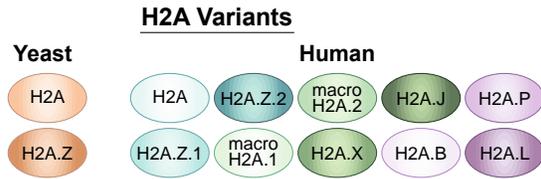


Supplementary Figure 1

A Genes encoding Histone H2A

<i>S. cerevisiae</i>	<i>S. pombe</i>
HTA1	HTA1
HTA2	HTA2
HTZ1	PHT1

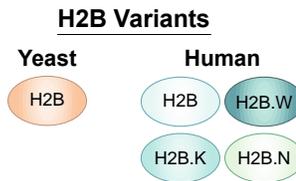


H. sapiens

H2AC1	H2AC12	H2AC18	H2AZ2	H2AB2
H2AC4	H2AC13	H2AC19	MACROH2A1	H2AB3
H2AC6	H2AC14	H2AC20	MACROH2A2	H2AP
H2AC7	H2AC15	H2AC21	H2AX	H2AL1Q
H2AC8	H2AC16	H2AC25	H2AJ	H2AL3
H2AC11	H2AC17	H2AZ1	H2AB1	

B Genes encoding Histone H2B

<i>S. cerevisiae</i>	<i>S. pombe</i>
HTB1	HTB1
HTB2	

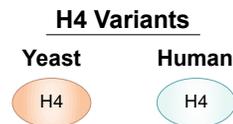


H. sapiens

H2BC1	H2BC7	H2BC12	H2BC18	H2BW1
H2BC3	H2BC8	H2BC13	H2BC21	H2BW2
H2BC4	H2BC9	H2BC14	H2BC26	H2BN1
H2BC5	H2BC10	H2BC15	H2BC12L	
H2BC6	H2BC11	H2BC17	H2BK1	

C Genes encoding Histone H4

<i>S. cerevisiae</i>	<i>S. pombe</i>
HHF1	HHF1
HHF2	HHF2
	HHF3



H. sapiens

H4C1	H4C4	H4C7*	H4C11	H4C14
H4C2	H4C5	H4C8	H4C12	H4C15
H4C3	H4C6	H4C9	H4C13	H4C16

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 SG**GKGGKAGSAAKASQ**SR**SAKAGLTF**PVGRVHRLLR**RGNYAQ**RI**SG**GAPVYL**TAV**LEYL**AAE**I**LEL** 66
H.s. H2A 1 SG-**RGKQGGKARAKAKTR**SR**AGLQ**FPVGRVHRLLR**KGNYAERV**GAGAPVYL**AAV**LEYL**TAE**I**LEL** 65

S.c. H2A 67 AGNAARDNKKTRII**PRHLQLAIRND**DELN**LLGNVTIAQ**GGVLP**PNIHQN**LLPK**SAKATKASQEL** 132
H.s. H2A 66 AGNAARDNKKTRII**PRHLQLAIRND**EELN**LLGKVTIAQ**GGVLP**PNIQAV**LLPK**TESH**H**KAKGK-** 130

S.p. H2Aa 1 SG-**GKSGGKA**AVAK**SAQ**SR**SAKAGLAF**FPVGRVHRLLR**KGNYAQ**RVGAGAPVYL**AAV**LEYL**AAE**I**LEL** 65
S.p. H2Ab 1 SG-**GKSGGKA**AVAK**SAQ**SR**SAKAGLAF**FPVGRVHRLLR**KGNYAQ**RVGAGAPVYL**AAV**LEYL**AAE**I**LEL** 65
H.s. H2A 1 S**GRGKQGGKARA--KAKTR**SR**AGLQ**FPVGRVHRLLR**KGNYAERV**GAGAPVYL**AAV**LEYL**TAE**I**LEL** 64

