

INDIVIDUAL LYSINE ACETYLATIONS ON THE N-TERMINUS OF *S. CEREVISIAE* H2A.Z ARE HIGHLY BUT NOT DIFFERENTIALLY REGULATED

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Running Title: Differential analysis of *S. cerevisiae* H2A.Z acetylation

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SUPPLEMENTARY TABLES / FIGURE LEGENDS

Suppl. Table 1	Antibodies used in this study
Suppl. Table 2	Strains used in this study
Suppl. Table 3	Mutants screened for differential regulation of Htz1 acetylation

Suppl. Fig. 1 *The generation of Htz1^{Ac}-specific antibodies*

(A) α Htz1-K8^{Ac} sera from rabbit 10818, or (B) α Htz1-K10^{Ac} sera from rabbit 10808, were tested against a comprehensive peptide panel (sample shown) in Luminex assays. PB, Pre-Bleed; RMF, Relative Mean Fluorescence.

Suppl. Fig. 2 *The acetylation of individual Htz1 N-terminal lysines is not interdependent*

Whole cell extracts from the indicated strains were immunoblotted as indicated. As an example *K8R* is the specific mutation of lysine 8 to arginine, while *K8Ac** is the mutation of all lysines other than K8 (i.e. *K3R*, *K10R*, *K14R*). WT, wild type; Δ is *htz1* Δ . Rpn8 is a loading control.

Suppl. Fig. 3 *The acetylation status of Htz1 does not regulate association of the variant with chromatin*

Htz1 acetylation is abolished in *4KR* or *4KQ* and increased in *hda1* Δ cells. (A - B) Indicated strains were spheroblasted (Total), fractionated into Cytoplasm, Nucleus and Chromatin, and immunoblotted as indicated. α HA monitors the localization of *htz1.HA₃*. Appropriate segregation of histone H2B and Rpn8 indicate efficient fractionation: the former is primarily localized in insoluble chromatin, the latter in soluble cytoplasm.

Suppl. Fig. 4 *Genetic interactions show that [htz1-N Δ \approx htz1-4KR] \neq htz1 Δ*

(A) Gene Ontology (GO) categories for the synthetic sick / synthetic lethal (SS/SL) interactors of *htz1* Δ , *N Δ* or *4KR*. This highlights the relative similarity between these mutants: i.e. the latter two are most closely related. Numbers in the center of each group indicate their respective SS/SL interactors identified. Note that *N Δ* and *4KR* were mated to the non-essential deletion and DAmP collections, while *htz1* Δ was only mated to the former (hence the reduced number of interactors identified). Each map was generated with the OSPREY network visualization system (1). (B) The top hits for over-represented GO functional categories within the SS/SL interactors of *htz1* Δ , *4KR*, or *N Δ* . Each list was generated with [GOstat](#), which considers and ranks the GO terms contained in the data (2). The precise SS/SL interrogation group differs from the Osprey list (e.g. *htz1* Δ : 269 or 272 interactors) as the gene space used by each program varies slightly.

Suppl. Fig. 5 *Efficient Htz1^{Ac} does not require individual Asf1-dependent acetylations on histones H3 or H4*

(A - B) WCEs from the indicated unacetylatable histone H3 or H4 point mutants (from the SHIMA collection (3)) were immunoblotted as indicated. H4-K12^{Ac} and Rpn8 are controls.

Suppl. Fig. 6 *Htz1^{Ac} is required for resistance to TBZ but not to Camptothecin*

(A) Growth curves on rich non-selective media (YPD) were analyzed on a Bioscreen (see Experimental Procedures). A*: Boxed area (from A) is re-plotted to facilitate comparison across strains. (B - C) *htz1Δ* shows a mild sensitivity to the topoisomerase inhibitor camptothecin (CPT) on plates (Fig. 5A) but not in liquid culture. Growth curves on YPD containing CPT (μM as indicated) were analyzed on a Bioscreen. C*: Boxed area (from C) is re-plotted to facilitate comparison across strains. (D - E) *htz1Δ*, and to a lesser degree *NA*, *4KR* or *4KQ*, are sensitive to the microtubule inhibitor TBZ. Growth curves on YPD containing TBZ (μg/ml as indicated) were analyzed on a Bioscreen. E*: Boxed area (from E) is re-plotted to facilitate comparison across strains.

Suppl. Fig. 7 *Htz1^{Ac} is regulated by benomyl via the Hda1 deacetylase complex*

(A) The reduction of Htz1^{Ac} on benomyl treatment is dependent on all members of the Hda1-complex. Strains were grown in YPD to OD₆₀₀ ~ 0.5 and benomyl (BEN; μg/ml) added. WCEs were harvested and immunoblotted as indicated. Rpn8 is a loading control. WT, Wild type. (B) Benomyl has no impact on the abundance of Hda1, Hda2 or Hda3. Strains containing C-terminally TAP-tagged forms were grown in YPD to OD₆₀₀ ~ 0.5 and benomyl (BEN; μg/ml) added for two hours. WCEs were immunoblotted and probed as indicated. PAP is Peroxidase anti-peroxidase to detect the immunoglobulin component of the TAP tag. Rpn8 is a loading control. (C) Hda1-complex subunits show no mobility shift (which could indicate post-translational modifications such as ubiquitylation or phosphorylation) after treatment of cells with benomyl (B; 40μg/ml) or MMS (M; 0.05%). Gels in the PAP panel were run for significantly longer than those in B to increase resolution. Rpn8 is a loading control. U, untreated.

