

Table SI. Basic characteristics of 212 patients with hepatocellular carcinoma.

Variable	Patients (n=212)	Recurrence-free survival				Overall survival			
		No. of events	MRT (months)	HR (95% CI)	P-value	No. of events	MST (months)	HR (95% CI)	P-value
Age (years)									
≤60	175	96	45.9	1		69	NA	1	
>60	37	20	48	0.974 (0.602-1.578)	0.916	13	NA	0.8643 (0.478-1.564)	0.63
Missing	0								
Sex									
Female	29	10	NA	1		8	NA	1	
Male	183	106	40.1	2.143 (1.120-4.100)	0.021	74	NA	1.704 (0.821-3.534)	0.152
Missing	0								
Multinodular									
Single	167	90	49.1	1		59	NA	1	
Multiple	45	26	28.7	1.216 (0.785-1.883)	0.382	23	47.9	1.607 (0.992-2.604)	0.054
Missing	0								
Tumor size (cm) ^a									
≤5	137	73	51.1	1		46	NA	1	
>5	74	43	28.4	1.409 (0.966-2.056)	0.075	36	53.3	1.975 (1.274-3.060)	0.002
Missing	1								
Cirrhosis									
No	17	5	NA	1		2	NA	1	
Yes	195	111	37.9	2.612 (1.066-6.402)	0.036	80	NA	4.335 (1.065-17.638)	0.041
Missing	0								
BCLC									
0	20	6	NA	1		2	NA	1	
A	143	74	51.6	2.050 (2.892-4.711)	0.091	48	NA	4.119 (1.001-16.951)	0.05
B	22	15	26.9	4.019 (1.550-10.421)	0.004	12	46.1	8.992 (2.005-40.320)	0.004
C	27	21	8.9	6.163 (2.477-15.333)	<0.001	20	13.6	18.993 (4.419-81.632)	<0.001
Missing	0								
Serum AFP (ng/ml) ^b									
≤300	115	62	48	1		39	NA	1	
>300	94	54	35.2	1.200 (0.833-1.728)	0.328	43	NA	1.546 (1.002-2.385)	0.049
Missing	3								

^aTumor size information was unavailable for one patient; ^bserum AFP information was unavailable for three patients. AFP, α-fetoprotein; BCLC, Barcelona Clinic Liver Cancer; CI, confidence interval; HR, hazard ratio; MRT, median recurrence time; MST, median survival time; NA, not available; OS, overall survival; RFS, recurrence-free survival.

Table SII. Gene set enrichment analysis results of c2-reference gene sets for groups with high cystatin 7 expression.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	124	0.6700854	2.418977	<0.0001	<0.0001	<0.0001	904	tags=26%, list=7%, signal=27%
REACTOME_IL_3_5_AND_GM-CSF_SIGNALING	43	0.7250032	2.3016274	<0.0001	<0.0001	<0.0001	939	tags=30%, list=7%, signal=32%
PID_CD8_TCR_DOWNSTREAM_PATHWAY	61	0.71487266	2.2981193	<0.0001	<0.0001	<0.0001	1,124	tags=31%, list=9%, signal=34%
REACTOME_COSTIMULATION_BY_THE_CD28_FAMILY	53	0.73543465	2.2892425	<0.0001	<0.0001	<0.0001	690	tags=34%, list=5%, signal=36%
KEGG_CHEMOKINE_SIGNALING_PATHWAY	167	0.6643665	2.2572207	<0.0001	5.39x10 ⁻⁴	0.002	705	tags=24%, list=5%, signal=25%
KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	104	0.6049423	2.2390716	<0.0001	0.001043906	0.004	904	tags=22%, list=7%, signal=24%
REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	243	0.61784405	2.2191133	<0.0001	0.001360615	0.004	1,825	tags=33%, list=14%, signal=38%
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	83	0.739056	2.2167673	<0.0001	0.001190538	0.004	1,124	tags=35%, list=9%, signal=38%
BIOCARTA_TCR_PATHWAY	43	0.66826797	2.2152076	<0.0001	0.001058256	0.004	915	tags=30%, list=7%, signal=32%
PID_CXCR4_PATHWAY	91	0.6927961	2.2011344	<0.0001	0.001267448	0.006	1,014	list=8%, signal=34%
MORI_MATURE_B_LYMPHOCYTE_UP	75	0.7956157	2.1999917	<0.0001	0.001152226	0.006	759	tags=40%, list=6%, signal=42%
REACTOME_NEGATIVE_REGULATORS_OF_RIG_I_MDA5_SIGNALING	24	0.771551	2.1896315	<0.0001	0.001056207	0.006	1,750	tags=46%, list=13%, signal=53%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
PID_TCR_PATHWAY	59	0.7711821	2.1871245	<0.0001	9.75x10 ⁻⁴	0.006	947	tags=44%, list=7%, signal=47%
PID_FCR1_PATHWAY	58	0.68035597	2.1700547	<0.0001	0.001276287	0.01	1,472	tags=34%, list=11%, signal=39%
REACTOME_ADAPTIVE_IMMUNE_SYSTEM	428	0.5552551	2.1671739	<0.0001	0.001191201	0.01	1,124	tags=23%, list=9%, signal=24%
PID_PTP1B_PATHWAY	51	0.6055136	2.1535213	<0.0001	0.001283075	0.011	1,112	tags=25%, list=9%, signal=28%
REACTOME_INTERFERON_SIGNALING	141	0.66810143	2.1455035	<0.0001	0.001403275	0.014	1,230	tags=33%, list=9%, signal=36%
DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_DN	279	0.6436554	2.1429987	<0.0001	0.001325316	0.014	1,543	tags=34%, list=12%, signal=38%
KEGG_AUTOIMMUNE_THYROID_DISEASE	49	0.8167898	2.1391838	<0.0001	0.001573633	0.016	736	tags=39%, list=6%, signal=41%
PID_CD8_TCR_PATHWAY	48	0.76430213	2.131344	<0.0001	0.001651528	0.018	947	tags=42%, list=7%, signal=45%
PID_PI3KCI_PATHWAY	41	0.6427355	2.1306095	<0.0001	0.001625356	0.019	897	tags=32%, list=7%, signal=34%
WIKMAN_ASBESTOS_LUNG_CANCER_DN	26	0.7454958	2.1214957	<0.0001	0.001787902	0.021	857	tags=35%, list=7%, signal=37%
FULCHER_INFLAMMATORY_RESPONSE_LLECTIN_VS_LPS_DN	340	0.6526421	2.121124	<0.0001	0.001757581	0.021	1,575	tags=39%, list=12%, signal=43%
QL_PLASMACYTOMA_UP	237	0.7042627	2.1206977	<0.0001	0.00173354	0.022	1,152	tags=39%, list=9%, signal=42%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
KEGG_HEMATOPOIETIC_CELL_LINEAGE	84	0.67801636	2.117748	<0.0001	0.001910393	0.025	1,157	tags=32%, list=9%, signal=35%
HAHTOLA_SEZARY_SYNDROM_DN	39	0.8047001	2.111656	<0.0001	0.002192868	0.03	849	tags=46%, list=7%, signal=49%
REACTOME_IL_RECEPTOR_SHC_SIGNALING	27	0.6906288	2.1059775	<0.0001	0.002196335	0.032	602	tags=22%, list=5%, signal=23%
REACTOME_IL_2_SIGNALING	40	0.6341163	2.0951881	<0.0001	0.002708581	0.043	939	list=7%, signal=24%
BASSO_CD40_SIGNALING_DN	65	0.6938557	2.0939598	<0.0001	0.002777111	0.046	956	tags=26%, list=7%, signal=28%
REACTOME_SIGNALING_BY_ILS	98	0.5843689	2.0855076	<0.0001	0.003096081	0.053	1,786	tags=30%, list=14%, signal=34%
REACTOME_REGULATION_OF_KIT_SIGNALING	16	0.70983475	2.0818813	<0.0001	0.003246295	0.057	620	tags=31%, list=5%, signal=33%
SMID_BREAST_CANCER_NORMAL_LIKE_UP	434	0.7756035	2.0803	<0.0001	0.003276045	0.06	1,369	tags=52%, list=11%, signal=56%
BIOCARTA_NKCELLS_PATHWAY	19	0.69670874	2.0669653	<0.0001	0.004057237	0.069	1,803	tags=53%, list=14%, signal=61%
PID_IL12_2PATHWAY	58	0.80070734	2.0653496	<0.0001	0.004028228	0.07	1,124	tags=52%, list=9%, signal=56%
REACTOME_REGULATION_OF_SIGNALING_BY_CBL	18	0.7474602	2.0628717	<0.0001	0.004190165	0.075	613	tags=33%, list=5%, signal=35%
SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A12	274	0.4904517	2.0562751	<0.0001	0.00444513	0.081	1,705	tags=23%, list=13%, signal=25%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
BOSCO_THI_CYTOTOXIC_MODULE	85	0.7583848	2.0546124	<0.0001	0.004386476	0.082	904	tags=47%, list=7%,
KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	48	0.64089316	2.0532193	<0.0001	0.004322809	0.083	1,786	signal=50% tags=31%, list=14%,
REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS	235	0.54707354	2.052783	<0.0001	0.004211968	0.083	906	signal=36% tags=16%, list=7%,
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	236	0.5895055	2.052139	<0.0001	0.004106668	0.083	1,302	signal=17% tags=24%, list=10%,
ONO_FOXP3_TARGETS_DN	34	0.74354357	2.0477428	<0.0001	0.004279079	0.088	890	signal=26% tags=32%, list=7%,
KEGG_FC_EPSILON_R1_SIGNALING_PATHWAY	74	0.5440681	2.0470314	<0.0001	0.004177196	0.088	897	signal=35% tags=20%, list=7%,
ST_T_CELL_SIGNAL_TRANSDUCTION	43	0.6790429	2.045881	<0.0001	0.00414046	0.088	947	signal=22% tags=30%, list=7%,
REACTOME_G_ALPHA_I_SIGNALLING_EVENTS	152	0.586476	2.0444236	<0.0001	0.004203389	0.093	906	signal=32% tags=19%, list=7%,
MARKEY_RB1_ACUTE_LOF_DN	182	0.74999624	2.0437574	<0.0001	0.004132054	0.094	874	signal=20% tags=42%, list=7%,
REACTOME_TCR_SIGNALING	45	0.774199	2.042535	<0.0001	0.004126125	0.095	947	signal=44% tags=47%, list=7%,
KEGG_VIRAL_MYOCARDITIS	67	0.75296587	2.0414639	<0.0001	0.004126378	0.097	736	signal=50% tags=31%, list=6%,
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	42	0.8559082	2.0349493	<0.0001	0.004322028	0.105	658	signal=33% tags=48%, list=5%, signal=50%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	148	0.610159	2.033433	<0.0001	0.004385575	0.107	880	tags=20%, list=7%, signal=21%
REACTOME_IMMUNOREGULATORY_INTERACTIONS _BETWEEN_A_LYMPHOID_AND_A_NON_LYMPHOID_CELL	58	0.7706169	2.0330207	<0.0001	0.004327929	0.107	958	tags=48%, list=7%, signal=52%
