Supplementary Table 3: Down-regulated gene ontology pathways in UC patients harboring remote neoplasia using DAVID webtool

Category	Term	Count	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_DIRECT	GO:0015701~bicarbonate transport	5	41.87	0.002	0.002	0.01
UP_SEQ_FEATURE	signal peptide	25	2.50	0.002	0.002	0.01
KEGG_PATHWAY	hsa04976:Bile secretion	5	19.21	0.01	0.01	0.10
UP_KEYWORDS	Signal	24	2.29	0.01	0.01	0.09
PIR_SUPERFAMILY	PIRSF001849:guanylin	2	237.14	0.04	0.04	3.41
SMART	SM01057:SM01057	3	53.85	0.05	0.05	1.16
KEGG_PATHWAY	hsa00910:Nitrogen metabolism	3	46.77	0.10	0.05	1.66
INTERPRO	IPR013098:Immunoglobulin I-set	5	10.04	0.21	0.06	1.74
KEGG_PATHWAY	hsa04964:Proximal tubule bicarbonate reclamation	3	34.57	0.17	0.06	3.03
GOTERM_MF_DIRECT	GO:0004089~carbonate dehydratase activity	3	69.26	0.07	0.07	0.87
INTERPRO	IPR001148:Alpha carbonic anhydrase	3	53.23	0.20	0.07	1.66
GOTERM_BP_DIRECT	GO:0055085~transmembrane transport	9	4.69	0.14	0.07	0.67
INTERPRO	IPR023561:Carbonic anhydrase, alpha-class	3	59.88	0.16	0.08	1.31
INTERPRO	IPR018338:Carbonic anhydrase, alpha-class, conserved site	3	79.85	0.09	0.09	0.73
SMART	SM00408:SM00408	5	6.84	0.18	0.09	4.54
UP_KEYWORDS	Transmembrane	26	1.65	0.52	0.12	6.00
UP_KEYWORDS	Glycoprotein	24	1.77	0.39	0.12	4.07
UP_KEYWORDS	Secreted	14	2.47	0.35	0.13	3.47
UP_KEYWORDS	Transmembrane helix	26	1.66	0.51	0.13	5.72
INTERPRO	IPR003598:Immunoglobulin subtype 2	5	7.16	0.55	0.15	5.77
UP_KEYWORDS	Membrane	33	1.55	0.28	0.15	2.74
INTERPRO	IPR000879:Guanylin	2	319.39	0.63	0.15	7.19
GOTERM_CC_DIRECT	GO:0070062~extracellular exosome	18	1.95	0.37	0.21	6.27
GOTERM_CC_DIRECT	GO:0016323~basolateral plasma membrane	5	7.98	0.22	0.22	3.45
GOTERM_BP_DIRECT	GO:0006730~one-carbon metabolic process	3	33.49	0.66	0.30	4.54
GOTERM_BP_DIRECT	GO:0034220~ion transmembrane transport	5	6.98	0.80	0.33	6.81
UP_SEQ_FEATURE	topological domain:Cytoplasmic	20	1.94	0.56	0.34	4.57
UP_KEYWORDS	Antibiotic	3	10.89	0.99	0.38	30.35
GOTERM_CC_DIRECT	GO:0045177~apical part of cell	3	11.54	0.87	0.40	24.99
UP_KEYWORDS	Cell membrane	16	1.74	0.99	0.41	29.99
UP_KEYWORDS	Transport	12	2.04	0.98	0.42	27.45
GOTERM_MF_DIRECT	GO:0004064~arylesterase activity	2	107.73	0.81	0.42	18.02
UP_KEYWORDS	Antimicrobial	3	9.54	1.00	0.43	37.02
GOTERM_MF_DIRECT	GO:0005254~chloride channel activity	3	17.31	0.68	0.44	12.83
INTERPRO	IPR026845:Neurexophilin/NXPE	2	79.85	0.98	0.44	25.81
GOTERM_CC_DIRECT	GO:0005615~extracellular space	10	2.34	0.82	0.44	21.49
UP_KEYWORDS	Polymorphism	43	1.19	1.00	0.48	45.51
KEGG_PATHWAY	hsa04972:Pancreatic secretion	3	8.64	0.93	0.49	35.97
UP_SEQ_FEATURE	transmembrane region	24	1.59	0.95	0.53	15.93
UP_KEYWORDS	Immunoglobulin domain	5	3.27	1.00	0.54	53.74
GOTERM_MF_DIRECT	GO:0005179~hormone activity	3	10.21	0.96	0.54	31.16
UP_KEYWORDS	Lyase	3	6.86	1.00	0.54	57.01
GOTERM_BP_DIRECT	GO:0007586~digestion	3	16.75	0.98	0.56	16.46
UP_KEYWORDS	Lectin	3	5.93	1.00	0.61	66.61
UP_SEQ_FEATURE	topological domain:Extracellular	16	1.92	0.95	0.63	15.49
GOTERM_CC_DIRECT	GO:0005886~plasma membrane	19	1.46	1.00	0.67	53.80
UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	20	1.58	1.00	0.76	33.11
GOTERM_BP_DIRECT	GO:0031284~positive regulation of guanylate cyclase activity	2	60.90	1.00	0.76	35.12
GOTERM_BP_DIRECT	GO:0002009~morphogenesis of an epithelium	2	51.53	1.00	0.77	40.03
GOTERM_BP_DIRECT	GO:1902476~chloride transmembrane transport	3	11.16	1.00	0.77	32.16
GOTERM_BP_DIRECT	GO:0051453~regulation of intracellular pH	2	39.40	1.00	0.82	48.76
GOTERM_BP_DIRECT	GO:0006810~transport	4	4.51	1.00	0.83	53.79
INTERPRO	IPR007110:Immunoglobulin-like domain	5	2.93	1.00	0.84	66.54
GOTERM_BP_DIRECT	GO:0006811~ion transport	3	6.79	1.00	0.87	62.03
GOTERM_BP_DIRECT	GO:0043552~positive regulation of phosphatidylinositol 3-kinase	2	22.33	1.00	0.88	69.29
GOTERM_BP_DIRECT	GO:0050832~defense response to fungus	2	23.92	1.00	0.88	66.77
UP_SEQ_FEATURE	metal ion-binding site:Zinc; catalytic	3	7.78	1.00	0.88	51.65
GOTERM_BP_DIRECT	GO:0045597~positive regulation of cell differentiation	2	19.14	1.00	0.90	74.78
UP_SEQ_FEATURE	sequence variant	43	1.16	1.00	0.95	70.86