

Table S1-1: List of “Biological Process” terms obtained from GO enrichment of identified biomarkers

GO_id	Term	Number Of Genes	p-value	p-value_fdr	p-value_bonferroni
GO:0051240	positive regulation of multicellular organismal process	14	1.22E-11	1.36E-07	1.64E-07
GO:0006954	inflammatory response	10	2.02E-11	1.36E-07	2.72E-07
GO:0001819	positive regulation of cytokine production	9	1.23E-10	4.77E-07	1.66E-06
GO:0001817	regulation of cytokine production	10	1.42E-10	4.77E-07	1.91E-06
GO:0007267	cell-cell signaling	12	3.34E-10	8.99E-07	4.5E-06
GO:0043408	regulation of MAPK cascade	10	6.14E-10	1.38E-06	8.25E-06
GO:0006952	defense response	13	9.28E-10	1.78E-06	1.25E-05
GO:0042327	positive regulation of phosphorylation	11	1.22E-09	2.06E-06	1.64E-05
GO:0071310	cellular response to organic substance	14	1.65E-09	2.47E-06	2.22E-05
GO:0009605	response to external stimulus	14	3E-09	4.04E-06	4.04E-05
GO:0002761	regulation of myeloid leukocyte differentiation	6	3.6E-09	4.35E-06	4.84E-05
GO:0031401	positive regulation of protein modification process	11	3.88E-09	4.35E-06	5.22E-05
GO:0042325	regulation of phosphorylation	12	4.75E-09	4.39E-06	6.39E-05
GO:0045937	positive regulation of phosphate metabolic process	11	5.08E-09	4.39E-06	6.83E-05
GO:0001934	positive regulation of protein phosphorylation	10	5.22E-09	4.39E-06	7.02E-05
GO:0001932	regulation of protein phosphorylation	11	9.75E-09	7.24E-06	0.000131
GO:0031399	regulation of protein modification process	12	9.75E-09	7.24E-06	0.000131
GO:0006955	immune response	12	1.02E-08	7.24E-06	0.000138
GO:0043410	positive regulation of MAPK cascade	8	1.67E-08	1.13E-05	0.000225
GO:0042221	response to chemical	17	2.09E-08	1.27E-05	0.000281
GO:0051239	regulation of multicellular organismal process	14	2.18E-08	1.27E-05	0.000293
GO:0048584	positive regulation of response to stimulus	13	2.22E-08	1.27E-05	0.000299

GO:0070887	cellular response to chemical stimulus	14	2.27E-08	1.27E-05	0.000305
GO:0019220	regulation of phosphate metabolic process	12	2.96E-08	1.59E-05	0.000398
GO:0051174	regulation of phosphorus metabolic process	12	3.28E-08	1.66E-05	0.000441
GO:1902531	regulation of intracellular signal transduction	12	3.33E-08	1.66E-05	0.000448
GO:0006950	response to stress	16	3.7E-08	1.72E-05	0.000497
GO:0032270	positive regulation of cellular protein metabolic process	11	3.7E-08	1.72E-05	0.000498
GO:0045637	regulation of myeloid cell differentiation	6	5.38E-08	2.41E-05	0.000724
GO:0009607	response to biotic stimulus	9	6.19E-08	2.68E-05	0.000832
GO:0051704	multi-organism process	14	8.08E-08	0.000034	0.00109
GO:0051247	positive regulation of protein metabolic process	11	8.75E-08	3.57E-05	0.00118
GO:0009967	positive regulation of signal transduction	11	9.48E-08	3.75E-05	0.00128
GO:0044700	single organism signaling	18	2.12E-07	7.78E-05	0.00285
GO:1902533	positive regulation of intracellular signal transduction	9	2.14E-07	7.78E-05	0.00288
GO:0023056	positive regulation of signaling	11	2.23E-07	7.89E-05	0.003
GO:0010647	positive regulation of cell communication	11	2.42E-07	8.33E-05	0.00325
GO:0007154	cell communication	18	2.95E-07	9.92E-05	0.00397
GO:1902105	regulation of leukocyte differentiation	6	3.18E-07	0.000104	0.00428
GO:0007165	signal transduction	17	4.3E-07	0.000138	0.00578
GO:0002763	positive regulation of myeloid leukocyte differentiation	4	4.5E-07	0.000141	0.00605
GO:0043434	response to peptide hormone	7	4.91E-07	0.000148	0.0066
GO:0010033	response to organic substance	13	4.97E-07	0.000148	0.00668
GO:0032268	regulation of cellular protein metabolic process	12	6.59E-07	0.000189	0.00887
GO:0043207	response to external biotic stimulus	8	6.74E-07	0.000189	0.00906
GO:0051707	response to other organism	8	6.74E-07	0.000189	0.00906
GO:1901652	response to peptide	7	7.88E-07	0.000216	0.0106
GO:0045670	regulation of osteoclast differentiation	4	8.43E-07	0.000227	0.0113

GO:1903706	regulation of hemopoiesis	6	1.39E-06	0.000366	0.0187
GO:0051716	cellular response to stimulus	18	1.78E-06	0.000455	0.0239
GO:0051246	regulation of protein metabolic process	12	1.79E-06	0.000455	0.0241
GO:0010557	positive regulation of macromolecule biosynthetic process	10	2.28E-06	0.000568	0.0307
GO:0045672	positive regulation of osteoclast differentiation	3	2.68E-06	0.000656	0.0361
GO:0008284	positive regulation of cell proliferation	8	3.01E-06	0.000719	0.0405
GO:0045639	positive regulation of myeloid cell differentiation	4	3.05E-06	0.000719	0.041
GO:0050729	positive regulation of inflammatory response	4	4.97E-06	0.00113	0.0668
GO:0051142	positive regulation of NK T cell proliferation	2	5.03E-06	0.00113	0.0676
GO:0034105	positive regulation of tissue remodeling	3	5.22E-06	0.00113	0.0703
GO:0040011	locomotion	9	5.23E-06	0.00113	0.0703
GO:0009891	positive regulation of biosynthetic process	10	5.34E-06	0.00114	0.0718
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	8	7.25E-06	0.00152	0.0975
GO:0032103	positive regulation of response to external stimulus	5	7.47E-06	0.00152	0.1
GO:0002376	immune system process	11	7.48E-06	0.00152	0.101
GO:0001775	cell activation	7	7.78E-06	0.00156	0.105
GO:0048608	reproductive structure development	6	8.92E-06	0.00175	0.12
GO:0048599	oocyte development	3	8.99E-06	0.00175	0.121
GO:0061458	reproductive system development	6	9.6E-06	0.00184	0.129
GO:0044332	Wnt signaling pathway involved in dorsal/ventral axis specification	2	0.00001	0.0019	0.135
GO:0009994	oocyte differentiation	3	1.09E-05	0.00204	0.147
GO:0090087	regulation of peptide transport	5	1.11E-05	0.00205	0.149
GO:0009617	response to bacterium	6	1.24E-05	0.00226	0.167
GO:0008283	cell proliferation	7	1.32E-05	0.00235	0.177

