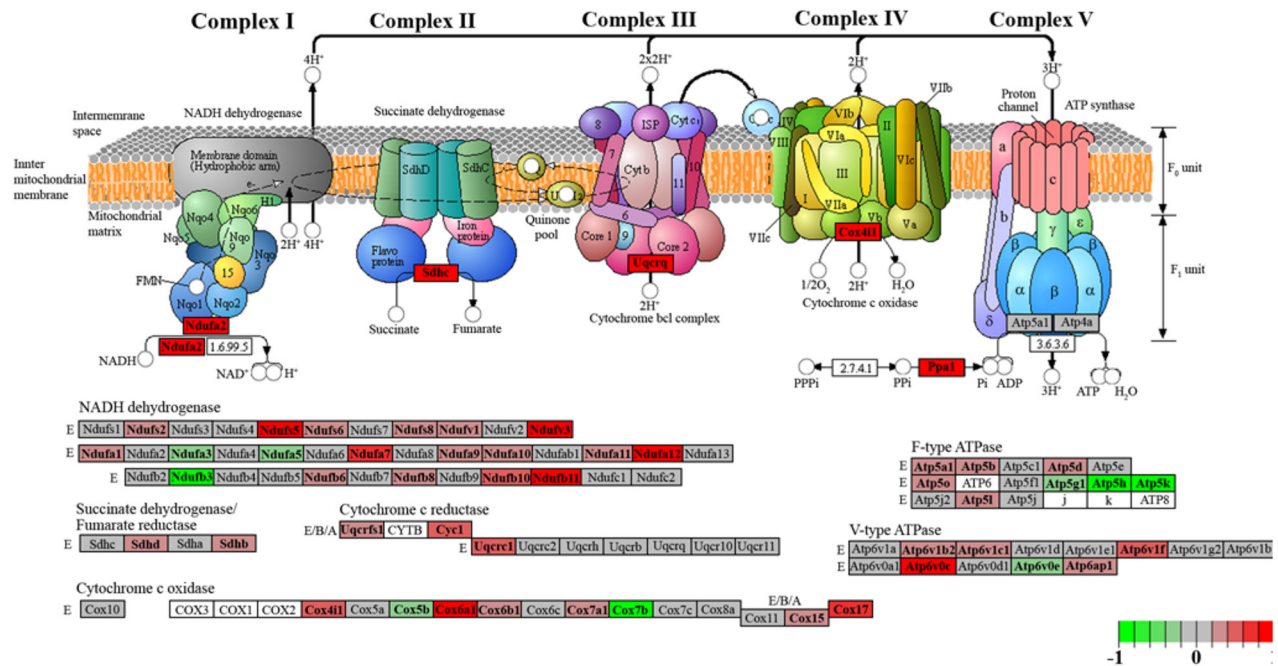


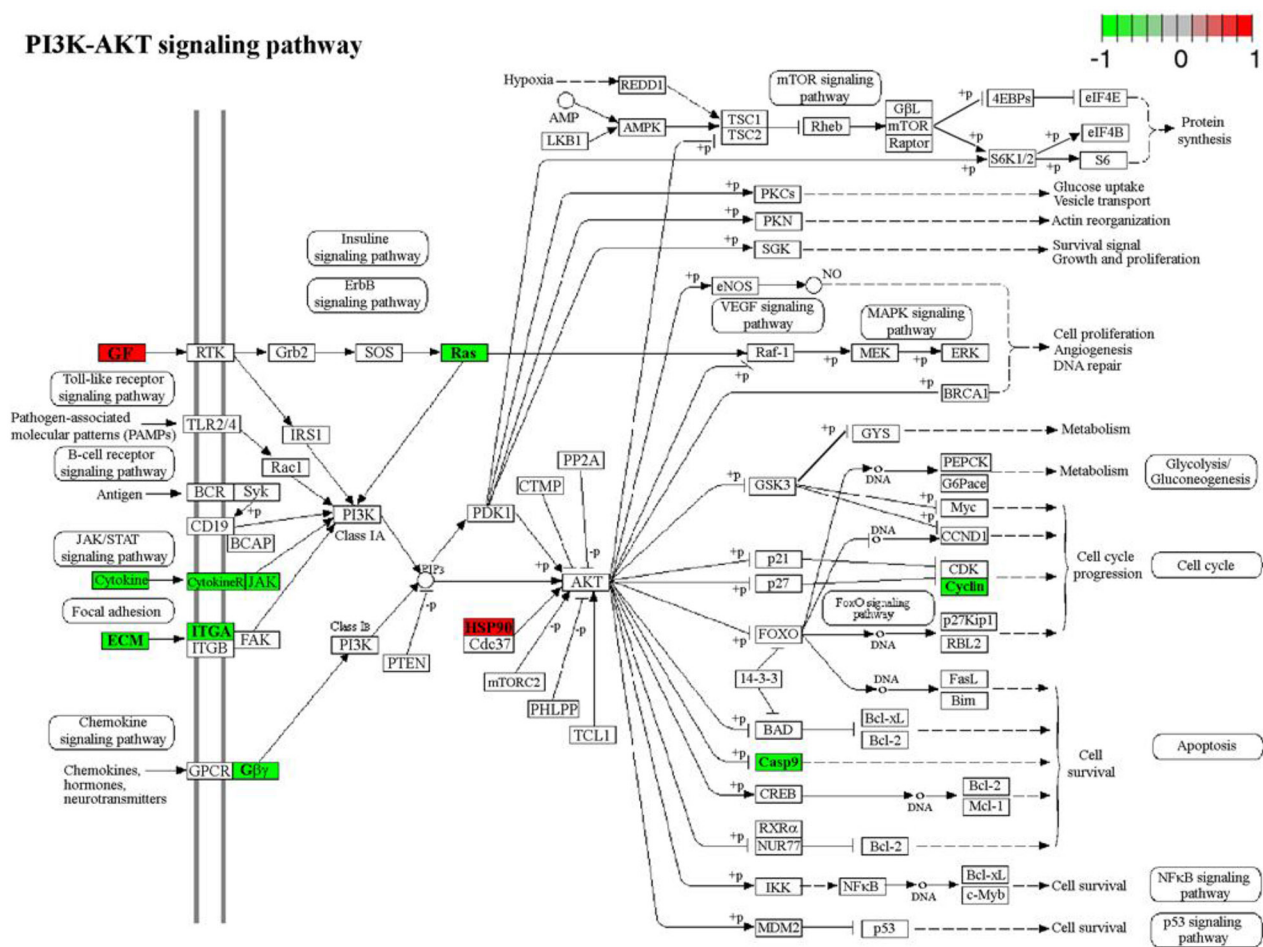
The systemic tumor response to RNase A treatment affects the expression of genes involved in maintaining cell malignancy

