

METHODS AND RESULTS

Sensitivity analysis of microarray data

We performed 36 independent microarray experiments on PBLs of 18 subjects at baseline and following exposure to CPAP. Subject-specific gene expression changes in response to treatment were modest, with no single gene reaching statistical significance. We performed paired analysis (baseline vs. CPAP) for each subject using significance analysis of microarrays algorithm (SAM, paired option,  $n = 1,000$  random permutations) and adjusted for multiple hypothesis testing using false discovery rate analysis (FDR < 5%).<sup>1,2</sup> SAM performs a random permutation analysis between the subjects' expression profiles to determine a null distribution that is then used for FDR determination. We performed sensitivity analyses to assess whether gender, race, baseline BMI or baseline AHI contributed to global changes in gene expression following CPAP therapy (Table S1). For each analysis, the subjects were segregated into two groups based on categorical groupings (gender, race) or based on a median split for continuous variables (BMI, AHI). The BMI and AHI measured at the pre-CPAP research visit were used for this analysis. No genes reached statistical significance (at FDR < 5%) when the subjects were segregated by gender, race, BMI or AHI (Table S1).

Transcription factor analysis

The ~1,400 leading edge genes identified by GSEA included several transcription factors (TFs). Indeed, a number of the key "neoplasm" network hubs are TFs including JUN, MYC, and SMAD3 (Figure S1). However microarrays only measure gene expression, whereas many TFs are post-transcriptionally modified and/or are differentially expressed for only a short duration after stimulation. Therefore, we explored an alternative method for identifying enriched TFs as we have previously described.<sup>3,4</sup> For this approach, we leveraged the leading edge genes from our GSEA to statistically identify over-represented putative common binding site motifs of 332 mammalian TFs based on their position weight matrices. A window of 1,000 base pairs upstream and 200 base pairs downstream of each gene's transcription start site was searched for TF binding sites. We chose a Bonferroni-corrected P-value < 0.05 to designate significant enrichment for a given TF. We identified 7 TFs that were overrepresented among the leading edge genes identified by GSEA (Table S2). Most of these TFs were not leading edge genes themselves, which is not surprising given the fact that most TFs are regulated through post-translational modification.

**Table S1**—Impact of baseline characteristics on the gene expression response to CPAP.

Covariate	Group 1	Group 2	Significant Genes
Gender	Male (n = 9)	Female (n = 9)	0
Race	African-American (n = 11)	Caucasian (n = 7)	0
BMI (kg/m <sup>2</sup> )	< 39 (n = 9)	> 39 (n = 9)	0
AHI (events/h)	< 40 (n = 9)	> 40 (n = 9)	0

BMI, body mass index; AHI, apnea hypopnea index.

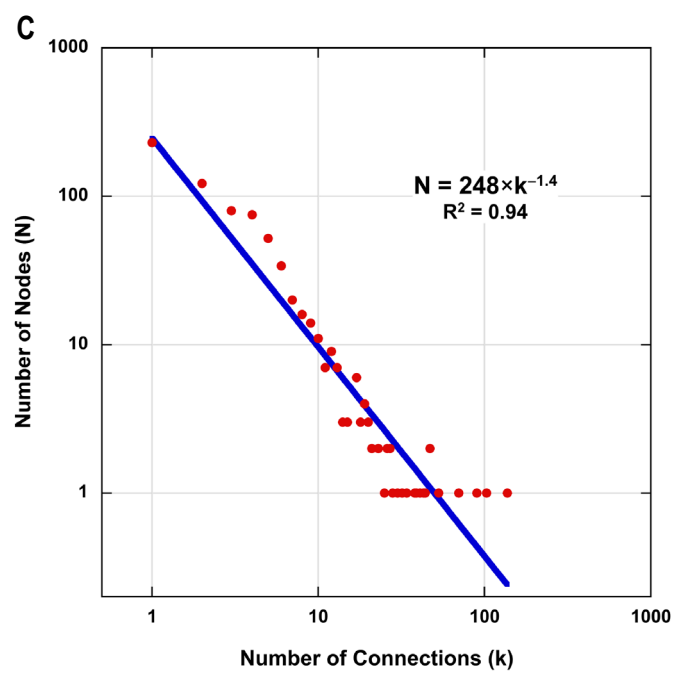
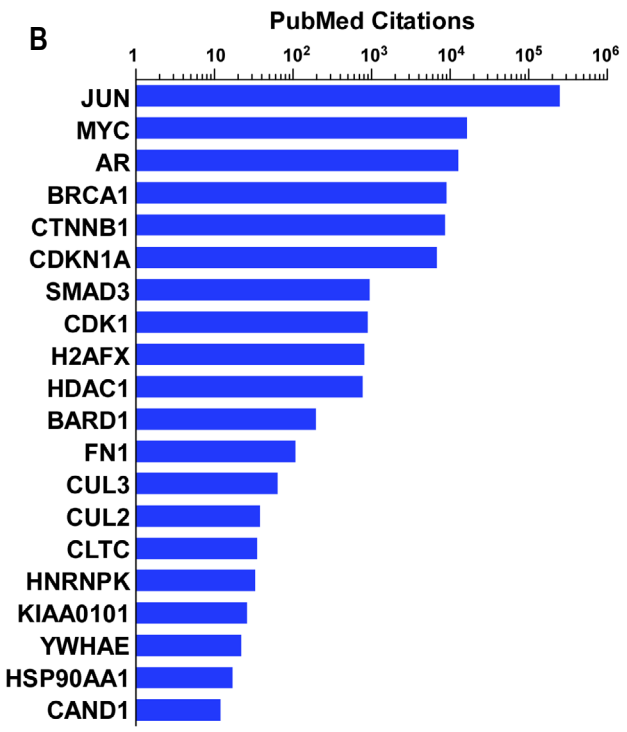
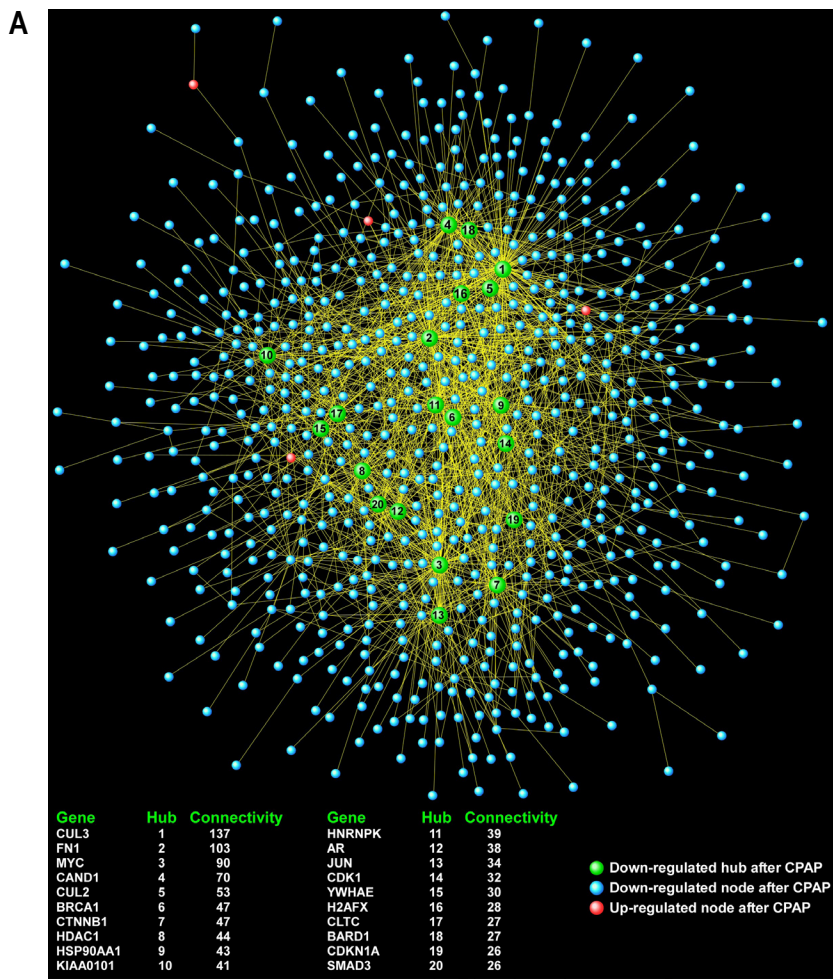
**Table S2**—Putative over-represented TFs among CPAP-responsive leading edge genes.

