



**Figure 9.** Coordinated methyllysine erasure between a Jumonji and a PHD. (A) Schematic representations of PHF8 and KIAA1718 domain structure. (B) A bent conformation of PHF8 bound to a histone H3 peptide (in red) containing K4me3 and K9me2 (circled in red; PDB 3KV4). (C) An extended conformation of KIAA1718 (PDB 3KV6). The position of the histone H3 peptide is taken from a cocrystal structure of *Caenorhabditis elegans* KIAA1718 (PDB 3N9P).