Table 3. **GOMiner Analysis for Genes Overexpressed in PTEN IHC– Tumors**

Rank	GO ID	Total	Under	Over	Change	P-Value (Over)	Term	Cell Cycle-related	Metabolism-related
1	6996	373	11	33	44	0	organelle organization and biogenesis		1
2	7017	63	2	12	14	0	microtubule-based process		
3	7049	416	10	49	59	0	cell cycle	1	
4	74	263	5	27	32	0	regulation of cell cycle	1	
5	7067	121	2	22	24	0	mitosis	1	
6	87	123	2	22	24	0	M phase of mitotic cell cycle	1	
7	279	141	2	25	27	0	M phase	1	
8	278	169	2	28	30	0	mitotic cell cycle	1	
9	910	112	1	17	18	0	cytokinesis	1	
10	51301	112	1	17	18	0	cell division	1	
11	7018	33	0	10	10	0	microtubule-based movement	1	
12	30705	33	0	10	10	0	cytoskeleton-dependent intracellular transport	1	
13	6270	12	0	5	5	0.0001	DNA replication initiation	1	
14	6261	45	0	9	9	0.0001	DNA-dependent DNA replication	1	
15	51329	56	0	10	10	0.0001	interphase of mitotic cell cycle	1	
16	51325	56	0	10	10	0.0001	interphase	1	
17	75	28	0	7	7	0.0001	cell cycle checkpoint	1	
18	16043	451	12	35	47	0.0003	cell organization and biogenesis		1
19	6259	311	7	27	34	0.0003	DNA metabolism		1
20	43283	804	15	54	69	0.0003	biopolymer metabolism		1
21	7093	10	0	4	4	0.0005	mitotic checkpoint	1	
22	7088	28	0	6	6	0.0009	regulation of mitosis	1	
23	6139	1408	31	81	112	0.0011	nucleobase, nucleoside, nucleotide and nucleic acid metabolism		1
24	6801	6	0	3	3	0.0014	superoxide metabolism		1
25	7089	6	0	3	3	0.0014	traversing start control point of mitotic cell cycle	1	
26	86	30	0	6	6	0.0014	G2/M transition of mitotic cell cycle	1	
27	8283	251	7	21	28	0.002	cell proliferation	1	
28	50875	4227	109	199	308	0.0021	cellular physiological process		
29	7001	125	4	13	17	0.0023	chromosome organization and biogenesis (sensu Eukaryota)	1	
30	46112	7	0	3	3	0.0023	nucleobase biosynthesis		1
31	6468	310	11	24	35	0.0028	protein amino acid phosphorylation		1
32	9987	4725	123	217	340	0.003	cellular process		
33	51258	15	0	4	4	0.003	protein polymerization		1
34	51276	147	4	14	18	0.0036	chromosome organization and biogenesis	1	
35	7059	36	0	6	6	0.0036	chromosome segregation	1	
36	9112	8	0	3	3	0.0036	nucleobase metabolism		1
37	6333	49	3	7	10	0.0042	chromatin assembly or disassembly	1	
38	7010	166	6	15	21	0.0043	cytoskeleton organization and biogenesis		1
39	19058	17	1	4	5	0.0048	viral infectious cycle		
40	6260	91	1	10	11	0.0049	DNA replication	1	
41	70	27	0	5	5	0.0049	mitotic sister chromatid segregation	1	
42	8150	5172	136	232	368	0.005	biological_process		
43	16310	361	11	26	37	0.0051	phosphorylation		1
44	6379	3	0	2	2	0.0052	mRNA cleavage		1
45	9113	3	0	2	2	0.0052	purine base biosynthesis		1
46	819	28	0	5	5	0.0058	sister chromatid segregation	1	
47	6396	172	2	15	17	0.006	RNA processing		1
48	46907	293	5	22	27	0.0061	intracellular transport		
49	51244	1284	32	71	103	0.0069	regulation of cellular physiological process		
50	6397	111	1	11	12	0.007	mRNA processing		1
51	6464	807	27	48	75	0.0079	protein modification		1
52	7582	4601	117	210	327	0.0096	physiological process		
53	67	11	0	3	3	0.0096	DNA replication and chromosome cycle	1	
54	7094	4	0	2	2	0.0101	mitotic spindle checkpoint	1	
55	6144	4	0	2	2	0.0101	purine base metabolism		1
56	16032	21	1	4	5	0.0106	viral life cycle		
57	7046	21	0	4	4	0.0106	ribosome biogenesis		1
58	44238	3044	79	147	226	0.0114	primary metabolism		1
59	50794	1355	34	73	107	0.0115	regulation of cellular process		
60	51318	12	0	3	3	0.0124	G1 phase	1	
61	80	12	0	3	3	0.0124	G1 phase of mitotic cell cycle	1	
62	42254	22	0	4	4	0.0126	ribosome biogenesis and assembly		1
63	16071	123	1	11	12	0.0147	mRNA metabolism		1
64	6378	5	0	2	2	0.0164	mRNA polyadenylylation		1
65	9067	5	0	2	2	0.0164	aspartate family amino acid biosynthesis		1
66	50791	1354	35	72	107	0.0165	regulation of physiological process		
67	79	24	0	4	4	0.0171	regulation of cyclin dependent protein kinase activity	1	
68	16070	214	2	16	18	0.0188	RNA metabolism		1
69	82	37	0	5	5	0.0188	G1/S transition of mitotic cell cycle	1	
70	6796	443	17	28	45	0.0202	phosphate metabolism		1
71	6793	443	17	28	45	0.0202	phosphorus metabolism		1
72	6041	6	0	2	2	0.0239	glucosamine metabolism		1
73	6040	6	0	2	2	0.0239	amino sugar metabolism		1
74	31124	6	0	2	2	0.0239	mRNA 3'-end processing		1
75	31123	6	0	2	2	0.0239	RNA 3'-end processing		1
76	50789	1474	38	76	114	0.0273	regulation of biological process		
77	6334	28	1	4	5	0.0289	nucleosome assembly	1	
78	42127	120	2	10	12	0.0302	regulation of cell proliferation	1	
79	6325	104	4	9	13	0.0314	establishment and/or maintenance of chromatin architecture	1	
80	50792	7	1	2	3	0.0326	regulation of viral life cycle		
81	6800	31	2	4	6	0.0403	oxygen and reactive oxygen species metabolism		1
82	7028	31	0	4	4	0.0403	cytoplasm organization and biogenesis		1
83	6323	109	4	9	13	0.0407	DNA packaging	1	

