

Additional data file 1. Supplementary Figures:

Figure S1. Cell division concentrations in cultures over the day-night cycle during the period of harvesting. Each symbol type represents a separate culture. The x-axis shows time (in hours) since dawn (lights on) on the first day of harvesting. The dark period (lights off) is shown by the grey box. A) Two 1N cultures grown on 14:10 light:dark over the whole experiment. RNA pools from one of these was used in 1N library construction and samples from both were used in RT-PCR tests. B) Four 2N cultures grown on 14:10 LD. RNA pools from one of these was used in 2N library construction and three were chosen at from each time point for RT-PCR testing. C) Two 1N cultures grown on 14:10 LD that experienced a failure of the light regulation one day prior to harvesting, causing them to grown in continuous light. These were not used in library construction but both were used for RT-PCR testing. Only the first 8 time points were used in pools of RNA for library construction and equal quantities of total RNA were mixed to give 100 µg of total RNA in each pool.

Figure S2. Bioanalyzer virtual gel image showing high quality of total RNA. RNA was tested after isolation, DNase treatment, and purification using the Qiagen RNeasy kit RNA clean-up protocol. The distinct 28s, 18s rRNA bands show lack of detectable degradation.

Figure S3. Histogram of EST reads per cluster. Distribution of ESTs across all clusters represented in the 1N library and all clusters represented in the 2N library.

Figure S4. Distribution of clusters by KOG functional class and library for clusters composed of ≥ 2 EST reads. * indicates KOG classes displaying significant differences between 1N-unique and 2N-unique clusters and @ indicates KOG classes displaying significant differences between 1N-unique and shared clusters.

Figure S5. Taxonomic distribution of clusters “best-hitting” to either Viridiplantae, Stramenopiles, or Metazoa. In each column of numbers, the top row refers to shared clusters, the second row refers to 1N-unique clusters, and the bottom row refers to 2N-unique clusters. Significant differences determined by Fishers Exact Test are marked (*, shared clusters different from both 1N unique and 2N unique; +, 1N-unique clusters different from both shared clusters and 2N-unique clusters; ^, 2N-unique clusters different from both shared clusters and 1N-unique clusters).

Figure S6. Example images of full gels showing absence of detectable genomic contamination in RT- samples. Top: GS00217 (Elongation factor 1 α), expressed in both cell types, amplified with primer pair e00217F2, e00217R2. Middle: GS09822 (GPA), expressed in both cell types, amplified with primer pair e09822F2/e09822R1. Bottom, GS02894, strongly differential expression in 1N (amplified with primer pair e02904F1/e02993). RT- reactions were tested in parallel with RT+ reactions with a total of 26 different primer combinations and in no case was a signal detected from RT- reactions.

Figure S7. MUSCLE alignment of phototropin homologs over the LOV2 domain

Included also is a sensor hybrid histidine kinase from the planctomycete bacterium *Gemmata obscuriglobus* identified as the second highest hit to the GS00132 predicted amino acid sequence in the nr protein database (E-value = 8e-22). The top hit to GS00132 was a PAS domain-containing predicted protein from *Ostreococcus tauri* (emb|CAL55375.1|) (E-value = 4e-23) but it was less conserved over the LOV2 domain. The following sequences were obtained from Genbank: At-PHOT2 (>gi|145362057|ref|NP_851212.2| PHOT2 (NON PHOTOTROPIC HYPOCOTYL 1-LIKE); kinase [Arabidopsis thaliana]), At-PHOT1 (>gi|15231245|ref|NP_190164.1| PHOT1 (phototropin 1); kinase [Arabidopsis thaliana]), Gemob (>gi|168702150|ref|ZP_02734427.1| multi-sensor hybrid histidine kinase [Gemmata obscuriglobus UQM 2246]), Chlre3 (>estExt_fgenes2_kg.C_190109 [Chlre3:183965]) was obtained from the *C. reinhardtii* protein catalog.

Figure S8. RT-PCR tests of expression pattern of further genes chosen by digital expression and not shown in Fig. 7-10 of the main test.

Figure S9. MUSCLE alignment of GS00273 and Myb transcription factor family members.

The following sequences were obtained from Swissprot: gi|127591|sp|P01103.1|MYB_CHICK, gi|1709195|sp|P52550.1|MYBA_CHICK, gi|417333|sp|Q03237.1|MYBB_CHICK, gi|75336839|sp|Q9S7L2.1|MYB98_ARATH, gi|75336831|sp|Q9S7G7.1|MB3R1_ARATH, gi|127590|sp|P01104.2|MYB_AVIMB. Conserved regularly repeating tryptophan residues are marked with arrows. The fourth tryptophan (the first in the R3 domain) has been substituted conservatively by phenylalanine in GS00273. This tryptophan is often substituted by other aromatic or hydrophobic residues in other plants (Martin and Paz-Ares, 1997).

Figure S10. CLUSTAL alignments of predicted amino acid sequences of clusters with GPA homology against GPA. A) Frame 3 ORF in GS09822 against GPA. B) Longest ORF of GS02894 translated frame 1 against GPA. C) A very strong homology to GPA is found over a 30 amino acid section of translated frame 2 of GS02894 against GPA, yet this frame is interrupted by multiple stop codons (marked in red), including two surrounding a methionine (potential start, marked in green). * marks perfect match, : marks strong conservation, and . marks weak conservation. The predicted EF-hand motif in GPA is underlined. The GPA sequence used was obtained from Genbank (>gi|4102565|gb|AAD01505.1| putative calcium binding protein [Emiliana huxleyi]).

Figure S11. MUSCLE alignment of VCX1 homologs. The following sequences were obtained from Swissprot: VCX1_SCHPO (>gi|74582235|sp|O59768.1|VCX1_SCHPO RecName: Full=Vacuolar calcium ion transporter), VCX1_YEAST (>gi|74623660|sp|Q99385.1|VCX1_YEAST RecName: Full=Vacuolar calcium ion transporter; AltName: Full=Vacuolar Ca(2+)/H(+) exchanger), CAX2_ARATH (>gi|122056116|sp|Q39254.2|CAX2_ARATH RecName: Full=Vacuolar cation/proton exchanger 2), CAX5_ARATH (>gi|75154113|sp|Q8L783.1|CAX5_ARATH RecName: Full=Vacuolar cation/proton exchanger 5).

Figure S12. MUSCLE alignment of partial sequences of V-type ATPase V0a subunits. The highly conserved arginine (R735 in VPH1_YEAST) is marked with an arrow. Two other clusters, GS08326 and GS12017, had hits against the KOG database to V-type ATPase V0a subunits but did not have strong homologs in the Uniprot or Swissprot databases and did not align over the conserved region shown here. The following sequences were obtained from Swissprot:

