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Project Title	Molecular mechanisms underlying eukaryotic chromosome segregation	
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Report

DNA lesions impact on local transcription and the damage-induced transcriptional repression facilitates efficient DNA repair. However, how chromatin dynamics cooperates with these two events remained largely unknown. We show that histone H2A acetylation at K118 is enriched in transcriptionally active regions. Under DNA damage, the RSF1 chromatin remodeling factor recruits HDAC1 to DSB sites. The RSF1-HDAC1 complex induces the deacetylation of H2A(X)-K118 and its deacetylation is indispensable for the ubiquitination of histone H2A at K119. Accordingly, the acetylation mimetic H2A-K118Q suppressed the H2A-K119ub level, perturbing the transcriptional repression at DNA lesions. Intriguingly, deacetylation of H2AX at K118 also licenses the propagation of γH2AX and recruitment of MDC1. Consequently, the H2AX-K118Q limits DNA repair. Together, the RSF1-HDAC1 complex controls the traffic of the DNA damage response and transcription simultaneously in transcriptionally active chromatins. The interplay between chromatin remodelers and histone modifiers highlights the importance of chromatin versatility in the maintenance of genome integrity.