PID_IL23_PATHWAY	34	0.73755795	2.0328944	<0.0001	0.004243068	0.107	1,076	tags=38%, list=8%, signal=42%
REACTOME_DOWNSTREAM_TCR_SIGNALING	29	0.78656214	2.030132	<0.0001	0.004346707	0.109	701	tags=41%, list=5%, signal=44%
THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_UP	73	0.68063325	2.0289345	<0.0001	0.004399982	0.111	1,498	tags=36%, list=11%, signal=40%
BIOCARTA_IL12_PATHWAY	22	0.8065115	2.0268521	<0.0001	0.004562236	0.116	1,076	tags=55%, list=8%, signal=59%
ZHENG_BOUND_BY_FOXP3	351	0.5287866	2.0260174	<0.0001	0.004561791	0.118	1,948	tags=32%, list=15%, signal=37%
JISON_SICKLE_CELL_DISEASE_UP	173	0.6571441	2.0259256	<0.0001	0.004522529	0.119	1,428	tags=35%, list=11%, signal=39%
PID_TXA2PATHWAY	54	0.5409585	2.0257428	0.001968504	0.004443186	0.119	1,647	tags=28%, list=13%, signal=41%
BIOCARTA_NKT_PATHWAY	29	0.76598537	2.0247128	<0.0001	0.00457588	0.124	1,275	tags=41%, list=10%, signal=46%
PID_IL12_STAT4_PATHWAY	33	0.8175582	2.023056	<0.0001	0.004583482	0.126	1,275	tags=55%, list=10%, signal=60%
DER_IFN_BETA_RESPONSE_UP	96	0.7125166	2.022621	<0.0001	0.004591095	0.129	1,803	tags=50%, list=14%, signal=58%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN	278	0.66001827	2.0207276	<0.0001	0.004719445	0.132	1,462	tags=39%, list=11%, signal=43%
TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN	36	0.78594035	2.0203354	<0.0001	0.004696077	0.134	1,397	tags=58%, list=11%, signal=65%
PID_EPO_PATHWAY	34	0.57240075	2.0185726	<0.0001	0.004788443	0.14	1,386	tags=29%, list=11%, signal=33%
REACTOME_GPV1_MEDIATED_ACTIVATION_CASCADE	30	0.75651973	2.0159783	<0.0001	0.004868356	0.143	1,014	tags=43%, list=8%, signal=47%
PID_IL2_STAT5_PATHWAY	30	0.6864737	2.0159328	<0.0001	0.004793458	0.143	939	tags=27%, list=7%, signal=29%
RUTELLA_RESPONSE_TO_HGF_DN	209	0.626869	2.015275	<0.0001	0.004756824	0.144	1,928	tags=42%, list=15%, signal=49%
FOSTER_TOLERANT_MACROPHAGE_UP	119	0.6535302	2.014641	<0.0001	0.004719574	0.145	1,151	tags=31%, list=9%, signal=34%
JAATINEN_HEMATOPOIETIC_STEM_CELL_DN	187	0.75003254	2.01044	<0.0001	0.00484378	0.15	965	tags=42%, list=7%, signal=45%
SANSOM_APC_TARGETS_DN	319	0.6056073	2.0090966	<0.0001	0.004950963	0.153	1,099	tags=28%, list=8%, signal=30%
REACTOME_THE_ROLE_OF_NEF_IN_HIV1 _REPLICATION_AND_DISEASE_PATHOGENESIS	25	0.74076796	2.0082731	<0.0001	0.004924512	0.155	1,124	tags=44%, list=9%, signal=48%
THUM_SYSTOLIC_HEART_FAILURE_UP	345	0.6548427	2.0066183	<0.0001	0.005008365	0.159	1,235	tags=31%, list=9%, signal=33%
LEE_DIFFERENTIATING_T_LYMPHOCYTE	136	0.7693926	2.0035505	<0.0001	0.00508248	0.164	978	tags=44%, list=8%, signal=47%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
BIOCARTA_STEM_PATHWAY	15	0.74357814	2.003312	<0.0001	0.005034613	0.164	627	tags=20%, list=5%, signal=21%
PID_IL27_PATHWAY	25	0.7034317	2.0032616	<0.0001	0.004966578	0.164	1,702	tags=52%, list=13%, signal=60%
MA_MYELOID_DIFFERENTIATION_DN	40	0.62849903	1.9984343	<0.0001	0.005291944	0.171	1,760	tags=33%, list=14%, signal=37%
ZHAN_MULTIPLE_MYELOMA_HP_UP	38	0.6937039	1.9964149	<0.0001	0.005327126	0.174	1,891	tags=50%, list=15%, signal=58%
FERRANDO_T_ALL_WITH_MLL_ENL_FUSION_UP	82	0.6563368	1.9960088	<0.0001	0.005272105	0.174	1,470	tags=38%, list=11%, signal=42%
RODWELL_AGING_KIDNEY_UP	356	0.7488766	1.99404	<0.0001	0.005433547	0.18	1,183	tags=41%, list=9%, signal=44%
BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_UP	153	0.6482563	1.9937571	<0.0001	0.005378933	0.181	1,210	tags=35%, list=9%, signal=38%
KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_GAMMA_IN_WS	30	0.6704363	1.9927937	<0.0001	0.005421504	0.182	613	tags=17%, list=5%, signal=17%
EHRlich_ICF_SYNDROM_DN	15	0.8451182	1.9927177	<0.0001	0.005365489	0.182	792	tags=60%, list=6%, signal=64%
DIRMEIER_LMP1_RESPONSE_LATE_DN	32	0.75991905	1.9915036	<0.0001	0.005426815	0.185	687	tags=31%, list=5%, signal=33%
PID_GMCSF_PATHWAY	37	0.67709476	1.991112	<0.0001	0.005437852	0.187	939	tags=30%, list=7%, signal=32%
BIOCARTA_TOB1_PATHWAY	20	0.72713375	1.9893457	0.001988072	0.005522257	0.192	1,275	tags=40%, list=10%, signal=44%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
WALLACE_PROSTATE_CANCER_RACE_UP	269	0.8637306	1.9870802	<0.0001	0.005659401	0.197	904	tags=65%, list=7%,
REACTOME_ANTIGEN_PROCESSING_CROSS_PRESENTATION	71	0.6552441	1.9867251	0.001972387	0.005631286	0.197	1,124	signal=68% tags=32%, list=9%,
HOFFMANN_SMALL_PRE_BII_TO_IMMATURE_B_LYMPHOCYTE_UP	63	0.6501147	1.9865862	<0.0001	0.005580373	0.198	1,331	signal=35% tags=30%, list=10%,
HUANG_GATA2_TARGETS_UP	122	0.65122175	1.9860891	<0.0001	0.005556206	0.2	1,251	signal=33% tags=35%, list=10%,
ONO_AML1_TARGETS_UP	22	0.8079194	1.9844471	<0.0001	0.005667009	0.203	904	signal=39% tags=55%, list=7%,
ZHU_CMV_ALL_UP	107	0.66071725	1.9837912	<0.0001	0.005666989	0.204	1,511	signal=59% tags=37%, list=12%,
BOSCO_INTERFERON_INDUCED_ANTIVIRAL_MODULE	56	0.803655	1.9802525	<0.0001	0.00604451	0.218	1,179	signal=42% tags=57%, list=9%,
REACTOME_EFFECTS_OF_PIP2_HYDROLYSIS	19	0.6800756	1.979058	0.001960784	0.006056576	0.221	807	signal=63% tags=21%, list=6%,
KEGG_PRIMARY_IMMUNODEFICIENCY	34	0.79014	1.9769104	<0.0001	0.006239482	0.227	1,055	signal=22% tags=47%, list=8%,
SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_DN	42	0.6923895	1.9711616	0.003913894	0.006737959	0.245	1,316	signal=51% tags=36%, list=10%,
BIOCARTA_CSK_PATHWAY	23	0.8401606	1.9697876	<0.0001	0.00687373	0.25	947	signal=40% tags=57%, list=7%,
PARK_HSC_MARKERS	38	0.6551438	1.968383	<0.0001	0.006944342	0.252	1,590	signal=61% tags=39%, list=12%, signal=45%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GAVIN_FOXP3_TARGETS_CLUSTER_P3	114	0.5866329	1.9673803	<0.0001	0.006982774	0.255	1,484	tags=32%, list=11%, signal=36%
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_UP	139	0.68276227	1.964433	<0.0001	0.00737273	0.265	1,473	tags=42%, list=11%, signal=47%
RAMALHO_STEMNESS_DN	61	0.695501	1.9634775	<0.0001	0.00750987	0.269	1,777	tags=46%, list=14%, signal=53%
CROONQUIST_NRAS_VS_STROMAL_STIMULATION_UP	37	0.73085093	1.9632356	<0.0001	0.007468425	0.27	1,413	tags=43%, list=11%, signal=48%
PID_BCR_5PATHWAY	62	0.5670457	1.9622028	<0.0001	0.007495965	0.272	947	tags=24%, list=7%, signal=26%
KUMAR_TARGETS_OF_MLL_AF9_FUSION	327	0.520633	1.9605663	<0.0001	0.007598224	0.278	1,339	tags=24%, list=10%, signal=26%
KLEIN_TARGETS_OF_BCR_ABL1_FUSION	43	0.70345825	1.958495	<0.0001	0.007799555	0.282	1,698	tags=44%, list=13%, signal=51%
BOYLAN_MULTIPLE_MYELOMA_PCA1_UP	87	0.73374027	1.9583962	<0.0001	0.00773431	0.282	857	tags=39%, list=7%, signal=42%
KEGG_GRAFT_VERSUS_HOST_DISEASE	38	0.8772354	1.957038	<0.0001	0.007825783	0.288	1,124	tags=63%, list=9%, signal=69%
REACTOME_RIG_I_MDA5_MEDIATED_INDUCCTION_OF_IFN_ALPHA_BETA_PATHWAYS	64	0.5283678	1.9562486	0.001996008	0.007826634	0.29	1,786	tags=25%, list=14%, signal=29%
FIGUEROA_AML_METHYLATION_CLUSTER_6_DN	21	0.752119	1.9560754	<0.0001	0.007789861	0.29	638	tags=29%, list=5%, signal=30%
RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP	367	0.635088	1.953906	<0.0001	0.007973054	0.292	1,791	tags=40%, list=14%, signal=45%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
ALTEMEIER_RESPONSE_TO_LPS_WITH_MECHANICAL_VENTILATION	109	0.7982782	1.9514147	<0.0001	0.00827307	0.303	1,291	tags=59%, list=10%, signal=65%
ONO_AML1_TARGETS_DN	33	0.7474124	1.9507478	<0.0001	0.008262963	0.307	2,005	tags=48%, list=15%, signal=57%
KEGG_ASTHMA	27	0.887867	1.9491012	<0.0001	0.008341211	0.31	179	tags=37%, list=1%, signal=37%
PENG_RAPAMYCIN_RESPONSE_UP	184	0.5160942	1.9488786	<0.0001	0.008280417	0.311	1,044	tags=17%, list=8%, signal=18%
BIOCARTA_CTLA4_PATHWAY	20	0.8698927	1.9487554	<0.0001	0.008221483	0.311	435	tags=50%, list=3%, signal=52%
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	97	0.5762038	1.9480231	<0.0001	0.008197175	0.313	1,868	tags=30%, list=14%, signal=35%
PID_IL2_PI3K_PATHWAY	30	0.60311985	1.9477732	0.001988072	0.008192862	0.315	164	tags=13%, list=1%, signal=13%
DIAZ_CHRONIC_MEYLOGENOUS_LEUKEMIA_DN	111	0.72519517	1.9470176	<0.0001	0.008131959	0.315	1,149	tags=40%, list=9%, signal=43%
