

Figure S1. Cluster analysis of the PPI network. A total of 1,085 DEGs were filtered into the DEGs PPI network complex that contained 1,012 nodes and 8,332 edges. PPI, protein-protein interaction; DEGs, differentially expressed genes.

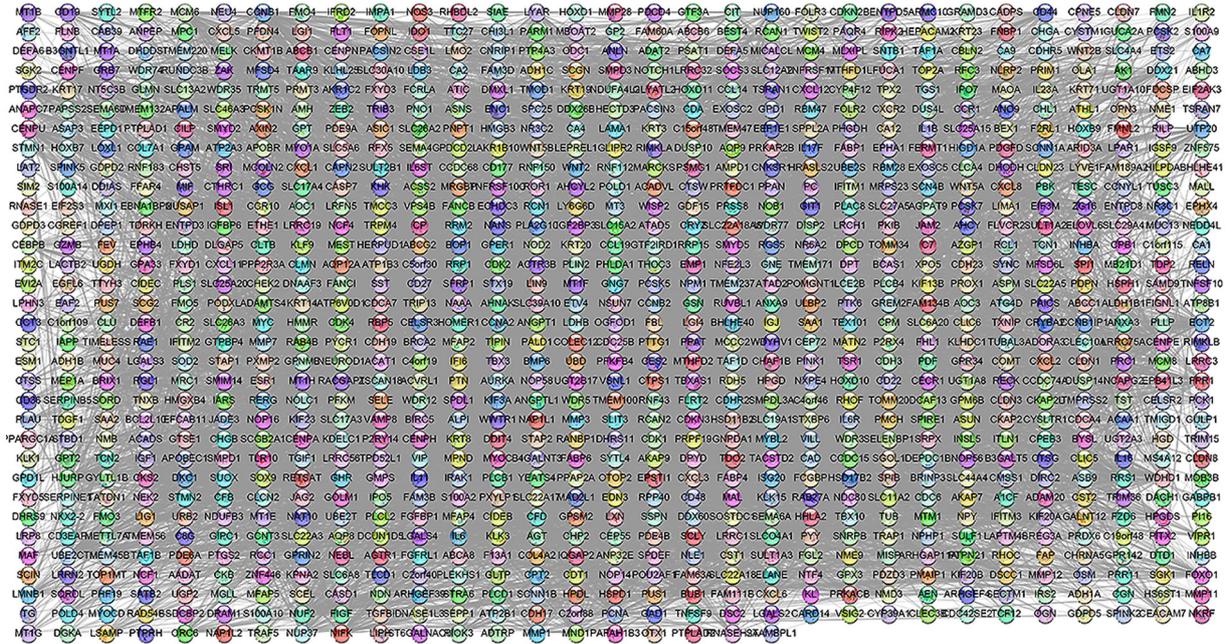


Table SI. Gene Ontology functional enrichment analyses of differently expressed genes associated with colorectal cancer.

