

Supplementary Information S1 (Table)| Functions and Distribution of Eukaryotic Histone Variants

Family	Variant	Function	Distribution	Mean number alignable	Mean conservation*
H4	Canonical	Genome packaging	Universal	94.5	89.5
H3	Canonical (H3.2**)	Genome packaging	Widespread	134.5	89
H3	H3.3	Replacement	Universal	134.5	89
H2A	Canonical	Genome packaging	Widespread	115.5	75
H2B	Canonical	Genome packaging	Universal	119.5	73
H2A	H2A.X	DNA ds break repair	Universal	131	67.5
H2A	H2A.Z	Promoter insulation	Universal	102.5	66
H3	CenH3 (CENP-A, others)	Centromere identity	Universal	56.5	52
H2A	macroH2A	Unknown	Animals		
H3	H3t	Testes-specific	Mammals		
H2B	TH2B	Testes-specific	Mammals		
H2A	H2A.Bbd	Unknown	Mammals		
H2B	H2BFWT	Testes-specific	Mammals		
H2A	H2AL1,L2	Testes-specific	Mammals		
H2A	H2Abd	DNA ds break repair	Bdelloids		
H3	H3V	Transcription termination	Trypanosomes		
H4	H4V	Transcription termination	Trypanosomes		
H2B	H2BV	Transcription initiation	Trypanosomes		

*The average percent of pairwise amino acid identities between human-*A. thaliana* and human-*T. thermophila*.

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