Table 2. **PTEN Signature Gene List: 246 genes with a consensus average P-value<0.02**

Rank	Clone ID	Accession	Unigene ID (Build 188)	Gene name	Symbol	Sign	Average P-value
1	366966	AA026562	Hs.500466	Phosphatase and tensin homolog (mutated in multiple advanced cancers 1)	PTEN	-30	0.000056
2	340722	W56360	Hs.85195	Myeloid leukemia factor 1	MLF1	30	0.000315
3	138168	N/A	N/A	N/A	N/A	-30	0.000551
4	2366057	AI740827	Hs.113684	Cadherin 12, type 2 (N-cadherin 2)	CDH12	30	0.000599
5	325600	W51744	Hs.437256	Glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	GRINL1A	-30	0.000715
6	462926	AA682321	Hs.153704	NIMA (never in mitosis gene a)-related kinase 2	NEK2	30	0.000753
7	415089	W93379	Hs.153704	NIMA (never in mitosis gene a)-related kinase 2	NEK2	30	0.000941
8	1472719	AA872379	Hs.474005	SMT3 suppressor of mif two 3 homolog 3 (yeast)	SUMO3	30	0.001363
9	811162	AA485748	Hs.519168	Fibromodulin	FMOD	-30	0.001646
10	510396	AA053694	MULTIPLE: Hs.211601|Hs.546271	Mitogen-activated protein kinase kinase kinase 12|Poly(rC) binding protein 2	MAP3K12|PCBP2	-30	0.001671
11	884653	AA629908	Hs.571666	Full-length cDNA clone CS0DN002YM12 of Adult brain of Homo sapiens (hum	N/A	30	0.001762
12	197888	R96220	Hs.5662	Guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	GNB2L1	-30	0.001835
13	270134	N27933	Hs.432548	Chromosome 10 open reading frame 18	C10orf18	30	0.001904
14	760344	AA426227	Hs.2057	Uridine monophosphate synthetase (orotate phosphoribosyl transferase and o	UMPS	30	0.001995
15	200136	R97785	Hs.53454	Topoisomerase (DNA) II binding protein 1	TOPBP1	30	0.002022
16	52031	H22936	Hs.556016	Chromosome 1 open reading frame 96	LOC126731	30	0.002073
17	1472719	AA872379	Hs.474005	SMT3 suppressor of mif two 3 homolog 3 (yeast)	SUMO3	30	0.002080
18	878259	AA775803	Hs.180909	Peroxiredoxin 1	PRDX1	30	0.002265
19	2566105	AW005923	Hs.211601	Mitogen-activated protein kinase kinase kinase 12	MAP3K12	-30	0.002296
20	428231	AA002125	Hs.127799	Baculoviral IAP repeat-containing 3	BIRC3	30	0.002300
21	345430	W76227	Hs.553498	Phosphoinositide-3-kinase, catalytic, alpha polypeptide	PIK3CA	30	0.002302
22	713886	AA284856	Hs.169718	Calponin 2	CNN2	-30	0.002493
23	823855	AA490464	Hs.438991	Chromosome 10 open reading frame 61	C10orf61	-30	0.002531
24	810035	AA455279	Hs.55918	Likely ortholog of mouse D11lgp2	LGP2	30	0.002701
25	824962	AA489087	Hs.159557	Karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	KPNA2	30	0.002839
26	BC DOX 5 A05	N/A	N/A	N/A	N/A	-30	0.003171
27	358083	W94774	Hs.478868	KIAA0226	KIAA0226	30	0.003206
28	2566903	AW072298	Hs.559132	Full-length cDNA clone CS0DE002YE21 of Placenta of Homo sapiens (huma	N/A	-30	0.003392
29	35105	R45413	MULTIPLE: Hs.18861|Hs.50984	KIAA1276 protein|Tetraspanin 31	KIAA1276|SAS	-30	0.003481
30	2496749	N/A	N/A	N/A	N/A	-30	0.003524
31	2220229	AI798411	Hs.371218	EPH receptor A4	EPHA4	-30	0.003593
32	284042	N53394	Hs.343664	ACA7 small nucleolar RNA	TIP120B	-30	0.003675
33	845321	AA773461	Hs.22857	Cysteine and histidine-rich domain (CHORD)-containing 1	CHORDC1	30	0.003874
34	30466	R42168	Hs.435948	ATPase family, AAA domain containing 1	ATAD1	-30	0.003895
