1.4	-1.4
orf19.2463	PRN2	-1.5	-2.1	-0.8	-1.1	-1.4
orf19.5749	SBA1	-0.9	-1.9	-1.3	-1.4	-1.4
orf19.4490.2	QCR8	-1.1	-2.3	-1.0	-1.2	-1.4
orf19.415	orf19.415	-1.8	-2.0	-0.9	-0.9	-1.4
orf19.388	CAF16	-1.8	-1.9	-1.0	-1.0	-1.4
orf19.4088	orf19.4088	-1.1	-1.9	-1.3	-1.4	-1.4
orf19.550	PDX3	-1.4	-2.2	-0.9	-1.2	-1.4
orf19.3122	ARR3	-1.0	-1.6	-1.5	-1.6	-1.4
orf19.4975	HYR1	-1.8	-1.1	-1.3	-1.5	-1.4
orf19.6062	orf19.6062	-0.7	-1.6	-1.6	-1.7	-1.4
orf19.276	orf19.276	-1.8	-2.1	-0.8	-1.0	-1.4
orf19.4170	orf19.4170	-1.5	-1.8	-0.9	-1.4	-1.4
orf19.431	orf19.431	-1.5	-1.4	-1.4	-1.4	-1.4
orf19.1277	orf19.1277	-1.4	-1.7	-1.3	-1.3	-1.4
orf19.2006.1	COX17	-0.4	-1.8	-1.6	-1.9	-1.4
orf19.6983	orf19.6983	-2.1	-1.6	-1.0	-1.1	-1.4
orf19.5742	ALS9	-1.3	-1.7	-1.4	-1.4	-1.4
orf19.89	orf19.89	-1.6	-2.0	-1.1	-1.1	-1.4
orf19.4734	orf19.4734	-1.1	-2.1	-1.3	-1.3	-1.4
orf19.2107	MUQ1	-1.6	-2.1	-1.2	-0.9	-1.4
orf19.3746	IFC1	-1.3	-1.9	-1.2	-1.4	-1.4

		CAP2/cap2Δ				
Systematic Name	**Standard Name**	***1a***	***1b***	***2a***	***2b***	**Ave.**
orf19.2498	orf19.2498	-2.0	-1.8	-1.1	-0.9	-1.4
orf19.1411	orf19.1411	-1.9	-2.1	-0.6	-1.1	-1.4
orf19.1364	orf19.1364	-1.6	-2.2	-0.9	-1.0	-1.4
orf19.6396	orf19.6396	-2.1	-1.7	-1.0	-1.0	-1.4
orf19.6065	orf19.6065	-1.4	-2.3	-1.0	-1.2	-1.4
orf19.3407	orf19.3407	-1.3	-1.7	-1.1	-1.6	-1.5
orf19.2220	orf19.2220	-1.5	-1.8	-1.6	-0.9	-1.5
orf19.2397.3	orf19.2397.3	-1.5	-2.0	-1.2	-1.2	-1.5
orf19.2076	orf19.2076	-1.4	-1.8	-1.5	-1.2	-1.5
orf19.4886	orf19.4886	-1.6	-2.2	-0.5	-1.5	-1.5
orf19.7638	PRO1	-1.9	-2.0	-1.0	-1.0	-1.5
orf19.2261	orf19.2261	-1.6	-2.1	-1.1	-1.0	-1.5
orf19.6973	orf19.6973	-1.7	-2.0	-1.0	-1.2	-1.5
orf19.6440	orf19.6440	-1.8	-1.9	-1.0	-1.2	-1.5
orf19.740	HAP41	-1.5	-2.0	-1.1	-1.2	-1.5
orf19.6126	KGD2	-1.9	-2.0	-1.1	-0.8	-1.5
orf19.6225.1	orf19.6225.1	-1.5	-1.9	-0.8	-1.6	-1.5
orf19.2107.1	STF2	-0.8	-1.6	-1.7	-1.9	-1.5
orf19.3026	MAS1	-1.8	-1.8	-1.2	-1.2	-1.5
orf19.4184	orf19.4184	-1.7	-1.8	-1.2	-1.3	-1.5
orf19.3922	orf19.3922	-1.7	-2.2	-1.0	-1.1	-1.5