GO:0010638	positive regulation of organelle organization	6	1.33E-05	0.00235	0.179
GO:0009719	response to endogenous stimulus	9	1.41E-05	0.00246	0.189
GO:0045595	regulation of cell differentiation	9	1.44E-05	0.00248	0.193
GO:0042981	regulation of apoptotic process	9	1.49E-05	0.00253	0.2
GO:0007548	sex differentiation	5	1.51E-05	0.00254	0.203
GO:0016477	cell migration	7	1.54E-05	0.00255	0.207
GO:0070374	positive regulation of ERK1 and ERK2 cascade	4	1.56E-05	0.00255	0.209
GO:0043067	regulation of programmed cell death	9	1.58E-05	0.00256	0.212
GO:0048583	regulation of response to stimulus	13	0.000017	0.00273	0.229
GO:0002237	response to molecule of bacterial origin	5	1.73E-05	0.00274	0.233
GO:1902107	positive regulation of leukocyte differentiation	4	1.78E-05	0.00278	0.239
GO:0051147	regulation of muscle cell differentiation	4	1.96E-05	0.00303	0.264
GO:0050678	regulation of epithelial cell proliferation	5	2.05E-05	0.00313	0.276
GO:2000107	negative regulation of leukocyte apoptotic process	3	2.27E-05	0.00344	0.306
GO:1903036	positive regulation of response to wounding	4	2.44E-05	0.00365	0.328
GO:0032819	positive regulation of natural killer cell proliferation	2	2.51E-05	0.00369	0.337
GO:0051674	localization of cell	7	2.53E-05	0.00369	0.34
GO:0048870	cell motility	7	2.55E-05	0.00369	0.344
GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	4	2.67E-05	0.00382	0.359
GO:0050793	regulation of developmental process	10	3.25E-05	0.0046	0.437
GO:0032817	regulation of natural killer cell proliferation	2	3.51E-05	0.00492	0.472
GO:0031328	positive regulation of cellular biosynthetic process	9	3.76E-05	0.00521	0.506
GO:0032844	regulation of homeostatic process	5	4.06E-05	0.0055	0.547
GO:1901698	response to nitrogen compound	7	4.08E-05	0.0055	0.549
GO:0051148	negative regulation of muscle cell differentiation	3	4.09E-05	0.0055	0.55
GO:1903708	positive regulation of hemopoiesis	4	4.39E-05	0.0058	0.59

GO:0002684	positive regulation of immune system process	7	0.000044	0.0058	0.592
GO:0033077	T cell differentiation in thymus	3	0.000046	0.00589	0.618
GO:0032729	positive regulation of interferon-gamma production	3	0.000046	0.00589	0.618
GO:1900017	positive regulation of cytokine production involved in inflammatory response	2	4.67E-05	0.00593	0.629
GO:0043065	positive regulation of apoptotic process	6	4.87E-05	0.00612	0.655
GO:0071363	cellular response to growth factor stimulus	6	5.03E-05	0.00626	0.676
GO:0043068	positive regulation of programmed cell death	6	5.14E-05	0.00634	0.691
GO:0009725	response to hormone	7	5.23E-05	0.0064	0.704
GO:0048477	oogenesis	3	5.42E-05	0.00651	0.73
GO:0034103	regulation of tissue remodeling	3	5.42E-05	0.00651	0.73
GO:0070372	regulation of ERK1 and ERK2 cascade	4	0.000055	0.00654	0.739
GO:0031325	positive regulation of cellular metabolic process	11	5.68E-05	0.0067	0.764
GO:0060548	negative regulation of cell death	7	5.86E-05	0.00685	0.788
GO:0070848	response to growth factor	6	5.95E-05	0.0069	0.8
GO:0010942	positive regulation of cell death	6	6.13E-05	0.00705	0.825
GO:0003006	developmental process involved in reproduction	6	6.26E-05	0.00714	0.842
GO:0002682	regulation of immune system process	8	6.95E-05	0.0078	0.935
GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signaling	4	6.96E-05	0.0078	0.936
GO:1901700	response to oxygen-containing compound	8	7.13E-05	0.00792	0.959
GO:0031349	positive regulation of defense response	5	7.26E-05	0.008	0.976
GO:0032740	positive regulation of interleukin-17 production	2	0.000075	0.0082	1
GO:0070663	regulation of leukocyte proliferation	4	7.79E-05	0.00845	1
GO:0034097	response to cytokine	6	7.95E-05	0.00856	1
GO:0050730	regulation of peptidyl-tyrosine phosphorylation	4	8.32E-05	0.00888	1

GO:1900015	regulation of cytokine production involved in inflammatory response	2	9.16E-05	0.0097	1
GO:0051571	positive regulation of histone H3-K4 methylation	2	0.00011	0.0114	1
GO:0032725	positive regulation of granulocyte macrophage colony-stimulating factor production	2	0.00011	0.0114	1
GO:0008406	gonad development	4	0.000111	0.0115	1
GO:0051094	positive regulation of developmental process	7	0.000116	0.0119	1
GO:2000106	regulation of leukocyte apoptotic process	3	0.00012	0.0122	1
GO:0045137	development of primary sexual characteristics	4	0.000123	0.0124	1
GO:0032645	regulation of granulocyte macrophage colony-stimulating factor production	2	0.00013	0.013	1
GO:2000026	regulation of multicellular organismal development	8	0.000131	0.013	1
GO:0032649	regulation of interferon-gamma production	3	0.000146	0.0144	1
GO:0033033	negative regulation of myeloid cell apoptotic process	2	0.000151	0.0148	1
GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	4	0.00016	0.0155	1
GO:0010941	regulation of cell death	8	0.000161	0.0155	1
GO:0048519	negative regulation of biological process	13	0.000161	0.0155	1
GO:0048518	positive regulation of biological process	14	0.000166	0.0157	1
GO:0022412	cellular process involved in reproduction in multicellular organism	4	0.000166	0.0157	1
GO:0045859	regulation of protein kinase activity	6	0.000167	0.0157	1
GO:0007292	female gamete generation	3	0.000169	0.0158	1
GO:0009950	dorsal/ventral axis specification	2	0.000174	0.0161	1
GO:0042035	regulation of cytokine biosynthetic process	3	0.000176	0.0161	1
GO:0007166	cell surface receptor signaling pathway	11	0.000176	0.0161	1
GO:0045597	positive regulation of cell differentiation	6	0.000178	0.0162	1