35	BC DDP 1 A08	N/A	N/A	NM_002266 karyopherin alpha 2 (RAG cohort 1 importin alpha 1) KPNA2(nuc	N/A	30	0.003964
36	725454	AA292964	Hs.83758	CDC28 protein kinase regulatory subunit 2	CKS2	30	0.004074
37	815564	N/A	Hs.525459	Transcribed locus	N/A	-30	0.004443
38	756769	AA425120	Hs.75238	Chromatin assembly factor 1, subunit B (p60)	CHAF1B	30	0.004817
39	2543539	AW029556	Hs.279766	Kinesin family member 4A	KIF4A	30	0.004865
40	882510	AA676460	Hs.159557	Karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	KPNA2	30	0.004945
41	BC TAX 2 F02	N/A	N/A	NM_002266 karyopherin alpha 2 (RAG cohort 1 importin alpha 1) KPNA2(nuc	N/A	30	0.004961
42	126393	R06466	Hs.446240	Protein kinase C binding protein 1	PRKCBP1	-30	0.005045
43	290560	N62372	Hs.388733	Polyribonucleotide nucleotidyltransferase 1	PNPT1	30	0.005269
44	742798	AA400450	Hs.69360	Kinesin family member 2C	KIF2C	30	0.005297
45	760299	AA425947	Hs.292156	Dickkopf homolog 3 (Xenopus laevis)	DKK3	-30	0.005404
46	320343	W04645	Hs.572642	CDNA FLJ46626 fis, clone TRACH2001612	N/A	-30	0.005512
47	108249	T70794	Hs.533124	SUMO1/sentrin specific peptidase 5	SENP5	30	0.005533
48	290263	N64406	Hs.549158	Phospholipase C, epsilon 1	PLCE1	-30	0.005591
49	248531	N78225	MULTIPLE: Hs.518345|Hs.546324	Transcribed locus, strongly similar to NP_003866.1 guanine monophosphate	N/A|GMPS	30	0.005600
50	283634	N52878	Hs.13997	Transcribed locus	N/A	-30	0.005638
51	838732	N/A	Hs.527193	ATG10 autophagy related 10 homolog (S. cerevisiae)	APG10L	-30	0.005657
52	795561	AA459681	Hs.188569	Zinc finger, DHHC-type containing 13	ZDHHC13	30	0.005751
53	72050	T52362	Hs.430733	Chloride channel, nucleotide-sensitive, 1A	CLNS1A	30	0.005973
54	727526	AA411850	Hs.75573	Centromere protein E, 312kDa	CENPE	30	0.006044
55	814350	AA458827	Hs.500546	Insulin-degrading enzyme	IDE	-30	0.006090
56	327289	W32362	Hs.184339	Maternal embryonic leucine zipper kinase	MELK	30	0.006105
57	BC DOX 5 D03	N/A	N/A	XM_004020.1 ribosomal protein S23(protein synthesis)	N/A	-30	0.006116
58	359119	AA010065	Hs.83758	CDC28 protein kinase regulatory subunit 2	CKS2	30	0.006124
59	430968	AA678335	Hs.486489	Ectonucleotide pyrophosphatase/phosphodiesterase 3	ENPP3	-30	0.006331
60	1621805	AI003892	Hs.125037	Ankyrin repeat and SOCS box-containing 6	ASB6	-30	0.006526
61	232670	H73313	Hs.503239	Mitochondrial ribosomal protein L48	MRPL48	30	0.006578
62	384670	AA709333	Hs.21958	Storkhead box 2	DKFZp762K2	-30	0.006613
63	BC DOX 5 H02	N/A	N/A	N/A	N/A	30	0.006650
64	135247	R31521	Hs.503315	Protein-kinase, interferon-inducible double stranded RNA dependent inhibitor,	PRKRIR	30	0.006721
65	248531	N78225	MULTIPLE: Hs.518345|Hs.546324	Transcribed locus, strongly similar to NP_003866.1 guanine monophosphate	N/A|GMPS	30	0.006742
66	506032	AA708446	Hs.20716	Translocase of inner mitochondrial membrane 17 homolog A (yeast)	TIMM17A	30	0.006749
67	796330	AA459735	Hs.165736	WD repeat domain 73	FLJ14888	-30	0.006829
68	796531	AA463824	Hs.453381	Transcribed locus, weakly similar to XP_517454.1 PREDICTED: similar to hy	N/A	-30	0.006838
69	BC DOX 1 F07	N/A	N/A	N/A	N/A	30	0.006905
70	1476065	AA873060	Hs.209983	Stathmin 1/oncoprotein 18	STMN1	30	0.007036
