A BRCA-2012-RTK-RAS-PI(3)K-pathway
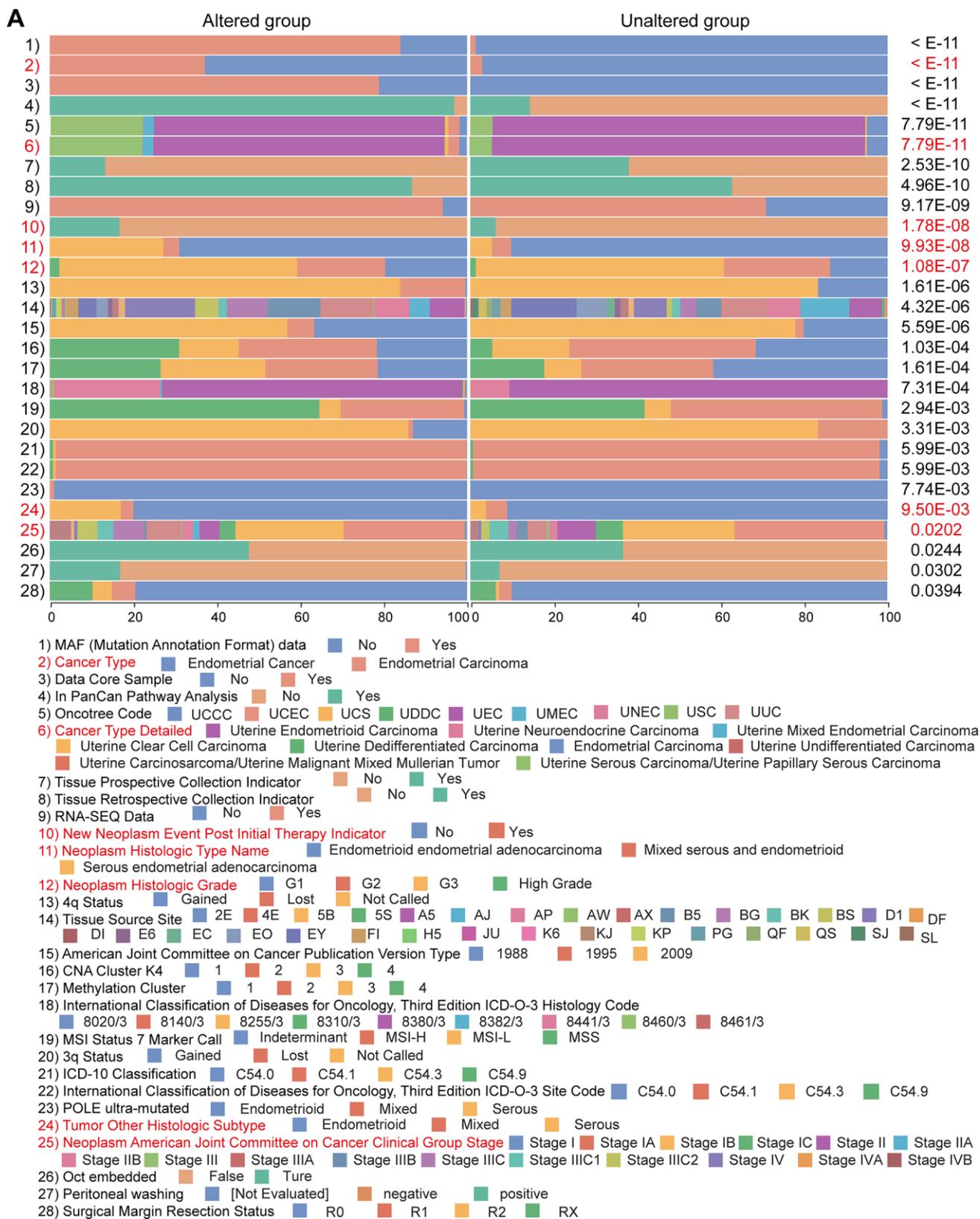

B COADREAD-2012-WNT-signaling-pathway
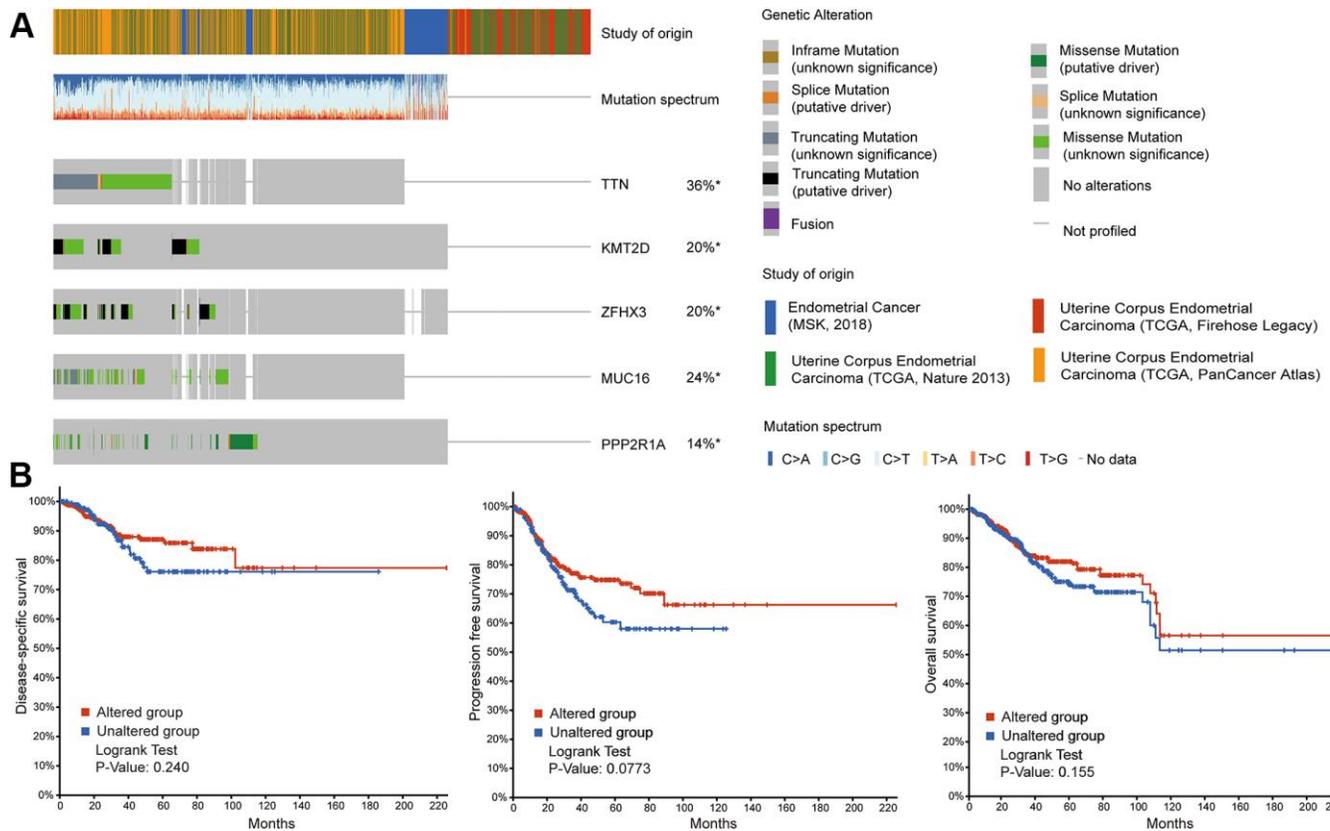

Supplementary Figure 1. Pathway enrichment analysis of 275 common mutation genes in EC. Pathway enrichment analysis of 275 common mutation genes in EC. The genes identified in the pink font were from 275 common mutation genes, percentage indicated the proportion of the gene mutated in EC. (**A**) BRCA-2012-RTK-RAS-PI(3)K-pathway. (**B**) COADREAD-2012-WNT-signaling-pathway.