Transcription Factor	Number of regulated genes	Adjusted P-value
E2F	781	3.86 × 10 <sup>-9</sup>
ETF	558	4.41 × 10 <sup>-6</sup>
NF-Y	332	5.47 × 10 <sup>-5</sup>
Nrf-1	405	1.00 × 10 <sup>-3</sup>
FOXJ2	182	3.00 × 10 <sup>-3</sup>
ZF5	233	2.30 × 10 <sup>-2</sup>
Pax-4	115	4.90 × 10 <sup>-2</sup>

However, one of the TFs, ETF, was a leading edge member. Several of the most enriched TFs have well-established roles in cancer biology, including E2F<sup>5</sup> and NF-Y.<sup>6</sup>

REFERENCES

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**Figure S1—(A)** Gene product interaction network of pathways mapping to neoplastic processes. This interactome was highlighted by a number of densely connected hubs (green, labeled 1-20). Note that the majority of the nodes had reduced expression after CPAP therapy (blue and green). **(B)** PubMed citation index of publications reporting the association of each network hub with the modifier term “cancer”. **(C)** Scale-free property of the neoplasm network is based on a power law relationship between nodal frequency distribution and connectivity.

**Table S3**—List of enriched gene sets (FDR < 0.05). Gene sets are hyperlinked for expanded details

Gene Set	Number of Genes	P-value	FDR	Gene Set	Number of Genes	P-value	FDR
<a href="#">RAGHAVACHARI_PLATELET_SPECIFIC_GENES</a>	69	> 0.001	> 0.001	<a href="#">GRAHAM_CML_QUIESCENT_VS_NORMAL_QUIESCENT_UP</a>	84	> 0.001	0.024
<a href="#">HAHTOLA_SEZARY_SYNDROM_DN</a>	39	> 0.001	> 0.001	<a href="#">PYEON_HPV_POSITIVE_TUMORS_UP</a>	90	> 0.001	0.03
<a href="#">PUJANA_XPRSS_INT_NETWORK</a>	167	> 0.001	0.001	<a href="#">BIOCARTA_CTCF_PATHWAY</a>	23	0.001	0.03
<a href="#">CHAN_INTERFERON_PRODUCING_DENDRITIC_CELL</a>	12	> 0.001	0.002	<a href="#">SHEN_SMARCA2_TARGETS_UP</a>	417	> 0.001	0.03
<a href="#">PUJANA_BRCA_CENTERED_NETWORK</a>	117	> 0.001	0.003	<a href="#">CHOW_RASSF1_TARGETS_UP</a>	27	0.001	0.03
<a href="#">REACTOME_RNA_POL_I_PROMOTER_OPENING</a>	54	> 0.001	0.004	<a href="#">GENTLES_LEUKEMIC_STEM_CELL_DN</a>	19	0.001	0.03
<a href="#">BIOCARTA_TOB1_PATHWAY</a>	20	> 0.001	0.006	<a href="#">BIOCARTA_PTC1_PATHWAY</a>	11	0.001	0.03
<a href="#">SCIBETTA_KDM5B_TARGETS_DN</a>	78	> 0.001	0.01	<a href="#">BIOCARTA_EDG1_PATHWAY</a>	27	> 0.001	0.03
<a href="#">ZHENG_FOXP3_TARGETS_IN_THYMUS_UP</a>	192	> 0.001	0.011	<a href="#">REACTOME_RNA_POL_I_TRANSCRIPTION</a>	76	> 0.001	0.03
<a href="#">TANG_SENESCENCE_TP53_TARGETS_DN</a>	56	> 0.001	0.013	<a href="#">BIOCARTA_STATHMIN_PATHWAY</a>	19	0.002	0.032
<a href="#">NELSON_RESPONSE_TO_ANDROGEN_DN</a>	19	> 0.001	0.013	<a href="#">REICHERT_MITOSIS_LIN9_TARGETS</a>	28	0.002	0.033
<a href="#">PUJANA_BRCA2_PCC_NETWORK</a>	416	> 0.001	0.012	<a href="#">GABRIELY_MIR21_TARGETS</a>	285	> 0.001	0.032
<a href="#">LY_AGING_OLD_DN</a>	56	> 0.001	0.013	<a href="#">REACTOME_MEIOSIS</a>	104	> 0.001	0.032
<a href="#">ZHANG_TLX_TARGETS_36HR_DN</a>	184	> 0.001	0.012	<a href="#">GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_DN</a>	84	> 0.001	0.032
<a href="#">ZHANG_BREAST_CANCER_PROGENITORS_UP</a>	417	> 0.001	0.012	<a href="#">REACTOME_CYCLIN_A_B1_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION</a>	15	0.002	0.032
<a href="#">REACTOME_MEIOTIC_SYNOPSIS</a>	67	> 0.001	0.015	<a href="#">REACTOME_MEIOTIC_RECOMBINATION</a>	77	> 0.001	0.033
<a href="#">REACTOME_PACKAGING_OF_TELOMERE_ENDS</a>	45	> 0.001	0.015	<a href="#">BIOCARTA_DREAM_PATHWAY</a>	14	0.003	0.033
<a href="#">GRABARCZYK_BCL11B_TARGETS_UP</a>	76	> 0.001	0.015	<a href="#">MISSIAGLIA_REGULATED_BY_METHYLATION_DN</a>	116	> 0.001	0.033
<a href="#">BIOCARTA_AKAP95_PATHWAY</a>	12	> 0.001	0.017	<a href="#">LY_AGING_MIDDLE_DN</a>	16	0.001	0.033
<a href="#">WU_APOPTOSIS_BY_CDKN1A_VIA_TP53</a>	55	> 0.001	0.018	<a href="#">MORI_PRE_BI_LYMPHOCYTE_UP</a>	78	> 0.001	0.033
<a href="#">REACTOME_AMYLOIDS</a>	73	> 0.001	0.017	<a href="#">ABRAMSON_INTERACT_WITH_AIRE</a>	43	0.001	0.033
<a href="#">KONG_E2F3_TARGETS</a>	97	> 0.001	0.017	<a href="#">BIOCARTA_CTL_PATHWAY</a>	14	0.001	0.033
<a href="#">REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWEEN_A_LYMPHOID_AND_A_NON_LYMPHOID_CELL</a>	60	> 0.001	0.016	<a href="#">CROONQUIST_NRAS_SIGNALING_DN</a>	72	> 0.001	0.034
<a href="#">IKEDA_MIR1_TARGETS_DN</a>	7	> 0.001	0.016	<a href="#">KEGG_CELL_CYCLE</a>	122	> 0.001	0.034
<a href="#">HAHTOLA_CTCL_PATHOGENESIS</a>	16	> 0.001	0.018	<a href="#">REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE</a>	41	> 0.001	0.034
<a href="#">GREENBAUM_E2A_TARGETS_UP</a>	33	> 0.001	0.018	<a href="#">ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_6HR</a>	82	> 0.001	0.034
<a href="#">DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN</a>	311	> 0.001	0.023	<a href="#">KIM_GERMINAL_CENTER_T_HELPER_UP</a>	65	> 0.001	0.036
<a href="#">LEE_EARLY_T_LYMPHOCYTE_UP</a>	104	> 0.001	0.023	<a href="#">REACTOME_CELL_CYCLE</a>	392	> 0.001	0.035
<a href="#">MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_DN</a>	73	> 0.001	0.023	<a href="#">BROWNE_HCMV_INFECTION_20HR_DN</a>	100	> 0.001	0.039
<a href="#">BIDUS_METASTASIS_UP</a>	213	> 0.001	0.022	<a href="#">ZHAN_MULTIPLE_MYELOMA_PR_UP</a>	44	0.001	0.038
<a href="#">BIOCARTA_G2_PATHWAY</a>	24	> 0.001	0.023	<a href="#">VANTVEER_BREAST_CANCER_METASTASIS_DN</a>	117	> 0.001	0.04
<a href="#">MANN_RESPONSE_TO_AMIFOSTINE_DN</a>	10	0.001	0.023	<a href="#">RAMALHO_STEMNESS_UP</a>	201	> 0.001	0.04
<a href="#">CAIRO_PML_TARGETS_BOUND_BY_MYC_UP</a>	23	> 0.001	0.023	<a href="#">MORI_IMMATURE_B_LYMPHOCYTE_DN</a>	89	> 0.001	0.04
<a href="#">REACTOME_G2_M_CHECKPOINTS</a>	41	> 0.001	0.024	<a href="#">MATZUK_FERTILIZATION</a>	8	0.001	0.039
<a href="#">MITSIADES_RESPONSE_TO_APLIDIN_DN</a>	246	> 0.001	0.023	<a href="#">RUIZ_TNC_TARGETS_DN</a>	140	> 0.001	0.042
<a href="#">RHODES_UNDIFFERENTIATED_CANCER</a>	68	> 0.001	0.024	<a href="#">REACTOME_MITOTIC_G2_G2_M_PHASES</a>	77	> 0.001	0.042
				<a href="#">PUJANA_BREAST_CANCER_LIT_INT_NETWORK</a>	100	> 0.001	0.046
				<a href="#">CROMER_METASTASIS_UP</a>	77	> 0.001	0.047
				<a href="#">ZHANG_TLX_TARGETS_60HR_DN</a>	276	> 0.001	0.048

