Cell Reports

Supplemental Information

Human *C6orf211* Encodes Armt1, a Protein Carboxyl Methyltransferase that Targets PCNA and Is Linked to the DNA Damage Response

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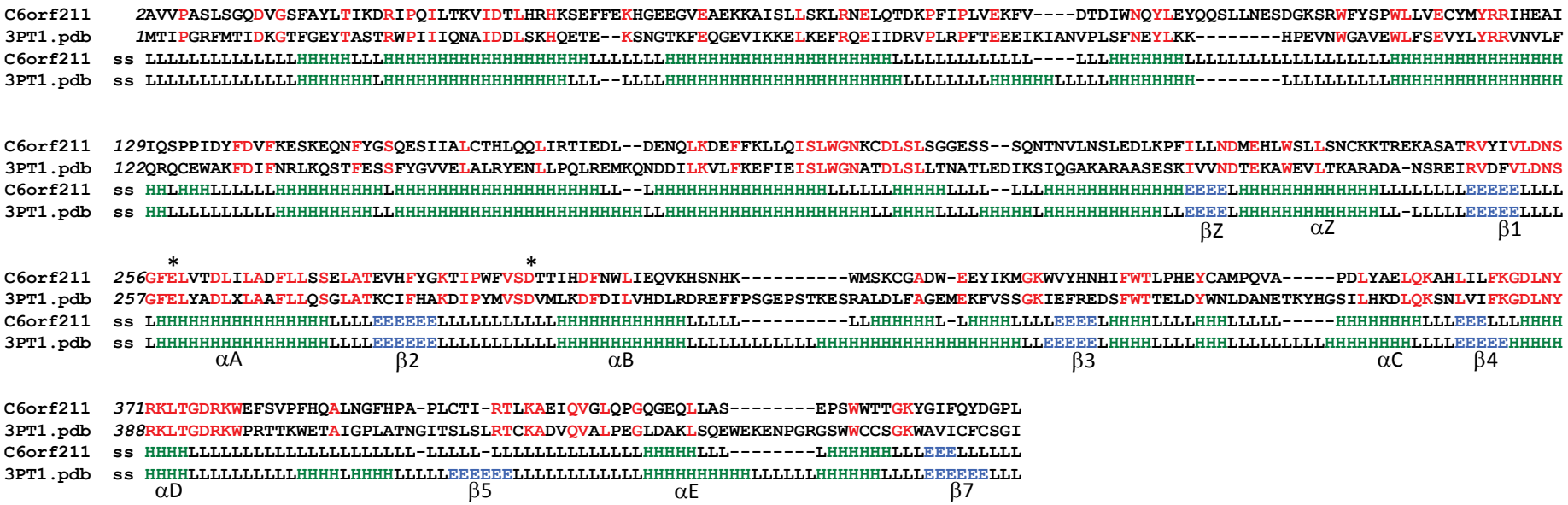

Figure S1 (related to Figure 1). Structure-based sequence alignment of human C6orf211 (Uniprot code: Q9H993) with DUF89 homolog 3PT1.pdb, and *S. cerevisiae* protein YMR027W (Uniprot code*:* Q04371). Conserved residues highlighted in red, stars indicate conserved active site acidic residues. I-Tasser predicted secondary structure shown for C6orf211 together with 3PT1.pdb secondary structure, as assigned by DSSP, green H indicates helix, blue E indicates strand and L is loop/coil. Conserved secondary structure elements in common with the core SAM-MT fold are labeled.

