SUPPLEMENTARY TABLE S3 B

Set B UP REGULATED GENES - GO TERMS AND KEGG PATHWAY

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:0006955~immune response	26	9.923664	2.88E-09	209555_S_	246	421	16792	4.215592	4.43E-06	4.43E-06	4.80E-06
GOTERM_	GO:0006910~phagocytosis, recognition	6	2.290076	4.74E-05	216491_X_	246	28	16792	14.62718	0.070369	0.035826	0.078991
GOTERM_	GO:0090026~positive regulation of monocyte chemotaxis	5	1.908397	7.01E-05	209687_A	246	16	16792	21.3313	0.102277	0.035326	0.116778
GOTERM_	GO:0070098~chemokine-mediated signaling pathway	8	3.053435	7.76E-05	209687_A	246	71	16792	7.691286	0.1126	0.029423	0.129288
GOTERM_	GO:0006783~heme biosynthetic process	5	1.908397	2.18E-04	222074_A	246	21	16792	16.25242	0.28469	0.064812	0.362181
GOTERM_	GO:0006782~protoporphyrinogen IX biosynthetic process	4	1.526718	2.42E-04	222074_A	246	9	16792	30.33785	0.31046	0.060075	0.401765
GOTERM_	GO:0050871~positive regulation of B cell activation	5	1.908397	5.13E-04	216491_X_	246	26	16792	13.12695	0.546355	0.106778	0.852371
GOTERM_	GO:0006911~phagocytosis, engulfment	5	1.908397	0.001623	216491_X_	246	35	16792	9.751452	0.917874	0.268339	2.670582
GOTERM_	GO:0006898~receptor-mediated endocytosis	10	3.816794	0.001671	209138_X_	246	186	16792	3.669901	0.923778	0.248746	2.749186
GOTERM_	GO:0006874~cellular calcium ion homeostasis	7	2.671756	0.002402	209687_A	246	93	16792	5.137862	0.975318	0.309381	3.929524
GOTERM_	GO:0051496~positive regulation of stress fiber assembly	5	1.908397	0.003204	210986_S_	246	42	16792	8.12621	0.992833	0.361693	5.207548
GOTERM_	GO:0006779~porphyrin-containing compound biosynthetic process	3	1.145038	0.005602	222074_A	246	8	16792	25.59756	0.999824	0.513482	8.938153
GOTERM_	GO:0034383~low-density lipoprotein particle clearance	3	1.145038	0.005602	217173_S_	246	8	16792	25.59756	0.999824	0.513482	8.938153
GOTERM_	GO:0001503~ossification	6	2.290076	0.006279	209585_S_	246	80	16792	5.119512	0.999938	0.525584	9.965776
GOTERM_	GO:0007166~cell surface receptor signaling pathway	11	4.198473	0.007117	217979_A	246	274	16792	2.740371	0.999983	0.543964	11.22334
GOTERM_	GO:0050853~B cell receptor signaling pathway	5	1.908397	0.007902	216491_X_	246	54	16792	6.320385	0.999995	0.556914	12.386
GOTERM_	GO:0030203~glycosaminoglycan metabolic process	4	1.526718	0.008473	212157_A	246	29	16792	9.415195	0.999998	0.558896	13.22242
GOTERM_	GO:0006935~chemotaxis	7	2.671756	0.009001	209687_A	246	122	16792	3.916567	0.999999	0.558926	13.98926
GOTERM_	GO:0044344~cellular response to fibroblast growth factor stimulus	4	1.526718	0.009315	203337_X_	246	30	16792	9.101355	0.999999	0.55073	14.44183
GOTERM_	GO:0055072~iron ion homeostasis	4	1.526718	0.009315	215863_A	246	30	16792	9.101355	0.999999	0.55073	14.44183

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:0016020~membrane	65	24.80916	4.65E-09	203337_X_	254	2200	18224	2.119828	1.44E-06	1.44E-06	6.25E-06
GOTERM_	GO:0009897~external side of plasma membrane	16	6.10687	3.06E-07	216491_X_	254	213	18224	5.389523	9.46E-05	4.73E-05	4.11E-04
GOTERM_	GO:0005874~microtubule	16	6.10687	3.15E-05	218602_S_	254	311	18224	3.691217	0.009697	0.003243	0.042323
GOTERM_	GO:0009986~cell surface	18	6.870229	0.001557	216491_X_	254	542	18224	2.382776	0.382052	0.113379	2.06932
GOTERM_	GO:0042571~immunoglobulin complex, circulating	4	1.526718	0.002173	209138_X_	254	19	18224	15.10485	0.489473	0.125814	2.878349
GOTERM_	GO:0045177~apical part of cell	6	2.290076	0.003883	217173_S_	254	75	18224	5.739843	0.699468	0.181569	5.088437
GOTERM_	GO:0005737~cytoplasm	93	35.49618	0.004521	221246_X_	254	5222	18224	1.27778	0.753478	0.181305	5.901726
GOTERM_	GO:0072562~blood microparticle	8	3.053435	0.005388	216491_X_	254	152	18224	3.776212	0.811645	0.188344	6.995412
GOTERM_	GO:0070062~extracellular exosome	55	20.99237	0.007208	203337_X_	254	2811	18224	1.403821	0.893058	0.219941	9.254471