Suppl. Fig. 8 *Htz1^{Ac} levels are unaffected by 6AU or MPA treatment*

URA⁺ wild type cells were grown in synthetic complete medium (lacking uracil) to OD₆₀₀ ~ 0.5 and 6-azauracil (6AU) or mycophenolic acid (MPA) added at concentration indicated before growth for another two hours. WCEs were harvested and immunoblotted as indicated. Rpn8 is a loading control. U, Untreated.

Supplementary Table 1: Antibodies used in this study

Anti-	Species	Info	Sera #	Source
Histone H2B	Rabbit	Polyclonal	39237	Active Motif
Histone H3-K9 ^{Ac}	Rabbit	Polyclonal	39137	Active Motif
Histone H3-K27 ^{Ac}	Rabbit	Polyclonal	39135	Active Motif
Histone H4-K12 ^{Ac}	Rabbit	Polyclonal	39165	Active Motif
Htz1-K8 ^{Ac}	Rabbit	Polyclonal	07-770	Millipore
Htz1-K10 ^{Ac}	Rabbit	Polyclonal	07-771	Millipore
Htz1-K14 ^{Ac}	Rabbit	Polyclonal	07-719	Millipore (4)
Peroxidase anti-Peroxidase (PAP)	Rabbit	Polyclonal	P1291	Sigma
HA epitope tag	Mouse	Monoclonal	12CA5	-
Rpn8 (YOR261C)	Rabbit	Polyclonal	sera4797	Dan Finley, HMS

Supplementary Table 2: Yeast strains used in this study

Name	Alt. name	Genotype	Used *	Ref.
KFY351	YSB1583	MAT α <i>ura3Δ0 leu2Δ0 his3Δ1 met15Δ0 trp1Δ::HIS3</i>	Throughout	Buratowski Lab
KFY471	BY4741	MAT α <i>ura3Δ0 leu2Δ0 his3Δ1 met15Δ0</i>	Throughout	Open Biosystems
KFY472	Y3656, YF1109	MAT α <i>ura3Δ0 leu2Δ0 his3Δ1 met15Δ0 lys2Δ0 can1Δ::MFA1ρ-HIS3-MFα1ρ-LEU2</i>	Throughout	(5)
KFY1069	YMS196	MAT α <i>ura3Δ0 leu2Δ0 his3Δ1 met15Δ0 lys2Δ0 LYS2+ can1Δ::STE2ρ-Sp.his5⁺ lyp1Δ::STE3ρ-LEU2 cyh2</i>	Throughout	(6)
KFY1129		KFY471 <i>hda1Δ::Kan.MX</i>	ST3	Open Biosystems
KLY391		KLY34 <i>hda1Δ::Kan.MX</i>	F1F, F6	This work
KFY1391		KFY471 <i>hda2Δ::Kan.MX</i>	ST3, SF7A	Open Biosystems
KFY1125		KFY471 <i>hda3Δ::Kan.MX</i>	ST3, SF7A	Open Biosystems
KFY1513		KFY471 <i>HDA1.TAP::HIS3.MX</i>	SF7B-C	(7)
KFY1514		KFY471 <i>HDA2.TAP::HIS3.MX</i>	SF7B-C	(7)
KFY1515		KFY471 <i>HDA3.TAP::HIS3.MX</i>	SF7B-C	(7)
KFY662	AT17	KFY472 <i>set3Δ::Kan.MX</i>	ST3	Greenblatt lab
KFY689	AT53	KFY472 <i>hst1Δ::Kan.MX</i>	ST3	Greenblatt lab
KFY695	AT61	KFY472 <i>hos2Δ::Kan.MX</i>	ST3	Greenblatt lab
KFY701	AT69	KFY472 <i>sap30Δ::Nat.MX</i>	ST3	Greenblatt lab
KFY699	AT66	KFY472 <i>rxt2Δ::Nat.MX</i>	ST3	Greenblatt lab
KFY705	AT74	KFY472 <i>pho23Δ::Nat.MX</i>	ST3	Greenblatt lab
KFY704	AT73	KFY472 <i>ume1Δ::Nat.MX</i>	ST3	Greenblatt lab
KFY431		KFY471 <i>rpd3Δ::Kan.MX</i>	ST3	Open Biosystems
KFY871	AT357	KFY472 <i>rpd3Δ::Nat.MX</i>	ST3	Greenblatt lab
KFY1368		KFY471 <i>sin3Δ::Kan.MX</i>	ST3	Open Biosystems
KFY879	AT352	KFY472 <i>sin3Δ::Nat.MX</i>	ST3	Greenblatt lab
KFY598		KFY471 <i>eaf3Δ::Kan.MX</i>	ST3	Open Biosystems
KFY800	AT243	KFY472 <i>eaf3Δ::Nat.MX</i>	ST3	Greenblatt lab
KFY432		KFY471 <i>rco1Δ::Kan.MX</i>	ST3	Open Biosystems
KFY841	AT321	KFY472 <i>rco1Δ::Nat.MX</i>	ST3	Greenblatt lab
KFY1072		KFY471 <i>sir2Δ::Kan.MX</i>	ST3	Open Biosystems
KFY908	AT409	KFY472 <i>hos3Δ::Nat.MX</i>	ST3	Greenblatt lab
KFY867	AT352	KFY472 <i>hos1Δ::Nat.MX</i>	ST3	Greenblatt lab
KFY681	AT43	KFY472 <i>eaf1Δ (vid21Δ)::Nat.MX</i>	ST3, F1E	Greenblatt lab
KFY392		KFY471 <i>eaf1Δ (vid21Δ)::Kan.MX</i>	ST3	Open Biosystems
KFY476	YF1115	KFY472 <i>yng2Δ::Nat.MX</i>	ST3, F1E	Greenblatt lab
KFY799	AT242	KFY472 <i>yaf9Δ::Nat.MX</i>	ST3, F1E	Greenblatt lab