Category	Term	Count	%	P-value
GOTERM_BP_DIRECT	GO:0007067~mitotic nuclear division	37	0.022902	5.10E-07
GOTERM_BP_DIRECT	GO:0008284~positive regulation of cell proliferation	53	0.032806	7.25E-06
GOTERM_BP_DIRECT	GO:0006730~one-carbon metabolic process	10	0.00619	3.88E-05
GOTERM_BP_DIRECT	GO:0051301~cell division	41	0.025378	4.75E-05
GOTERM_BP_DIRECT	GO:0006955~immune response	46	0.028473	6.21E-05
GOTERM_BP_DIRECT	GO:0008285~negative regulation of cell proliferation	44	0.027235	8.35E-05
GOTERM_BP_DIRECT	GO:0006260~DNA replication	23	0.014237	1.14E-04
GOTERM_BP_DIRECT	GO:0008283~cell proliferation	41	0.025378	1.27E-04
GOTERM_BP_DIRECT	GO:0007059~chromosome segregation	14	0.008666	1.47E-04
GOTERM_BP_DIRECT	GO:0000086~G2/M transition of mitotic cell cycle	21	0.012999	1.56E-04
GOTERM_BP_DIRECT	GO:0042493~response to drug	35	0.021664	2.58E-04
GOTERM_BP_DIRECT	GO:0048146~positive regulation of fibroblast proliferation	12	0.007428	2.63E-04
GOTERM_BP_DIRECT	GO:0042517~positive regulation of tyrosine phosphorylation of Stat3 protein	10	0.00619	2.89E-04
GOTERM_BP_DIRECT	GO:0050731~positive regulation of peptidyl-tyrosine phosphorylation	15	0.009285	2.89E-04
GOTERM_BP_DIRECT	GO:0000082~G1/S transition of mitotic cell cycle	17	0.010523	3.02E-04
GOTERM_BP_DIRECT	GO:0032496~response to lipopolysaccharide	22	0.013618	6.68E-04
GOTERM_BP_DIRECT	GO:0070098~chemokine-mediated signaling pathway	13	0.008047	8.46E-04
GOTERM_BP_DIRECT	GO:0007062~sister chromatid cohesion	16	0.009904	0.001022
GOTERM_BP_DIRECT	GO:0060326~cell chemotaxis	12	0.007428	0.00136
GOTERM_BP_DIRECT	GO:0071456~cellular response to hypoxia	15	0.009285	0.001465
GOTERM_BP_DIRECT	GO:0006364~rRNA processing	25	0.015475	0.001894
GOTERM_BP_DIRECT	GO:0030855~epithelial cell differentiation	12	0.007428	0.002514
GOTERM_BP_DIRECT	GO:0033138~positive regulation of peptidyl-serine phosphorylation	12	0.007428	0.002514
GOTERM_BP_DIRECT	GO:0006814~sodium ion transport	13	0.008047	0.002723
GOTERM_BP_DIRECT	GO:0001822~kidney development	13	0.008047	0.004499
