Supplementary Material

Supplementary Figure 1. The forest map of 34 pyroptosis-related lncRNAs that is considered to be significantly correlated with the overall survival of patients with ovarian cancer after univariate-cox regression analysis.

Supplementary Table 1. The 52 pyroptosis-related genes included in our research.

Supplementary Table 2. The 1122 lncRNAs that have significant expression correlation with pyroptosis-related genes.

Supplementary Table 3. The 712 lncRNAs that are significantly different expressed between normal and malignant ovarian tissues.

Supplementary Table 4. The 29 pyroptosis-related genes that are dysregulated between ovarian cancer and normal ovarian tissues.