

Supplementary Materials: Camptothecin Induces PD-L1 and Immunomodulatory Cytokines in Colon Cancer Cells

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Table S1. Cytokines with an overall downregulation by treatment of SW620 cells with CPT. The list was sorted in decreasing order for fold expression reduced by 1 μ M CPT.

Gene	Overall Down by CPT Treatment vs Control		Major functions summary
	1 μ M	5 μ M	
XCL1	-10.9	-13.4	X-C Motif Chemokine Ligand 1; Chemotactic for T-cells; antimicrobial
C5	-4.6	-5.1	Complement component 5
IL-27	-2.9	-4.8	Interleukin 27; Potentiate TH1 response; suppress pro-inflammatory cytokines IL2, IL4, IL5, IL6; Inhibit TH17 activity and IL17 production
VEGFA	-2.0	-3.4	Vascular Endothelial Growth Factor A; Endothelial cell mitogen; Induces endothelial cell migration, and angiogenesis; Increase permeability
FASLG	-1.9	-3.0	Fas Ligand; T-cell apoptosis
HPRT1	-1.5	-2.4	Hypoxanthine Phosphoribosyltransferase 1; Purine nucleotide synthesis

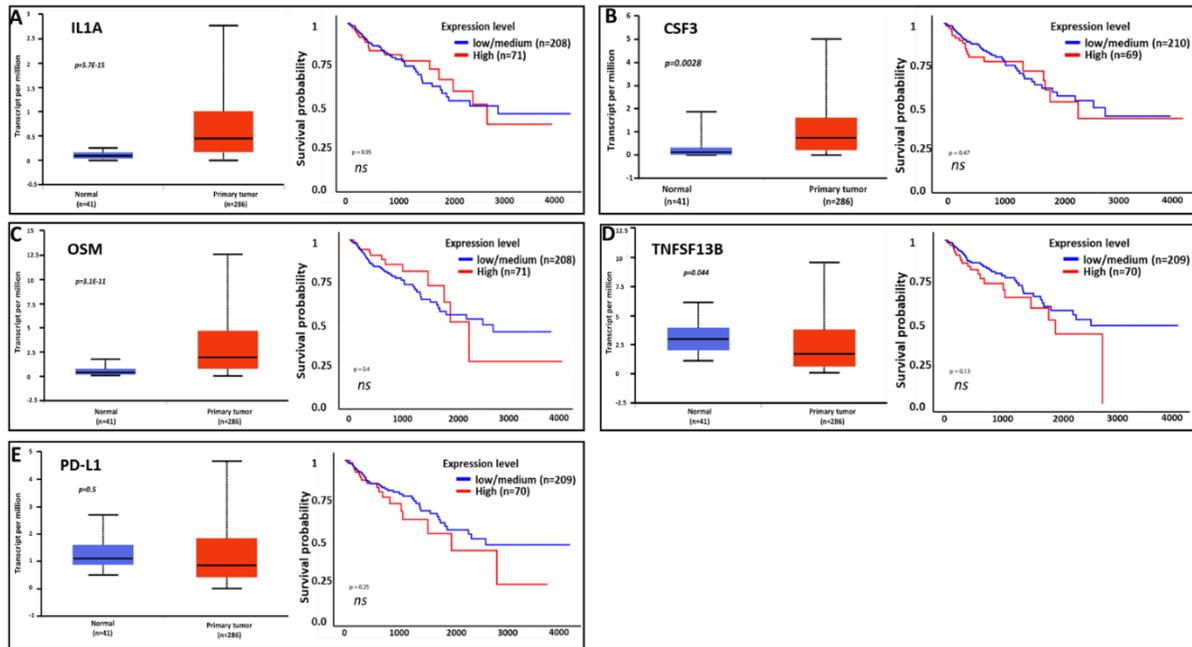


Figure S1. Expression profiles and patient survival probabilities for additional CPT-responsive cytokine genes. The TCGA database was probed for clinical significance by using the UALCAN portal. Graphs (A–E) for 5 additional genes, IL-1A, CSF3, OSM, TNFSF13B, and PD-L1, respectively, with their corresponding significance values in expression and/or survival probability are shown. Bar graphs show comparison of gene expression between normal and primary tumor, whereas the line graphs show effect of gene expression level on COAD patient survival. *n* is the sample size. *ns* = not significant. Note that, in the COAD dataset, PD-L1 expression is not significantly different between normal and primary tumors, nor are its expression levels associated with patient survival.