**Table S4**—Cancer-associated network genes.

Gene Symbol	Gene Name	Entrez Gene ID	Log <sub>2</sub> [postCPAP/preCPAP]
AARS	alanyl-tRNA synthetase	16	-0.017
AASDHPPT	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	60496	-0.028
ABCB1	ATP-binding cassette, sub-family B (MDR/TAP), member 1	5243	-0.082
ACAT1	acetyl-CoA acetyltransferase 1	38	-0.042
ACVR1B	activin A receptor, type IB	91	-0.029
ADD3	adducin 3 (gamma)	120	-0.033
ADH1B	alcohol dehydrogenase 1B (class I), beta polypeptide	125	-0.063
AEBP2	AE binding protein 2	121536	-0.026
AHNAK	AHNAK nucleoprotein	79026	-0.044
AK4	adenylate kinase 4	205	-0.070
AKAP11	A kinase (PRKA) anchor protein 11	11215	-0.030
AKR1C3	aldo-keto reductase family 1, member C3	8644	-0.106
AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	10000	-0.053
AKTIP	AKT interacting protein	64400	-0.037
ALCAM	activated leukocyte cell adhesion molecule	214	-0.039
ANAPC1	anaphase promoting complex subunit 1	64682	-0.046
ANKRD28	ankyrin repeat domain 28	23243	-0.084
ANKRD32	ankyrin repeat domain 32	84250	-0.172
ANP32E	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	81611	-0.051
APAF1	apoptotic peptidase activating factor 1	317	-0.025
AR	androgen receptor	367	-0.064
ARFGEF1	ADP-ribosylation factor guanine nucleotide-exchange factor 1 (brefeldin A-inhibited)	10565	-0.022
ARFGEF2	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited)	10564	-0.018
ARFIP1	ADP-ribosylation factor interacting protein 1	27236	-0.040
ARHGEF10	Rho guanine nucleotide exchange factor (GEF) 10	9639	-0.060
ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	23365	-0.065
ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7	8874	-0.043
ARL6IP1	ADP-ribosylation factor-like 6 interacting protein 1	23204	-0.056
ARMC1	armadillo repeat containing 1	55156	-0.074
ARMC8	armadillo repeat containing 8	25852	-0.055
ARMCX3	armadillo repeat containing, X-linked 3	51566	-0.077
ARNT2	aryl-hydrocarbon receptor nuclear translocator 2	9915	-0.017
ASCC2	activating signal cointegrator 1 complex subunit 2	84164	-0.062
ASF1A	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	25842	-0.090
ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	259266	-0.076
ATAD2	ATPase family, AAA domain containing 2	29028	-0.019
ATF1	activating transcription factor 1	466	-0.018
ATF2	activating transcription factor 2	1386	-0.039
ATG16L1	autophagy related 16-like 1 (S. cerevisiae)	55054	-0.027
ATM	ataxia telangiectasia mutated	472	-0.044
ATP2B4	ATPase, Ca <sup>++</sup> transporting, plasma membrane 4	493	-0.050
ATR	ataxia telangiectasia and Rad3 related	545	-0.046
ATRX	alpha thalassemia/mental retardation syndrome X-linked	546	-0.117

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**Table S4** (continued)—Cancer-associated network genes.

Gene Symbol	Gene Name	Entrez Gene ID	Log <sub>2</sub> [postCPAP/preCPAP]
AURKA	aurora kinase A	6790	-0.056
AZI2	5-azacytidine induced 2	64343	-0.016
BARD1	BRCA1 associated RING domain 1	580	-0.049
BAX	BCL2-associated X protein	581	-0.028
BCAS2	breast carcinoma amplified sequence 2	10286	-0.077
BCCIP	BRCA2 and CDKN1A interacting protein	56647	-0.041
BCLAF1	BCL2-associated transcription factor 1	9774	-0.031
BIRC2	baculoviral IAP repeat containing 2	329	-0.023
BLM	Bloom syndrome, RecQ helicase-like	641	-0.030
BLMH	bleomycin hydrolase	642	-0.056
BMI1	BMI1 polycomb ring finger oncogene	648	-0.036
BNIP3	BCL2/adenovirus E1B 19kDa interacting protein 3	664	-0.045
BPTF	bromodomain PHD finger transcription factor	2186	-0.035
BRCA1	breast cancer 1, early onset	672	-0.043
BRD7	bromodomain containing 7	29117	-0.018
C11orf30	chromosome 11 open reading frame 30	56946	-0.042
CA2	carbonic anhydrase II	760	-0.119
CALD1	caldesmon 1	800	-0.101
CALM1	calmodulin 1 (phosphorylase kinase, delta)	801	-0.051
CAND1	cullin-associated and neddylation-dissociated 1	55832	-0.058
CAPN2	calpain 2, (m/II) large subunit	824	-0.053
CAPRN1	cell cycle associated protein 1	4076	-0.033
CASP8AP2	caspase 8 associated protein 2	9994	-0.044
CAV2	caveolin 2	858	-0.050
CBFB	core-binding factor, beta subunit	865	-0.024
CBLL1	Cbl proto-oncogene, E3 ubiquitin protein ligase-like 1	79872	-0.017
CBX3	chromobox homolog 3	11335	-0.023
CCL4	chemokine (C-C motif) ligand 4	6351	-0.070
CCL5	chemokine (C-C motif) ligand 5	6352	-0.105
CCNA1	cyclin A1	8900	-0.104
CCNB1	cyclin B1	891	-0.116
CCND2	cyclin D2	894	-0.054
CCND3	cyclin D3	896	-0.019
CCT6A	chaperonin containing TCP1, subunit 6A (zeta 1)	908	-0.039
CD160	CD160 molecule	11126	-0.029
CD2	CD2 molecule	914	-0.086
CD244	CD244 molecule, natural killer cell receptor 2B4	51744	-0.044
CD247	CD247 molecule	919	-0.098
CD28	CD28 molecule	940	-0.062
CD2AP	CD2-associated protein	23607	-0.022
CD38	CD38 molecule	952	-0.094
CD3E	CD3e molecule, epsilon (CD3-TCR complex)	916	-0.037
CD47	CD47 molecule	961	-0.037

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**Table S4** (continued)—Cancer-associated network genes.

Gene Symbol	Gene Name	Entrez Gene ID	Log <sub>2</sub> [postCPAP/preCPAP]
CD52	CD52 molecule	1043	-0.054
CD9	CD9 molecule	928	-0.058
CDC25A	cell division cycle 25A	993	-0.045
CDC40	cell division cycle 40	51362	-0.027
CDC45	cell division cycle 45	8318	-0.020
CDK1	cyclin-dependent kinase 1	983	-0.084
CDK3	cyclin-dependent kinase 3	1018	-0.024
CDK8	cyclin-dependent kinase 8	1024	-0.058
CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	1026	-0.042
CDKN2AIP	CDKN2A interacting protein	55602	-0.033
CDKN3	cyclin-dependent kinase inhibitor 3	1033	-0.034
CDYL	chromodomain protein, Y-like	9425	-0.026
CEBPG	CCAAT/enhancer binding protein (C/EBP), gamma	1054	-0.024
CENPC1	centromere protein C 1	1060	-0.113
CENPJ	centromere protein J	55835	-0.065
CENPK	centromere protein K	64105	-0.112
CENPN	centromere protein N	55839	0.014
CEP192	centrosomal protein 192kDa	55125	-0.046
CEP350	centrosomal protein 350kDa	9857	-0.018
CEP57	centrosomal protein 57kDa	9702	-0.057
CEP97	centrosomal protein 97kDa	79598	-0.043
CHEK1	checkpoint kinase 1	1111	-0.079
CHEK2	checkpoint kinase 2	11200	-0.154
CHN1	chimerin 1	1123	-0.107
CHTOP	chromatin target of PRMT1	26097	-0.010
CKAP5	cytoskeleton associated protein 5	9793	-0.043
CKS1B	CDC28 protein kinase regulatory subunit 1B	1163	-0.034
CLGN	calmegin	1047	-0.032
CLOCK	clock circadian regulator	9575	-0.028
CLSPN	claspin	63967	-0.060
CLTC	clathrin, heavy chain (Hc)	1213	-0.021
CMPK1	cytidine monophosphate (UMP-CMP) kinase 1, cytosolic	51727	-0.047
CNN3	calponin 3, acidic	1266	-0.050
CNOT7	CCR4-NOT transcription complex, subunit 7	29883	-0.033
COL4A5	collagen, type IV, alpha 5	1287	-0.049
COPS2	COP9 signalosome subunit 2	9318	-0.034
COPS8	COP9 signalosome subunit 8	10920	-0.035
CPA3	carboxypeptidase A3 (mast cell)	1359	-0.121
CPSF4	cleavage and polyadenylation specific factor 4, 30kDa	10898	-0.027
CPSF6	cleavage and polyadenylation specific factor 6, 68kDa	11052	-0.034
CRKL	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	1399	-0.029
CRY1	cryptochrome 1 (photolyase-like)	1407	-0.042
CRYZ	crystallin, zeta (quinone reductase)	1429	-0.065