71	418126	W90505	Hs.365116	U2(RNU2) small nuclear RNA auxiliary factor 1	U2AF1	30	0.007176
72	796161	AA461092	Hs.380118	RNA binding motif protein, X-linked	RBMX	30	0.007338
73	26910	R37743	Hs.503666	G patch domain and KOW motifs	GPKOW	30	0.007362
74	128337	R12567	Hs.243596	Katanin p60 subunit A-like 1	KATNAL1	30	0.007393
75	1631253	AA994305	Hs.348326	Stathmin-like 3	STMN3	-30	0.007480
76	248531	N78225	MULTIPLE: Hs.518345|Hs.546324	Transcribed locus, strongly similar to NP_003866.1 guanine monophosphate	N/A|GMPS	30	0.007545
77	46182	H09614	Hs.473087	CTP synthase	CTPS	30	0.007583
78	BC TAX 3 D02	N/A	N/A	N/A	N/A	-30	0.007740
79	363966	AA021381	MULTIPLE: Hs.489811|Hs.552128	Inhibitor of growth family, member 3|Transcribed locus	ING3|N/A	-30	0.007771
80	713886	AA284856	Hs.169718	Calponin 2	CNN2	-30	0.008235
81	898062	AA598776	Hs.494347	Full-length cDNA clone CS0DD006YE20 of Neuroblastoma Cot 50-normalize	N/A	30	0.008279
82	1942271	AI203233	Hs.385998	WD repeat and HMG-box DNA binding protein 1	WDHD1	30	0.008384
83	2280715	AI669374	Hs.179565	MCM3 minichromosome maintenance deficient 3 (S. cerevisiae)	MCM3	30	0.008512
84	754355	AA436278	Hs.321637	Sema domain, seven thrombospondin repeats (type 1 and type 1-like), transm	SEMA5A	-30	0.008614
85	1636876	AI000256	Hs.433615	Tubulin, beta 2C	TUBB2	30	0.008740
86	50882	H18535	MULTIPLE: Hs.195080|Hs.371312	Endothelin converting enzyme 1|Transcribed locus	ECE1|N/A	-30	0.008796
87	1635384	AI014416	Hs.153961	ARP1 actin-related protein 1 homolog A, centractin alpha (yeast)	ACTR1A	-30	0.008910
88	BC DOX 2 A01	N/A	N/A	N/A	N/A	-30	0.008953
89	291974	N73091	Hs.567333	Ribosomal protein S23	RPS23	-30	0.008956
90	160573	H22171	Hs.446350	Transforming growth factor, beta receptor associated protein 1	TGFBRAP1	30	0.009145
91	357373	W93717	Hs.77695	Discs, large homolog 7 (Drosophila)	DLG7	30	0.009331
92	814995	AA465090	Hs.44269	Shugoshin-like 2 (S. pombe)	SGOL2	30	0.009394
93	1850925	AI241434	Hs.308122	Inositol 1,3,4-triphosphate 5/6 kinase	ITPK1	-30	0.009395
94	2963100	AW732908	Hs.23960	Cyclin B1	CCNB1	30	0.009445
95	1554167	AA931102	Hs.150718	Junctional adhesion molecule 3	JAM3	-30	0.009594
96	309288	N93924	Hs.518475	Replication factor C (activator 1) 4, 37kDa	RFC4	30	0.009709
97	488404	AA046679	Hs.27621	CDNA FLJ12815 fis, clone NT2RP2002546	N/A	-30	0.009773
98	823598	AA497132	Hs.4295	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	PSMD12	30	0.009784
99	289977	N79964	MULTIPLE: Hs.534783|Hs.557630	Hypothetical gene supported by AK056895|Transcribed locus	N/A|N/A	-30	0.010159
100	841610	AA487669	Hs.522995	Eukaryotic translation initiation factor 4E binding protein 2	EIF4EBP2	-30	0.010263
101	2338797	AI692949	Hs.376032	Platelet-derived growth factor alpha polypeptide	PDGFA	-30	0.010270
102	279905	N38860	Hs.440414	Spastic paraplegia 20, spartin (Troyer syndrome)	SPG20	-30	0.010278
103	773183	AA425682	Hs.532755	Gene trap locus 3 (mouse)	GTL3	30	0.010315
104	BC DDP 3 B09	N/A	N/A	NM_018098 FLJ10461(unknown)	N/A	30	0.010438

Rank	Clone ID	Accession	Unigene ID (Build 188)	Gene name	Symbol	Sign	Average P-value
105	564771	AA136551	Hs.432548	Chromosome 10 open reading frame 18	C10orf18	30	0.010556
