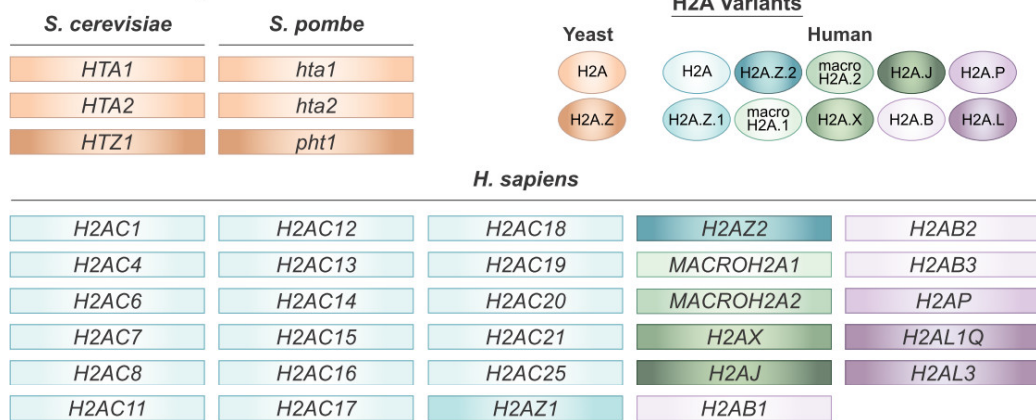
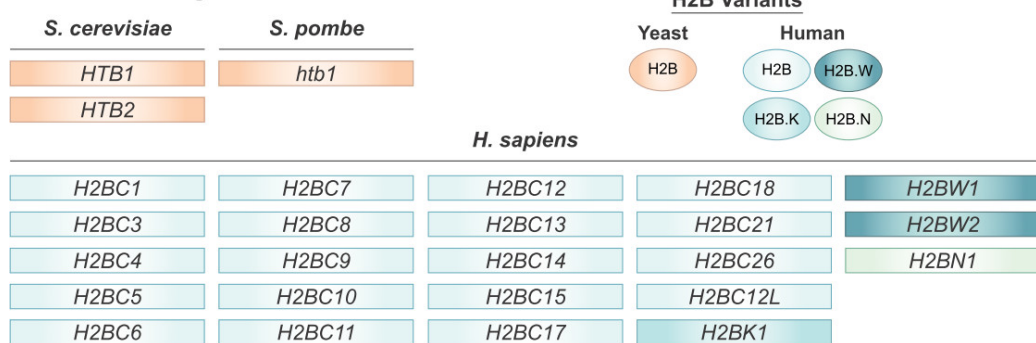


## Supplemental Figure 1

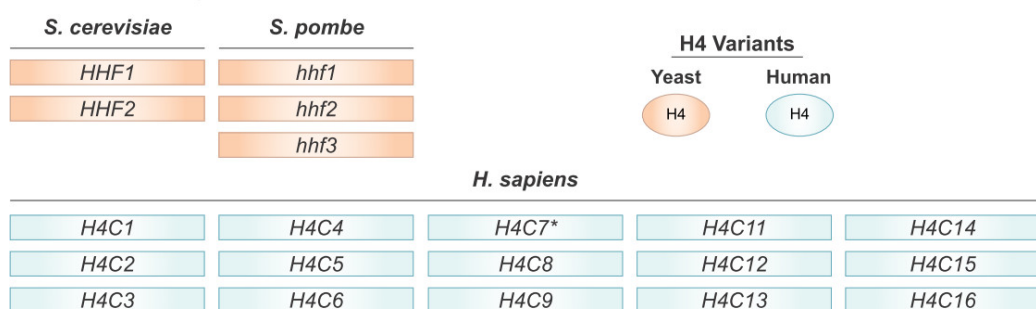
### A Genes encoding Histone H2A



### B Genes encoding Histone H2B



### C Genes encoding Histone H4



**Figure S1: A comparison of histones H2A, H2B, and H4 from *S. cerevisiae*, *S. pombe*, and *H. sapiens*.** Humans have many more gene copies and protein variants for (A) H2A, (B) H2B, or (C) H4 than either yeast species. The genes that encode each variant are color coordinated with their respective Histone Variants. The genes for H2A and H2B result in minor amino acid sequence variations for the canonical protein products which are not reflected here. \*The existence of the protein encoded by this gene is uncertain, though there is evidence that it expresses the histone H4G variant .