Name	Alt. name	Genotype	Used *	Ref.
KFY391	YSB1758	MATa <i>ura3Δ0 leu2Δ0 his3Δ1 met15Δ0 trp1Δ::URA3 yaf9Δ::Kan.MX</i>	ST3	Buratowski lab
KFY712	AT87	KFY472 <i>swc2Δ (vps72Δ)::Nat.MX</i>	ST3	Greenblatt lab
KFY356	YSB1599	MATa <i>ura3Δ0 leu2Δ0 his3Δ1 met15Δ0 trp1Δ::HIS3 swc2Δ::Kan.MX</i>	ST3	Buratowski lab
KFY357	YSB1610	KFY351 <i>swc6Δ (vps71Δ)::Kan.MX HTZ1.HA₃.KI-TRP</i>	ST3	Buratowski lab
KFY1140		KFY471 <i>swr1Δ::Kan.MX</i>	ST3, F1D	Open Biosystems
KFY589	YF526	KFY471 <i>htz1Δ::Kan.MX</i>		(8)
KFY628	NJK1172	KFY472 <i>htz1Δ::Nat.MX</i>	F1E	(9)
KLY36		MATα <i>ura3Δ0 leu2Δ0 his3Δ1 met15Δ0 htz1Δ::Nat.MX</i>	F1D, SF2	This work
KLY400		KLY34 <i>Nat.NT2-GAL1_p-HTZ1.HA₃.KI-TRP</i>	F3B-C	This work
KLY726		KLY400 <i>hda1Δ::Kan.MX</i>	F3C	This work
KLY727		KLY34 <i>Nat.NT2-GAL1_p-htz1-4KR.HA₃.KI-TRP</i>	F3C	This work
KFY582	LPY3498	MATa <i>ura3-52 leu2-3,112 trp1Δ1 his3Δ200</i>	F1D	(10)
KFY583	LPY4345	KFY582 <i>esa1-L327S +/- [pLP795: ESA1, URA3, CEN/ARS]</i>	F1D ^{NS}	(10)
KFY584	LPY4346	KFY582 <i>esa1-L254P +/- [pLP795: ESA1, URA3, CEN/ARS]</i>	F1D	(10)
KFY585	LPY4346	KFY582 <i>esa1Δ414 +/- [pLP795: ESA1, URA3, CEN/ARS]</i>	F1D ^{NS}	(10)
KFY1136		KFY471 <i>gcn5Δ::Kan.MX</i>	F1D	Open Biosystems
KFY935	AT461	KFY472 <i>sgf73Δ::Nat.MX</i>	ST3	Greenblatt lab
KFY602		KFY471 <i>sas3Δ::Kan.MX</i>	ST3	Open Biosystems
KFY910	AT411	KFY472 <i>sas3Δ::Nat.MX</i>	ST3	Greenblatt lab
KFY635		KFY471 <i>sas2Δ::Kan.MX</i>	ST3	Open Biosystems
KFY913	AT415	KFY472 <i>sas2Δ::Nat.MX</i>	ST3	Greenblatt lab
KFY634		KFY471 <i>hat1Δ::Kan.MX</i>	ST3	Open Biosystems
KFY929	AT441	KFY472 <i>hat2Δ::Nat.MX</i>	ST3	Greenblatt lab
KFY1392		KFY471 <i>hpa2Δ::Kan.MX</i>	ST3	Open Biosystems
KFY1135		KFY471 <i>rtt109Δ::Kan.MX</i>	ST3	Open Biosystems
KFY900	AT398	KFY472 <i>rtt109Δ::Nat.MX</i>	ST3	Greenblatt lab
KFY1138		KFY471 <i>vps75Δ::Kan.MX</i>	ST3	Open Biosystems
KFY1010	AT678	KFY472 <i>vps75Δ::Nat.MX</i>	ST3	Greenblatt lab
KFY1137		KFY471 <i>asf1Δ::Kan.MX</i>	ST3	Open Biosystems
KFY742	AT131	KFY472 <i>asf1Δ::Nat.MX</i>	ST3	Greenblatt lab
KLY396		KLY34 <i>asf1Δ::Kan.MX</i>	F4A-B	This work
KFY1438	SRH001	MATa <i>ura3-1 leu2-3,112 trp1-1 his3-11 lys2Δ can1-100 TELVIII::URA3 bar1Δ::LEU2 Kan.MX6-GAL1_p-3HA-ASF1</i>	F4D-E	(11)
KFY1439	SRH014	MATa <i>ura3-1 leu2-3,112 trp1-1 his3-11 lys2Δ can1-100 gal1::hisG bar1Δ::LEU2 Kan.MX6-GAL1_p-ASF1-3HA-PEST-HIS3</i>	F4D-E	(11)
KFY498	FY2162,	MATa <i>ura3-52 leu2Δ1 trp1Δ63 his3Δ200 lys2-126δ Ty912Δ35-LacZ::his4</i>	SF5A-B	(12)

