SUPPLEMENTARY TABLE S3 A

Set A UP REGULATED GENES - GO TERMS AND KEGG PATHWAY

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enric	Bonferroni	Benjamini	FDR
GOTERM_BP_DIREC	GO:0098532~histone H3-K27 trimethylation	3	3.26087	3.75E-04	214537_A	86	6	16792	97.62791	0.251608	0.251608	0.571298
GOTERM_BP_DIREC	GO:0016584~nucleosome positioning	3	3.26087	6.95E-04	214537_A	86	8	16792	73.22093	0.415819	0.235682	1.057
GOTERM_BP_DIREC	GO:0001525~angiogenesis	7	7.608696	9.37E-04	201464_X	86	223	16792	6.129106	0.515409	0.214538	1.4219
GOTERM_BP_DIREC	GO:0080182~histone H3-K4 trimethylation	3	3.26087	0.002547	214537_A	86	15	16792	39.05116	0.860783	0.389167	3.822751
GOTERM_BP_DIREC	GO:0006334~nucleosome assembly	5	5.434783	0.003121	214537_A	86	119	16792	8.204026	0.910778	0.383271	4.66492

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enric	Bonferroni	Benjamini	FDR
GOTERM_CC_DIREC	GO:0005615~extracellular space	19	20.65217	3.99E-05	214315_X	86	1347	18224	2.989037	0.004896	0.004896	0.046
GOTERM_CC_DIREC	GO:0000786~nucleosome	5	5.434783	9.77E-04	214537_A	86	94	18224	11.27165	0.113258	0.05833	1.120504
GOTERM_CC_DIREC	GO:0005576~extracellular region	17	18.47826	0.00288	214315_X	86	1610	18224	2.237527	0.298636	0.11152	3.270713
GOTERM_CC_DIREC	GO:0030141~secretory granule	4	4.347826	0.005001	212171_X	86	74	18224	11.45443	0.460281	0.142879	5.617362
GOTERM_CC_DIREC	GO:0005719~nuclear euchromatin	3	3.26087	0.006996	201464_X	86	27	18224	23.54522	0.578337	0.158618	7.776315
GOTERM_CC_DIREC	GO:0005578~proteinaceous extracellular matrix	6	6.521739	0.008361	212171_X	86	268	18224	4.744186	0.643963	0.158122	9.227352

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enric	Bonferroni	Benjamini	FDR
GOTERM_MF_DIREC	GO:0031490~chromatin DNA binding	4	4.347826	0.003114	214537_A	86	58	16881	13.53729	0.496455	0.496455	3.891976
GOTERM_MF_DIREC	GO:0044822~poly(A) RNA binding	14	15.21739	0.004096	201464_X	86	1129	16881	2.434074	0.594651	0.36333	5.090731
GOTERM_MF_DIREC	GO:0004386~helicase activity	4	4.347826	0.009044	220586_A	86	85	16881	9.237209	0.86449	0.486362	10.92104

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enric	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	hsa00340:Histidine metabolism	3	3.26087	0.006402	207067_S	39	22	6879	24.05245	0.503465	0.503465	6.988378