orf19.5521	ISA1	-0.8	-2.0	-1.3	-1.9	-1.5
orf19.836.1	orf19.836.1	-0.8	-2.2	-1.0	-1.9	-1.5
orf19.2883	CSO99	-1.6	-2.2	-1.1	-1.1	-1.5
orf19.7276.1	TLO4	-0.8	-1.8	-1.7	-1.6	-1.5
orf19.4013	orf19.4013	-1.9	-2.1	-1.0	-1.0	-1.5
orf19.5408	orf19.5408	-1.9	-1.9	-1.0	-1.2	-1.5
orf19.2839	CIRT4B	-2.1	-2.0	-1.1	-0.9	-1.5
orf19.6406	orf19.6406	-0.6	-2.0	-1.6	-1.7	-1.5
orf19.2779	orf19.2779	-1.9	-2.3	-0.9	-0.9	-1.5
orf19.2618	MET2	-2.1	-1.9	-1.0	-1.0	-1.5
orf19.922	ERG11	-1.6	-2.5	-1.1	-0.8	-1.5
orf19.3433	OYE23	-1.1	-2.1	-1.4	-1.5	-1.5
orf19.5527	orf19.5527	-1.9	-2.0	-1.2	-1.0	-1.5
orf19.6690	orf19.6690	-1.8	-1.7	-1.2	-1.3	-1.5
orf19.2284	orf19.2284	-1.8	-2.4	-1.0	-0.9	-1.5
orf19.92	orf19.92	-2.0	-2.2	-0.9	-1.0	-1.5
orf19.3307	orf19.3307	-1.8	-1.8	-1.3	-1.2	-1.5
orf19.5629	QCR7	-1.2	-2.3	-1.2	-1.4	-1.5
orf19.1354	UCF1	-1.9	-1.7	-1.0	-1.7	-1.6
orf19.7437	orf19.7437	-1.7	-2.0	-1.4	-1.2	-1.6

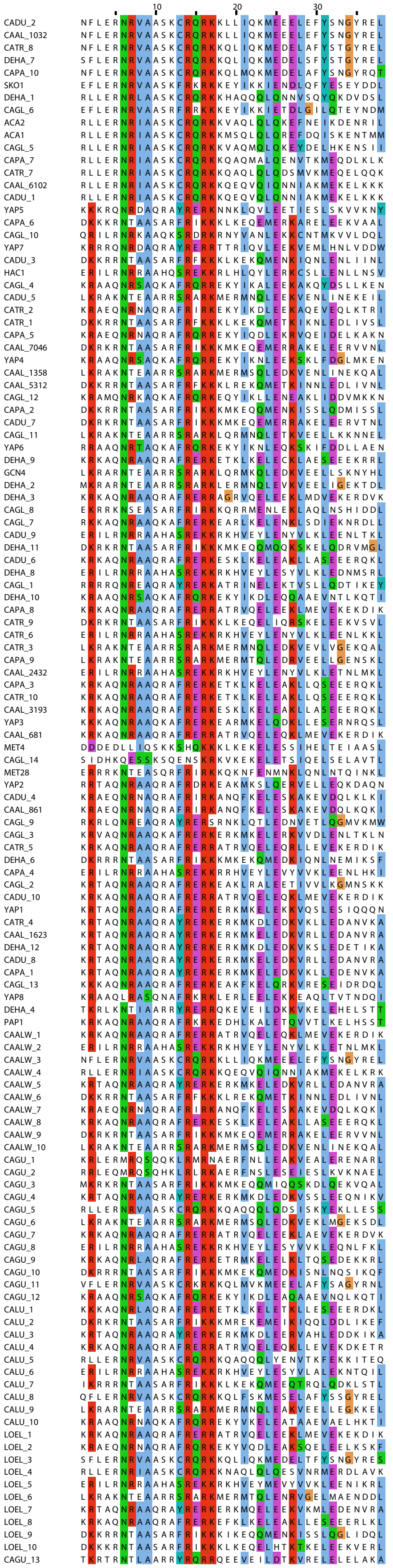
		CAP2/cap2Δ				
Systematic Name	**Standard Name**	***1a***	***1b***	***2a***	***2b***	**Ave.**
orf19.3915	orf19.3915	-2.1	-2.1	-1.1	-1.0	-1.6
orf19.1471	COX4	-1.7	-2.3	-1.3	-1.0	-1.6
orf19.5159	orf19.5159	-1.4	-1.9	-1.5	-1.6	-1.6
orf19.1473	orf19.1473	-1.2	-1.7	-1.4	-1.9	-1.6
orf19.111	CAN2	-2.1	-2.1	-1.0	-1.0	-1.6
orf19.1034	orf19.1034	-1.5	-2.5	-1.1	-1.3	-1.6
orf19.7325	orf19.7325	-1.5	-2.0	-1.5	-1.3	-1.6
orf19.3923	PGA37	-0.9	-2.7	-1.2	-1.6	-1.6
orf19.717	HSP60	-1.9	-2.1	-1.3	-1.1	-1.6
orf19.4828	orf19.4828	-2.0	-2.2	-1.1	-1.1	-1.6
orf19.3734	GEF2	-2.1	-1.8	-1.3	-1.2	-1.6
orf19.592	orf19.592	-1.9	-2.4	-1.0	-1.2	-1.6
orf19.7637	YHB4	-2.0	-2.3	-1.1	-1.0	-1.6
orf19.3518	orf19.3518	-1.9	-2.6	-1.1	-0.9	-1.6
orf19.2954	orf19.2954	-1.6	-2.6	-1.1	-1.1	-1.6
orf19.225	orf19.225	-2.1	-2.1	-1.3	-1.0	-1.6
orf19.125	EBP1	-1.6	-2.2	-1.4	-1.3	-1.6
orf19.2047	orf19.2047	-1.6	-2.3	-1.3	-1.3	-1.6
orf19.2248	ARE2	-2.0	-2.3	-1.1	-1.2	-1.6
orf19.7098	orf19.7098	-1.2	-2.4	-1.6	-1.4	-1.6
orf19.6296	orf19.6296	-1.1	-2.3	-1.4	-1.8	-1.7
