

Supplementary Information S2 (Table)|Conservation of Histone Variants in Selected Model Organisms

Family	Variant	Conservation*													
		<i>Homo sapiens</i>		<i>Mus musculus</i>		<i>Drosophila melanogaster</i>		<i>Caenorhabditis elegans</i>		<i>Saccharomyces cerevisiae</i>		<i>Arabidopsis thaliana</i>		<i>Tetrahymena thermophila</i>	
		%	number aligned	%	number aligned	%	number aligned	%	number aligned	%	number aligned	%	number aligned	%	number aligned
H4	Canonical	100	102	100	102	99	102	99	102	90	86	98	102	81	87
H3	Canonical (H3.2**)	100	135	100	135	100	135	97	135			97	135	81	134
H3	H3.3	100	135	100	135	100	135	99	135	90	135	94	135	84	134
H2A	Canonical	100	129	98	129	92	106	90	105			78	121	72	110
H2B	Canonical	100	125	99	125	93	91	85	107	85	104	84	123	62	116
H2A	H2A.X	100	142	97	142	***	***	***	***	75	127	65	146	70	116
H2A	H2A.Z	100	127	100	127	98	119	89	120	73	107	72	91	60	114
H3	CenH3 (CENP-A, others)	100	139	100	71	50	67	50	50	57	51	56	49	48	64
H2A	macroH2A	100	368	91	368										
H3	H3t	100	135	100	135										
H2B	TH2B	100	126	94	126										
H2A	H2A.Bbd	100	114	49	114										
H2B	H2BFWT	100	174												
H2A	H2A1,L2			100	223										

*The percent identity and number of aligned residues when searched using the human ortholog with BLAST.

**H3.1 is a mammalian-specific variant that differs from the ancestral version by a single amino acid residue (S96C).

****D. melanogaster* H2A.X is also the organism's H2A.Z (referred to as "H2Av"), and *C. elegans* lacks an H2A.X