GOTERM_BP_DIRECT	GO:0022617~extracellular matrix disassembly	12	0.007428	0.004829
GOTERM_BP_DIRECT	GO:0006954~inflammatory response	36	0.022283	0.005838
GOTERM_BP_DIRECT	GO:0043065~positive regulation of apoptotic process	30	0.018569	0.00617
GOTERM_BP_DIRECT	GO:0042127~regulation of cell proliferation	21	0.012999	0.00652
GOTERM_BP_DIRECT	GO:0055114~oxidation-reduction process	51	0.031568	0.006796
GOTERM_BP_DIRECT	GO:0050679~positive regulation of epithelial cell proliferation	10	0.00619	0.008198
GOTERM_BP_DIRECT	GO:0006810~transport	33	0.020426	0.008653
GOTERM_BP_DIRECT	GO:0030336~negative regulation of cell migration	13	0.008047	0.009931
GOTERM_BP_DIRECT	GO:0007586~digestion	10	0.00619	0.011222
GOTERM_BP_DIRECT	GO:0030335~positive regulation of cell migration	20	0.01238	0.01255
GOTERM_BP_DIRECT	GO:0006935~chemotaxis	15	0.009285	0.012783
GOTERM_BP_DIRECT	GO:0030324~lung development	11	0.006809	0.013557
GOTERM_BP_DIRECT	GO:0014068~positive regulation of phosphatidylinositol 3-kinase signaling	10	0.00619	0.013657
GOTERM_BP_DIRECT	GO:0030593~neutrophil chemotaxis	10	0.00619	0.015011
GOTERM_BP_DIRECT	GO:0070374~positive regulation of ERK1 and ERK2 cascade	19	0.011761	0.015393
GOTERM_BP_DIRECT	GO:0043066~negative regulation of apoptotic process	39	0.02414	0.019381
GOTERM_BP_DIRECT	GO:0035690~cellular response to drug	10	0.00619	0.019668
GOTERM_BP_DIRECT	GO:0051091~positive regulation of sequence-specific DNA binding transcription factor activity	13	0.008047	0.020818
GOTERM_BP_DIRECT	GO:1902476~chloride transmembrane transport	12	0.007428	0.02086
GOTERM_BP_DIRECT	GO:0071347~cellular response to interleukin-1	10	0.00619	0.023301
GOTERM_BP_DIRECT	GO:0034220~ion transmembrane transport	21	0.012999	0.023731
GOTERM_BP_DIRECT	GO:0016485~protein processing	10	0.00619	0.025287
GOTERM_BP_DIRECT	GO:0007204~positive regulation of cytosolic calcium ion concentration	15	0.009285	0.026814
GOTERM_BP_DIRECT	GO:0050729~positive regulation of inflammatory response	10	0.00619	0.02739

