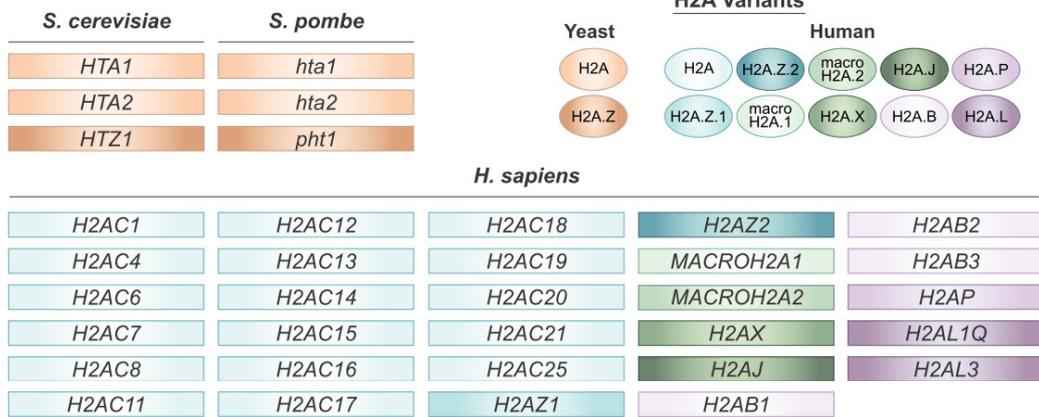
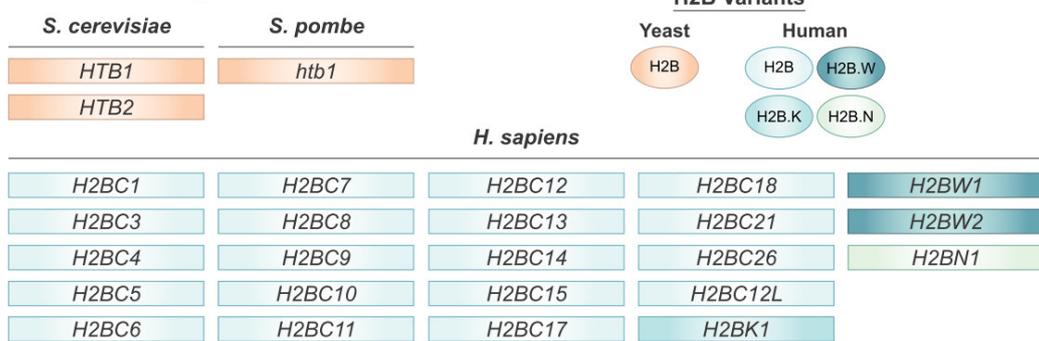


Supplemental Figure 1

A Genes encoding Histone H2A



B Genes encoding Histone H2B



C Genes encoding Histone H4

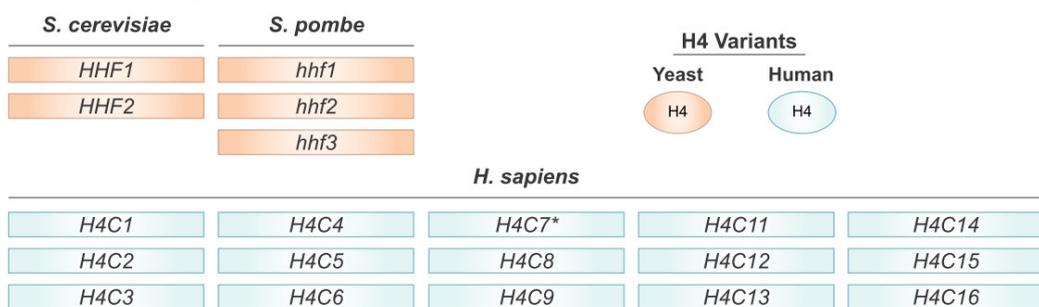


Figure S1: A comparison of histones H2A, H2B, and H4 from *S. cerevisiae*, *S. pombe*, and *H. sapiens*. Humans have many more gene copies and protein variants for (A) H2A, (B) H2B, or (C) H4 than either yeast species. The genes that encode each variant are color coordinated with their respective Histone 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 SGGKGGKAGSAAKASQSRSAKAGLTFPVGRVHRLLRKGNYAQRIGSGAPVYLTAVLEYLAEEILEL 66
H.s. H2A 1 SG-RGKQGGKARAKAKTRSSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAHVLEYLTAEILEL 65

S.c. H2A 67 AGNAARDNKKTRIPRHLQLAIRNDELNKLKGNVTIAQGGVLPNQHQNLLPKKSAKATKASQEL 132
H.s. H2A 66 AGNAARDNKKTRIPRHLQLAIRNDELNKLKGVVTIAQGGVLPNIAQVLLPKKTESHHKAKGK- 130

S.p. H2A α 1 SG-GKSGGKA AVAKSAQSRSAKAGLAFPVGRVHRLLRKGNYAQRVGAGAPVYLAHVLEYLAEEILE 65
S.p. H2A β 1 SG-GKSGGKA AVAKSAQSRSAKAGLAFPVGRVHRLLRKGNYAQRVGAGAPVYLAHVLEYLAEEILE 65
H.s. H2A 1 SGRGKQGGKARA--KAKTRSSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAHVLEYLTAEILE 64

S.p. H2A α 66 LAGNAARDNKKTRIPRHLQLAIRNDELNKLKGVVTIAQGGVLPNINAHLLPKTSGRTCKPSQEL 131
S.p. H2A β 66 LAGNAARDNKKTRIPRHLQLAIRNDELNKLKGVVTIAQGGVLPNINAHLLPKQSGK-GKPSQEL 130
H.s. H2A 65 LAGNAARDNKKTRIPRHLQLAIRNDELNKLKGVVTIAQGGVLPNIAQVLLPKKTESHHKAKGK- 129

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

	Sequence Identity with <i>S. pombe</i> H2A
H2A α	78%
H2A β	78%

B H2B Protein Sequence Alignments

S.c. H2B 1 SAKAEKKPASKAPAEKKPAKKTSTST--DGKKRSKARKETYSSYIYKVLKQTHPDTGISQKSMSEI 64
H.s. H2B 1 -----PEPAKSAPAPKKGSKKAVTKAQKKGKKRKRSRKESYSIYVYKVLKQVHPDTGISSKAMGI 61

S.c. H2B 65 LNSFVNDIFERIA TEASKLAAYNKSTISSAREIQTAVRLILPGELAKHAVSEGTRAVTKYSSSTQA 130
H.s. H2B 62 MNSFVNDIFERIA GEASRLAHYNKRSTITTSREIQTAVRLILPGELAKHAVSEGTKAVTKYTSSK-- 125

S.p. H2B 1 -SAAEKKPASKAPAGKAPRDTMKSADKKRGNRKE TYSSYIYKVLKQVHPDTGISNQAMRILNSFV 65
H.s. H2B 1 PEPAKSAPAPKKGSKKAVTKAQKKGKKRKRSRKESYSIYVYKVLKQVHPDTGISSKAMGIMNSFV 66

S.p. H2B 66 NDIFERIA TEASKLAAYNKSTISSREIQTAVRLILPGELAKHAVTEGTKSVTKYSSSAQ 125
H.s. H2B 67 NDIFERIA GEASRLAHYNKRSTITTSREIQTAVRLILPGELAKHAVSEGTKAVTKYTSSK- 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 SGRGKGGKGLGKGGAKRHRKVLRDNIQGITKPAIRRLARRGGVKRISGLIYEEETRGVLVFLENVI 66

S.c. H4 67 RDSVITYTEHAKRKTVTSLDVVYALKRQGRITLYGFGG 102
H.s. H4 67 RDAVITYTEHAKRKTVTAMDVVYALKRQGRITLYGFGG 102

S.p. H4 1 SGRGKGGKGLGKGGAKRHRKILRDNIQGITKPAIRRLARRGGVKRISALVYEEETRAVLKLFLENVI 66
H.s. H4 1 SGRGKGGKGLGKGGAKRHRKVLRDNIQGITKPAIRRLARRGGVKRISGLIYEEETRGVLVFLENVI 66

S.p. H4 67 RDAVITYTEHAKRKTVTSLDVVYSLKRQGRITLYGFGG 102
H.s. H4 67 RDAVITYTEHAKRKTVTAMDVVYALKRQGRITLYGFGG 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.