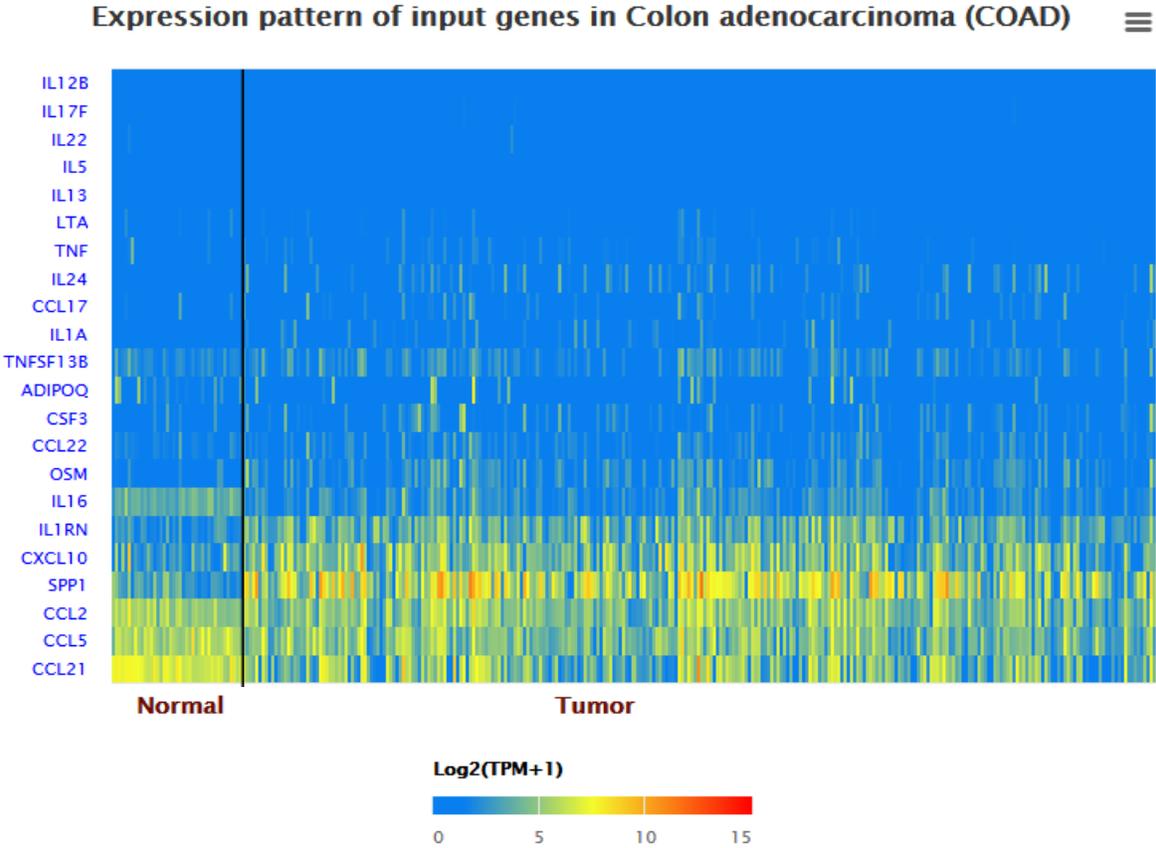


Figure S2. Expression profile heat map for 22 CPT-responsive cytokine genes identified using the TCGA COAD dataset showing differential expression between normal and tumor tissues of a number of CPT-responsive genes.