



Supplementary Figure S4. Validation of new classifications using The Cancer Genome Atlas dataset. (A) Classification of TCGA data set based on TP53 inactivation score.

The data set of endometrial carcinomas was extracted from an available public database (cBioPortal; <https://www.cbioportal.org/>). [2] This analysis was performed using 507 samples containing clinical characteristics, somatic mutations, and gene expression profiling registered in the cBioPortal. TCGA classification was based on the available subtypes in the database. The endometrial carcinomas with TP53 inactivation scores greater than the 75th percentile ($\geq Q3$) or with *TP53* nonsynonymous mutations were defined as TP53-inactive and others as TP53-active. Pie charts represent the distribution of TCGA classifications within the TP53 inactivation and activation subgroups.

(B) Progression-free survival curve of patients in new subgroups including TP53 status. (C) Expression of core genes in the gene set identified by gene set enrichment analysis (GSEA). Among the ten significant pathways identified by GSEA, 11 core genes involved in multiple pathways ($>3/10$ pathways) are shown (see Figure 5).

Samples ($n = 310$) excluding polymerase-epsilon (POLE) and microsatellite instability (MSI) subgroups are displayed in ascending order of TP53 inactivation score.

The Pearson correlation (r) between each gene and the TP53 inactivation score is represented on the right of the heatmap. CN, copy number.