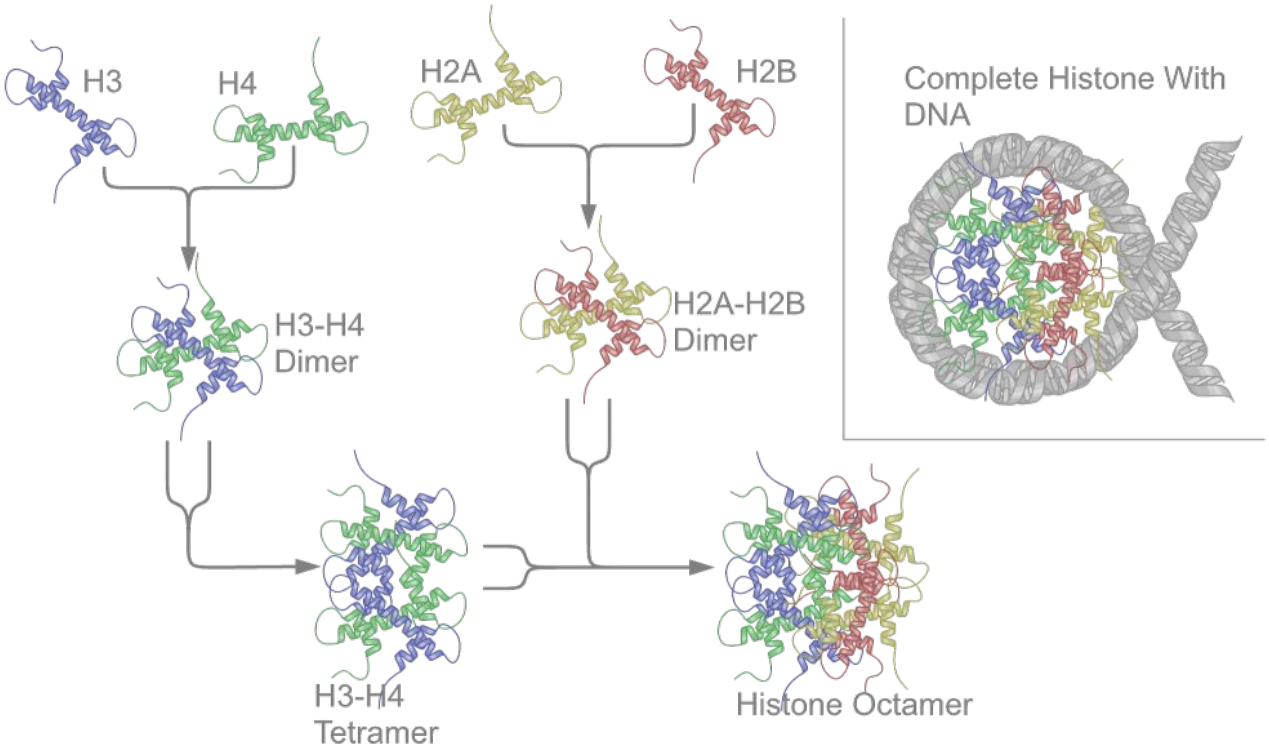
Гистоновые варианты и их изоформы

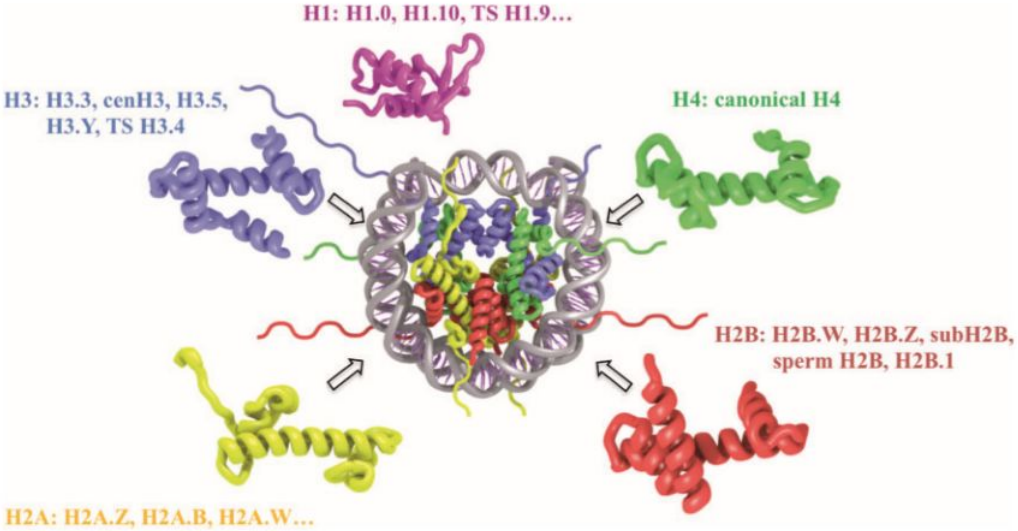
Кафедра биоинженерии
Сингх Лавприт

Москва
2020

Гистоны

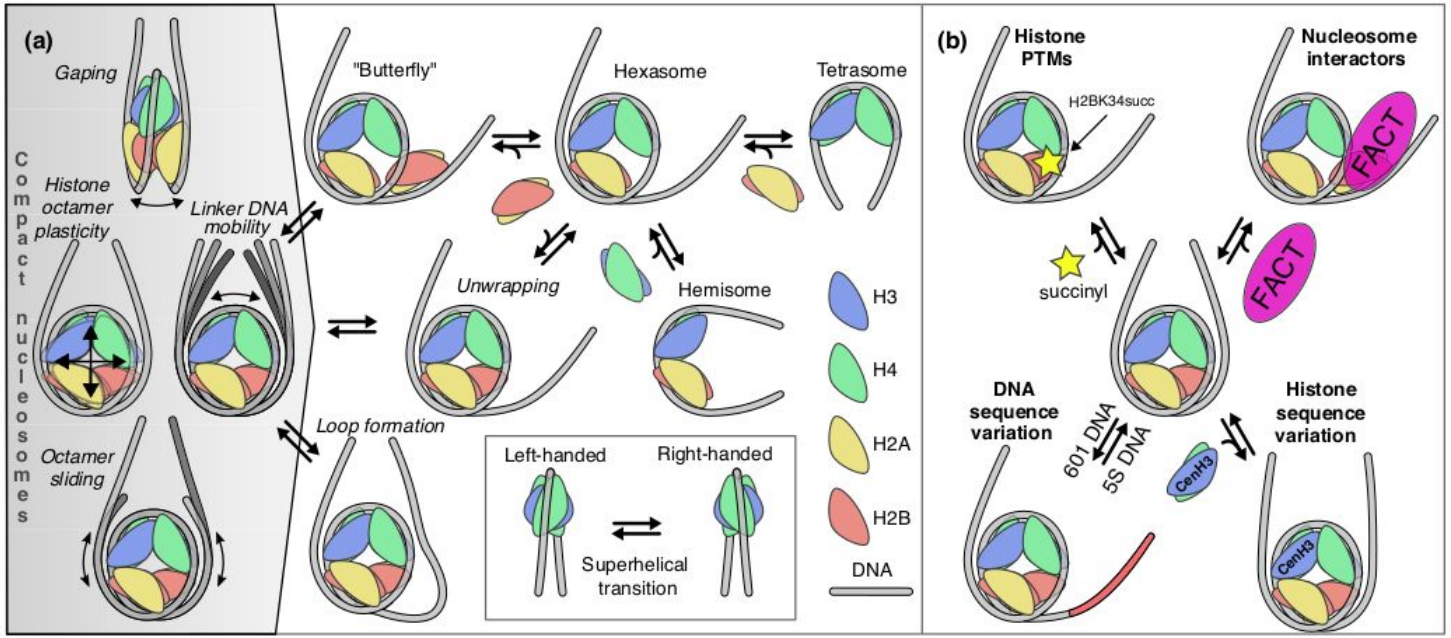

H3
H4
H3-H4
Dimer
H2A
H2B
H2A-H2B
Dimer
H3-H4
Tetramer
Histone Octamer
Complete Histone With
DNA

Гистоновые варианты



E.J. Draizen, A.K. Shaytan, L. Marino-Ramirez, P.B. Talbert, D. Landsman, A.R. Panchenko. "HistoneDB 2.0: a histone database with variants—an integrated resource to explore histones and their variants." Database (2016). PMID: 26989147.

Роль гистоновых вариантов в динамике хроматина



Armeev GA, Gribkova AK, Pospelova I, Komarova GA, Shaytan AK. Linking chromatin composition and structural dynamics at the nucleosome level. Current Opinion in Structural Biology. 2019 Jun;56:46-55. DOI: 10.1016/j.sbi.2018.11.006.