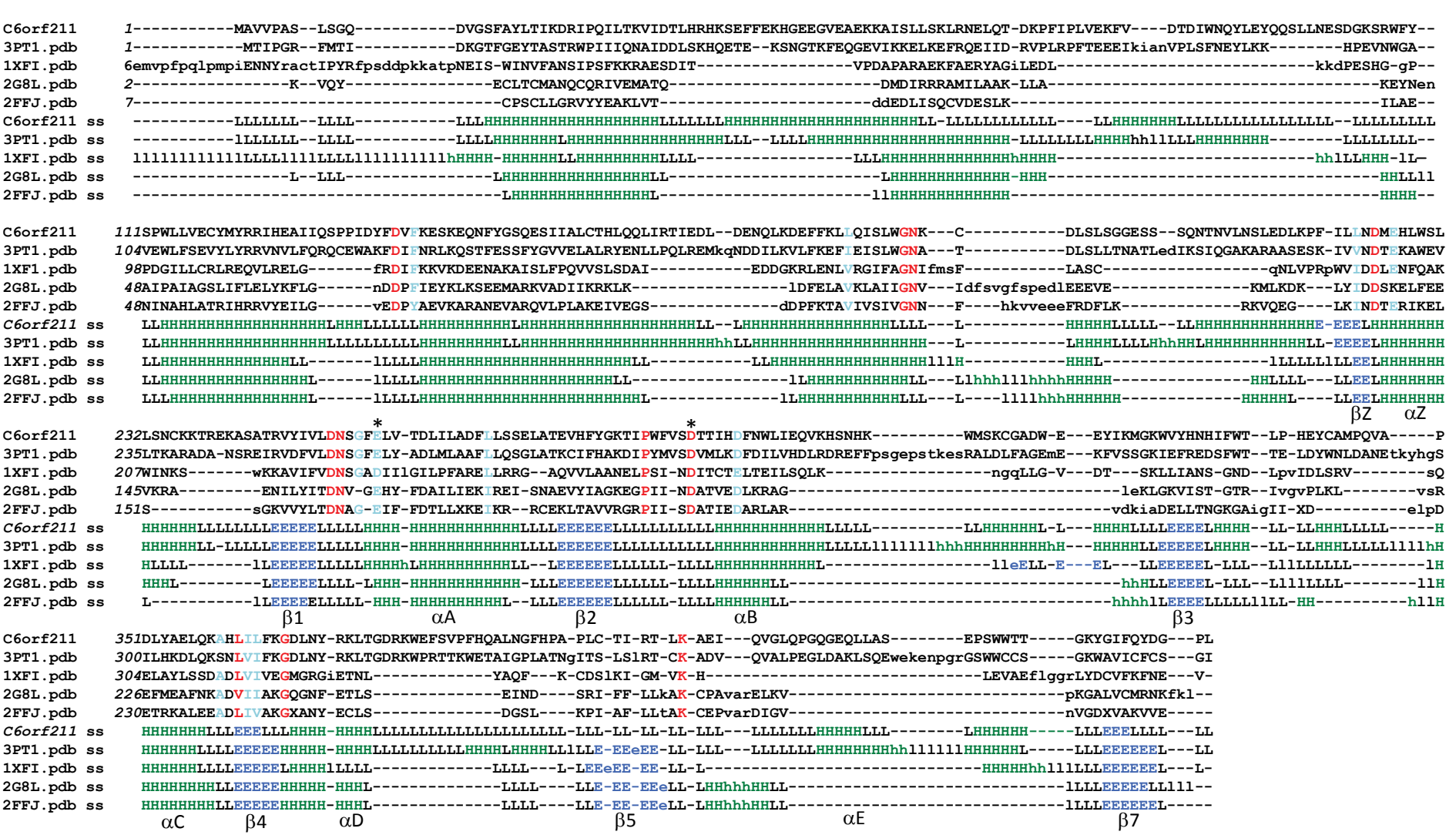

Figure S2 (related to Figure 2). Structure-based sequence alignment of human C6orf211 with known DUF89 structures, 3PT1.pdb, *S. cerevisiae* protein YMR027W (Uniprot code: Q04371); 1XFI.pdb (and 2Q40.pdb), *A. thaliana* gene product At2g17340 (Uniprot code: Q949P3); 2G8L.pdb, *P. horikoshii* protein ph1575 (Uniprot code: O59272); 2FFJ.pdb, *A. fulgidus* protein AF1104 (Uniprot code: O29161). Conserved residues highlighted in red, well-conserved in cyan, stars indicate conserved active site acidic residues, Uppercase indicates structurally equivalent positions, lowercase indicates insertions. I-Tasser predicted secondary structure are shown for C6orf211 together with the DUF89 secondary structures, as defined by DSSP. Green H indicates helix, blue E indicates strand and L is loop/coil. The conserved secondary structure elements in common with the core SAM-MT fold are labeled.