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:0005515~protein binding	162	61.83206	1.26E-05	213152_S_	247	8785	16881	1.260302	0.00623	0.00623	0.01809
GOTERM_	GO:0034987~immunoglobulin receptor binding	6	2.290076	3.23E-05	216491_X_	247	26	16881	15.77172	0.015933	0.007998	0.046487
GOTERM_	GO:0031727~CCR2 chemokine receptor binding	3	1.145038	6.28E-04	207794_A	247	3	16881	68.34413	0.268326	0.098901	0.900383
GOTERM_	GO:0008009~chemokine activity	6	2.290076	7.13E-04	209687_A	247	49	16881	8.368669	0.298559	0.084838	1.021373
GOTERM_	GO:0003823~antigen binding	7	2.671756	0.003974	216491_X_	247	103	16881	4.644747	0.861767	0.326834	5.567707
GOTERM_	GO:0042803~protein homodimerization activity	21	8.015267	0.005194	212768_S_	247	730	16881	1.966064	0.924858	0.350398	7.219508
GOTERM_	GO:0045236~CXCR chemokine receptor binding	3	1.145038	0.007117	209687_A	247	9	16881	22.78138	0.97127	0.397769	9.76631

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
KEGG_PA	hsa05144:Malaria	8	3.053435	1.64E-05	209555_S_	118	49	6879	9.517814	0.003511	0.003511	0.020747
KEGG_PA	hsa04062:Chemokine signaling pathway	12	4.580153	3.01E-04	209687_A	118	186	6879	3.761072	0.062603	0.031807	0.380617
KEGG_PA	hsa04060:Cytokine-cytokine receptor interaction	12	4.580153	0.002711	209687_A	118	243	6879	2.878845	0.442169	0.176808	3.384486
KEGG_PA	hsa04145:Phagosome	9	3.435115	0.003894	209555_S_	118	150	6879	3.497797	0.567787	0.18918	4.827657
KEGG_PA	hsa00860:Porphyrin and chlorophyll metabolism	5	1.908397	0.005406	222074_A	118	42	6879	6.940073	0.688228	0.207923	6.64388

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Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:0000122~negative regulation of transcription from RNA polymer	21	9.859155	3.64E-04	209636_A	200	720	16792	2.448833	0.398501	0.398501	0.597593
GOTERM_	GO:0044344~cellular response to fibroblast growth factor stimulus	5	2.347418	4.12E-04	201368_A	200	30	16792	13.99333	0.437652	0.250101	0.676446
GOTERM_	GO:0030155~regulation of cell adhesion	5	2.347418	0.001645	201407_S_	200	43	16792	9.762791	0.899795	0.535524	2.676156
GOTERM_	GO:0006954~inflammatory response	13	6.103286	0.001907	209636_A	200	379	16792	2.879894	0.930545	0.486635	3.09588
GOTERM_	GO:0045766~positive regulation of angiogenesis	7	3.286385	0.002481	219028_A	200	115	16792	5.110609	0.9689	0.50048	4.0096
GOTERM_	GO:1904628~cellular response to phorbol 13-acetate 12-myristate	3	1.408451	0.002822	213277_A	200	7	16792	35.98286	0.980702	0.482091	4.548199
GOTERM_	GO:0043066~negative regulation of apoptotic process	14	6.57277	0.003067	203627_A	200	455	16792	2.583385	0.986306	0.458261	4.933522
GOTERM_	GO:0000288~nuclear-transcribed mRNA catabolic process, deader	3	1.408451	0.003733	213277_A	200	8	16792	31.485	0.99462	0.479587	5.975047
GOTERM_	GO:0032355~response to estradiol	6	2.816901	0.004538	209580_S_	200	91	16792	5.535824	0.99826	0.50638	7.218263
GOTERM_	GO:0043524~negative regulation of neuron apoptotic process	7	3.286385	0.004897	209678_S_	200	132	16792	4.452424	0.998948	0.496274	7.767277
GOTERM_	GO:0000398~mRNA splicing, via spliceosome	9	4.225352	0.005066	201071_X_	200	222	16792	3.403784	0.999171	0.475348	8.025752
GOTERM_	GO:0071456~cellular response to hypoxia	6	2.816901	0.005689	213277_A	200	96	16792	5.2475	0.999654	0.485306	8.969761
GOTERM_	GO:0061024~membrane organization	4	1.877934	0.006314	209678_S_	200	32	16792	10.495	0.999857	0.493745	9.908492
GOTERM_	GO:0007050~cell cycle arrest	7	3.286385	0.006718	214315_X_	200	141	16792	4.168227	0.999919	0.489618	10.50885
GOTERM_	GO:0006369~termination of RNA polymerase II transcription	5	2.347418	0.006988	208672_S_	200	64	16792	6.559375	0.999944	0.479555	10.90864
GOTERM_	GO:0006468~protein phosphorylation	13	6.103286	0.008272	207540_S_	200	456	16792	2.393596	0.999991	0.515784	12.78736
GOTERM_	GO:0061158~3'-UTR-mediated mRNA destabilization	3	1.408451	0.00853	213277_A	200	12	16792	20.99	0.999994	0.505363	13.1601
GOTERM_	GO:0016032~viral process	10	4.694836	0.009541	200786_A	200	299	16792	2.808027	0.999998	0.524815	14.60812
GOTERM_	GO:0016192~vesicle-mediated transport	7	3.286385	0.009555	214257_S_	200	152	16792	3.866579	0.999999	0.506359	14.62832
GOTERM_	GO:0043065~positive regulation of apoptotic process	10	4.694836	0.009676	207574_S_	200	300	16792	2.798667	0.999999	0.492942	14.79889