GO:0048522	positive regulation of cellular process	13	0.000184	0.0166	1
GO:0046425	regulation of JAK-STAT cascade	3	0.000188	0.0169	1
GO:0042127	regulation of cell proliferation	8	0.000191	0.017	1
GO:0002407	dendritic cell chemotaxis	2	0.000199	0.0172	1
GO:0060788	ectodermal placode formation	2	0.000199	0.0172	1
GO:0071696	ectodermal placode development	2	0.000199	0.0172	1
GO:0071697	ectodermal placode morphogenesis	2	0.000199	0.0172	1
GO:0010628	positive regulation of gene expression	8	0.0002	0.0172	1
GO:0050900	leukocyte migration	4	0.000202	0.0173	1
GO:0010604	positive regulation of macromolecule metabolic process	10	0.00021	0.0179	1
GO:0010243	response to organonitrogen compound	6	0.000225	0.0191	1
GO:0045860	positive regulation of protein kinase activity	5	0.000233	0.0196	1
GO:0050727	regulation of inflammatory response	4	0.000234	0.0196	1
GO:1901701	cellular response to oxygen-containing compound	6	0.000238	0.0198	1
GO:0043549	regulation of kinase activity	6	0.00024	0.0198	1
GO:0030595	leukocyte chemotaxis	3	0.000246	0.0201	1
GO:0045935	positive regulation of nucleobase-containing compound metabolic process	8	0.000247	0.0201	1
GO:0032940	secretion by cell	5	0.000248	0.0201	1
GO:0009966	regulation of signal transduction	10	0.000253	0.0203	1
GO:0042089	cytokine biosynthetic process	2	0.000253	0.0203	1
GO:0032496	response to lipopolysaccharide	4	0.000262	0.0209	1
GO:0051093	negative regulation of developmental process	6	0.000273	0.0216	1
GO:0051173	positive regulation of nitrogen compound metabolic process	8	0.000276	0.0216	1
GO:0014031	mesenchymal cell development	3	0.000278	0.0216	1

GO:1903037	regulation of leukocyte cell-cell adhesion	4	0.000279	0.0216	1
GO:0036336	dendritic cell migration	2	0.000283	0.0216	1
GO:0046641	positive regulation of alpha-beta T cell proliferation	2	0.000283	0.0216	1
GO:0032660	regulation of interleukin-17 production	2	0.000283	0.0216	1
GO:0006874	cellular calcium ion homeostasis	4	0.000302	0.0229	1
GO:0046330	positive regulation of JNK cascade	3	0.000304	0.023	1
GO:0033674	positive regulation of kinase activity	5	0.000308	0.0231	1
GO:0032816	positive regulation of natural killer cell activation	2	0.000314	0.0234	1
GO:0080134	regulation of response to stress	7	0.000315	0.0234	1
GO:0044089	positive regulation of cellular component biogenesis	4	0.000325	0.024	1
GO:0055082	cellular chemical homeostasis	5	0.000327	0.024	1
GO:0055074	calcium ion homeostasis	4	0.000345	0.0252	1
GO:0051569	regulation of histone H3-K4 methylation	2	0.000347	0.0252	1
GO:0048523	negative regulation of cellular process	12	0.000348	0.0252	1
GO:0072503	cellular divalent inorganic cation homeostasis	4	0.00035	0.0252	1
GO:0001101	response to acid chemical	4	0.000366	0.0262	1
GO:0002819	regulation of adaptive immune response	3	0.000371	0.0263	1
GO:0043066	negative regulation of apoptotic process	6	0.000372	0.0263	1
GO:0032880	regulation of protein localization	6	0.000375	0.0264	1
GO:0042107	cytokine metabolic process	2	0.000381	0.0267	1
GO:0043069	negative regulation of programmed cell death	6	0.000383	0.0267	1
GO:0001525	angiogenesis	4	0.000393	0.0272	1
GO:0032879	regulation of localization	9	0.000415	0.0283	1
GO:0042104	positive regulation of activated T cell proliferation	2	0.000417	0.0283	1
GO:0033032	regulation of myeloid cell apoptotic process	2	0.000417	0.0283	1
GO:0045662	negative regulation of myoblast differentiation	2	0.000417	0.0283	1

GO:0097305	response to alcohol	4	0.000433	0.0292	1
GO:0030217	T cell differentiation	3	0.000436	0.0292	1
GO:0032874	positive regulation of stress-activated MAPK cascade	3	0.000436	0.0292	1
GO:0044087	regulation of cellular component biogenesis	5	0.000446	0.0295	1
GO:0070304	positive regulation of stress-activated protein kinase signaling cascade	3	0.000447	0.0295	1
GO:0072507	divalent inorganic cation homeostasis	4	0.000452	0.0295	1
GO:0046640	regulation of alpha-beta T cell proliferation	2	0.000455	0.0295	1
GO:0042346	positive regulation of NF-kappaB import into nucleus	2	0.000455	0.0295	1
GO:0045992	negative regulation of embryonic development	2	0.000455	0.0295	1
GO:0071219	cellular response to molecule of bacterial origin	3	0.000459	0.0297	1
GO:0035556	intracellular signal transduction	8	0.000462	0.0297	1
GO:0050680	negative regulation of epithelial cell proliferation	3	0.000471	0.0301	1
GO:0042592	homeostatic process	7	0.000494	0.0315	1
GO:0051130	positive regulation of cellular component organization	6	0.000507	0.032	1
GO:0034284	response to monosaccharide	3	0.000507	0.032	1
GO:0060326	cell chemotaxis	3	0.000532	0.0334	1
GO:0031062	positive regulation of histone methylation	2	0.000535	0.0334	1
GO:0051338	regulation of transferase activity	6	0.000541	0.0337	1
GO:0070665	positive regulation of leukocyte proliferation	3	0.000545	0.0338	1
GO:0030155	regulation of cell adhesion	5	0.000548	0.0338	1
GO:0042129	regulation of T cell proliferation	3	0.000558	0.0341	1
GO:0002685	regulation of leukocyte migration	3	0.000558	0.0341	1
GO:0046649	lymphocyte activation	4	0.000565	0.0344	1
GO:0090279	regulation of calcium ion import	2	0.000577	0.0348	1
GO:0032814	regulation of natural killer cell activation	2	0.000577	0.0348	1

