# **Supplementary Figures**



Supplementary Figure 1: Maximum likelihood phylogenetic tree of all nucleus-coded H2A protein variants in cryptophytes and chlorarachniophytes. The tree was generated using MUSCLE (Edgar 2004) multiple sequence alignments and RAxML (Stamatakis 2014; version 8.0.26) under the LG+G model and with 100 bootstrap replicates, and visualized using MEGA (Tamura et al. 2013). H2A sequences were obtained from available genome assemblies for *Bigelowiella natans* and *Guillardia theta* and from transcriptome assemblies for *Lotharella* sp., *Hemiselmis andersenii*, *Cryptomonas paramecium*, and *Chroomonas mesostigmatica* provided by the Marine Microbial Eukaryote Transcriptome Sequencing Project (MMETSP) (Keeling et al. 2014) (after filtering out incompletely assembled proteins). Canonical H2A sequences from several other eukaryotes were also included.



#### Н 0.10

Supplementary Figure 2: Maximum likelihood phylogenetic tree of all nucleus- and nucleomorph-coded H2B protein variants in cryptophytes and chlorarachniophytes. The tree was generated using MUSCLE (Edgar 2004) multiple sequence alignments and RAxML (Stamatakis 2014; version 8.0.26) under the LG+G model and with 100 bootstrap replicates, and visualized using MEGA (Tamura et al. 2013). H2B sequences were obtained from nucleomorph genome assemblies, from available genome assemblies for *Bigelowiella natans* and *Guillardia theta* and from transcriptome assemblies for *Lotharella* sp., *Hemiselmis andersenii, Cryptomonas paramecium*, and *Chroomonas mesostigmatica* provided by the Marine Microbial Eukaryote Transcriptome Sequencing Project (MMETSP) (Keeling et al. 2014) (after filtering out incompletely assembled proteins). Canonical H2A sequences from several other eukaryotes were also included.



Supplementary Figure 3 (preceding page): Maximum likelihood phylogenetic tree of all nucleus- and nucleomorph-coded H3 protein variants in cryptophytes and chlorarachniophytes. The tree was generated using MUSCLE (Edgar 2004) multiple sequence alignments and RAxML (Stamatakis 2014; version 8.0.26) under the LG+G model and with 100 bootstrap replicates, and visualized using MEGA (Tamura et al. 2013). H3 sequences were obtained from nucleomorph genome assemblies, from available genome assemblies for *Bigelowiella natans* and *Guillar-dia theta* and from transcriptome assemblies for *Lotharella* sp., *Hemiselmis andersenii, Cryptomonas paramecium*, and *Chroomonas mesostigmatica* provided by the Marine Microbial Eukaryote Transcriptome Sequencing Project (MMETSP) (Keeling et al. 2014) (after filtering out incompletely assembled proteins). Canonical H2A sequences from several other eukaryotes were also included.



#### H 0.05

Supplementary Figure 4: Maximum likelihood phylogenetic tree of all nucleus- and nucleomorph-coded H4 protein variants in cryptophytes and chlorarachniophytes. The tree was generated using MUSCLE (Edgar 2004) multiple sequence alignments and RAxML (Stamatakis 2014; version 8.0.26) under the LG+G model and with 100 bootstrap replicates, and visualized using MEGA (Tamura et al. 2013). H4 sequences were obtained from nucleomorph genome assemblies, from available genome assemblies for *Bigelowiella natans* and *Guillardia theta* and from transcriptome assemblies for *Lotharella* sp., *Hemiselmis andersenii, Cryptomonas paramecium*, and *Chroomonas mesostigmatica* provided by the Marine Microbial Eukaryote Transcriptome Sequencing Project (MMETSP) (Keeling et al. 2014) (after filtering out incompletely assembled proteins). Canonical H2A sequences from several other eukaryotes were also included.

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Cryptomonas\_paramecium\_histone\_H2B/1-113 histone\_H2B\_[Saccharomyces\_cerevisiae]/1-131 histone\_H2B\_(Arabidopsis\_thaliana]/1-150 histone\_H2B\_[Drosophila\_melanagaster]/1-123 histone\_H2B\_[Homo\_sapiens]/1-126

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  | P A<br>P V<br><br>E R<br>E R   | A -<br>E E  <br><br>L V :  | <br>K S  <br><br>S E :<br>T E /  | <br>K A E<br><br>S Y N<br>A S K   | K A<br><br>                     | A P A   | <br>E K<br><br>S R  | <br>K P K<br><br>S K <mark>T</mark><br>K S T                         | A G<br>A G<br>G S   | <br>K K L<br>K<br>K K A<br>A R E<br>A R E  
  | K K<br>P K I<br>A Q I<br>V T I   | S T<br>A G<br>N I<br>A Q<br>S V  | - MT<br>SVD<br>AGG<br>TKT<br>KKD<br>RLV<br>RLI  | D K<br>G K<br>D K<br>G K<br>I P<br>L P  | IT<br>KR<br>KK<br>KR<br>GE<br>GE  | K K I<br>S K V<br>K M I<br>K R I<br>K R I<br>L A I  | K R N<br>V R K<br>K K K<br>K R K<br>S R K<br>K H S<br>K H A  | <br>S V<br><br><br>V S<br>V S                                      | E T `<br>E T `<br>E S `<br>E S `<br>E G T<br>E G T  | (SI<br>(SS<br>(KI<br>(AI<br>(SI<br>(SI<br>(SA  
  | YI<br>YI<br>YI<br>YV<br>VA<br>VT   | Y K \<br>Y K \<br>F K \<br>Y K \<br>Y K \<br>Y K \<br>K Y F<br>K Y S  | / L F<br>/ L F<br>/ L F<br>/ L F<br>/ L F<br>R S S  |   
   | H P K I<br>H P D T<br>H P D I<br>H P D T<br>H P D T<br>-  | 29<br>56<br>78<br>50<br>53<br>102<br>131   |
| 1<br>1<br>1<br>1<br>30<br>57<br>79  | M<br>M<br>G<br>G   | <br>S S<br>A P<br><br><br>V S<br>I S (  | A A<br>R A<br><br><br>S K<br>Q K<br>S K  | E K H<br>E K H<br>MP E<br>A MN<br>S MS   |   | SKA<br>EKK<br>TSG<br>KSA<br>NSF<br>NSF  | P A E<br>P A Z<br>K A Z<br>P A F<br>V N E<br>V N E  | E K K<br>A E K<br>A K K<br>P K K<br>D L F<br>D I F  
   
