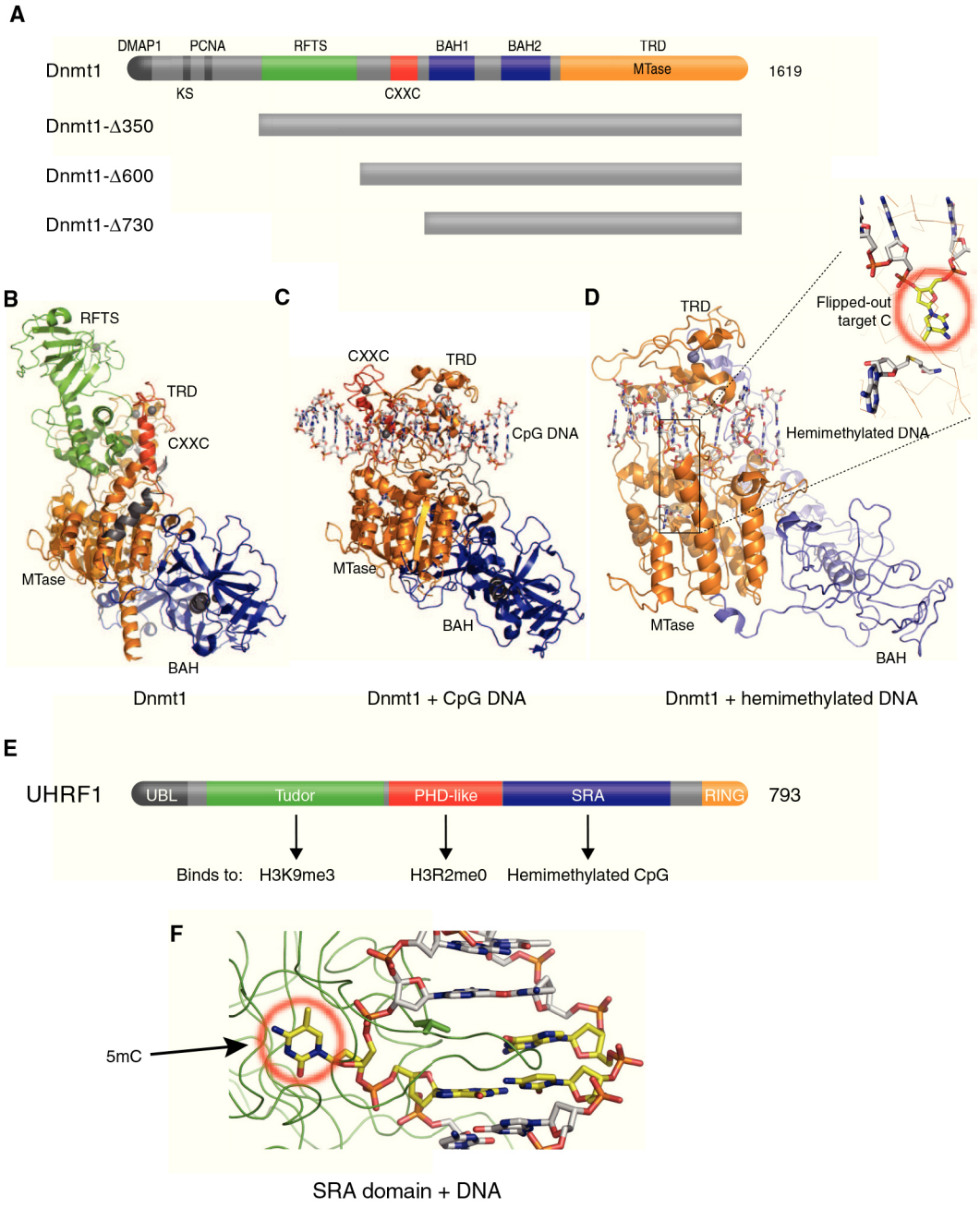

Figure 6. Structures of maintenance Dnmt1 and UHRF1. (*A*) Schematic representation of mouse Dnmt1 domain organization and available Dnmt1 amino-terminal deletion mutants. An amino-terminal region interacts with Dnmt1-associated protein(s) (DMAP1; Rountree et al. 2000). Then an adjacent lysine and serine are subject to a methylation and phosphorylation switch that determines Dnmt1 stability (Esteve et al. 2011), a PCNA (proliferating cell nuclear antigen) interacting sequence (Chuang et al. 1997), and an RFTS (Leonhardt et al. 1992) that interacts with the SET- and RING-associated (SRA) domain of UHRF1 (Achour et al. 2008). This is followed by a CpG-interacting CXXC domain (Song et al. 2011), a tandem BAH (bromo-adjacent homology) domain (Callebaut et al. 1999), and the catalytic DNA methyltransferase domain that includes the target-recognizing domain (Lauster et al. 1989) at the carboxyl terminus. (*B*) Structure of Dnmt1 in the absence of DNA (PDB 3AV4). (*C*) Structure of Dnmt1 in the presence of unmethylated CpG (PDB 3PT6). (*D*) Structure of Dnmt1 with hemimethylated CpG DNA oligonucleotides (PDB 4DA4). (*E*) UHRF1 harbors at least five recognizable functional domains: an ubiquitin-like domain at the amino terminus, followed by a tandem tudor domain recognizing H3K9me3 (Rothbart et al. 2012), a plant homeodomain (PHD) recognizing H3R2me0 (Rajakumara et al. 2011), an SRA domain recognizing hemimethylated CpG, and really interesting new gene (RING) domain at the carboxyl terminus that may endow UHRF1 with E3 ubiquitin ligase activity to histones (Citterio et al. 2004). (*F*) Structure of SRA-DNA complex illustrates 5mC flipped out from the DNA helix and bound in a cage-like pocket (circled in red; PDB 2ZO1). (Adapted from Hashimoto et al. 2009).