GO:0046903	secretion	5	0.000607	0.0364	1
GO:0090263	positive regulation of canonical Wnt signaling pathway	3	0.000613	0.0366	1
GO:0006928	movement of cell or subcellular component	7	0.000616	0.0366	1
GO:0042517	positive regulation of tyrosine phosphorylation of Stat3 protein	2	0.000621	0.0366	1
GO:0010623	developmental programmed cell death	2	0.000621	0.0366	1
GO:0048469	cell maturation	3	0.000627	0.0368	1
GO:0031334	positive regulation of protein complex assembly	3	0.000656	0.0384	1
GO:0035116	embryonic hindlimb morphogenesis	2	0.000666	0.0386	1
GO:0072676	lymphocyte migration	2	0.000666	0.0386	1
GO:0071216	cellular response to biotic stimulus	3	0.000686	0.0396	1
GO:0051347	positive regulation of transferase activity	5	0.000705	0.0405	1
GO:0007155	cell adhesion	6	0.000711	0.0407	1
GO:0022407	regulation of cell-cell adhesion	4	0.000723	0.0412	1
GO:0022610	biological adhesion	6	0.000729	0.0414	1
GO:0071495	cellular response to endogenous stimulus	6	0.000756	0.0426	1
GO:0031347	regulation of defense response	5	0.000758	0.0426	1
GO:0010453	regulation of cell fate commitment	2	0.000762	0.0427	1
GO:0046328	regulation of JNK cascade	3	0.00078	0.0435	1
GO:0031128	developmental induction	2	0.000812	0.045	1
GO:0009743	response to carbohydrate	3	0.000814	0.045	1
GO:0006935	chemotaxis	5	0.00082	0.045	1
GO:0048514	blood vessel morphogenesis	4	0.000832	0.0452	1
GO:1903034	regulation of response to wounding	4	0.000832	0.0452	1
GO:0019725	cellular homeostasis	5	0.000833	0.0452	1
GO:0007204	positive regulation of cytosolic calcium ion concentration	3	0.000848	0.0457	1

GO:0045785	positive regulation of cell adhesion	4	0.000851	0.0457	1
GO:0008285	negative regulation of cell proliferation	5	0.00086	0.0457	1
GO:0035115	embryonic forelimb morphogenesis	2	0.000864	0.0457	1
GO:0046006	regulation of activated T cell proliferation	2	0.000864	0.0457	1
GO:0045168	cell-cell signaling involved in cell fate commitment	2	0.000864	0.0457	1
GO:0032101	regulation of response to external stimulus	5	0.000894	0.0471	1
GO:0042516	regulation of tyrosine phosphorylation of Stat3 protein	2	0.000917	0.0482	1
GO:2000243	positive regulation of reproductive process	2	0.000972	0.0506	1
GO:0000578	embryonic axis specification	2	0.000972	0.0506	1
GO:0046661	male sex differentiation	3	0.000974	0.0506	1
GO:0044702	single organism reproductive process	6	0.000993	0.0514	1
GO:0008543	fibroblast growth factor receptor signaling pathway	3	0.00101	0.0522	1
GO:0002053	positive regulation of mesenchymal cell proliferation	2	0.00103	0.0526	1
GO:0002711	positive regulation of T cell mediated immunity	2	0.00103	0.0526	1
GO:0006875	cellular metal ion homeostasis	4	0.00105	0.0534	1
GO:0051223	regulation of protein transport	5	0.00105	0.0535	1
GO:0065008	regulation of biological quality	10	0.00106	0.0538	1
GO:0007186	G-protein coupled receptor signaling pathway	6	0.00108	0.0541	1
GO:0031667	response to nutrient levels	4	0.00108	0.0541	1
GO:0035137	hindlimb morphogenesis	2	0.00109	0.0541	1
GO:0032330	regulation of chondrocyte differentiation	2	0.00109	0.0541	1
GO:0050789	regulation of biological process	18	0.00114	0.0564	1
GO:0030177	positive regulation of Wnt signaling pathway	3	0.00118	0.0581	1
GO:0045321	leukocyte activation	4	0.00119	0.0586	1
GO:0035136	forelimb morphogenesis	2	0.00121	0.0588	1
GO:0021795	cerebral cortex cell migration	2	0.00121	0.0588	1

GO:0046686	response to cadmium ion	2	0.00121	0.0588	1
GO:2001233	regulation of apoptotic signaling pathway	4	0.00123	0.0595	1
GO:0032872	regulation of stress-activated MAPK cascade	3	0.00124	0.06	1
GO:0010464	regulation of mesenchymal cell proliferation	2	0.00127	0.0603	1
GO:0001954	positive regulation of cell-matrix adhesion	2	0.00127	0.0603	1
GO:0045661	regulation of myoblast differentiation	2	0.00127	0.0603	1
GO:0042345	regulation of NF-kappaB import into nucleus	2	0.00127	0.0603	1
GO:0051480	cytosolic calcium ion homeostasis	3	0.00133	0.0627	1
GO:0050796	regulation of insulin secretion	3	0.00133	0.0627	1
GO:0060401	cytosolic calcium ion transport	2	0.00133	0.0627	1
GO:0032504	multicellular organism reproduction	5	0.00135	0.0635	1
GO:0050670	regulation of lymphocyte proliferation	3	0.00138	0.0641	1
GO:0051924	regulation of calcium ion transport	3	0.00138	0.0641	1
GO:0006915	apoptotic process	6	0.0014	0.0641	1
GO:0031060	regulation of histone methylation	2	0.0014	0.0641	1
GO:0009948	anterior/posterior axis specification	2	0.0014	0.0641	1
GO:0032944	regulation of mononuclear cell proliferation	3	0.0014	0.0641	1
GO:0009893	positive regulation of metabolic process	10	0.0014	0.0641	1
GO:0060341	regulation of cellular localization	6	0.00141	0.0644	1
GO:0012501	programmed cell death	6	0.00143	0.0649	1
GO:0030003	cellular cation homeostasis	4	0.00145	0.0658	1
GO:0009991	response to extracellular stimulus	4	0.00147	0.0662	1
GO:0044344	cellular response to fibroblast growth factor stimulus	3	0.0015	0.0674	1
GO:0046635	positive regulation of alpha-beta T cell activation	2	0.00153	0.0685	1
GO:0010862	positive regulation of pathway-restricted SMAD protein phosphorylation	2	0.00153	0.0685	1