Table S4 continues on the following page

**Table S4** (continued)—Cancer-associated network genes.

Gene Symbol	Gene Name	Entrez Gene ID	Log <sub>2</sub> [postCPAP/preCPAP]
CSE1L	CSE1 chromosome segregation 1-like (yeast)	1434	-0.048
CSTF2	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa	1478	-0.051
CSTF3	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa	1479	-0.054
CTBP1	C-terminal binding protein 1	1487	-0.042
CTLA4	cytotoxic T-lymphocyte-associated protein 4	1493	-0.083
CTNNB1	catenin (cadherin-associated protein), beta 1, 88kDa	1499	-0.025
CTPS1	CTP synthase 1	1503	-0.046
CTSL1	cathepsin L1	1514	-0.068
CUL2	cullin 2	8453	-0.059
CUL3	cullin 3	8452	-0.033
CXCR4	chemokine (C-X-C motif) receptor 4	7852	-0.034
CYB5A	cytochrome b5 type A (microsomal)	1528	-0.055
CYP2J2	cytochrome P450, family 2, subfamily J, polypeptide 2	1573	-0.034
DBF4	DBF4 homolog (S. cerevisiae)	10926	-0.095
DCAF6	DDB1 and CUL4 associated factor 6	55827	-0.020
DCK	deoxycytidine kinase	1633	-0.030
DDB2	damage-specific DNA binding protein 2, 48kDa	1643	-0.050
DDR2	discoidin domain receptor tyrosine kinase 2	4921	-0.046
DDX1	DEAD (Asp-Glu-Ala-Asp) box helicase 1	1653	-0.033
DDX21	DEAD (Asp-Glu-Ala-Asp) box helicase 21	9188	-0.039
DDX39A	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39A	10212	-0.056
DEPTOR	DEP domain containing MTOR-interacting protein	64798	-0.055
DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	1660	-0.031
DLAT	dihydrolipoamide S-acetyltransferase	1737	-0.015
DLGAP5	discs, large (Drosophila) homolog-associated protein 5	9787	-0.080
DMD	dystrophin	1756	-0.019
DNAJC9	DnaJ (Hsp40) homolog, subfamily C, member 9	23234	-0.051
DNTT	deoxynucleotidyltransferase, terminal	1791	-0.026
DPM1	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	8813	-0.040
DPY30	dpy-30 homolog (C. elegans)	84661	-0.056
DROSHA	drosha, ribonuclease type III	29102	-0.031
DSC1	desmocollin 1	1823	-0.054
DUSP11	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	8446	-0.014
DUT	deoxyuridine triphosphatase	1854	-0.057
DYRK1A	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	1859	-0.020
EAPP	E2F-associated phosphoprotein	55837	-0.036
ECT2	epithelial cell transforming sequence 2 oncogene	1894	-0.064
EFTUD2	elongation factor Tu GTP binding domain containing 2	9343	0.020
EIF2S1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	1965	-0.032
EIF3H	eukaryotic translation initiation factor 3, subunit H	8667	-0.027
EIF4A3	eukaryotic translation initiation factor 4A3	9775	-0.023
EIF4B	eukaryotic translation initiation factor 4B	1975	-0.035
EIF5	eukaryotic translation initiation factor 5	1983	-0.045

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**Table S4** (continued)—Cancer-associated network genes.

Gene Symbol	Gene Name	Entrez Gene ID	Log <sub>2</sub> [postCPAP/preCPAP]
EIF5B	eukaryotic translation initiation factor 5B	9669	-0.030
EPHA4	EPH receptor A4	2043	-0.047
EPRS	glutamyl-prolyl-tRNA synthetase	2058	-0.045
ERCC3	excision repair cross-complementing rodent repair deficiency, complementation group 3	2071	-0.016
ERCC6L	excision repair cross-complementing rodent repair deficiency, complementation group 6-like	54821	-0.048
ESCO2	establishment of cohesion 1 homolog 2 ( <i>S. cerevisiae</i> )	157570	-0.052
ESPL1	extra spindle pole bodies homolog 1 ( <i>S. cerevisiae</i> )	9700	-0.036
ESYT2	extended synaptotagmin-like protein 2	57488	-0.028
EZH2	enhancer of zeste homolog 2 ( <i>Drosophila</i> )	2146	-0.079
F2R	coagulation factor II (thrombin) receptor	2149	-0.035
FAM13B	family with sequence similarity 13, member B	51306	-0.026
FAM208B	family with sequence similarity 208, member B	54906	-0.025
FANCD2	Fanconi anemia, complementation group D2	2177	-0.035
FANCG	Fanconi anemia, complementation group G	2189	-0.022
FANCL	Fanconi anemia, complementation group L	55120	-0.061
FASTKD2	FAST kinase domains 2	22868	-0.045
FBL	fibrillarin	2091	-0.030
FBXO11	F-box protein 11	80204	-0.017
FBXO28	F-box protein 28	23219	-0.035
FBXO3	F-box protein 3	26273	-0.039
FBXO5	F-box protein 5	26271	-0.046
FBXW11	F-box and WD repeat domain containing 11	23291	-0.026
FEM1A	fem-1 homolog a ( <i>C. elegans</i> )	55527	-0.040
FEM1B	fem-1 homolog b ( <i>C. elegans</i> )	10116	-0.025
FEN1	flap structure-specific endonuclease 1	2237	-0.024
FGFR10P	FGFR1 oncogene partner	11116	-0.008
FH	fumarate hydratase	2271	-0.057
FN1	fibronectin 1	2335	-0.057
FNBP1	formin binding protein 1	23048	-0.015
FUBP1	far upstream element (FUSE) binding protein 1	8880	-0.030
FYN	FYN oncogene related to SRC, FGR, YES	2534	-0.048
G3BP1	GTPase activating protein (SH3 domain) binding protein 1	10146	-0.037
G3BP2	GTPase activating protein (SH3 domain) binding protein 2	9908	-0.066
GABPB2	GA binding protein transcription factor, beta subunit 2	126626	-0.033
GALE	UDP-galactose-4-epimerase	2582	-0.029
GANAB	glucosidase, alpha; neutral AB	23193	-0.046
GCLM	glutamate-cysteine ligase, modifier subunit	2730	-0.047
GCN1L1	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	10985	-0.045
GIN1	gypsy retrotransposon integrase 1	54826	-0.049
GINS1	GINS complex subunit 1 (Psf1 homolog)	9837	-0.132
GINS2	GINS complex subunit 2 (Psf2 homolog)	51659	-0.031
GINS3	GINS complex subunit 3 (Psf3 homolog)	64785	-0.091
GLCCI1	glucocorticoid induced transcript 1	113263	-0.018

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**Table S4** (continued)—Cancer-associated network genes.

Gene Symbol	Gene Name	Entrez Gene ID	Log <sub>2</sub> [postCPAP/preCPAP]
GLS2	glutaminase 2 (liver, mitochondrial)	27165	-0.023
GMPS	guanine monphosphate synthetase	8833	-0.018
GNAQ	guanine nucleotide binding protein (G protein), q polypeptide	2776	-0.046
GNB5	guanine nucleotide binding protein (G protein), beta 5	10681	-0.060
GNG11	guanine nucleotide binding protein (G protein), gamma 11	2791	-0.090
GPR137B	G protein-coupled receptor 137B	7107	-0.071
GPR56	G protein-coupled receptor 56	9289	-0.115
GRAP2	GRB2-related adaptor protein 2	9402	-0.093
GTF2A1	general transcription factor IIA, 1, 19/37kDa	2957	-0.015
GTF3C3	general transcription factor IIIC, polypeptide 3, 102kDa	9330	-0.027
GTPBP10	GTP-binding protein 10 (putative)	85865	-0.046
GZMA	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)	3001	-0.102
GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	3002	-0.147
GZMK	granzyme K (granzyme 3; tryptase II)	3003	-0.096
H2AFX	H2A histone family, member X	3014	-0.067
HACE1	HECT domain and ankyrin repeat containing E3 ubiquitin protein ligase 1	57531	-0.060
HAPLN1	hyaluronan and proteoglycan link protein 1	1404	-0.033
HAT1	histone acetyltransferase 1	8520	-0.054
HBS1L	HBS1-like ( <i>S. cerevisiae</i> )	10767	-0.047
HDAC1	histone deacetylase 1	3065	-0.036
HEATR1	HEAT repeat containing 1	55127	-0.040
HECTD1	HECT domain containing E3 ubiquitin protein ligase 1	25831	-0.029
HELLS	helicase, lymphoid-specific	3070	-0.028
HERC2	HECT and RLD domain containing E3 ubiquitin protein ligase 2	8924	-0.046
HIBCH	3-hydroxyisobutyryl-CoA hydrolase	26275	-0.032
HIPK1	homeodomain interacting protein kinase 1	204851	-0.037
HLTF	helicase-like transcription factor	6596	-0.053
HMGB1	high mobility group box 1	3146	-0.038
HMGB3	high mobility group box 3	3149	-0.036
HNMT	histamine N-methyltransferase	3176	-0.036
HNRNPA1	heterogeneous nuclear ribonucleoprotein A1	3178	-0.096
HNRNPA3	heterogeneous nuclear ribonucleoprotein A3	220988	-0.019
HNRNPAB	heterogeneous nuclear ribonucleoprotein A/B	3182	-0.037
HNRNPH3	heterogeneous nuclear ribonucleoprotein H3 (2H9)	3189	-0.032
HNRNPK	heterogeneous nuclear ribonucleoprotein K	3190	-0.044
HNRNPR	heterogeneous nuclear ribonucleoprotein R	10236	-0.020
HNRNPU	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	3192	-0.033
HNRPDL	heterogeneous nuclear ribonucleoprotein D-like	9987	-0.021
HOXA9	homeobox A9	3205	-0.038
HPRT1	hypoxanthine phosphoribosyltransferase 1	3251	-0.053
HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member 1	3320	-0.066
HUWE1	HECT, UBA and WWE domain containing 1, E3 ubiquitin protein ligase	10075	-0.020
ICOS	inducible T-cell co-stimulator	29851	-0.092

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**Table S4** (continued)—Cancer-associated network genes.

