

**Supplemental Data 4: Most Specific GO Biological Process Term per Gene**

<b>Affymetrix ID</b>	<b>GO ID</b>	<b>GO Term</b>	<b>p-value</b>
99099_at	GO:0007259	JAK-STAT cascade	0.0358529
100730_at	GO:0006955	immune response	3.44E-13
102401_at	GO:0045893	positive regulation of transcription, DNA-dependent	0.1986299
104531_at	GO:0042100	B cell proliferation	0.0133264
102879_s_at	GO:0050776	regulation of immune response	0.0226872
93315_at	GO:0042035	regulation of cytokine biosynthesis	0.0416229
96185_at	GO:0051138	positive regulation of NK T cell differentiation	0.0002099
95529_at	GO:0051017	actin filament bundle formation	0.1493277
98038_at	GO:0045638	negative regulation of myeloid cell differentiation	0.1493277
103422_at	GO:0051138	positive regulation of NK T cell differentiation	0.0168579
101475_at	GO:0006959	humoral immune response	9.84E-09
94881_at	GO:0045736	negative regulation of cyclin dependent protein kinase activity	0.0084641
100611_at	GO:0042742	defense response to bacteria	0.4911458
101555_at	GO:0030838	positive regulation of actin filament polymerization	3.46E-58
98562_at	GO:0006958	complement activation, classical pathway	0.0014377
92223_at	GO:0006958	complement activation, classical pathway	0.0014377
96020_at	GO:0006958	complement activation, classical pathway	0.0014377
94425_at	GO:0006955	immune response	3.44E-13
93917_at	GO:0030154	cell differentiation	0.0109693
160511_at	GO:0050930	induction of positive chemotaxis	4.31E-05
98390_at	GO:0046651	lymphocyte proliferation	1.17E-08
101923_at	GO:0016042	lipid catabolism	0.1047075
98892_at	GO:0045598	regulation of fat cell differentiation	0.0407207
96886_at	GO:0007155	cell adhesion	0.4434236
94993_f_at	GO:0006957	complement activation, alternative pathway	2.84E-09
101853_f_at	GO:0006957	complement activation, alternative pathway	2.84E-09
102639_at	GO:0006954	inflammatory response	0.156549
93874_s_at	GO:0007166	cell surface receptor linked signal transduction	0.2530902
160809_at	GO:0006955	immune response	3.44E-13
96953_at	GO:0006955	immune response	3.44E-13
104388_at	GO:0007600	sensory perception	0.2828597
104597_at	GO:0006955	immune response	3.44E-13
97540_f_at	GO:0019885	antigen processing, endogenous antigen via MHC class I	0.0003588
93120_f_at	GO:0019885	antigen processing, endogenous antigen via MHC class I	0.0003588
93956_at	GO:0006955	immune response	3.44E-13
97541_f_at	GO:0019885	antigen processing, endogenous antigen via MHC class I	0.0003588
103202_at	GO:0006955	immune response	3.44E-13
104431_at	GO:0050870	positive regulation of T cell activation	0.0416229
99081_at	GO:0007596	blood coagulation	0.0011052
100981_at	GO:0006955	immune response	3.44E-13
103634_at	GO:0045351	interferon type I biosynthesis	2.84E-08
103639_at	GO:0006955	immune response	3.44E-13
102726_at	GO:0048265	response to pain	0.0334368
93088_at	GO:0019885	antigen processing, endogenous antigen via MHC class I	0.0003588
103033_at	No Information Available		
93497_at	GO:0050766	positive regulation of phagocytosis	0.0036843
102802_at	GO:0006955	immune response	3.44E-13

93412_at	GO:0007186	G-protein coupled receptor protein signaling pathway	0.4454595
99133_at	GO:0006952	defense response	2.74E-18
101876_s_at	GO:0006952	defense response	2.74E-18
98579_at	GO:0030217	T cell differentiation	0.1047075
92925_at	GO:0045444	fat cell differentiation	0.0416229
93865_s_at	GO:0006952	defense response	2.74E-18
103759_at	GO:0006952	defense response	2.74E-18
103648_at	GO:0006952	defense response	2.74E-18
95415_f_at	GO:0006958	complement activation, classical pathway	0.0014377
96221_at	GO:0048305	immunoglobulin secretion	0.025182
102299_at	GO:0050930	induction of positive chemotaxis	0.0334368