GO:0030324	lung development	3	0.00155	0.0689	1
GO:0070201	regulation of establishment of protein localization	5	0.00155	0.0689	1
GO:0007281	germ cell development	3	0.00157	0.0696	1
GO:0071774	response to fibroblast growth factor	3	0.0016	0.0705	1
GO:0042993	positive regulation of transcription factor import into nucleus	2	0.0016	0.0705	1
GO:0006873	cellular ion homeostasis	4	0.00163	0.0713	1
GO:0008219	cell death	6	0.00163	0.0714	1
GO:0033993	response to lipid	5	0.00165	0.0714	1
GO:0044093	positive regulation of molecular function	7	0.00165	0.0714	1
GO:0030323	respiratory tube development	3	0.00165	0.0714	1
GO:0042531	positive regulation of tyrosine phosphorylation of STAT protein	2	0.00168	0.0716	1
GO:0016265	death	6	0.00168	0.0716	1
GO:0006816	calcium ion transport	3	0.00168	0.0716	1
GO:0030098	lymphocyte differentiation	3	0.00168	0.0716	1
GO:0001568	blood vessel development	4	0.00171	0.0726	1
GO:0071900	regulation of protein serine/threonine kinase activity	4	0.00172	0.073	1
GO:0050865	regulation of cell activation	4	0.00174	0.0732	1
GO:0001541	ovarian follicle development	2	0.00175	0.0732	1
GO:0002709	regulation of T cell mediated immunity	2	0.00175	0.0732	1
GO:0072358	cardiovascular system development	5	0.00176	0.0732	1
GO:0072359	circulatory system development	5	0.00176	0.0732	1
GO:0021700	developmental maturation	3	0.00176	0.0732	1
GO:0090276	regulation of peptide hormone secretion	3	0.00179	0.0741	1
GO:0001837	epithelial to mesenchymal transition	2	0.00182	0.0754	1

GO:0055065	metal ion homeostasis	4	0.00185	0.0764	1
GO:0022414	reproductive process	6	0.00188	0.0774	1
GO:0030858	positive regulation of epithelial cell differentiation	2	0.0019	0.0779	1
GO:0065007	biological regulation	18	0.00191	0.0782	1
GO:0001944	vasculature development	4	0.00192	0.0782	1
GO:0002791	regulation of peptide secretion	3	0.00193	0.0783	1
GO:0051049	regulation of transport	7	0.00196	0.0795	1
GO:0009952	anterior/posterior pattern specification	3	0.00199	0.0802	1
GO:0022029	telencephalon cell migration	2	0.00206	0.0823	1
GO:0060395	SMAD protein signal transduction	2	0.00206	0.0823	1
GO:0061035	regulation of cartilage development	2	0.00206	0.0823	1
GO:0042509	regulation of tyrosine phosphorylation of STAT protein	2	0.00222	0.088	1
GO:0021885	forebrain cell migration	2	0.00222	0.088	1
GO:0072089	stem cell proliferation	2	0.00222	0.088	1
GO:0043406	positive regulation of MAP kinase activity	3	0.00226	0.0893	1
GO:0060541	respiratory system development	3	0.00226	0.0893	1
GO:0042110	T cell activation	3	0.0023	0.0901	1
GO:0071593	lymphocyte aggregation	3	0.00236	0.0924	1
GO:0042108	positive regulation of cytokine biosynthetic process	2	0.00239	0.093	1
GO:0045893	positive regulation of transcription, DNA-templated	6	0.00242	0.0937	1
GO:1903508	positive regulation of nucleic acid-templated transcription	6	0.00242	0.0937	1
GO:0051050	positive regulation of transport	5	0.00246	0.0949	1
GO:0060393	regulation of pathway-restricted SMAD protein phosphorylation	2	0.00247	0.0953	1
GO:0048878	chemical homeostasis	5	0.00251	0.0966	1
GO:0023051	regulation of signaling	9	0.00256	0.098	1

GO:0070486	leukocyte aggregation	3	0.00257	0.098	1
GO:0055080	cation homeostasis	4	0.00259	0.0985	1
GO:0009615	response to virus	3	0.00264	0.0995	1
GO:0046427	positive regulation of JAK-STAT cascade	2	0.00265	0.0995	1
GO:0031058	positive regulation of histone modification	2	0.00265	0.0995	1
GO:0046634	regulation of alpha-beta T cell activation	2	0.00265	0.0995	1
GO:0042733	embryonic digit morphogenesis	2	0.00265	0.0995	1
GO:0010646	regulation of cell communication	9	0.00267	0.0998	1
GO:0048864	stem cell development	3	0.00267	0.0998	1
GO:1902680	positive regulation of RNA biosynthetic process	6	0.00272	0.101	1
GO:0070542	response to fatty acid	2	0.00274	0.102	1
GO:0060828	regulation of canonical Wnt signaling pathway	3	0.00282	0.104	1
GO:0098771	inorganic ion homeostasis	4	0.00282	0.104	1
GO:0045740	positive regulation of DNA replication	2	0.00283	0.104	1
GO:0009880	embryonic pattern specification	2	0.00283	0.104	1
GO:0070838	divalent metal ion transport	3	0.00285	0.105	1
GO:1903310	positive regulation of chromatin modification	2	0.00293	0.107	1
GO:0045165	cell fate commitment	3	0.00297	0.108	1
GO:0051254	positive regulation of RNA metabolic process	6	0.00313	0.113	1
GO:0044703	multi-organism reproductive process	5	0.00321	0.116	1
GO:0071345	cellular response to cytokine stimulus	4	0.00327	0.118	1
GO:0046883	regulation of hormone secretion	3	0.00332	0.119	1
GO:0007423	sensory organ development	4	0.00337	0.121	1
GO:0002690	positive regulation of leukocyte chemotaxis	2	0.00342	0.122	1
GO:0050801	ion homeostasis	4	0.00345	0.123	1
GO:0043085	positive regulation of catalytic activity	6	0.00349	0.124	1