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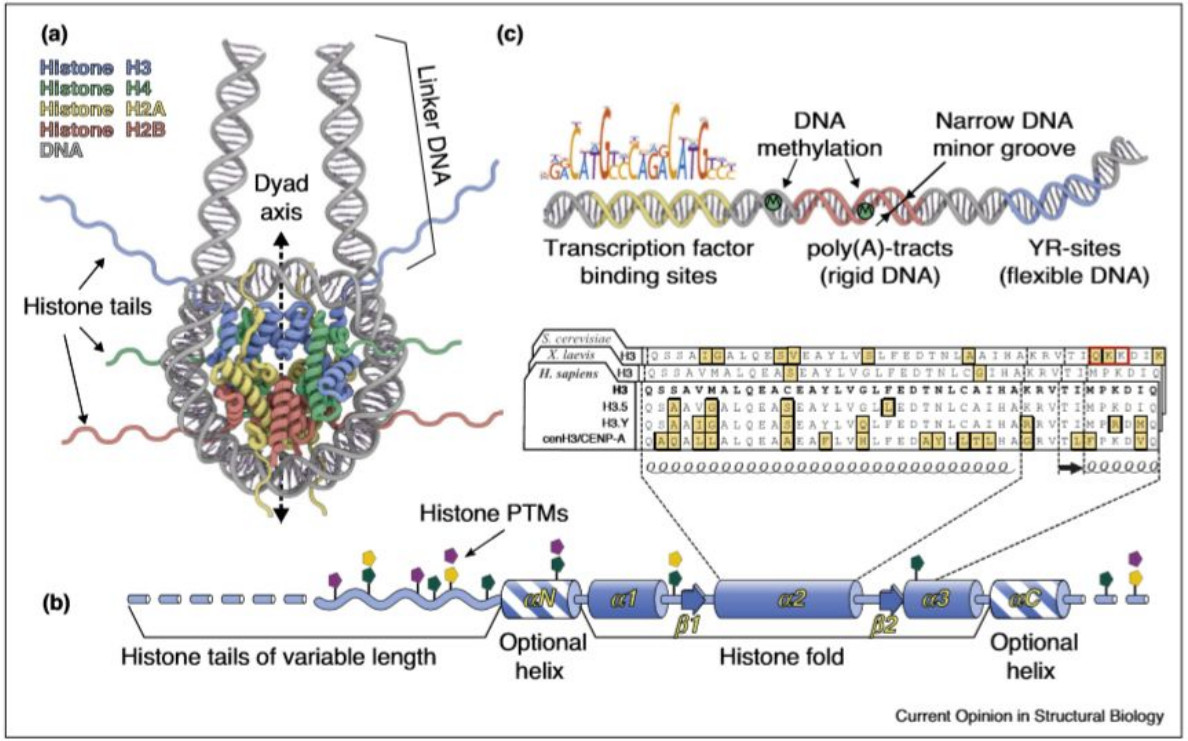


Armeev GA, Gribkova AK, Pospelova I, Komarova GA, Shaytan AK. Linking chromatin composition and structural dynamics at the nucleosome level. Current Opinion in Structural Biology. 2019 Jun;56:46-55. DOI: 10.1016/j.sbi.2018.11.006.

Номенклатура гистоновых вариантов

Naming feature	Recommendation	Examples
Core histone name	Use in an inclusive sense for the protein family. Specify subgroups with a descriptor, prefix, letter suffix, or number suffix.	'H2A can be ubiquitylated.' 'H3 can be methylated on K4.'
Capitalization	Upper and lower case are equivalent in meaning, but upper case is preferred for designating core histones, their suffixes, and modifiable amino acids. Use lowercase for modifications and for prefixes.	H3.3K4me3, H2BK123ub1, cenH3
Descriptors	Descriptors can be used before the core histone name to specify a feature, group variants developmentally or functionally, indicate the species of origin, or other uses. There should be a space between the descriptor and the core histone name. There is no requirement that a descriptor specifies a clade.	RC H2A, early H4, testis-specific H3.4 or TS H3.4, *Hs* H2A.X or human H2A.X, GC H2As, oocyte H1s
Prefixes	These should be few in number and specify a structurally distinct clade of a core histone that is universal or characteristic of a high-level taxonomic clade. Lower case is preferred for prefixes.	macroH2A, cenH3, subH2B
Letter suffixes	These should be preceded by a period (.) and specify a structurally distinct monophyletic clade of a histone family (exception: H2A.X). A suffix may be applied judiciously at any taxon level.	H2A.Z, H3.X, H2A.B
Number suffixes	These should be preceded by a period (.) and specify a particular variant of a core histone, without constraint as to distinctiveness and without implication as to phylogeny. Number suffixes should be assumed to be species-specific, but it is convenient to name variants in related species consistently where unique orthologies are clear. A number suffix should be the default designation of new variants.	H3.5, H2A.1, macroH2A.2, H1.0
Punctuation	Use a period (.) after core histone names to indicate a subtype (letter or number suffix). Use additional periods as necessary to separate finer divisions of subtypes. A period is equivalent to a branch point in a phylogenetic tree.	H2A.Z.1, H2A.L.1
Splice variants	Use a period (.) before a splice variant number. Treat the same as paralog number suffixes, except that a lowercase 's' may precede the number to indicate that the isoform is a splice variant.	macroH2A.1.2, H2A.Z.s3