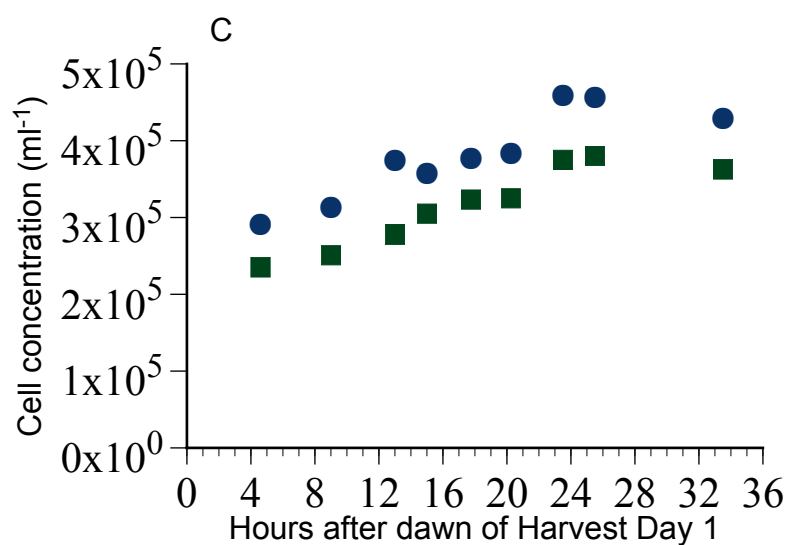
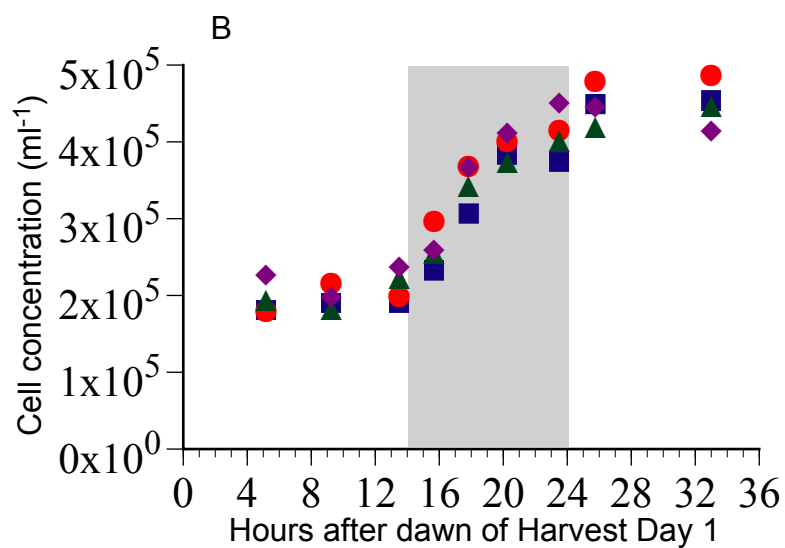
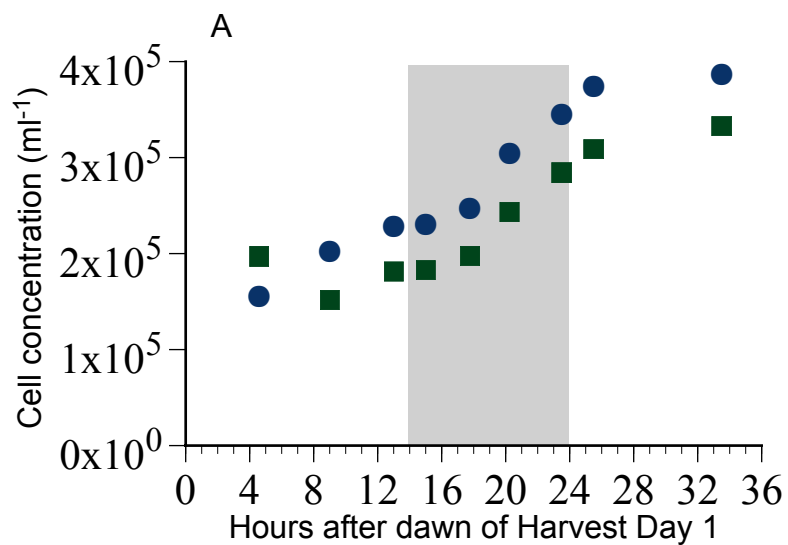
gi|1711568|sp|P37296.2|STV1_YEAST, gi|418296|sp|P32563.3|VPH1_YEAST, gi|3929395|sp|Q01290.1|VPH1_NEUCR, gi|3929385|sp|O13742.1|VPH1_SCHPO, gi|182702220|sp|Q54E04.2|VATM_DICDI, gi|59803038|sp|Q93050.3|VPP1_HUMAN, gi|172046607|sp|Q9Y487.2|VPP2_HUMAN, gi|12643719|sp|Q13488.2|VPP3_HUMAN, gi|38372616|sp|Q9HBG4.1|VPP4_HUMAN, gi|15226542|ref|NP_179736.1| VHA-A2 [Arabidopsis thaliana], gi|30683925|ref|NP_850122.1| VHA-A1 [Arabidopsis thaliana], gi|18420373|ref|NP_568051.1| VHA-A3 [Arabidopsis thaliana], gi|74502607|sp|Q5JDS2.1|VATI_PYRKO [Thermococcus kodakarensis].

Figure S13. MUSCLE alignment of histone H4 homologs. Possible initiator methionines of GS02435 are marked with arrows. The following sequences were obtained from Swissprot: gi|28202123|sp|P59259.2|H4_ARATH [Arabidopsis thaliana], gi|51317339|sp|P62805.2|H4_HUMAN, >gi|74752149|sp|Q99525.1|H4G_HUMA, gi|122107|sp|P02309.2|H4_YEAST, gi|59799579|sp|P69152.2|H42_TETTH [Tetrahymena thermophila]. To increase phylogenetic coverage the following sequences were obtained from the Genbank nr protein dataset: gi|72389584|ref|XP_845087.1| histone H4 [Trypanosoma brucei TREU927], gi|219116983|ref|XP_002179286.1| histone H4 isoform 1b [Phaeodactylum tricornutum CCAP 1055/1], gi|159464912|ref|XP_001690685.1| histone H4 [Chlamydomonas reinhardtii], gi|159480048|ref|XP_001698098.1| histone H4 variant [Chlamydomonas reinhardtii].

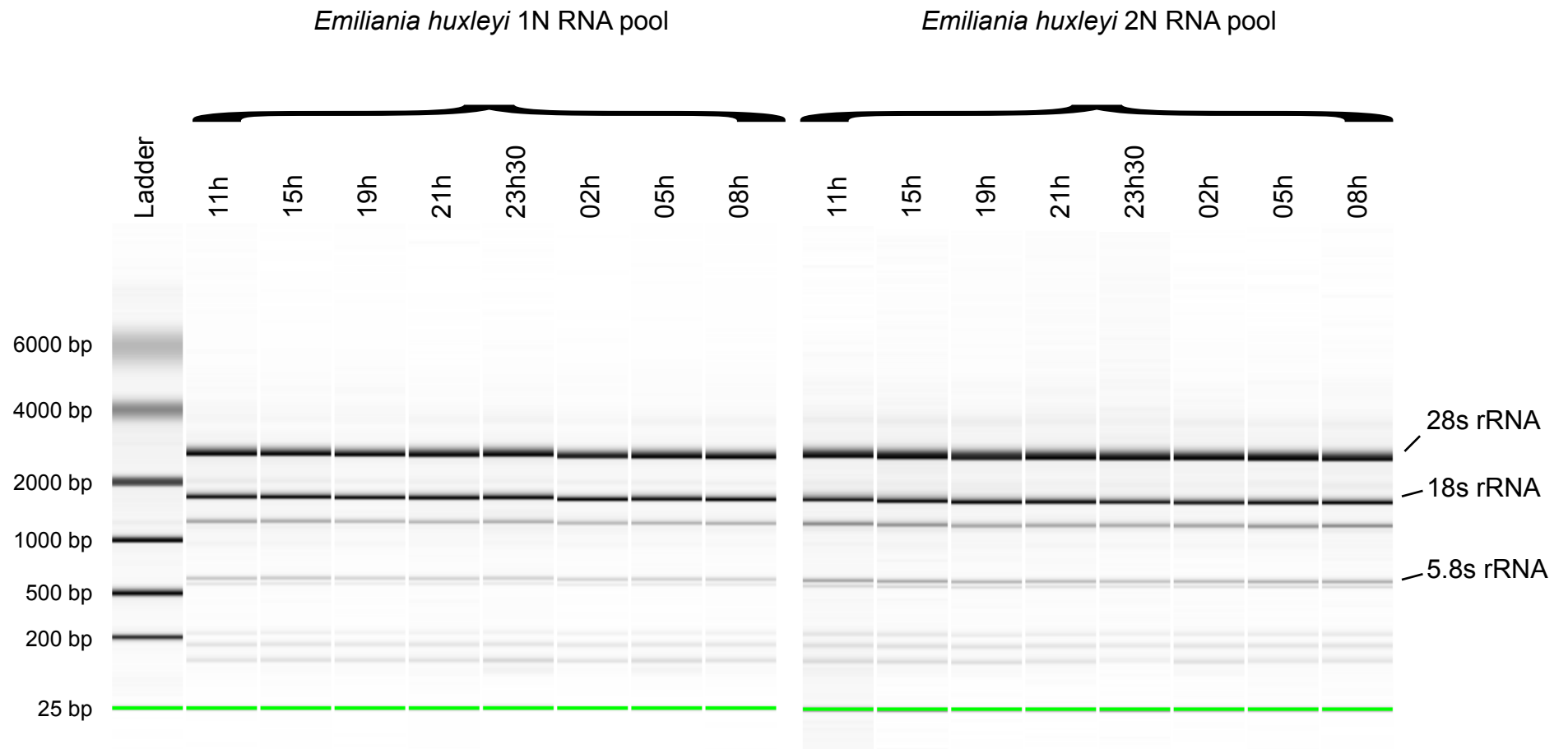
Figure S14. Partial MUSCLE alignment of histone H2A homologs. The C terminals, which are extremely variable in length and sequence, are not included. Two mini-clusters that composed cluster GS07501 differed slightly in predicted aa sequence. These are shown by e07501.1 and e07501.2. The following *Arabidopsis thaliana*, *Homo sapiens*, *C. reinhardtii*, and *Tetrahymena thermophila* sequences were obtained from Swissprot: gi|75306451|sp|Q94F49.1|H2A5_ARATH, gi|75276926|sp|O04848.1|H2AXA_ARATH, gi|75313113|sp|Q9S9K7.1|H2AXB_ARATH, gi|75308805|sp|Q9C681.1|H2A1_ARATH, gi|75311179|sp|Q9LHQ5.1|H2A2_ARATH, gi|75311051|sp|Q9LD28.1|H2A6_ARATH, gi|75279005|sp|O81826.1|H2A3_ARATH, gi|75309136|sp|Q9FJE8.1|H2A7_ARATH, gi|75311717|sp|Q9LZ46.1|H2A4_ARATH, gi|75313476|sp|Q9SII0.1|H2AV2_ARATH, gi|75277395|sp|O23628.1|H2AV1_ARATH, gi|75308904|sp|Q9C944.1|H2AV3, gi|75314165|sp|Q9T0H7.1|H2A8_ARATH, gi|74752099|sp|Q96QV6.3|H2A1A_HUMAN, gi|74750623|sp|Q8IUE6.3|H2A2B_HUMAN, gi|121992|sp|P16104.2|H2AX_HUMAN, gi|12643341|sp|Q93077.3|H2A1C_HUMAN, gi|47117890|sp|Q16777.4|H2A2C_HUMAN, gi|74733131|sp|Q9BTM1.1|H2AJ_HUMAN, gi|74751984|sp|Q96KK5.3|H2A1H_HUMAN,

