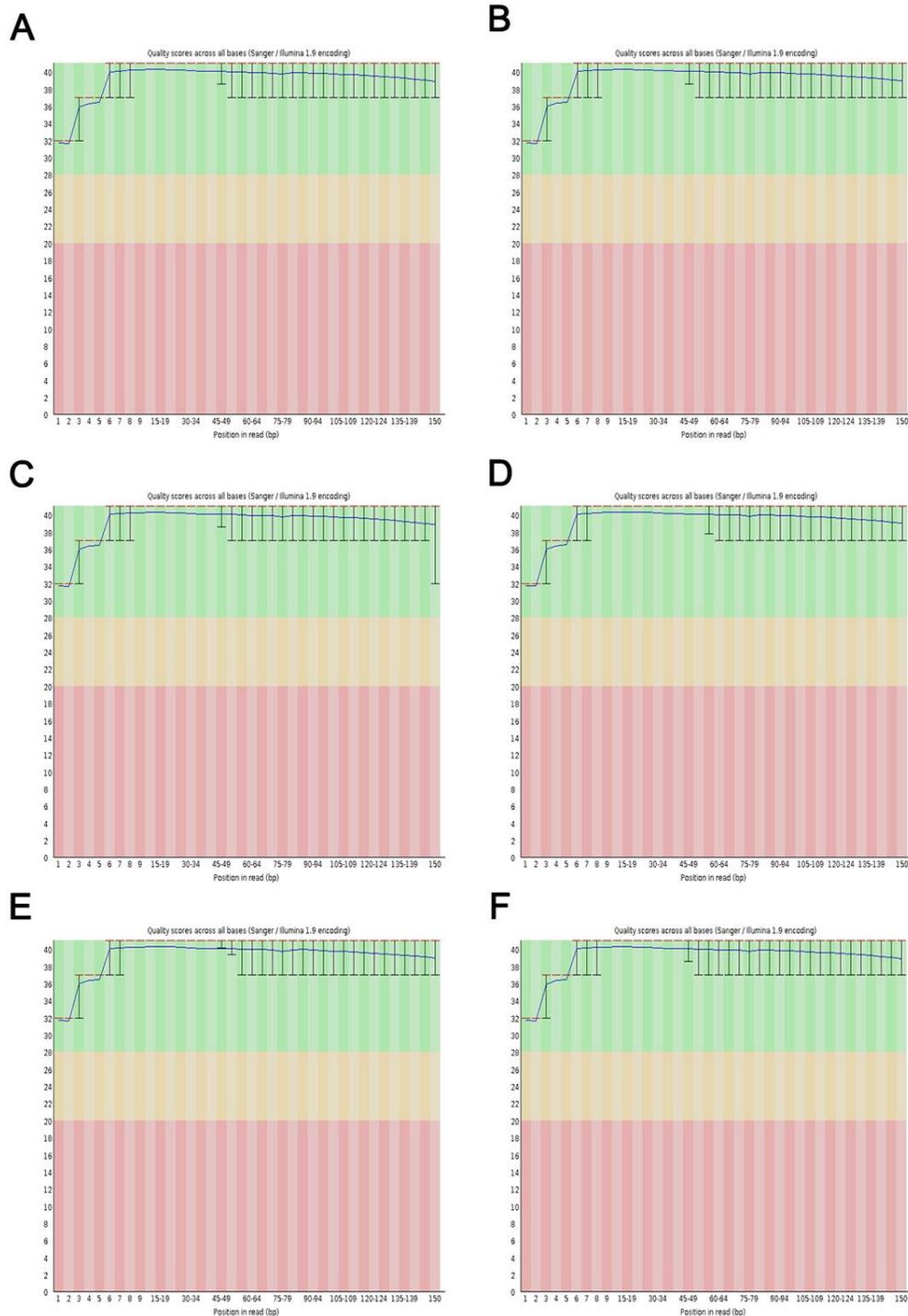
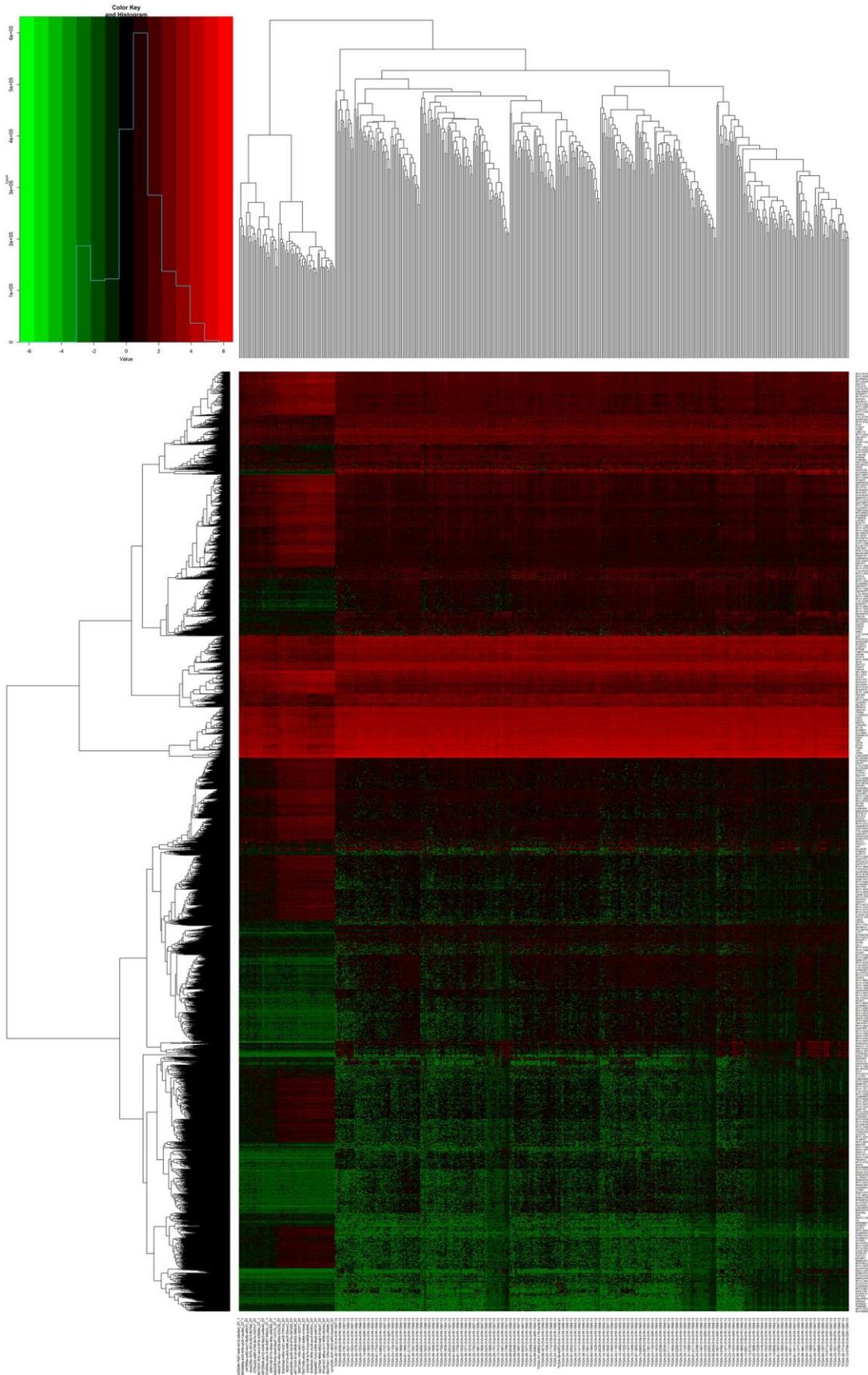


## SUPPLEMENTARY FIGURES



**Supplementary Figure 1. The BoxWhisker map shows all the base mass ranges in the FastQ sequencing file.** The Y axis shows the base mass score, and the higher the score is, the better the base sequencing quality is. The background color of the map divides the Y axis into regions with high sequencing base quality (green), qualified regions (orange) and poor-quality regions (red). (A–F) represented control group (6 kPa) 1, 2, high group (60 kPa) 1, 2 and low group (1 kPa) 1, 2, respectively.



**Supplementary Figure 2. Heatmap of TCGA EOC data.** Red corresponds to up-regulation and green to down-regulation.