Figure S1. Expression profile of the glutathione gene set was analyzed across various cancer types and their stages using publicly available transcriptomic data from The Cancer Genome Atlas database, with a focus on comparing normal tissues, early-stage tumors (pathological T1/T2) and advanced-stage tumors (pathological T3/T4). The expression of the glutathione gene set was significantly higher in normal tissues than in tumor tissues across multiple cancer types, including BRCA, LUSC, READ, STAD, HNSC and KICH, when compared with both pathological T1/T2 and pathological T3/T4 stages. However, in KIRP, this elevated expression in normal tissues was only significant when compared with pathological T1/T2 stage tumors. However, no significant differences were observed in other cancer types (Kruskal-Wallis test followed by Dunn's test; ns, not significant; $^{**}P<0.01$, $^{***}P<0.001$, $^{****}P<0.0001$). BRCA, breast invasive carcinoma; LUSC, lung squamous cell carcinoma; READ, rectal adenocarcinoma; STAD, stomach adenocarcinoma; HNSC, head and neck squamous cell carcinoma; KICH, kidney chromophobe; KIRP, kidney renal papillary cell carcinoma; CESC, cervical squamous cell carcinoma and endocervical adenocarcinoma; ESCA, esophageal carcinoma; CHOL, cholangiocarcinoma; LIHC, liver hepatocellular carcinoma; PAAD, pancreatic adenocarcinoma; THCA, thyroid carcinoma; FPKM, fragments per kilobase of exon model per million mapped fragments.

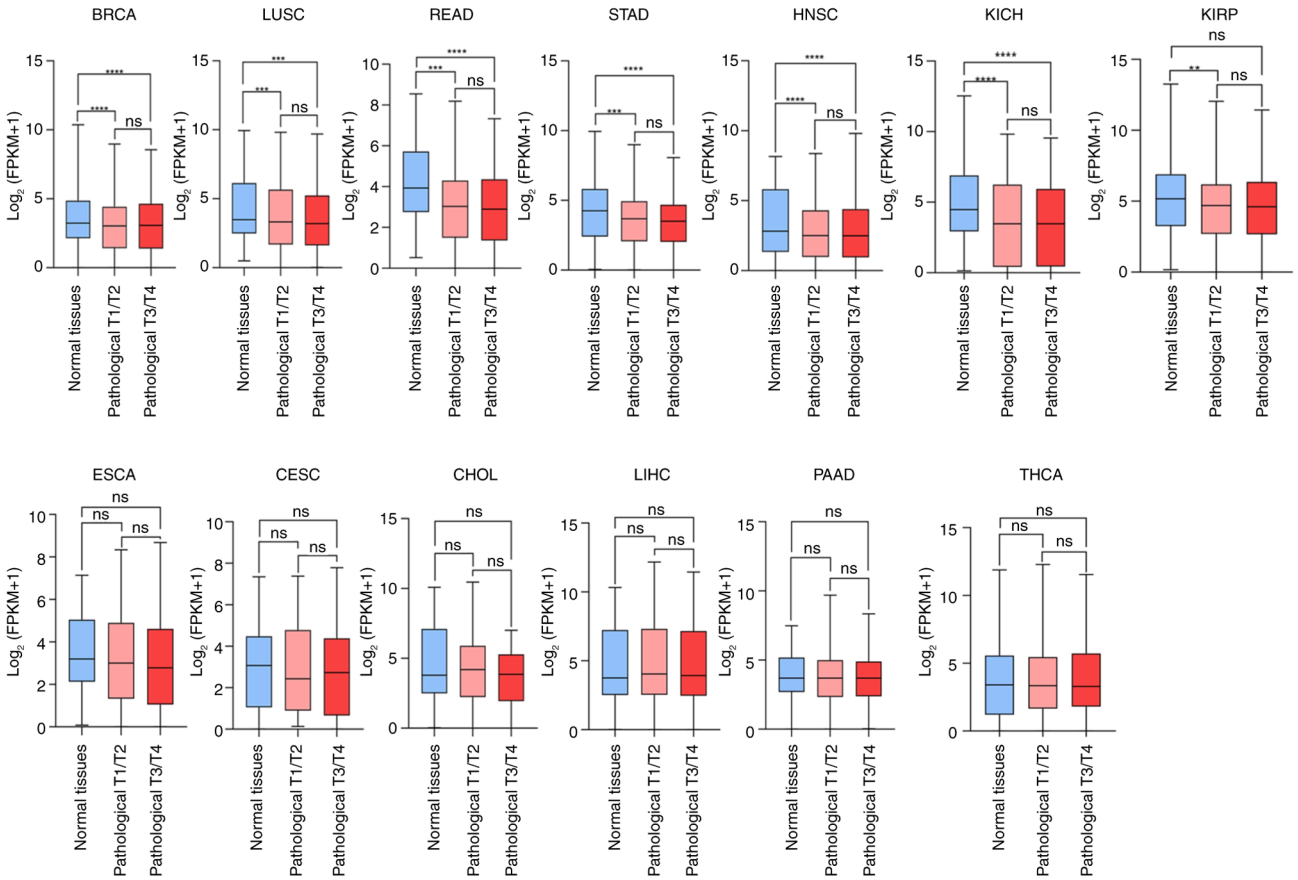

Figure S2. Enrichment differences of the glutathione gene set between high and low expression samples in 14 pathways within The Cancer Genome Atlas-Colon Adenocarcinoma dataset show distinct patterns. In the EGFR, estrogen, p53 and Trail pathways, the enrichment of the high expression samples was significantly higher than that of the low expression samples. Conversely, in the PI3K and VEGF pathways, the opposite trend was observed, with low expression samples exhibiting higher enrichment. No significant differences were detected in the remaining pathways. (two-tailed unpaired t-test; *P<0.05, **P<0.01, ***P<0.001, ****P<0.0001). ns, not significant.