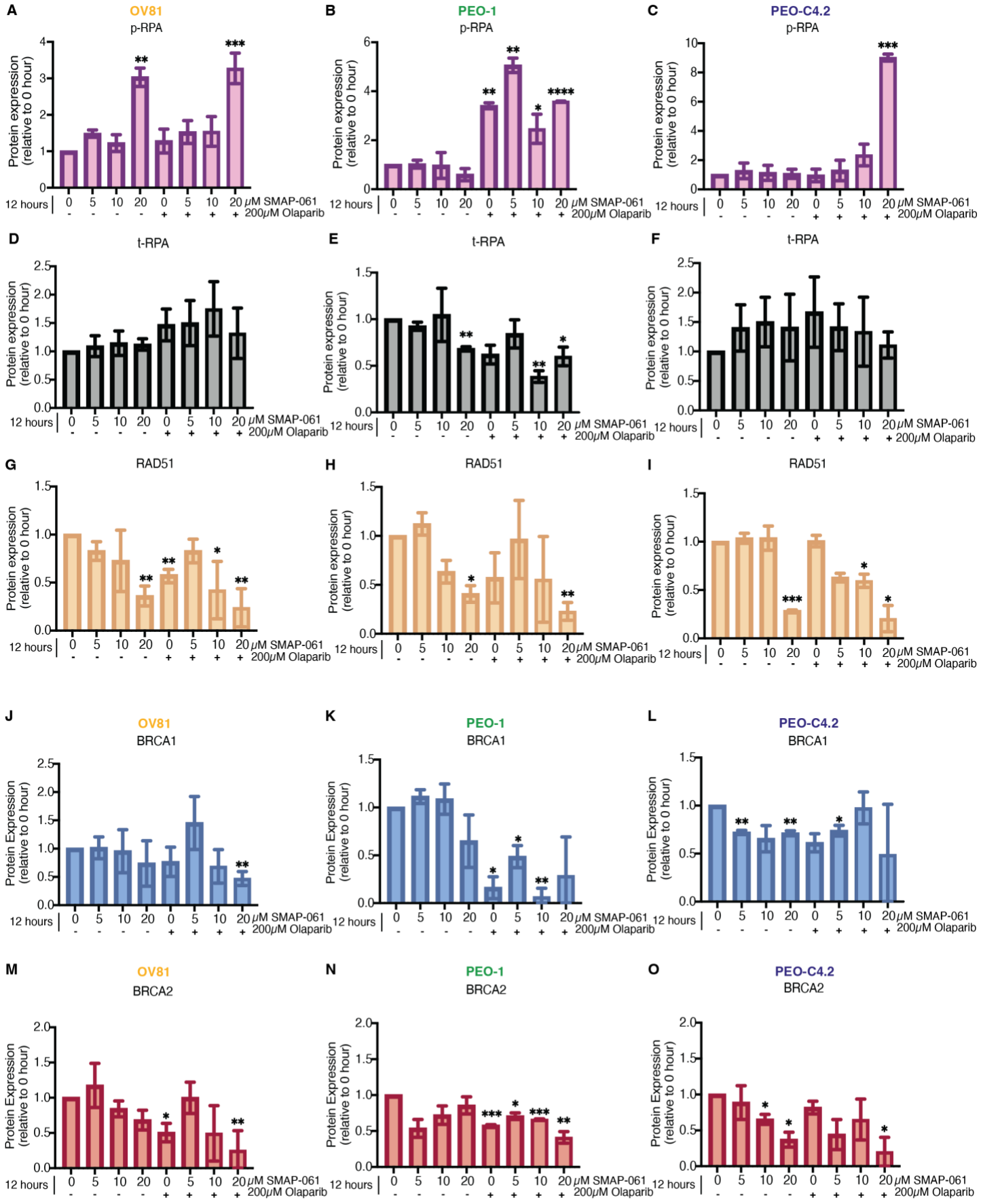
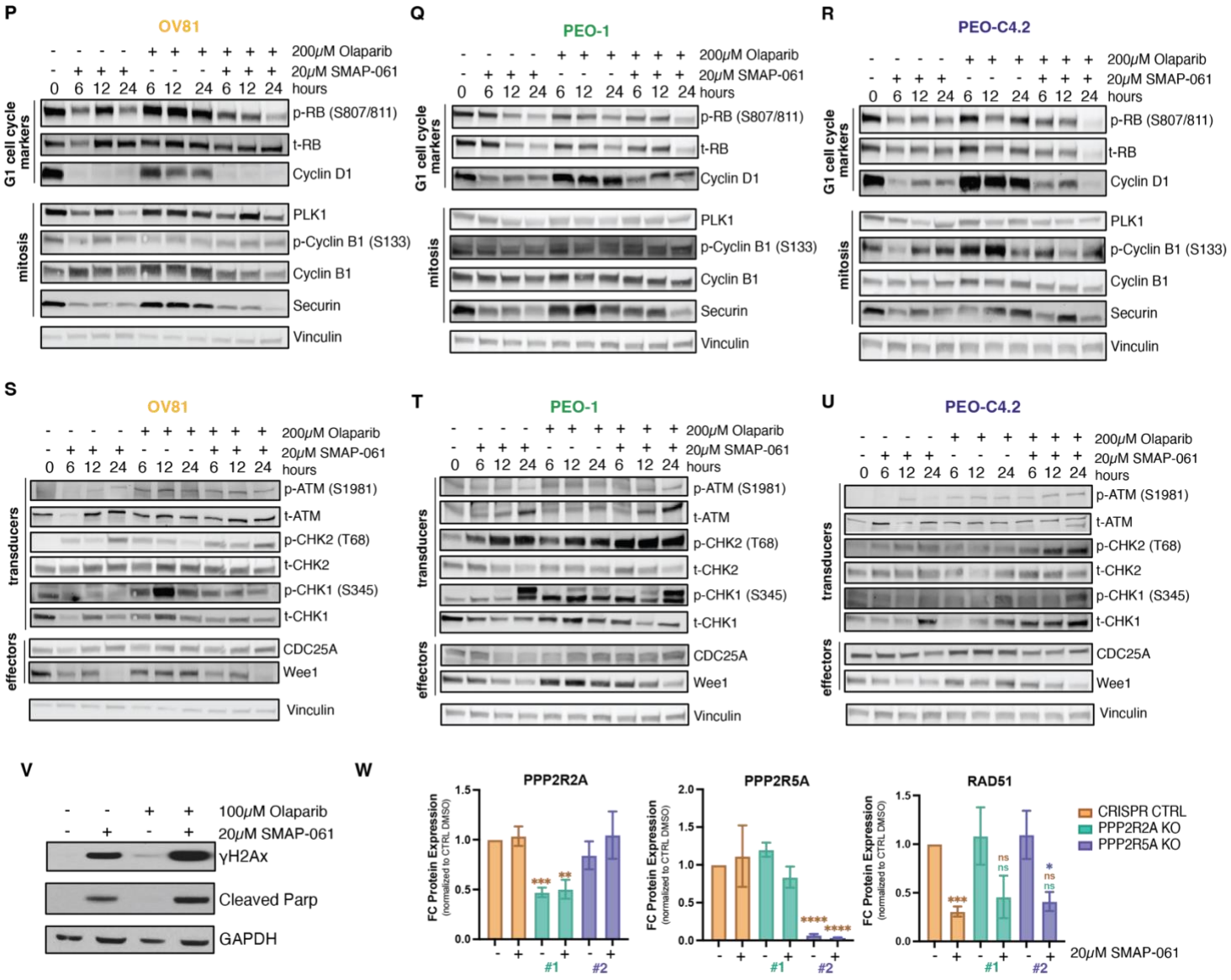
Supplementary Figure 5