Old name	Organism(s)	New unified name
H2A (with SPKK motifs)	plants	H2A.W
H2A.Bbd	mammals	H2A.B
H2Abd1, H2Abd2, H2Abd	bdelloid rotifers	(bdelloid) H2A.1 to (bdelloid) H2A.3
H2AL	mammals	H2A.L
H2Av, H2AvD, D2, hv1, Htz1p	*Drosophila, Tetrahymena, Saccharomyces*	H2A.Z
SubH2Bv	mammals	subH2B
H2BL1	mammals	subH2B
H2Bv	apicomplexans	H2B.Z
H2BV	trypanosomes	H2B.V
H2BFWT	mammals	H2B.W
TH2B, hTSH2B	mammals	(TS) H2B.1
H3(P)	*Moneuplotes*	H3.P
H3t	mammals	(TS) H3.4
H3v1 to H3v10	*Stylonychia*	H3.1 to H3.10
H3V	trypanosomes	H3.V
H3.X	human	H3.Y.2
H3.Y	human	H3.Y.1
H4V	trypanosomes	H4.V
H1°	animals	H1.0
H5	birds	H1.0
H1δ	echinoderms	H1.0
H1t	mammals	(TS) H1.6
H1T2	mammals	(TS) H1.7

Talbert PB, Ahmad K, et al. "A unified phylogeny-based nomenclature for histone variants." Epigenetics Chromatin, 2012. PMID: 22650316

Номенклатура гистоновых вариантов

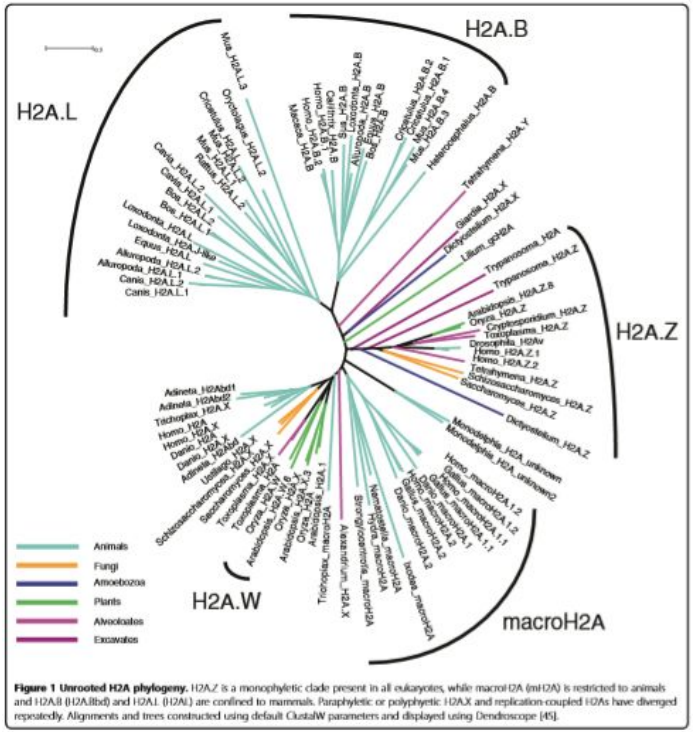


Figure 1 Unrooted H2A phylogeny. H2A.Z is a monophyletic clade present in all eukaryotes, while macroH2A (mH2A) is restricted to animals and H2A.B (H2A.Bbd) and H2A.L (H2AL) are confined to mammals. Paraphyletic or polyphyletic H2A.X and replication-coupled H2As have diverged repeatedly. Alignments and trees constructed using default ClustalW parameters and displayed using Dendroscope [45].