LENAOUR_DENDRITIC_CELL_MATURATION_UP	109	0.68466026	1.9467955	<0.0001	0.008094185	0.315	1,029	tags=34%, list=8%, signal=37%
REACTOME_GPCR_LIGAND_BINDING	321	0.48436344	1.9467652	<0.0001	0.00802559	0.315	1,404	tags=18%, list=11%, signal=19%
REACTOME_INTERFERON_ALPHA_BETA_SIGNALING	59	0.7737068	1.9453894	<0.0001	0.008089338	0.317	1,230	tags=49%, list=9%, signal=54%
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	85	0.5763175	1.9448123	<0.0001	0.008031326	0.317	785	tags=24%, list=6%, signal=25%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GRAESSMANN_RESPONSE_TO_MC_AND_SERUM_DEPRIVATION_UP	159	0.62990665	1.9447184	<0.0001	0.007985185	0.317	1,295	tags=36%, list=10%, signal=39% tags=29%, list=10%, signal=32% tags=56%, list=9%, signal=61% tags=59%, list=13%, signal=67% tags=51%, list=5%, signal=54% tags=31%, list=7%, signal=32% tags=45%, list=8%, signal=49% tags=49%, list=10%, signal=53% tags=23%, list=15%, signal=27% tags=13%, list=9%, signal=14% tags=34%, list=11%, signal=38%
BIOCARTA_DC_PATHWAY	21	0.6524375	1.9439574	0.001953125	0.007971761	0.318	1,333	
REACTOME_INTERFERON_GAMMA_SIGNALING	52	0.78658515	1.941863	0.001988072	0.008100026	0.32	1,124	
BASSO_CD40_SIGNALING_UP	94	0.7589262	1.9399799	<0.0001	0.008246092	0.325	1,744	
MORI_LARGE_PRE_BII_LYMPHOCYTE_DN	49	0.8555237	1.9398167	<0.0001	0.008180124	0.325	680	
BOYLAN_MULTIPLE_MYELOMA_C_D_DN	205	0.61319804	1.9396458	<0.0001	0.008131666	0.325	890	
KEGG_LEISHMANIA_INFECTION	64	0.7779623	1.939126	<0.0001	0.008151233	0.326	992	
LINDSTEDT_DENDRITIC_CELL_MATURATION_D	66	0.7626605	1.9379492	<0.0001	0.008222343	0.332	1,109	
LINDGREN_BLADDER_CANCER_CLUSTER_2B	333	0.7518384	1.9378318	<0.0001	0.008158605	0.332	1,331	
KEGG_JAK_STAT_SIGNALING_PATHWAY	140	0.45775196	1.9365288	<0.0001	0.008254158	0.338	1,986	
REACTOME_GPCR_DOWNSTREAM_SIGNALING	422	0.4391505	1.9362597	<0.0001	0.008200162	0.338	1,109	
CASORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_UP	157	0.59998417	1.9359336	<0.0001	0.008191769	0.341	1,459	

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
WORSCHER_TUMOR_EVASION_AND_TOLEROGENICITY_UP	27	0.83010393	1.9338772	<0.0001	0.008285183	0.345	491	tags=37%, list=4%, signal=38%
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	106	0.6641962	1.9334054	0.002024292	0.008257918	0.346	587	tags=21%, list=5%, signal=22%
ZHU_CMV_24_HR_UP	82	0.6285993	1.9308506	<0.0001	0.008553432	0.357	1,511	tags=34%, list=12%, signal=38%
DER_IFN_GAMMA_RESPONSE_UP	68	0.72224826	1.9307958	<0.0001	0.008499504	0.357	1,803	tags=54%, list=14%, signal=63%
PID_ALPHA_SYNUCLEIN_PATHWAY	33	0.60488594	1.927592	<0.0001	0.008717939	0.366	1,652	tags=30%, list=13%, signal=35%
JIANG_AGING_HYPOTHALAMUS_UP	43	0.5515347	1.9273968	0.001941748	0.008685018	0.366	2,848	tags=40%, list=22%, signal=50%
BIOCARTA_IL2_PATHWAY	22	0.68709916	1.9273645	<0.0001	0.008630943	0.367	939	tags=27%, list=7%, signal=29%
ODONNELL_TARGETS_OF_MYC_AND_TFRC_UP	68	0.7300543	1.9270438	<0.0001	0.008627145	0.369	1,240	tags=49%, list=10%, signal=53%
BIOCARTA_IL2RB_PATHWAY	38	0.5951162	1.9269944	<0.0001	0.008573026	0.369	1,922	tags=34%, list=15%, signal=40%
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_UP	118	0.6941652	1.9267529	<0.0001	0.008521856	0.37	1,397	tags=44%, list=11%, signal=49%
ACOSTA_PROLIFERATION_INDEPENDENT_MYC_TARGETS_DN	110	0.5410576	1.9265679	<0.0001	0.008501268	0.372	1,735	tags=33%, list=13%, signal=37%
BIOCARTA_TH1TH2_PATHWAY	19	0.7720923	1.9264101	0.001964637	0.008448698	0.372	1,076	tags=37%, list=8%, signal=40%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
SIG_BCR_SIGNALING_PATHWAY	45	0.5761704	1.9253132	0.001915709	0.008525036	0.375	1,032	tags=27%, list=8%, signal=29%
BIOCARTA_INFLAM_PATHWAY	29	0.6588244	1.9247168	<0.0001	0.008538385	0.376	1,275	tags=24%, list=10%, signal=27%
GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_DN	51	0.658176	1.9246249	<0.0001	0.008486317	0.376	1,792	tags=41%, list=14%, signal=48%
PID_EPHRINB_REV_PATHWAY	30	0.62993944	1.9245567	0.001972387	0.008438663	0.377	477	tags=20%, list=4%, signal=21%
FAELT_B_CLL_WITH_VH_REARRANGEMENTS_UP	40	0.6646283	1.9240855	<0.0001	0.008439016	0.378	1,317	tags=25%, list=10%, signal=28%
MUNSHI_MULTIPLE_MYELOMA_UP	79	0.5445495	1.9240245	<0.0001	0.008390026	0.378	1,237	tags=20%, list=9%, signal=22%
KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	68	0.56813663	1.9236557	0.001945525	0.008370584	0.378	2,078	tags=34%, list=16%, signal=40%
MCBRYAN_PUBERTAL_BREAST_3_4WK_DN	31	0.6685308	1.9218705	<0.0001	0.008545194	0.386	1,425	tags=26%, list=11%, signal=29%
BOSCO_ALLERGEN_INDUCED_TH2_ASSOCIATED_MODULE	112	0.53646797	1.9213156	<0.0001	0.008534083	0.386	1,566	tags=30%, list=12%, signal=34%
PID_IL2_1PATHWAY	54	0.55637467	1.9200182	<0.0001	0.008638539	0.392	1,914	tags=30%, list=15%, signal=35%
KYNG_DNA_DAMAGE_BY_GAMMA_RADIATION	72	0.5251719	1.9199648	<0.0001	0.008582807	0.392	1,656	tags=26%, list=13%, signal=30%
GRABARCZYK_BCL11B_TARGETS_UP	52	0.6378625	1.9178146	<0.0001	0.008780249	0.4	810	tags=27%, list=6%, signal=29%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
LINDGREN_BLADDER_CANCER_CLUSTER_2A_DN	110	0.6157384	1.9167874	0.001968504	0.008828919	0.402	1,344	tags=31%, list=10%, signal=34%, tags=43%, list=12%, signal=49%, tags=54%, list=11%, signal=61%, tags=34%, list=7%, signal=37%, tags=29%, list=7%, signal=31%, tags=48%, list=16%, signal=58%, tags=53%, list=13%, signal=61%, tags=51%, list=6%, signal=54%, tags=32%, list=9%, signal=35%, tags=15%, list=3%, signal=16%, tags=32%, list=15%, signal=38%, tags=35%, list=7%, signal=37%
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_16D_UP	127	0.64754355	1.9140574	<0.0001	0.009144057	0.412	1,579	
HESS_TARGETS_OF_HOXA9_AND_MEIS1_DN	70	0.76431483	1.9123045	<0.0001	0.009383039	0.42	1,459	
MARSON_FOXP3_TARGETS_DN	44	0.6610218	1.9095497	0.00203252	0.009680946	0.431	904	
LEE_DOUBLE_POLAR_THYMOCYTE	21	0.68074447	1.9073901	<0.0001	0.009969217	0.442	858	
ZHENG_FOXP3_TARGETS_IN_T_LYMPHOCYTE_DN	31	0.63481355	1.9072326	0.005859375	0.009940853	0.443	2,130	
BIOCARTA_IL7_PATHWAY	17	0.74882793	1.9062543	<0.0001	0.010099273	0.451	1,652	
GAURNIER_PSMD4_TARGETS	67	0.8332363	1.9055825	<0.0001	0.010122686	0.452	759	
AMUNDSON_POOR_SURVIVAL_AFTER_GAMMA_RADIATION_8G	88	0.6435357	1.9053472	<0.0001	0.010088497	0.452	1,217	
PID_CXCR3_PATHWAY	39	0.65316415	1.9045306	<0.0001	0.010142478	0.454	339	
REACTOME_INNATE_IMMUNE_SYSTEM	207	0.5390503	1.9042536	<0.0001	0.010098323	0.454	1,971	
REACTOME_ANTIGEN_ACTIVATES_B_CELL_RECEPTOR_LEADING_TO_GENERATION_OF_SECOND_MESSENGERS	26	0.64241767	1.9026444	0.001988072	0.010283887	0.457	915	

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
BIOCARTA_IL3_PATHWAY	15	0.7445913	1.9000741	<0.0001	0.010500046	0.47	939	tags=33%, list=7%, signal=36%
SENGUPTA_EBNA1_ANTICORRELATED	101	0.47900975	1.8980525	<0.0001	0.010825371	0.481	2,101	tags=29%, list=16%, signal=34%
HECKER_IFNB1_TARGETS	75	0.833121	1.897393	<0.0001	0.010879834	0.483	849	tags=60%, list=7%, signal=64%
GALINDO_IMMUNE_RESPONSE_TO_ENTEROTOXIN	77	0.67788815	1.8971406	<0.0001	0.010851593	0.484	1,401	tags=42%, list=11%, signal=46%
KEGG_TYPE_I_DIABETES_MELLITUS	40	0.8060022	1.8952875	<0.0001	0.011041909	0.491	1,124	tags=55%, list=9%, signal=60%
DER_IFN_ALPHA_RESPONSE_UP	71	0.75934815	1.8951756	<0.0001	0.01099644	0.492	1,803	tags=62%, list=14%, signal=72%
WORSCHER_TUMOR_REJECTION_UP	48	0.77221507	1.8948137	<0.0001	0.010954069	0.493	1,159	tags=48%, list=9%, signal=52%
RASHI_RESPONSE_TO_IONIZING_RADIATION_6	70	0.68319464	1.8929658	<0.0001	0.01112367	0.501	680	tags=31%, list=5%, signal=40%
VERHAAK_AML_WITH_NPM1_MUTATED_UP	171	0.63885045	1.888218	<0.0001	0.011799057	0.512	1,534	list=12%, signal=44%
HELLER_SILENCED_BY_METHYLATION_UP	263	0.65021944	1.8878821	<0.0001	0.011790025	0.515	1,265	tags=34%, list=10%, signal=37%
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_UP	131	0.70281667	1.8873605	<0.0001	0.011796167	0.518	1,294	tags=44%, list=10%, signal=49%
WINTER_HYPOXIA_DN	39	0.8459356	1.885792	<0.0001	0.011924157	0.526	675	tags=59%, list=5%, signal=62%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
