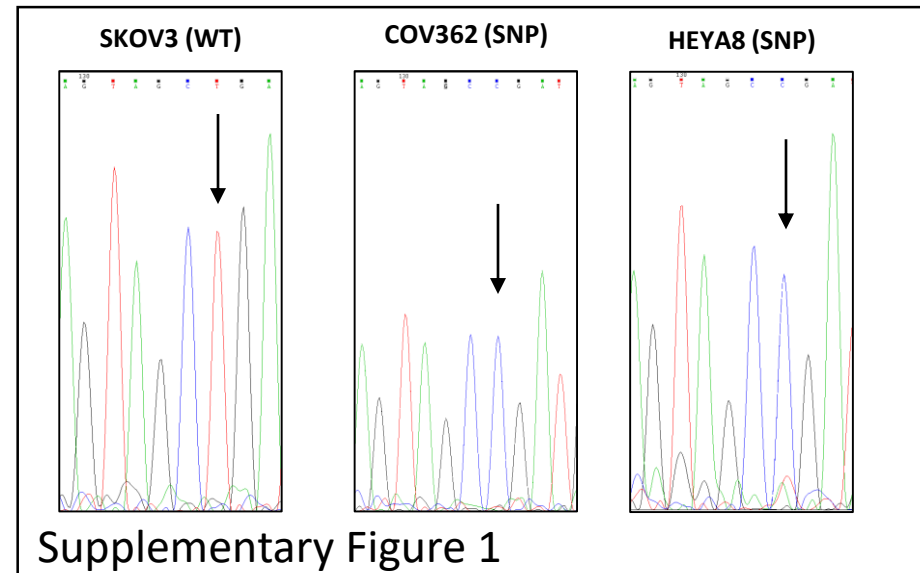
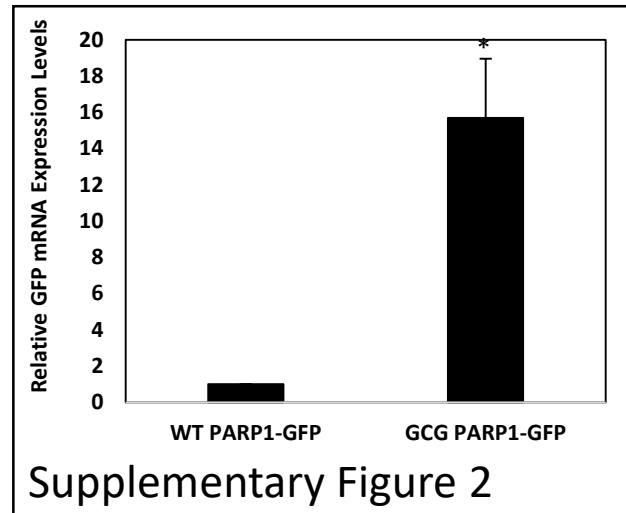
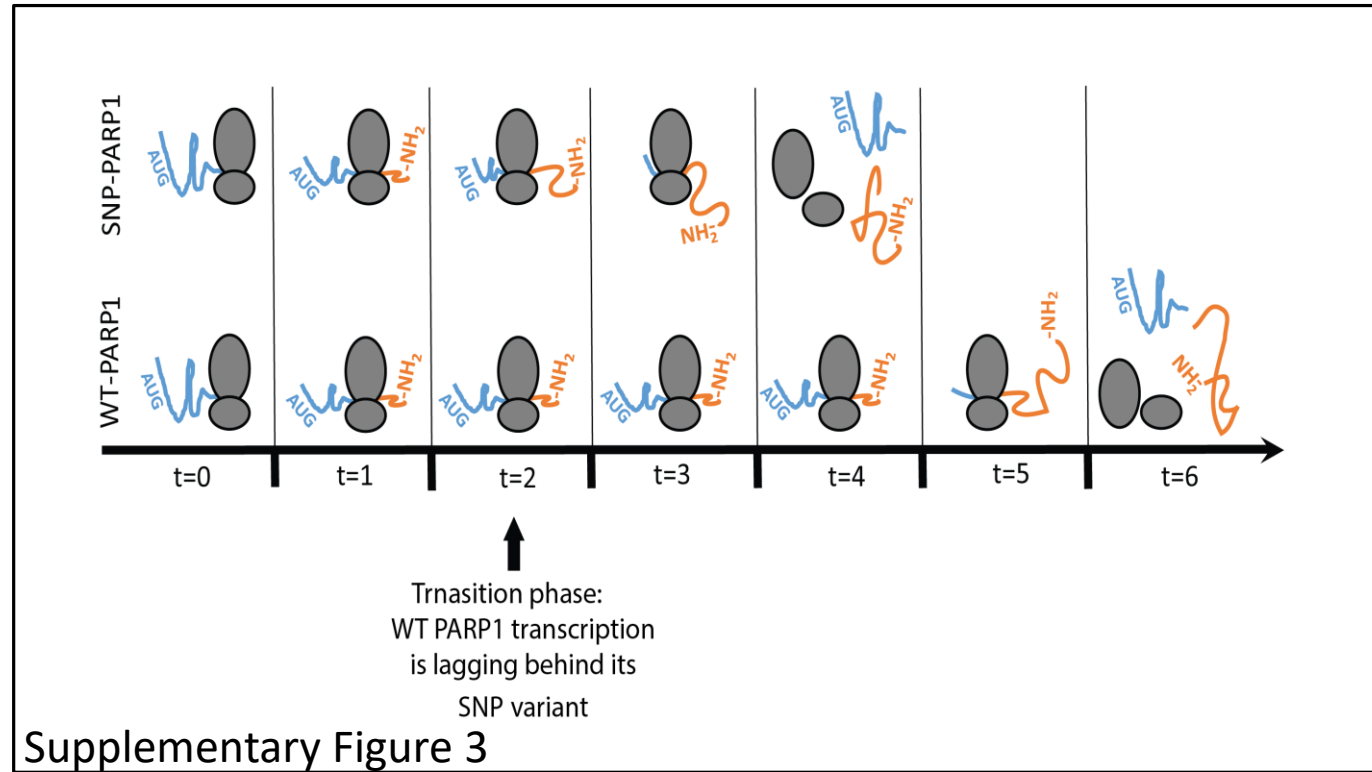