  | PA<br>PV<br><br>ER<br>ER   | A -<br>E E I<br><br>L V :<br>I A <sup>-</sup>  | <br>K S  <br><br>S E :<br>T E /  | K A E<br><br>S Y N<br>A S K   | K 4                             | A P A<br><br><br><br><br><br><br><br><br><br><br><br><br><br><br><br><br><br><br><br><br><br><br><br><br><br><br><br><br><br><br><br> | <br>E K<br><br>S R<br>N K   | <br>K P k<br><br>S K T<br>K S T<br>K P T                             | A G<br>A G<br>G S   | <br>K K L<br>K<br>K K A<br>A R E<br>S R F  
  | K K<br>P K I<br>A Q I<br>V T I<br>I Q 1  | S T<br>A G<br>N I<br>A Q<br>S V  | - MT<br>SVD<br>AGG<br>TKT<br>KKD<br>RLV<br>RLI<br>RLV   | D K<br>G K<br>D K<br>G K<br>I P<br>L P  | IT<br>KR<br>KK<br>KR<br>GE<br>GE  | K K I<br>S K M<br>K R I<br>K R I<br>L A I<br>L A I  | K R N<br>V R K<br>K K K<br>K R K<br>S R K<br>K H S<br>K H A  | <br>S V<br><br>V S<br>V S<br>V S                                   | E T `<br>E T `<br>E S `<br>E S `<br>E G T<br>E G T  | (SI<br>(SS<br>(KI<br>(AI<br>(SI<br>- KA<br>- KA  
  | YI<br>YI<br>YI<br>YV<br>VA<br>VT   | Y K \<br>Y K \<br>F K \<br>Y K \<br>Y K \<br>Y K Y<br>K Y S<br>K F T  | / L F<br>/ L F<br>/ L F<br>/ L F<br>/ L F<br>R S S<br>S S S   | QVI<br>QVI<br>QVI<br>QVI<br>QVI<br>QVI<br>1 -   
   | + P K I<br>+ P D T<br>+ P D I<br>+ P D T<br>+ P D T<br>- A  | 29<br>56<br>78<br>50<br>53<br>102<br>131   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 1<br>1<br>1<br>1<br>30<br>57<br>79<br>51  | M<br>M<br>G<br>G<br>G  | SS<br>AP<br><br>VS<br>IS<br>IS<br>IS  | A A<br>R A<br><br>S K<br>Q K<br>S K  | E K H<br>E K H<br>MP E<br>MP E<br>A MN<br>S MS   |   | SKA<br>EKK<br>TSG<br>KSA<br>NSF<br>NSF  | PAE<br>PAZ<br>KAZ<br>VNC<br>VNC   |  | P A<br>P V<br><br>E R<br>E R<br>E R<br>E R   | A -<br>E E I<br><br>I V :<br>I A -   | K S<br>S E S<br>S E S<br>S E S   |   |                                 | N S<br>A Y<br>A Y   | <br>E K<br><br>S R<br>N K<br>N K  | <br>K P k<br><br>S K T<br>K S T<br>K P T<br>R S T                    | A G<br>A G<br>G S<br>I T<br>I T   | <br>K K L<br>K<br>K K A<br>R E<br>S R E<br>S R F  | K K<br>P K I<br>A Q I<br>V T I<br>I Q 1<br>I Q 1   | S T<br>A G<br>A G<br>A Q<br>S V<br>A V   | - M T<br>S V D<br>A G G<br>T K T<br>K K D<br>R L V<br>R L I<br>R L V<br>R L I   | D K<br>G K<br>D K<br>G K<br>I P<br>L P  | IT<br>KR<br>KK<br>KR<br>GE<br>GE  | К К I<br>S К I<br>K R I<br>K R I<br>L A I<br>L A I<br>L A I   | K R N<br>V R K<br>K K K<br>K R K<br>S R K<br>K H A<br>K H A  | S V<br><br><br>V S<br>V S<br>V S<br>V S                            | E T `<br>E T `<br>E S `<br>E S `<br>E G T<br>E G T<br>E G T   | ( S I<br>( S S<br>( K I<br>( A I<br>( S I<br>(S I<br>( | YI<br>YI<br>YI<br>YV<br>VA<br>VT<br>VT   | Y K \<br>Y K \<br>F K \<br>Y K \<br>Y K \<br>K Y F<br>K Y T   | / L F<br>/ S S<br>S S<br>S S<br>S S<br>S S  |   | H P K I<br>H P D T<br>H P D T<br>H P D T<br>H P D T<br>-<br>-   | 29<br>56<br>78<br>50<br>53<br>102<br>131<br>150<br>123   |
| 1<br>1<br>1<br>1<br>30<br>57<br>79<br>51<br>54  | M<br>M<br>G<br>G<br>G<br>G<br>G<br>G   | <br>S S<br>A P<br><br>V S<br>I S<br>I S<br>I S<br>I S   | A A<br>R A<br><br>C -<br>S K<br>S K<br>S K<br>S K  | E K F<br>E K F<br>MP E<br>A M<br>S M S<br>A M<br>S<br>A M<br>S   |   | SKA<br>EKK<br>TSG<br>KSA<br>NSF<br>NSF<br>NSF   | PAE<br>PAA<br>KAA<br>VNC<br>VNC<br>VNC  |  | PA<br>PV<br><br>ER<br>ER<br>ER<br>ER   | A -<br>E E I<br><br>I A 1<br>I A 1<br>I A 2  | K S<br><br>S E :<br>S E :<br>S E :<br>A E /  |   |                                 | A P A<br>N S<br>A Y<br>R Y<br>H Y   | <br>E K<br><br>S R<br>N K<br>N K<br>N K                                   | <br>K P k<br><br>S K T<br>K S T<br>K P T<br>R S T<br>R S T           | A G<br>A G<br>G S<br>I T<br>I T   | <br>K K L<br>K<br>K K A<br>R E<br>A R E<br>S R E<br>S R E   | K K<br>P K I<br>A Q I<br>V T I<br>I Q I<br>I Q I<br>I Q I  | S T<br>A G<br>N I<br>C A Q<br>S V<br>A V<br>A V  | - MT<br>S V D<br>A G G<br>T K T<br>K K D<br>R L V<br>R L I<br>R L I<br>R L I  | D K<br>G K<br>D K<br>G K<br>I P<br>L P<br>L P   | IT<br>KR<br>KK<br>KR<br>GE<br>GE<br>GE  | K K I<br>S K N<br>K R I<br>K R I<br>L A I<br>L A I<br>L A I   | K R N<br>V R K<br>K K K<br>K R K<br>S R K<br>K H S<br>K H A<br>K H A   | <br>S V<br><br>V S<br>V S<br>V S<br>V S<br>V S                     | E T `<br>E T `<br>E S `<br>E S `<br>E G T<br>E G T<br>E G T<br>E G T  | ( S I<br>( S S<br>( K I<br>( A I<br>( S I<br>(S I<br>( | YI<br>YI<br>YI<br>YV<br>VA<br>VT<br>VT   | Y K \<br>Y K \<br>Y K \<br>Y K \<br>Y K Y<br>Y K Y<br>K Y T<br>K Y T  | / L F<br>/ S S<br>S S<br>S S<br>S S<br>S S<br>S S<br>S S<br>S S<br>S S<br>S   | QVI<br>QVI<br>QVI<br>QVI<br>QVI<br>QVI<br>GVI<br>GVI<br>GVI<br>GVI<br>GVI<br>GVI<br>GVI<br>GVI<br>GVI<br>G  | H P K I<br>H P D T<br>H P D T<br>H P D T<br>H P D T<br>-<br>-<br>-  | 29<br>56<br>78<br>50<br>53<br>102<br>131<br>150<br>123<br>126  |