YU_MYC_TARGETS_DN	46	0.78404427	1.884448	<0.0001	0.012077848	0.533	961	tags=41%, list=7%, signal=44%
DAUER_STAT3_TARGETS_DN	48	0.82020366	1.8839335	<0.0001	0.012143111	0.537	1,171	tags=60%, list=9%, signal=66%
KUROZUMI_RESPONSE_TO_ONCOCYTIC_VIRUS	40	0.8255674	1.8825356	<0.0001	0.012316334	0.543	992	tags=55%, list=8%, signal=59%
KUROZUMI_RESPONSE_TO_ONCOCYTIC_VIRUS_AND_CYCLIC_RGD	18	0.8356495	1.8824006	<0.0001	0.012278887	0.543	904	tags=44%, list=7%, signal=48%
BROCKE_APOPTOSIS_REVERSED_BY_IL6	126	0.6283308	1.8823662	<0.0001	0.012230679	0.543	2,015	tags=43%, list=15%, signal=50%
PID_IL8_CXCR2_PATHWAY	29	0.62744766	1.8797376	<0.0001	0.012560218	0.559	1,880	tags=41%, list=14%, signal=48%
KEGG_CELL_ADHESION_MOLECULES_CAMS	117	0.6291447	1.8796904	<0.0001	0.012501677	0.559	1,356	tags=35%, list=10%, signal=39%
BEIER_GLIOMA_STEM_CELL_DN	48	0.7326362	1.8791966	<0.0001	0.012508696	0.563	110	tags=23%, list=1%, signal=23%
ICHIBA_GRAFT_VERSUS_HOST_DISEASE_D7_UP	92	0.8309729	1.8787957	<0.0001	0.012504083	0.565	1,157	tags=61%, list=9%, signal=66%
VALK_AML_CLUSTER_5	29	0.65561426	1.8771297	0.002012072	0.012766216	0.572	1,686	tags=38%, list=13%, signal=43%
KEGG_ALLOGRAFT_REJECTION	34	0.86662096	1.8760606	<0.0001	0.012863869	0.576	904	tags=59%, list=7%, signal=63%
CROONQUIST_NRAS_SIGNALING_UP	39	0.8029513	1.8756968	<0.0001	0.012892186	0.58	628	tags=44%, list=5%, signal=46%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
AMUNDSON_POOR_SURVIVAL_AFTER_GAMMA_RADIATION_2G	152	0.5257576	1.8749653	<0.0001	0.012956167	0.581	1,941	tags=30%, list=15%, signal=35%
WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_UP	234	0.51684517	1.8741645	<0.0001	0.013033052	0.584	1,612	tags=29%, list=12%, signal=33%
MARSHALL_VIRAL_INFECTION_RESPONSE_DN	24	0.6724754	1.869751	<0.0001	0.013630409	0.592	658	tags=21%, list=5%, signal=22%
ZHU_CMV_8_HR_UP	44	0.78426814	1.8693166	<0.0001	0.013633918	0.592	1,202	tags=57%, list=9%, signal=62%
HELLER_HDAC_TARGETS_DN	261	0.54229254	1.8687338	<0.0001	0.013683402	0.597	1,493	tags=29%, list=11%, signal=32%
TAVOR_CEBPA_TARGETS_DN	29	0.72297996	1.8682587	<0.0001	0.013707494	0.598	1,645	tags=48%, list=13%, signal=55%
BILBAN_B_CLL_LPL_DN	35	0.8042244	1.8673261	<0.0001	0.013798443	0.601	1,241	tags=49%, list=10%, signal=54%
LIAN_LIPA_TARGETS_6M	62	0.7311148	1.867036	0.001923077	0.013805707	0.601	1,438	tags=50%, list=11%, signal=56%
BOYLAN_MULTIPLE_MYELOMA_PCA3_DN	48	0.57796687	1.8659272	0.001912046	0.013957976	0.605	2,360	tags=42%, list=18%, signal=51%
LIU_VAV3_PROSTATE_CARCINOGENESIS_UP	84	0.74916893	1.8655751	<0.0001	0.013938091	0.605	1,224	tags=45%, list=9%, signal=50%
MARSON_FOXP3_TARGETS_STIMULATED_UP	21	0.7822219	1.8653507	0.001996008	0.013896602	0.605	602	tags=43%, list=5%, signal=45%
LEE_AGING_CEREBELLUM_UP	75	0.62351054	1.8637369	<0.0001	0.014111627	0.607	1,202	tags=31%, list=9%, signal=34%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
YAN_ESCAPE_FROM_ANOIKIS	22	0.8575384	1.8631272	<0.0001	0.014126941	0.61	770	tags=59%, list=6%, signal=63%
BIOCARTA_FCR1_PATHWAY	36	0.577888	1.8620169	<0.0001	0.014270583	0.617	915	tags=22%, list=7%, signal=24%
DIRMEIER_LMP1_RESPONSE_LATE_UP	54	0.66819495	1.8606541	<0.0001	0.01441626	0.621	1,253	tags=41%, list=10%, signal=45%
MORI_PRE_BI_LYMPHOCYTE_DN	57	0.65273666	1.8604358	0.001980198	0.014400296	0.622	736	tags=28%, list=6%, signal=30%
WUNDER_INFLAMMATORY_RESPONSE_AND_CHOLESTEROL_UP	49	0.819089	1.8589706	<0.0001	0.014528788	0.628	668	tags=47%, list=5%, signal=49%
PID_IL3_PATHWAY	26	0.5905009	1.8588505	<0.0001	0.014480655	0.628	1,401	tags=27%, list=11%, signal=30%
SEKI_INFLAMMATORY_RESPONSE_LPS_UP	66	0.7656708	1.857571	<0.0001	0.014595765	0.631	1,678	tags=56%, list=13%, signal=64%
MARKEY_RB1_CHRONIC_LOF_DN	97	0.6657857	1.8571403	<0.0001	0.014595551	0.633	1,331	tags=35%, list=10%, signal=39%
TSAL_RESPONSE_TO_IONIZING_RADIATION	138	0.5543843	1.8570824	<0.0001	0.014537087	0.633	1,751	tags=31%, list=13%, signal=36%
HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_DN	252	0.5409827	1.8562641	<0.0001	0.014604745	0.634	1,493	tags=29%, list=11%, signal=32%
LENAOUR_DENDRITIC_CELL_MATURATION_DN	121	0.6687963	1.8554671	<0.0001	0.014662415	0.638	1,686	tags=46%, list=13%, signal=53%
FIGUEROA_AML_METHYLATION_CLUSTER_5_DN	32	0.67255414	1.854948	<0.0001	0.01469881	0.64	1,009	tags=31%, list=8%, signal=34%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GEISS_RESPONSE_TO_DSRNA_UP	36	0.7714594	1.8549111	<0.0001	0.014653301	0.641	1,534	tags=56%, list=12%,
MORI_PLASMA_CELL_DN	27	0.7223458	1.8538646	0.003875969	0.014786687	0.644	1,152	signal=63% tags=41%, list=9%,
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULOCYTE_DN	16	0.80407745	1.8506019	<0.0001	0.015429189	0.657	1,065	signal=45% tags=38%, list=8%,
GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN	88	0.72480327	1.8499864	<0.0001	0.015463089	0.658	1,294	signal=41% tags=44%, list=10%,
REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	48	0.80780745	1.8495884	<0.0001	0.015479926	0.658	662	signal=49% tags=44%, list=5%,
SHIN_B_CELL_LYMPHOMA_CLUSTER_3	26	0.70851654	1.8495547	0.001960784	0.015420365	0.658	2,003	signal=46% tags=62%, list=15%,
KYNG_DNA_DAMAGE_DN	181	0.52549773	1.849237	<0.0001	0.015380932	0.66	1,477	signal=73% tags=25%, list=11%,
BIOCARTA_NO2IL12_PATHWAY	16	0.8823501	1.8487095	<0.0001	0.015384919	0.663	904	signal=28% tags=63%, list=7%,
KAAB_FAILED_HEART_VENTRICLE_DN	38	0.6928702	1.8466244	<0.0001	0.015793573	0.673	1,261	signal=67% tags=37%, list=10%,
PID_NFAT_TFPATHWAY	44	0.5879703	1.8461223	<0.0001	0.015801504	0.675	2,129	signal=41% tags=45%, list=16%,
LEE_EARLY_T_LYMPHOCYTE_DN	41	0.73808104	1.8459971	0.00203252	0.015746087	0.675	1,614	signal=54% tags=54%, list=12%,
ICHIBA_GRAFT_VERSUS_HOST_DISEASE_35D_UP	112	0.80668795	1.8459655	<0.0001	0.015680771	0.675	769	signal=61% tags=49%, list=6%, signal=52%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
BOYLAN_MULTIPLE_MYELOMA_D_DN	56	0.5783557	1.844585	<0.0001	0.015795397	0.677	1,633	tags=32%, list=13%, signal=37%
MATSUDA_NATURAL_KILLER_DIFFERENTIATION	383	0.49010202	1.8438399	<0.0001	0.015843885	0.677	1,534	tags=25%, list=12%, signal=28%
LINDSTEDT_DENDRITIC_CELL_MATURATION_A	65	0.7904196	1.8434682	<0.0001	0.015847774	0.679	1,288	tags=54%, list=10%, signal=59%
LIAN_LIPA_TARGETS_3M	49	0.78805196	1.8427782	0.001937985	0.015934201	0.684	1,333	tags=59%, list=10%, signal=66%
BOQUEST_STEM_CELL_DN	196	0.6337001	1.8425993	<0.0001	0.015888013	0.684	1,473	tags=39%, list=11%, signal=43%
REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS	115	0.48079264	1.8423454	0.022357723	0.015870005	0.684	1,699	tags=22%, list=13%, signal=25%
GRAESSMANN_APOPTOSIS_BY_SERUM_DEPRIVATION_UP	415	0.48459163	1.8406252	<0.0001	0.016117867	0.69	1,373	tags=23%, list=11%, signal=25%
ZHAN_MULTIPLE_MYELOMA_LB_DN	32	0.80940676	1.8376911	<0.0001	0.016611272	0.702	1,845	tags=78%, list=14%, signal=91%
VILIMAS_NOTCH1_TARGETS_UP	47	0.7901841	1.8373729	<0.0001	0.016593078	0.704	785	tags=47%, list=6%, signal=50%
VALK_AML_CLUSTER_6	27	0.71698797	1.8332983	0.001968504	0.017290745	0.725	998	tags=33%, list=8%, signal=36%
CHYLA_CBFA2T3_TARGETS_UP	284	0.5352139	1.8328282	<0.0001	0.0172938	0.728	1,552	tags=30%, list=12%, signal=33%
LI_INDUCED_T_TO_NATURAL_KILLER_UP	229	0.59281254	1.8325953	<0.0001	0.0172739	0.728	1,586	tags=33%, list=12%, signal=37%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
LU_IL4_SIGNALING	75	0.64473253	1.8323021	<0.0001	0.017290892	0.728	898	tags=27%, list=7%,
GAZDA_DIAMOND_BLACKFAN_ANEMIA_PROGENITOR_UP	36	0.664745	1.8317058	<0.0001	0.017336057	0.729	1,303	signal=28% tags=39%, list=10%,
ROSS_AML_WITH_MLL_FUSIONS	74	0.57117873	1.83069	<0.0001	0.017484652	0.733	1,633	signal=43% tags=30%, list=13%,
BIOCARTA_IL17_PATHWAY	16	0.89071023	1.8306425	<0.0001	0.017412994	0.733	881	signal=34% tags=56%, list=7%,
KIM_GERMINAL_CENTER_T_HELPER_UP	53	0.6144749	1.8303864	<0.0001	0.017406544	0.736	1,529	signal=60% tags=36%, list=12%,
REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR_WALL	82	0.58419	1.8298017	<0.0001	0.017466936	0.737	1,409	signal=40% tags=32%, list=11%,