A

Altered group | Unaltered group

1) < E-11
2) < E-11
3) < E-11
4) < E-11
5) 7.79E-11
6) 7.79E-11
7) 2.53E-10
8) 4.96E-10
9) 9.17E-09
10) 1.78E-08
11) 9.93E-08
12) 1.08E-07
13) 1.61E-06
14) 4.32E-06
15) 5.59E-06
16) 1.03E-04
17) 1.61E-04
18) 7.31E-04
19) 2.94E-03
20) 3.31E-03
21) 5.99E-03
22) 5.99E-03
23) 7.74E-03
24) 9.50E-03
25) 0.0202
26) 0.0244
27) 0.0302
28) 0.0394

1) MAF (Mutation Annotation Format) data ■ No ■ Yes
2) Cancer Type ■ Endometrial Cancer ■ Endometrial Carcinoma
3) Data Core Sample ■ No ■ Yes
4) In PanCan Pathway Analysis ■ No ■ Yes
5) Oncotree Code ■ UCCC ■ UCEC ■ UCS ■ UDDC ■ UEC ■ UMEC ■ UNEC ■ USC ■ UUC
6) Cancer Type Detailed ■ Uterine Endometrioid Carcinoma ■ Uterine Neuroendocrine Carcinoma ■ Uterine Mixed Endometrial Carcinoma
  ■ Uterine Clear Cell Carcinoma ■ Uterine Dedifferentiated Carcinoma ■ Endometrial Carcinoma ■ Uterine Undifferentiated Carcinoma
  ■ Uterine Carcinosarcoma/Uterine Malignant Mixed Mullerian Tumor ■ Uterine Serous Carcinoma/Uterine Papillary Serous Carcinoma
7) Tissue Prospective Collection Indicator ■ No ■ Yes
8) Tissue Retrospective Collection Indicator ■ No ■ Yes
9) RNA-SEQ Data ■ No ■ Yes
10) New Neoplasm Event Post Initial Therapy Indicator ■ No ■ Yes
11) Neoplasm Histologic Type Name ■ Endometrioid endometrial adenocarcinoma ■ Mixed serous and endometrioid
  ■ Serous endometrial adenocarcinoma
12) Neoplasm Histologic Grade ■ G1 ■ G2 ■ G3 ■ High Grade
13) 4q Status ■ Gained ■ Lost ■ Not Called