Set A DOWN REGULATED GENES - GO TERMS AND KEGG PATHWAY

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enric	Bonferroni	Benjamini	FDR
GOTERM_BP_DIREC	GO:0006955~immune response	45	18	2.45E-26	207565_S	232	421	16792	7.736506	3.73E-23	3.73E-23	4.08E-23
GOTERM_BP_DIREC	GO:0031295~T cell costimulation	16	6.4	1.54E-13	206545_A	232	78	16792	14.84704	2.34E-10	1.17E-10	2.56E-10
GOTERM_BP_DIREC	GO:0002250~adaptive immune response	19	7.6	2.03E-12	216491_X	232	148	16792	9.291938	3.10E-09	1.03E-09	3.39E-09
GOTERM_BP_DIREC	GO:0050852~T cell receptor signaling pathway	18	7.2	2.16E-11	206545_A	232	148	16792	8.802889	3.29E-08	8.22E-09	3.59E-08
GOTERM_BP_DIREC	GO:0007166~cell surface receptor signaling pathway	23	9.2	3.09E-11	206545_A	232	274	16792	6.075636	4.71E-08	9.42E-09	5.15E-08
GOTERM_BP_DIREC	GO:0050776~regulation of immune response	18	7.2	4.08E-10	209138_X	232	178	16792	7.319256	6.22E-07	1.04E-07	6.80E-07
GOTERM_BP_DIREC	GO:0045087~innate immune response	26	10.4	1.31E-09	207565_S	232	430	16792	4.376423	1.99E-06	2.84E-07	2.17E-06
GOTERM_BP_DIREC	GO:0060333~interferon-gamma-mediated signaling pathway	12	4.8	3.26E-09	217523_A	232	71	16792	12.23312	4.97E-06	6.21E-07	5.43E-06
GOTERM_BP_DIREC	GO:0006968~cellular defense response	11	4.4	1.15E-08	221602_S	232	62	16792	12.84149	1.75E-05	1.94E-06	1.91E-05
GOTERM_BP_DIREC	GO:0019882~antigen processing and presentation	10	4	5.54E-08	207565_S	232	55	16792	13.15987	8.43E-05	8.43E-06	9.22E-05
GOTERM_BP_DIREC	GO:0006954~inflammatory response	21	8.4	3.04E-07	209687_A	232	379	16792	4.010463	4.62E-04	4.20E-05	5.06E-04
GOTERM_BP_DIREC	GO:0006959~humoral immune response	9	3.6	1.05E-06	206545_A	232	57	16792	11.42831	0.001598	1.33E-04	0.001749
GOTERM_BP_DIREC	GO:0042102~positive regulation of T cell proliferation	9	3.6	1.57E-06	211108_S	232	60	16792	10.8569	0.002387	1.84E-04	0.002614
GOTERM_BP_DIREC	GO:0002504~antigen processing and presentation of peptide or polysaccharide antig	6	2.4	2.55E-06	212999_X	232	17	16792	25.54564	0.003875	2.77E-04	0.004246
GOTERM_BP_DIREC	GO:0042110~T cell activation	8	3.2	3.35E-06	205686_S	232	47	16792	12.31988	0.005089	3.40E-04	0.00558
GOTERM_BP_DIREC	GO:0032729~positive regulation of interferon-gamma production	7	2.8	3.76E-05	213537_A	232	46	16792	11.01424	0.055554	0.003566	0.062487
GOTERM_BP_DIREC	GO:0070098~chemokine-mediated signaling pathway	8	3.2	5.36E-05	206366_X	232	71	16792	8.155415	0.078328	0.004787	0.089161
GOTERM_BP_DIREC	GO:0050870~positive regulation of T cell activation	5	2	9.18E-05	213537_A	232	18	16792	20.10536	0.130343	0.007729	0.152612
GOTERM_BP_DIREC	GO:0050853~B cell receptor signaling pathway	7	2.8	9.45E-05	216491_X	232	54	16792	9.382503	0.133943	0.00754	0.157142
GOTERM_BP_DIREC	GO:0046641~positive regulation of alpha-beta T cell proliferation	4	1.6	2.03E-04	207794_A	232	9	16792	32.16858	0.265867	0.015334	0.337424
GOTERM_BP_DIREC	GO:0060337~type I interferon signaling pathway	7	2.8	2.45E-04	204562_A	232	64	16792	7.916487	0.310917	0.017577	0.406422
GOTERM_BP_DIREC	GO:0006874~cellular calcium ion homeostasis	8	3.2	2.96E-04	204253_S	232	93	16792	6.226177	0.362437	0.020251	0.491024