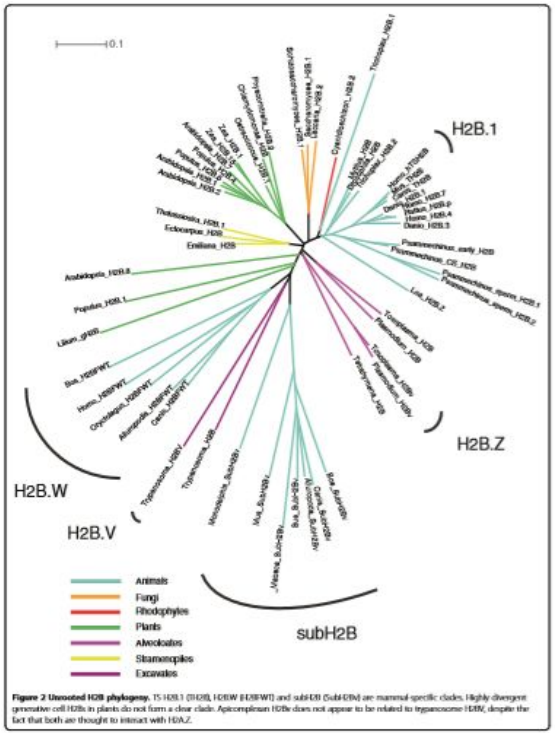
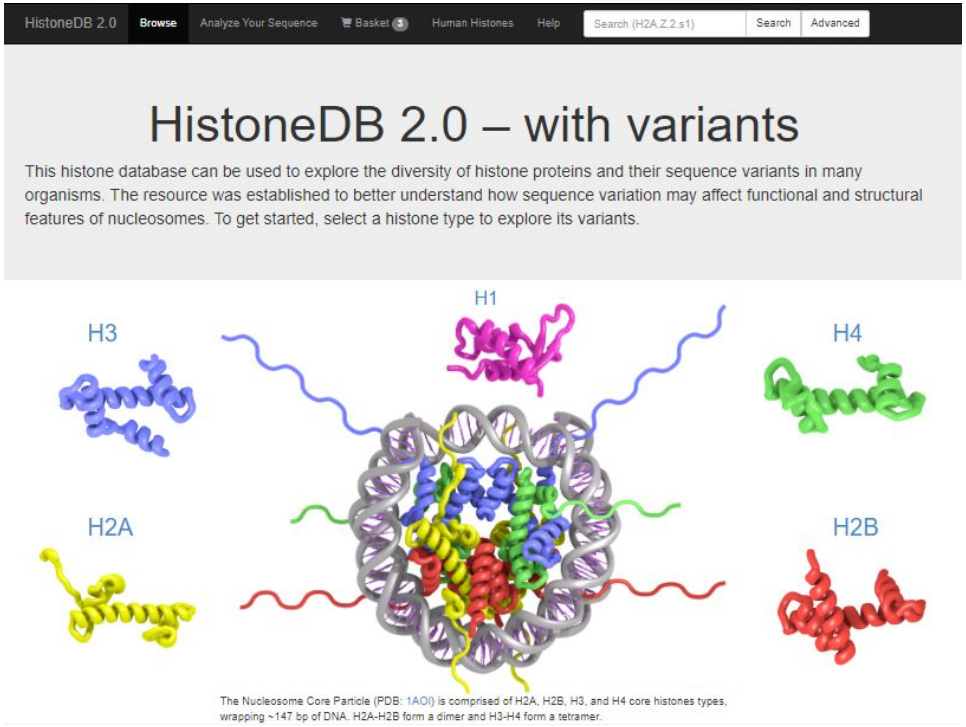
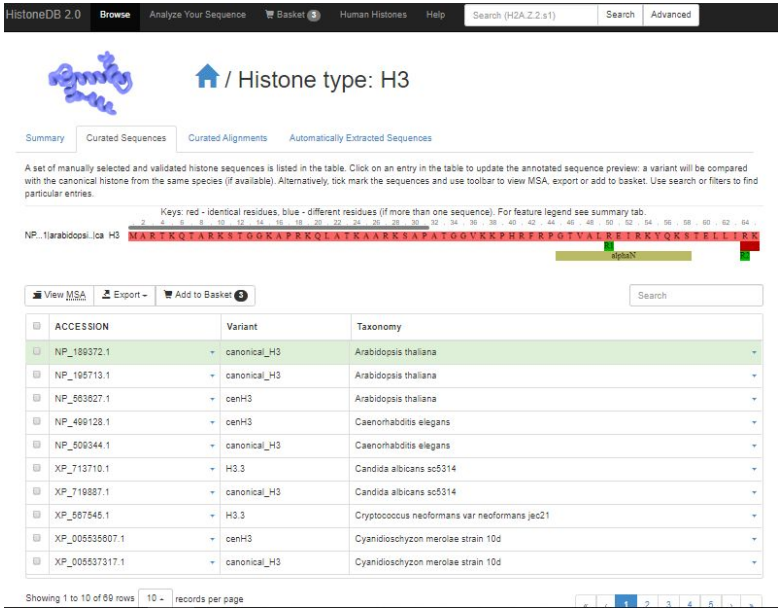


Figure 2 Unrooted H2B phylogeny. TS H2B.1 (H2B), H2BW (H2BFWT) and subH2B (SubH2Bv) are mammal-specific clades. Highly divergent germinative cell H2Bs in plants do not form a clear clade. Apicomplexan H2Bs does not appear to be related to trypanosome H2BV, despite the fact that both are thought to interact with H2A.Z.