14) Tissue Source Site ■ 2E ■ 4E ■ 5B ■ 5S ■ A5 ■ AJ ■ AP ■ AW ■ AX ■ B5 ■ BG ■ BK ■ BS ■ D1 ■ DF
  ■ DI ■ E6 ■ EC ■ EO ■ EY ■ FI ■ H5 ■ JU ■ K6 ■ KJ ■ KP ■ PG ■ QF ■ QS ■ SJ ■ SL
15) American Joint Committee on Cancer Publication Version Type ■ 1988 ■ 1995 ■ 2009
16) CNA Cluster K4 ■ 1 ■ 2 ■ 3 ■ 4
17) Methylation Cluster ■ 1 ■ 2 ■ 3 ■ 4
18) International Classification of Diseases for Oncology, Third Edition ICD-O-3 Histology Code
  ■ 8020/3 ■ 8140/3 ■ 8255/3 ■ 8310/3 ■ 8380/3 ■ 8382/3 ■ 8441/3 ■ 8460/3 ■ 8461/3
19) MSI Status 7 Marker Call ■ Indeterminant ■ MSI-H ■ MSI-L ■ MSS
20) 3q Status ■ Gained ■ Lost ■ Not Called
21) ICD-10 Classification ■ C54.0 ■ C54.1 ■ C54.3 ■ C54.9
22) International Classification of Diseases for Oncology, Third Edition ICD-O-3 Site Code ■ C54.0 ■ C54.1 ■ C54.3 ■ C54.9
23) POLE ultra-mutated ■ Endometrioid ■ Mixed ■ Serous
24) Tumor Other Histologic Subtype ■ Endometrioid ■ Mixed ■ Serous
25) Neoplasm American Joint Committee on Cancer Clinical Group Stage ■ Stage I ■ Stage IA ■ Stage IB ■ Stage IC ■ Stage II ■ Stage IIA
  ■ Stage IIB ■ Stage III ■ Stage IIIA ■ Stage IIIB ■ Stage IIIC ■ Stage IIIC1 ■ Stage IIIC2 ■ Stage IV ■ Stage IVA ■ Stage IVB
26) Oct embedded ■ False ■ Ture
27) Peritoneal washing ■ [Not Evaluated] ■ negative ■ positive
28) Surgical Margin Resection Status ■ R0 ■ R1 ■ R2 ■ RX