Table SI. Continued. Gene Ontology functional enrichment analyses of differently expressed genes associated with colorectal cancer.

Category	Term	Count	%	P-value
GOTERM_BP_DIRECT	GO:0050900~leukocyte migration	14	0.008666	0.027873
GOTERM_BP_DIRECT	GO:0006508~proteolysis	41	0.025378	0.031161
GOTERM_BP_DIRECT	GO:0006629~lipid metabolic process	16	0.009904	0.044643
GOTERM_BP_DIRECT	GO:0001764~neuron migration	12	0.007428	0.04541
GOTERM_BP_DIRECT	GO:0007267~cell-cell signaling	23	0.014237	0.046196
GOTERM_CC_DIRECT	GO:0005615~extracellular space	153	0.094704	1.90E-16
GOTERM_CC_DIRECT	GO:0070062~extracellular exosome	248	0.153507	3.86E-13
GOTERM_CC_DIRECT	GO:0005576~extracellular region	135	0.083562	4.92E-06
GOTERM_CC_DIRECT	GO:0016324~apical plasma membrane	37	0.022902	1.08E-05
GOTERM_CC_DIRECT	GO:0005829~cytosol	241	0.149174	2.92E-05
GOTERM_CC_DIRECT	GO:0031526~brush border membrane	11	0.006809	5.35E-04
GOTERM_CC_DIRECT	GO:0030141~secretory granule	13	0.008047	9.40E-04
GOTERM_CC_DIRECT	GO:0000777~condensed chromosome kinetochore	14	0.008666	0.001287
GOTERM_CC_DIRECT	GO:0005578~proteinaceous extracellular matrix	29	0.01795	0.00154
GOTERM_CC_DIRECT	GO:0031225~anchored component of membrane	16	0.009904	0.001939
GOTERM_CC_DIRECT	GO:0045177~apical part of cell	12	0.007428	0.003435
GOTERM_CC_DIRECT	GO:0000922~spindle pole	15	0.009285	0.00367
GOTERM_CC_DIRECT	GO:0005813~centrosome	39	0.02414	0.004448
GOTERM_CC_DIRECT	GO:0000775~chromosome, centromeric region	10	0.00619	0.004762
GOTERM_CC_DIRECT	GO:0005730~nucleolus	68	0.042091	0.005708
GOTERM_CC_DIRECT	GO:0005886~plasma membrane	269	0.166506	0.008509
GOTERM_CC_DIRECT	GO:0005737~cytoplasm	334	0.206739	0.008805
GOTERM_CC_DIRECT	GO:0031012~extracellular matrix	28	0.017331	0.01134
GOTERM_CC_DIRECT	GO:0048471~perinuclear region of cytoplasm	50	0.030949	0.013934
GOTERM_CC_DIRECT	GO:0045121~membrane raft	21	0.012999	0.014552
GOTERM_CC_DIRECT	GO:0030496~midbody	15	0.009285	0.015673
GOTERM_CC_DIRECT	GO:0005887~integral component of plasma membrane	100	0.061898	0.020456
GOTERM_CC_DIRECT	GO:0005654~nucleoplasm	184	0.113892	0.021124
GOTERM_CC_DIRECT	GO:0005938~cell cortex	14	0.008666	0.023639
GOTERM_CC_DIRECT	GO:0009986~cell surface	43	0.026616	0.028033
GOTERM_CC_DIRECT	GO:0000776~kinetochore	10	0.00619	0.041291
GOTERM_CC_DIRECT	GO:0005796~Golgi lumen	11	0.006809	0.047491
GOTERM_MF_DIRECT	GO:0005179~hormone activity	18	0.011142	2.70E-05
GOTERM_MF_DIRECT	GO:0017080~sodium channel regulator activity	10	0.00619	6.21E-05
GOTERM_MF_DIRECT	GO:0051287~NAD binding	10	0.00619	2.63E-04
GOTERM_MF_DIRECT	GO:0042803~protein homodimerization activity	66	0.040853	4.18E-04
GOTERM_MF_DIRECT	GO:0005515~protein binding	563	0.348486	5.65E-04
GOTERM_MF_DIRECT	GO:0008201~heparin binding	21	0.012999	0.001033
GOTERM_MF_DIRECT	GO:0005125~cytokine activity	22	0.013618	0.001425
GOTERM_MF_DIRECT	GO:0008009~chemokine activity	10	0.00619	0.001865
GOTERM_MF_DIRECT	GO:0008083~growth factor activity	20	0.01238	0.002856
GOTERM_MF_DIRECT	GO:0005215~transporter activity	23	0.014237	0.003536
GOTERM_MF_DIRECT	GO:0004252~serine-type endopeptidase activity	24	0.014856	0.025162
GOTERM_MF_DIRECT	GO:0005509~calcium ion binding	55	0.034044	0.03151