106	856135	AA630604	Hs.443861	SFRS protein kinase 1	SRPK1	30	0.010583
107	191007	H37930	Hs.503222	RAB6A, member RAS oncogene family	RAB6A	30	0.010742
108	809557	AA456608	Hs.179565	MCM3 minichromosome maintenance deficient 3 (S. cerevisiae)	MCM3	30	0.010772
109	200402	R96998	Hs.472716	Chromosome 20 open reading frame 129	C20orf129	30	0.010861
110	1650535	AI023118	Hs.533291	MRS2-like, magnesium homeostasis factor (S. cerevisiae)	MRS2L	30	0.010887
111	BC DOX 4 C03	N/A	N/A	N/A	N/A	-30	0.010953
112	502669	AA127093	Hs.3352	Histone deacetylase 2	HDAC2	30	0.010962
113	898123	AA598487	Hs.473648	Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide syn	GART	30	0.010969
114	815279	AA481540	Hs.555925	Armadillo repeat containing 8	ARMC8	30	0.011084
115	110307	T82022	Hs.63795	Coiled-coil domain containing 21	DKFZP434L0	30	0.011095
116	33299	R43961	Hs.372099	Nucleoporin 160kDa	NUP160	30	0.011134
117	47542	H16454	MULTIPLE: Hs.464734|Hs.561101	Small nuclear ribonucleoprotein D1 polypeptide 16kDa|Transcribed locus	SNRPD1|N/A	30	0.011268
118	786202	AA448691	Hs.74137	Transmembrane emp24-like trafficking protein 10 (yeast)	TMP21	-30	0.011341
119	2512014	AI963347	Hs.102914	Cullin 4B	CUL4B	-30	0.011343
120	868308	AA634008	Hs.567333	Ribosomal protein S23	RPS23	-30	0.011563
121	2457449	AI932735	Hs.194698	Cyclin B2	CCNB2	30	0.011651
122	277339	N34418	Hs.523968	Tumor protein p53 binding protein, 2	TP53BP2	30	0.011653
123	47681	H11720	Hs.533122	Splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	SFRS10	30	0.011731
124	510845	AA099969	Hs.518201	Deltex 3-like (Drosophila)	DTX3L	30	0.011785
125	295446	W04294	MULTIPLE: Hs.134859|Hs.445387	V-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)|Ribosoma	MAF|RPS6KA3	-30	0.012021
126	251717	H97847	Hs.516468	ADP-ribosylation-like factor 6 interacting protein 6	ARL6IP6	30	0.012074
127	156324	R72619	Hs.460109	Myosin, heavy polypeptide 11, smooth muscle	MYH11	-30	0.012199
128	1639531	AI032392	Hs.493512	RAB27A, member RAS oncogene family	RAB27A	30	0.012243
129	1606345	AA995670	Hs.348264	Granzyme H (cathepsin G-like 2, protein h-CCPX)	GZMH	30	0.012341
130	343699	W69183	MULTIPLE: Hs.198161|Hs.554815	Phospholipase A2, group IVB (cytosolic)|Spectrin, beta, non-erythrocytic 5	PLA2G4B|SPTBN5	-30	0.012393
131	789182	AA450265	Hs.147433	Proliferating cell nuclear antigen	PCNA	30	0.012419
132	BC TAX 2 H10	N/A	N/A	AB019568 clone SMAP83(unknown)	N/A	-30	0.012432
133	489320	AA058514	Hs.130759	Phospholipid scramblase 1	PLSCR1	30	0.012489
134	280233	N49198	Hs.533323	Mannosidase, endo-alpha	MANEA	30	0.012574
135	730412	AA469966	Hs.445386	Chromosome 1 open reading frame 75	FLJ10874	30	0.012589
136	259950	N32587	Hs.558577	NudC domain containing 1	CML66	30	0.012589
137	2131592	AI431878	Hs.156486	CDNA FLJ45626 fis, clone BRTHA3028782	N/A	-30	0.012645
138	273546	N44764	MULTIPLE: Hs.518774|Hs.571466	Phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole s	PAICS|N/A	30	0.012684
139	124298	R02196	Hs.191734	Microsomal glutathione S-transferase 3	MGST3	30	0.012811
140	1589488	AA975785	Hs.109520	Vacuolar protein sorting 36 (yeast)	C13orf9	-30	0.012857