Gene Symbol	Gene Name	Entrez Gene ID	Log <sub>2</sub> [postCPAP/preCPAP]
ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	3398	-0.066
IDE	insulin-degrading enzyme	3416	-0.031
IGFBP5	insulin-like growth factor binding protein 5	3488	-0.045
IK	IK cytokine, down-regulator of HLA II	3550	-0.029
IKBKAP	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase complex-associated protein	8518	-0.027
IKZF2	IKAROS family zinc finger 2 (Helios)	22807	-0.029
IKZF3	IKAROS family zinc finger 3 (Aiolos)	22806	-0.055
IL12RB2	interleukin 12 receptor, beta 2	3595	-0.084
IL18R1	interleukin 18 receptor 1	8809	-0.094
IL23A	interleukin 23, alpha subunit p19	51561	-0.029
IL2RB	interleukin 2 receptor, beta	3560	-0.064
IL7R	interleukin 7 receptor	3575	-0.077
INSIG1	insulin induced gene 1	3638	-0.099
INTS6	integrator complex subunit 6	26512	-0.036
INTS7	integrator complex subunit 7	25896	-0.066
IPO5	importin 5	3843	-0.048
IPO8	importin 8	10526	-0.028
ITFG1	integrin alpha FG-GAP repeat containing 1	81533	-0.051
ITGA6	integrin, alpha 6	3655	-0.057
ITGB3BP	integrin beta 3 binding protein (beta3-endonexin)	23421	-0.107
ITGB4	integrin, beta 4	3691	-0.050
IVNS1ABP	influenza virus NS1A binding protein	10625	-0.038
JAK1	Janus kinase 1	3716	-0.022
JUN	jun proto-oncogene	3725	-0.058
KANK1	KN motif and ankyrin repeat domains 1	23189	-0.024
KAT2B	K(lysine) acetyltransferase 2B	8850	-0.036
KBTBD7	kelch repeat and BTB (POZ) domain containing 7	84078	-0.043
KCTD15	potassium channel tetramerisation domain containing 15	79047	-0.043
KDM1A	lysine (K)-specific demethylase 1A	23028	-0.014
KIAA0101	KIAA0101	9768	-0.100
KIAA1109	KIAA1109	84162	-0.022
KIAA1279	KIAA1279	26128	-0.034
KIAA1430	KIAA1430	57587	-0.064
KIDINS220	kinase D-interacting substrate, 220kDa	57498	-0.015
KIF11	kinesin family member 11	3832	-0.089
KIF14	kinesin family member 14	9928	-0.069
KIF21A	kinesin family member 21A	55605	-0.074
KIF21B	kinesin family member 21B	23046	-0.032
KIF2C	kinesin family member 2C	11004	-0.074
KIFAP3	kinesin-associated protein 3	22920	-0.069
KIR2DS4	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 4	100132285	-0.166
KIR3DL2	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2	3812	-0.103
KLHDC2	kelch domain containing 2	23588	-0.025

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**Table S4** (continued)—Cancer-associated network genes.

Gene Symbol	Gene Name	Entrez Gene ID	Log <sub>2</sub> [postCPAP/preCPAP]
KLHL23	kelch-like family member 23	151230	-0.029
KLHL24	kelch-like family member 24	54800	-0.028
KLHL8	kelch-like family member 8	57563	-0.047
KNTC1	kinetochore associated 1	9735	-0.069
KTN1	kinectin 1 (kinesin receptor)	3895	-0.032
LANCL1	LanC lantibiotic synthetase component C-like 1 (bacterial)	10314	-0.050
LARP4	La ribonucleoprotein domain family, member 4	113251	-0.028
LARP7	La ribonucleoprotein domain family, member 7	51574	-0.031
LATS1	LATS, large tumor suppressor, homolog 1 (Drosophila)	9113	-0.011
LBR	lamin B receptor	3930	-0.078
LCK	lymphocyte-specific protein tyrosine kinase	3932	-0.043
LEF1	lymphoid enhancer-binding factor 1	51176	-0.050
LPIN1	lipin 1	23175	-0.028
LRBA	LPS-responsive vesicle trafficking, beach and anchor containing	987	-0.072
LUC7L3	LUC7-like 3 ( <i>S. cerevisiae</i> )	51747	-0.047
LUZP1	leucine zipper protein 1	7798	-0.021
MAGED2	melanoma antigen family D, 2	10916	-0.061
MAN2A1	mannosidase, alpha, class 2A, member 1	4124	-0.059
MAP3K5	mitogen-activated protein kinase kinase kinase 5	4217	-0.029
MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5	11183	-0.043
MAPRE1	microtubule-associated protein, RP/EB family, member 1	22919	-0.017
MAPRE2	microtubule-associated protein, RP/EB family, member 2	10982	-0.039
MAT2A	methionine adenosyltransferase II, alpha	4144	-0.024
MATK	megakaryocyte-associated tyrosine kinase	4145	-0.026
MBNL1	muscleblind-like splicing regulator 1	4154	-0.049
MCAM	melanoma cell adhesion molecule	4162	-0.033
MCM10	minichromosome maintenance complex component 10	55388	-0.040
MCM3	minichromosome maintenance complex component 3	4172	-0.063
MCM4	minichromosome maintenance complex component 4	4173	-0.052
MCM5	minichromosome maintenance complex component 5	4174	-0.062
MCM6	minichromosome maintenance complex component 6	4175	-0.078
MCM8	minichromosome maintenance complex component 8	84515	-0.057
MDC1	mediator of DNA-damage checkpoint 1	9656	-0.039
MDF1	MyoD family inhibitor	4188	-0.031
MDH1	malate dehydrogenase 1, NAD (soluble)	4190	-0.036
MDN1	MDN1, midasin homolog (yeast)	23195	-0.037
MECP2	methyl CpG binding protein 2 (Rett syndrome)	4204	-0.022
MED1	mediator complex subunit 1	5469	-0.048
MED17	mediator complex subunit 17	9440	-0.053
MED21	mediator complex subunit 21	9412	-0.047
MED4	mediator complex subunit 4	29079	-0.068
MEIS1	Meis homeobox 1	4211	-0.052
MELK	maternal embryonic leucine zipper kinase	9833	-0.102

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**Table S4** (continued)—Cancer-associated network genes.

Gene Symbol	Gene Name	Entrez Gene ID	Log <sub>2</sub> [postCPAP/preCPAP]
MET	met proto-oncogene (hepatocyte growth factor receptor)	4233	-0.029
METAP1	methionyl aminopeptidase 1	23173	-0.035
METTL9	methyltransferase like 9	51108	-0.036
MFGE8	milk fat globule-EGF factor 8 protein	4240	-0.042
MGA	MGA, MAX dimerization protein	23269	-0.057
MID1	midline 1 (Opitz/BBB syndrome)	4281	-0.048
MKL2	MKL/myocardin-like 2	57496	-0.044
MLLT3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3	4300	-0.090
MMD	monocyte to macrophage differentiation-associated	23531	-0.122
MMP16	matrix metalloproteinase 16 (membrane-inserted)	4325	-0.116
MOB4	MOB family member 4, phocein	25843	-0.039
MPDZ	multiple PDZ domain protein	8777	-0.054
MPHOSPH6	M-phase phosphoprotein 6	10200	-0.058
MPHOSPH9	M-phase phosphoprotein 9	10198	-0.044
MPP5	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	64398	-0.022
MRE11A	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)	4361	-0.058
MRPL42	mitochondrial ribosomal protein L42	28977	-0.040
MRPL9	mitochondrial ribosomal protein L9	65005	-0.035
MSH6	mutS homolog 6 (E. coli)	2956	-0.036
MST4	serine/threonine protein kinase MST4	51765	-0.052
MT1E	metallothionein 1E	4493	-0.030
MT1H	metallothionein 1H	4496	-0.067
MT2A	metallothionein 2A	4502	-0.098
MTDH	metadherin	92140	-0.016
MTHFD1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methylenetetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	4522	-0.029
MYBL1	v-myb myeloblastosis viral oncogene homolog (avian)-like 1	4603	-0.105
MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	4605	-0.030
MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	4609	-0.084
MYCBP2	MYC binding protein 2, E3 ubiquitin protein ligase	23077	-0.029
MYO9A	myosin IXA	4649	-0.045
NAP1L1	nucleosome assembly protein 1-like 1	4673	-0.058
NBEA	neurobeachin	26960	-0.029
NCAPD2	non-SMC condensin I complex, subunit D2	9918	-0.034
NCAPD3	non-SMC condensin II complex, subunit D3	23310	-0.061
NCAPG	non-SMC condensin I complex, subunit G	64151	-0.050
NCK1	NCK adaptor protein 1	4690	-0.026
NCKAP1	NCK-associated protein 1	10787	-0.099
NCL	nucleolin	4691	-0.024
NCOA6	nuclear receptor coactivator 6	23054	-0.023
NCOR1	nuclear receptor corepressor 1	9611	-0.017
NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)	4724	-0.067
NEK1	NIMA-related kinase 1	4750	-0.028
NEK7	NIMA-related kinase 7	140609	-0.036

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**Table S4** (continued)—Cancer-associated network genes.