| 1<br>1<br>1<br>1<br>30<br>57<br>79<br>51<br>54  | M<br>M<br>G<br>G<br>G<br>G<br>G  | S S .<br>A P<br><br><br>I S<br>I S<br>I S<br>I S<br>I S   | A A<br>R A<br><br>Q K<br>S K<br>S K<br>S K   | E K F<br>MP<br>MP E<br>AMN<br>S MS<br>AMS<br>AMS   |   | S K A<br>E K K<br>T S G<br>K S A<br>N S F<br>N S F<br>N S F<br>N S F<br>N S F   | P A E<br>P A Z<br>K A Z<br>V N C<br>V N C<br>V N C<br>V N C   | E K K<br>A E K<br>A K K<br>P K K<br>D L F<br>D I F<br>D I F<br>D I F   | P A<br>P V<br><br>E R<br>E R<br>E R<br>E R<br>E R<br>E R   | A -<br>E E I<br><br>I A -<br>I A -<br>I A /<br>I A /   | K S<br>S E S<br>S E S<br>S E S<br>S E S<br>S E S<br>S E S  | <br>K A E<br><br>S Y N<br>A S K<br>S S K<br>A S F<br>A S F  | K A<br>K A<br>L S<br>L A<br>L A | N S<br>A Y<br>A Y<br>A Y<br>A Y<br>A Y<br>A Y   | <br>E K<br><br><br>S R<br>N K<br>N K<br>N K<br>N K                        | <br>K P K<br><br>S K T<br>K S T<br>K P T<br>R S T<br>R S T           | A G<br>A G<br>G S<br>L T<br>I S<br>I T<br>I T<br>I T  | <br>K K L<br>K<br>K K A<br>A R E<br>S R E<br>S R E<br>S R E<br>S R E  | K K <sup>-</sup><br>P K I<br>A Q I<br>V T I<br>I Q 1<br>I Q 1<br>I Q 1<br>I Q 1  | S T<br>A G<br>A I<br>A Q<br>S V<br>A V<br>A V<br>A V   | - MT<br>S V D<br>A G G<br>T K T<br>K K D<br>R L V<br>R L V<br>R L L<br>R L L  | D K<br>G K<br>D K<br>G K<br>I P<br>L P<br>L P<br>L P  | IT<br>KR<br>KK<br>KR<br>GE<br>GE<br>GE<br>GE  | K K I<br>K M I<br>K R I<br>K R I<br>L A I<br>L A I<br>L A I<br>L A I  | K R N<br>V R K<br>K K K<br>K R K<br>S R K<br>K H A<br>K H A<br>K H A   | <br>S V<br><br>V S<br>V S<br>V S<br>V S<br>V S<br>V S<br>V S       | E T `<br>E T `<br>E S `<br>E G T<br>E G T<br>E G T<br>E G T<br>E G T  | ( S I<br>( S S<br>( A I<br>( S I<br>(S I<br>( | Y I<br>Y I<br>Y I<br>Y V<br>V A<br>V T<br>V T<br>V T<br>V T  | Y K \<br>Y K \<br>Y K \<br>Y K \<br>Y K Y<br>K Y T<br>K Y T<br>K Y T  | / L F<br>/ L F  | R Q V I<br>Q V I<br>Q V I<br>Q V I<br>C Q | H P K I<br>H P D T<br>H P D I<br>H P D T<br>H P D T<br>H P D T  | 29<br>56<br>78<br>50<br>53<br>102<br>131<br>150<br>123<br>126  |
| 1<br>1<br>1<br>1<br>30<br>57<br>79<br>51<br>54  | M<br>M<br>G<br>G<br>G<br>G<br>G  | S S A P<br><br><br><br><br><br><br><br><br><br>-  | A A<br>R A<br><br><br>S K<br>Q K<br>S K<br>S K<br>S K  | E K F<br>E K F<br>MP E<br>AMP E<br>AMS<br>AMS  |   | S K A<br>E K K<br>K S A<br>N S F<br>N S F<br>N S F<br>N S F   | P A E<br>P A A<br>K A A<br>P A F<br>V N C<br>V N C<br>V N C<br>V N C  | K K<br>A E K<br>K K<br>C I F<br>D I F<br>D I F<br>D I F  | P A<br>P V<br><br>E R<br>E R<br>E R<br>E R<br>E R  | A -<br>E E I<br><br>I A -<br>I A -<br>I A -<br>I A -   | K S<br>S E :<br>S E :<br>S E :<br>A E ;<br>G E ;   | <br><br>S Y N<br>A S K<br>S S K<br>A S F<br>A S F   |                                 | N S<br>A P A<br>A C<br>A Y<br>A Y<br>A Y<br>A Y<br>A Y<br>A Y<br>A Y<br>A Y   | <br>E K<br><br>S R<br>N K<br>N K<br>N K<br>N K                            | <br>K P K<br><br>S K T<br>K S T<br>K P T<br>R S T<br>R S T           | A G<br>A G<br>G S<br>I T<br>I T<br>I T  | <br>K K L<br>K<br>K K A<br>R E<br>S R E<br>S R E<br>S R E   | K K <sup>-</sup><br>P K I<br>A Q I<br>V T I<br>I Q 1<br>I Q 1<br>I Q 1<br>I Q 1<br>I Q 1   | S T<br>A G<br>A U<br>A U<br>A V<br>A V<br>A V<br>A V   | - MT<br>S V D<br>A G G<br>T K T<br>K K D<br>R L V<br>R L U<br>R L L   | D K<br>G K<br>D K<br>G K<br>I P<br>L P<br>L P<br>L P  | IT<br>KR<br>KK<br>KR<br>GE<br>GE<br>GE<br>GE  | K K I<br>S K M<br>K R I<br>K R I<br>L A I<br>L A I<br>L A I<br>L A I<br>L A I   | K R N<br>V R K<br>K K K<br>K R K<br>S R K<br>K H S<br>K H A<br>K H A   | <br>S V<br><br>V S<br>V S<br>V S<br>V S<br>V S                     | E T Y<br>E T Y<br>E S Y<br>E G I<br>E G I<br>E G I<br>E G I   | ( S I<br>( S S<br>( K I<br>( S S)<br>( S I<br>( S I)))))))))))))))))))))))))))))))))))   | YI<br>YI<br>YI<br>YV<br>VA<br>VT<br>VT<br>VT<br>VT   | Y K \<br>Y K \<br>F K \<br>Y K \<br>Y K \<br>Y K Y<br>F K<br>Y F<br>K Y T<br>K Y T  | / L F<br>/ L H<br>/ L H<br>/ L H<br>/ L H<br>/ L H<br>/ L H<br>- S S<br>S S<br>S S<br>S S<br>S S<br>S<br>S S<br>S<br>S<br>S<br>S<br>S<br>S  | R Q V I<br>C Q  | H P K I<br>H P D T<br>H P D T<br>H P D T<br>H P D T<br>-<br>-<br>-<br>-   | 29<br>56<br>78<br>50<br>53<br>102<br>131<br>150<br>123<br>126  |
| 1<br>1<br>1<br>1<br>30<br>57<br>79<br>51<br>54  | M<br>M<br>G<br>G<br>G<br>G<br>G<br>G<br>G<br>G   | S S<br>A P<br><br><br>I S<br>I S<br>I S<br>I S<br>  | A A<br>R A<br><br>S K<br>Q K<br>S K<br>S K<br>S K  |  |   | S K A<br>E K K<br>T S G<br>K S A<br>N S F<br>N S F<br>N S F<br>N S F  | P A E<br>P A Z<br>P A F<br>V N C<br>V N C<br>V N C<br>V N C   | K K<br>A E K<br>A K K<br>C I F<br>D I F<br>D I F<br>D I F   
   