GOTERM_BP_DIREC	GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway	8	3.2	3.59E-04	207655_S	232	96	16792	6.031609	0.421296	0.023501	0.596377
GOTERM_BP_DIREC	GO:0045060~negative thymic T cell selection	4	1.6	3.91E-04	206545_A	232	11	16792	26.31975	0.44838	0.024483	0.648468
GOTERM_BP_DIREC	GO:0097190~apoptotic signaling pathway	7	2.8	4.31E-04	211282_X	232	71	16792	7.135988	0.481505	0.025931	0.71573
GOTERM_BP_DIREC	GO:0051607~defense response to virus	10	4	4.73E-04	220832_A	232	165	16792	4.386625	0.513041	0.027297	0.783842
GOTERM_BP_DIREC	GO:0045086~positive regulation of interleukin-2 biosynthetic process	4	1.6	5.16E-04	204562_A	232	12	16792	24.12644	0.543974	0.028663	0.855027
GOTERM_BP_DIREC	GO:0002755~MyD88-dependent toll-like receptor signaling pathway	5	2	0.001044	220832_A	232	33	16792	10.96656	0.795969	0.055186	1.723241
GOTERM_BP_DIREC	GO:0090026~positive regulation of monocyte chemotaxis	4	1.6	0.001261	209687_A	232	16	16792	18.09483	0.853359	0.064055	2.077573
GOTERM_BP_DIREC	GO:0019886~antigen processing and presentation of exogenous peptide antigen via	7	2.8	0.001692	212999_X	232	92	16792	5.507121	0.924018	0.082322	2.779142
GOTERM_BP_DIREC	GO:0002503~peptide antigen assembly with MHC class II protein complex	3	1.2	0.001833	215666_A	232	5	16792	43.42759	0.938769	0.08616	3.008358
GOTERM_BP_DIREC	GO:0002260~lymphocyte homeostasis	3	1.2	0.001833	206937_A	232	5	16792	43.42759	0.938769	0.08616	3.008358
GOTERM_BP_DIREC	GO:0038083~peptidyl-tyrosine autophosphorylation	5	2	0.002163	211108_S	232	40	16792	9.047414	0.96293	0.097844	3.539223
GOTERM_BP_DIREC	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	26	10.4	0.002197	206966_S	232	981	16792	1.91831	0.964836	0.09647	3.594875
GOTERM_BP_DIREC	GO:0006915~apoptotic process	18	7.2	0.002236	218000_S	232	567	16792	2.297756	0.966871	0.095358	3.657712
GOTERM_BP_DIREC	GO:0050850~positive regulation of calcium-mediated signaling	4	1.6	0.002464	214032_A	232	20	16792	14.47586	0.9766	0.101731	4.02331
GOTERM_BP_DIREC	GO:0007165~signal transduction	29	11.6	0.002665	207565_S	232	1161	16792	1.807924	0.982781	0.106694	4.344711
GOTERM_BP_DIREC	GO:0019835~cytolysis	4	1.6	0.002846	210321_A	232	21	16792	13.78654	0.986931	0.11062	4.632802
GOTERM_BP_DIREC	GO:0050729~positive regulation of inflammatory response	6	2.4	0.003316	206366_X	232	73	16792	5.948984	0.993627	0.124574	5.378852
GOTERM_BP_DIREC	GO:0010628~positive regulation of gene expression	11	4.4	0.003478	209723_A	232	262	16792	3.038826	0.995022	0.127129	5.634122
GOTERM_BP_DIREC	GO:0032760~positive regulation of tumor necrosis factor production	5	2	0.003916	201743_A	232	47	16792	7.699927	0.997451	0.138694	6.322496
GOTERM_BP_DIREC	GO:0009615~response to virus	7	2.8	0.004146	206366_X	232	110	16792	4.605956	0.998205	0.142909	6.680832
GOTERM_BP_DIREC	GO:0006898~receptor-mediated endocytosis	9	3.6	0.004272	216233_A	232	186	16792	3.502225	0.998521	0.143711	6.878122
GOTERM_BP_DIREC	GO:0014066~regulation of phosphatidylinositol 3-kinase signaling	6	2.4	0.004411	206545_A	232	78	16792	5.567639	0.998803	0.144835	7.093386