XU_RESPONSE_TO_TRETINOIN_UP	16	0.74604374	1.8295184	0.001980198	0.017425824	0.738	1,652	signal=35% tags=56%, list=13%,
REACTOME_GENERATION_OF_SECOND_MESSENGER_MOLECULES	24	0.8701391	1.8279849	<0.0001	0.017668929	0.745	785	signal=64% tags=71%, list=6%,
MCLACHLAN_DENTAL_CARIES_UP	233	0.82637423	1.8277487	<0.0001	0.017648596	0.745	933	signal=75% tags=59%, list=7%,
CHUNG_BLISTER_CYTOTOXICITY_DN	30	0.60096836	1.8268017	0.006198347	0.017745027	0.75	1,908	signal=62% tags=27%, list=15%,
WANG_IMMORTALIZED_BY_HOXA9_AND_MEIS1_DN	21	0.7807198	1.8251785	<0.0001	0.017922595	0.753	2,084	signal=31% tags=71%, list=16%,
FOSTER_TOLERANT_MACROPHAGE_DN	306	0.5437809	1.8249834	<0.0001	0.017863031	0.753	2,241	signal=85% tags=40%, list=17%, signal=47%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
BIOCARTA_CYTOKINE_PATHWAY	21	0.63714975	1.8241495	0.008097166	0.017969713	0.757	904	tags=24%, list=7%, signal=26% tags=19%, list=3%, signal=20% tags=27%, list=9%, signal=29% tags=27%, list=10%, signal=30% tags=38%, list=2%, signal=38% tags=46%, list=11%, signal=51% tags=22%, list=7%, signal=23% tags=23%, list=13%, signal=26% tags=54%, list=4%, signal=56% tags=42%, list=7%, signal=45% tags=47%, list=5%, signal=50% tags=34%, list=16%, signal=41%
REACTOME_CTLA4_INHIBITORY_SIGNALING	21	0.55945486	1.8232888	0.004008016	0.018079959	0.757	348	
PELLICCIOTTA_HDAC_IN_ANTIGEN_PRESENTATION_DN	45	0.60995084	1.8230942	0.007874016	0.018052226	0.757	1,124	
ROSS_LEUKEMIA_WITH_MLL_FUSIONS	73	0.5995688	1.8226752	<0.0001	0.01805731	0.758	1,253	
BIOCARTA_CCR5_PATHWAY	16	0.8198571	1.8225982	<0.0001	0.017994963	0.758	203	
LINDSTEDT_DENDRITIC_CELL_MATURATION_B	50	0.6930687	1.8200787	<0.0001	0.018455118	0.766	1,417	
LOPES_METHYLATED_IN_COLON_CANCER_UP	23	0.6106799	1.8172947	0.008247423	0.018985868	0.774	904	
KYNG_DNA_DAMAGE_UP	198	0.44628885	1.816318	<0.0001	0.01908913	0.775	1,656	
KRASNOSELSKAYA_ILF3_TARGETS_UP	37	0.83493096	1.8162335	<0.0001	0.019029304	0.775	505	
DUNNE_TARGETS_OF_AML1_MTG8_FUSION_UP	48	0.7168509	1.8153728	<0.0001	0.01917511	0.778	962	
RADAEVA_RESPONSE_TO_IFNA1_UP	51	0.78351384	1.815338	<0.0001	0.019120611	0.778	701	
ROSS_ACUTE_MYELOID_LEUKEMIA_CBF	76	0.57754797	1.8149384	0.001912046	0.019109536	0.778	2,146	

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
BIDUS_METASTASIS_DN	116	0.5643114	1.8125494	<0.0001	0.01953964	0.786	1,970	tags=32%, list=15%, signal=37%
FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP	83	0.87925446	1.8121463	<0.0001	0.019592479	0.788	801	tags=69%, list=6%, signal=73%
VERHAAK_GLIOMASTOMA_MESENCHYMAL	205	0.6766388	1.8114138	0.001908397	0.019667825	0.79	1,723	tags=47%, list=13%, signal=53%
IIZUKA_LIVER_CANCER_PROGRESSION_L0_L1_DN	20	0.7384535	1.8088436	<0.0001	0.020216892	0.798	1,575	tags=45%, list=12%, signal=51%
WEST_ADRENOCORTICAL_CARCINOMA_VS_ADENOMA_DN	24	0.7710381	1.808751	0.003937008	0.020181984	0.798	912	tags=38%, list=7%, signal=40%
MITSIADES_RESPONSE_TO_APLIDIN_UP	396	0.44629458	1.806758	<0.0001	0.020556536	0.803	2,276	tags=33%, list=17%, signal=39%
PID_AMB2_NEUTROPHILS_PATHWAY	41	0.7072758	1.8049272	0.001923077	0.020871319	0.806	1,937	tags=51%, list=15%, signal=60%
PANGAS_TUMOR_SUPPRESSION_BY_SMAD1_AND_SMAD5_UP	90	0.5962016	1.8048581	<0.0001	0.020818848	0.806	1,141	tags=26%, list=9%, signal=28%
BIOCARTA_BCR_PATHWAY	32	0.52786195	1.8048409	0.003921569	0.020742588	0.806	915	tags=22%, list=7%, signal=23%
WIERENGA_STAT5A_TARGETS_GROUP2	47	0.70774025	1.8024337	0.001964637	0.021163603	0.807	1,395	tags=47%, list=11%, signal=52%
BROWN_MYELOID_CELL_DEVELOPMENT_UP	134	0.61019695	1.8018422	0.001904762	0.021254744	0.807	1,651	tags=39%, list=13%, signal=44%
RIZKI_TUMOR_INVASIVENESS_3D_DN	241	0.45354772	1.8013254	<0.0001	0.021294374	0.807	1,118	tags=19%, list=9%, signal=20%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
PID_GLYPICAN_IPATHWAY	27	0.6471933	1.8010365	0.001908397	0.021273037	0.807	1,275	tags=37%, list=10%, signal=41% tags=56%, list=4%, signal=57% tags=27%, list=12%, signal=30% tags=35%, list=13%, signal=40% tags=18%, list=8%, signal=19% tags=41%, list=12%, signal=46% tags=30%, list=13%, signal=35% tags=52%, list=10%, signal=58% tags=26%, list=7%, signal=28% tags=32%, list=6%, signal=34% tags=29%, list=8%, signal=31% tags=59%, list=10%, signal=66%
SANA_RESPONSE_TO_IFNG_UP	54	0.8551751	1.8006413	<0.0001	0.021289887	0.809	491	
TORCHIA_TARGETS_OF_EWSR1_FLI1_FUSION_DN	240	0.50711095	1.8005271	<0.0001	0.021247778	0.81	1,553	
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_8D_DN	159	0.60944134	1.8004872	0.00189394	0.021181487	0.81	1,653	
MARTENS_BOUND_BY_PML_RARA_FUSION	335	0.442084	1.7996053	0.001890359	0.021314245	0.812	1,027	
MIKKELSEN_MEF_LCP_WITH_H3K4ME3	93	0.63868296	1.7988261	<0.0001	0.021463936	0.812	1,553	
MORI_SMALL_PRE_BII_LYMPHOCYTE_DN	66	0.57224494	1.7974055	0.005758158	0.021712506	0.815	1,689	
GRAHAM_CML_QUIESCENT_VS_NORMAL_QUIESCENT_DN	44	0.78063196	1.7946684	<0.0001	0.022274943	0.822	1,294	
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_DN	178	0.56735826	1.793819	<0.0001	0.02241227	0.824	968	
NEMETH_INFLAMMATORY_RESPONSE_LPS_UP	81	0.6583546	1.7932236	<0.0001	0.02252854	0.827	743	
HOFMANN_MYELODYSPLASTIC_SYNDROM_RISK_DN	21	0.7148868	1.7928544	0.004056795	0.022570834	0.828	1,035	
SANA_TNF_SIGNALING_UP	74	0.76752245	1.7927177	<0.0001	0.02250336	0.828	1,331	

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
PID_RAC1_REG_PATHWAY	31	0.5711298	1.7914284	0.002040816	0.022666527	0.829	1,515	tags=29%, list=12%, signal=33%
HAHTOLA_CTCL_CUTANEOUS	26	0.68084615	1.7903894	0.001964637	0.022853889	0.829	2,293	tags=54%, list=18%, signal=65%
XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_UP	17	0.80849737	1.7902796	<0.0001	0.022795891	0.829	958	tags=53%, list=7%, signal=57%
KANG_GIST_WITH_PDGFR_A_UP	47	0.7234339	1.789657	<0.0001	0.022834286	0.831	1,205	tags=49%, list=9%, signal=54%
DEBOSSCHER_NFKB_TARGETS_REPRESSED_BY_GLUCOCORTICOIDS	23	0.7380656	1.7893282	<0.0001	0.022798996	0.831	1,647	tags=39%, list=13%, signal=45%
REACTOME_CD28_CO_STIMULATION	27	0.55825824	1.7883971	0.00390625	0.022985274	0.836	504	tags=22%, list=4%, signal=23%
HOLLMANN_APOPTOSIS_VIA_CD40_UP	183	0.46070507	1.7882193	<0.0001	0.022971947	0.836	2,178	tags=31%, list=17%, signal=37%
REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES	46	0.5962853	1.7878172	0.016032064	0.022980595	0.836	1,067	tags=22%, list=8%, signal=24%
MORI_IMMATURE_B_LYMPHOCYTE_UP	45	0.7590807	1.7872685	<0.0001	0.02299846	0.836	680	tags=42%, list=5%, signal=44%
CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_DN	370	0.59568197	1.7870091	<0.0001	0.02302154	0.836	2,127	tags=41%, list=16%, signal=48%
REACTOME_HEMOSTASIS	407	0.4188244	1.7848563	<0.0001	0.023505295	0.841	1,702	tags=23%, list=13%, signal=25%
THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN	207	0.4188539	1.7845442	0.002024292	0.023479138	0.841	1,633	tags=21%, list=13%, signal=23%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GAVIN_FOXP3_TARGETS_CLUSTER_T7	83	0.5160771	1.7837238	0.003875969	0.023602726	0.844	982	tags=19%, list=8%, signal=21%
PID_ANTHRAX_PATHWAY	16	0.67968863	1.7833146	0.010288066	0.023623908	0.844	1,107	tags=31%, list=8%, signal=34%
BIOCARTA_STATHMIN_PATHWAY	18	0.7522538	1.7810302	<0.0001	0.024150234	0.852	355	tags=33%, list=3%, signal=34%
BIOCARTA_IL10_PATHWAY	17	0.7318343	1.7806389	<0.0001	0.024165018	0.853	2,995	tags=71%, list=23%, signal=34%
GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_UP	52	0.7399325	1.7801032	<0.0001	0.024183154	0.853	992	tags=37%, list=8%, signal=92%
IZADPANAH_STEM_CELL_ADIPOSE_VS_BONE_UP	99	0.63356227	1.7796326	<0.0001	0.024236802	0.857	933	tags=32%, list=7%, signal=39%
BIOCARTA_CASPASE_PATHWAY	22	0.6900894	1.7790536	0.004008016	0.02433503	0.86	630	tags=27%, list=5%, signal=35%
HENDRICKS_SMARCA4_TARGETS_DN	44	0.64673597	1.7782682	0.001912046	0.024449294	0.862	1,638	tags=32%, list=13%, signal=29%
BYSTROEM_CORRELATED_WITH_IL5_DN	60	0.48363012	1.7777481	0.001984127	0.024499254	0.862	1,579	tags=28%, list=12%, signal=36%