Name	Alt. name	Genotype	Used *	Ref.
	YBL574	<i>[hht1-hhf1]Δ::LEU2 [hht2-hhf2]Δ::HIS3 [pDM9: HHT1-HHF1, URA3, CEN/ARS]</i>		
KFY1379		KFY498 [pDM9 shuffled] + [hht2-K9A, HHF1, TRP1, CEN/ARS]	SF5A	(3)
KFY1380		KFY498 [pDM9 shuffled] + [hht2-K27A, HHF1, TRP1, CEN/ARS]	SF5A	(3)
KFY1382		KFY498 [pDM9 shuffled] + [hht2-K56A, HHF1, TRP1, CEN/ARS]	SF5A	(3)
KFY1384		KFY498 [pDM9 shuffled] + [HHT2, hhf1-K5A, TRP1, CEN/ARS]	SF5B	(3)
KFY1385		KFY498 [pDM9 shuffled] + [HHT2, hhf1-K8A, TRP1, CEN/ARS]	SF5B	(3)
KFY1386		KFY498 [pDM9 shuffled] + [HHT2, hhf1-K12A, TRP1, CEN/ARS]	SF5B	(3)
KFY590		KFY471 <i>elp1Δ::Kan.MX</i>	ST3	Open Biosystems
KFY837	AT315	KFY472 <i>elp2Δ::Nat.MX</i>	ST3	Greenblatt lab
KFY591		KFY471 <i>elp3Δ::Kan.MX</i>	ST3	Open Biosystems
KFY720	AT101	KFY472 <i>elp3Δ::Nat.MX</i>	ST3	Greenblatt lab
KFY734	AT121	KFY472 <i>elp4Δ::Nat.MX</i>	ST3	Greenblatt lab
KFY732	AT118	KFY472 <i>elp6Δ::Nat.MX</i>	ST3	Greenblatt lab
KFY1314		KFY471 <i>hir1Δ::Kan.MX</i>	ST3	Open Biosystems
KFY1315		KFY471 <i>hir2Δ::Kan.MX</i>	ST3	Open Biosystems
KFY1510		KFY471 <i>hir3Δ::Kan.MX</i>	ST3	Open Biosystems
KFY1471		KFY471 <i>rtt106Δ::Kan.MX</i>	ST3	Open Biosystems
KLY66		KFY471 <i>spe1Δ::Kan.MX</i>	ST3	This work
KLY67		KFY471 <i>spe2Δ::Kan.MX</i>	ST3	This work
KLY81		KFY471 <i>spe3Δ::Kan.MX</i>	ST3	This work
KLY68		KFY471 <i>spe4Δ::Kan.MX</i>	ST3	This work
KLY34		KFY351 <i>HTZ1.HA₃.KI-TRP</i>	Throughout	This work
KFY358		KLY34 <i>swr1Δ::Kan.MX</i>	ST3, F1C	(4)
KLY270		KLY34 <i>pho85Δ::Nat.MX</i>	ST3	This work
KLY269		KLY34 <i>ado1Δ::Nat.MX</i>	ST3	This work
KLY289		KLY34 <i>bem1Δ::Kan.MX</i>	ST3	This work
KLY268		KLY34 <i>rts1Δ::Nat.MX</i>	ST3	This work
KLY299		KLY34 <i>pho13Δ::Kan.MX</i>	ST3	This work
KLY20		KFY1069 <i>htz1Δ::Nat.MX</i>	F2, F5, SF4, SF6, SF8	This work
KLY185		KFY1069 <i>htz1-K3R</i>	SF2	This work
KLY186		KFY1069 <i>htz1-K8R</i>	SF2	This work
KLY187		KFY1069 <i>htz1-K10R</i>	SF2	This work
KLY192		KFY1069 <i>htz1-K14R</i>	SF2, SF6	This work
KLY188		KFY1069 <i>htz1-K14Q</i>	SF2, SF6	This work
KLY711		KFY1069 <i>htz1-K8R,K10R,K14R</i>	SF2	This work
KLY193		KFY1069 <i>htz1-K3R,K10R,K14R</i>	SF2	This work
KLY712		KFY1069 <i>htz1-K3R,K8R,K14R</i>	SF2	This work
KLY713		KFY1069 <i>htz1-K3R,K8R,K10R</i>	SF2	This work