orf19.6600	orf19.6600	-1.7	-1.9	-1.4	-1.5	-1.7
orf19.287	orf19.287	-1.5	-2.6	-1.3	-1.2	-1.7
orf19.3444	orf19.3444	-1.1	-2.0	-1.5	-2.0	-1.7
orf19.2989	orf19.2989	-1.9	-2.2	-1.4	-1.2	-1.7
orf19.91	orf19.91	-1.3	-2.4	-1.3	-1.7	-1.7
orf19.3167	orf19.3167	-1.9	-2.0	-1.5	-1.2	-1.7
orf19.4607	orf19.4607	-1.7	-2.2	-1.4	-1.4	-1.7
orf19.7158	orf19.7158	-1.3	-2.0	-1.5	-1.9	-1.7
orf19.336	YAH1	-1.3	-2.5	-1.4	-1.5	-1.7
orf19.516	XKS1	-1.7	-2.2	-1.3	-1.6	-1.7
orf19.1290	orf19.1290	-2.4	-2.3	-1.0	-1.1	-1.7
orf19.1617	orf19.1617	-1.8	-2.1	-1.4	-1.5	-1.7
orf19.7313	SSU1	-1.4	-1.7	-1.9	-1.8	-1.7
orf19.2754	orf19.2754	-1.2	-2.5	-1.5	-1.6	-1.7
orf19.93	orf19.93	-1.5	-2.5	-1.2	-1.6	-1.7
orf19.136	orf19.136	-1.9	-2.1	-1.4	-1.5	-1.7
orf19.7130	orf19.7130	-1.3	-2.5	-2.0	-1.1	-1.7
orf19.297	DTD2	-1.2	-2.4	-1.7	-1.6	-1.7
orf19.5547	orf19.5547	-1.2	-2.7	-1.4	-1.7	-1.7
orf19.867	orf19.867	-2.1	-2.5	-1.2	-1.2	-1.7

		CAP2/cap2Δ				
Systematic Name	**Standard Name**	***1a***	***1b***	***2a***	***2b***	**Ave.**
orf19.3340	SOD2	-1.2	-1.9	-1.9	-2.0	-1.7
orf19.1932	CFL4	-2.2	-2.0	-1.5	-1.5	-1.8
orf19.5805	DLD1	-2.3	-2.3	-1.4	-1.2	-1.8
orf19.1616	FGR23	-2.4	-2.3	-1.4	-1.2	-1.8
orf19.2938	orf19.2938	-2.1	-2.4	-1.3	-1.5	-1.8
orf19.5098	NTG1	-2.1	-2.5	-1.2	-1.5	-1.8
orf19.260	SLD1	-1.9	-2.3	-1.5	-1.6	-1.8
orf19.4358	orf19.4358	-1.6	-2.2	-2.0	-1.6	-1.8
orf19.669	PRM1	-1.9	-3.1	-1.1	-1.3	-1.9
orf19.6554	orf19.6554	-1.8	-2.6	-1.4	-1.6	-1.9
orf19.1412	orf19.1412	-1.6	-2.8	-1.4	-1.7	-1.9
orf19.1682	orf19.1682	-2.5	-2.6	-1.2	-1.1	-1.9
orf19.913.2	orf19.913.2	-2.0	-2.6	-1.5	-1.4	-1.9
orf19.4016	orf19.4016	-2.5	-2.6	-1.2	-1.2	-1.9
orf19.279	orf19.279	-1.4	-2.3	-2.0	-1.8	-1.9
orf19.4056	GAT2	-2.5	-2.2	-1.4	-1.3	-1.9
orf19.2863.1	orf19.2863.1	-1.2	-2.5	-1.8	-2.1	-1.9
orf19.4869	SFU1	-2.4	-1.8	-1.7	-1.7	-1.9
orf19.7596	orf19.7596	-1.1	-2.6	-2.1	-1.8	-1.9
orf19.2324	UBA4	-2.0	-2.4	-1.7	-1.5	-1.9
orf19.4736	orf19.4736	-2.3	-2.6	-1.4	-1.4	-1.9
orf19.4907	orf19.4907	-2.0	-2.3	-1.7	-1.7	-1.9
orf19.2091	orf19.2091	-2.0	-2.5	-1.7	-1.5	-1.9