SUPPLEMENTARY MATERIALS



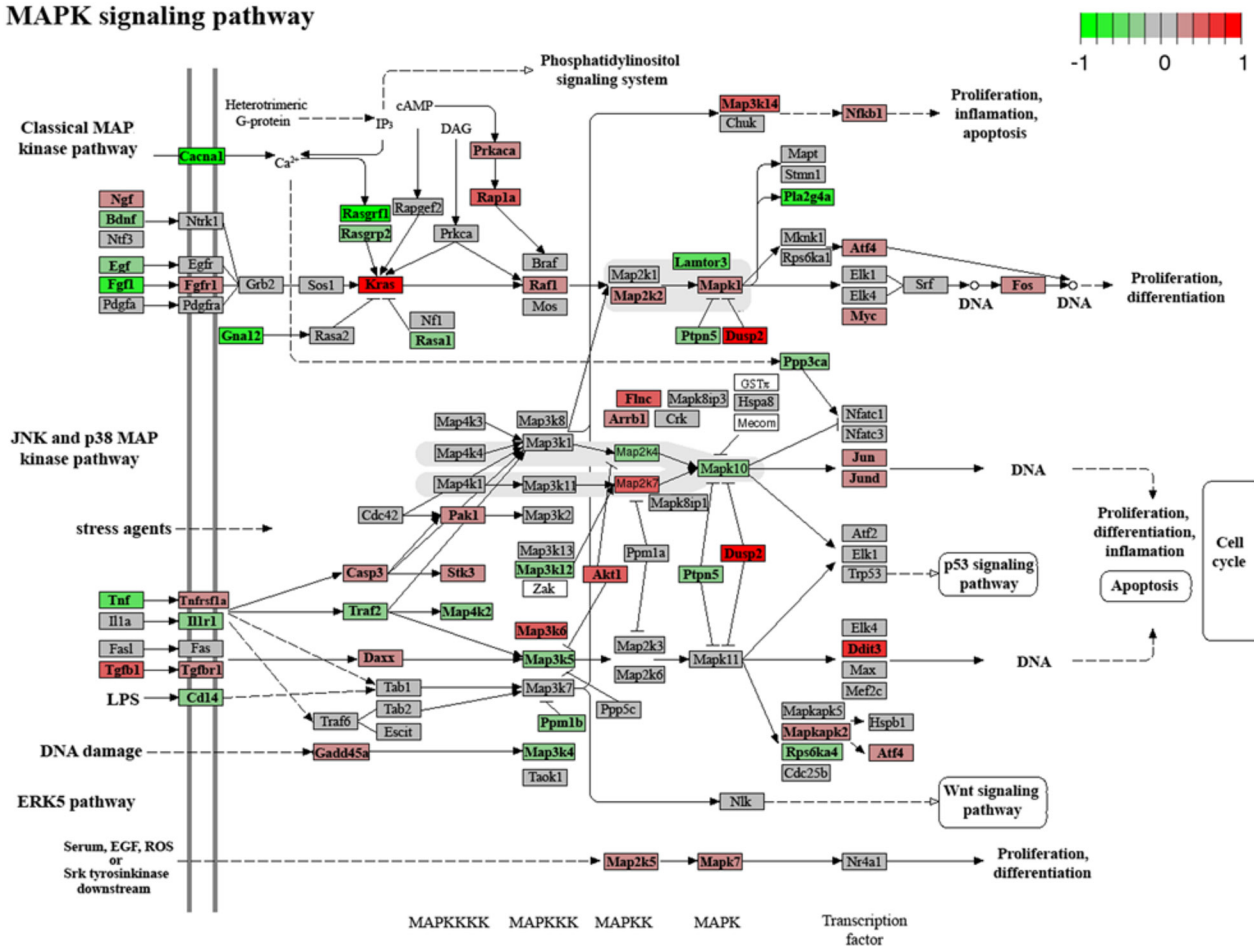
Supplementary Figure 1: Genes and components involved in oxidative phosphorylation.