gi|74757558|sp|Q6FI13.3|H2A2A_HUMAN,
gi|12585257|sp|Q99878.3|H2A1J_HUMAN, gi|83288406|sp|P0C0S8.2|H2A1_HUMAN,
gi|74749897|sp|Q7L7L0.3|H2A3_HUMAN, >gi|121978|sp|P20671.2|H2A1D_HUMAN,
gi|124028530|sp|P04908.2|H2A1B_HUMAN,
gi|90110023|sp|O75367.4|H2AY_HUMAN,
gi|12585260|sp|Q9P0M6.3|H2AW_HUMAN,
gi|74749787|sp|Q71UI9.3|H2AV_HUMAN, gi|83288408|sp|P0C0S5.2|H2AZ_HUMAN,
gi|161784333|sp|P0C5Z0.1|H2AB2_HUMAN,
gi|161784332|sp|P0C5Y9.1|H2AB1_HUMAN, gi|1708102|sp|P50567.1|H2A_CHLRE,
gi|462229|sp|P35064.2|H2A1_TETTH, gi|462230|sp|P35065.2|H2A2_TETTH,
gi|121991|sp|P08992.2|H2AV_TETTH. Four diatom sequences were obtained from
Thalassiosira pseudonana and *Phaeodactylum tricornutum* via the Genbank nr protein
database. H2A_Tpseud (gi|209585850|gb|ACI64535.1|), H2A-1_Ptric
(gi|219122004|ref|XP_002181345.1| histone H2A isoform 1), H2A-2_Ptric
(gi|219119185|ref|XP_002180358.1| histone H2A isoform 2), H2A-3_Ptric
(gi|219116815|ref|XP_002179202.1| histone H2A isoform 3a).

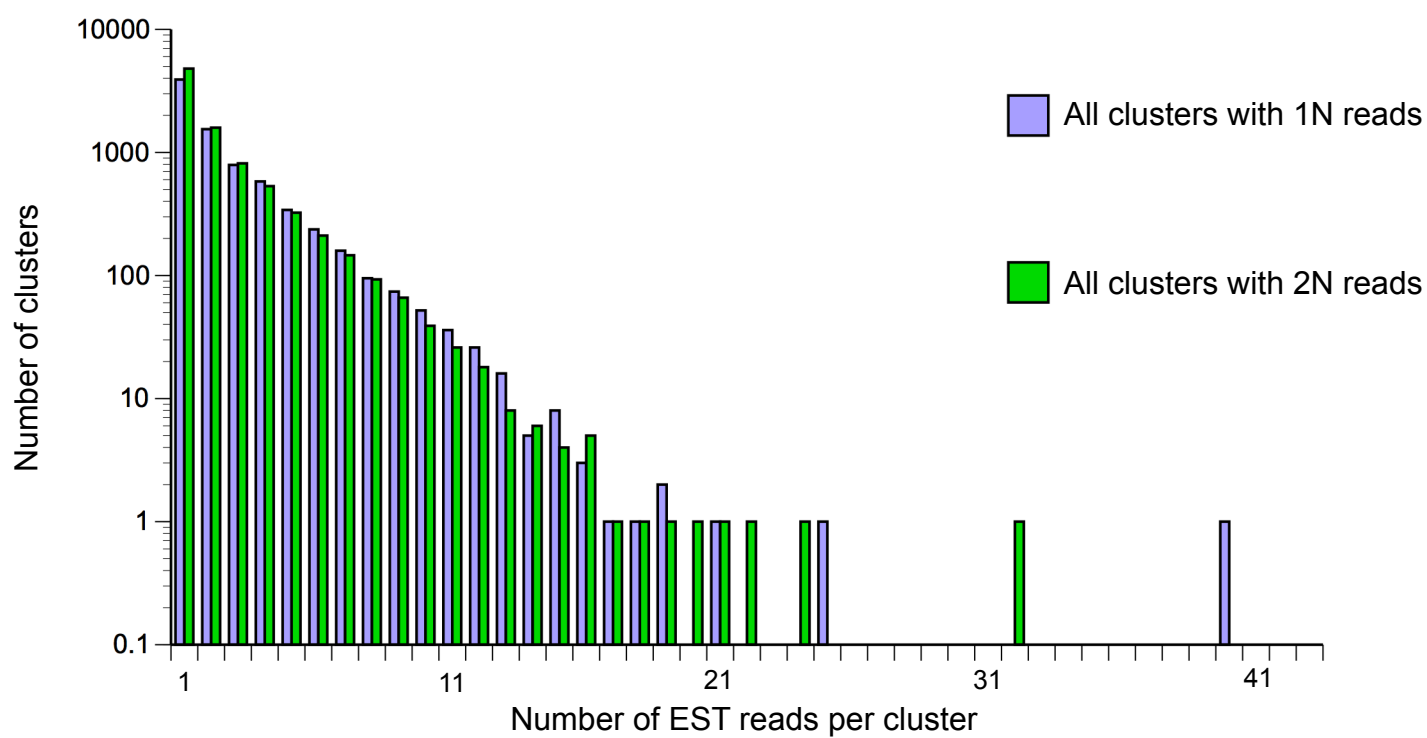
Figure S15. Phylogenetic tree classifying different H2A homologs. MUSCLE-aligned sequences were curated with GBLOCKS and aligned using the PhyML method and the Approximate Likelihood Ratio Test. Branch nodes with support <50% have been collapsed.



