

Figure S1. NCOA4-related genes hallmark enrichment pathway of COAD in the

TCGA database.

The relationship between NCOA4-related genes and traditional pathways, including Tumor_Inflammation_Signature, Cellular_response_to_hypoxia, Tumor_proliferation_signature, EMT_markers, ECM-related_genes, Angiogenesis, Apoptosis, DNA_repair, G2M_checkpoint, Inflammatory_response, PI3K_AKT_mTOR_pathway, P53_pathway, MYC_targets, TGFB, IL-10_Anti-inflammatory_Signaling_Pathway, Genes_up-regulated_by_reactive_oxygen_species_(ROS), DNA_replication, Collagen_formation, Degradation_of_ECM. The r range from -1 to 1, where $|r| \geq 0.7$ signifies a high positive correlation, $0.5 \leq |r| < 0.7$ is a moderate positive correlation, $0.3 \leq |r| < 0.5$ is a low positive correlation, and $|r| < 0.3$ is a negligible correlation.

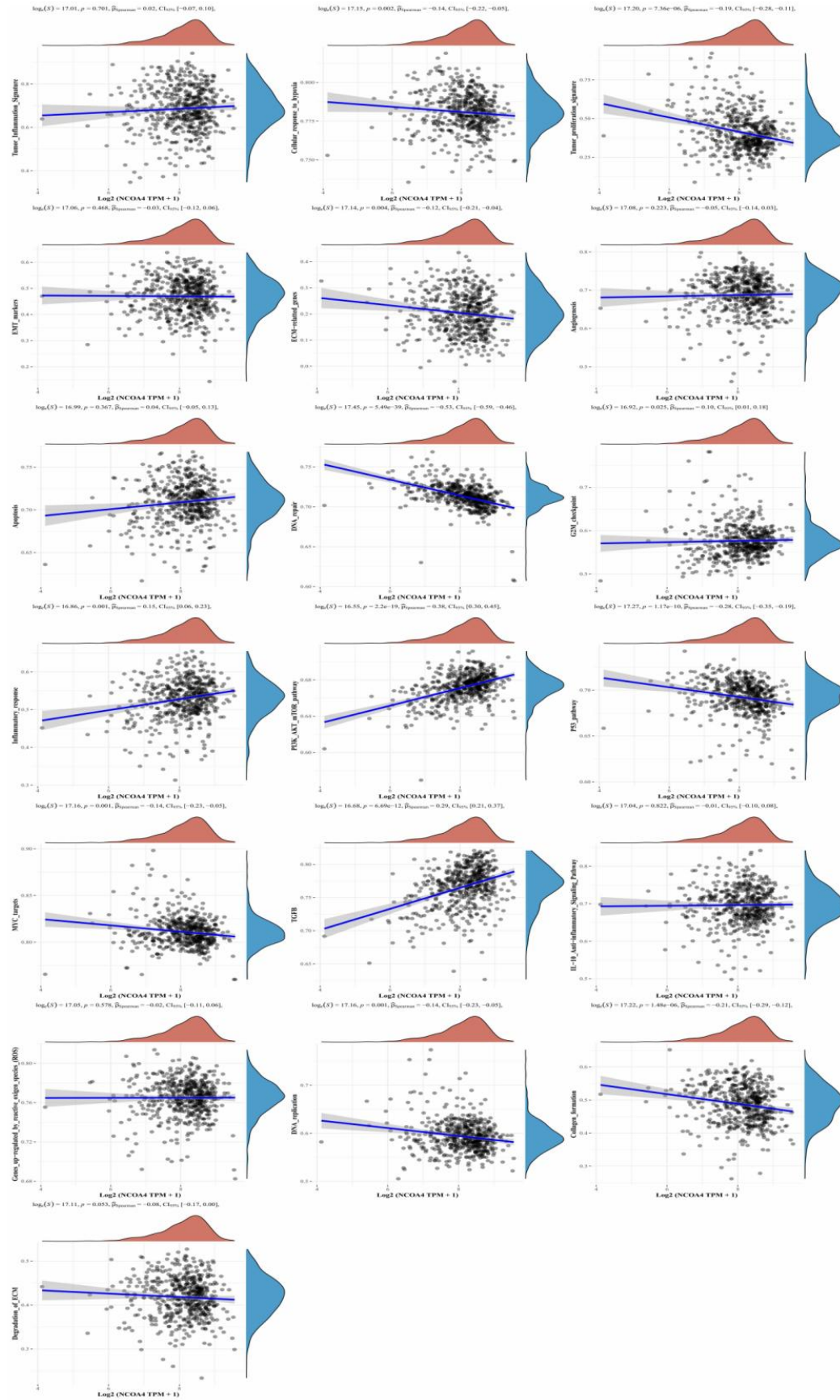


Figure S2. NCOA4-related genes hallmark enrichment pathway of KIRC in the

TCGA database.

Tumor_Inflammation_Signature, Cellular_response_to_hypoxia,
Tumor_proliferation_signature, EMT_markers, ECM-related_genes, Angiogenesis,
Apoptosis, DNA_repair, G2M_checkpoint, Inflammatory_response,
PI3K_AKT_mTOR_pathway, P53_pathway, MYC_targets, TGFB,
IL-10_Anti-inflammatory_Signaling_Pathway,
Genes_up-regulated_by_reactive_oxygen_species_(ROS), DNA_replication,
Collagen_formation, Degradation_of_ECM. The r range from -1 to 1, where $|r| \geq 0.7$
signifies a high positive correlation, $0.5 \leq |r| < 0.7$ is a moderate positive correlation,
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