141	2393810	AI760459	Hs.4930	Low density lipoprotein receptor-related protein 4	LRP4	-30	0.013097
142	136431	N/A	Hs.167167	Tyrosylprotein sulfotransferase 2	TPST2	-30	0.013116
143	323644	W45678	Hs.473087	CTP synthase	CTPS	30	0.013295
144	262251	N/A	N/A	N/A	N/A	-30	0.013465
145	327461	W20438	Hs.529272	Membrane-associated ring finger (C3HC4) 7	AXOT	30	0.013552
146	127193	R08266	Hs.407482	Hypothetical protein LOC388931	N/A	-30	0.013589
147	BC TAX 1 A07	N/A	N/A	BC010494 tubulin alpha 1(cytoskeleton)	N/A	30	0.013714
148	646057	AA204873	Hs.59332	Sprouty-related, EVH1 domain containing 2	SPRED2	-30	0.013717
149	825013	AA504222	Hs.494604	Acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	ANP32B	30	0.013724
150	138165	R53900	Hs.572704	CDNA FLJ44256 fis, clone TKIDN2013287	N/A	-30	0.013733
151	295781	N74574	Hs.33922	Chromosome 1 open reading frame 156	MGC9084	30	0.013768
152	452635	AA779148	Hs.59584	Chromosome 1 open reading frame 176	FLJ21144	30	0.013958
153	40704	R55992	Hs.464184	SEC14-like 1 (S. cerevisiae)	SEC14L1	30	0.014042
154	506646	AA708793	Hs.274329	TP53 activated protein 1	TP53AP1	-30	0.014157
155	2497644	AI989914	Hs.500526	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, 170kDa (	BTAF1	-30	0.014171
156	781089	AA430241	Hs.350966	Pituitary tumor-transforming 1	PTTG1	30	0.014188
157	155227	R69522	MULTIPLE: Hs.12084|Hs.25318	Tu translation elongation factor, mitochondrial|RAB27B, member RAS oncoge	TUFM|RAB27B	-30	0.014206
158	506032	AA708446	Hs.20716	Translocase of inner mitochondrial membrane 17 homolog A (yeast)	TIMM17A	30	0.014329
159	137058	N/A	N/A	N/A	N/A	-30	0.014495
160	786084	AA448667	Hs.77254	Chromobox homolog 1 (HP1 beta homolog Drosophila)	CBX1	30	0.014556
161	250678	H95976	Hs.487471	RNA binding motif protein 35A	FLJ20171	30	0.014659
162	121621	T97593	Hs.166463	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	HNRPU	30	0.014696
163	124242	R02010	Hs.500897	Chromosome 10 open reading frame 26	C10orf26	-30	0.014750
164	814818	AA455254	Hs.298654	Dual specificity phosphatase 6	DUSP6	-30	0.014789
165	BC DDP 2 A04	N/A	N/A	NM_006082 K-ALPHA-1 tubulin(cytoskeleton)	N/A	30	0.014833
166	841334	AA487427	Hs.337295	Stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	STIP1	30	0.014926
167	840691	AA488075	Hs.470943	Signal transducer and activator of transcription 1, 91kDa	STAT1	30	0.014949
168	2016414	N/A	Hs.572708	Transcribed locus	N/A	-30	0.014980
169	418279	W90323	Hs.486401	Chromosome 6 open reading frame 173	C6orf173	30	0.015011
170	BC TAX 2 F03	N/A	N/A	XM_011743 similar to eukaryotic translation elongation factor 1 alpha 1-like 1	N/A	-30	0.015022
171	80399	T65786	Hs.68714	Splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor	SFRS1	30	0.015039
172	79808	T63998	Hs.515056	Guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	GNA11	-30	0.015047
173	2106953	AI380323	Hs.270043	KIAA0196	KIAA0196	-30	0.015177
174	1493390	AA894687	Hs.75117	Interleukin enhancer binding factor 2, 45kDa	ILF2	30	0.015220
175	854899	AA630374	Hs.298654	Dual specificity phosphatase 6	DUSP6	-30	0.015308
176	BC DDP 1 E10	N/A	N/A	NM_002973 spinocerebellar ataxia 2(unknown)	N/A	30	0.015328