Name	Alt. name	Genotype	Used *	Ref.
KLY229		KFY1069 <i>htz1-4KR</i>	Throughout	This work
KLY230		KFY1069 <i>htz1-4KQ</i>	Throughout	This work
KLY28		KFY1069 <i>HTZ1::Nat.NT2</i> (Tracking)	F2	This work
KLY35		KFY1069 <i>htz1-NΔ::LoxP::Nat.NT2</i>	F2	This work
KLY262		KFY1069 <i>htz1-4KR::Nat.NT2</i>	F2	This work
KLY263		KFY1069 <i>htz1-4KQ::Nat.NT2</i>	F2	This work
KLY231		KFY1069 <i>htz1-K3R::Nat.NT2</i>	F2	This work
KLY232		KFY1069 <i>htz1-K8R::Nat.NT2</i>	F2	This work
KLY199		KFY1069 <i>htz1-K10R::Nat.NT2</i>	F2	This work
KLY233		KFY1069 <i>htz1-K14R::Nat.NT2</i>	F2	This work
KLY506		KFY1069 <i>htz1-K3Q::Nat.NT2</i>	F2	This work
KLY507		KFY1069 <i>htz1-K8Q::Nat.NT2</i>	F2	This work
KLY530		KFY1069 <i>htz1-K10Q::Nat.NT2</i>	F2	This work
KLY200		KFY1069 <i>htz1-K14Q::Nat.NT2</i>	F2	This work
KLY717		KFY1069 <i>htz1-K8R, K10R, K14R::Nat.NT2</i>	F2	This work
KLY714		KFY1069 <i>htz1-K3R, K10R, K14R::Nat.NT2</i>	F2	This work
KLY715		KFY1069 <i>htz1-K3R, K8R, K14R::Nat.NT2</i>	F2	This work
KLY716		KFY1069 <i>htz1-K3R, K8R, K10R::Nat.NT2</i>	F2	This work

* F1D, Figure 1D (etc); ^{NS}, not shown; ST3, Supplementary Table 3.

Supplementary Table 3: Strains used for proteomic screening to identify novel Htz1^{Ac} regulators

Complex: Activity ^a	Genes annotated	# Checked	Specific mutants ^b	Effect on Htz1 ^{Ac}
NuA4: Acetyltransferase	13	Unique: 3 Shared: 2	<i>eaf1, yng2, esa1^c yaf9, eaf3^d</i>	Strongly reduced ^e (3/3) (e.g. Fig. 1D-E) Reduced ^e (1/2); No change (1/2)
SWR-C: Snf2-family ATPase	14	Unique: 3	<i>swc2, swc6, swr1</i>	Strongly reduced (1/3); Reduced (2/3)
Rpd3L: Deacetylase	14	Unique: 3 Shared: 3	<i>pho23, rxt2, sap30 rpd3, sin3, ume1</i>	Reduced (3/3) Reduced (3/3)
Rpd3S: Deacetylase	5	Unique: 2	<i>rco1, eaf3^d</i>	No change (2/2)
SAGA: Acetyltransferase	20	Shared: 1	<i>gcn5, sgf73</i>	No change (2/2) (e.g. Fig. 1D)
ADA: Acetyltransferase	3	Shared: 1	<i>gcn5</i>	No change (1/1)
SLIK: Acetyltransferase	18	Shared: 2	<i>gcn5, sgf73</i>	No change (2/2)
HDA1: Deacetylase	3	3	<i>hda1-3</i>	Increased (1/3); No change (2/3) (e.g. Fig. 1F)
Elongator: Acetyltransferase	6	5	<i>elp1-4, elp6</i>	Reduced (5/5)
SET3-C: Deacetylase	7	3	<i>set3, hst1, hos2</i>	Reduced (1/3); No change (2/3)
HIR: Histone chaperone	4	3	<i>hir1-3</i>	Reduced (1/3); No change (2/3)
NuA3: Acetyltransferase	5	1	<i>sas3</i>	No change (1/1)
SAS: Acetyltransferase	3	1	<i>sas2</i>	No change (1/1)
HAT: Acetyltransferase	2	2	<i>hat1-2</i>	No change (2/2)
Miscellaneous (includes acetyltransferases, deacetylases & histone chaperones)		20	<i>ado1, asf1, bem1, H3^f, H4^f, hos1, hos3, hpa2, pho13, pho85, rts1, rtt106, rtt109, vps75, sir2, spe1-4, ydl025c</i>	Reduced (8/20); No change (12/20) Asf1 (see Fig. 4)

^a Not intended as an exhaustive description of the enzymatic activities in many of these complexes

^b Deletion unless stated otherwise

^c Temperature sensitive allele

^d Eaf3 is a member of the NuA4 acetyltransferase and Rpd3S deacetylase complexes (13)