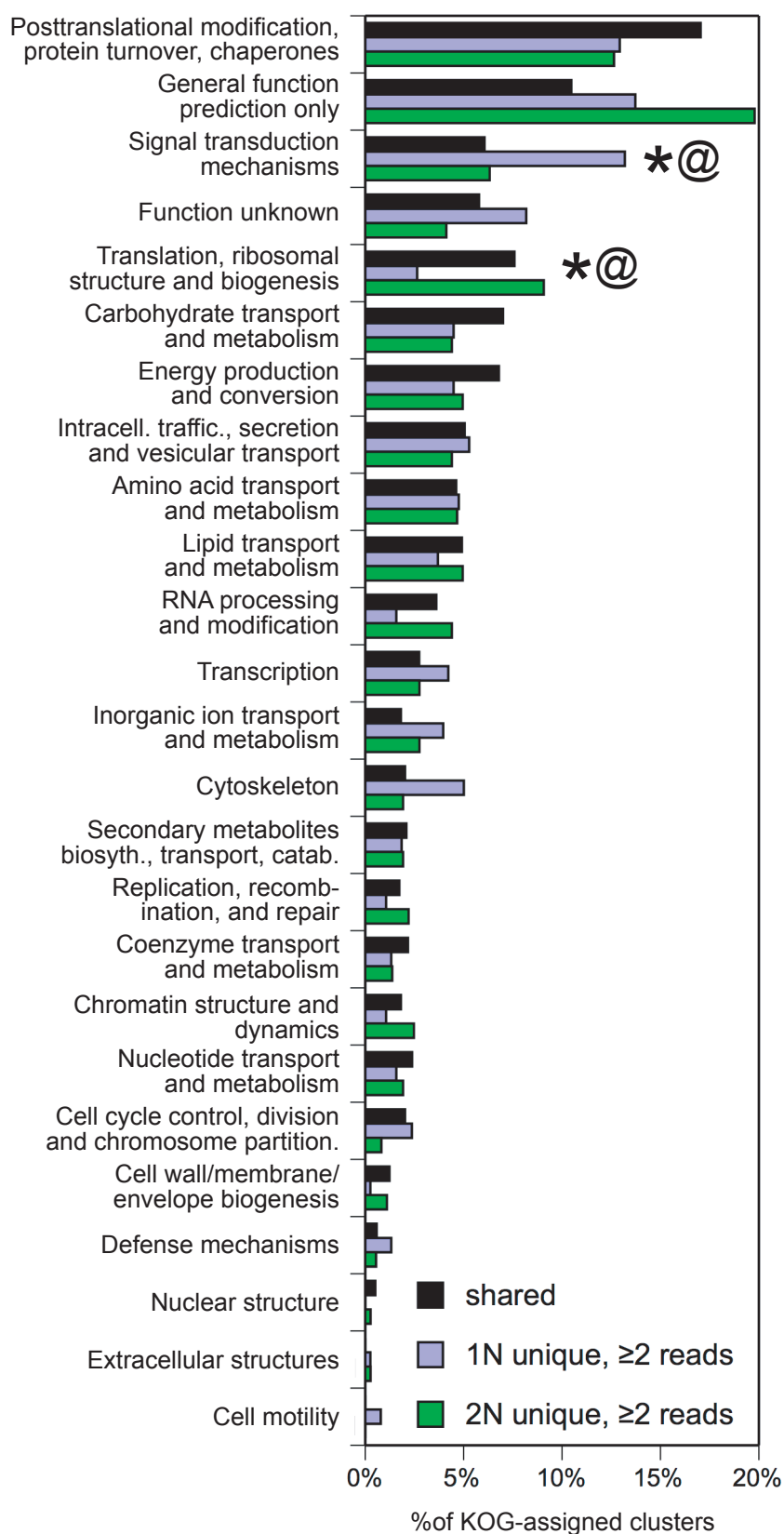
Supplementary Figure S1.



Supplementary Figure S2. Bioanalyzer analysis of total purified RNA samples pooled for construction of 1N and 2N libraries.



Supplementary Figure S3.



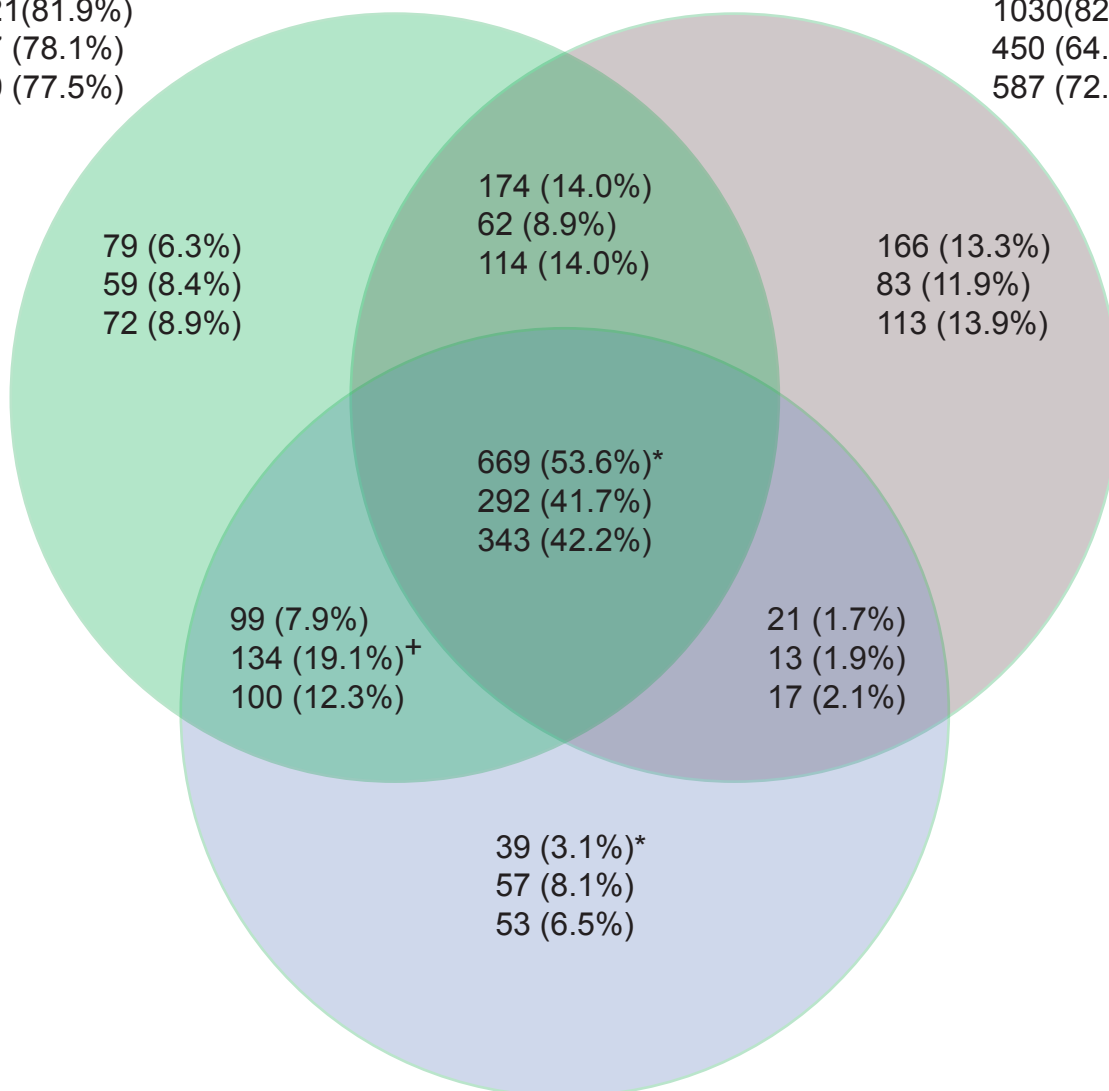
Supplementary Figure S4.

Viridiplantae

1021(81.9%)
547 (78.1%)
629 (77.5%)