Supplementary Figure 2. Molecular differences in EC patients with/without 275 common mutation genes. (**A**) Molecular differences in EC patients with/without 275 common mutation genes. EC patients with 275 common mutation genes were classified as the altered group, and those without the 275 common mutation genes as the unaltered group.

Supplementary Figure 3. Oncoprint a of TTN, KMT2D, ZFHX3, MUC16, PPP2R1A and their association with prognosis in EC patients. (**A**) Oncoprint of TTN, KMT2D, ZFHX3, MUC16, PPP2R1A in EC. (**B**) Kaplan–Meier plots comparing prognostic value (DFS, PFS and OS) in EC patients with/without TTN, KMT2D, ZFHX3, MUC16, PPP2R1A mutation genes. EC patients with TTN, KMT2D, ZFHX3, MUC16, PPP2R1A mutation genes were classified as the altered group, and those without the TTN, KMT2D, ZFHX3, MUC16, PPP2R1A mutation genes as the unaltered group.
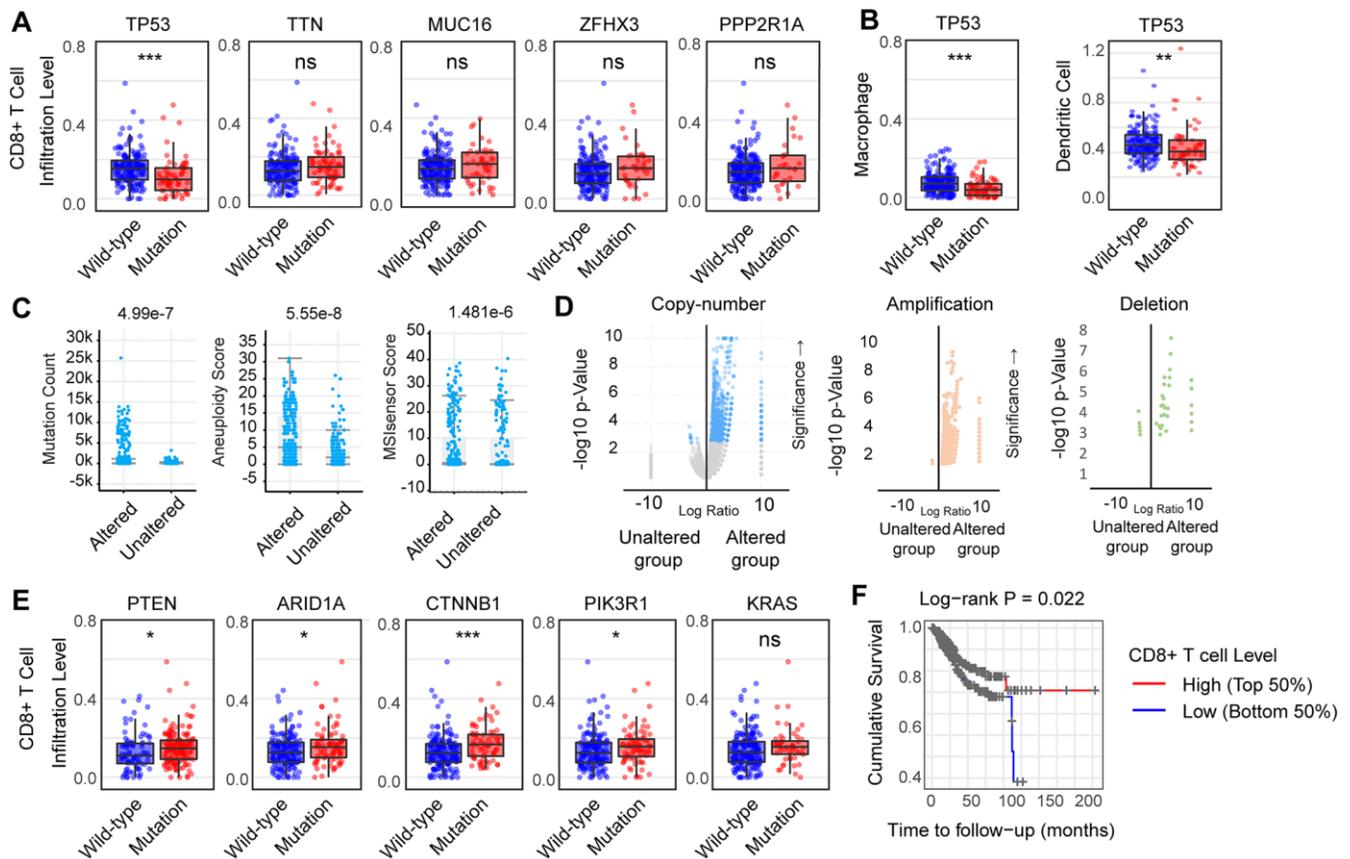
Supplementary Figure 4. Different immune cell infiltrates and genomic characteristics in the two clusters of EC patients with different mutation signatures. (**A**) The infiltration level of CD8+ T cells and mutation status in EC. (**B**) The infiltration level of macrophage and dendritic cells and mutation status of *TP53* in EC (**C**) The mutation count, aneuploidy score, and MSIsensor Score of EC patients clustered by Signature 1. (**D**) The copy-number, amplification, and deletion of EC patients clustered by Signature 1. (**E**) The infiltration level of CD8+ T cells mutation status of *PTEN ARID1A*, *CTNNB1*, *PIK3R1*, and *KRAS* in EC. (**F**) The cumulative survival and CD8+ T cell infiltration level.
