

Supplementary Table 1: Functional annotation of the differentially expressed classification genes in S1 vs. non-S1, S2 vs. non-S2, and S3 vs. non-S3. Annotations are based on Gene Ontology (GO) Biological Process terms

Top upregulated functions based on differential expression in S1 versus non-S1 tumors	Count	P value	Fold enrichment	FDR
GO:0007165~signal transduction	50	2.63E-10	2.698394333	4.49E-07
GO:0030198~extracellular matrix organization	19	2.42E-09	6.073865367	4.12E-06
GO:0030574~collagen catabolic process	12	4.72E-09	11.74813433	8.05E-06
GO:0030199~collagen fibril organization	9	1.48E-07	14.45924225	2.52E-04
GO:0006935~chemotaxis	12	3.95E-06	6.162955713	0.006737382
GO:0006955~immune response	21	1.40E-05	3.125394406	0.023884388
GO:0019886~antigen processing and presentation of exogenous peptide antigen via MHC class II	10	1.56E-05	6.810512654	0.026613043
GO:0050900~leukocyte migration	11	2.52E-05	5.64937607	0.042981754
GO:0044319~wound healing, spreading of cells	5	2.80E-05	26.10696517	0.047727495
GO:0006915~apoptotic process	24	3.96E-05	2.652136145	0.067470714
GO:0001817~regulation of cytokine production	5	3.99E-05	24.09873708	0.068072539
GO:0071407~cellular response to organic cyclic compound	8	4.00E-05	8.495825955	0.068232494
GO:0038063~collagen-activated tyrosine kinase receptor signaling pathway	4	7.67E-05	41.77114428	0.130840782
GO:0031100~organ regeneration	7	9.49E-05	9.331851381	0.161850239
GO:0006954~inflammatory response	18	1.25E-04	2.975780727	0.212296707
GO:0050852~T cell receptor signaling pathway	11	1.30E-04	4.656918112	0.22120312
GO:0007155~cell adhesion	20	1.45E-04	2.730140149	0.247475496
GO:0001934~positive regulation of protein phosphorylation	10	1.96E-04	4.933599718	0.334635146
GO:0007568~aging	11	3.14E-04	4.177114428	0.535065098
GO:0001501~skeletal system development	10	3.46E-04	4.57348295	0.588855402
GO:0090023~positive regulation of neutrophil chemotaxis	5	3.65E-04	14.24016282	0.620536602
GO:0043066~negative regulation of apoptotic process	19	3.70E-04	2.616434312	0.629515617
GO:0042102~positive regulation of T cell proliferation	7	3.73E-04	7.309950249	0.6337275
GO:0030168~platelet activation	9	5.02E-04	4.903569111	0.853256233

GO:0042476~odontogenesis	5	8.22E-04	11.60309563	1.393550657
GO:0035987~endodermal cell differentiation	5	8.22E-04	11.60309563	1.393550657
GO:0045860~positive regulation of protein kinase activity	6	8.70E-04	7.998729755	1.474423546
GO:0048010~vascular endothelial growth factor receptor signaling pathway	7	9.92E-04	6.091625207	1.679372145
GO:0007229~integrin-mediated signaling pathway	8	0.001018849	5.063169003	1.724157042
GO:0043123~positive regulation of I-kappaB kinase/NF-kappaB signaling	10	0.001109028	3.891721517	1.875407228
GO:0042554~superoxide anion generation	4	0.001270723	17.90191898	2.146057397
GO:0031295~T cell costimulation	7	0.001507087	5.623038653	2.540428077
GO:0007166~cell surface receptor signaling pathway	13	0.001508464	2.972763918	2.542720326
GO:0031663~lipopolysaccharide-mediated signaling pathway	5	0.001582962	9.79011194	2.66670673
GO:0001503~ossification	7	0.001717383	5.482462687	2.890045071
GO:0001666~response to hypoxia	10	0.001755459	3.64283235	2.953219528
GO:0070374~positive regulation of ERK1 and ERK2 cascade	10	0.001975823	3.580383795	3.318084739
GO:0033572~transferrin transport	5	0.002220543	8.950959488	3.721762454
GO:0002504~antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	4	0.002291624	14.7427568	3.838717843
GO:0042531~positive regulation of tyrosine phosphorylation of STAT protein	3	0.002440338	37.59402985	4.082973256
GO:0006928~movement of cell or subcellular component	7	0.002483154	5.09996529	4.15318774
GO:0048013~ephrin receptor signaling pathway	7	0.002483154	5.09996529	4.15318774
GO:0034142~toll-like receptor 4 signaling pathway	4	0.002717864	13.92371476	4.537236849
GO:0030335~positive regulation of cell migration	10	0.002772964	3.405256327	4.627184178

Top upregulated functions based on differential expression in S2 versus non-S2 tumors	Count	P value	Fold enrichment	FDR
GO:0019083~viral transcription	10	4.37E-05	5.997142857	0.074534848
GO:0000184~nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	10	7.03E-05	5.644369748	0.119916941
GO:0007165~signal transduction	35	1.08E-04	2.024875108	0.18480215
GO:0006413~translational initiation	10	2.07E-04	4.902773723	0.352320222