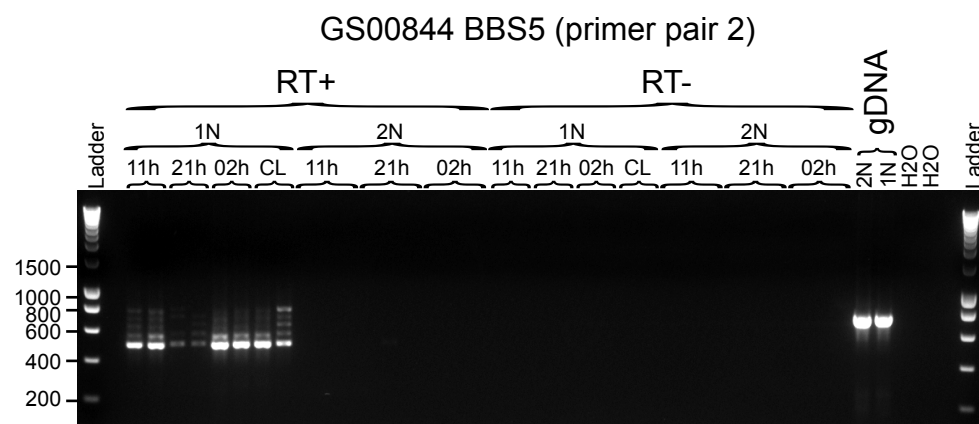
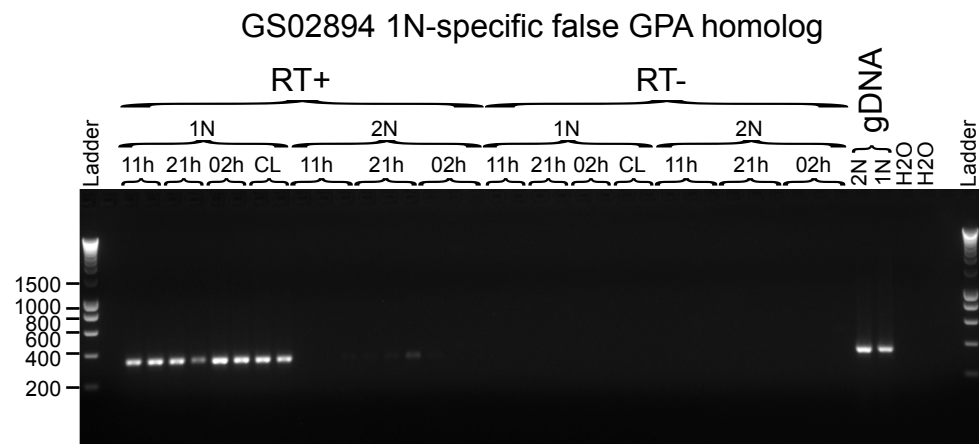
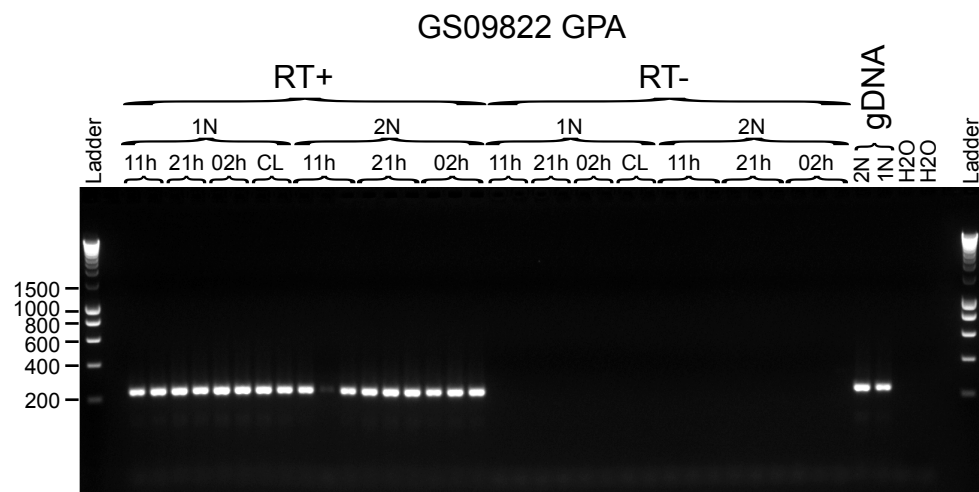
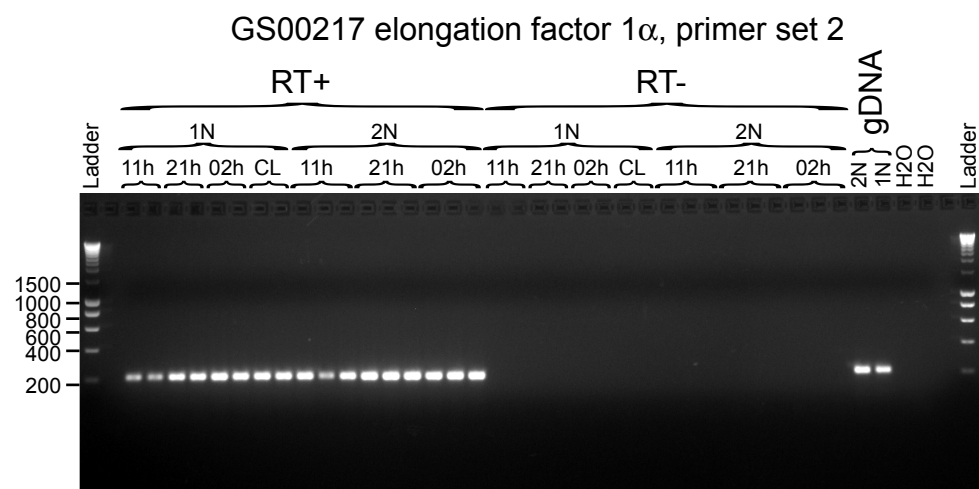
Stramenopiles

1030(82.6%)*
450 (64.3%)+
587 (72.3%)^



Metazoa

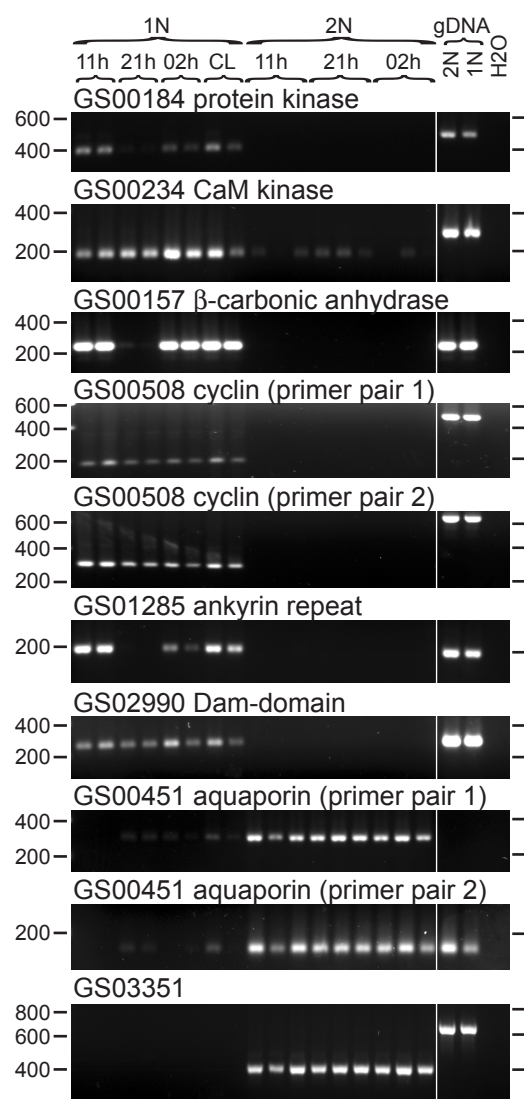
828 (66.4%)
496 (70.9%)
513 (63.2%)



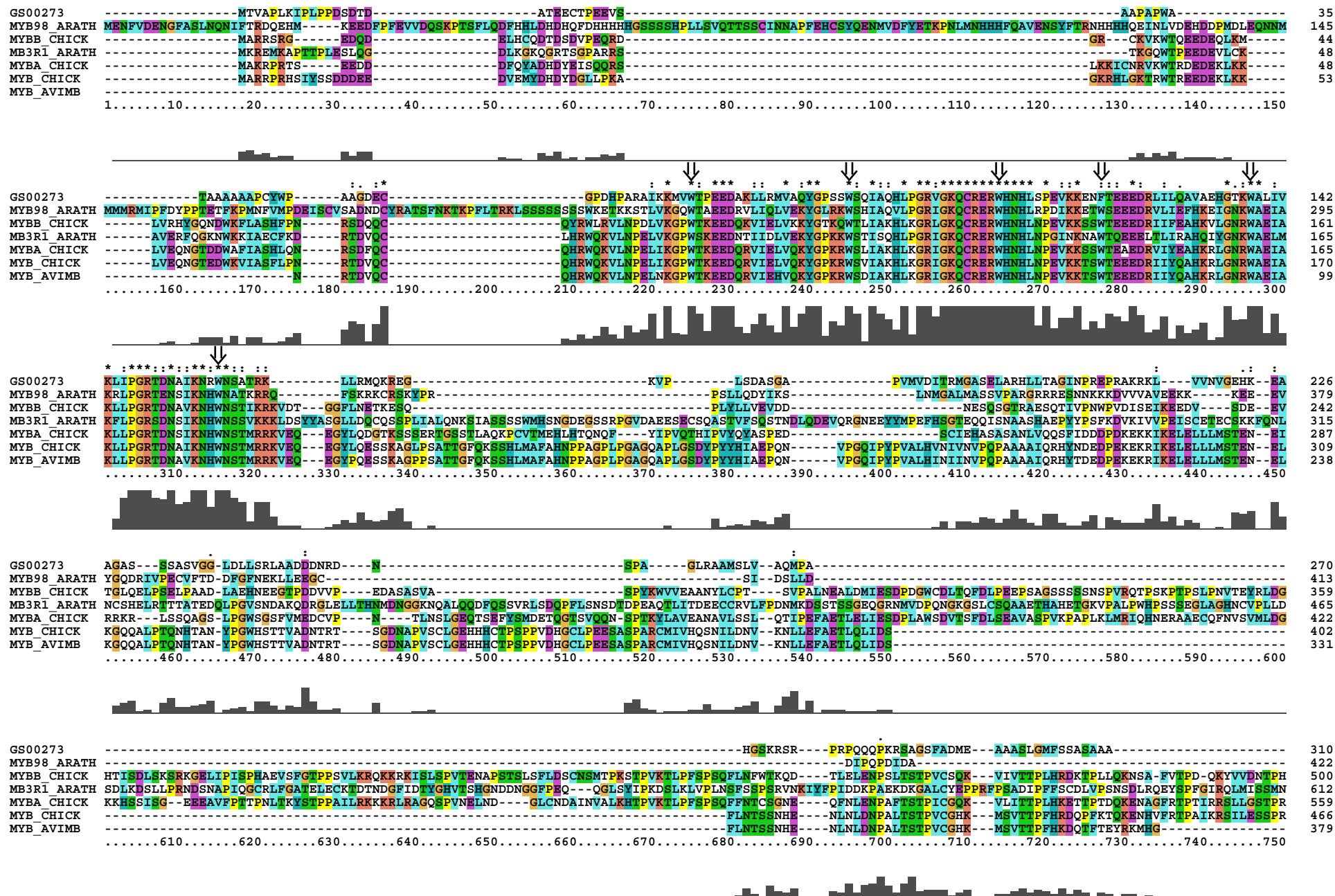
Supplementary Figure S6.