GO:0033273	response to vitamin	2	0.00352	0.125	1
GO:0000003	reproduction	5	0.00352	0.125	1
GO:0051241	negative regulation of multicellular organismal process	5	0.00356	0.126	1
GO:0007167	enzyme linked receptor protein signaling pathway	5	0.00366	0.129	1
GO:0050863	regulation of T cell activation	3	0.0037	0.13	1
GO:0010556	regulation of macromolecule biosynthetic process	10	0.00372	0.13	1
GO:0002708	positive regulation of lymphocyte mediated immunity	2	0.00373	0.13	1
GO:0007159	leukocyte cell-cell adhesion	3	0.00374	0.13	1
GO:0032481	positive regulation of type I interferon production	2	0.00383	0.133	1
GO:0002824	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	2	0.00383	0.133	1
GO:0007276	gamete generation	4	0.00405	0.14	1
GO:0022602	ovulation cycle process	2	0.00405	0.14	1
GO:0002821	positive regulation of adaptive immune response	2	0.00416	0.143	1
GO:0035050	embryonic heart tube development	2	0.00416	0.143	1
GO:0034110	regulation of homotypic cell-cell adhesion	3	0.0042	0.144	1
GO:0048145	regulation of fibroblast proliferation	2	0.00427	0.146	1
GO:0030334	regulation of cell migration	4	0.0044	0.15	1
GO:0043254	regulation of protein complex assembly	3	0.00444	0.151	1
GO:0097306	cellular response to alcohol	2	0.0045	0.153	1
GO:0071902	positive regulation of protein serine/threonine kinase activity	3	0.00454	0.153	1
GO:0034109	homotypic cell-cell adhesion	3	0.00454	0.153	1
GO:0048660	regulation of smooth muscle cell proliferation	2	0.00462	0.155	1
GO:2001252	positive regulation of chromosome organization	2	0.00462	0.155	1

GO:0001952	regulation of cell-matrix adhesion	2	0.00474	0.158	1
GO:0010959	regulation of metal ion transport	3	0.00474	0.158	1
GO:0050867	positive regulation of cell activation	3	0.00484	0.161	1
GO:0002688	regulation of leukocyte chemotaxis	2	0.00485	0.161	1
GO:0042698	ovulation cycle	2	0.00498	0.165	1
GO:0043405	regulation of MAP kinase activity	3	0.005	0.165	1
GO:0006887	exocytosis	3	0.00505	0.166	1
GO:0045778	positive regulation of ossification	2	0.0051	0.167	1
GO:0009798	axis specification	2	0.0051	0.167	1
GO:0008585	female gonad development	2	0.0051	0.167	1
GO:0045087	innate immune response	5	0.00516	0.169	1
GO:0032845	negative regulation of homeostatic process	2	0.00522	0.17	1
GO:2000145	regulation of cell motility	4	0.00527	0.171	1
GO:0042990	regulation of transcription factor import into nucleus	2	0.00534	0.173	1
GO:0042307	positive regulation of protein import into nucleus	2	0.00534	0.173	1
GO:0043200	response to amino acid	2	0.00547	0.176	1
GO:0042102	positive regulation of T cell proliferation	2	0.00547	0.176	1
GO:0002705	positive regulation of leukocyte mediated immunity	2	0.00547	0.176	1
GO:0043010	camera-type eye development	3	0.00554	0.177	1
GO:0002576	platelet degranulation	2	0.0056	0.178	1
GO:0046545	development of primary female sexual characteristics	2	0.0056	0.178	1
GO:0045787	positive regulation of cell cycle	3	0.00571	0.18	1
GO:0050896	response to stimulus	14	0.00571	0.18	1
GO:0090100	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	2	0.00573	0.18	1
GO:0048771	tissue remodeling	2	0.00573	0.18	1

GO:0051928	positive regulation of calcium ion transport	2	0.00573	0.18	1
GO:0009889	regulation of biosynthetic process	10	0.00575	0.181	1
GO:0071375	cellular response to peptide hormone stimulus	3	0.00582	0.182	1
GO:2000241	regulation of reproductive process	2	0.00612	0.191	1
GO:0002687	positive regulation of leukocyte migration	2	0.00612	0.191	1
GO:0045596	negative regulation of cell differentiation	4	0.00614	0.191	1
GO:1900182	positive regulation of protein localization to nucleus	2	0.00639	0.198	1
GO:0030335	positive regulation of cell migration	3	0.00641	0.199	1
GO:1901653	cellular response to peptide	3	0.00653	0.202	1
GO:0046887	positive regulation of hormone secretion	2	0.00666	0.206	1
GO:0050790	regulation of catalytic activity	7	0.00668	0.206	1
GO:0033043	regulation of organelle organization	5	0.00676	0.208	1
GO:0032355	response to estradiol	2	0.0068	0.208	1
GO:0010811	positive regulation of cell-substrate adhesion	2	0.0068	0.208	1
GO:0009953	dorsal/ventral pattern formation	2	0.0068	0.208	1
GO:0040012	regulation of locomotion	4	0.00714	0.217	1
GO:0051128	regulation of cellular component organization	7	0.00723	0.218	1
GO:0002683	negative regulation of immune system process	3	0.00723	0.218	1
GO:0051272	positive regulation of cellular component movement	3	0.00723	0.218	1
GO:0003002	regionalization	3	0.0073	0.22	1
GO:0046824	positive regulation of nucleocytoplasmic transport	2	0.00738	0.221	1
GO:0051270	regulation of cellular component movement	4	0.00739	0.221	1
GO:0051099	positive regulation of binding	2	0.00752	0.224	1
GO:0002822	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	2	0.00752	0.224	1

GO:0001654	eye development	3	0.00763	0.227	1
GO:0046660	female sex differentiation	2	0.00767	0.227	1
GO:0002706	regulation of lymphocyte mediated immunity	2	0.00767	0.227	1
GO:0006357	regulation of transcription from RNA polymerase II promoter	6	0.00775	0.229	1
GO:0050921	positive regulation of chemotaxis	2	0.00782	0.23	1
GO:0031056	regulation of histone modification	2	0.00782	0.23	1
GO:0032479	regulation of type I interferon production	2	0.00782	0.23	1
GO:0071396	cellular response to lipid	3	0.00791	0.232	1
GO:0040017	positive regulation of locomotion	3	0.00798	0.233	1
GO:0050708	regulation of protein secretion	3	0.0084	0.245	1
GO:0048609	multicellular organismal reproductive process	4	0.00857	0.249	1
GO:0007160	cell-matrix adhesion	2	0.00858	0.249	1
GO:0051249	regulation of lymphocyte activation	3	0.00862	0.25	1
GO:0048762	mesenchymal cell differentiation	2	0.00874	0.253	1
GO:0019953	sexual reproduction	4	0.00876	0.253	1
GO:0050794	regulation of cellular process	16	0.00878	0.253	1
GO:0071222	cellular response to lipopolysaccharide	2	0.00889	0.255	1
GO:0051493	regulation of cytoskeleton organization	3	0.00891	0.255	1
GO:0009749	response to glucose	2	0.00921	0.264	1
GO:0009746	response to hexose	2	0.00987	0.281	1
GO:1903308	regulation of chromatin modification	2	0.00987	0.281	1
GO:0006275	regulation of DNA replication	2	0.01	0.285	1
GO:0019221	cytokine-mediated signaling pathway	3	0.0101	0.288	1
GO:0050671	positive regulation of lymphocyte proliferation	2	0.0104	0.294	1
GO:0032946	positive regulation of mononuclear cell proliferation	2	0.0105	0.297	1