Table SII. Gene Ontology functional enrichment analyses of upregulated genes associated with colorectal cancer.

Category	Term	Count	%	P-value
GOTERM_CC_DIRECT	GO:0005654~nucleoplasm	143	28.88889	6.32E-17
GOTERM_BP_DIRECT	GO:0007067~mitotic nuclear division	34	6.868687	4.25E-14
GOTERM_BP_DIRECT	GO:0051301~cell division	38	7.676768	1.62E-12
GOTERM_CC_DIRECT	GO:0005730~nucleolus	60	12.12121	5.94E-12
GOTERM_CC_DIRECT	GO:0005829~cytosol	137	27.67677	6.33E-09
GOTERM_BP_DIRECT	GO:0006260~DNA replication	21	4.242424	8.13E-09
GOTERM_BP_DIRECT	GO:0000082~G1/S transition of mitotic cell cycle	17	3.434343	1.54E-08
GOTERM_MF_DIRECT	GO:0005515~protein binding	298	60.20202	1.84E-08
GOTERM_BP_DIRECT	GO:0006364~rRNA processing	23	4.646465	9.69E-08
GOTERM_BP_DIRECT	GO:0007062~sister chromatid cohesion	16	3.232323	1.21E-07
GOTERM_CC_DIRECT	GO:0005634~nucleus	192	38.78788	2.48E-07
GOTERM_CC_DIRECT	GO:0000777~condensed chromosome kinetochore	14	2.828283	3.49E-07
GOTERM_BP_DIRECT	GO:0000086~G2/M transition of mitotic cell cycle	17	3.434343	1.01E-06
GOTERM_BP_DIRECT	GO:0007059~chromosome segregation	12	2.424242	2.04E-06
GOTERM_CC_DIRECT	GO:0005813~centrosome	30	6.060606	2.27E-06
GOTERM_BP_DIRECT	GO:0008283~cell proliferation	27	5.454545	8.73E-06
GOTERM_BP_DIRECT	GO:0032496~response to lipopolysaccharide	17	3.434343	1.07E-05
GOTERM_CC_DIRECT	GO:0000775~chromosome, centromeric region	10	2.020202	1.43E-05
GOTERM_CC_DIRECT	GO:0000922~spindle pole	13	2.626263	2.50E-05
GOTERM_CC_DIRECT	GO:0030496~midbody	14	2.828283	3.00E-05
GOTERM_BP_DIRECT	GO:0042493~response to drug	23	4.646465	3.22E-05
GOTERM_BP_DIRECT	GO:0008284~positive regulation of cell proliferation	30	6.060606	3.25E-05
GOTERM_CC_DIRECT	GO:0005615~extracellular space	59	11.91919	8.51E-05
GOTERM_BP_DIRECT	GO:0008285~negative regulation of cell proliferation	26	5.252525	9.03E-05
GOTERM_BP_DIRECT	GO:0030324~lung development	10	2.020202	2.14E-04
GOTERM_CC_DIRECT	GO:0000776~kinetochore	10	2.020202	2.39E-04
GOTERM_CC_DIRECT	GO:0005737~cytoplasm	169	34.14141	4.88E-04
GOTERM_MF_DIRECT	GO:0005524~ATP binding	63	12.72727	5.26E-04
GOTERM_MF_DIRECT	GO:0044822~poly(A) RNA binding	50	10.10101	7.96E-04
GOTERM_CC_DIRECT	GO:0015630~microtubule cytoskeleton	11	2.222222	0.002986
GOTERM_MF_DIRECT	GO:0005125~cytokine activity	13	2.626263	0.003203
GOTERM_BP_DIRECT	GO:0051092~positive regulation of NF-kappaB transcription factor activity	11	2.222222	0.003469
GOTERM_BP_DIRECT	GO:0045766~positive regulation of angiogenesis	10	2.020202	0.004181
GOTERM_MF_DIRECT	GO:0008083~growth factor activity	12	2.424242	0.004822
GOTERM_CC_DIRECT	GO:0016020~membrane	77	15.55556	0.004938
GOTERM_MF_DIRECT	GO:0042803~protein homodimerization activity	33	6.666667	0.005599
GOTERM_MF_DIRECT	GO:0019901~protein kinase binding	20	4.040404	0.007379
GOTERM_MF_DIRECT	GO:0042802~identical protein binding	33	6.666667	0.007923
GOTERM_BP_DIRECT	GO:0006954~inflammatory response	20	4.040404	0.008146
GOTERM_BP_DIRECT	GO:0042127~regulation of cell proliferation	12	2.424242	0.012602
GOTERM_BP_DIRECT	GO:0045893~positive regulation of transcription, DNA-templated	24	4.848485	0.014224
GOTERM_BP_DIRECT	GO:0051607~defense response to virus	11	2.222222	0.014997
GOTERM_BP_DIRECT	GO:0043066~negative regulation of apoptotic process	21	4.242424	0.024687
GOTERM_BP_DIRECT	GO:0043065~positive regulation of apoptotic process	15	3.030303	0.035789
GOTERM_CC_DIRECT	GO:0031965~nuclear membrane	12	2.424242	0.036373
GOTERM_BP_DIRECT	GO:0006955~immune response	19	3.838384	0.040212
GOTERM_CC_DIRECT	GO:0005576~extracellular region	54	10.90909	0.040649
GOTERM_MF_DIRECT	GO:0003723~RNA binding	23	4.646465	0.044868
GOTERM_BP_DIRECT	GO:0007267~cell-cell signaling	13	2.626263	0.045952

Table SIII. Gene Ontology functional enrichment analyses of down-regulated genes associated with colorectal cancer.