  | E R<br>E R<br>E R<br>E R   | A -<br>E E I<br><br>I A 1<br>I A 1<br>I A 2<br>I A 2   | S E :<br>S E :<br>S E :<br>S E :<br>S E :<br>G E /   |   | ILS<br>LA                       | A P A   | E K<br>S R<br>N K<br>N K<br>N K   |  | A G<br>A G<br>G S<br>I T<br>I T<br>I T  | <br>K K L<br>K<br>K K A<br>R E<br>S R E<br>S R E<br>S R E  
  | K K <sup>-</sup><br>P K I<br>A Q I<br>V T I<br>I Q 1<br>I Q 1<br>I Q 1<br>I Q 1<br>I Q 1<br>I Q 1<br>- K I   | S T<br>A G<br>A Q<br>S V<br>A V<br>A V<br>A V  | - MT<br>S V D<br>A G G<br>T K T<br>K K D<br>R L V<br>R L I<br>R L I<br>R L I<br>R L I<br>R L I  | D K<br>G K<br>D K<br>G K<br>I P<br>L P<br>L P<br>L P  | IT<br>KR<br>KK<br>KR<br>GE<br>GE<br>GE  | K K I<br>K MI<br>K R I<br>K R I<br>L A I                             | K R N<br>V R K<br>K K K<br>K R K<br>S R K<br>K H S<br>K H A<br>K H A<br>K H A  | <br>S V<br><br>V S<br>V S<br>V S<br>V S<br>V S                     |   | S I<br>S S<br>K I<br>K A<br>K A<br>K A<br>K A<br>K A  
   | YI<br>YI<br>YV<br>VV<br>VT<br>VT<br>VT<br>VT   | Y K \<br>Y K \<br>Y K \<br>Y K \<br>Y K Y<br>F T<br>K Y T<br>K Y T<br>K Y T   | / L F<br>/ L F<br>/ L F<br>/ L F<br>/ L F<br>/ L F<br>/ L F   | R     Q     F       K     Q     F       K     Q     F       K     Q     F       K     Q     F       K     Q     F       K     Q     F       K     Q     F  
  | H P K I<br>H P D T<br>H P D T<br>H P D T<br>H P D T<br>-<br>-<br>-<br>-<br>-<br>-<br>-  | 29<br>56<br>78<br>50<br>53<br>102<br>131<br>150<br>123<br>126<br>46  |
| 1<br>1<br>1<br>1<br>30<br>57<br>79<br>51<br>54<br>1<br>1                                  | M<br>M<br>G<br>G<br>G<br>G<br>G<br>G<br>G<br>G<br>G<br>G<br>G<br>G<br>G                          | S S A P<br>   | A A<br>R A<br><br><br>S K<br>Q K<br>S K<br>S K<br>S K<br>S K   | E K H<br>MP E<br>AMN<br>S MS<br>AMG<br>AMS<br>AMG  |   | S K A<br>E K K<br>T S G<br>K S A<br>N S F<br>N S F<br>N S F<br>N S F<br>N S F<br>N S F<br>N S F   | P A E<br>P A Z<br>P A Z<br>V N C<br>V N C<br>V N C<br>V N C<br>V N C  | E K K<br>A E K<br>A K K<br>F K K<br>D I F<br>D I F<br>D I F<br>D I F<br>D I F  | E R<br>E R<br>E R<br>E R<br>E R  | A -<br>E E I<br>I A<br>I A<br>I A<br>I A<br>A -  | K S I<br>S E S<br>S E S<br>S E S<br>S E S<br>G E S   | K A E<br>   | I L S<br>L A                    | A P A<br>N S<br>A Y<br>A Y<br>A Y<br>A Y<br>A Y   | E K<br>S R<br>N K<br>N K<br>N K   | K P K<br><br>K S K<br>K S T<br>K S T<br>R S T                        | A G<br>A G<br>G S<br>I T<br>I T<br>I T  | K K L<br>K<br>K K A<br>R E<br>A R E<br>A R E<br>S R E<br>S R E<br>S R E<br>S R E  | K K <sup>2</sup><br>P K I<br>A Q I<br>V T I<br>I Q 1<br>I Q |  | - MT<br>S V D<br>A G G<br>T K T<br>K K D<br>R L V<br>R L I<br>R L V<br>R L L<br>E K S<br>S V D  | D K<br>G K<br>D K<br>G K<br>L P<br>L P<br>L P<br>C R<br>G K   | IT<br>KR<br>KK<br>KR<br>GE<br>GE<br>GE<br>GE  | K K I<br>K MI<br>K R I<br>K R I<br>L A I<br>S K I                             | K R N<br>V R K<br>K K K K<br>K R K<br>K H S<br>K H A<br>K H A<br>K H A<br>K H A<br>K R V<br>V R K  | <br>S V<br><br>V S<br>V S<br>V S<br>V S<br>V S                     | E T `<br>E T `<br>E S `<br>E S `<br>E G I<br>E G I<br>E G I<br>E G I<br>I S `<br>E T `  | ( S I<br>( S S<br>( K I<br>( A I)))))))))))))))))))))))))))))))))))  | Y I<br>Y I<br>Y I<br>Y V<br>V V<br>V T<br>V T<br>V T<br>V T<br>V T<br>V T  | Y K \<br>Y K \<br>Y K \<br>Y K \<br>Y K \<br>K Y T<br>K Y T<br>K Y T<br>Y K \<br>Y K \  | / L F<br>/ L F  |   | + P K I<br>+ P D T<br>+ P D T<br>+ P D T<br>-<br>-<br>-<br>-<br>-<br>-<br>-<br>-<br>-<br>-<br>-<br>-<br>-<br>-<br>-<br>-<br>-<br>-<br>-   | 29<br>56<br>78<br>50<br>53<br>102<br>131<br>150<br>123<br>126<br>46<br>56  |
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   | / L F<br>/ L F<br>/ L F<br>/ L F<br>/ L F<br>S S<br>S S<br>S S<br>S S<br>S<br>S<br>S<br>S<br>S<br>S<br>S<br>S<br>S<br>S<br>S  | R     Q     V       K     Q     V       K     Q     V       G     T     Q       G     T     Q       G     T     Q       G     T     Q       G     T     Q       G     T     Q       G     T     Q       G     T     Q       G     T     Q       G     T     Q       G     Q     V       G     Q     V       G     Q     V   | + P K I<br>+ P D T<br>+ P D T<br>+ P D T<br>+ P D T<br>+ P D T<br>-<br>-<br>-<br>-<br>-<br>-<br>-<br>-<br>-<br>-<br>-<br>-<br>-<br>-<br>-<br>-<br>-<br>-<br>-   
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Supplementary Figure 5: Alignment of cryptophyte nucleomorph H2B histones and the nuclear H2B histones from several representative eukaryotes. (A) Chroomonas mesostigmatica histone H2B; (B) Cryptomonas paramecium histone H2B; (C) Guillardia theta histone H2B; (D) Hemiselmis andersenii histone H2B.