BOYLAN_MULTIPLE_MYELOMA_D_CLUSTER_DN	33	0.5607214	1.776771	0.007722008	0.024658348	0.863	1,576	tags=30%, list=12%, signal=32%
LEE_TARGETS_OF_PTCH1_AND_SUFU_UP	44	0.6613485	1.776682	0.003960396	0.02461021	0.863	714	tags=27%, list=5%, signal=34%
SMITH_TERT_TARGETS_DN	83	0.53873533	1.7762809	0.001912046	0.024598194	0.863	2,058	tags=29%, list=16%, signal=38%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
PID_IFNG_PATHWAY	38	0.5051456	1.7749149	0.006369427	0.024918387	0.867	2,006	tags=29%, list=15%, signal=34%
KIM_L=RR3B_TARGETS	29	0.87620133	1.7745247	<0.0001	0.024968684	0.87	661	tags=62%, list=5%, signal=65%
KYNG_DNA_DAMAGE_BY_UV	55	0.565297	1.7744726	<0.0001	0.024899475	0.87	1,305	tags=25%, list=10%, signal=28%
WIELAND_UP_BY_HBV_INFECTION	96	0.8737821	1.77175	<0.0001	0.025545118	0.874	668	tags=73%, list=5%, signal=76%
KORKOLA_SEMINOMA_UP	37	0.64233595	1.7697034	0.009784736	0.025988322	0.877	2,128	tags=49%, list=16%, signal=58%
BOHN_PRIMARY_IMMUNODEFICIENCY_SYNDROM_DN	39	0.62928927	1.7695061	0.001956947	0.02593264	0.877	824	tags=26%, list=6%, signal=27%
REACTOME_TOLL_RECEPTOR_CASCADES	100	0.491197	1.7684855	<0.0001	0.02616506	0.879	2,097	tags=33%, list=16%, signal=39%
MAHAJAN_RESPONSE_TO_IL1A_UP	80	0.58507556	1.768274	<0.0001	0.026137555	0.879	1,607	tags=38%, list=12%, signal=43%
WIERENGA_STAT5A_TARGETS_UP	152	0.55412674	1.7681146	<0.0001	0.026107734	0.879	1,546	tags=29%, list=12%, signal=32%
KEGG_PRION_DISEASES	34	0.7098382	1.7661515	0.001923077	0.02668996	0.883	1,180	tags=35%, list=9%, signal=39%
TARTE_PLASMA_CELL_VS_PLASMA_BLAST_UP	365	0.48281285	1.7656004	0.001919386	0.026803898	0.887	1,643	tags=23%, list=13%, signal=26%
LIAN_NEUTROPHIL GRANULE CONSTITUENTS	21	0.7704184	1.765072	<0.0001	0.026907256	0.888	717	tags=43%, list=6%, signal=45%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
MARSON_FOXP3_CORE_DIRECT_TARGETS	16	0.86882865	1.7649894	<0.0001	0.02683952	0.888	1,420	tags=88%, list=11%, signal=98%
HOLLMANN_APOPTOSIS_VIA_CD40_DN	238	0.5014861	1.7640723	<0.0001	0.02703688	0.891	1,165	tags=23%, list=9%, signal=25%
STAMBOLSKY_TARGETS_OF_MUTATED_TP53_DN	35	0.75252837	1.7639178	0.00742115	0.026981149	0.891	668	tags=46%, list=5%, signal=48%
DEMAGALHAES_AGING_UP	47	0.7613472	1.7627994	0.001912046	0.027289025	0.895	736	tags=36%, list=6%, signal=38%
GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_UP	61	0.6975179	1.7612286	0.001964637	0.027717516	0.899	1,294	tags=43%, list=10%, signal=47%
ZHAN_MULTIPLE_MYELOMA_DN	40	0.68836457	1.7611636	<0.0001	0.027643627	0.899	884	tags=38%, list=7%, signal=40%
GEORGANTAS_HSC_MARKERS	62	0.6721612	1.7608416	<0.0001	0.027662836	0.899	1,702	tags=39%, list=13%, signal=44%
ONO_FOXP3_TARGETS_UP	20	0.75303173	1.7594348	0.001968504	0.027935885	0.905	1,137	tags=50%, list=9%, signal=55%
CHUNG_BLISTER_CYTOTOXICITY_UP	96	0.49029857	1.7584655	0.002008032	0.028108593	0.905	1,600	tags=24%, list=12%, signal=27%
REACTOME_ER_PHAGOSOME_PATHWAY	57	0.55513	1.7570969	0.04509804	0.02850356	0.906	1,124	tags=23%, list=9%, signal=25%
SIG_PIP3_SIGNALING_IN_B_LYMPHOCYTES	33	0.56227964	1.7564526	0.001919386	0.0285614	0.908	2,097	tags=39%, list=16%, signal=47%
WANG_ESOPHAGUS_CANCER_VS_NORMAL_UP	112	0.62280995	1.756184	0.001919386	0.028556874	0.908	1,331	tags=36%, list=10%, signal=39%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
ALCALA_APOPTOSIS	77	0.51747185	1.7561767	0.012145749	0.028477538	0.908	639	tags=18%, list=5%,
RUTELLA_RESPONSE_TO_HGF_UP	385	0.54416883	1.7556546	0.001934236	0.028555062	0.909	2,055	signal=19% tags=37%, list=16%,
MULLIGHAN_MLL_SIGNATURE_1_UP	350	0.44453374	1.7555844	<0.0001	0.02851989	0.911	1,706	signal=43% tags=24%, list=13%,
REACTOME_ANTIGEN_PRESENTATION_FOLDING _ASSEMBLY_AND_PEPTIDE_LOADING_OF_CLASS_I_MHC	19	0.6880818	1.7552711	0.011428571	0.02855893	0.912	1,124	signal=27% tags=42%, list=9%,
HUANG_DASATINIB_RESISTANCE_UP	68	0.71904784	1.7531924	<0.0001	0.0291859	0.914	1,473	signal=46% tags=49%, list=11%,
REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION	182	0.4575602	1.7527269	0.001883239	0.029230664	0.914	1,973	signal=54% tags=26%, list=15%,
ODONNELL_TFRC_TARGETS_UP	287	0.46491387	1.7521096	<0.0001	0.029342433	0.916	2,291	signal=30% tags=28%, list=18%,
REACTOME_SEMA4D_IN_SEMAPHORIN_SIGNALING	27	0.64045584	1.7504613	0.003984064	0.029752403	0.918	1,014	signal=33% tags=26%, list=8%,
PID_PDGFRB_PATHWAY	119	0.4611439	1.750182	0.003921569	0.029767126	0.918	947	signal=28% tags=15%, list=7%,
HINATA_NFKB_TARGETS_KERATINOCYTE_UP	91	0.6749507	1.7500949	<0.0001	0.029692546	0.918	1,395	signal=16% tags=37%, list=11%,
HAHTOLA_CTCL_PATHOGENESIS	16	0.9191198	1.7500852	<0.0001	0.029616114	0.918	229	signal=42% tags=50%, list=2%,
COATES_MACROPHAGE_M1_VS_M2_UP	56	0.5908495	1.7499219	<0.0001	0.02958626	0.918	1,516	signal=51% tags=38%, list=12%, signal=42%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
EINAV_INTERFERON_SIGNATURE_IN_CANCER	24	0.88151026	1.7482404	<0.0001	0.030036142	0.922	668	tags=67%, list=5%, signal=70%
VANTVEER_BREAST_CANCER_BRCA1_UP	31	0.64133257	1.7466357	0.001988072	0.03046595	0.925	1,292	tags=39%, list=10%, signal=43%
KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	53	0.6114497	1.7458327	0.001941748	0.030669652	0.927	1,789	tags=34%, list=14%, signal=39%
REACTOME_SIGNALING_BY_THE_B_CELL_RECEPTOR_BCR	105	0.44227856	1.7457997	0.011406845	0.03058504	0.927	1,202	tags=17%, list=9%, signal=19%
DUNNE_TARGETS_OF_AML1_MTG8_FUSION_DN	18	0.74430877	1.7457865	<0.0001	0.030505914	0.927	1,239	tags=44%, list=10%, signal=49%
EBAUER_TARGETS_OF_PAX3_FOXP01_FUSION_UP	187	0.48520434	1.7450467	<0.0001	0.03066642	0.928	1,316	tags=21%, list=10%, signal=23%
SA_MMP_CYTOKINE_CONNECTION	15	0.69739425	1.7446601	0.001972387	0.030698137	0.928	1,275	tags=40%, list=10%, signal=44%
BROWNE_INTERFERON_RESPONSIVE_GENES	64	0.8332484	1.7437094	<0.0001	0.030892827	0.928	716	tags=63%, list=5%, signal=66%
SEITZ_NEOPLASTIC_TRANSFORMATION_BY_8P_DELETION_UP	70	0.727096	1.7432961	0.001992032	0.03094025	0.93	1,388	tags=54%, list=11%, signal=60%
HOSHIDA_LIVER_CANCER_SUBCLASS_S1	228	0.7526549	1.742123	0.003802281	0.031205622	0.93	1,166	tags=46%, list=9%, signal=49%
MARSON_FOXP3_TARGETS_UP	56	0.68122125	1.7418817	0.001960784	0.031215372	0.931	1,420	tags=43%, list=11%, signal=48%
BAUS_TFF2_TARGETS_UP	28	0.7286062	1.7413157	0.001879699	0.031338096	0.932	1,116	tags=50%, list=9%, signal=55%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
SU_THYMUS	19	0.7286238	1.7411581	0.004024145	0.031300947	0.932	858	tags=42%, list=7%, signal=45%
RASHI_RESPONSE_TO_IONIZING_RADIATION_4	48	0.51323086	1.7409105	0.001941748	0.031331155	0.932	1,035	tags=23%, list=8%, signal=25%
MULLIGHAN_MLL_SIGNATURE_1_DN	217	0.46774575	1.7406081	<0.0001	0.031338736	0.932	1,823	tags=29%, list=14%, signal=33%
DIRMEIER_LMP1_RESPONSE_EARLY	62	0.62963605	1.7398162	0.009689922	0.031503625	0.934	1,678	tags=42%, list=13%, signal=48%
FERRANDO_LYL1_NEIGHBORS	15	0.7423757	1.7393774	0.003853565	0.03156096	0.934	495	tags=47%, list=4%, signal=28%
DEBIASI_APOPTOSIS_BY_REOVIRUS_INFECTION_UP	280	0.5064155	1.738799	<0.0001	0.03169604	0.935	1,544	list=12%, signal=31%
MAHADEVAN_IMATINIB_RESISTANCE_DN	19	0.79335093	1.7386535	0.003960396	0.031660028	0.935	1,209	tags=47%, list=9%, signal=52%
IWANAGA_CARCIANOGENESIS_BY_KRAS_DN	89	0.46474978	1.7383258	<0.0001	0.03169261	0.935	1,509	tags=24%, list=12%, signal=27%
AKL_HTLV1_INFECTION_DN	59	0.6032486	1.7367967	0.007952286	0.032170746	0.938	1,141	tags=29%, list=9%, signal=31%
HAHTOLA_MYCOSIS_FUNGOIDES_DN	15	0.83124834	1.7365973	<0.0001	0.032166693	0.939	937	tags=53%, list=7%, signal=57%
GAVIN_PDE3B_TARGETS	20	0.7222673	1.7341075	0.007858546	0.03293287	0.941	1,520	tags=55%, list=12%, signal=62%
ROSS_AML_WITH_CBFEB_MYH11_FUSION	49	0.72583085	1.7340872	0.001923077	0.03285752	0.941	926	tags=39%, list=7%, signal=42%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_UP	72	0.88042754	1.7335479	<0.0001	0.032929953	0.942	810	tags=71%, list=6%, signal=75% tags=30%, list=3%, signal=31% tags=31%, list=15%, signal=35% tags=41%, list=7%, signal=44% tags=16%, list=9%, signal=17% tags=39%, list=13%, signal=45% tags=36%, list=22%, signal=45% tags=26%, list=11%, signal=29% tags=33%, list=12%, signal=38% tags=20%, list=7%, signal=21% tags=54%, list=15%, signal=64% tags=31%, list=15%, signal=36%