Gene Symbol	Gene Name	Entrez Gene ID	Log <sub>2</sub> [postCPAP/preCPAP]
NF1	neurofibromin 1	4763	-0.022
NF2	neurofibromin 2 (merlin)	4771	-0.021
NFATC3	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	4775	-0.025
NFIA	nuclear factor I/A	4774	-0.079
NFYB	nuclear transcription factor Y, beta	4801	-0.102
NMT2	N-myristoyltransferase 2	9397	-0.073
NNT	nicotinamide nucleotide transhydrogenase	23530	-0.023
NONO	non-POU domain containing, octamer-binding	4841	-0.012
NPAT	nuclear protein, ataxia-telangiectasia locus	4863	-0.031
NQO1	NAD(P)H dehydrogenase, quinone 1	1728	-0.06
NR1D2	nuclear receptor subfamily 1, group D, member 2	9975	-0.04
NR2C1	nuclear receptor subfamily 2, group C, member 1	7181	-0.023
NR3C2	nuclear receptor subfamily 3, group C, member 2	4306	-0.030
NRGN	neurogranin (protein kinase C substrate, RC3)	4900	-0.076
NSFL1C	NSFL1 (p97) cofactor (p47)	55968	-0.050
NSMCE4A	non-SMC element 4 homolog A ( <i>S. cerevisiae</i> )	54780	-0.013
NUDT21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	11051	-0.037
NUP107	nucleoporin 107kDa	57122	-0.019
NUP155	nucleoporin 155kDa	9631	-0.034
NUP85	nucleoporin 85kDa	79902	-0.042
NVL	nuclear VCP-like	4931	-0.061
ODC1	ornithine decarboxylase 1	4953	-0.091
OGT	O-linked N-acetylglucosamine (GlcNAc) transferase	8473	-0.026
OPTN	optineurin	10133	-0.051
ORC4	origin recognition complex, subunit 4	5000	-0.027
ORC6	origin recognition complex, subunit 6	23594	-0.073
OSBPL3	oxysterol binding protein-like 3	26031	-0.065
OVOS/OVOS2	ovostatin 2	144203	-0.037
OXCT1	3-oxoacid CoA transferase 1	5019	-0.062
P4HA1	prolyl 4-hydroxylase, alpha polypeptide I	5033	-0.032
PAFAH1B1	platelet-activating factor acetylhydrolase 1b, regulatory subunit 1 (45kDa)	5048	-0.025
PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	10606	-0.043
PALB2	partner and localizer of BRCA2	79728	-0.026
PARP1	poly (ADP-ribose) polymerase 1	142	-0.031
PAXIP1	PAX interacting (with transcription-activation domain) protein 1	22976	-0.031
PBK	PDZ binding kinase	55872	-0.104
PBX1	pre-B-cell leukemia homeobox 1	5087	-0.041
PCM1	pericentriolar material 1	5108	-0.034
PCNP	PEST proteolytic signal containing nuclear protein	57092	-0.040
PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)	27250	-0.024
PDE4B	phosphodiesterase 4B, cAMP-specific	5142	-0.033
PDLIM1	PDZ and LIM domain 1	9124	-0.085
PDS5A	PDS5, regulator of cohesion maintenance, homolog A ( <i>S. cerevisiae</i> )	23244	-0.050

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**Table S4** (continued)—Cancer-associated network genes.

Gene Symbol	Gene Name	Entrez Gene ID	Log <sub>2</sub> [postCPAP/preCPAP]
PEX7	peroxisomal biogenesis factor 7	5191	-0.046
PF4	platelet factor 4	5196	-0.156
PFDN4	prefoldin subunit 4	5203	-0.062
PFKP	phosphofructokinase, platelet	5214	-0.039
PFN2	profilin 2	5217	-0.055
PGRMC1	progesterone receptor membrane component 1	10857	-0.137
PGRMC2	progesterone receptor membrane component 2	10424	-0.026
PHB2	prohibitin 2	11331	-0.035
PHF17	PHD finger protein 17	79960	-0.018
PHF20L1	PHD finger protein 20-like 1	51105	-0.042
PHF6	PHD finger protein 6	84295	-0.025
PIK3C2A	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 alpha	5286	-0.025
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	5295	-0.073
PIK3R3	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	8503	-0.029
PKP4	plakophilin 4	8502	-0.024
PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)	23236	-0.059
PLEKHA1	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	59338	-0.058
PLK4	polo-like kinase 4	10733	-0.071
PLS3	plastin 3	5358	-0.061
PNP	purine nucleoside phosphorylase	4860	-0.054
POLD3	polymerase (DNA-directed), delta 3, accessory subunit	10714	-0.028
POLR2B	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa	5431	-0.032
POLR2G	polymerase (RNA) II (DNA directed) polypeptide G	5436	-0.052
POLR3B	polymerase (RNA) III (DNA directed) polypeptide B	55703	-0.025
POLR3H	polymerase (RNA) III (DNA directed) polypeptide H (22.9kD)	171568	-0.095
POT1	protection of telomeres 1	25913	-0.044
PPAT	phosphoribosyl pyrophosphate amidotransferase	5471	-0.042
PPBP	pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)	5473	-0.128
PPID	peptidylprolyl isomerase D	5481	-0.103
PPP1CC	protein phosphatase 1, catalytic subunit, gamma isozyme	5501	-0.036
PPP1R16B	protein phosphatase 1, regulatory subunit 16B	26051	-0.075
PRF1	perforin 1 (pore forming protein)	5551	-0.127
PRIM1	primase, DNA, polypeptide 1 (49kDa)	5557	-0.055
PRKAB2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	5565	-0.042
PRKACB	protein kinase, cAMP-dependent, catalytic, beta	5567	-0.086
PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha	5573	-0.017
PRKAR1B	protein kinase, cAMP-dependent, regulatory, type I, beta	5575	-0.041
PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha	5576	-0.050
PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta	5577	-0.136
PRKCB	protein kinase C, beta	5579	-0.013
PRKCQ	protein kinase C, theta	5588	-0.071
PRKD3	protein kinase D3	23683	-0.008
PRKDC	protein kinase, DNA-activated, catalytic polypeptide	5591	-0.055

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**Table S4** (continued)—Cancer-associated network genes.

