Supplementary Figure 1

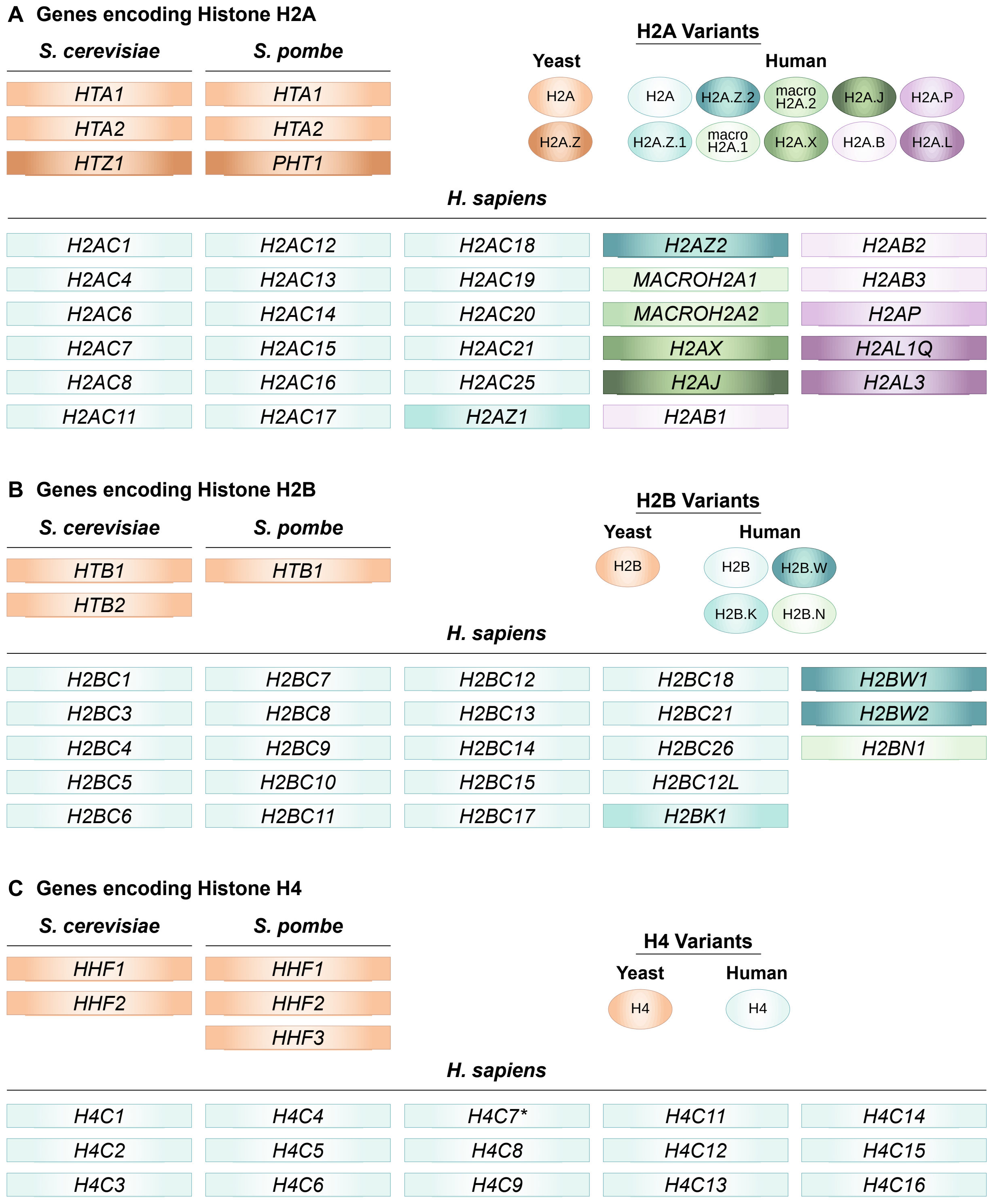

Fig. S1: A comparison of histones H2A, H2B, and H4 from *S. cerevisiae*, *S. pombe*, and *H. sapiens*. Humans have many more gene copies and protein variants for **(A)** H2A, **(B)** H2B, or **(C)**

H4 than either yeast species. The genes that encode each variant are color coordinated with their respective Variants. *The existence of the protein encoded by this gene is uncertain (11).