PI3K-AKT signaling pathway

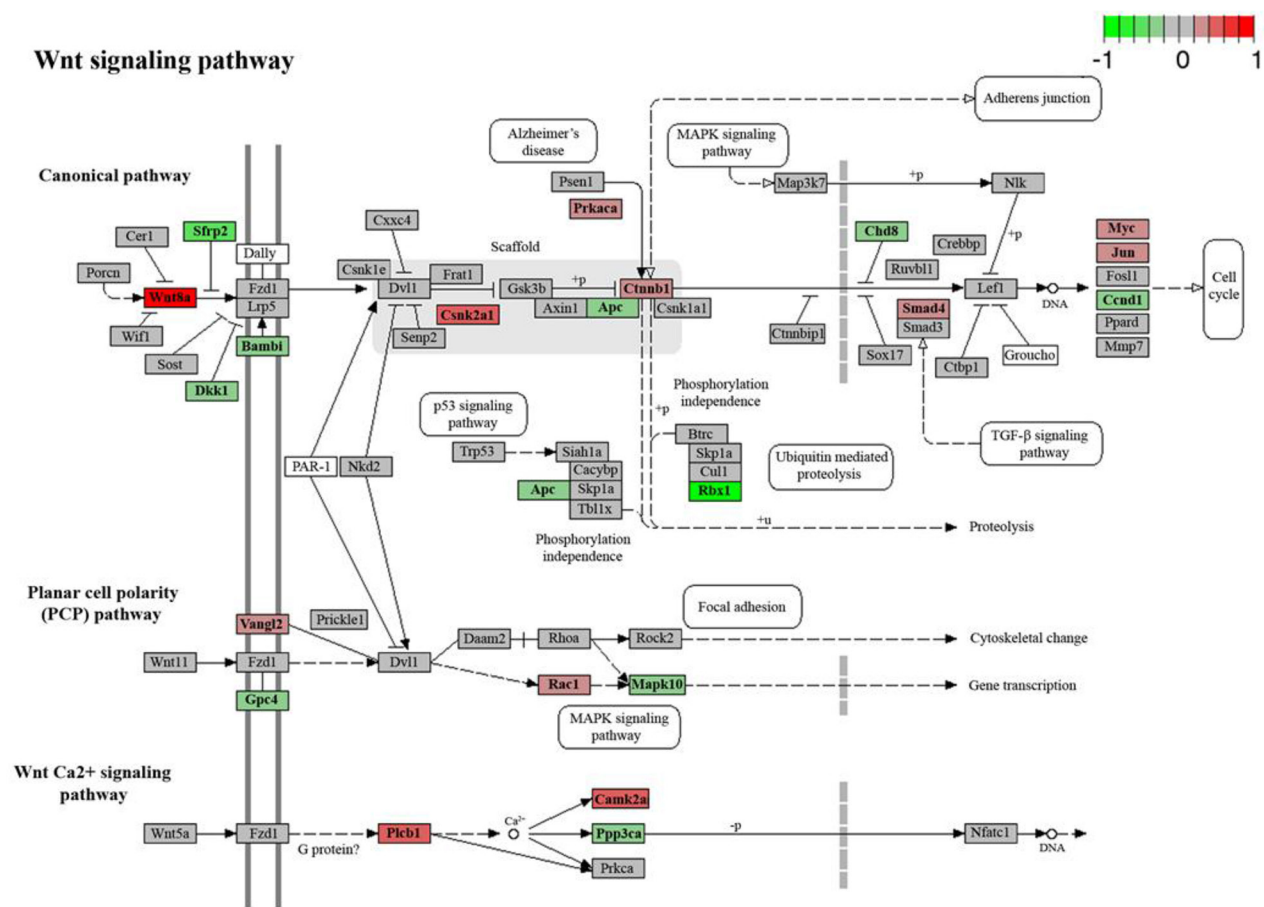


Supplementary Figure 2: Genes involved in the PI3K-AKT signaling pathway.