GO:0048520	positive regulation of behavior	2	0.0105	0.297	1
GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	2	0.0107	0.301	1
GO:0051222	positive regulation of protein transport	3	0.0108	0.303	1
GO:1902275	regulation of chromatin organization	2	0.0109	0.305	1
GO:0044057	regulation of system process	3	0.011	0.309	1
GO:0010035	response to inorganic substance	3	0.0112	0.311	1
GO:0046546	development of primary male sexual characteristics	2	0.0112	0.311	1
GO:0008584	male gonad development	2	0.0112	0.311	1
GO:0021543	pallium development	2	0.0112	0.311	1
GO:0001701	in utero embryonic development	3	0.0114	0.315	1
GO:0051054	positive regulation of DNA metabolic process	2	0.0116	0.32	1
GO:0048015	phosphatidylinositol-mediated signaling	2	0.0121	0.334	1
GO:0010001	glial cell differentiation	2	0.0123	0.338	1
GO:0009611	response to wounding	4	0.0124	0.341	1
GO:0002694	regulation of leukocyte activation	3	0.0125	0.343	1
GO:0032846	positive regulation of homeostatic process	2	0.0129	0.351	1
GO:0002703	regulation of leukocyte mediated immunity	2	0.0131	0.355	1
GO:0050920	regulation of chemotaxis	2	0.0132	0.359	1
GO:0001667	ameboidal-type cell migration	2	0.0132	0.359	1
GO:0040007	growth	3	0.0133	0.359	1
GO:0051495	positive regulation of cytoskeleton organization	2	0.0138	0.373	1
GO:0009913	epidermal cell differentiation	2	0.014	0.377	1
GO:0002699	positive regulation of immune effector process	2	0.0142	0.382	1
GO:0048568	embryonic organ development	3	0.0145	0.39	1

GO:0031589	cell-substrate adhesion	2	0.0146	0.391	1
GO:0051607	defense response to virus	2	0.0148	0.395	1
GO:0050679	positive regulation of epithelial cell proliferation	2	0.0152	0.405	1
GO:0050776	regulation of immune response	4	0.0154	0.411	1
GO:0016337	single organismal cell-cell adhesion	3	0.0155	0.413	1
GO:0031960	response to corticosteroid	2	0.0156	0.414	1
GO:0042306	regulation of protein import into nucleus	2	0.016	0.424	1
GO:1903827	regulation of cellular protein localization	3	0.0163	0.43	1
GO:0007584	response to nutrient	2	0.0166	0.438	1
GO:0010810	regulation of cell-substrate adhesion	2	0.0166	0.438	1
GO:0031326	regulation of cellular biosynthetic process	9	0.0168	0.441	1
GO:0007187	G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	2	0.0168	0.441	1
GO:0098602	single organism cell adhesion	3	0.0174	0.455	1
GO:0042063	gliogenesis	2	0.0175	0.455	1
GO:0002250	adaptive immune response	2	0.0175	0.455	1
GO:0042594	response to starvation	2	0.0179	0.466	1
GO:0065009	regulation of molecular function	7	0.0181	0.47	1
GO:0001894	tissue homeostasis	2	0.0183	0.475	1
GO:0051726	regulation of cell cycle	4	0.0187	0.484	1
GO:0060348	bone development	2	0.0192	0.496	1
GO:1900180	regulation of protein localization to nucleus	2	0.0194	0.501	1
GO:0030278	regulation of ossification	2	0.0197	0.506	1
GO:0044763	single-organism cellular process	16	0.02	0.512	1
GO:0030522	intracellular receptor signaling pathway	2	0.0201	0.515	1
GO:0010605	negative regulation of macromolecule metabolic process	6	0.0201	0.515	1

GO:0010564	regulation of cell cycle process	3	0.021	0.537	1
GO:0030001	metal ion transport	3	0.0214	0.545	1
GO:0038095	Fc-epsilon receptor signaling pathway	2	0.022	0.558	1
GO:0045765	regulation of angiogenesis	2	0.0222	0.562	1
GO:0050870	positive regulation of T cell activation	2	0.0222	0.562	1
GO:0002764	immune response-regulating signaling pathway	3	0.0224	0.566	1
GO:0048839	inner ear development	2	0.0227	0.571	1
GO:1903039	positive regulation of leukocyte cell-cell adhesion	2	0.0227	0.571	1
GO:0034112	positive regulation of homotypic cell-cell adhesion	2	0.0229	0.576	1
GO:2001235	positive regulation of apoptotic signaling pathway	2	0.0232	0.581	1
GO:0080135	regulation of cellular response to stress	3	0.0233	0.583	1
GO:0050795	regulation of behavior	2	0.0239	0.597	1
GO:0001818	negative regulation of cytokine production	2	0.0241	0.602	1
GO:0030097	hemopoiesis	3	0.0242	0.603	1
GO:0046822	regulation of nucleocytoplasmic transport	2	0.0244	0.605	1
GO:0009612	response to mechanical stimulus	2	0.0244	0.605	1
GO:0043269	regulation of ion transport	3	0.0249	0.616	1
GO:0021537	telencephalon development	2	0.0251	0.621	1
GO:1901342	regulation of vasculature development	2	0.0254	0.625	1
GO:0090092	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	2	0.0254	0.625	1
GO:0043270	positive regulation of ion transport	2	0.0259	0.635	1
GO:0009790	embryo development	4	0.0259	0.635	1
GO:0030182	neuron differentiation	4	0.026	0.636	1
GO:2001234	negative regulation of apoptotic signaling pathway	2	0.0261	0.639	1
GO:0007173	epidermal growth factor receptor signaling pathway	2	0.0266	0.65	1

