

GSEA enrichment of Cox-PH associated cancer pathways

List of significantly enriched pathways (p < 0.05)

Pathway	E.score	P.value	P.adjusted
KEGG cell cycle	-0.407	0.000	0.003
KEGG citrate cycle tca cycle	0.607	0.000	0.003
KEGG fatty acid metabolism	0.561	0.000	0.003
KEGG lysosome	0.410	0.000	0.003
KEGG oxidative phosphorylation	0.418	0.000	0.003
KEGG proximal tubule bicarbonate reclamation	0.633	0.000	0.003
KEGG valine leucine and isoleucine degradation	0.577	0.000	0.003
KEGG olfactory transduction	0.294	0.000	0.005
KEGG cytokine cytokine receptor interaction	-0.330	0.000	0.005
KEGG proteasome	-0.540	0.000	0.005
KEGG vascular smooth muscle contraction	0.391	0.000	0.005
KEGG peroxisome	0.415	0.000	0.006
KEGG tight junction	0.343	0.000	0.006
KEGG propanoate metabolism	0.518	0.001	0.009
KEGG ppar signaling pathway	0.406	0.001	0.011
KEGG renin angiotensin system	0.645	0.001	0.011
KEGG systemic lupus erythematosus	-0.377	0.001	0.014
KEGG prostate cancer	0.368	0.002	0.016
KEGG pathogenic escherichia coli infection	-0.433	0.003	0.034
KEGG endometrial cancer	0.409	0.004	0.040
KEGG butanoate metabolism	0.458	0.005	0.042
KEGG epithelial cell signaling in helicobacter pylori infection	0.361	0.006	0.047
KEGG nod like receptor signaling pathway	-0.407	0.006	0.047
KEGG beta alanine metabolism	0.521	0.006	0.047
KEGG complement and coagulation cascades	-0.393	0.007	0.047

Pathway	E.score	P.value	P.adjusted
KEGG tryptophan metabolism	0.427	0.007	0.047
KEGG arginine and proline metabolism	0.381	0.007	0.047
KEGG calcium signaling pathway	0.272	0.007	0.047
KEGG spliceosome	-0.333	0.007	0.047
KEGG parkinsons disease	0.304	0.008	0.048