Supplementary Figure S7.



Supplementary Figure S8.



Supplementary Figure S9.

A

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GS09822 -----
GPA      MGVCSSSTPKDQPVAEPTYDPAPAPAPEVPEVPEVPEGAVDTAIDKLETKVGSDLDGDGQV

GS09822 -----
GPA      AGVPVVEVPADAPAEAADAVEPAEDKNILQKAADYVKSFSGRVEPEPAAEEPAVEPEAAP

GS09822 -----
GPA      EGGYEAPKEEASAEEAPAEEPEPEPETASFLDKVKSYLSPRPEVPEGAVDTAIDKLETK

GS09822 -----
GPA      VGSDLDGDGEVAGVPVEAAAEVEAATEAAAEVPVEAAAEAVEAAVEAAPAVPEKKESY

GS09822 -----EPVAEEAEAAPEVAPEAEEEKPSL
GPA      LGKVASILSPRKAASDASAADAPAADDAAEAAEEPVAEEAEAAPEVAPEAEEEKPSL
                                           *****

GS09822 IQKLSKAFSSIIIPATPQCLPGRPSESTLNASETSADAPSAAEEEEAAPAYKAEAPAEV
GPA      IQKLSKAFSSIIIPATPQCLPGRPSESTLNASETSADAPSAAEEEEAAPAYKAEAPAEV
                                           *****

GS09822 A
GPA      A
           *
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B

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GS02894frame1 MGCSGK-----MATAEPATALHLRTMGTCSSKSINNTIADPVKPEQIDTPADATI
GPA      MGVCSSSTPKDQPVAEPTYDPAPAPAPEVPEVPEVPEGAVDTAIDKLETKVGSDLDGDGQV
           ** .*. . . . . **.* .: : .. :*: . . * .*. :

GS02894frame1 VDATTDIAPTEMPADAAP-----
GPA      AGVPVVEVPADAPAEAADAVEPAEDKNILQKAADYVKSFSGRVEPEPAAEEPAVEPEAAP
           ..... :.*: **:*

GS02894frame1 -SDYAKPEAEVAVAEPEALG-----SAAFLWERLGFLTR-----
GPA      EGGYEAPKEEASAEEAPAEEPEPEPETASFLDKVKSYLSPRPEVPEGAVDTAIDKLETK
           ..* *: *. . * * . :*:*: : .*:

GS02894frame1 -----
GPA      VGSDLDGDGEVAGVPVEAAAEVEAATEAAAEVPVEAAAEAVEAAVEAAPAVPEKKESY

GS02894frame1 -----SAEAAPEAAPEAAPEVAVEAAPEVAVEAAPEAAVEEALA
GPA      LGKVASILSPRKAASDASAADAPAADDAAEAAEEPVAEEAEAAPEVAPEAEEEKPSL
                                           .* ** :** * .*. .*. *.* ** *:.

GS02894frame1 VHHLDR-----
GPA      IQKLSKAFSSIIIPATPQCLPGRPSESTLNASETSADAPSAAEEEEAAPAYKAEAPAEV
           ::*:

GS02894frame1 -
GPA      A
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Supplementary Figure S10.

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GS02894frame2          -----KEVSQDVVCAGFGCLV[X]-----
GPA                    MGVCSSSTPKDQPVAEPTYDPAPAPAPEVPEVPEVPEGAVDTAIDKLETKVGSDLDGDGQV
                               **. . . . * . . . *

GS02894frame2          -----FCTPLFAGNLWAVRAERWRPPNRRLLFIYEPWVPAAPSRRSTT
GPA                    AGVPVEEVPADAPAEAAADAVEPAEDKNILQKAADYKVSFSGRVEPEPAEEFPAVEPEAAP
                               *      *:      *:      . . . *:      . ** . . : . .

GS02894frame2          PSPIR[X]SRSRSTLPQTPRSSTPRPTSRLLPRCPPMRRPRITQSPQR[X]-----
GPA                    EGGYEAPKEEASAEAPAEAAPEPEPETASFLDDKVKSYLSSPRPEVPEGAVDTAIDKLETK
                               . . . . : . : * . . . * . . . . . : . : * .

GS02894frame2          -----RWQRSPRRSQAQPRSCGSASASSHGLLRPLLRLRPRWRLRLRPR---W
GPA                    VGSDLDGDGGEVAGVPVEAAAEVEEAATEAAAEVPEVAAAEAVEAAVEAAPAVPEKKESY
                               .      * . . * . . : . : * : . :      . .      : : :

GS02894frame2          RLRLRPLRLSRRRRSRITWIANVIKAGSFVVDGEHTPELIDEVDE-----EEDKPTL
GPA                    LGKVASILSPRKKASDASAAADAPAAADAAEAAEAPVAAEAAEAAPEVAPEAAEEKPSL
                               : . . * . * : : * : * : . . * . * * : :      * : : * :

GS02894frame2          VQKLSKAFSNILPAAPKCMPSHP----ELNEEPADAPTA[X]SRQVCVCAVAVIXTYQCL
GPA                    IQKLSKAFSSIIIPATPQCLGRPSESTLNASETSADAPSAAEEEEAAPAYKAEAPAEVVK
                               : * : * : * : * : * :      : . * . * : * : . . . . . * : :

GS02894frame2          LC
GPA                    A-

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CAX2_ARATH -----MSCKVPVLI^{EAQ}VEMVSANELENKSLFRQ^{EE}EDATQTK^{EA}SLMEQ^{GS}LSLTSF^{FP}CHTPKAPKNSVLN^S-----TKIVIFC^NKNL^NLLLP^{FG}PLAILVHYMIDSKGWVFL^LLLVGI^{IT}PLAERLGYATE^{EQ}LACYT^{GP}TVGG 132

CAX5_ARATH -----MGCKVP^{AL}IAQ^QVEMGLVNDVEH^KSLFRRDTDSPERKAASLMEQ^{GS}LSL^SASF^{RE}CSKT^{PN}NSVLN^S-----FKIVIL^SKNL^NLLLP^{FG}PLAILLHYLTDNKGWIFL^LSLVGI^{IT}PLAERLGYATE^{EQ}LACYT^{GS}TVGG 132

VCX1_YEAST -----MDATTE^{LL}TVAN^{SH}-----PARN-----PKHTA^WRAAVYD^{LO}VILKAS^{PL}NFL^{LV}FV^{PL}LGLI^{WG}H^QFLSHTL^LFLFN^{FL}AI^{IP}PLAAILANATE^{EE}LADKAGN^{TI}GG 95

VCX1_SCHPO -----MIERLKI^{AK}NRLEAMNS^{FN}FP^{AC}DRHERA^{PL}LLGS^{EY}DHSMARQ^LSL^{LN}VV^{GM}TK^{SV}LMSS^{YF}NLM^{LV}FV^{PL}TGLI^{AG}WFEWNAK^SVFIL^{NM}LAI^{IP}PLASL^{SF}ATE^{EQ}LSI^{IS}GP^{IL}GA 117

GS00019 ^{TT}CKKRL^{LA}CL^{QA}RSAR^{CL}WL^{HT}FP^{VG}Q^{GG}PP^{DC}CAV^{GP}MKTA^{ER}TH^{GM}SV^{IG}LR^{DS}SA^{AG}SS^{AS}ERQ^{LL}ARE^{DF}SL^{LP}SPAY^{WR}RALD^{AL}FL^{HN}AL^{NL}ML^{LC}PL^{AI}FA^{PK}KRD^{WD}AG^TVFF^LSL^{VA}IA^{PF}AE^{RL}SY^{VT}EQ^{AL}LHT^{SE}AL^{GG} 150

