

Figure S1. Identification of DEGs after MNP treatment. (a) Heat map of the whole transcriptome, DEGs with false discovery rate of 5% and fold change cut-off at 0.5. Lanes 1-3 indicate control samples, lanes 4-6 indicate MNP treated samples. (b) Volcano plots of the DEGs. Red and green dots indicated upregulated and downregulated genes, respectively, in MNP treated samples compared with control. Abbreviations: DEGs, differentially expressed genes.

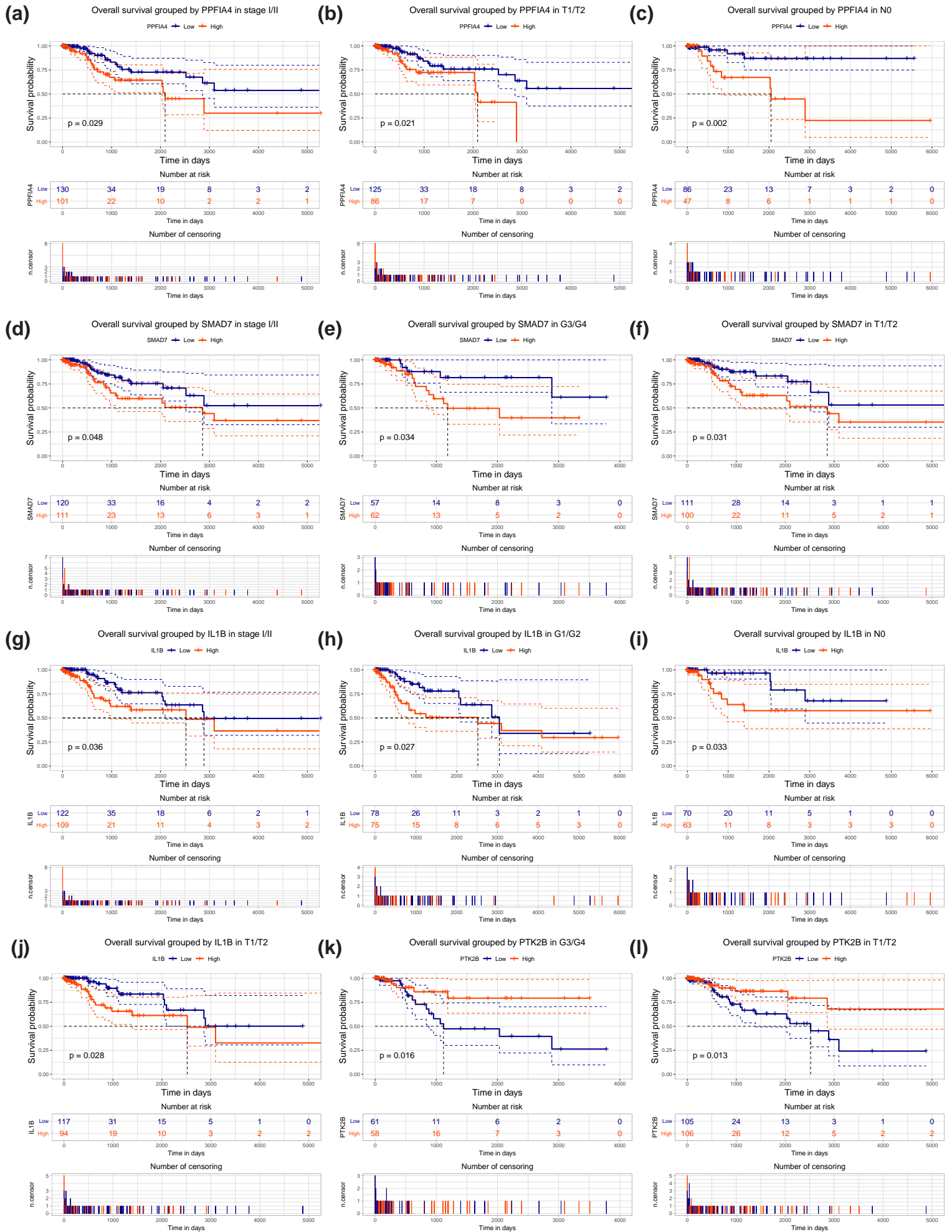


Figure S2. Subgroup survival analysis of the four key genes were conducted in different clinical stage, histologic grade, tumor (T) and (N) classification among TCGA cervical cancer patients. The patients were divided into 2 groups, based on median gene expression value as a cut-off point. (a-c) High PPFIA4 expression correlated with a poor overall survival in patients in clinical stage I/II, T1/T2 and N0. (d-f) High SMAD7 expression correlated with a poor overall survival in patients in clinical stage I/II, histologic grade G3/G4 and T1/T2. (g-j) High IL1B expression correlated with a poor overall survival in patients in clinical stage I/II (P=0.036), histologic grade G1/G2 (P=0.027), T1/T2 (P=0.028) and N0 (P=0.033). (k,l) High PTK2B expression correlated with a better overall survival in patients in histologic grade G3/G4 (P=0.016) and T1/T2 (P=0.013)