Figure S1. Transcriptome analysis identifies DEGs and enriched pathways in hepatocellular carcinoma. (A) Volcano plot of DEGs between control and drug-treated HCC cells, showing 324 upregulated (red) and 869 downregulated (blue) genes. (B) Gene expression heatmap comparing transcriptional profiles of the control and drug-treated groups. (C) KEGG pathway enrichment analysis of upregulated DEGs, highlighting top pathways such as 'Cytoskeleton in muscle cells' and 'Pathways in cancer'. (D) GO term enrichment analysis of upregulated DEGs, showing enriched biological processes such as 'Collagen-containing extracellular matrix' and 'Endothelium development'. (E) KEGG pathway enrichment analysis of downregulated DEGs, featuring major pathways such as 'Metabolic pathways' and 'Retinol metabolism'. (F) GO term enrichment analysis of downregulated DEGs, encompassing key biological processes such as 'Small molecule catabolic process' and 'Fatty acid metabolic process'. DEGs, differentially expressed genes; KEGG, Kyoto Encyclopedia of Genes and Genomes; GO, Gene Ontology.

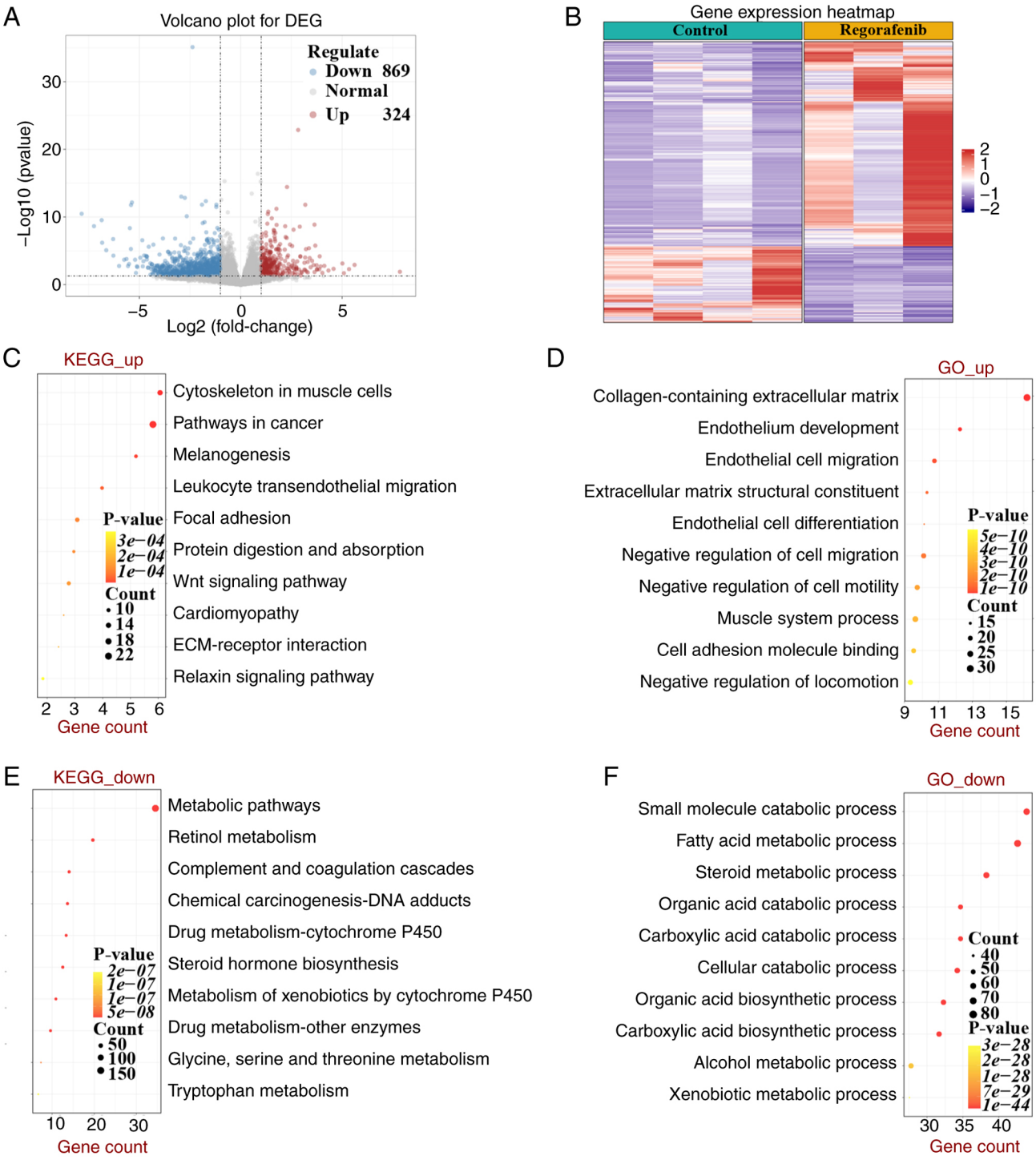

Figure S2. Original uncropped western blot images corresponding to Fig. 2. This figure presents the original, uncropped western blot images for all target proteins and their paired internal reference proteins (GAPDH or TUBULIN) analyzed in Fig. 2. Groups (left to right): Control, Regorafenib, Nifuroxazide, Regorafenib + Nifuroxazide. Although the strips were cropped for concise presentation in Fig. 2, each target protein and its paired internal reference strip originate from the same initial intact membrane, ensuring consistent loading across detections. The molecular weights (kDa) of each protein are labeled on the right side of the corresponding blot.