Talbert PB, Ahmad K, et al. "A unified phylogeny-based nomenclature for histone variants." Epigenetics Chromatin, 2012. PMID: 22650316

Ресурсы анализа гистоновых вариантов





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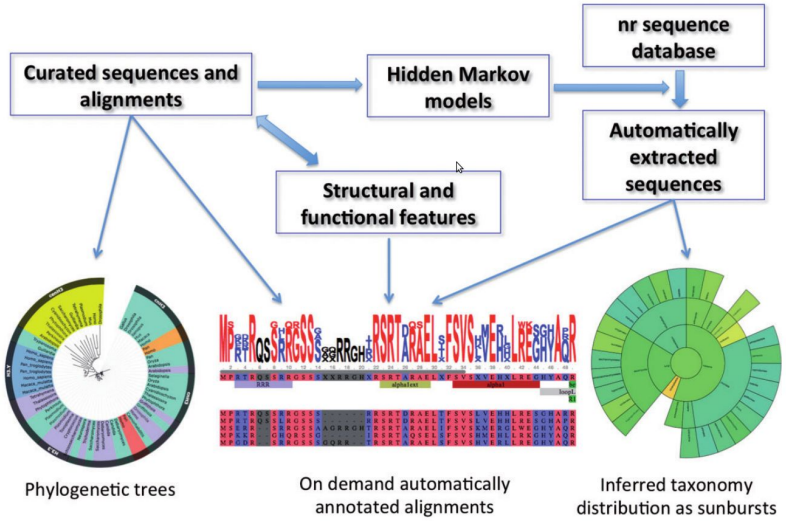
HistoneDB 2.0



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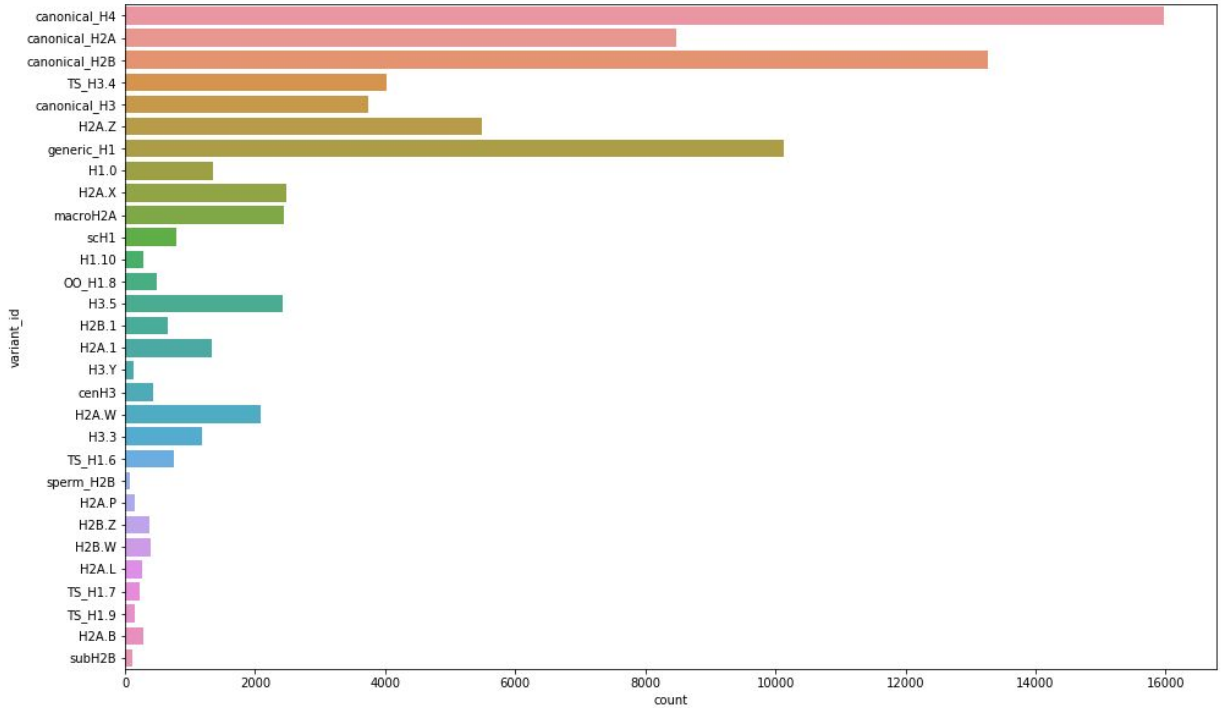
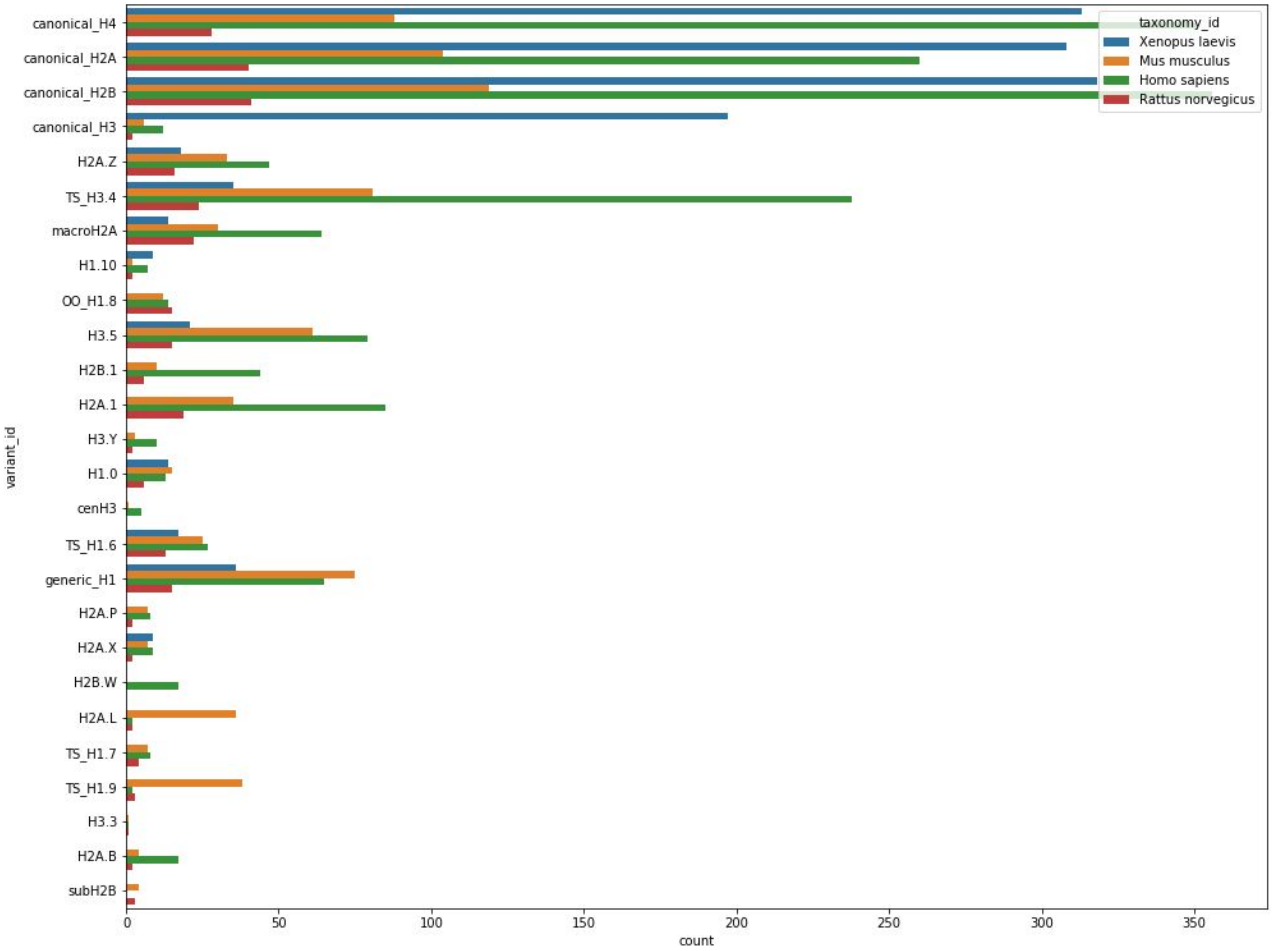
HistoneDB 2.0