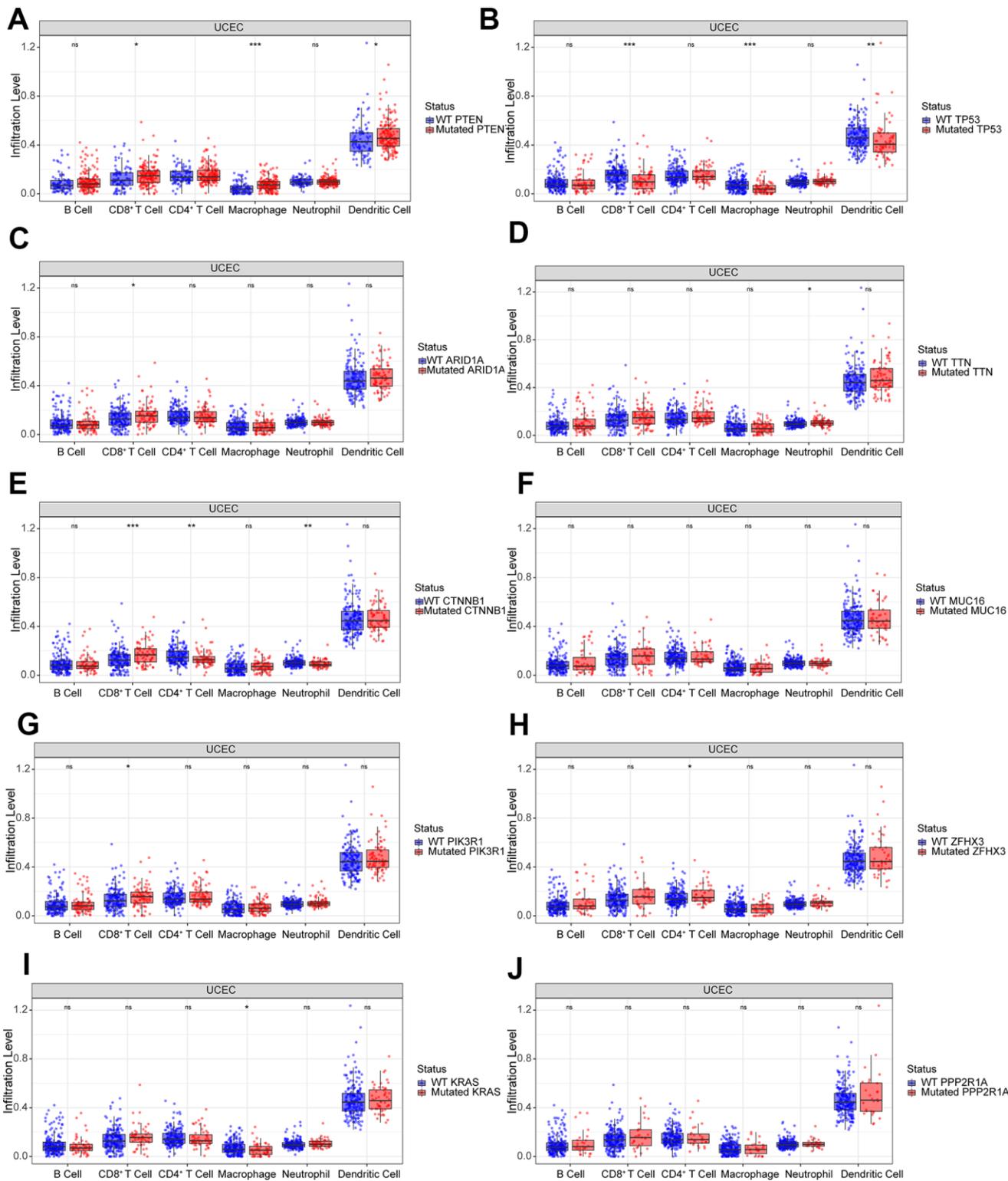
Supplementary Figure 5. Tumor-infiltrating lymphocytes in wild-type or mutation group. (**A**–**J**) The infiltration of B Cell, CD8+ T Cell, CD4+ T Cell, Macrophage, Neutrophil, Dendritic Cell in EC tumors with wild-type or mutation of PTEN, TP53, ARID1A, TTN, CTNNB1, MUC16, PIK3R1, ZFHX3, KRAS and PPP2R1A genes, * P<0.05; ** P<0.01; ***P<0.001; ****P<0.0001, ns indicated that there was no significant statistical difference.