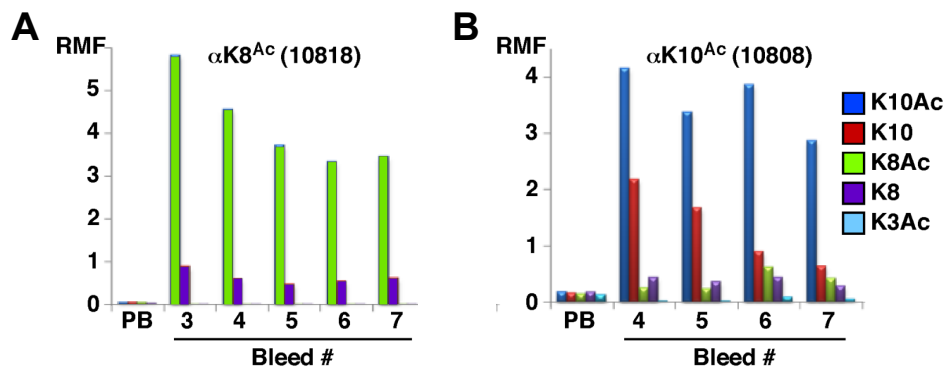
^e Strongly reduced is defined as below the level of detection in Western analysis

^f Histone H3 / H4 point mutants were from the SHIMA collection (see Supplementary Figure 5)

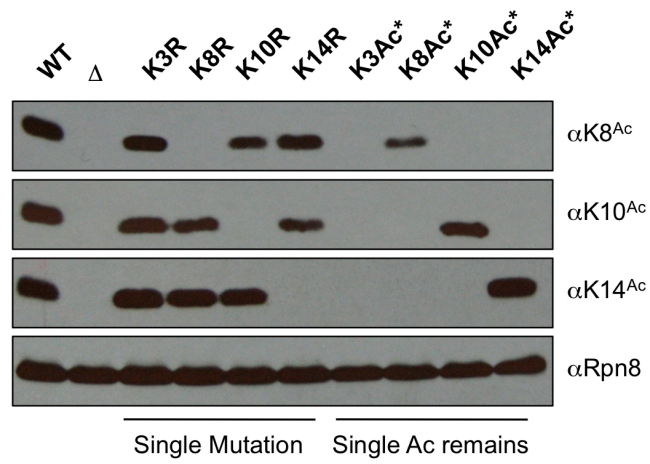
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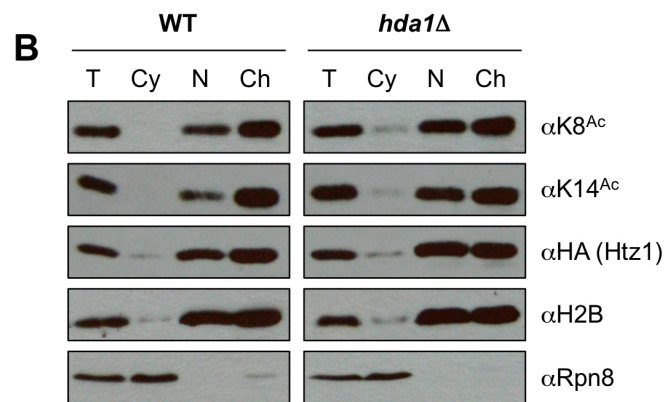
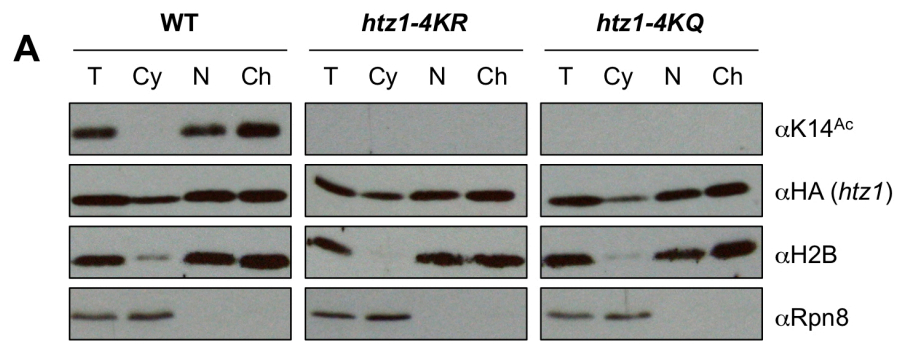
Suppl Fig 1: Mehta *et al*