MAPK signaling pathway

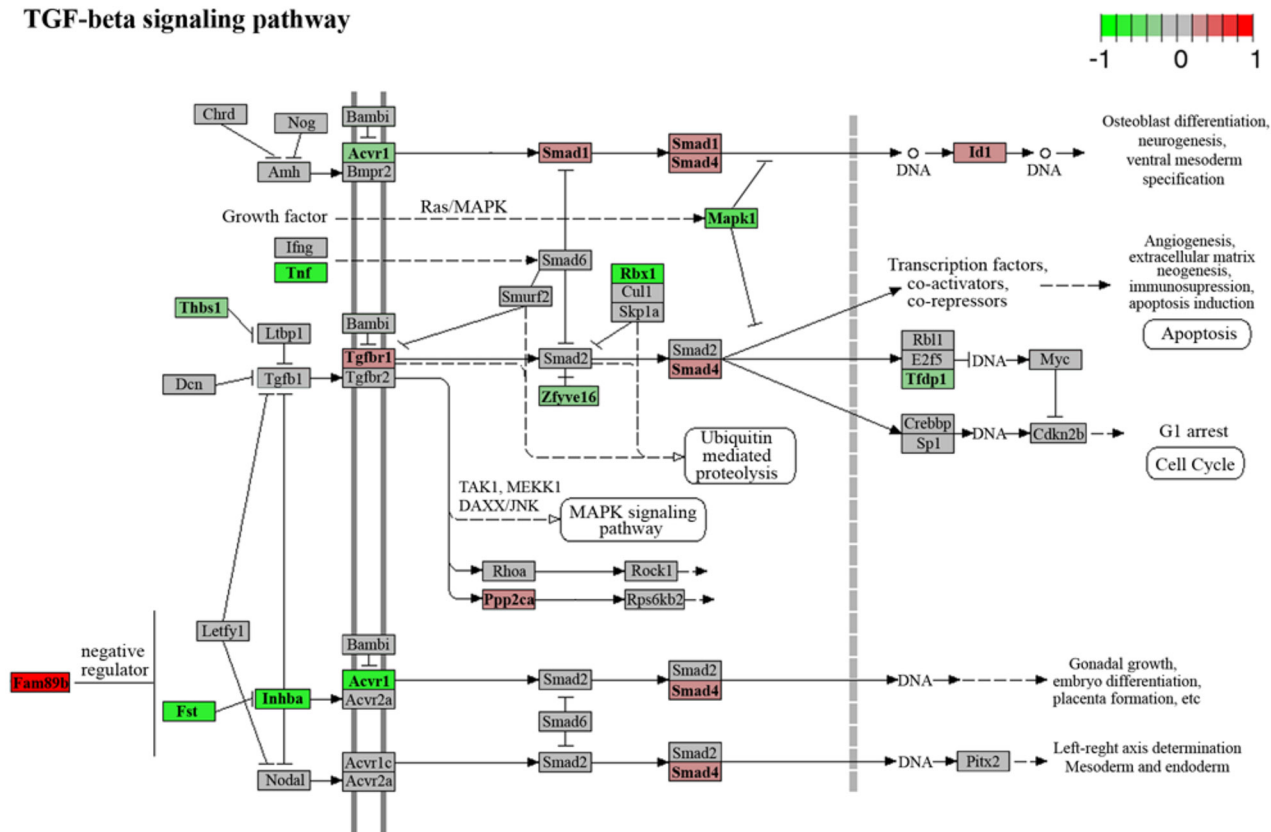


Supplementary Figure 3: Genes involved in the MAPK signaling pathway.



Supplementary Figure 4: Genes involved in the Wnt signaling pathway.

TGF-beta signaling pathway



Supplementary Figure 5: Genes involved in the TGF-β signaling pathway.

Supplementary Table 1: Up-regulated genes in tumor of mice with LLC after RNase A treatment (L_U)

See Supplementary File 1

Supplementary Table 2: Down-regulated genes in tumor of mice with LLC after RNase A treatment (sorted by Value L_D)

See Supplementary File 2

Supplementary Table 3: Upregulated transcription-related genes in tumor of mice with LLC after RNase A treatment (sorted by Value L_R)

See Supplementary File 3

Supplementary Table 4: Down-regulated transcription-related genes in tumor of mice with LLC after RNase A treatment (sorted by Value L_D)

See Supplementary File 4