OKAMOTO_LIVER_CANCER_MULTICENTRIC_OCCURRENCE_UP	23	0.72145486	1.7326522	0.005802708	0.033123426	0.942	437	
FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_UP	432	0.47882813	1.7322935	0.001908397	0.033197954	0.942	1,925	
RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_UP	29	0.7330047	1.7321578	<0.0001	0.033143684	0.942	907	
REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRESENTATION	189	0.4208921	1.731708	0.019569471	0.033209987	0.943	1,124	
GOLUB_ALL_VS_AML_DN	23	0.6405188	1.7316664	0.007575758	0.03314262	0.943	1,651	
BROWN_MYELOID_CELL_DEVELOPMENT_DN	109	0.47631997	1.7308618	0.001949318	0.033356648	0.944	2,849	
STAEGE_EWING_FAMILY_TUMOR	23	0.6453716	1.7293487	<0.0001	0.03378742	0.945	1,484	
BORCZUK_MALIGNANT_MESOTHELIOMA_DN	90	0.5549147	1.7289671	<0.0001	0.033837248	0.945	1,597	
REACTOME_MHC_CLASS_II_ANTIGEN_PRESENTATION	76	0.5846587	1.7284379	0.006048387	0.03394887	0.945	864	
VALK_AML_CLUSTER_11	35	0.6651151	1.7281586	0.001872659	0.033956368	0.945	1,977	
WIERENGA_STAT5A_TARGETS_DN	156	0.51239514	1.72436	0.003824092	0.035204653	0.95	1,952	

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
NIELSEN_GIST_AND_SYNOVIAL_SARCOMA_DN	19	0.8985647	1.7238094	<0.0001	0.035315663	0.952	516	tags=63%, list=4%, signal=66%
STEARMAN_LUNG_CANCER_EARLY_VS_LATE_DN	51	0.6369746	1.7234098	0.007434944	0.035361093	0.952	613	tags=25%, list=5%, signal=27%
PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN	117	0.520399	1.7228887	0.00203252	0.035393856	0.954	1,159	tags=26%, list=9%, signal=29%
FINAK_BREAST_CANCER_SDPP_SIGNATURE	22	0.88164973	1.7225785	<0.0001	0.035403155	0.956	906	tags=68%, list=7%, signal=73%
ZHAN_LATE_DIFFERENTIATION_GENES_UP	32	0.6458564	1.7208401	0.003773585	0.03590983	0.957	1,661	tags=38%, list=13%, signal=43%
CHIARETTI_T_ALL_REFRACTORY_TO_THERAPY	28	0.5904494	1.7206157	0.005952381	0.03591437	0.959	1,227	tags=36%, list=9%, signal=39%
REACTOME_REGULATION_OF_IFNA_SIGNALING	24	0.46583027	1.719662	0.02079002	0.036160596	0.96	1,914	tags=21%, list=15%, signal=24%
SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP	330	0.751901	1.7195085	0.003838772	0.036098026	0.96	1,468	tags=54%, list=11%, signal=59%
BURTON_ADIPOGENESIS_PEAK_AT_8HR	35	0.61337894	1.7190031	0.001964637	0.03624148	0.962	2,110	tags=40%, list=16%, signal=48%
KYNG_ENVIRONMENTAL_STRESS_RESPONSE_UP	53	0.5766342	1.7184927	0.005535055	0.0363227	0.962	1,014	tags=21%, list=8%, signal=22%
KLEIN_PRIMARY EFFUSION_LYMPHOMA_DN	53	0.66302437	1.7181574	0.007936508	0.036344986	0.963	1,320	tags=42%, list=10%, signal=46%
NAKAJIMA_EOSINOPHIL	29	0.6065777	1.7165697	0.003891051	0.03689071	0.963	1,490	tags=31%, list=11%, signal=35%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
HOLLERN_EMT_BREAST_TUMOR_UP	85	0.61598444	1.7158613	0.005780347	0.037063926	0.963	1,745	tags=42%, list=13%, signal=49%
HILLION_HMGA1B_TARGETS	86	0.46194524	1.714092	0.015625	0.037686147	0.966	1,840	tags=23%, list=14%, signal=27%
NABA_SECRETED_FACTORS	266	0.47077364	1.7129903	0.002004008	0.03802902	0.966	1,427	tags=17%, list=11%, signal=19%
KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_GAMMA_IN_OLD	28	0.60025054	1.7122416	0.009633912	0.03821797	0.968	1,014	tags=18%, list=8%, signal=19%
POOLA_INVASIVE_BREAST_CANCER_UP	263	0.7267956	1.7117763	0.002008032	0.038287666	0.969	842	tags=47%, list=6%, signal=49%
REACTOME_TRAF6_MEDIATED_IRF7_ACTIVATION	27	0.49619648	1.7116549	0.01996008	0.03825851	0.969	1,116	tags=19%, list=9%, signal=20%
BERTUCCI_INVASIVE_CARCINOMA_DUCTAL_VS_LOBULAR_DN	39	0.69546723	1.7087489	0.006060606	0.039229557	0.971	1,295	tags=44%, list=10%, signal=48%
ZHANG_INTERFERON_RESPONSE	22	0.8952988	1.7082994	<0.0001	0.039298434	0.972	1,331	tags=82%, list=10%, signal=91%
KORKOLA_TERATOMA_UP	15	0.8012303	1.7081842	0.001934236	0.039233014	0.972	1,830	tags=67%, list=14%, signal=77%
ZUCCHI_METASTASIS_UP	37	0.5455448	1.707441	0.002008032	0.03940712	0.972	803	tags=19%, list=6%, signal=20%
ZHANG_TLX_TARGETS_UP	89	0.55319846	1.7069052	<0.0001	0.039533257	0.972	1,651	tags=28%, list=13%, signal=32%
WILENSKY_RESPONSE_TO_DARAPLADIB	28	0.8644438	1.7051078	<0.0001	0.040104955	0.972	930	tags=71%, list=7%, signal=77%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
PID_CASPASE_PATHWAY	49	0.5062632	1.7049117	0.010162601	0.040092092	0.972	1,056	tags=20%, list=8%, signal=22%
XU_CREBBP_TARGETS_DN	39	0.50918394	1.7040157	0.00390625	0.04034269	0.973	2,271	tags=33%, list=17%, signal=40%
REACTOME_ACTIVATED_TLR4_SIGNALLING	82	0.4598218	1.7030658	0.001855288	0.040624768	0.973	1,898	tags=29%, list=15%, signal=34%
MA_MYELOID_DIFFERENTIATION_UP	38	0.5615038	1.70166	<0.0001	0.04111289	0.975	186	tags=13%, list=1%, signal=13%
KORKOLA_YOLK_SAC_TUMOR_UP	17	0.6533804	1.7012594	0.02	0.041178998	0.975	2,801	tags=59%, list=21%, signal=75%
KANG_IMMORTALIZED_BY_TERT_UP	86	0.51656663	1.7010999	<0.0001	0.041160613	0.975	2,120	tags=36%, list=16%, signal=43%
KIM_GLI2_TARGETS_UP	79	0.79741025	1.7006894	0.003838772	0.041234143	0.975	1,205	tags=59%, list=9%, signal=65%
FARMER_BREAST_CANCER_CLUSTER_1	39	0.92837775	1.7006824	<0.0001	0.04113502	0.975	521	tags=87%, list=4%, signal=91%
MAHADEVAN_RESPONSE_TO_MP470_UP	17	0.9248654	1.700565	<0.0001	0.04109356	0.975	627	tags=65%, list=5%, signal=68%
PID_TCR_CALCIIUM_PATHWAY	25	0.564401	1.6994342	0.01734104	0.04147301	0.978	2,129	tags=40%, list=16%, signal=48%
PID_EPHA_FWDPATHWAY	30	0.48915708	1.6991166	0.004081633	0.04150356	0.978	1,639	tags=27%, list=13%, signal=30%
MIKKELSEN_MCV6_LCP_WITH_H3K4ME3	110	0.54747605	1.6987374	0.009191177	0.041569684	0.978	2,020	tags=38%, list=16%, signal=45%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER	52	0.6845687	1.6980498	0.003717472	0.041717973	0.978	1,598	tags=48%, list=12%, signal=55%
SAKAI_CHRONIC_HEPATITIS_VS_LIVER_CANCER_UP	73	0.5155493	1.6970264	0.008080808	0.042020947	0.978	1,591	tags=21%, list=12%, signal=23%
MULLIGHAN_MLL_SIGNATURE_2_UP	378	0.43299124	1.6962023	<0.0001	0.042254735	0.979	1,735	tags=25%, list=13%, signal=28%
MARTINEZ_TP53_TARGETS_UP	479	0.41511053	1.6959928	<0.0001	0.042262036	0.979	1,803	tags=21%, list=14%, signal=24%
EBAUER_MYOGENIC_TARGETS_OF_PAX3_FOXO1_FUSION	49	0.58462787	1.6959118	0.015503876	0.04218954	0.979	1,147	tags=22%, list=9%, signal=25%
PAPASPYRIDONOS_UNSTABLE_ATEROSCLEROTIC_PLAQUE_UP	44	0.7074725	1.6957142	0.003780718	0.04217144	0.979	1,534	tags=52%, list=12%, signal=59%
AMUNDSON_RESPONSE_TO_ARSENITE	189	0.43931702	1.695131	0.001890359	0.04229757	0.979	1,581	tags=24%, list=12%, signal=27%
IWANAGA_CARCINOGENESIS_BY_KRAS_PTEN_DN	245	0.47391787	1.6948675	<0.0001	0.04233783	0.979	1,925	tags=27%, list=15%, signal=31%
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_DN	28	0.6825798	1.6946826	0.007633588	0.042315282	0.979	1,514	tags=50%, list=12%, signal=56%
GOLDRATH_IMMUNE_MEMORY	54	0.5052515	1.6942847	<0.0001	0.042387173	0.979	2,215	tags=30%, list=17%, signal=36%
BAKKER_FOXO3_TARGETS_UP	44	0.54469544	1.6936927	<0.0001	0.04249861	0.979	1,908	tags=32%, list=15%, signal=37%
ZHAN_MULTIPLE_MYELOMA_SPIKED	21	0.71425295	1.6929226	0.004008016	0.04276671	0.979	880	tags=43%, list=7%, signal=46%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GHANDHI_BYSTANDER_IRRADIATION_UP	71	0.6799454	1.6927686	0.005681818	0.042727306	0.981	1,653	tags=49%, list=13%, signal=56%
KAYO_CALORIE_RESTRICTION_MUSCLE_UP	91	0.5791742	1.6924282	0.005791506	0.04277855	0.982	1,146	tags=25%, list=9%, signal=28%
NAKAYAMA_FRA2_TARGETS	35	0.60187316	1.6922172	0.004016064	0.04275412	0.982	1,118	tags=34%, list=9%, signal=37%
MARTINEZ_RB1_AND_TP53_TARGETS_UP	484	0.4248983	1.6918204	<0.0001	0.042788614	0.982	1,934	tags=24%, list=15%, signal=26%
CASTELLANO_NRAS_TARGETS_UP	58	0.62247694	1.6913432	0.007518797	0.042874955	0.982	491	tags=26%, list=4%, signal=27%