orf19.6794	FESUR1	-2.2	-2.5	-1.9	-1.2	-1.9
orf19.176	OPT4	-2.9	-1.7	-1.6	-1.6	-2.0
orf19.1873	orf19.1873	-1.7	-2.8	-1.8	-1.5	-2.0
orf19.5000	CYB2	-2.7	-1.9	-2.1	-1.3	-2.0
orf19.84	CAN3	-2.7	-2.5	-1.5	-1.3	-2.0
orf19.6550	orf19.6550	-1.8	-2.9	-1.5	-1.9	-2.0
orf19.4495	NDH51	-2.6	-2.7	-1.4	-1.4	-2.0
orf19.4449	orf19.4449	-2.0	-2.6	-1.9	-1.7	-2.0
orf19.2419	orf19.2419	-2.3	-2.6	-1.7	-1.7	-2.0
orf19.3822	SCS7	-2.4	-2.4	-1.9	-1.5	-2.1
orf19.780	DUR1,2	-3.0	-2.8	-1.3	-1.3	-2.1
orf19.3021	orf19.3021	-2.1	-2.5	-2.0	-1.8	-2.1
orf19.2108	SOD6	-1.9	-3.3	-1.6	-1.7	-2.1
orf19.4580	orf19.4580	-1.7	-2.9	-1.7	-2.1	-2.1
orf19.2149	orf19.2149	-2.6	-2.2	-1.7	-2.0	-2.1
orf19.6531	NUC2	-2.8	-2.8	-1.5	-1.3	-2.1
orf19.822	orf19.822	-1.6	-2.4	-2.2	-2.2	-2.1
orf19.5893	RIP1	-2.6	-3.0	-1.5	-1.4	-2.1

		CAP2/cap2Δ				
Systematic Name	**Standard Name**	***1a***	***1b***	***2a***	***2b***	**Ave.**
orf19.6948	CCC1	-2.2	-2.6	-1.8	-2.1	-2.1
orf19.3846	LYS4	-3.1	-2.9	-1.3	-1.2	-2.2
orf19.4468	orf19.4468	-2.0	-3.0	-1.7	-1.9	-2.2
orf19.6249	HAK1	-2.9	-3.2	-1.2	-1.4	-2.2
orf19.1477	orf19.1477	-1.5	-2.6	-2.1	-2.5	-2.2
orf19.6559	orf19.6559	-2.5	-3.0	-1.7	-1.7	-2.2
orf19.1433	orf19.1433	-2.3	-3.1	-1.6	-1.7	-2.2
orf19.3527	CYT1	-3.0	-2.9	-1.5	-1.4	-2.2
orf19.1868	RNR22	-3.1	-3.3	-1.3	-1.2	-2.2
orf19.3290	orf19.3290	-1.9	-3.1	-2.1	-2.0	-2.3
orf19.1413	YFH1	-2.0	-3.4	-1.7	-1.9	-2.3
orf19.2601	HEM1	-2.3	-2.1	-2.4	-2.3	-2.3
orf19.670.2	orf19.670.2	-1.5	-2.8	-2.3	-2.5	-2.3
orf19.2570	MCI4	-1.8	-3.5	-2.1	-1.9	-2.3
orf19.3366.1	orf19.3366.1	-1.9	-3.1	-2.1	-2.3	-2.4
orf19.100	orf19.100	-2.9	-3.3	-1.5	-1.8	-2.4
orf19.5215	TES15	-2.3	-2.8	-2.1	-2.3	-2.4
orf19.1179	orf19.1179	-1.6	-3.5	-2.1	-2.4	-2.4
orf19.4040	ILV3	-3.4	-3.1	-1.8	-1.3	-2.4
orf19.1867	orf19.1867	-2.8	-3.0	-2.2	-1.8	-2.4
orf19.1744	HEM4	-1.8	-3.5	-2.0	-2.5	-2.4
orf19.1770	CYC1	-2.5	-3.3	-2.0	-2.1	-2.5
orf19.5205	orf19.5205	-2.8	-2.7	-2.3	-2.1	-2.5
orf19.866	RAD32	-2.6	-3.2	-1.9	-2.2	-2.5
orf19.2067	orf19.2067	-2.1	-3.5	-1.9	-2.4	-2.5