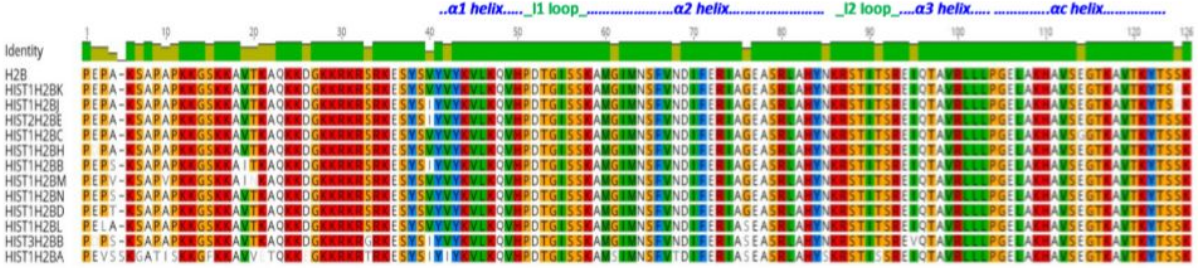


HistoneDB 2.0



Гистоновые изоформы

A



B

	H2B	HIST1H2BK	HIST1H2BJ	HIST2H2BE	HIST1H2BC	HIST1H2BH	HIST1H2BB	HIST1H2BM	HIST1H2BN	HIST1H2BD	HIST1H2BL	HIST3H2BB	HIST1H2BA
H2B		99.200%	98.400%	99.200%	99.200%	99.200%	97.600%	96.800%	99.200%	99.200%	98.400%	95.200%	84.127%
HIST1H2BK	99.200%		99.200%	98.400%	98.400%	98.400%	96.800%	96.000%	98.400%	98.400%	97.600%	94.400%	83.333%
HIST1H2BJ	98.400%	99.200%		99.200%	97.600%	97.600%	97.600%	95.200%	97.600%	97.600%	96.800%	95.200%	84.127%
HIST2H2BE	99.200%	98.400%	99.200%		98.400%	98.400%	98.400%	96.000%	98.400%	98.400%	97.600%	96.000%	84.921%
HIST1H2BC	99.200%	98.400%	97.600%	98.400%		98.400%	96.800%	96.000%	98.400%	98.400%	97.600%	94.400%	83.333%
HIST1H2BH	99.200%	98.400%	97.600%	98.400%	98.400%		96.800%	96.000%	98.400%	98.400%	97.600%	96.000%	83.333%
HIST1H2BB	97.600%	96.800%	97.600%	98.400%	96.800%	96.800%		96.800%	98.400%	97.600%	96.000%	96.000%	84.921%
HIST1H2BM	96.800%	96.000%	95.200%	96.000%	96.000%	96.000%	96.800%		96.800%	96.800%	95.200%	92.800%	83.333%
HIST1H2BN	99.200%	98.400%	97.600%	98.400%	98.400%	98.400%	98.400%	96.800%		99.200%	97.600%	96.000%	84.921%
HIST1H2BD	99.200%	98.400%	97.600%	98.400%	98.400%	98.400%	97.600%	96.800%	99.200%		97.600%	95.200%	84.127%
HIST1H2BL	98.400%	97.600%	96.800%	97.600%	97.600%	97.600%	96.000%	95.200%	97.600%	97.600%		95.200%	84.921%
HIST3H2BB	95.200%	94.400%	95.200%	96.000%	94.400%	96.000%	96.000%	92.800%	96.000%	95.200%	95.200%		84.921%
HIST1H2BA	84.127%	83.333%	84.127%	84.921%	83.333%	83.333%	84.921%	83.333%	84.921%	84.127%	84.921%	84.921%	

Figure 2. Comparison of H2B isoforms. **(A)** Sequence alignment of H2B isoforms. Residues that are different among the isoforms are shown. **(B)** Percentage similarity among the H2B isoforms based on their primary sequence. Images were created using the Geneious software.

Rajbir Singh, Emily Bassett, Arnab Chakravarti, Mark R Parthun, Replication-dependent histone isoforms: a new source of complexity in chromatin structure and function, Nucleic Acids Research, Volume 46, Issue 17, 28 September 2018, Pages 8665–8678, https://doi.org/10.1093/nar/gky768

Онкогистоны

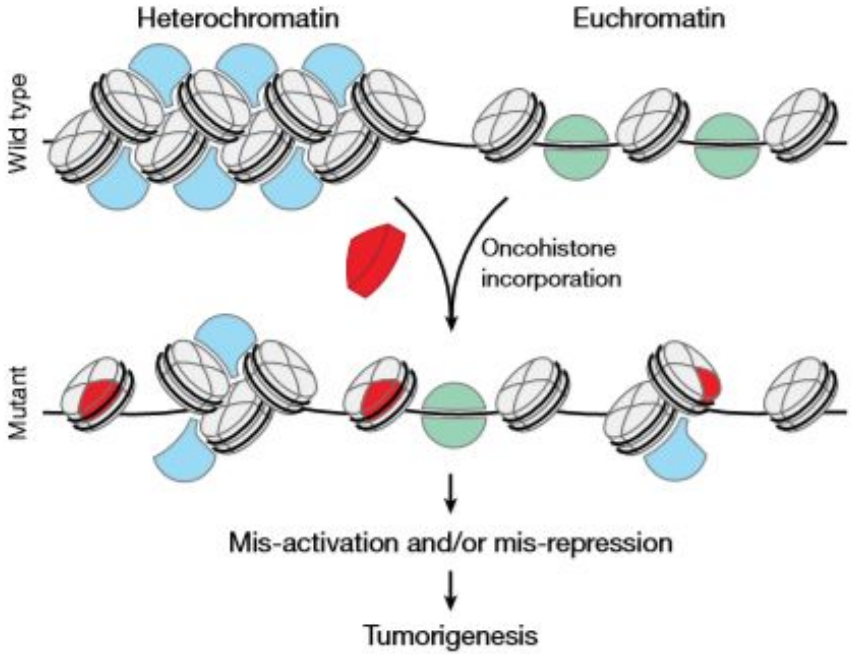


Fig. 4 | A model for the effect of oncohistones on the chromatin polymer. By incorporation into the chromatin polymer, mutated histone proteins (oncohistones, in red) may cause functional effects by altering the biophysical and/or functional properties of chromatin. We propose that these effects will occur when the mutant histone is present even at low concentrations and that mutating even one of many histone gene copies can have dominant effects.

Nacev, B.A., Feng, L., Bagert, J.D. et al. The expanding landscape of ‘oncohistone’ mutations in human cancers. Nature 567, 473–478 (2019). https://doi.org/10.1038/s41586-019-1038-1