Figure S1. Analysis of miRNA and BLM expression in patients with PCa in TCGA dataset. (A) miR-27b-3p, miR-152-3p and miR-23b-3p expression levels in PCa tumor samples and normal prostate tissue. (B) Correlations between the expression of PVT1 and that of overlapping target miRNAs. (C) c-myc expression following miR-27b-3p overexpression. (D) BLM upregulation was observed in PCa tissue samples relative to normal prostate tissue in the Oncomine database. These datasets were all regarding prostate carcinoma vs. normal tissue [1 (33); 2 (45); 3 (46); 4 (38); 5 (42); the numbers in parentheses refer to references in the main manuscript]. (E) BLM expression in paired PCa tumors and paracancerous tissue samples in the TCGA-PRAD database. *P<0.05, **P<0.01 and ***P<0.001. BLM, bloom syndrome protein; PVT1, plasmacytoma variant translocation 1; PCa, prostate cancer; TCGA, The Cancer Genome Atlas; PRAD, prostate adenocarcinoma; CR, complete response; PR, partial response; SD, stable disease; PD, progressive disease.



Figure S2. BLM promotes PVT1 expression. (A) BLM expression in PCa cells and the control RWPE-2 cell line was assessed using RT-qPCR and western blot analysis. (B) The expression of miR-27b-3p in PC3 cells and LNCap cells was assessed using RT-qPCR after the transfection with NC mimic or miR-27b-3p mimic. (C) BLM and (D) PVT1 expression in PC3 cells and LNCap cells was assessed using RT-qPCR after transfection with empty vector or BLM overexpression vector. **P<0.01 and ***P<0.001. BLM, bloom syndrome protein; PVT1, plasmacytoma variant translocation 1; PCa, prostate cancer; RT-qPCR, reverse transcription-quantitative polymerase chain reaction.