## Supplemental Figure 2

### A H2A Protein Sequence Alignments

S.c. H2A 1 SGGKGGKAGSAAKASQSRSAKAGLTFPVGRVHRLLRGNYAQRIGSGAPVYLTA VLEYLA AEILEL 66  
H.s. H2A 1 SG-RGKQGGKARAKAKTRSSRAGLQFPVGRVHRLLRGNYAERVGAGAPVYLA VLEYLTAEILEL 65

S.c. H2A 67 AGNAARDNKKTRIIPRHLQLAIRNDELNKLGNVTIAQGGVLPNQHQNLLPKKSAKATKASQEL 132  
H.s. H2A 66 AGNAARDNKKTRIIPRHLQLAIRNDELNKLKGVTIAQGGVLPNIQAVLLPKKTESHHKAKGK- 130

S.p. H2A $\alpha$  1 SG-GKSGGKA AVAKSAQSRSAKAGLAFPVGRVHRLLRGNYAQRVGAGAPVYLA AVLEYLA AEILE 65  
S.p. H2A $\beta$  1 SG-GKSGGKA AVAKSAQSRSAKAGLAFPVGRVHRLLRGNYAQRVGAGAPVYLA AVLEYLA AEILE 65  
H.s. H2A 1 SGRGKQGGKARA--KAKTRSSRAGLQFPVGRVHRLLRGNYAERVGAGAPVYLA AVLEYLTAEILE 64

S.p. H2A $\alpha$  66 LAGNAARDNKKTRIIPRHLQLAIRNDELNKLGHVTIAQGGVVPNINAHLLPKTSGRTCKPSQEL 131  
S.p. H2A $\beta$  66 LAGNAARDNKKTRIIPRHLQLAIRNDELNKLGHVTIAQGGVVPNINAHLLPKQSGK-GKPSQEL 130  
H.s. H2A 65 LAGNAARDNKKTRIIPRHLQLAIRNDELNKLKGVTIAQGGVLPNIQAVLLPKKTESHHKAKGK- 129

	Sequence Identity with <i>S. cerevisiae</i> H2A
H2A	73%

	Sequence Identity with <i>S. pombe</i> H2A
H2A $\alpha$	78%
H2A $\beta$	78%

### B H2B Protein Sequence Alignments

S.c. H2B 1 SAKAEKKPASAPAEKKPAKKTTST--DGKKRSKARKETYSSYIYKVLKQTHPDTGISQKSM SI 64  
H.s. H2B 1 -----PEPAKSAPAPKKGSKKAVTKAQKKDGKKRKR SRKESYSIYVYKVLKQVHPDTGISSKAMGI 61

S.c. H2B 65 LNSFVNDIFERIA TEASKLAAYNKKSTISAREIQTAVRLILPGELAKHAVSEGTRAVTKYSSSTQA 130  
H.s. H2B 62 MNSFVNDIFERIA GEASRLAHYNKRSTITSREIQTAVRLILPGELAKHAVSEGTKAVTKYTSSK-- 125

S.p. H2B 1 -SAAEKKPASAPAGKAPRDTMK SADKKRGKNRKETYSYIYKVLKQVHPDTGISNQAMRILNSFV 65  
H.s. H2B 1 PEPAKSAPAPKKGSKKAVTKAQKKDGKKRKR SRKESYSIYVYKVLKQVHPDTGISSKAMGIMNSFV 66

S.p. H2B 66 NDIFERIA TEASKLAAYNKKSTISSREIQTAVRLILPGELAKHAVTEGTSVTKYSSSAQ 125  
H.s. H2B 67 NDIFERIA GEASRLAHYNKRSTITSREIQTAVRLILPGELAKHAVSEGTKAVTKYTSSK- 125

	Sequence Identity with <i>S. cerevisiae</i> H2B
H2B	67%

	Sequence Identity with <i>S. pombe</i> H2B
H2B	69%

### C H4 Protein Sequence Alignments

S.c. H4 1 SGRGKGGKGLGKGGAKRHRKILRDNIQGITKPAIRRLARRGGVKRISGLIYEEVRAVLKSFLESVI 66  
H.s. H4 1 SGRGKGGKGLGKGGAKRHRKVLRDNIQGITKPAIRRLARRGGVKRISGLIYEE TRGVLKVFLENVI 66

S.c. H4 67 RDSVTYTEHAKRKTVTSLDVVYALKRQGRITLYGFGG 102  
H.s. H4 67 RDAVTYTEHAKRKTVTAMDVVYALKRQGRITLYGFGG 102

S.p. H4 1 SGRGKGGKGLGKGGAKRHRKILRDNIQGITKPAIRRLARRGGVKRISALVYEETRAVLKLFLENVI 66  
H.s. H4 1 SGRGKGGKGLGKGGAKRHRKVLRDNIQGITKPAIRRLARRGGVKRISGLIYEE TRGVLKVFLENVI 66

S.p. H4 67 RDAVTYTEHAKRKTVTSLDVVYS LKRQGRITLYGFGG 102  
H.s. H4 67 RDAVTYTEHAKRKTVTAMDVVYALKRQGRITLYGFGG 102

	Sequence Identity with <i>S. cerevisiae</i> H4
H4	92%

	Sequence Identity with <i>S. pombe</i> H4
H4	91%

**Figure S2: Protein alignment comparing histones H2A, H2B, and H4 sequences from *S. cerevisiae*, *S. pombe*, and *H. sapiens*. (A, B, C) The canonical protein sequences for each histone are compared between the *S. cerevisiae* or *S. pombe* protein and the human protein. Blue residues represent conservative changes, where the biochemical properties of the amino acid are maintained, and orange residues represent non conservative changes, where the biochemical properties are altered.**