GS00304 -----LVP^{FA}CF^QEL^{GL}DDA^QTF^{IL}AATA^{IL}PL^{AG}L^LGE^{AT}EQ^{VA}FHT^{NE}TVGG 50

GS00617 -----

GS00976 -----

GS06500 -----

1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

CAX2_ARATH LLNATFGN^{VT}ELI^{IS}IFALK^{NG}MIR^{VV}QLT^{LL}GSIL^{SN}MML^{VL}VGCAFF^{CG}GLV^{FY}QK^{DV}FDK^{GI}ATV^{NS}GLL^{MA}VMG^{IL}FP^{AV}LHYTHSE^{VH}-----GSSEL^{AL}S^{RF}SS^{CI}MLI^{AY}AA^{YL}FF^{OL}K^SQ^{SN}SV^{PL}DEES^{NO}NE----- 272

CAX5_ARATH LLNATFGN^{VT}ELI^{IS}IFALK^{SG}MIR^{VV}QLT^{LL}GSIL^{SN}MML^{VL}VGCAFF^{CG}GLV^{FS}QK^{EO}VP^{DK}GN^{AV}VNS^{GL}LL^{MA}VMG^{LL}FP^{AV}LHYTHSE^{VH}-----GSSEL^{AL}S^{RF}SS^{CI}MLV^{AY}AA^{YL}FF^{OL}K^SQ^{PS}Y^{TP}LEET^{NO}NE----- 272

VCX1_YEAST LLNATFGN^{AV}ELI^{VS}IIALK^{KG}Q^{VR}IVQ^{AS}ML^{GS}LL^{SN}LL^{VL}GLCF^{IF}GGY^{NR}VO-----CTFN^{QT}AAQTMSS^{LL}AA^{TAC}AS^{LL}IP^{AA}FRAT^{LP}PH^{GK}ED^{HF}ID^{GK}IL^{EL}SRG^{TS}IVIL^{IV}V^{LV}FL^{YF}Q^{LG}SH^{HA}LF^{EQ}QEE----- 231

VCX1_SCHPO LLNASFGN^{AT}ELI^{VG}VLAK^{RG}EL^{RI}VQSS^{LL}GSIL^{SN}LL^{VL}FGM^{CL}VTG^{IR}REI-----TTFN^{IT}VAQTMIA^{ML}AL^{IS}TAT^{IL}IPAT^{PH}YS^{LP}DNAN-----SEN^{AL}LHV^{SR}GT^{AV}IV^{LV}V^{LV}LL^{LV}Q^{LG}TH^{KV}CH^{DP}SE----- 250

GS00019 LLNATFGN^{VT}ELI^{VS}FFALK^{KG}M^{LR}IVQV^{LL}GSIL^{SN}LL^{VL}VGCAFF^{EG}GIR^{HK}H-----GYFN^{VH}GS^{AV}NV^{GL}LV^{IS}V^{MA}LL^{FP}MM^{LE}AS-----HEV^{LA}-----PGAV^{MA}VS^{RS}VS^{CL}LL^{LL}YAG^YIFF^{QM}ST^{HP}HL^{YD}Q^{PG}EG^{EG}GG^{GA}DANG 293

GS00304 -LNATFGN^{VT}ELI^{VS}LFALK^YG^{ML}RIVQ^{CS}LL^{GS}IL^{SN}ML^{VL}VGCAFF^{AG}GIV^{TK}C-----QK^{FS}AP^{AS}SV^{NY}SL^{LV}LG^{AS}SS^{LL}PC^{AI}DAN^{PE}EG^{AP}-----PGSG^{LV}VS^{RV}LS^{CM}ML^{VV}V^{CV}Y^{VT}Q^{LV}TH^{TF}FL^{YD}ED^{DD}DD^{DE}EAG----- 137

GS00617 LLNATFGN^{AT}ELI^{VC}YFAL^QRGL^{LL}VVQV^{SL}GSIL^{SN}LL^{VL}VGCS^{MA}AGIR^{QM}C-----SKFN^{LV}AAQ^{SN}TLL^QTAI^{LG}LV^{VP}TAMESTGQ^{FA}EH-----SFND^{LT}LAG^{IS}IV^{LL}L^{IV}LV^{YV}Q^{LG}FS^{HA}AL^{FED}SG----- 182

GS00976 -----NTVA^{AI}SN^{AA}LL^QTA^{VL}GL^{LL}PT^{IM}HY^{AK}DD^{MD}F-----MQP-----L^{SH}GIS^{IG}LL^{LL}Y^{LY}IY^{YF}Q^{LG}TH^{HF}FL^{EA}PL^{EG}DK^{SL}Q-----DQ 78

GS06500 -----

.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

CAX2_ARATH --ETSA^{ED}ED^{PE}-----ISKWE^{AI}IW^{LS}IL^{TA}W^{VS}LL^{SG}YL^{VD}AI^{EG}AS^VSW^{NI}PIA^{FI}S-----TILL^{PI}V^{GN}AAE^HAG^{AI}MFAM^{KD}KLD^{LS}LG^{VA}IG^{SS}IQ^{IS}MF^{AV}PP^{CV}VI^{GW}MMG^QQMD^{LN}FQ^{LF}ET^{AM}LFI^{TV}IV^{VA}FF^{FL}QEG^{SN}Y 413

CAX5_ARATH --ETSD^{DE}DE^{PE}-----ISKWE^{AI}IW^{LS}IL^{TA}W^{VS}LL^{SG}YL^{VD}AI^{EG}AS^VSW^{NI}PIA^{FI}S-----TILL^{PI}V^{GN}AAE^HAG^{AI}MFAM^{KD}KLD^{LS}LG^{VA}IG^{SS}IQ^{IS}MF^{AV}PP^{CV}VI^{GW}MMG^QQMD^{LN}FQ^{LF}ET^{AM}LFI^{TV}IV^{VA}FF^{FL}QEG^{SN}Y 413

VCX1_YEAST ---ETD^{EV}MT^{IS}SN^{PH}SL^{SV}K^SSL^{VL}ILL^{GT}TV^{II}SFC^{AD}FL^{VG}TD^{IN}V^{VE}STGL^{SK}TF^{IG}L^{VI}PI^{VG}NAAE^{HV}TV^{SV}LAM^{KD}KMD^{AL}LG^{VA}IG^{SS}IQ^{IA}LF^{VP}TP^{FM}VL^{VG}MM^{ID}VP^{MT}LN^{FS}TF^{ET}AT^{LF}IA^{VF}LS^{NY}L^{LD}DG^{ES}NW 378

VCX1_SCHPO ---VEETE^{EP}RI-----LGLRS^{IA}ML^{AI}VT^{VF}SL^{CAD}Y^{LV}GS^{ID}Q^{LV}EE^{VNI}SK^{TF}VG^{LV}IL^{PV}GNAAE^{HV}TA^{IV}VS^{YR}GQ^{MD}AL^{LG}VA^{IG}SS^{IQ}IA^{LF}VP^{FL}VI^{VG}W^{II}IS-----PL^{TL}YF^{ES}LE^{TV}IL^{VS}V^{FL}V^{NY}L^{LD}GATHW 390

GS00019 EEEEEEEEE^{EA}V-----LGVAG^{SI}LW^{AI}IT^{TV}VI^{GL}SE^{YM}VD^{AL}ED^{AA}EG^{WG}VP^{NL}FG^{AI}II^{PI}V^{GN}AAE^{HAA}II^{FA}V^{KN}KM^{EL}AV^{GI}AV^{GS}SS^{IQ}IA^{IF}CV^{PL}LV^{TV}AW^{AL}GI^{EL}SL^{NF}Q^{PF}ET^{GV}LL^VTV^{ML}V^{LG}FT^{IL}NG^{ES}SW 436

GS00304 -EEEEEEEE^{EA}V-----LGVAG^{SV}FW^{LA}VI^{TV}VI^{SIL}SE^{YM}VD^{SL}EAA^{AV}GV^{PD}FL^{GT}II^{PI}V^{GN}AAE^{HAA}II^{FA}V^{KN}KM^{EL}AL^{GI}AV^{GS}SS^{IQ}IG^{VF}CV^{PL}LC^{VF}AW^{SI}DI^{EL}SL^{NF}GV^{FE}CL^{TY}LIT^{AL}LV^{GA}IT^{SG}Q^{SN}W 279

GS00617 ---EDE^{EE}E^{EE}E-----VLL^{PM}SG^{AI}AW^{LA}FAT^{VL}IA^{FL}SE^{KL}TGA^{IE}GT^{TAT}Y^{GI}SET^{FS}V^{SV}II^{PI}V^{GN}AAE^{HST}AI^{VM}MA^{WG}KMD^{LA}FG^{VA}LG^{SS}Q^{IA}LF^{VP}VL^{MV}II^{GW}AI^{DP}PL^{TL}YF^{GV}YET^{II}IF^{LS}SV^{LV}SH^{IV}SD^{GE}TNW 324