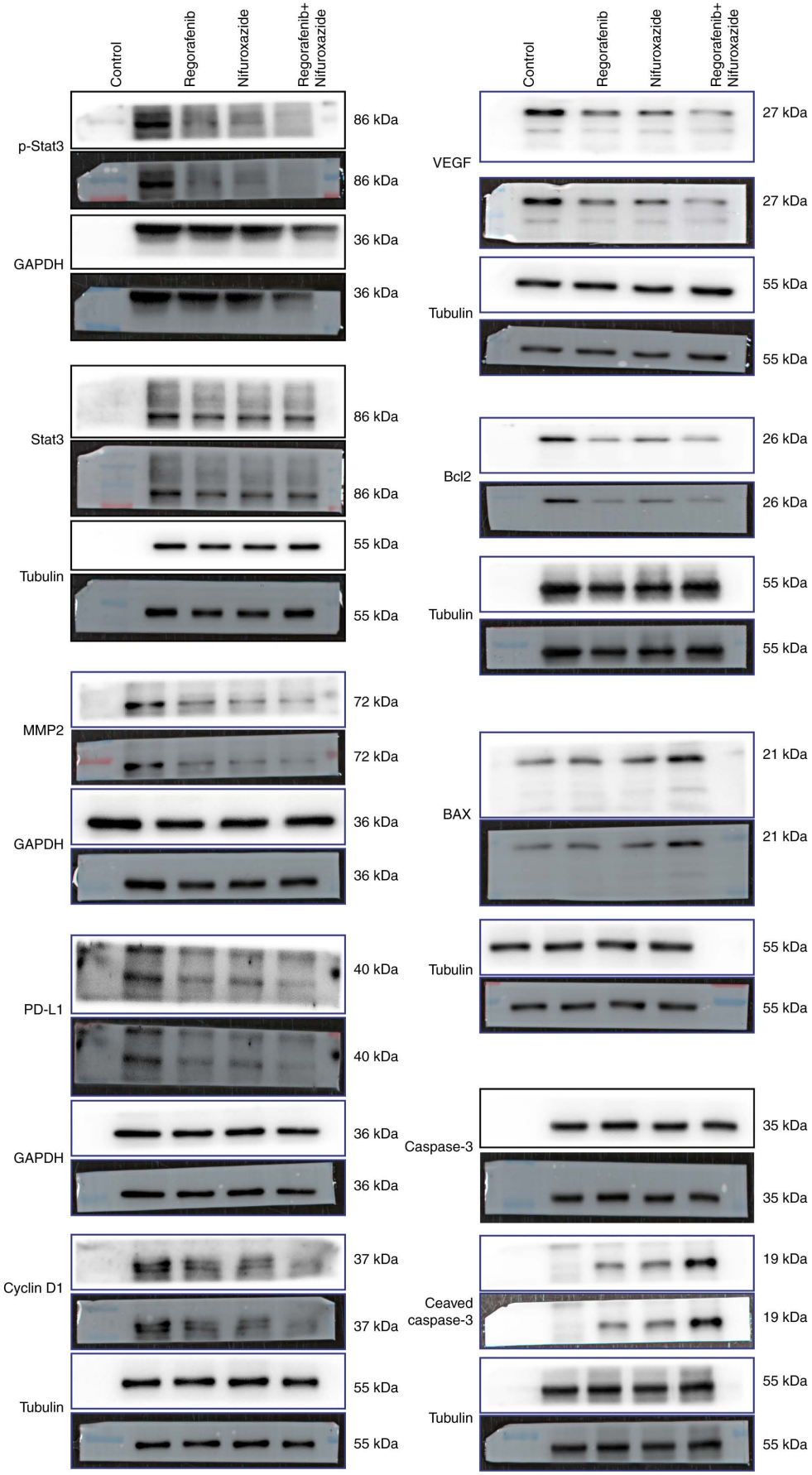

Figure S3. Expression of JAK2/SHP-1 pathway-related proteins in cells and tumor tissues. (A) Western blotting results of p-JAK2, total JAK2 and internal reference Tubulin in HepG2 cells. (B) Quantitative analysis of p-JAK2 expression (normalized to total JAK2). (C) Western blotting results of SHP-1 and internal reference GAPDH in HepG2 cells. (D) Quantitative analysis of SHP-1 expression. (E) Western blotting results of p-JAK2, total JAK2 and internal reference Tubulin in tumor tissues. (F) Quantitative analysis of p-JAK2 expression (normalized to total JAK2). (G) Western blotting results of SHP-1 and internal reference GAPDH in tumor tissues. (H) Quantitative analysis of SHP-1 expression. Data are presented as mean ± standard deviation (n=3). *P<0.05 vs. the Control group; #P<0.05 vs. the Regorafenib group; $P<0.05 vs. the Nifuroxazide group. JAK2, Janus kinase 2; SHP-1, Src homology region 2 domain-containing phosphatase 1; p-, phosphorylated.