Gene Symbol	Gene Name	Entrez Gene ID	Log <sub>2</sub> [postCPAP/preCPAP]
PRKRA	protein kinase, interferon-inducible double stranded RNA dependent activator	8575	-0.017
PRPF38B	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	55119	-0.036
PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	8899	-0.018
PRPF8	PRP8 pre-mRNA processing factor 8 homolog ( <i>S. cerevisiae</i> )	10594	-0.044
PRPS1	phosphoribosyl pyrophosphate synthetase 1	5631	-0.057
PRR14L	proline rich 14-like	253143	-0.013
PRSS23	protease, serine, 23	11098	-0.044
PSIP1	PC4 and SFRS1 interacting protein 1	11168	-0.116
PSMD14	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	10213	-0.062
PSMD2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	5708	-0.059
PSMG2	proteasome (prosome, macropain) assembly chaperone 2	56984	-0.019
PTBP3	polypyrimidine tract binding protein 3	9991	-0.023
PTCH1	patched 1	5727	-0.069
PTMA	prothymosin, alpha	5757	-0.041
PTPN14	protein tyrosine phosphatase, non-receptor type 14	5784	-0.030
PTPN22	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	26191	-0.032
PTPN3	protein tyrosine phosphatase, non-receptor type 3	5774	-0.047
PUM2	pumilio homolog 2 ( <i>Drosophila</i> )	23369	-0.016
PURB	purine-rich element binding protein B	5814	-0.014
RAB11A	RAB11A, member RAS oncogene family	8766	-0.064
RAB1A	RAB1A, member RAS oncogene family	5861	-0.021
RAB22A	RAB22A, member RAS oncogene family	57403	-0.019
RAB40B	RAB40B, member RAS oncogene family	10966	-0.020
RAB7A	RAB7A, member RAS oncogene family	7879	-0.100
RACGAP1	Rac GTPase activating protein 1	29127	-0.067
RAD50	RAD50 homolog ( <i>S. cerevisiae</i> )	10111	-0.036
RAD51	RAD51 homolog ( <i>S. cerevisiae</i> )	5888	-0.052
RAD54L	RAD54-like ( <i>S. cerevisiae</i> )	8438	-0.044
RAE1	RAE1 RNA export 1 homolog ( <i>S. pombe</i> )	8480	-0.026
RAG1	recombination activating gene 1	5896	-0.029
RAG2	recombination activating gene 2	5897	-0.058
RAP2A	RAP2A, member of RAS oncogene family	5911	-0.066
RASGRP1	RAS guanyl releasing protein 1 (calcium and DAG-regulated)	10125	-0.052
RBM15	RNA binding motif protein 15	64783	-0.023
RBM34	RNA binding motif protein 34	23029	-0.023
RBMX	RNA binding motif protein, X-linked	27316	-0.032
RBPJ	recombination signal binding protein for immunoglobulin kappa J region	3516	-0.035
RDX	radixin	5962	-0.052
RFC1	replication factor C (activator 1) 1, 145kDa	5981	-0.022
RFC4	replication factor C (activator 1) 4, 37kDa	5984	-0.073
RFWD3	ring finger and WD repeat domain 3	55159	-0.071
RFX3	regulatory factor X, 3 (influences HLA class II expression)	5991	-0.062
RGCC	regulator of cell cycle	28984	-0.053

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**Table S4** (continued)—Cancer-associated network genes.

Gene Symbol	Gene Name	Entrez Gene ID	Log <sub>2</sub> [postCPAP/preCPAP]
RHOBTB3	Rho-related BTB domain containing 3	22836	-0.092
RIF1	RAP1 interacting factor homolog (yeast)	55183	-0.034
RIOK3	RIO kinase 3	8780	-0.067
RLIM	ring finger protein, LIM domain interacting	51132	-0.081
RMND5A	required for meiotic nuclear division 5 homolog A ( <i>S. cerevisiae</i> )	64795	-0.037
RNASEH2B	ribonuclease H2, subunit B	79621	-0.034
RNF14	ring finger protein 14	9604	-0.046
RNF19A	ring finger protein 19A, E3 ubiquitin protein ligase	25897	-0.042
RNF6	ring finger protein (C3H2C3 type) 6	6049	-0.03
RNF7	ring finger protein 7	9616	-0.022
RNMT	RNA (guanine-7-) methyltransferase	8731	-0.030
RORA	RAR-related orphan receptor A	6095	-0.091
RPL15	ribosomal protein L15	6138	-0.054
RPN2	ribophorin II	6185	-0.030
RPP30	ribonuclease P/MRP 30kDa subunit	10556	-0.032
RRM1	ribonucleotide reductase M1	6240	-0.029
RRM2	ribonucleotide reductase M2	6241	-0.113
RRN3	RRN3 RNA polymerase I transcription factor homolog ( <i>S. cerevisiae</i> )	54700	-0.088
RSF1	remodeling and spacing factor 1	51773	-0.018
RTCA	RNA 3'-terminal phosphate cyclase	8634	-0.026
RTF1	Rtf1, Paf1/RNA polymerase II complex component, homolog ( <i>S. cerevisiae</i> )	23168	-0.048
RWDD3	RWD domain containing 3	25950	-0.020
RYK	receptor-like tyrosine kinase	6259	-0.040
SCAMP1	secretory carrier membrane protein 1	9522	-0.045
SCAPER	S-phase cyclin A-associated protein in the ER	49855	-0.027
SEC23A	Sec23 homolog A ( <i>S. cerevisiae</i> )	10484	-0.046
SEC23IP	SEC23 interacting protein	11196	-0.011
SERINC3	serine incorporator 3	10955	-0.022
SERPINE2	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2	5270	-0.061
SERTAD4	SERTA domain containing 4	56256	-0.039
SFPQ	splicing factor proline/glutamine-rich	6421	-0.030
SGOL2	shugoshin-like 2 ( <i>S. pombe</i> )	151246	-0.115
SH2D1A	SH2 domain containing 1A	4068	-0.057
SH3BP4	SH3-domain binding protein 4	23677	-0.054
SH3BP5	SH3-domain binding protein 5 (BTK-associated)	9467	-0.028
SHFM1	split hand/foot malformation (ectrodactyly) type 1	7979	-0.028
SKP1	S-phase kinase-associated protein 1	6500	-0.041
SKP2	S-phase kinase-associated protein 2, E3 ubiquitin protein ligase	6502	-0.073
SLC16A1	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	6566	-0.098
SLC25A12	solute carrier family 25 (aspartate/glutamate carrier), member 12	8604	-0.051
SLC26A2	solute carrier family 26 (sulfate transporter), member 2	1836	-0.043
SLC30A5	solute carrier family 30 (zinc transporter), member 5	64924	-0.021
SLC38A1	solute carrier family 38, member 1	81539	-0.046

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**Table S4** (continued)—Cancer-associated network genes.

Gene Symbol	Gene Name	Entrez Gene ID	Log <sub>2</sub> [postCPAP/preCPAP]
SLC38A2	solute carrier family 38, member 2	54407	-0.052
SLC5A3	solute carrier family 5 (sodium/myo-inositol cotransporter), member 3	6526	-0.111
SLTM	SAFB-like, transcription modulator	79811	-0.017
SMAD2	SMAD family member 2	4087	-0.036
SMAD3	SMAD family member 3	4088	-0.035
SMAD4	SMAD family member 4	4089	-0.032
SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	6595	-0.020
SMARCA5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	8467	-0.045
SMC1A	structural maintenance of chromosomes 1A	8243	-0.042
SMC2	structural maintenance of chromosomes 2	10592	-0.050
SMC3	structural maintenance of chromosomes 3	9126	-0.043
SMC4	structural maintenance of chromosomes 4	10051	-0.055
SMCHD1	structural maintenance of chromosomes flexible hinge domain containing 1	23347	-0.028
SMS	spermine synthase	6611	-0.027
SNRNP27	small nuclear ribonucleoprotein 27kDa (U4/U6.U5)	11017	-0.032
SNRNP40	small nuclear ribonucleoprotein 40kDa (U5)	9410	-0.047
SNRPA	small nuclear ribonucleoprotein polypeptide A	6626	-0.042
SNRPB	small nuclear ribonucleoprotein polypeptides B and B1	6628	-0.065
SNRPN	small nuclear ribonucleoprotein polypeptide N	6638	-0.041
SNX5	sorting nexin 5	27131	-0.044
SPIN1	spindlin 1	10927	-0.027
SPTBN1	spectrin, beta, non-erythrocytic 1	6711	-0.067
SRSF1	serine/arginine-rich splicing factor 1	6426	-0.013
SRSF11	serine/arginine-rich splicing factor 11	9295	-0.028
SRSF2	serine/arginine-rich splicing factor 2	6427	-0.026
SRSF3	serine/arginine-rich splicing factor 3	6428	-0.045
SS18	synovial sarcoma translocation, chromosome 18	6760	-0.061
SSBP2	single-stranded DNA binding protein 2	23635	-0.035
ST13	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	6767	-0.030
STAG1	stromal antigen 1	10274	-0.021
STAM2	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	10254	-0.045
STAR	steroidogenic acute regulatory protein	6770	-0.077
STAT4	signal transducer and activator of transcription 4	6775	-0.069
STAU2	staufen, RNA binding protein, homolog 2 (Drosophila)	27067	-0.024
STRBP	spermatid perinuclear RNA binding protein	55342	-0.047
STXBP3	syntaxin binding protein 3	6814	-0.031
SUCLA2	succinate-CoA ligase, ADP-forming, beta subunit	8803	-0.048
SUCLG1	succinate-CoA ligase, alpha subunit	8802	-0.015
SUCLG2	succinate-CoA ligase, GDP-forming, beta subunit	8801	-0.129
SYCP2	synaptonemal complex protein 2	10388	-0.047
SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	10492	-0.051
SYNE1	spectrin repeat containing, nuclear envelope 1	23345	-0.044

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**Table S4** (continued)—Cancer-associated network genes.

