Table 4. **GOMiner Analysis for Genes Overexpressed in PTEN IHC+ Tumors**

Rank	GO ID	Total	Under	Over	Change	P-Value (Over)	Term	Muscle-related	MAPK-related
1	165	51	0	7	7	0.0003	MAPKKK cascade		1
2	6940	2	0	2	2	0.0007	regulation of smooth muscle contraction	1	
3	6937	9	0	3	3	0.0012	regulation of muscle contraction	1	
4	6939	12	0	3	3	0.003	smooth muscle contraction	1	
5	188	13	0	3	3	0.0039	inactivation of MAPK		1
6	7243	147	5	10	15	0.0042	protein kinase cascade		
7	7154	1346	44	48	92	0.0064	cell communication		
8	6936	49	0	5	5	0.0079	muscle contraction	1	
9	7165	1093	38	40	78	0.0091	signal transduction		
10	7167	101	4	7	11	0.0145	enzyme linked receptor protein signaling pathway		
11	9190	9	0	2	2	0.0208	cyclic nucleotide biosynthesis		
12	7254	24	0	3	3	0.0224	JNK cascade		1
13	31098	24	0	3	3	0.0224	stress-activated protein kinase signaling pathway		
14	6960	1	0	1	1	0.0256	antimicrobial humoral response (sensu Protostomia)		
15	6911	1	0	1	1	0.0256	phagocytosis, engulfment		
16	6909	10	0	2	2	0.0256	phagocytosis		
17	6651	1	0	1	1	0.0256	diacylglycerol biosynthesis		
18	6627	1	0	1	1	0.0256	mitochondrial protein processing		
19	6610	1	0	1	1	0.0256	ribosomal protein-nucleus import		
20	6581	1	0	1	1	0.0256	acetylcholine catabolism		
21	6573	1	0	1	1	0.0256	valine metabolism		
22	1507	1	0	1	1	0.0256	acetylcholine catabolism in synaptic cleft		
23	51294	1	0	1	1	0.0256	establishment of spindle orientation		
24	16572	1	0	1	1	0.0256	histone phosphorylation		
25	132	1	0	1	1	0.0256	establishment of mitotic spindle orientation		
26	48016	1	0	1	1	0.0256	inositol phosphate-mediated signaling		
27	16065	1	0	1	1	0.0256	humoral defense mechanism (sensu Protostomia)		
28	8291	1	0	1	1	0.0256	acetylcholine metabolism		
29	45947	1	0	1	1	0.0256	negative regulation of translational initiation		
30	9653	499	11	20	31	0.0285	morphogenesis		
31	6897	68	0	5	5	0.0294	endocytosis		
32	9310	27	0	3	3	0.0306	amine catabolism		
33	7205	11	0	2	2	0.0307	protein kinase C activation		1
34	1503	11	0	2	2	0.0307	ossification		
35	31214	11	0	2	2	0.0307	biomineral formation		
36	7169	69	3	5	8	0.0311	transmembrane receptor protein tyrosine kinase signaling pathway		
37	9887	383	9	16	25	0.0348	organogenesis		
38	48513	383	9	16	25	0.0348	organ development		
39	7173	12	0	2	2	0.0363	epidermal growth factor receptor signaling pathway		
40	46849	12	0	2	2	0.0363	bone remodeling		
41	44267	1414	71	46	117	0.0384	cellular protein metabolism		
42	7166	390	14	16	30	0.0401	cell surface receptor linked signal transduction		
43	7275	719	20	26	46	0.0413	development		
44	6470	75	2	5	7	0.0423	protein amino acid dephosphorylation		
45	19538	1424	71	46	117	0.0428	protein metabolism		
46	16311	76	2	5	7	0.0444	dephosphorylation		

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. Muscle and MAPK pathway-related categories were identified manually.