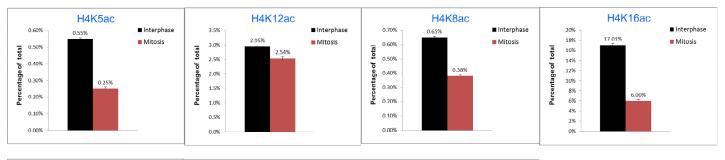
	H4(4to17)ac0me0	H4(4to17)K5ac1me0 leftpeak	H4(4to17)K12ac1_left peak	H4(4to17)K16ac1me0	H4(4to17)K5ac1K8ac1me0_left peak	H4(4to17)K5ac1K16ac1me0_right peak	 H4(4to17)K12ac1K16ac1me0	H4(4to17)K8ac1K12ac1K16ac1me0_right peak	H4(4to17)K5ac1K8ac1K12ac1me0_left peak	H4(4to17)K5ac1K8ac1K16ac1me0_right peak	m l	H4(68-78)AltNorm	H4(20to23)K20me0	H4(20to23)K20me1	H4(20to23)K20me2	H4(20to23)K20me3	H4(20to23)K20me2	H4(20to23)K20me3							
unSynch_exp3																									
unSynch_exp2																									
unSynch_exp1																				Lo	g ₂ f	old-ch	nange		
Synch_exp3																			-5.00	-2.5	50	0.00	2.50	5	.00
Synch_exp2 Synch_exp1		-														_									

В



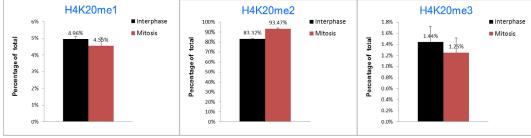


Figure S2. Identification of global changes in histone H4 modifications by quantitative targeted mass spectrometry analysis. (A) Heat map (log2 of fold change) of the different histone modifications as detailed on top. Data was normalized to average signal of interphase samples. (B) Relative abundance of selected modifications on H4 tails from interphase or mitotic HeLa-S3 cells. The data was obtained by quantitative targeted mass spectrometry analysis. Each bar represents the percentage of the H4 peptides with the indicated modifications within the total H4 tail peptide population.

Α