Supplementary Figure 6: Conservation of key posttranscriptionally modified residues in the cryptophyte nucleomorph histone H2B. The radius r refers to the size of the context considered when scoring conservation. When r = 1, only the residue itself is considered; when r = 1, a perfect match to the three-amino acid peptide also including the flanking residues on each side is required; when r = 2, the five-amino acid peptide also including the two flanking residues on each side is considered. A score of 1 means conservation according to these criteria, while a score of 0 means lack of conservation. Conservation was scored against the *Homo sapiens* histone H2B sequence.

RPB1\_Saccharomyces\_cerevisiae/1-1733 Bigolowiela\_natans/1-1510 Lotharella\_oceonica/1-1502 Guillardia\_theta/1-1473 Crystomanas\_paramecium/1-1452 Chroannaas\_mesostigmatica/1-1473 Hemiselmis\_anderseni/1-1464

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RPB1\_Saccharomyces\_cerevisioe/1-1733 Bigelowiella\_natans/1-1510 Lotharella\_oceanica/1-1502 Guillardia\_theta/1-1473 Crystomonas\_parameeium/1-1452 Chroamonas\_mesostigmatica/1-1473 Hemiselmis\_anderseni/1-1464

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227 AR LK GK EGR I RGN LMG KR VD F SART VI SG DPN LE LD QVG VFK SI AKTL TY PE VYTPYN I D LT QL VR NG PN H PEAKY VI RD SG DH D L RY SK RAGD I QL QVG WK 12 QRL KGK FG FFR RN LMG KR VD F FG RT VI TG DS YI NL DE LG I PK LI AKKL TL PE VYNK FN I D RL SY LI D ST GHE LK MY I LG KYNK VI D L RY KS SN SI LL LKYG FI 13 QRL NG KFG FFR RN LMG KR VD FFG RT VI TG DS YI NL DE LG I PK I SKL TI PT V WK FN I D RL SY LI D ST GHE LK MY I LG KYNK VI D L RY KS SN SI LL LKYG FI 13 QRL QG KEG RI RGN LMG KR VD FFG RT VI T PD PN I LD E LG I PK I SKL TI PT VWK FN I EWNST LV D SI SKD LKANS I LG VYNK VI D L RY KS AT SI I LLKYG FI 14 QRL QG KEG RI RGN LMG KR VD FFS ART VI TP PD NI LL E LG I PWN VALNITY PE I VT SFN I E YMSF LL VNG PY KH PGAKY LI RND GT RLD L RY VK VL SNN VL E I G QV 13 ERL QG KEG RI RGN LMG KR VD FFS ART VI TP PD NI LL E LG I PWN VALNITY PE I VT SFN FEKLK LV NG PI H PGAKY LI RND GS RLD L RY VKL SNV I E I G QV 14 QG KEG RI RGN LMG KR VD FFS ART VI TP PD NI LL E LG I PWN VALNITY PE I VT SFN FEKLK LV NG PI H PGAKY LI RND GS RLD L RY VKL SNV I E I G QV 14 QR LQ GKEG RV RGN LMG KR VD FFS ART VI TP PD NI LL E LG I PWN SL ALNITY PE I VT SFN FEKLKK LV NG PI H PGAKY LI RND GS RLD L RY KKL SNV I E I G QV 14 QR LQ GKEG RV RGN LMG KR VD FFS ART VI TP PD NI LL E LG I PWN SL ALNITY PE I VSE FNMK KMK I VUNG PI H PGAKY LI RND GS RLD L RY KKL SNV I E I G QV 14 QR LQ GKEG RV RGN LMG KR VD FFS ART VI TP PD NI LL E LG I PWN SL ALNITY PE I VSE FNMK KMK I VONG PI H PGAKY I I RND GS RLD L RY KKL SNV L E I G QV 14 QR LQ GKEG RV RGN LMG KR VD FFS ART VI TP PD NI LL E LG I PWN SL ALNITY PE I VSE FNMK KMK I VONG PI H PGAKY I I RND GS RLD L RY KKL SNV L E I G QV 14 QR LG GKEG RV RGN LMG KR VD FFS ART VI TP PD NI LL E LG I PWN SL ALNITY PE I VSE FNMK KMK I VONG PI H PGAKY I I RND GS RLD L RY KKN LSE I FNMK LG I PH LG LG L RY SN L R LE I G RY	E R H I MD 438 E R H I Q S 422 E K H L E D 423 YE R H L Q N 423 YE R H L Q D 424 E R H L Q D 424 E R H L Q D 425
439 NDP VLENRQPSLHKMSMMAHRVKVI PYSTFRLNLSVT SPYNAD PGDEMNLH PQSELTRAELSQLCAVPLQIVSPQSNRPCMGIVQDTLCGIRKLTLRDTFIELD 423 GDIVILNRQPSLHKMSMMGHRVKI PSTFRLNLSVT PYNAD PGDEMNIH PQSELTRSESTFINNVINNINSPQANRPVIG UVQDTLSTVTLSRDSFLNSL 424 GDVLLLNRQPSLHKMSMMGHRVKI KILPVLT FRLNLSVT PYNAD PGDEMNIH PQTLLTRSESTFLNSLLMVINNINSPQANRPVIG IVQDSLLGSVDIFKNNFLTK 425 GDIVILNRQPSLHKMSMMGHIVKI MIDYSTFRMNLSAT SPYNAD PGDEMNIH PQTLELTRSESTFLSLLNLLWSNCIVSPQANRPVIG IVQDSLLGSFLLSRDSFLNSL 426 GDVLLNRQPSLHKMSMMGHIVKI MIDYSTFRMNLSAT SPYNAD PGDEMNLH PQTLESTSELLNLLUNSNCIVSQLGARPVIG IVQDSLLGSFLLSRDSFLNSL 426 GDVLLNRQPSLHKMSMMGHIVKIMH PSTFRMNLSAT SPYNAD PGDEMNLH PQTLESTSELLNLLUNSNCIVSQLGARPVIG IVQDSLLGSFLLSRDSFLNS 426 GDVLLNRQPSLHKMSMMGHIVKIMH PSTFRMNLSAT SPYNAD PGDEMNLH PQTLESTSELLNLLUNSNCIVSQQQNRPVIG IVQDSLLGSFLLSRDSFLNS 426 GDVLLFNRQPSLHKMSMMGHIVKIMH PSTFRMNLSAT SPYNAD PGDEMNLH PQTLESKSELKNLLUN PNCI ISQQNRPVIG IVQDSLLGSFLLSRDSFLNS 426 GDVLLFNRQPSLHKMSMMGHIVKIMH PSTFRMNLSAT SPYNAD