orf19.2475	PGA26	-1.7	-3.4	-2.1	-2.8	-2.5
orf19.6257	GLT1	-2.9	-2.8	-2.2	-2.2	-2.5
orf19.6996	orf19.6996	-3.2	-3.3	-1.7	-1.9	-2.5
orf19.7396	orf19.7396	-2.9	-3.1	-2.0	-2.1	-2.5
orf19.7498	LEU1	-3.2	-2.8	-2.2	-2.0	-2.5
orf19.4617	orf19.4617	-2.4	-3.5	-2.0	-2.3	-2.5
orf19.3395	orf19.3395	-2.4	-3.3	-2.1	-2.4	-2.6
orf19.4099	ECM17	-3.2	-3.0	-2.3	-1.8	-2.6
orf19.2397	orf19.2397	-2.5	-2.9	-2.4	-2.5	-2.6
orf19.2462	PRN3	-2.9	-3.7	-1.9	-1.8	-2.6
orf19.5077	orf19.5077	-2.5	-3.6	-2.0	-2.3	-2.6
orf19.6555	orf19.6555	-2.8	-3.1	-2.1	-2.4	-2.6
orf19.3749	IFC3	-3.2	-2.6	-2.5	-2.2	-2.6
orf19.1745	orf19.1745	-3.0	-3.4	-1.5	-2.5	-2.6
orf19.4041	PEX4	-1.8	-3.3	-2.6	-2.8	-2.6
orf19.5811	MET1	-2.7	-3.1	-2.4	-2.2	-2.6

		CAP2/cap2Δ				
Systematic Name	**Standard Name**	***1a***	***1b***	***2a***	***2b***	**Ave.**
orf19.3733	IDP2	-3.5	-3.3	-1.7	-2.0	-2.6
orf19.4773	AOX2	-2.5	-3.1	-2.0	-3.0	-2.6
orf19.6385	ACO1	-2.9	-2.9	-2.6	-2.2	-2.6
orf19.2674	orf19.2674	-2.2	-4.3	-1.6	-2.5	-2.6
orf19.5674	PGA10	-2.3	-3.2	-2.8	-2.3	-2.6
orf19.4758	orf19.4758	-3.2	-3.8	-1.8	-1.8	-2.7
orf19.2496	orf19.2496	-3.1	-3.7	-1.9	-1.9	-2.7
orf19.2414	orf19.2414	-2.5	-3.2	-2.2	-2.8	-2.7
orf19.4747	HEM14	-2.3	-3.4	-2.4	-2.7	-2.7
orf19.508	QDR1	-3.5	-3.5	-2.1	-1.9	-2.7
orf19.2871	SDH12	-4.0	-3.4	-2.3	-2.1	-2.9
orf19.392	orf19.392	-2.4	-3.6	-2.8	-2.9	-2.9
orf19.633	orf19.633	-3.5	-3.7	-2.3	-2.3	-3.0
orf19.5005	OSM2	-3.7	-3.1	-2.8	-2.4	-3.0
orf19.2803	HEM13	-4.1	-3.4	-2.4	-2.2	-3.0
orf19.1480	orf19.1480	-2.6	-3.7	-2.9	-3.0	-3.1
orf19.6229	CAT1	-3.6	-3.2	-2.9	-2.5	-3.1
orf19.5282	orf19.5282	-3.7	-3.9	-2.6	-2.0	-3.1
orf19.238	CCP1	-3.4	-3.8	-2.5	-2.6	-3.1
orf19.3656	COX15	-4.0	-4.3	-2.6	-2.4	-3.3
orf19.637	SDH2	-3.7	-4.3	-2.6	-2.7	-3.3
orf19.7514	PCK1	-4.2	-4.2	-2.6	-2.4	-3.3
orf19.4450.1	orf19.4450.1	-3.6	-5.2	-2.6	-2.7	-3.5
orf19.6747	orf19.6747	-3.6	-4.7	-2.7	-3.3	-3.6
orf19.489	DAP1	-3.8	-4.8	-3.0	-2.7	-3.6
orf19.7231	FTR2	-3.9	-4.1	-3.5	-3.7	-3.8
orf19.2590	orf19.2590	-3.3	-4.7	-3.7	-4.2	-4.0