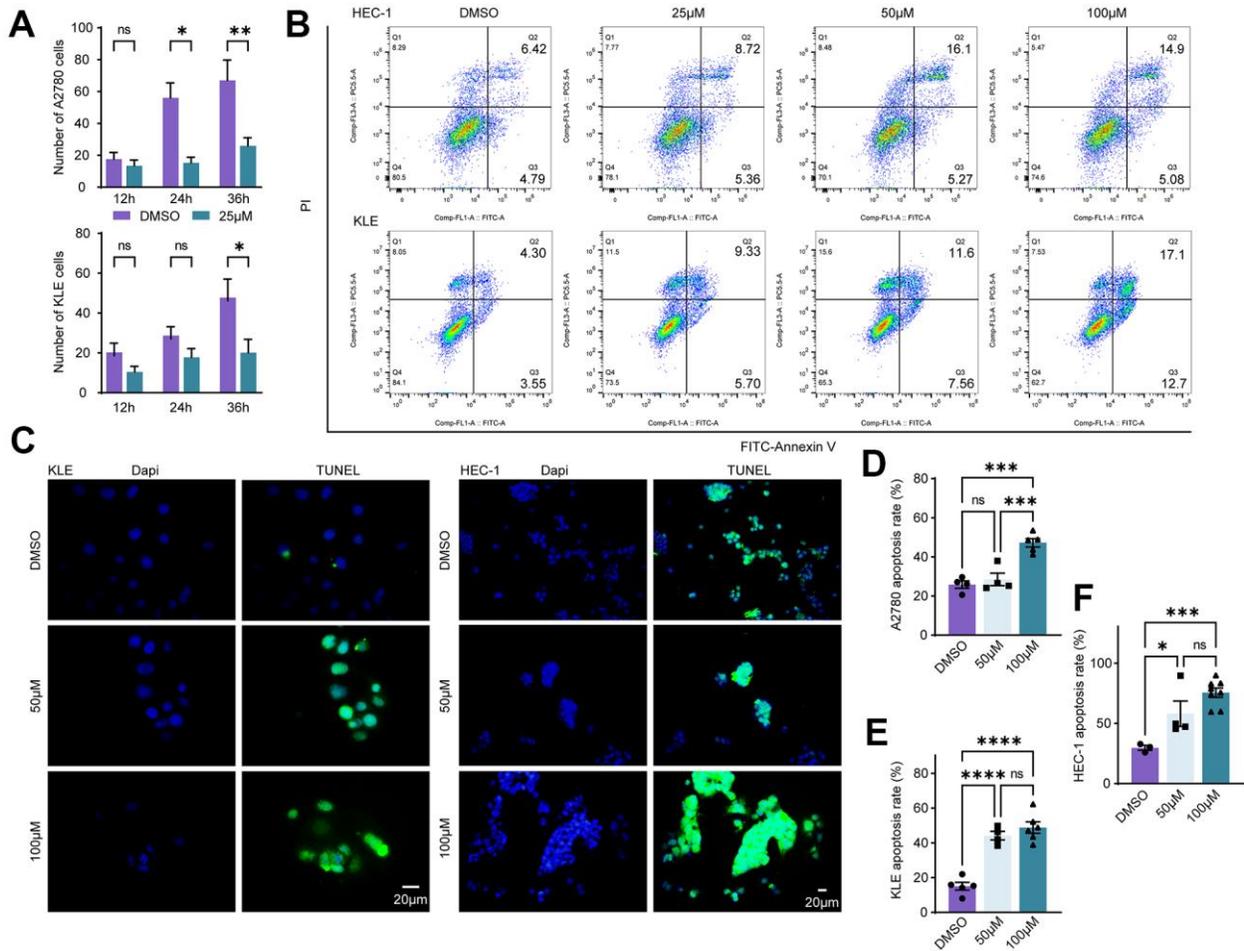
Supplementary Figure 6. Olaparib inhibits cell migration and promotes apoptosis in EC and EnOC *in vitro*. (**A**) The quantification of cell migration assay. (**B**) Apoptosis assay in HEC-1 and KLE. (**C**–**F**) TUNEL assays and their quantifications.