PGDEMNLH PQTLEGKSELLNLLNUPNCI ISQQNRPVIG IVQDSLLGSFLLSRDSFLNS 426 GDVLFNRQPSLHKMSMMGHIVKIMH PSTFRMNLSAT SPYNAD PGDEMNLH PQTLEGKSELLNLLNUPNCI ISQQNRPVIG IVQDSLLGSFLLSRDSFLNS 426 GDVLFNRQPSLHKMSMMGHIVKIMH PSTFRMNLSAT SPYNAD PGDEMNLH PQTLEGKSELLNLLNUPNCI ISQQNRPVIG IVQDSLUGSFLLSRDSFLNS 426 GDVLFNRQPSLHKMSMMGHIVKIMH PSTFRMNLSAT SPYNAD PGDEMNLH PQTLEGKSELLNLLNUPNCI ISQQNRPVIG IVQDSLUGSFLLSRDSFLNS 426 GDVLFNRQPSLHKMSMMGHIVKIMH PSTFRMNLSAT SPYNAD PGDEMNLH PQTLEGKSELLNLM PNCI ISQQNRPVIG IVQDSLUGSFLLSRDSFLLSRDSFLNS 426 GDVLFNRQPSLHKMSMMGHIVKIMH PSTFRMNLSAT SPYNAD PGDEMNLH PQTLEGKSELLNLM PNCI ISQQNRPVIG IVQDSLUGSFLLSRDSFLLSRDSFLNS 426 GDVLFNRQPSLHKMSMMGHIVKIMANGHIVKIM PNCI PTFRMNLSAT SPYNAD PGDEMNLH PQTLEGKSELLNLM PNCI ISQQNAT PNGINGND PNGING 446 GDVLFNRQP	QVLNM- 549 EKDYL- 533 (SLNIVS 535 EIMAY- 534 CTLNML- 529 SQFMLL- 535 SKFMLL- 536
550 - LIVWQP DWDGVIR TPAIIRP KPLWSGKGILS VAIPNGIHLQRFPEGTTLLSPKDRAML ID GQIIF GVVEKKTVGSSNGGL HVVTREKGRQVCAKLFGNL 534	1 K V V N F 656 1 T A R H T 641 1 Y S T K Q 645 1 I V N N 645 2 W M I N H 637 2 L I V N T 646 2 T I V N S 647
657 LINN GFSTGIGDTIAD GPTIMREITETIAEAK KKU DVY KEAGANLUTAKH GMTIRESFEDNV KFLNEARD KAG RIAEVN KDINNV KOMVMAG SKOSFI G2N IK NGFTS SLMOVENEKKIEN I FVNIK KFVI HNWIK LME KKOLKKIKI (K NEKF-NTITKINN LSTTKKYFS LINIEN LINNM KOKOSKOS G40 I FLKGF SLAD LELDVSMIEI VCTSIEN I EKLWIE U STELVD LKFFGKNK QQY L KVKTINEEI KKFDKILSYY LNKGN LMAN SLINMK SG SGSE G40 LQL GFSVGIDCI PTKMVK KDVSII I KTAKLYKK SIX RULSKK FNGFENKOSNY NLENNIK VV UNARDMAG SJAQKCISYNNLKMI FSGSKGSE G48 LQL GFSVGIDCI PTKMVK KDVSII I KTAKLYKK SIX RULSKK FNGFENKOSNY NLENNIK VV UNARDMAG SJAQKCISYNNLKMI FSGSKGSE G48 LQL GFSVGIDCI PTKMVK KDVSII I KTAKLYKR SIX RULSKK FNGFENKOSNY NLENNIK VV UNARDMAG SJAQKCISYNNLKKMI FSGSKGSE G48 LQL GFSVGIDCI PTKMVK KDVSII I KTAKLYKR RULSKK SIX RULSKK FNGFENKOSNY NLENNIK VV UNARDMAG SJAQKCISYNNLKKMI FSGSKGSE G48 LQL GFSVGIDCI PTANEI NIKI VISI I KTAKLYKR RULSKK SIX RULSKK FNGFENKOSNY NLENNIK VV UNARDMAG SJAQKCISYNNLKKMI FSGSKGSE G48 LQL GFSVGIDTIAD KKTMNNI I KTIKK KK RULSKK SIX RULSKK SIX RULSKA SLSVNANNIK KMV GGSKGSFI G48 LL FEGFSVGIDTIAD KKTMNNI I KTIK KAK KA RULSKA SLSV RULSKK SK RULSKA SLSVNANNIK KMV GGSKGSFI	N   A QMS 762 N   Q   V 748 N   MQ   I 752 N   S Q   V 751 N   S Q   I 752 N   S Q   I 752 N   S Q   I 753
763 ACV G QQ SVE GKR I Å FG FV D KTLPH FS KD DV S ÞE SKG FVEN SVLRG LT POLEFFHAMG GREGL I DT AV KTA ET GYLORR FLVKA LED I MVH D M TT KN SLGNI OF LV 793 G LLG KQS SLK I NNMMH HG K LEGNNI TEM I TEM SLG FI STA LSKA SKAREGLI DT SLKTA ET GYLORR FSK SMENNI GYVD GSK 753 G LLG QQ SLV LSEF SR DV KA R LF SH YT FFEI D LEI KGYLKNNFLKG LSPYEFFHSI A GREGLI DT SI KTA ET GYLORR FSK SMENNI SYVD GSK RNS KNFL I GYV 753 G LLG QQ SLV LSEF SR DV KA R LF SH YT FFEI D LEI KGYLKNNFLKG LSPYEFFHSI A GREGLI DT SI KTA ET GYLORR LSK SMENNI SYVD GSK RNS KNFL I GYV 753 G CV G QQ NV B GKR I D SA FG SR SL PH FLFBD KET KGFVQN SY SS G L PD EFFHAMG GREGLI DT AI KT SET GYLQ RR LSK AMED I V EV D LT VR NA GKEL LEFF 753 A CV G QQ NV B GKR I D SA FG SR CL PH FLFBD KOP TK GFVQ NSY SS G L PD EFFHAMG GREGLI DT AI KT SET GYLQ RR LSK AMED I V EV D LT VR NA GKEL LEFF 754 A CV G QQ NV B GKR I D SA FG SR SL PH FLFB KQ NG NSY SS G L PD EFFHAMG GREGLI DT AI KT SET GYLQ RR LSK AMEN W SV D T VR NA GKEL LEFF 754 A CV G QQ NV B GKR I D SA FG SR SL PH FS KD NG PET RG FVQ NSY I SG L PD EFFHAMG GREGLI DT AI KT SET GYLQ RR LSK AMEN W SV D D T VR NA GKEL LEFF 754 A CV G QQ NV E GKR I PM G FN KR SL PH FS KD NG PET RG FVQ NSY I SG L PD EFFH SM GREGLI DT AI KT SET GYLQ RR LSK AMEN W SV D D T VR NA GKEL LEFFY	GEDGMD 874 (GEDGLD 860 (GEDGFD 864 (GEDCFD 863 (GEDSID 854 (GEDGMD 864 (GEDGMD 865
875 MAHIE KQSLDTIGGSDAAF EKRY RVDLINTDHTLDSLLESGSEILGDLK LQULDE EYKQLVKDRKFL REVFVDG. EAWWPLPVNIRTI ONAQOTHI 801 PTELESTITS KNHKARTNKNLGSNKLKTYT TKOLGFSNP SHIHFINT NFKKYYTODKILN IKGTKNTCYIPVNI FII IAHT SSLO 865 PTLIESSCVENKNFFMKIFINNKK FNFNILCNNK IN KNYK KNYSKI OGEF YHNI INI I KRKNFLIKKKFYJPLNIEN IFR SMFT- 864 AVVLENG KIFLGKNSDI EMMWYKYTOSSPCGLAI-DSLIFLSKSVN SKI ANIE YNDLLKDEEF RKIMLGOND IN PLYVNLDRI ISK SVI FK 855 AVFLENG YN IFRAN TYEELN SKWFTNSPCGLAI-DSLIFLSKSVN SKI ANIE YNDLLKDEEF RKIMLGONFIN PLYVNLDRI ISK SVI FK 855 AVFLENG YN IFRAN TYEELN SKWFTKSPCYGLNT-K RFFLLK IN SKOFFE KLGGLOFFFLQT FDRHI LOQI FSSGIEINLEJPVNI ORLIMNANN FF 866 ALNLENG MANTI KKNREIEI YFR NSSPCIGLOZ-KSMIT KNIK SKOFFE KLGGLOFFFLQT FDRHI LQN FNSGFNI PLYVNI SKI INN FF 866 ALNLENG MNTI KKNREIEI YFR FNINSPLI GMAY-DGKEVSELKI FKDKNTKKKI VE-FFLQI KKDREILROMI INNYELTI PLYVNI DRI IKNAEK FF	I D H T K P S 979 955 - N H K N S S 966 - N I E T S T 961 - K I S K Y S 971 - Q E K N C 970