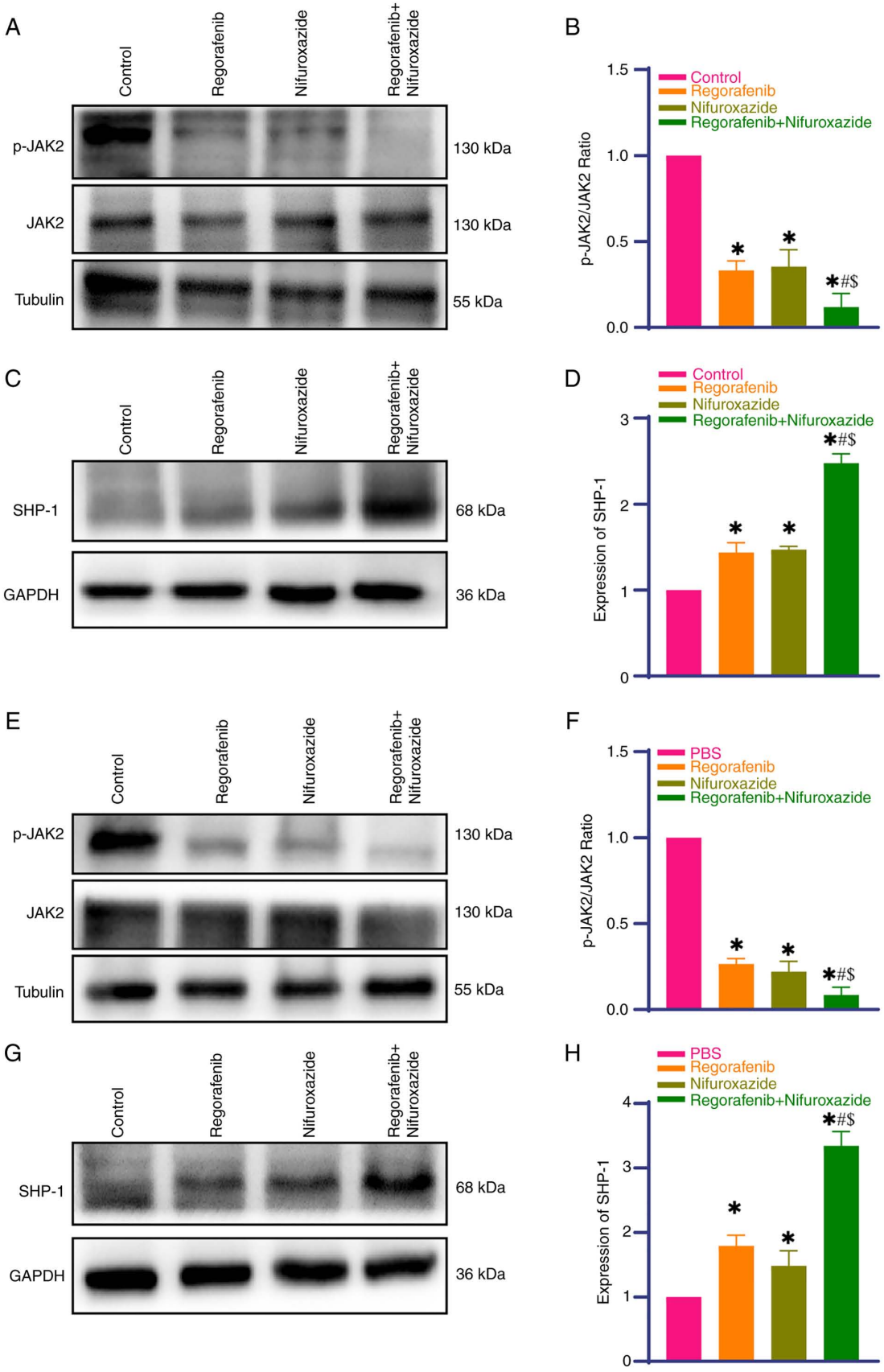

Figure S4. Original uncropped Western blot images corresponding to Fig. 4. This figure presents the original, uncropped Western blot images for all target proteins and their paired internal reference proteins (GAPDH or Tubulin) analyzed in Fig. 4. Groups (left to right): Control, Regorafenib, Nifuroxazide, Regorafenib + Nifuroxazide. Although the strips were cropped for concise presentation in Fig. 4, each target protein and its paired internal reference strip originate from the same initial intact membrane, ensuring consistent loading across detections. The molecular weights (kDa) of each protein are labeled on the right side of the corresponding blot.