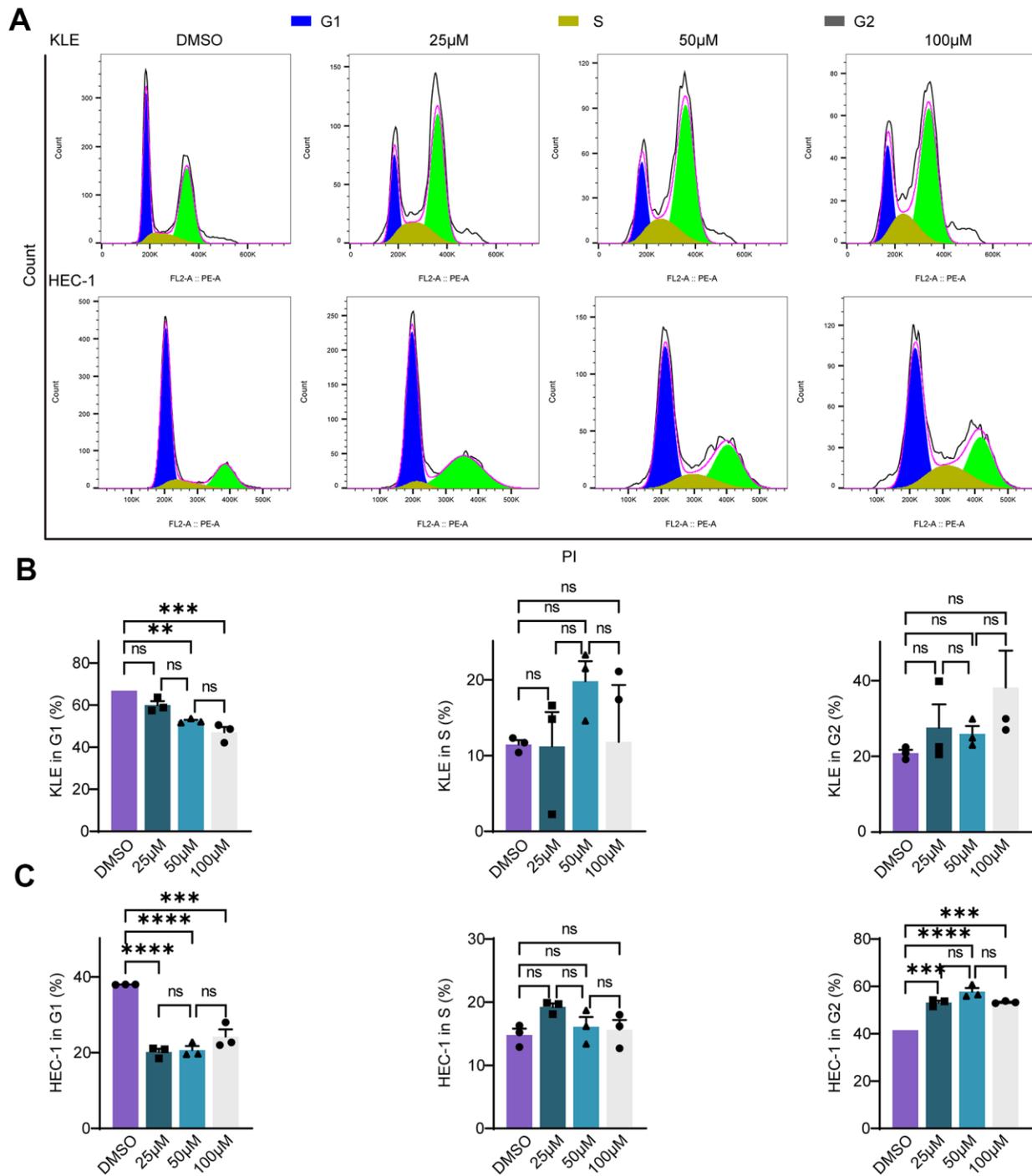
Supplementary Figure 7. Olaparib interferes with the cell cycle in KLE and HEC-1. (**A**–**C**) Cell cycle analysis and their quantifications in KLE and HEC-1.