

Figure S1. Gene expression changes in the carboplatin- and lobaplatin-treated groups. (A-a) A total of 123,683 genes were evaluated in the NC vs. carboplatin group comparison and are shown in the volcano plot. The red dots represent the 1,353 genes with upregulated expression, the blue dots represent the 1,172 genes with downregulated expression, and the gray dots represent genes without differential expression. (A-b) A total of 33,280 genes were evaluated in the NC vs. lobaplatin group comparison, as shown in the plot. The red dots represent the 2,582 genes with upregulated expression, the blue dots represent the 2,971 genes with downregulated expression, and the gray dots represent the genes without differential expression. (A-c) A total of 125,628 genes were evaluated in the carboplatin vs lobaplatin group comparison, as shown in the plot. The red dots represent the 1,534 genes with upregulated expression, the blue dots represent the 2,190 genes with downregulated expression, and the gray dots represent the genes without differential expression. (B-a-c) The main GO categories impacted by carboplatin or lobaplatin treatment were identified according to the adjusted P-values. Red, green and blue reflect terms relating to biological processes, cellular components, and molecular functions, respectively.