177	2329679	AI703219	Hs.118555	Fascin homolog 2, actin-bundling protein, retinal (Strongylocentrotus purpurat	FSCN2	-30	0.015425
178	739983	AA477501	Hs.3104	Kinesin family member 14	KIF14	30	0.015502
179	416075	W85962	Hs.555894	Transcription factor 19 (SC1)	TCF19	30	0.015570
180	BC DDP 1 H08	N/A	N/A	BC006838 hypothetical protein FLJ10461(unknown)	N/A	30	0.015645
181	204483	H58234	Hs.370834	ATPase family, AAA domain containing 2	ATAD2	30	0.015661
182	292933	N90985	Hs.436912	Kinesin family member C1	KIFC1	30	0.015725
183	855715	AA663944	Hs.50749	Tripartite motif-containing 4	TRIM4	-30	0.015752
184	704290	AA279429	Hs.195080	Endothelin converting enzyme 1	ECE1	-30	0.015803
185	1602088	AA988857	Hs.489118	Sterile alpha motif domain containing 9-like	C7orf6	30	0.015930
186	781047	AA446462	Hs.469649	BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast)	BUB1	30	0.015963
187	1569156	AA973494	Hs.153003	Serine/threonine kinase 16	STK16	-30	0.016041
188	770462	AA427724	Hs.78068	Carboxypeptidase Z	CPZ	30	0.016139
189	509484	AA056504	Hs.423935	RD RNA binding protein	RDBP	30	0.016201
190	754538	AA421977	Hs.356742	DR1-associated protein 1 (negative cofactor 2 alpha)	DRAP1	30	0.016311
191	451937	AA707195	Hs.523698	Hypothetical protein LOC219988	FLJ36874	30	0.016383
192	182797	H45262	Hs.465475	ATPase, Class II, type 9B	ATP9B	-30	0.016404
193	868630	AA664389	Hs.507916	TSC22 domain family, member 1	TGFB1I4	-30	0.016438
194	725335	AA291959	Hs.289123	Dynactin 2 (p50)	DCTN2	-30	0.016543
195	2516036	AI982577	Hs.438236	Actin binding LIM protein 1	ABLIM1	-30	0.016591
196	26997	R37145	Hs.412587	RAD51 homolog C (S. cerevisiae)	RAD51C	30	0.016646
197	592410	AA158532	Hs.435948	ATPase family, AAA domain containing 1	ATAD1	-30	0.016651
198	129865	R19158	Hs.250822	Serine/threonine kinase 6	STK6	30	0.016678
199	501880	AA129902	Hs.8372	Ubiquinol-cytochrome c reductase, 6.4kDa subunit	UQCR	-30	0.016682
200	842765	AA486299	Hs.435741	IQ motif and WD repeats 1	IQWD1	30	0.016693
201	356883	W84638	Hs.238432	GC-rich promoter binding protein 1-like 1	SP192	30	0.016747
202	823634	AA490565	Hs.547286	Full-length cDNA clone CS0DL007YI24 of B cells (Ramos cell line) Cot 25-nor	N/A	-30	0.016797
203	868308	AA634008	Hs.567333	Ribosomal protein S23	RPS23	-30	0.016809
204	647435	AA199585	Hs.101891	KIAA1193	KIAA1193	-30	0.016836
205	BC DOX 1 A01	N/A	N/A	NM_000018 acyl-Coenzyme A dehydrogenase nuclear gene encoding mitoch	N/A	-30	0.016843
206	826135	AA521346	Hs.409578	Serine/threonine kinase 38	STK38	-30	0.016997
207	951230	AA620571	Hs.546299	Small nuclear RNA activating complex, polypeptide 3, 50kDa	SNAPC3	30	0.017092
208	430973	AA678348	Hs.33366	Cell division cycle associated 2	CDCA2	30	0.017143
209	810741	AA457725	Hs.84359	GABA(A) receptor-associated protein	GABARAP	-30	0.017161
210	40643	R56294	Hs.509067	Platelet-derived growth factor receptor, beta polypeptide	PDGFRB	-30	0.017220
211	162199	H26353	Hs.49774	Protein tyrosine phosphatase, receptor type, M	PTPRM	-30	0.017221

Rank	Clone ID	Accession	Unigene ID (Build 188)	Gene name	Symbol	Sign	Average P-value
212	32781	R20405	Hs.558351	Kinesin heavy chain member 2	KIF2	30	0.017254