GO:0006935~chemotaxis	9	4.70E-04	4.955016393	0.799275817
GO:0006614~SRP-dependent cotranslational protein targeting to membrane	8	4.96E-04	5.716425532	0.842413348
GO:0000165~MAPK cascade	13	5.60E-04	3.332763359	0.950898159
GO:0044319~wound healing, spreading of cells	4	6.42E-04	22.38933333	1.089830338
GO:0006915~apoptotic process	20	8.26E-04	2.369241623	1.400770371
GO:0002576~platelet degranulation	8	8.57E-04	5.216932039	1.453013146
GO:0051091~positive regulation of sequence-specific DNA binding transcription factor activity	8	9.61E-04	5.117561905	1.626655399
GO:0043085~positive regulation of catalytic activity	7	0.001284174	5.804641975	2.16908021
GO:0006468~protein phosphorylation	17	0.001321192	2.504070175	2.230945146
GO:0006364~rRNA processing	11	0.001378797	3.452560748	2.32714044

Top upregulated functions based on differential expression in S3 versus non-S3 tumors	Count	P value	Fold enrichment	FDR
GO:0002576~platelet degranulation	17	1.67E-11	9.758785724	2.85E-08
GO:0055114~oxidation-reduction process	37	2.48E-11	3.695422535	4.22E-08
GO:0042730~fibrinolysis	9	9.92E-10	25.34004024	1.69E-06
GO:0006635~fatty acid beta-oxidation	11	2.36E-09	14.78169014	4.02E-06
GO:0055088~lipid homeostasis	10	1.31E-08	15.16070784	2.24E-05
GO:0033539~fatty acid beta-oxidation using acyl-CoA DH	7	3.40E-07	22.99374022	5.80E-04
GO:0006559~L-phenylalanine catabolic process	6	5.58E-07	32.25096031	9.51E-04
GO:0010951~negative regulation of endopeptidase activity	13	9.51E-07	6.352461879	0.001619858
GO:0006520~cellular amino acid metabolic process	8	4.15E-06	11.82535211	0.00707326
GO:0006805~xenobiotic metabolic process	10	6.37E-06	7.580353918	0.010853044
GO:0031639~plasminogen activation	5	9.31E-06	32.84820031	0.015859123
GO:0007597~blood coagulation, intrinsic pathway	6	9.39E-06	19.70892019	0.016000634
GO:0009636~response to toxic substance	10	1.30E-05	6.956089478	0.022108705
GO:0051918~negative regulation of fibrinolysis	5	1.53E-05	29.56338028	0.026080105
GO:0042493~response to drug	18	1.67E-05	3.500926612	0.028428535
GO:0006069~ethanol oxidation	5	3.51E-05	24.63615023	0.059846669
GO:0006695~cholesterol biosynthetic process	7	3.81E-05	10.89177168	0.064915886

GO:0006572~tyrosine catabolic process	4	4.62E-05	47.30140845	0.078659675
GO:0032496~response to lipopolysaccharide	12	1.08E-04	4.326348334	0.183593096
GO:0030168~platelet activation	10	1.43E-04	5.14145744	0.243076378
GO:0030855~epithelial cell differentiation	8	1.74E-04	6.757344064	0.295244223
GO:0006810~transport	17	2.90E-04	2.888376234	0.4922843
GO:0032869~cellular response to insulin stimulus	8	3.15E-04	6.143040059	0.535257814
GO:0010043~response to zinc ion	6	3.22E-04	9.854460094	0.547922892
GO:0045471~response to ethanol	9	4.00E-04	5.068008048	0.67992556
GO:0001523~retinoid metabolic process	7	5.55E-04	6.785038097	0.94053746
GO:0006081~cellular aldehyde metabolic process	4	7.07E-04	21.5006402	1.197449915
GO:0006094~gluconeogenesis	6	8.32E-04	8.062740077	1.408594575
GO:0030212~hyaluronan metabolic process	4	9.31E-04	19.70892019	1.573934437
GO:0006107~oxaloacetate metabolic process	4	9.31E-04	19.70892019	1.573934437
GO:0007596~blood coagulation	11	0.001152302	3.53475199	1.944859039
GO:2000145~regulation of cell motility	5	0.001175468	10.5583501	1.983591255
GO:0042311~vasodilation	4	0.001502192	16.89336016	2.528322315
GO:0030449~regulation of complement activation	5	0.0015323	9.854460094	2.578376156
GO:0001889~liver development	7	0.00154232	5.593071945	2.595028866
GO:0051919~positive regulation of fibrinolysis	3	0.001660614	44.34507042	2.791424306
GO:0019626~short-chain fatty acid catabolic process	3	0.002736895	35.47605634	4.561254542
GO:0019439~aromatic compound catabolic process	3	0.002736895	35.47605634	4.561254542
GO:0005975~carbohydrate metabolic process	10	0.002829521	3.398089688	4.712142956
GO:0055085~transmembrane transport	12	0.002927661	2.90787347	4.871767182