S.p. H2Aa 66 LAGNAARDNKKTRII**PRHLQLAIRNDEELN**KLLG**HVTIAQ**GGV**VP**NI**NAHLLPKTS**GRTG**KPSQEL** 131
S.p. H2Ab 66 LAGNAARDNKKTRII**PRHLQLAIRNDEELN**KLLG**HVTIAQ**GGV**VP**NI**NAHLLPKQ**SGK-**GKPSQEL** 130
H.s. H2A 65 LAGNAARDNKKTRII**PRHLQLAIRNDEELN**KLLG**KVTIAQ**GGV**LP**NI**QAV**LLPK**TESH**H**KAKGK-** 129

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

	Sequence Identity with <i>S. pombe</i> H2A
H2Aa	78%
H2Ab	78%

B H2B Protein Sequence Alignments

S.c. H2B 1 **SAKA**EKK**PA**SK**APAEKKPA**AK**KTSTST--**DG**KKRSK**ARKETYS**SYI**YKVL**KQ**THPDTGIS**QK**SMS**I** 64
H.s. H2B 1 -----**PE**PA**KS**AP**PKGSK**AV**TKAQ**KKDG**KKRKR**SRKESYS**IYV**YKVL**KQ**VHPDTGIS**SK**AM**G**I 61

S.c. H2B 65 **LNS**FVNDIFERIA**TEAS**K**LAA**YN**KKSTIS**AREI**QTAVRL**IL**PGELAKH**AVSEGT**RA**VTKY**SS**S**TQA** 130
H.s. H2B 62 **MNS**FVNDIFERIA**GEAS**R**LAA**YN**KKSTITS**REI**QTAVRL**LL**PGELAKH**AVSEGT**KAV**TKY**TSS**K-- 125

S.p. H2B 1 -**SAA**EKK**PA**SK**APAGKA**PRD**TMKSAD**KKR**GKNRKE**TY**SSYI**YKVL**KQ**VHPDTGIS**NQ**AMR**ILNS**FV 65
H.s. H2B 1 **PE**PA**KS**AP**PKGSK**KA**VTKAQ**KKDG**KKRKR**SRKESYS**IYV**YKVL**KQ**VHPDTGIS**SK**AM**GIMNS**FV 66

S.p. H2B 66 NDIFERIA**TEAS**K**LAA**YN**KKSTIS**SREI**QTAVRL**IL**PGELAKH**AV**TEG**TK**SV**TKY**SS**SA**Q** 125
H.s. H2B 67 NDIFERIA**GEAS**R**LAA**YN**KKSTITS**REI**QTAVRL**LL**PGELAKH**AV**SEG**TK**AV**TKY**TSS**K- 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 SGRGKGGKGLGKGGAKRHRK**IL**RDNIQGITKPAIRRLARRGGV**KRISGLI**YEE**VRA**VL**KSFLE**SVI 66
H.s. H4 1 SGRGKGGKGLGKGGAKRHRK**VL**RDNIQGITKPAIRRLARRGGV**KRISGLI**YEE**TRG**VL**KVFLE**NVI 66

S.c. H4 67 RD**SV**TYTEHA**KR**KT**VTSL**DVVYAL**KRQ**GRTLYG**FGG** 102
H.s. H4 67 RD**AV**TYTEHA**KR**KT**VTAM**DVVYAL**KRQ**GRTLYG**FGG** 102

S.p. H4 1 SGRGKGGKGLGKGGAKRHRK**IL**RDNIQGITKPAIRRLARRGGV**KRISAL**VYE**ETRA**VL**KLFLE**NVI 66
H.s. H4 1 SGRGKGGKGLGKGGAKRHRK**VL**RDNIQGITKPAIRRLARRGGV**KRISGLI**YEE**TRG**VL**KVFLE**NVI 66

S.p. H4 67 RD**AV**TYTEHA**KR**KT**VTSL**DVVY**SL**KRQ**GRTI**YG**FGG** 102
H.s. H4 67 RD**AV**TYTEHA**KR**KT**VTAM**DVVYAL**KRQ**GRTLYG**FGG** 102

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

	Sequence Identity with <i>S. pombe</i> 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.