213	788256	AA454098	Hs.270845	Kinesin family member 23	KIF23	30	0.017391
214	824117	AA490617	Hs.468623	Vaccinia related kinase 2	VRK2	30	0.017439
215	292882	N69460	Hs.9589	Ubiquilin 1	UBQLN1	30	0.017475
216	44255	H06113	Hs.205163	Mitochondrial ribosomal protein L3	MRPL3	30	0.017646
217	2018131	AI364509	Hs.505469	Rac GTPase activating protein 1	RACGAP1	30	0.017670
218	788558	AA452824	Hs.511265	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (sema	SEMA6D	-30	0.017740
219	2018976	AI362866	Hs.350966	Pituitary tumor-transforming 1	PTTG1	30	0.017842
220	712895	AA282219	Hs.195080	Endothelin converting enzyme 1	ECE1	-30	0.017922
221	BC DOX 2 A06	N/A	N/A	N/A	N/A	-30	0.017960
222	814975	AA465717	Hs.314338	Bromodomain and WD repeat domain containing 1	WDR9	30	0.017961
223	810844	AA459164	Hs.521151	Zinc finger protein 672	FLJ22301	30	0.018020
224	BC DOX 5 C02	N/A	N/A	N/A	N/A	-30	0.018065
225	280375	N47113	Hs.370834	ATPase family, AAA domain containing 2	ATAD2	30	0.018154
226	2418897	AI826909	Hs.226307	Apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3D (putative	APOBEC3B	30	0.018301
227	823598	AA497132	Hs.4295	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	PSMD12	30	0.018592
228	1476065	AA873060	Hs.209983	Stathmin 1/oncoprotein 18	STMN1	30	0.018742
229	262264	H99426	Hs.49774	Protein tyrosine phosphatase, receptor type, M	PTPRM	-30	0.018796
230	309081	N92895	Hs.120855	KIAA0960 protein	KIAA0960	-30	0.018935
231	1587847	AA976533	Hs.444118	MCM6 minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (	MCM6	30	0.018943
232	258966	N31641	Hs.510225	Ribosomal protein S6 kinase, 90kDa, polypeptide 5	RPS6KA5	-30	0.018987
233	1540729	AA907689	Hs.507916	TSC22 domain family, member 1	TGFB1I4	-30	0.019080
234	128792	R16760	Hs.420229	Hepatitis B virus x associated protein	HBXAP	30	0.019190
235	277528	N34518	Hs.371886	CDNA FLJ45534 fis, clone BRTHA2031517	N/A	-30	0.019324
236	435415	AA700090	Hs.288224	Mitochondrial ribosomal protein L50	MRPL50	30	0.019341
237	193383	H48097	Hs.529609	ATPase type 13A3	ATP13A3	30	0.019514
238	841398	AA487544	Hs.518203	Poly (ADP-ribose) polymerase family, member 14	PARP14	30	0.019521
239	BC DDP 1 A09	N/A	N/A	AF141348 alpha-tubulin(cytoskeleton)	N/A	30	0.019649
240	399143	AA774619	Hs.351099	Hypothetical protein FLJ10241	FLJ10241	-30	0.019655
241	309515	N94385	Hs.1584	Cartilage oligomeric matrix protein	COMP	-30	0.019701
242	753692	AA406601	Hs.438236	Actin binding LIM protein 1	ABLIM1	-30	0.019756
243	287749	N79336	Hs.533573	CDC7 cell division cycle 7 (S. cerevisiae)	CDC7	30	0.019780
244	1669563	AI056710	Hs.436922	Ret finger protein 2	RFP2	-30	0.019798
245	760299	AA425947	Hs.292156	Dickkopf homolog 3 (Xenopus laevis)	DKK3	-30	0.019904
246	810974	AA459407	Hs.3068	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, s	SMARCA3	30	0.019931

Note: 'Clone ID', if numeric, is the IMAGE consortium cDNA clone #, otherwise, it reflects an internally-generated cDNA clone. 'Accession' is the GenBank accession #. 'Sign' represents the sum of signs as described in the methods section. Unavailable data is denoted as 'N/A'. The complete list of all ranked genes is available upon request.