



B

Chromatin Enrichment/Depletion
Open Reading Frame

Histone Modification	Rank Percentile	Trend*	P-value*	Ranked Gene List
H3K4 Di-Methylation	54.4 %	none	0.0598	■
H3K36 Di-Methylation	36.3 %	Depleted	$< 10^{-8}$	■
H2AK7 Acetylation	63.0 %	none	0.0010	■
H2AZK14 Acetylation	63.0 %	Enriched	$< 10^{-6}$	■
H2BK11 Acetylation	57.7 %	none	0.0536	■
H2BK16 Acetylation	58.4 %	none	0.0346	■
H3Nterm Acetylation	65.0 %	Enriched	$< 10^{-9}$	■
H3K9 Acetylation	64.0 %	Enriched	$< 10^{-3}$	■
H3K14 Acetylation	69.0 %	Enriched	$< 10^{-5}$	■
H3K18 Acetylation	70.8 %	Enriched	$< 10^{-6}$	■
H3K23 Acetylation	66.6 %	Enriched	$< 10^{-4}$	■
H3K27 Acetylation	67.0 %	Enriched	$< 10^{-4}$	■
H3K56 Acetylation	59.4 %	Enriched	$< 10^{-3}$	■
H4Nterm Acetylation	66.9 %	Enriched	$< 10^{-12}$	■
H4K8 Acetylation	61.0 %	none	0.0058	■
H4K12 Acetylation	64.4 %	Enriched	$< 10^{-3}$	■
H4K16 Acetylation	45.8 %	none	0.2908	■
H2A Occupancy	-- %	--	--	■
H2B Occupancy	-- %	--	--	■
H3 Occupancy	37.5 %	Depleted	$< 10^{-7}$	■
H4 Occupancy	42.3 %	none	$< 10^{-3}$	■
H2AZ Occupancy	59.0 %	Enriched	$< 10^{-3}$	■

*At least 5 genes (with data) are needed to calculate p-values for enrichment or depletion

Supplemental Figure S11: (A,B) Chromatin modifications associated with the open reading frame (ORF) of genes with slower repair on the non-transcribed strand in the *snf5Δ* and/or *snf6Δ* mutants relative to WT. Enrichment of histone modifications is derived from published chromatin IP-microarray data (ChIP-chip) and analyzed using the ChromatinDB database (O'Connor and Wyrick 2007).