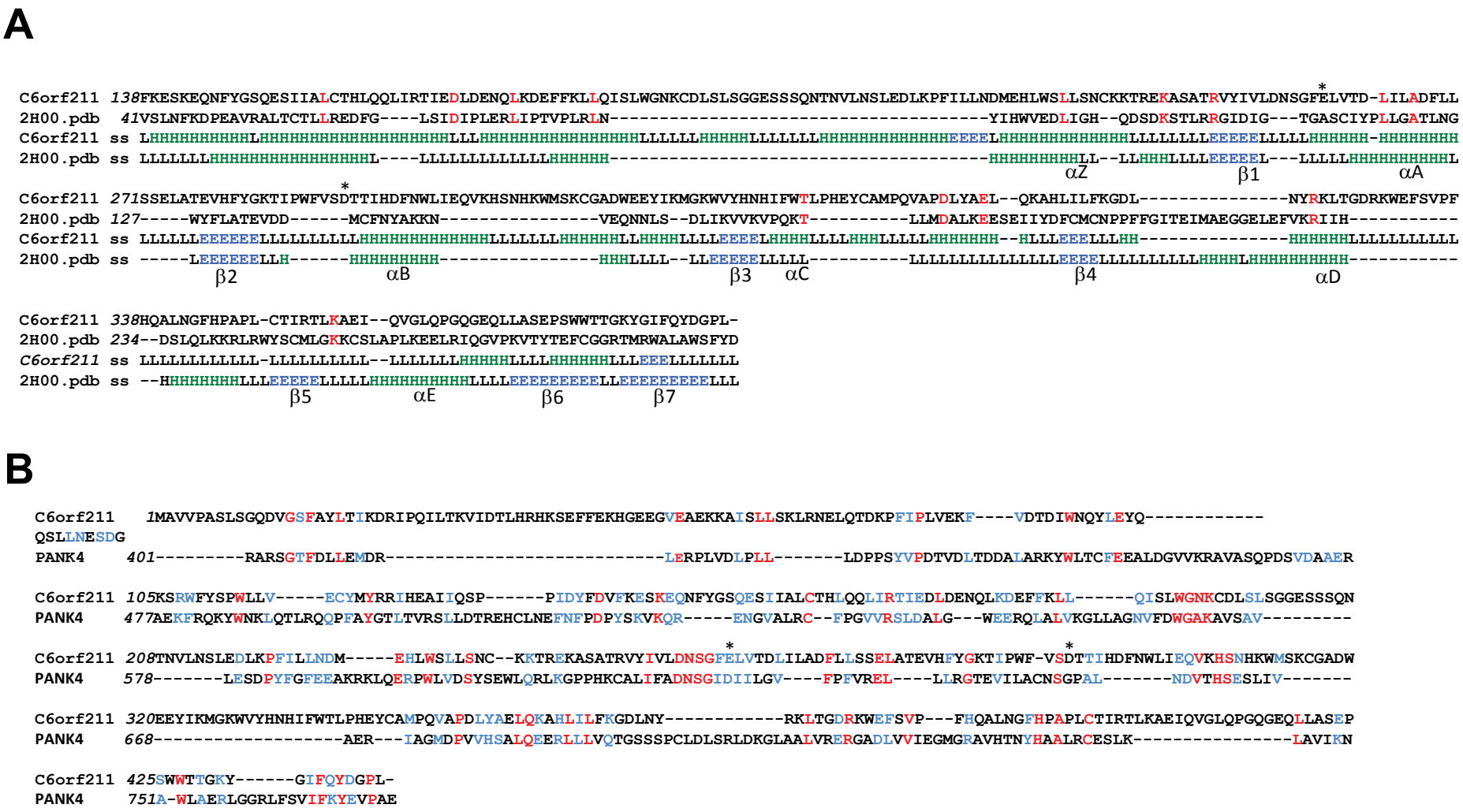

Figure S3 (related to Figure 3). (A) Structure-based sequence alignment of human C6orf211 with the human methyltransferase 10 domain containing protein (PDB code: 2H00.pdb; Uniprot code: Q86W50). Conserved residues are highlighted in red, stars indicate predicted C6orf211 active site acidic residues. I-Tasser predicted secondary structure shown for C6orf211 together with 2H00.pdb secondary structure as defined by DSSP, green H indicates helix, blue E indicates strand and L is loop/coil. The conserved secondary structure elements in common with the core SAM-MT fold are labeled. (B) Sequence alignment of C6orf211, residues 1-441 with DUF89 sequence from human PANK4, residues 401-773 (Uniprot code: Q9NVE7). Conserved residues are highlighted in red, well conserved in cyan. Predicted conserved active site site acidic residues of C6orf211 highlighted by stars.

