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2 **Supplementary Material**

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

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

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

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

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

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