Rank	GO ID	Total	Under	Over	Change	P-Value (Over)	Term	Cell Cycle-related	Metabolism-related
84	46049	1	0	1	1	0.0424	UMP metabolism		1
85	7130	1	0	1	1	0.0424	synaptonemal complex formation	1	
86	7129	1	0	1	1	0.0424	synapsis	1	
87	7128	1	0	1	1	0.0424	meiotic prophase I	1	
88	7095	1	0	1	1	0.0424	mitotic G2 checkpoint	1	
89	7079	1	0	1	1	0.0424	mitotic chromosome movement towards spindle pole	1	
90	6597	1	0	1	1	0.0424	spermine biosynthesis		1
91	6547	1	0	1	1	0.0424	histidine metabolism		1
92	45071	1	0	1	1	0.0424	negative regulation of viral genome replication		
93	6222	1	0	1	1	0.0424	UMP biosynthesis		1
94	1315	1	0	1	1	0.0424	age-dependent response to reactive oxygen species		
95	6048	1	0	1	1	0.0424	UDP-N-acetylglucosamine biosynthesis		1
96	6045	1	0	1	1	0.0424	N-acetylglucosamine biosynthesis		1
97	6042	1	0	1	1	0.0424	glucosamine biosynthesis		1
98	51324	1	0	1	1	0.0424	prophase	1	
99	51305	1	0	1	1	0.0424	chromosome movement towards spindle pole	1	
100	48525	1	0	1	1	0.0424	negative regulation of viral life cycle		
101	305	1	0	1	1	0.0424	response to oxygen radicals		
102	303	1	0	1	1	0.0424	response to superoxide		
103	17121	1	0	1	1	0.0424	phospholipid scrambling		
104	50434	1	0	1	1	0.0424	positive regulation of viral transcription		
105	30838	1	0	1	1	0.0424	positive regulation of actin filament polymerization		1
106	105	1	0	1	1	0.0424	histidine biosynthesis		1
107	9301	1	0	1	1	0.0424	snRNA transcription		1
108	72	1	0	1	1	0.0424	M phase specific microtubule process	1	
109	9174	1	0	1	1	0.0424	pyrimidine ribonucleoside monophosphate biosynthesis		1
110	9173	1	0	1	1	0.0424	pyrimidine ribonucleoside monophosphate metabolism		1
111	9089	1	0	1	1	0.0424	lysine biosynthesis via diaminopimelate		1
112	9085	1	0	1	1	0.0424	lysine biosynthesis		1
113	9076	1	0	1	1	0.0424	histidine family amino acid biosynthesis		1
114	9075	1	0	1	1	0.0424	histidine family amino acid metabolism		1
115	15680	1	0	1	1	0.0424	intracellular copper ion transport		
116	19877	1	0	1	1	0.0424	diaminopimelate biosynthesis		1
117	8215	1	0	1	1	0.0424	spermine metabolism		1
118	46451	1	0	1	1	0.0424	diaminopimelate metabolism		1
119	46349	1	0	1	1	0.0424	amino sugar biosynthesis		1
120	8054	1	0	1	1	0.0424	cyclin catabolism	1	
121	45869	1	0	1	1	0.0424	negative regulation of retroviral genome replication		
122	44237	3133	80	146	226	0.0485	cellular metabolism		1

Note: Gene Ontology (GO) analysis was performed using the top 785 signature genes with APV<0.05. Only 'biological process' GO categories overrepresented as upregulated in PTEN IHC– tumors and with *P* <0.05 are shown. 'Total' = total # of genes annotated to the given category; 'Under' = # of these genes underexpressed in PTEN IHC– group; 'Over' = # of genes overexpressed in PTEN IHC– group; 'Changed' = total # of genes that are under- or overexpressed. Cell cycle and metabolism-related categories were identified manually.