Gene Symbol	Gene Name	Entrez Gene ID	Log <sub>2</sub> [postCPAP/preCPAP]
SYNE2	spectrin repeat containing, nuclear envelope 2	23224	-0.057
SYT11	synaptotagmin XI	23208	-0.047
SYTL2	synaptotagmin-like 2	54843	-0.024
TACC1	transforming, acidic coiled-coil containing protein 1	6867	-0.019
TAF1	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 250kDa	6872	-0.018
TAF1D	TATA box binding protein (TBP)-associated factor, RNA polymerase I, D, 41kDa	79101	-0.025
TAF9B	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	51616	-0.039
TANK	TRAF family member-associated NFKB activator	10010	-0.048
TARP	TCR gamma alternate reading frame protein	445347	-0.063
TASP1	taspase, threonine aspartase, 1	55617	-0.028
TBC1D4	TBC1 domain family, member 4	9882	-0.030
TBCA	tubulin folding cofactor A	6902	-0.017
TBL1XR1	transducin (beta)-like 1 X-linked receptor 1	79718	-0.056
TCEA1	transcription elongation factor A (SII), 1	6917	-0.027
TCN2	transcobalamin II	6948	-0.029
TCP1	t-complex 1	6950	-0.026
TDP2	tyrosyl-DNA phosphodiesterase 2	51567	-0.046
TERF2	telomeric repeat binding factor 2	7014	-0.024
TFCP2	transcription factor CP2	7024	-0.021
TFDP2	transcription factor Dp-2 (E2F dimerization partner 2)	7029	-0.049
TGFA	transforming growth factor, alpha	7039	-0.039
TGFB2	transforming growth factor, beta 2	7042	-0.054
TGFBR3	transforming growth factor, beta receptor III	7049	-0.099
THAP11	THAP domain containing 11	57215	-0.054
THBS1	thrombospondin 1	7057	-0.070
THOC1	THO complex 1	9984	-0.04
THOC2	THO complex 2	57187	-0.024
THUMPD1	THUMP domain containing 1	55623	-0.025
TIA1	TIA1 cytotoxic granule-associated RNA binding protein	7072	-0.036
TIAL1	TIA1 cytotoxic granule-associated RNA binding protein-like 1	7073	-0.023
TIMELESS	timeless circadian clock	8914	-0.045
TIMM17A	translocase of inner mitochondrial membrane 17 homolog A (yeast)	10440	-0.043
TIPIN	TIMELESS interacting protein	54962	-0.027
TLK1	tousled-like kinase 1	9874	-0.068
TLK2	tousled-like kinase 2	11011	-0.016
TMED10	transmembrane emp24-like trafficking protein 10 (yeast)	10972	-0.017
TMED7	transmembrane emp24 protein transport domain containing 7	51014	-0.018
TMEM2	transmembrane protein 2	23670	-0.043
TMEM48	transmembrane protein 48	55706	-0.036
TMF1	TATA element modulatory factor 1	7110	-0.025
TNIK	TRAF2 and NCK interacting kinase	23043	-0.051
TNPO1	transportin 1	3842	-0.023
TOMM70A	translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	9868	-0.048

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**Table S4** (continued)—Cancer-associated network genes.

Gene Symbol	Gene Name	Entrez Gene ID	Log <sub>2</sub> [postCPAP/preCPAP]
TOP1	topoisomerase (DNA) I	7150	-0.033
TOP2A	topoisomerase (DNA) II alpha 170kDa	7153	-0.062
TPX2	TPX2, microtubule-associated, homolog ( <i>Xenopus laevis</i> )	22974	-0.073
TRA	T cell receptor alpha locus	6955	-0.078
TRAF3IP3	TRAF3 interacting protein 3	80342	-0.026
TRAK2	trafficking protein, kinesin binding 2	66008	-0.056
TRAPPC2	trafficking protein particle complex 2	6399	-0.116
TRAPPC4	trafficking protein particle complex 4	51399	-0.034
TRAT1	T cell receptor associated transmembrane adaptor 1	50852	-0.101
TRIM2	tripartite motif containing 2	23321	-0.028
TRIM24	tripartite motif containing 24	8805	-0.038
TRIM37	tripartite motif containing 37	4591	-0.039
TRIP12	thyroid hormone receptor interactor 12	9320	-0.016
TRIP4	thyroid hormone receptor interactor 4	9325	-0.022
TRMT1L	tRNA methyltransferase 1 homolog ( <i>S. cerevisiae</i> )-like	81627	-0.038
TROVE2	TROVE domain family, member 2	6738	-0.041
TRPC1	transient receptor potential cation channel, subfamily C, member 1	7220	-0.098
TRPM7	transient receptor potential cation channel, subfamily M, member 7	54822	-0.047
TRRAP	transformation/transcription domain-associated protein	8295	-0.024
TRUB1	TruB pseudouridine (psi) synthase homolog 1 ( <i>E. coli</i> )	142940	-0.047
TSC22D3	TSC22 domain family, member 3	1831	-0.022
TSR1	TSR1, 20S rRNA accumulation, homolog ( <i>S. cerevisiae</i> )	55720	-0.055
TTC3	tetratricopeptide repeat domain 3	7267	-0.045
TTC37	tetratricopeptide repeat domain 37	9652	-0.043
TTI1	TELO2 interacting protein 1	9675	-0.062
TUBB4B	tubulin, beta 4B class IVb	10383	0.019
TUBG1	tubulin, gamma 1	7283	-0.059
TULP4	tubby like protein 4	56995	-0.054
TXK	TXK tyrosine kinase	7294	-0.086
TYMS	thymidylate synthetase	7298	0.056
U2SURP	U2 snRNP-associated SURP domain containing	23350	-0.035
UBE2C	ubiquitin-conjugating enzyme E2C	11065	-0.080
UBE2D2	ubiquitin-conjugating enzyme E2D 2	7322	-0.057
UBE2I	ubiquitin-conjugating enzyme E2I	7329	-0.027
UBE2K	ubiquitin-conjugating enzyme E2K	3093	-0.025
UBQLN2	ubiquilin 2	29978	-0.019
UCHL5	ubiquitin carboxyl-terminal hydrolase L5	51377	-0.026
UGDH	UDP-glucose 6-dehydrogenase	7358	-0.058
UGGT1	UDP-glucose glycoprotein glucosyltransferase 1	56886	-0.035
UPF3B	UPF3 regulator of nonsense transcripts homolog B (yeast)	65109	-0.023
USO1	USO1 vesicle transport factor	8615	-0.073
USP34	ubiquitin specific peptidase 34	9736	-0.031
USP44	ubiquitin specific peptidase 44	84101	-0.097

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**Table S4** (continued)—Cancer-associated network genes.

Gene Symbol	Gene Name	Entrez Gene ID	Log <sub>2</sub> [postCPAP/preCPAP]
USP47	ubiquitin specific peptidase 47	55031	-0.046
USP9X	ubiquitin specific peptidase 9, X-linked	8239	-0.020
UTP15	UTP15, U3 small nucleolar ribonucleoprotein, homolog (S. cerevisiae)	84135	-0.026
UTRN	utrophin	7402	-0.033
UVRAG	UV radiation resistance associated	7405	-0.026
VBP1	von Hippel-Lindau binding protein 1	7411	-0.105
VDAC3	voltage-dependent anion channel 3	7419	-0.086
VEGFA	vascular endothelial growth factor A	7422	-0.053
VPS13A	vacuolar protein sorting 13 homolog A (S. cerevisiae)	23230	-0.048
VPS26A	vacuolar protein sorting 26 homolog A (S. pombe)	9559	-0.036
VPS45	vacuolar protein sorting 45 homolog (S. cerevisiae)	11311	-0.008
WAC	WW domain containing adaptor with coiled-coil	51322	-0.017
WBP11	WW domain binding protein 11	51729	-0.024
WDR3	WD repeat domain 3	10885	-0.033
WDR75	WD repeat domain 75	84128	-0.040
WDR76	WD repeat domain 76	79968	-0.066
WHSC1	Wolf-Hirschhorn syndrome candidate 1	7468	-0.081
WNK1	WNK lysine deficient protein kinase 1	65125	-0.039
WRN	Werner syndrome, RecQ helicase-like	7486	-0.072
XPA	xeroderma pigmentosum, complementation group A	7507	-0.051
XPO1	exportin 1 (CRM1 homolog, yeast)	7514	-0.073
YES1	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	7525	-0.05
YTHDC1	YTH domain containing 1	91746	-0.011
YTHDF1	YTH domain family, member 1	54915	-0.061
YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	7529	-0.012
YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	7531	-0.025
ZAP70	zeta-chain (TCR) associated protein kinase 70kDa	7535	-0.067
ZBED1	zinc finger, BED-type containing 1	9189	-0.026
ZBTB20	zinc finger and BTB domain containing 20	26137	-0.029
ZBTB5	zinc finger and BTB domain containing 5	9925	-0.035
ZC3H13	zinc finger CCCH-type containing 13	23091	-0.032
ZCCHC10	zinc finger, CCHC domain containing 10	54819	-0.095
ZMYND11	zinc finger, MYND-type containing 11	10771	-0.040
ZNF22	zinc finger protein 22	7570	-0.063
ZNF318	zinc finger protein 318	24149	-0.043
ZNF667	zinc finger protein 667	63934	-0.067
ZRANB2	zinc finger, RAN-binding domain containing 2	9406	-0.035