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:0005654~nucleoplasm	70	32.86385	6.48E-11	207983_S_	208	2784	18224	2.202973	2.05E-08	2.05E-08	8.73E-08
GOTERM_	GO:0005829~cytosol	75	35.21127	1.29E-09	207983_S_	208	3315	18224	1.982249	4.08E-07	2.04E-07	1.74E-06
GOTERM_	GO:0005925~focal adhesion	20	9.389671	1.14E-07	201087_A	208	391	18224	4.481605	3.61E-05	1.20E-05	1.54E-04
GOTERM_	GO:0016607~nuclear speck	14	6.57277	5.23E-07	204095_S_	208	201	18224	6.102564	1.65E-04	4.13E-05	7.04E-04
GOTERM_	GO:0016020~membrane	49	23.00469	5.40E-06	207983_S_	208	2200	18224	1.951434	0.001704	3.41E-04	0.007268
GOTERM_	GO:0005634~nucleus	92	43.19249	8.89E-06	207983_S_	208	5415	18224	1.488572	0.002804	4.68E-04	0.011969
GOTERM_	GO:0005737~cytoplasm	89	41.78404	1.28E-05	206919_A	208	5222	18224	1.493253	0.004048	5.79E-04	0.017289
GOTERM_	GO:0072357~PTW/PP1 phosphatase complex	3	1.408451	0.002597	201407_S_	208	7	18224	37.54945	0.560328	0.097617	3.441815
GOTERM_	GO:0015630~microtubule cytoskeleton	7	3.286385	0.004794	207941_S_	208	137	18224	4.476698	0.781001	0.155274	6.268049
GOTERM_	GO:0016605~PML body	6	2.816901	0.00521	219028_A	208	98	18224	5.364207	0.808104	0.152174	6.794374

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:0005515~protein binding	153	71.83099	1.05E-10	207983_S_	207	8785	16881	1.420292	4.20E-08	4.20E-08	1.46E-07
GOTERM_	GO:0044822~poly(A) RNA binding	32	15.02347	1.80E-05	219041_S_	207	1129	16881	2.311447	0.007203	0.003608	0.025098
GOTERM_	GO:0003677~DNA binding	36	16.90141	0.001079	209636_A	207	1674	16881	1.753779	0.352145	0.134715	1.495931
GOTERM_	GO:0001046~core promoter sequence-specific DNA binding	5	2.347418	0.001832	214732_A	207	43	16881	9.482642	0.521446	0.168269	2.526486
GOTERM_	GO:0019901~protein kinase binding	13	6.103286	0.002302	207540_S_	207	376	16881	2.819573	0.60404	0.169135	3.165592
GOTERM_	GO:0031625~ubiquitin protein ligase binding	11	5.164319	0.002816	214315_X_	207	287	16881	3.125638	0.67819	0.172185	3.86026
GOTERM_	GO:0004674~protein serine/threonine kinase activity	12	5.633803	0.006595	207540_S_	207	376	16881	2.602683	0.930061	0.316152	8.822763

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
KEGG_PA	hsa04380:Osteoclast differentiation	9	4.225352	8.81E-04	209636_A	107	131	6879	4.416851	0.144428	0.144428	1.076617
KEGG_PA	hsa05132:Salmonella infection	7	3.286385	0.001678	208728_S_	107	83	6879	5.422025	0.257139	0.138106	2.041606
KEGG_PA	hsa05203:Viral carcinogenesis	10	4.694836	0.004198	209636_A	107	205	6879	3.136084	0.525052	0.219783	5.03559
KEGG_PA	hsa04666:Fc gamma R-mediated phagocytosis	6	2.816901	0.009314	207540_S_	107	84	6879	4.592123	0.809164	0.339056	10.85819