GS00976 EPEE^{DE}E^{DE}E-----VLL^{FS}GG^{LL}WL^{GI}AT^{VA}IA^{FL}SE^{EL}TGA^{LE}PAAA^{AW}GL^{PQ}AF^{VG}FCL^{LP}IV^{GN}AAE^{HST}AI^{VC}AY^{KQ}KMD^{AL}LG^{VA}LG^{SS}Q^{IA}LF^{VP}VM^{VV}IG^{WV}IQ^{PL}DL^{FF}GP^{FP}PT^{AV}FLSTNL^{VF}FM^{VV}Q^{NG}ETNW 223

GS06500 -----EE-----LSFRQSTVAL^{ALL}CA^{AT}AG^{LS}EV^{VV}GS^{IG}AAA^{AG}AK^{VPL}AF^{VS}TILL^{PI}V^{GN}AAE^{HAS}AV^{MF}AV^{RN}KPD^{LA}IG^{VA}GS^{AT}QIT^{LL}GF^{PA}SV^{LA}AW^{AY}GE^{PL}SL^{DM}LP^{FE}TA^{CL}VL^{TL}IG^{VA}TV^{LP}SG^{RS}NW 133

.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

CAX2_ARATH FKGLML^{IL}CYL^{IV}AA^SFFV^{HE}D^{PH}QD^{GI}----- 441

CAX5_ARATH FKGLML^{IL}CYL^{IV}AA^SFFV^{HE}D^{PH}QDD^I----- 441

VCX1_YEAST LEGVMS^{LA}MY^{LI}IA^{MA}FF^{YV}PD^{EK}TL^{DS}IG^{NS}L----- 411

VCX1_SCHPO LEGVQL^{LA}LY^{AI}VL^{AF}FF^{YV}PQ----- 412

GS00019 LIGAM^{LI}VA^{YC}SLAA^{AF}V^{VH}KD^{PP}GL^{PR}PP^{SI}PP^{SY}TY^{DS}RGL^{SA}RAL^{AR}AG^{VV}YL^{PQ}TP^{FS}SIL^{PR}SL^{LR}RPSMDAL^{PP}AR^{AS}PO^{DP}PR^{RR}WS^{LF}RE^{YV}AC^{SS}W 540

GS00304 LQGV^{VL}IT^{GY}AF^VSA^{AF}V^{HA}DP^{PE}ELAS-----HA^{EH}HH^{HE}----- 314

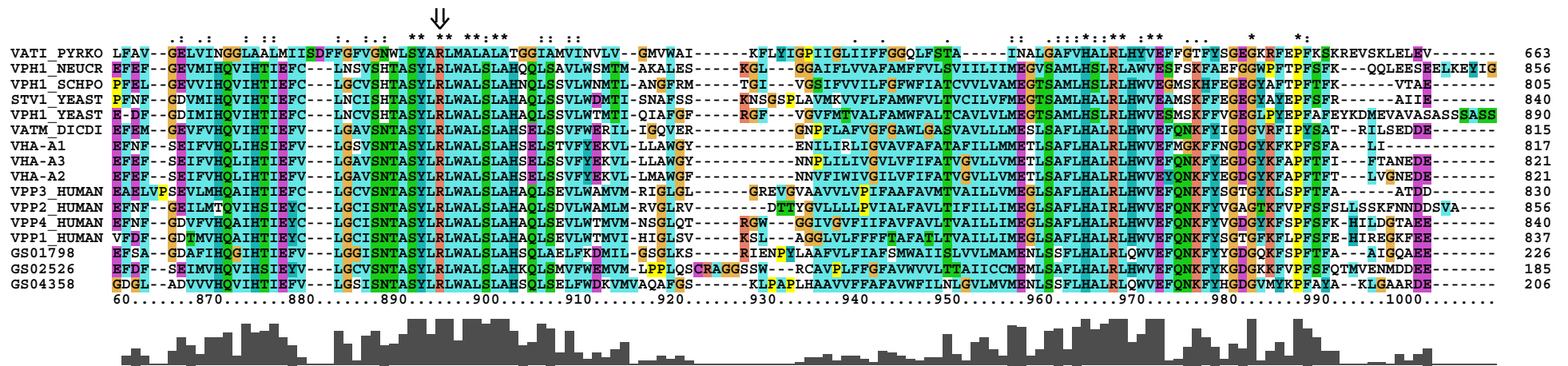
GS00617 LEGT^{ML}LFT^{YF}II^{CF}AF^{FF}Y^{HH}QEA^LPDD^{HP}MK^{HA}----- 359

GS00976 LEGAM^{LL}FS^{YAI}IC^{FS}FL^{EV}----- 243

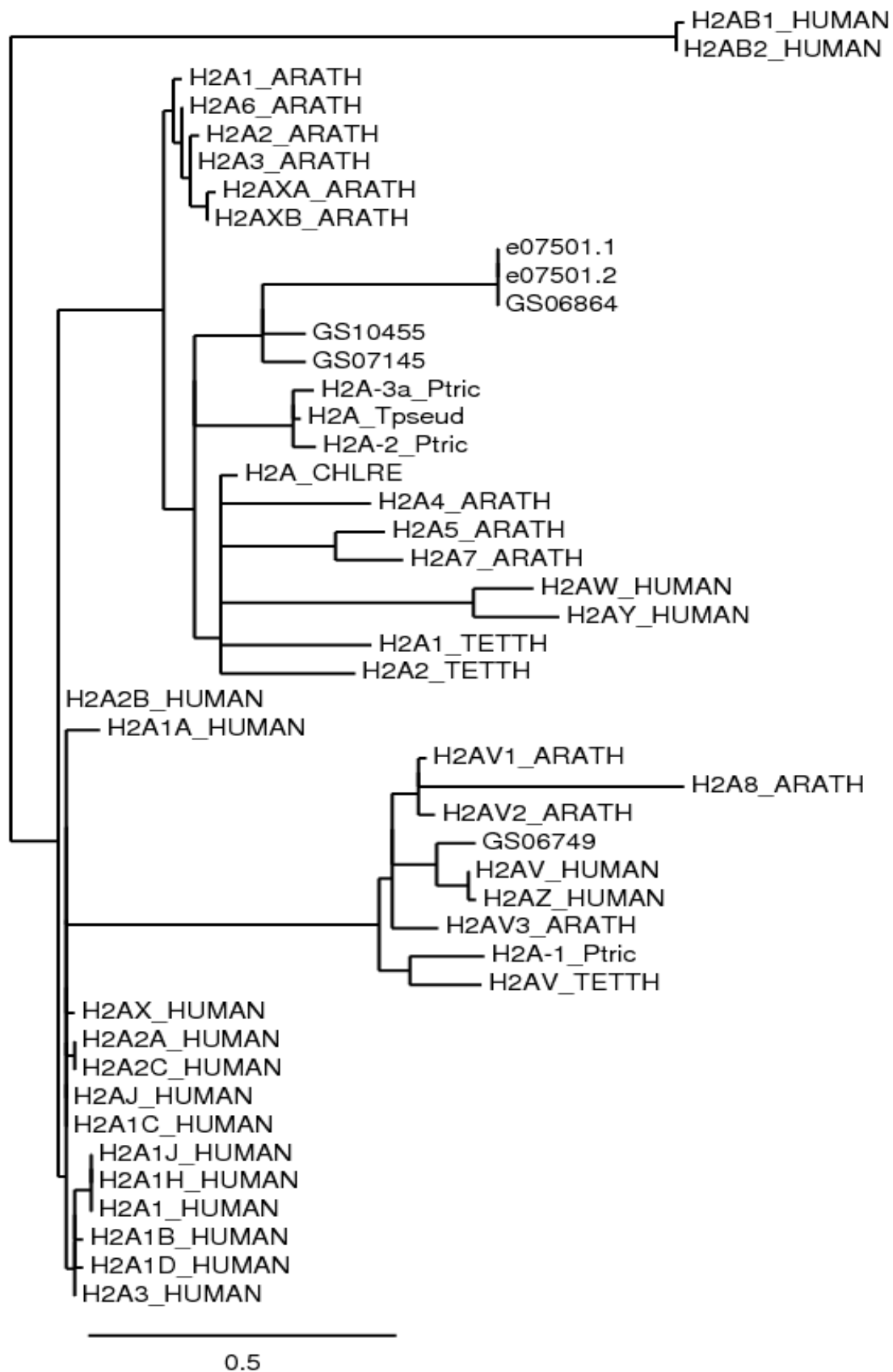
GS06500 LKGL^{TL}IS^{LV}VV^{IAL}AF^{LF}HDS^{SE}TRAP^{AA}AK^{HK}RL^{LG}----- 170

.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....

Supplementary Figure S11.



Supplementary Figure S12.



Supplementary Figure S15.