orf19.2048	orf19.2048	-3.0	-4.4	-4.3	-4.3	-4.0
orf19.3707	YHB1	-5.5	-5.6	-3.0	-2.7	-4.2
orf19.2591	orf19.2591	-4.1	-4.9	-3.9	-4.0	-4.2
orf19.2587	HNM3	-5.8	-5.3	-5.4	-4.8	-5.3
orf19.2593	BIO2	-5.9	-6.1	-4.9	-4.6	-5.4

Fig. S1



CADU_2	NFLERNRVAASKCRQRKKLLIQKMEEELEFYSNGYREL
CAAL_1032	NFLERNRVAASKCRQRKKLLIQKMEEELEFYSNGYREL
CATR_8	NFLERNRVAASKCRQRKKQLIQKMEDELAFYSTGYREL
DEHA_7	SFLERNRVAASKCRQRKKQLIQKMEDELSFYSTGYREL
CAPA_10	NFLERNRVAASKCRQRKKQLMQKMEDELAFYSNGYRQT
SKO1	EFLERNRVAASKFRKRKKEYIKKIENDLQFYESEYDDL
DEHA_1	RLLERNRLAASKCRQRKKHAQQQLQNNVSQYQKDVDSL
CAGL_6	EFLERNRVAASRFRRKKKEYIKKIETDLGILQTEYNDM
ACA2	RLLERNRIAASKCRQRKKVAQLQLQKEFNEIKDENRIL
ACA1	RLLERNRIAASKCRQRKKMSQLQLQREFDQISKENTMM
CAGL_5	RLLERNRIAASKCRQRKKVAQMQLQKEYDELHKENSII
CAPA_7	RLLERNRIAASKCRQRKKQAQMALQENVTKMEQDLKLK
CATR_7	RLLERNRIAASKCRQRKKQAQLQLQDSMVKMEQELQQK
CAAL_6102	RLLERNRIAASKCRQRKKQEQVQIQNNIAKMEKELKKK
CADU_1	RLLERNRIAASKCRQRKKQEQVQLQNNIAKMEKELKKK
YAP5	KKKRQNRDAQRAYRERKNNKLQVLEETIESLSKVVKNY
CAPA_6	DKKKRNTAASARFRIKKKLKEQEMERKARELEEKVAAL
CAGL_10	QRILRNRKAAQKSRDRKRNYVANLEKKCNTMKVVLDQL
YAP7	KRRRQNRDAQRAYRERRTTRIQVLEEKVEMLHNLVDDW
CADU_3	DKKRRNTAASARFRFKKKLKEKQMENKIQNLENLIINL
HAC1	ERILRNRRAAHQSREKKRLHLQYLERKCSLLENLLNSV
CAGL_4	KRAAQNRSAQKAFRQRREKYIKALEEKAKQYDSLLKEN
CADU_5	LKRAKNTEAARRSRARKMERMNQLEEKVENLINEKEIL
CATR_2	KRAEQNRNAQRAFRIRKEKYIKDLEEKAQEVEQLKTRI
CATR_1	DKKRRNTAASARFRFKKKLKEKQMETKIKNLEDLIVSL
CAPA_5	KRAEQNRNAQRAFRQRREKYIQDLEKRVQEIDELKAKN
CAAL_7046	DKRKRNTAASARFRIKKKMKEQEMERRAKELEERVVNL
YAP4	KRAAQNRSAQKAFRQRREKYIKNLEEKSKLFDGLMKEN
CAAL_1358	LKRAKNTEAARRSRARKMERMSQLEDKVENLINEKQAL
CAAL_5312	DKKRRNTAASARFRFKKKLREKQMETKINNLEDLIVNL
CAGL_12	KRAMQNRKAQKAFRQRKEQYIKLLENEAKLIDDVMKKN
CAPA_2	DKKRRNTAASARFRIKKKMKEQQMENKISSLQDMISSL
CADU_7	DKRKRNTAASARFRIKKKMKEQEMERRAKELEERVTNL
CAGL_11	LKRAKNTEAARRSRARKLQRMNQLETKVEELLKKNNEL
YAP6	RRAAQNRTAQKAFRQRKEKYIKNLEQKSKIFDDLLAEN
DEHA_9	KRKAQNRAAQRAFRERKETKLKELECKLAESEEEKRRL
GCN4	LKRARNTEAARRSRARKLQRMKQLEDKVEELLSKNYHL
DEHA_2	MKRARNTEAARRSRARKLERMNQLEVKVEELIGEKTDL