980 DLTIKO IVLGVKDLQENLLVLRGKNE I QNAQRO AVTLFCLLRSRLATRRVQEY NLTKQAEDWULSNIE AQELRSVVHPGEMVGVLAAQSIGE 956 RVGKLQKNCTCPLLUSVLSUSKTVGKUFYRALFNEI - NPSILLVYI NFTLAUKIFYKLI-SKLINLFQLKVKFRQIENXKNSLTPGECVGVIAAQSIGE 950 DRALKQTVCD - NNLLALFLNTLI - KVLILKTNGVIFNNFKNF- INFSLLVYI NFTLAUKINYKKSNITPSSLWIIHKIEKKILKSLICPGLCLGVIAAQSIGE 967 JLNFKET RSIKFIRMYTELIN- FKISFNQKKSDNGUINN- DNFLLAIYI NFTLAUKISNITPSSLWIIHKIEKKILKSLICPGLCLGVIAAQSIGE 967 JLNFKET NSIKFIRMYTELIN- FKISFNQKKSDNGUINN- DNFLLAIYI NFTLAIYI NFTLAIYI NFTLAIYI 967 JLNFKET NSIKFIRMYTELIN- FKISFNQKKSDNGUINN- DNFLLAIYI NFTLAIYI NFTLAIYI NFTLAIYI NFTLAIYI NFTLAIYI 967 JLNFKET NSIKFIRMYTELIN- FKISFNQKKSDNGUINN- DNFLLAIYI NFTLAIYI NFTLAIYI NFTLAIYI NFTLAIYI 967 JLNFKET NSIKFIRMYTELIN- FKISFNQKKSDNGUINN- SOSIGQ 972 DLSPTEI JGVKKI ENV CFDSLGPKKNEECSGFCNCCKCESRLNATLFFTYLRSMLASKIVIFFKYKFSKVAFLWVLNE ICTVYRKSIN SASIGQ 971 RSPIE I JGGVKKIENY CFDSLGPKKNEECSGFCNCCKCESRLNATLFFTYLRSMLASKI IFFKYKFSKVAFLWVLNE ICTVYRKSI ASPGEWVGTI SAQSIGQP	ATQMTL 1081 TTQMTL 1064 TTQMTL 1067 ATQMTL 1067 ATQMTL 1072 ATQMTL 1083 ATQMTL 1082
1082 NT FH FAGVASK KYT SGVPRLKEIL IN VAK NMKT PSLTYVLEP GHAADQCAKLIR SALEHTTLKSYT I ASE IYD DPRSTVIPEDEE I QLHESLDDELARQSFDO 606 NT FH HAGILDKNYT VGVPR NEI I NYSKNIKHTI YN YCH SNSKEIE STOFI I SRLEET KLEFFYKEIT LKSYT I ASE IYD SNYT FI IYD DDR IN IN FKMPLMN YFLMYN 1068 NT FH HAGILDKNYT VGVPR NEI I NYSKNIKHTI YN YCH SNSKEIE STOFI I SRLEET KLEFFYKEIT LKSYT I AD DPR I SNIK SN 1070 NT FH FAGVASKNYT LGIPRLKEI I NYSKNIKHTI YN YCH SNSKEIE STOFI 1071 NT FH YAGY SAKNYT LGIPRLKEI I NYLKIT KT PSLTYIK KEYN SY FKVTYL QCHLEFYT LKOMMSSIS FFYD PD FFYSIS KKNE I PDELON I DYNK I SNSKEI PT DI DON IN SNSKEI PT DI DON SNSKEI PT DI DON IN SNSKEI PT DON SNSKEI PT DON SNSKEI PT DON IN SNSKEI PT DON SNSKEI PT SNSKE	1Q S P W 1191 1N P R W 1172 3K D A F V N 1175 2A S S W 1183 H I G T W - 1180 S L G T W - 1191 C I G T W - 1190
1192 - LLR LE LDRAAMNDKOLTMOQVGERIKGTFKN       -DLFVIWSEDNDEKLIIRCRVVRFSLDAETEAEBOHMIK         1172 - LLKLIISRWALFEKKISIVKLEKKLSDKLKNVGNIQISFADKFEIAIITSNIKNLERVSID       -DLFVIWSEDNDEKKINK         1172 - LLKLIISRWALFEKKISIVKLEKKLSDKLKNVGNIQISFADKFEIAIITSDNIKNLERVSID	<ul> <li>K S K 1259</li> <li>K S K 1242</li> <li>K F LE PN 1281</li> <li>LE I Q 1260</li> <li>F E R Q 1271</li> <li>F E R K 1270</li> </ul>
1262	G S Y VNY 1365 D N S Y I NQ 1370 3 S T Y I NM 1353 D G S Y VNY 1391 D G S Y VNY 1369 D G S Y VNY 1380 D G S Y VNS 1380 D G S Y VNS 1379
1306 RH MALL VOYMT TAGGUT SVT RHGFNRSNT GALMACSFEET VEILFEKGÅ SAELDOCRGVSTAVILGGMAPIGTGAFD VMIDE ESLVK VMPEOKITE I EDGOGGOV 1371 HH SCLAD VSNT KAFNA IN RYGLKVQIST LOCSFEET MKT LIKASVET KVD RFSSITETI I FOKESNFGT GFNPF VKPQLGANE 1384 HH LC TOPMTNLGFINS IN RYGLKVQIST LOCSFEET AKT FIKASINT KADE INSITENVILGKLIKLGTGFFNP VKPQLGANE I KN. – I VKQTLQQT KEI 1392 RHLTVULIT FRGINSNIN RYGLKVQIST LOCSFEET AKT FIKASINT KADE INSITENVILGKLIKLGTGFFNP VKPQLGANE I KN. – I VKQTLQQT KEI 1392 RHLTVULIT FRGINSNIN RYGLKVGIST LOCKSFEET AKT FIKASINT KADE INSITENVILGKLIKLGTGFFNP VKPQLGANE I KN. – I VKQTLQQT KEI 1392 RHLTVULIT FRGINSNIN RYGLKVGISTEN LOKSFEET VDIF I VSVLGANA FISTONIKSISANI MVGNLUSVGTGKVDLFVDDF 1393 RHIFLU ADI MTHGGKLMSIT RHGISKIE GFIAKSFEET VDIF VQAAAFGVCDNLKGVSANI MVGNLUSVGTGKVDLFVDDF 1383 RHIFLU VDI MTHRGKLISIT RHGINRTDIG PIAKCSFEET I EVLYQAAAFGVCDNLKGVSGSILVGQVSSLGTGKIDLFLGEKK F	PYSNES 1477 PSFNQS 1476 NNNSLVI 1463 1473 - 1475 - 1473 - 1473 - 1474 - 1473 - 1464
1478 GLVNAD LDVKDE LMF SFLVDSG SNOAMAGG FTA YGGAD YGGAT SPFGAYGEAPT SPGFGV SSPGF SPT SPT SPAY SPT SPSY SPT SPSY SPT SPSY SPT SPSY SPT SPS 1477 KSSY K U VSYY K	YSPTSP 1589
1590 SY SPT SP SY SP	NYSPTSP 1701
1702 SY SPT SPGY SPG SPAY SPKQDE QKHNENENSR	1733