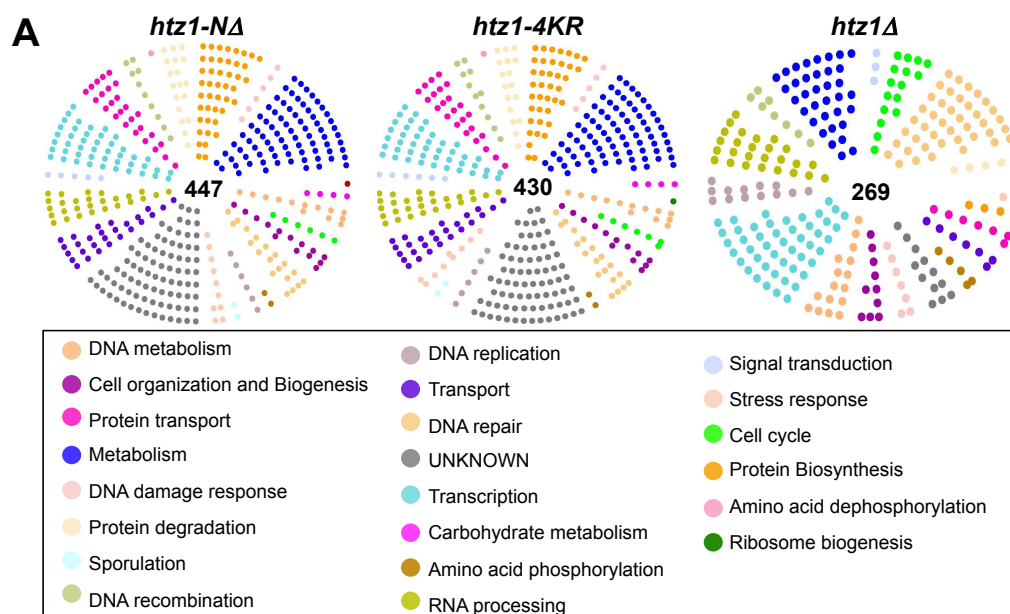
Suppl Fig 2: Mehta *et al*



Suppl Fig 3: Mehta *et al*



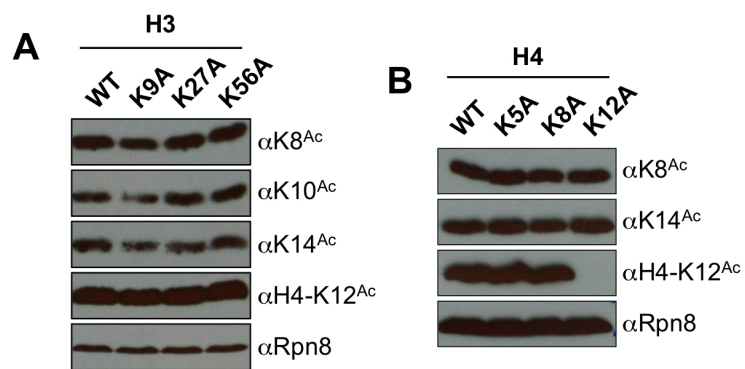
Suppl Fig 4: Mehta *et al*



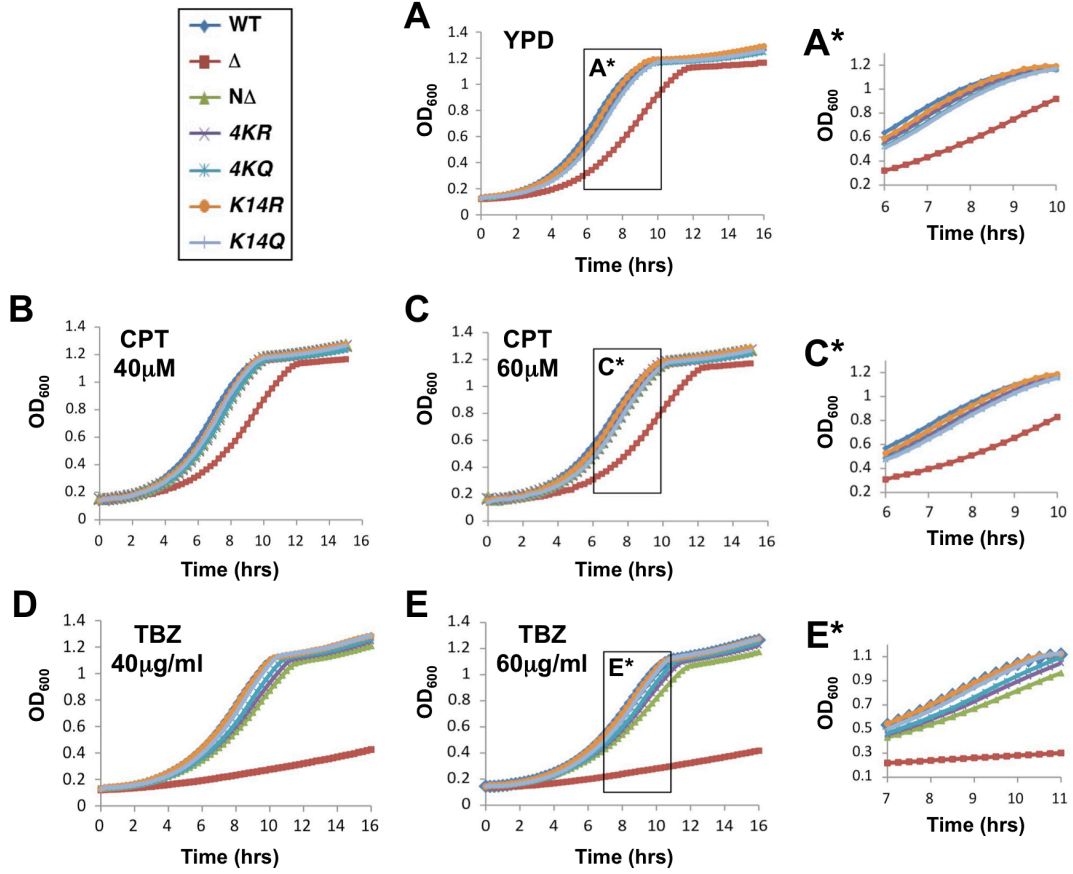
B

<i>htz1</i>	SS/SL	GO term	Category	P-value
Δ	272	GO:0006325	Establishment &/or maintenance of chromatin architecture	0
		GO:0016568	chromatin modification	0
		GO:0051276	chromosome organization & biogenesis	0
		GO:0006323	DNA packaging	0
		GO:0005667	transcription factor complex	1.11E-77
		GO:0006351	transcription, DNA-dependent	2.21E-62
		GO:0016570	histone modification	8.84E-54
		GO:0006974	response to DNA damage stimulus	2.00E-47
		GO:0032200	telomere organization & biogenesis	1.90E-45
		GO:0006366	transcription from RNA polymerase II promoter	3.83E-43
		GO:0006338	chromatin remodeling	5.79E-35
GO:0045449	regulation of transcription	6.12E-35		
4KR	386	GO:0032200	telomere organization and biogenesis	2.39E-45
		GO:0051276	chromosome organization and biogenesis	1.43E-43
		GO:0016570	histone modification	1.43E-22
		GO:0006351	transcription, DNA dependent	3.86E-20
		GO:0016568	chromatin modification	8.85E-20
		GO:0006323	DNA packaging	1.10E-17
