



Figure 8. Model for maintenance of histone modifications by the concerted action of multiple chromatin regulators via RI replacement with H3.3. We address the question of how a histone modification can be inherited when a nucleosome is lost and replaced. (A) The Suv39h H3K9 methyltransferase (an ortholog of fly Su(var)3-9) is recruited by HP-1 protein, which binds specifically to methylated H3K9. To perpetuate this mark when the nucleosome turns over, we speculate that the ATRX ATPase is recruited to the site via its ATRX-DNMT3-DNMT3L (ADD) domain, which binds with high specificity to methylated H3K9 on tails that entirely lack H3K4 methylation (because there are no H3K4 methyltransferases in this region of the genome). (B) ATRX provides the energy of ATP and works together with the H3.3-specific DAXX histone chaperone complex to incorporate the new nucleosome (Goldberg et al. 2010), or half-nucleosome in the case of partial eviction (Xu et al. 2010). The high local concentration of Suv39h results in a new nucleosome with the same H3K9 methylation as the nucleosome that was lost.