Supplementary Figure 7 (preceding page): Multiple sequence alignment of RNA Pol II largest subunits (Rpb1) from nucleomorphs and *Saccharomyces cerevisiae* (top row). The CTD tail domain and its heptad YSPTSPS repeats are absent from all nucleomorph polymerases.



Supplementary Figure 8: Presence and absence of epigenetic mark depositing and reading domains as well as histone chaperons, chromatin remodellers, DNA methylation-related proteins and the FACT complex in nucleomorph genomes. Domains were identified using HMMER3.0, the number of proteins containing a significant match to each domain/protein is shown.

### Supplementary References

- Edgar RC. 2004. MUSCLE: multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Res 32(5):1792–1797.
- Keeling PJ, Burki F, Wilcox HM, Allam B, Allen EE, Amaral-Zettler LA, Armbrust EV, Archibald JM, Bharti AK, Bell CJ, Beszteri B, Bidle KD, Cameron CT, Campbell L, Caron DA, Cattolico RA, Collier JL, Coyne K, Davy SK, Deschamps P, Dyhrman ST, Edvardsen B, Gates RD, Gobler CJ, Greenwood SJ, Guida SM, Jacobi JL, Jakobsen KS, James ER, Jenkins B, John U, Johnson MD, Juhl AR, Kamp A, Katz LA, Kiene R, Kudryavtsev A, Leander BS, Lin S, Lovejoy C, Lynn D, Marchetti A, McManus G, Nedelcu AM, Menden-Deuer S, Miceli C, Mock T, Montresor M, Moran MA, Murray S, Nadathur G, Nagai S, Ngam PB, Palenik

B, Pawlowski J, Petroni G, Piganeau G, Posewitz MC, Rengefors K, Romano G, Rumpho ME, Rynearson T, Schilling KB, Schroeder DC, Simpson AG, Slamovits CH, Smith DR, Smith GJ, Smith SR, Sosik HM, Stief P, Theriot E, Twary SN, Umale PE, Vaulot D, Wawrik B, Wheeler GL, Wilson WH, Xu Y, Zingone A, Worden AZ. 2014. The Marine Microbial Eukaryote Transcriptome Sequencing Project (MMETSP): illuminating the functional diversity of eukaryotic life in the oceans through transcriptome sequencing. *PLoS Biol* **12**(6):e1001889.

- Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics* **30**(9):1312–1313.
- Tamura K, Stecher G, Peterson D, Filipski A, Kumar S. 2013. MEGA6: Molecular Evolutionary Genetics Analysis Version 6.0. Mol Biol Evol 30(12):2725–2729.