DEHA_3	KRKAQNRAAQRAFRERRAGRVQELEEKLMDVEKERDVK
CAGL_8	EKRRKNSEASARFRIRKKQRRMENLEKLAQLNSHIDDL
CAGL_7	RKKAQNRAAQKAFRERKEARLKELENKLSDIEKNRDLL
CADU_9	ERILRNRRAAHASREKKRKHVEYLENYVLKLEENLTKL
DEHA_11	DKRKRNTAASARFRIKKKMKEQQMQQKSKELQDRVMGL
CADU_6	KRKAQNRAAQRAFRERKESKLKELEAKLLASEEERQKL
DEHA_8	ERILRNRRAAHASREKKRKHVEYLESYVLKLEDNMSRL
CAGL_1	RRRRQNREAQRAYRERKATRINELEKTVSLLQDTIKEY
DEHA_10	KRAAQNRSAQKAFRQRKEKYIKDLEQQAAEVNTLKQTI
CAPA_8	KRKAQNRAAQRAFRERRATRVQELEEKLMEVEKEKDIK
CATR_9	DKRKRNTAASARFRIKKKLKEQELIQRSKELEEKVSVL
CATR_6	ERILRNRRAAHASREKKRKHVEYLENYVLKLEENLKKL
CATR_3	LKRAKNTEAARRSRARKMERMNQLEDKVEVLVGEKQAL
CAPA_9	LKRAKNTEAARRSRARKMERMTQLEDRVEELLGENSKL
CAAL_2432	ERILRNRRAAHASREKKRKHVEYLENYVLKLETNLMKL
CAPA_3	KRKAQNRAAQRAFRERKETKLKELEAKLLQSEEERQKL
CATR_10	KRKAQNRAAQRAFRERKETKLKELEAKLLQSEEERQKL
CAAL_3193	KRKAQNRAAQRAFRERKESKLKELEAKLLASEEERQKL
YAP3	KKKAQNRAAQKAFRERKEARMKELQDKLLESERNRQSL
CAAL_681	KRKAQNRAAQRAFRERRATRVQELEQKLMEVEKERDIK
MET4	DDDEDLLIQSKKSHQKKKLKEKELESSIHELTEIAASL
CAGL_14	SIDHKQESSKSQENSKRKVKEKELETSIQELSELAVTL
MET28	ERRRKNTEASQRFRIRKKQKNFENMNKLQNLNTQINKL
YAP2	RRTAQNRAAQRAFRDRKEAKMKSLQERVELLEQKDAQN
CADU_4	KRAEQNRNAQRAFRIRKANQFKELESKAKEVDQLKLKI
CAAL_861	KRAEQNRNAQRAFRIRKANQFKELESKAKEVDQLKQKI
CAGL_9	RKRLQNREAQRAYRERSRNKLQTLEDNVETLQGMVKMW
CAGL_3	KRVAQNRAAQKAFRERKERKMKELERKVVDLENLTKLN
CATR_5	KRKAQNRAAQRAFRERRATRVQELEQRLLEVEKERDIK
DEHA_6	DKRRRNTAASARFRIKKKMKEKQMEDKIQNLNEMIKSF
CAPA_4	ERILRNRRAAHASREKKRRHVEYLEVYVVKLEENLHKI
CAGL_2	KRTAQNRAAQRAFRERKEAKLRALEETIVVLKGMNSKK
CADU_10	KRKAQNRAAQRAFRERRATRVQELEQKLMEVEKERDIK
YAP1	KRTAQNRAAQRAFRERKERKMKELEKKVQSLESIQQQN
CATR_4	KRTAQNRAAQRAYRERKERKMKDLEDKVKLLEDANVKA
CAAL_1623	KRTAQNRAAQRAYRERKERKMKELEDKVRLLEDANVRA
DEHA_12	KRTAQNRAAQRAYRERKERKMKDLEDKVKSLEDETIKA
CADU_8	KRTAQNRAAQRAYRERKERKMKELEDKVRLLEDANVRA
CAPA_1	KRTAQNRAAQRAYRERKERKMKELEDKVKLLEDENVKA
CAGL_13	KKKAQNRAAQRAFRERKEAKFKELQRKVRESEIDRDQL
YAP8	KRAAQLRASQNAFRKRKLERLEELEKKEAQLTVTNDQI
DEHA_4	TKRLKNTIAARRYRERRQKEVEILDKKVKELEHELSTT
PAP1	KRKAQNRAAQRAFRKRKEDHLKALETQVVTLKELHSST