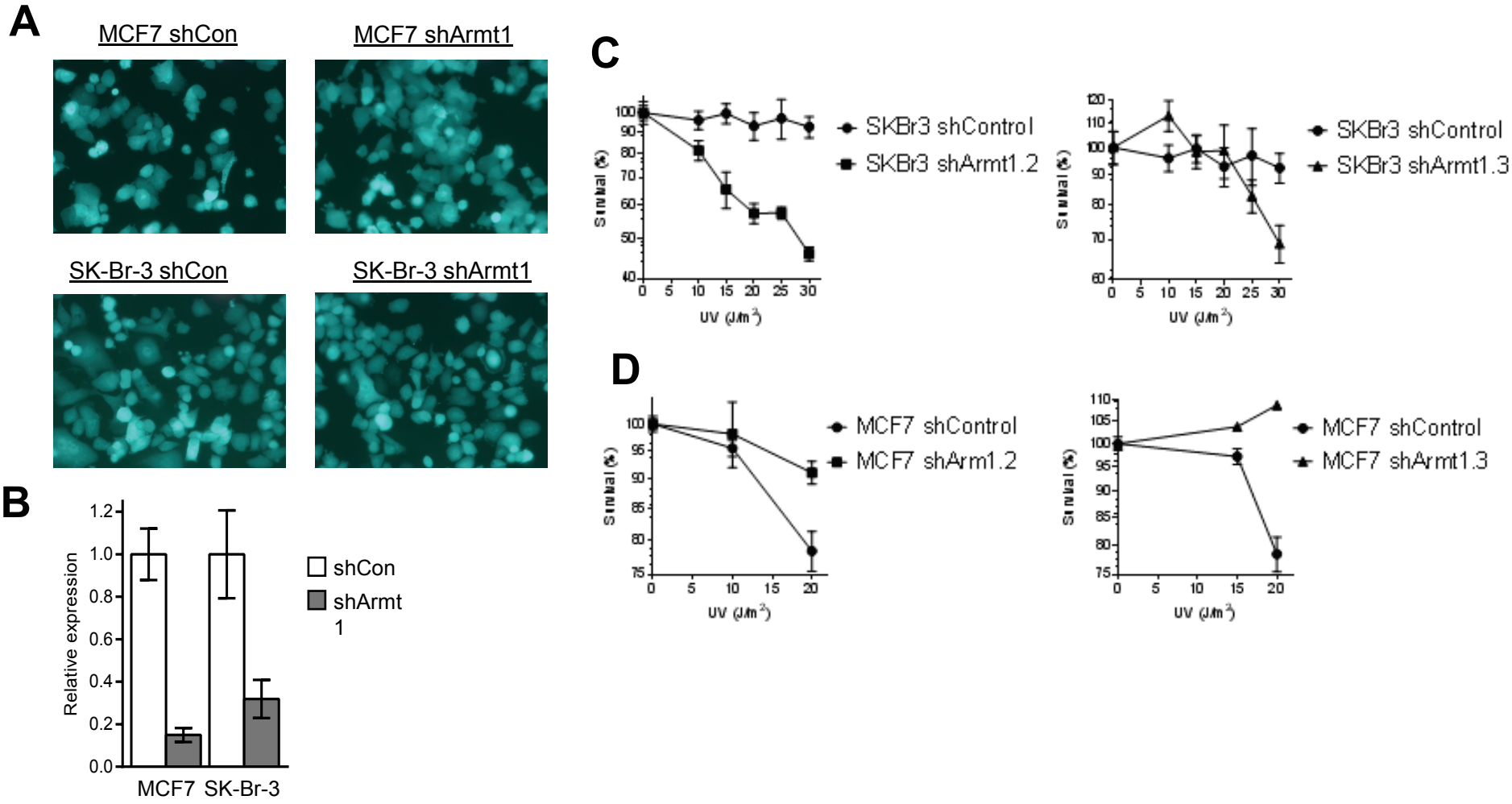

Figure S4 (related to Figure 5). (A) MCF7 and SK-Br-3 cells were infected with lentiviral particles expressing shRNA and TurboGFP from a bicistronic promoter, and stable clones selected with puromycin. Expression of TurboGFP was confirmed by microscopy. (B) Armt1 expression levels were determined by Q-PCR. Average mRNA expression levels were normalized to non-targeting controls and are presented ± SD. MCF7 and SK-Br-3 cells were infected with lentiviral particles and clones stably expressing two alternative shRNA constructs (shArmt1.2, or shArmt1.3) were selected. SK-Br-3 cells (C) and MCF7 cells (D) expressing either control or Armt1 knockdown shRNA were exposed to increasing doses of UV radiation and survival assessed by clonogenic assays. Average colony numbers were normalized to the non-irradiated controls and are presented ± SEM.