Category	Term	Count	%	P-value
GOTERM_CC_DIRECT	GO:0070062~extracellular exosome	173	29.57265	7.97E-20
GOTERM_CC_DIRECT	GO:0005615~extracellular space	94	16.06838	2.62E-13
GOTERM_CC_DIRECT	GO:0005886~plasma membrane	190	32.47863	3.11E-09
GOTERM_CC_DIRECT	GO:0016324~apical plasma membrane	25	4.273504	1.62E-05
GOTERM_CC_DIRECT	GO:0005576~extracellular region	81	13.84615	2.15E-05
GOTERM_CC_DIRECT	GO:0016021~integral component of membrane	207	35.38462	2.39E-05
GOTERM_CC_DIRECT	GO:0005887~integral component of plasma membrane	73	12.47863	2.72E-05
GOTERM_MF_DIRECT	GO:0008201~heparin binding	16	2.735043	1.41E-04
GOTERM_BP_DIRECT	GO:0030855~epithelial cell differentiation	10	1.709402	3.55E-04
GOTERM_BP_DIRECT	GO:0034220~ion transmembrane transport	18	3.076923	3.98E-04
GOTERM_MF_DIRECT	GO:0005179~hormone activity	11	1.880342	6.66E-04
GOTERM_BP_DIRECT	GO:0006955~immune response	27	4.615385	9.91E-04
GOTERM_BP_DIRECT	GO:0006814~sodium ion transport	10	1.709402	0.001047
GOTERM_BP_DIRECT	GO:0006810~transport	23	3.931624	0.001767
GOTERM_CC_DIRECT	GO:0048471~perinuclear region of cytoplasm	34	5.811966	0.002209
GOTERM_BP_DIRECT	GO:1902476~chloride transmembrane transport	10	1.709402	0.002764
GOTERM_CC_DIRECT	GO:0031225~anchored component of membrane	11	1.880342	0.002876
GOTERM_CC_DIRECT	GO:0005578~proteinaceous extracellular matrix	18	3.076923	0.004736
GOTERM_BP_DIRECT	GO:0006508~proteolysis	28	4.786325	0.005253
GOTERM_BP_DIRECT	GO:0070374~positive regulation of ERK1 and ERK2 cascade	13	2.222222	0.010117
GOTERM_MF_DIRECT	GO:0005215~transporter activity	14	2.393162	0.010499
GOTERM_CC_DIRECT	GO:0005783~endoplasmic reticulum	39	6.666667	0.01177
GOTERM_CC_DIRECT	GO:0045121~membrane raft	14	2.393162	0.013092
GOTERM_BP_DIRECT	GO:0007166~cell surface receptor signaling pathway	17	2.905983	0.014413
GOTERM_CC_DIRECT	GO:0005938~cell cortex	10	1.709402	0.015181
GOTERM_BP_DIRECT	GO:0055085~transmembrane transport	15	2.564103	0.024294
GOTERM_BP_DIRECT	GO:0007204~positive regulation of cytosolic calcium ion concentration	10	1.709402	0.027109
GOTERM_MF_DIRECT	GO:0005102~receptor binding	19	3.247863	0.027331
GOTERM_MF_DIRECT	GO:0004252~serine-type endopeptidase activity	15	2.564103	0.028217
GOTERM_BP_DIRECT	GO:0006629~lipid metabolic process	11	1.880342	0.028299
GOTERM_MF_DIRECT	GO:0042803~protein homodimerization activity	33	5.641026	0.032042
GOTERM_BP_DIRECT	GO:0030335~positive regulation of cell migration	12	2.051282	0.033109
GOTERM_BP_DIRECT	GO:0055114~oxidation-reduction process	28	4.786325	0.037941
GOTERM_BP_DIRECT	GO:0008284~positive regulation of cell proliferation	23	3.931624	0.042122
GOTERM_MF_DIRECT	GO:0005198~structural molecule activity	14	2.393162	0.044876

Table SIV. KEGG enrichment analyses of upregulated genes associated with CRC.

Category	Term	Count	%	P-value
KEGG_PATHWAY	hsa04110:Cell cycle	19	3.83	2.41E-8
KEGG_PATHWAY	hsa04115:p53 signaling pathway	11	2.22	2.71E-5
KEGG_PATHWAY	hsa04668:TNF signaling pathway	12	2.42	3.46E-4

KEGG, Kyoto Encyclopedia of Genes and Genomes.

Table SV. KEGG enrichment analyses of down-regulated genes associated with colorectal.

Category	Term	Count	%	P-value
KEGG_PATHWAY	hsa04110: Retinol metabolism	10	1.71	5.15E-4
KEGG_PATHWAY	hsa04115: Drug metabolism-cytochrome P450	10	1.71	8.10E-4
KEGG_PATHWAY	hsa04668: Metabolic pathways	64	10.96	2.39E-3

KEGG, Kyoto Encyclopedia of Genes and Genomes.