		GO:0006366	transcription from RNA polymerase II promoter	7.26E-17
		GO:0007035	vacuolar acidification	5.46E-09
		GO:0045449	regulation of transcription	1.10E-08
		GO:0005667	transcription factor complex	1.71E-08
		GO:0006338	chromatin remodelling	7.89E-08
GO:0006885	regulation of cellular pH	8.61E-08		
NA	398	GO:0032200	telomere organization and biogenesis	1.85E-46
		GO:0051276	chromosome organization and biogenesis	1.67E-44
		GO:0016570	histone modification	1.08E-21
		GO:0016568	chromatin modification	6.67E-20
		GO:0006351	transcription, DNA dep	1.12E-19
		GO:0006323	DNA packaging	9.94E-18
		GO:0006366	transcription from RNA polymerase II promoter	8.22E-16
		GO:0007034	vacuolar transport	5.24E-09
		GO:0005667	transcription factor complex	6.03E-09
		GO:0007035	vacuolar acidification	7.50E-09
		GO:0007033	vacuole organization and biogenesis	7.55E-09
GO:0045449	regulation of transcription	1.31E-08		

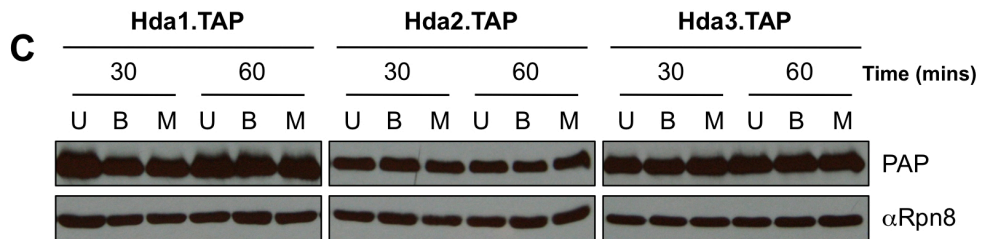
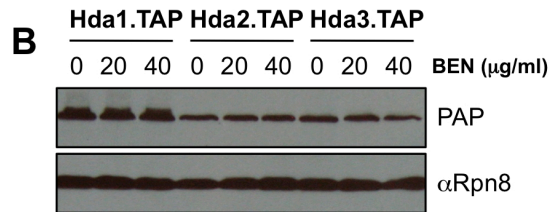
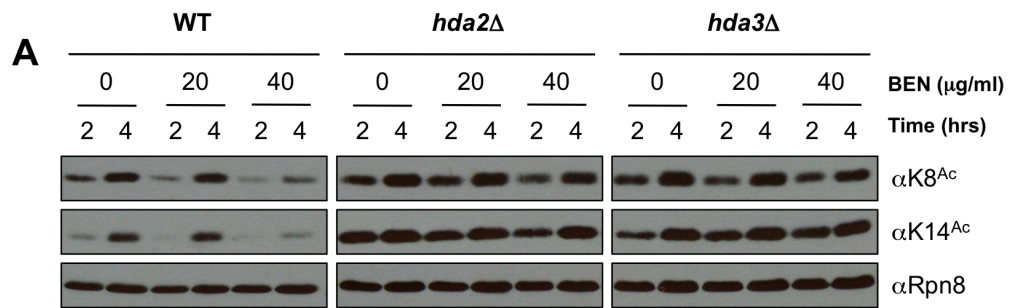
Suppl Fig 5: Mehta *et al*



Suppl Fig 6: Mehta *et al*



Suppl Fig 7: Mehta *et al*



Suppl Fig 8: Mehta *et al*