CAALW_1	KRKAQNRAAQRAFRERRATRVQELEQKLMEVEKERDIK
CAALW_2	ERILRNRRAAHASREKKRKHVEYLENYVLKLETNLMKL
CAALW_3	NFLERNRVAASKCRQRKKLLIQKMEEELEFYSNGYREL
CAALW_4	RLLERNRIAASKCRQRKKQEQVQIQNNIAKMEKELKRK
CAALW_5	KRTAQNRAAQRAYRERKERKMKELEDKVRLLEDANVRA
CAALW_6	DKKRRNTAASARFRFKKKLREKQMETKINNLEDLIVNL
CAALW_7	KRAEQNRNAQRAFRIRKANQFKELESKAKEVDQLKQKI
CAALW_8	KRKAQNRAAQRAFRERKESKLKELEAKLLASEEERQKL
CAALW_9	DKRKRNTAASARFRIKKKMKEQEMERRAKELEERVVNL
CAALW_10	LKRAKNTEAARRSRARKMERMSQLEDKVENLINEKQAL
CAGU_1	KRLERMRQSQQKLRMRNAERFNLLEAKVEALERENARL
CAGU_2	RRLEQMRQSQHKLRLRKAERFNSLESEIESLKVKNAEL
CAGU_3	MKRKRNTAASARFRIKKKMKEQQMIQQSKDLQEKVQAL
CAGU_4	KRTAQNRAAQRAYRERKERKMKDLEDKVSSLEEQNIKV
CAGU_5	RLLERNRVAASKCRQRKKQAQQQLQDSISKYEKLLESS
CAGU_6	LKRAKNTEAARRSRARKMERMSQLEDKVEKLMGEKSDL
CAGU_7	KRKAQNRAAQRAFRERRATRVQELEEKLAEVEKERDVK
CAGU_8	ERILRNRRAAHASREKKRKHVEYLESYVVKLEQNLFKL
CAGU_9	KRKAQNRLAQRAFRERKETRMKELELKLTQSEDEKKRL
CAGU_10	DKRRRNTAASARFRIKKKMKEKQMEDKISNLNQSIKQF
CAGU_11	VFLERNRVAASKCRKRKKQLMVKMEEELAFYSAGYRNL
CAGU_12	KRAAQNRSAQKAFRQRKEKYIKDLEAQAAEVNQLKQTI
CALU_1	KKKAQNRLAQRAFRERKETKLKELETKLLESEEERDKL
CALU_2	DKRKRNTAASARFRIKKKMREKEMEIKIQQLDDLIKEF
CALU_3	KRTAQNRAAQRAYRERKERKMKDLEERVAHLEDDKIKA
CALU_4	KRKAQNRAAQRAFRERRATRVQELEQKLLEVEKDKETR
CALU_5	RLLERNRVAASKCRQRKKQAQQQLYENVTKFEKKITEQ
CALU_6	ERILRNRRAAHASREKKRKHVEYLESYVLALEKNTQIL
CALU_7	IKRRRNTAASARFRIKKKLKEKQMEEQTRQLQDKLSTL
CALU_8	QFLERNRVAASKCRQRKKQLFSKMESELAFYSSGYREL
CALU_9	LKRARNTEAARRSRARKMERMNQLEAKVEELLEGKKEL
CALU_10	KRAAQNRNAQKAFRQRREKYVKELEATAAEVAELHKTI
LOEL_1	KRKAQNRAAQRAFRERRATRVQELEEKLMEVEKEKDIK
LOEL_2	KRAEQNRNAQRAFRQRKEKYVQDLEAKSQELEELKSKF
LOEL_3	SFLERNRVAASKCRQRKKQLIQKMEDELTFYSNGYRES
LOEL_4	RLLERNRIAASKCRQRKKNAQLQLQESVNRMERDLAVK
LOEL_5	ERILRNRRAAHASREKKRKHVEYMEVYVVKLEENIKRL
LOEL_6	LKRAKNTEAARRSRARKMERMTQLENRVGELMAENDDL
LOEL_7	KRTAQNRAAQRAYRERKERKMQELEEKVKMLEDENVRA
LOEL_8	KRKAQNRAAQRAFRERKEFKLKELEAKLLESEEERLKL
LOEL_9	DKKRRNTAASARFRIKKKIKEQQMENKISSLQGLIDQL
LOEL_10	DKKKRNTAASARFRIKKKLKEQELHTKTKELEEKVERL
CAGU_13	TKRTRNTLAARRYRQRRQEEVEILDTKVRELELELAKA