GO:0038127	ERBB signaling pathway	2	0.0274	0.668	1
GO:0032870	cellular response to hormone stimulus	3	0.0275	0.668	1
GO:0051961	negative regulation of nervous system development	2	0.0277	0.671	1
GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	2	0.0279	0.675	1
GO:0048871	multicellular organismal homeostasis	2	0.0279	0.675	1
GO:0043583	ear development	2	0.0284	0.687	1
GO:0090316	positive regulation of intracellular protein transport	2	0.0287	0.692	1
GO:0043588	skin development	2	0.029	0.697	1
GO:1903530	regulation of secretion by cell	3	0.0296	0.712	1
GO:0048534	hematopoietic or lymphoid organ development	3	0.0299	0.718	1
GO:0022409	positive regulation of cell-cell adhesion	2	0.0306	0.731	1
GO:0032956	regulation of actin cytoskeleton organization	2	0.0314	0.75	1
GO:0050778	positive regulation of immune response	3	0.0314	0.75	1
GO:1903651	positive regulation of cytoplasmic transport	2	0.0325	0.773	1
GO:0002520	immune system development	3	0.0338	0.802	1
GO:0090068	positive regulation of cell cycle process	2	0.0342	0.81	1
GO:0016192	vesicle-mediated transport	4	0.0346	0.82	1
GO:0080090	regulation of primary metabolic process	10	0.0349	0.825	1
GO:0048468	cell development	5	0.035	0.826	1
GO:0030168	platelet activation	2	0.0356	0.838	1
GO:0051098	regulation of binding	2	0.0359	0.843	1
GO:0038093	Fc receptor signaling pathway	2	0.0367	0.862	1
GO:0051251	positive regulation of lymphocyte activation	2	0.037	0.868	1
GO:0051046	regulation of secretion	3	0.0373	0.873	1
GO:0001503	ossification	2	0.0376	0.878	1

GO:0009628	response to abiotic stimulus	4	0.0381	0.887	1
GO:0060249	anatomical structure homeostasis	2	0.0385	0.896	1
GO:0006812	cation transport	3	0.0394	0.914	1
GO:1903533	regulation of protein targeting	2	0.0403	0.934	1
GO:0006367	transcription initiation from RNA polymerase II promoter	2	0.0409	0.947	1
GO:0009892	negative regulation of metabolic process	6	0.0412	0.953	1
GO:0071496	cellular response to external stimulus	2	0.0415	0.957	1
GO:0023057	negative regulation of signaling	4	0.0416	0.957	1
GO:0048511	rhythmic process	2	0.0418	0.961	1
GO:0008544	epidermis development	2	0.0424	0.973	1
GO:0010648	negative regulation of cell communication	4	0.0425	0.973	1
GO:0032970	regulation of actin filament-based process	2	0.0433	0.991	1
GO:0010038	response to metal ion	2	0.0437	0.995	1
GO:0002696	positive regulation of leukocyte activation	2	0.0437	0.995	1
GO:0002521	leukocyte differentiation	2	0.0449	1	1
GO:0051052	regulation of DNA metabolic process	2	0.0449	1	1
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	3	0.0454	1	1
GO:0048863	stem cell differentiation	2	0.0462	1	1
GO:0051649	establishment of localization in cell	5	0.0468	1	1
GO:1903829	positive regulation of cellular protein localization	2	0.0468	1	1
GO:1903532	positive regulation of secretion by cell	2	0.0474	1	1
GO:0002697	regulation of immune effector process	2	0.0487	1	1
GO:0006352	DNA-templated transcription, initiation	2	0.0494	1	1

Table S1-2: List of “Molecular Function” terms obtained from GO enrichment of identified biomarkers

GO_id	Term	NumberOfGenes	p-value	p-value_fdr	p-value_bonferroni
GO:0008083	growth factor activity	7	2.55E-10	0.000001	0.000001
GO:0005125	cytokine activity	7	2.2E-09	4.32E-06	8.64E-06
GO:0005102	receptor binding	9	1.01E-05	0.0133	0.0399
GO:0019957	C-C chemokine binding	2	2.51E-05	0.0247	0.0987
GO:0042813	Wnt-activated receptor activity	2	0.000075	0.059	0.295
GO:0019956	chemokine binding	2	0.00011	0.072	0.432
GO:0048020	CCR chemokine receptor binding	2	0.000253	0.142	0.997
GO:0005179	hormone activity	3	0.000304	0.15	1
GO:0001102	RNA polymerase II activating transcription factor binding	2	0.00103	0.45	1
GO:0033613	activating transcription factor binding	2	0.00222	0.799	1
GO:0005126	cytokine receptor binding	3	0.00223	0.799	1
GO:0019955	cytokine binding	2	0.00362	1	1
GO:0001085	RNA polymerase II transcription factor binding	2	0.00612	1	1
GO:0070851	growth factor receptor binding	2	0.00797	1	1
GO:0003690	double-stranded DNA binding	2	0.00827	1	1
GO:0001664	G-protein coupled receptor binding	2	0.029	1	1
GO:0043566	structure-specific DNA binding	2	0.0373	1	1
GO:0046983	protein dimerization activity	4	0.0442	1	1

Table S1-3: List of “Cellular Component” terms obtained from GO enrichment of identified biomarkers

GO_id	Term	NumberOfGenes	p-value	p-value_fdr	p-value_bonferroni
GO:0005615	extracellular space	15	8.57E-13	1.36E-09	1.36E-09
GO:0044421	extracellular region part	14	2.22E-05	0.0176	0.0352
GO:0034774	secretory granule lumen	3	7.36E-05	0.0389	0.117
GO:0060205	cytoplasmic membrane-bounded vesicle lumen	3	0.000152	0.0489	0.24
GO:0031983	vesicle lumen	3	0.000157	0.0489	0.249
GO:0005576	extracellular region	14	0.000185	0.0489	0.294
GO:0009986	cell surface	5	0.00129	0.292	1
GO:0031093	platelet alpha granule lumen	2	0.0019	0.376	1
GO:0009897	external side of plasma membrane	3	0.00297	0.509	1
GO:0031091	platelet alpha granule	2	0.00322	0.509	1
GO:0044433	cytoplasmic vesicle part	4	0.00413	0.595	1
GO:0048471	perinuclear region of cytoplasm	4	0.00637	0.668	1
GO:0098552	side of membrane	3	0.00666	0.668	1
GO:0005923	tight junction	2	0.00695	0.668	1
GO:0031901	early endosome membrane	2	0.00695	0.668	1
GO:0030141	secretory granule	3	0.00717	0.668	1
GO:0031410	cytoplasmic vesicle	5	0.00894	0.755	1
GO:0043296	apical junction complex	2	0.00905	0.755	1
GO:0010008	endosome membrane	3	0.0113	0.895	1
GO:0044440	endosomal part	3	0.0133	1	1
GO:0005938	cell cortex	2	0.0284	1	1

GO:0030139	endocytic vesicle	2	0.0325	1	1
GO:0016023	cytoplasmic membrane-bounded vesicle	4	0.0325	1	1
GO:0005886	plasma membrane	10	0.0364	1	1
GO:0071944	cell periphery	10	0.04	1	1