Supplementary Figure 2

A H2A Protein Sequence Alignments

```
S.c. H2A    1 SGGKGGKAGSAAKASQSRSAKAGLTFPVGRVHRLLRRGNYAQRIGSGAPVYLTAVLEYLAAEILEL 66
H.s. H2A    1 SG-RGKQGGKARAKAKTRSSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAAVLEYLTAEILEL 65

S.c. H2A   67 AGNAARDNKKTRIIPRHLQLAIRNDDELNKLLGNVTIAQGGVLPPNIHQNLLPKKSAKATKASQEL 132
H.s. H2A   66 AGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVTIAQGGVLPPNIQAVLLPKKTESHHKAKGK- 130
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
S.p. H2Aa   1 SG-GKSGGKAAVAKSAQSRSAKAGLAFPVGRVHRLLRKGNYAQRVGAGAPVYLAAVLEYLAAEILE 65
S.p. H2Ab   1 SG-GKSGGKAAVAKSAQSRSAKAGLAFPVGRVHRLLRKGNYAQRVGAGAPVYLAAVLEYLAAEILE 65
H.s. H2A    1 SGRGKQGGKARA--KAKTRSSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAAVLEYLTAEILE 64

S.p. H2Aa  66 LAGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGHVTIAQGGVVPNINAHLLPKTSGRTGKPSQEL 131
S.p. H2Ab  66 LAGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGHVTIAQGGVVPNINAHLLPKQSGK-GKPSQEL 130
H.s. H2A   65 LAGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVTIAQGGVLPNIQAVLLPKKTESHHKAKGK- 129
```

	Sequence Identity with *S. cerevisiae* H2A
H2A	73%

	Sequence Identity with *S. pombe* H2A
H2Aa	78%
H2Ab	78%

B H2B Protein Sequence Alignments

```
S.c. H2B    1 SAKAEKKPASKAPAEKKPAAKKTSTST--DGKKRSKARKETYSSYIYKVLKQTHPDTGISQKSMSI 64
H.s. H2B    1 -----PEPAKSAPAPKKGSKKAVTKAQKKDGKKRKRSRKESYSIYVYKVLKQVHPDTGISSKAMGI 61

S.c. H2B   65 LNSFVNDIFERIATEASKLAAYNKKSTISAREIQTAVRLILPGELAKHAVSEGTRAVTKYSSSTQA 130
H.s. H2B   62 MNSFVNDIFERIAGEASRLAHYNKRSTITSREIQTAVRLLLPGELAKHAVSEGTKAVTKYTSSK-- 125
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
S.p. H2B    1 -SAAEKKPASKAPAGKAPRDTMKSADKKRGKNRKETYSSYIYKVLKQVHPDTGISNQAMRILNSFV 65
H.s. H2B    1 PEPAKSAPAPKKGSKKAVTKAQKKDGKKRKRSRKESYSIYVYKVLKQVHPDTGISSKAMGIMNSFV 66

S.p. H2B   66 NDIFERIATEASKLAAYNKKSTISSREIQTAVRLILPGELAKHAVTEGTKSVTKYSSSAQ 125
H.s. H2B   67 NDIFERIAGEASRLAHYNKRSTITSREIQTAVRLLLPGELAKHAVSEGTKAVTKYTSSK- 125
```

	Sequence Identity with *S. cerevisiae* H2B
H2B	67%

	Sequence Identity with *S. pombe* H2B
H2B	69%

C H4 Protein Sequence Alignments

```
S.c. H4   1 SGRGKGGKGLGKGGAKRHRKILRDNIQGITKPAIRRLARRGGVKRISGLIYEEVRAVLKSFLESVI 66
H.s. H4   1 SGRGKGGKGLGKGGAKRHRKVLRDNIQGITKPAIRRLARRGGVKRISGLIYEETRGVLKVFLENVI 66

S.c. H4  67 RDSVTYTEHAKRKTVTSLDVVYALKRQGRTLYGFGG 102
H.s. H4  67 RDAVTYTEHAKRKTVTAMDVVYALKRQGRTLYGFGG 102
```

	Sequence Identity with *S. cerevisiae* H4
H4	92%

```
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
S.p. H4   1 SGRGKGGKGLGKGGAKRHRKILRDNIQGITKPAIRRLARRGGVKRISALVYEETRAVLKLFLENVI 66
H.s. H4   1 SGRGKGGKGLGKGGAKRHRKVLRDNIQGITKPAIRRLARRGGVKRISGLIYEETRGVLKVFLENVI 66

S.p. H4  67 RDAVTYTEHAKRKTVTSLDVVYSLKRQGRTIYGFGG 102
H.s. H4  67 RDAVTYTEHAKRKTVTAMDVVYALKRQGRTLYGFGG 102
```

	Sequence Identity with *S. pombe* H4
H4	91%

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