Supplementary Figure 5



Supplementary Figure 5 – Co-treatment of SMAP-061 and PARPi synergistically engages the cell cycle and the DDR pathways in a time dependent manner. A) – O) Quantitation of protein targets expression evaluated on the western blot analysis from Fig. 5A, for OV81, PEO-1 and PEO-C4.2, respectively – A), B), C) p-RPA, D), E), F) t-RPA, G), H), I) RAD51, J), K), L) BRCA1, and M), N), O) BRCA2. Data is presented as the mean ± SEM (n=3), (unpaired Student T-tests, comparing each condition relative to DMSO, *p < 0.05, **p < 0.01, ***p < 0.001, ****p < 0.0001). P)-U) Western blot analysis evaluating cell cycle protein expression regulation upon 20μM SMAP-061, 200μM Olaparib or SMAP + Olaparib treatments for P) OV81, Q) PEO-1 and R) PEO-C4.2 during 6, 12 and 24 hours of exposure. **Transducer** and **effector** proteins (Fig. 3A schematic) are also affected by SMAP-061 treatment and significantly more engaged when in combination with PARPi for S) OV81, T) PEO-1 and U) PEO-C42 cell lines. V) Western blot analysis evaluating Cleaved PARP and γH2Ax expression levels upon 20μM SMAP-061, 100μM Olaparib or SMAP + Olaparib treatments. GAPDH was used as housekeeping. W) CRISPR Cas9 KO of 2 specific B-subunits (PPP2R2A and PPP2R5A) rescue experiments quantification in Fig. 5I for PPP2R2A, PPP2R5A and RAD51 protein expression. Data presented as the mean ± SD (n=3), (unpaired

Student T-tests, comparing each treatment group to distinct groups, *p < 0.05, **p < 0.01, ***p < 0.001, ****p < 0.0001). Data is presented as the mean ± SD (n=3).