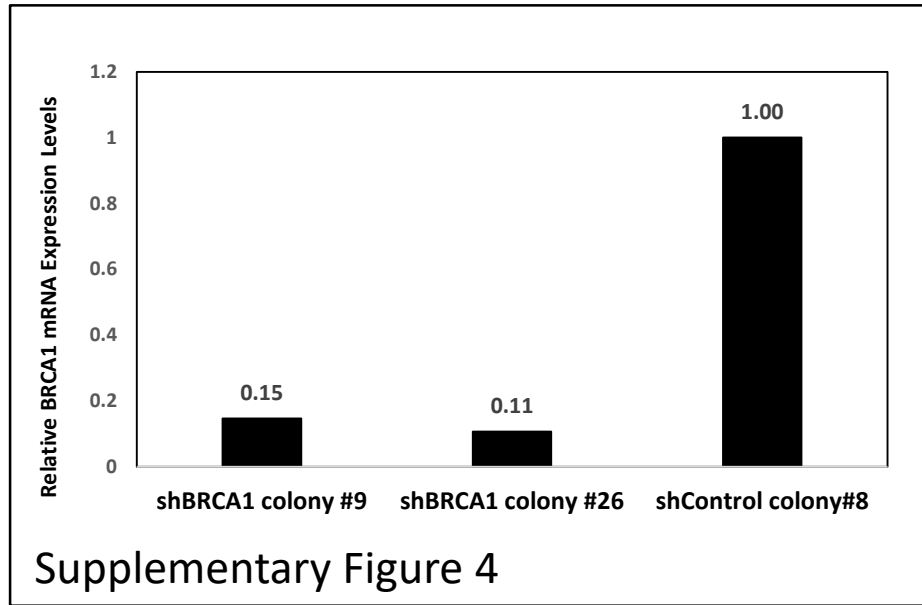
Supplementary Figure 1. Sanger sequencing was employed to verify PARP1 status of SKOV3, COV362 and Heya8 Ovarian cell lines, by using the indicated primers (in the Methods section), which surround the SNP position from both sides.



Supplementary Figure 2. We introduced a GCG artificial variant of PARP1 to the WT-PARP1 vector by SDM manipulation. GCG-PARP1-GFP and WT-(GCT)-PARP1-GFP plasmids were over expressed in HEK293T cells. 48h later, mRNA levels of these PARP1 variants, demonstrated **high** levels of PARP1 mRNA compare to WT PARP1 GFP (p Value < 0.05).



Supplementary Figure 3. A schematic illustration of translation. SNP versus WT –PARP1 mRNAs are being processed through ribosomes machinery to obtain the mature protein. A lagging phase in WT-PARP1 translation, contributed by lack of an appropriate tRNA, results in delay on ribosome and rearrangement of the newly synthesized peptide. While the SNP-PARP1 mRNA complicates an entire cycle of translation, ready to initiate an additional cycle, the WT-PARP1 repairs its tRNA and continues a first cycle, forming a new protein structure compared to its SNP-PARP1 version.



Supplementary Figure 4. HEK293T cells were transfected with 2 μ g of a specific short hairpin vector, sh-BRCA1 or sh-Control to generate a stable system of silenced endogenous BRCA1. 48h post transfection, cells were exposed to 2 μ g/ μ l puromycin selection, until stable colonies were generated. RNA was extracted from the stable cells and mRNA levels of BRCA1 were analyzed by qRT-PCR, normalized to β -actin (primers are indicated in the Methods section).