VERHAAK_AML_WITH_NPM1_MUTATED_DN	224	0.5635732	1.691269	<0.0001	0.042810272	0.982	1,825	tags=33%, list=14%, signal=37%
BIOCARTA_T1D_PATHWAY	19	0.5975407	1.6910425	0.011472276	0.042790603	0.982	1,830	tags=32%, list=14%, signal=37%
WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_DN	51	0.65893567	1.690721	0.003875969	0.042803857	0.982	2,121	tags=45%, list=16%, signal=54%
ZHANG_RESPONSE_TO_CANTHARIDIN_UP	17	0.58666265	1.6901171	0.007662835	0.04296949	0.982	1,415	tags=41%, list=11%, signal=46%
HADDAD_B_LYMPHOCYTE_PROGENITOR	257	0.44846317	1.6882474	<0.0001	0.04358251	0.982	2,012	tags=28%, list=15%, signal=33%
KYNG_DNA_DAMAGE_BY_GAMMA_AND_UV_RADIATION	77	0.47315755	1.6874143	0.003795066	0.04381605	0.982	1,569	tags=26%, list=12%, signal=29%
BIOCARTA_IL22BP_PATHWAY	15	0.6662058	1.6873823	0.015779093	0.043729182	0.982	939	tags=33%, list=7%, signal=36%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
KEGG_LEUKOCYTE_TRANSENDOTHELIAL_MIGRATION	102	0.514625	1.68709	0.009652509	0.043780368	0.982	1,652	tags=30%, list=13%, signal=35% tags=18%, list=10%, signal=20% tags=23%, list=5%, signal=24% tags=55%, list=7%, signal=59% tags=39%, list=9%, signal=43% tags=44%, list=5%, signal=46% tags=33%, list=14%, signal=39% tags=47%, list=12%, signal=54% tags=75%, list=6%, signal=80% tags=24%, list=15%, signal=27% tags=41%, list=13%, signal=47% tags=32%, list=11%, signal=36%
LEE_AGING_NEOCORTEX_DN	71	0.44435933	1.6857544	0.001941748	0.04430153	0.982	1,264	
PAL_PRMT5_TARGETS_DN	26	0.63207346	1.6853899	0.001919386	0.04437644	0.983	685	
CHEN_ETV5_TARGETS_SERTOLI	20	0.85559356	1.6852117	0.001988072	0.04436702	0.983	965	
REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL_SURFACE_ RECEPTORS_BY_RECRUITING_THEM_TO_CLATHRIN_ADAPTERS	18	0.6393202	1.6851513	0.024096385	0.04428424	0.983	1,124	
NIELSEN_LEIOMYOSARCOMA_UP	16	0.8174637	1.6845305	0.003861004	0.044483777	0.983	657	
PID_IL8_CXCR1_PATHWAY	24	0.54305357	1.6839004	0.024242423	0.044666313	0.983	1,880	
NADLER_OBESITY_UP	57	0.741864	1.6836388	0.003802281	0.04468314	0.983	1,553	
BOYVAULT_LIVER_CANCER_SUBCLASS_G5_DN	24	0.91114795	1.6820859	<0.0001	0.045210842	0.984	790	
FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP	499	0.44246918	1.6820463	0.001960784	0.045130104	0.984	1,932	
HERNANDEZ_MITOTIC_ARREST_BY_DOCETAXEL_2_UP	56	0.6342981	1.6806353	0.007874016	0.04577765	0.984	1,702	
FLECHNER_PBL_KIDNEY_TRANSPLANT_OK_VS_DONOR_DN	37	0.5414466	1.6795874	0.015564202	0.046136774	0.985	1,473	

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
FOSTER_KDM1A_TARGETS_UP	179	0.5218091	1.6778886	<0.0001	0.04675004	0.985	1,214	tags=23%, list=9%,
OSWALD_HEMATOPOIETIC_STEM_CELL_IN_COLLAGEN_GEL_UP	214	0.50844526	1.6777422	<0.0001	0.046689864	0.985	1,712	signal=26% tags=32%, list=13%,
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_6HR_UP	63	0.6254153	1.6777403	<0.0001	0.04658836	0.985	1,641	signal=36% tags=38%, list=13%,
TIAN_TNF_SIGNALING_VIA_NFKB	28	0.74635106	1.676348	0.009596929	0.047110636	0.985	1,459	signal=43% tags=50%, list=11%,
LEE_AGING_NEOCORTEX_UP	79	0.5280288	1.6762354	0.001872659	0.047064986	0.985	1,651	signal=56% tags=32%, list=13%,
BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS	27	0.7900871	1.6753426	0.009596929	0.047415216	0.985	1,192	signal=36% tags=59%, list=9%,
TAVOR_CEBPA_TARGETS_UP	46	0.6668075	1.6748055	0.001901141	0.047539007	0.985	1,397	signal=65% tags=39%, list=11%,
PARK_TRETINOIN_RESPONSE_AND_PML_RARA_FUSION	30	0.7230047	1.6746821	0.009633912	0.04747864	0.985	1,639	signal=44% tags=57%, list=13%,
FURUKAWA_DUSP6_TARGETS_PCI35_UP	58	0.609457	1.6740732	0.007858546	0.047580928	0.985	718	signal=65% tags=31%, list=6%,
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYTE_DN	51	0.57719916	1.6734052	0.014344262	0.04785641	0.985	958	signal=33% tags=29%, list=7%,
MARZEC_IL2_SIGNALING_UP	105	0.529831	1.6724205	0.007462686	0.0481549	0.985	1,401	signal=32% tags=30%, list=11%,
YAGI_AML_WITH_T_8_21_TRANSLOCATION	333	0.4283847	1.6718524	0.001949318	0.048334077	0.985	1,553	signal=33% tags=20%, list=12%, signal=22%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
MUELLER_COMMON_TARGETS_OF_AML_FUSIONS_DN	27	0.5672096	1.6713928	0.004192872	0.04848945	0.985	1,401	tags=30%, list=11%, signal=33%
PID_P38_ALPHA_BETA_PATHWAY	28	0.5332849	1.6706636	0.007968128	0.048768166	0.986	819	tags=21%, list=6%, signal=23%
WATTEL_AUTONOMOUS_THYROID_ADENOMA_DN	49	0.6975249	1.668294	<0.0001	0.049697146	0.986	1,286	tags=49%, list=10%, signal=54%
MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_23	18	0.6729596	1.668001	0.019569471	0.049722545	0.986	446	tags=22%, list=3%, signal=23%
NIELSEN_SYNOVIAL_SARCOMA_DN	18	0.9160624	1.6678935	<0.0001	0.04968663	0.986	601	tags=83%, list=5%, signal=87%
RIZKI_TUMOR_INVASIVENESS_3D_UP	197	0.39905632	1.6669698	<0.0001	0.049994644	0.986	1,425	tags=18%, list=11%, signal=20%
GNATENKO_PLATELET_SIGNATURE	44	0.53072053	1.6669377	0.023076924	0.04990691	0.986	1,973	tags=27%, list=15%, signal=32%
LEE_RECENT_THYMIC_EMIGRANT	148	0.49439046	1.6657883	0.001992032	0.050291236	0.987	1,301	tags=23%, list=10%, signal=25%
TSAI_RESPONSE_TO_RADIATION_THERAPY	32	0.7814172	1.6656498	0.001838235	0.050244078	0.987	1,230	signal=65%, tags=37%, list=9%, signal=40%
ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_UP	30	0.69585204	1.6648805	0.007843138	0.05050422	0.988	1,116	tags=26%, list=5%, signal=27%
FUJII_YBX1_TARGETS_UP	35	0.6980574	1.6637748	0.005791506	0.050917745	0.988	671	tags=41%, list=12%, signal=46%
GREENBAUM_E2A_TARGETS_DN	17	0.70118034	1.663572	0.011472276	0.05090592	0.988	1,505	

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
HOFFMANN_IMMATURE_TO_MATURE_B_LYMPHOCYTE_UP	35	0.5780713	1.6632864	0.001972387	0.050934512	0.988	602	tags=20%, list=5%,
LI_PROSTATE_CANCER_EPIGENETIC	28	0.6522721	1.6630021	0.008048289	0.050926484	0.988	880	signal=21% tags=32%, list=7%,
TRACEY_RESISTANCE_TO_IFNA2_DN	28	0.6516444	1.662246	0.007751938	0.05117796	0.988	1,224	signal=34% tags=36%, list=9%,
RICKMAN_HEAD_AND_NECK_CANCER_D	30	0.6711334	1.6621183	0.009689922	0.051120143	0.988	717	signal=39% tags=37%, list=6%,
BROWNE_HCMV_INFECTION_30MIN_UP	51	0.5603894	1.6619488	0.005597015	0.051111914	0.988	1,924	signal=39% tags=35%, list=15%,
GRUETZMANN_PANCREATIC_CANCER_UP	329	0.55240405	1.6617109	0.003802281	0.0511067	0.988	1,395	signal=41% tags=30%, list=11%,
LANDIS_ERBB2_BREAST_TUMORS_324_DN	132	0.5734535	1.661706	0.003663004	0.051004987	0.988	1,886	signal=33% tags=38%, list=14%,
LEIN_ASTROCYTE_MARKERS	34	0.59392965	1.660859	0.011857707	0.051358253	0.989	767	signal=44% tags=24%, list=6%,
BYSTRYKH_HEMATOPOIESIS_STEM_CELL_AND_BRAIN_QTL_CIS	40	0.47409573	1.6586426	0.010080645	0.052318476	0.99	1,840	signal=25% tags=30%, list=14%,
NAGASHIMA_EGF_SIGNALING_UP	52	0.75496596	1.6578116	0.005836576	0.052660655	0.99	1,459	signal=35% tags=56%, list=11%,
BIOCARTA_GLEEVEC_PATHWAY	23	0.5740117	1.6576612	0.009861933	0.05260678	0.99	939	signal=63% tags=22%, list=7%,
ENGELMANN_CANCER_PROGENITORS_UP	42	0.638543	1.6532383	0.003875969	0.054728355	0.993	1,968	signal=23% tags=48%, list=15%, signal=56%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
FIGUEROA_AML_METHYLATION_CLUSTER_3_DN	25	0.5482084	1.652405	0.01980198	0.05504817	0.993	2,788	tags=48%, list=21%, signal=61%
SERVITJA_ISLET_HNF1A_TARGETS_UP	147	0.62535816	1.6515567	0.003816794	0.05533842	0.993	1,294	tags=30%, list=10%, signal=33%
PID_API1_PATHWAY	68	0.582522	1.6514632	0.009708738	0.05526824	0.993	2,061	tags=38%, list=16%, signal=45%
SWEET_KRAS_ONCOGENIC_SIGNATURE	83	0.5110869	1.6506968	0.017077798	0.055583	0.994	1,053	tags=18%, list=8%, signal=20%
BUKANOVICH_T_LYMPHOCYTE_HOMING_ON_TUMOR_UP	19	0.6816369	1.6504899	0.01532567	0.0555478	0.994	2,166	tags=37%, list=17%, signal=44%
OUYANG_PROSTATE_CANCER_PROGRESSION_UP	16	0.67517805	1.6503515	0.025390625	0.05551536	0.994	613	tags=25%, list=5%, signal=26%
ZHAN_MULTIPLE_MYELOMA_PR_DN	32	0.5868099	1.6499485	0.012345679	0.05561188	0.995	2,142	tags=50%, list=16%, signal=60%
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_6HR_DN	32	0.6363554	1.6497763	0.005905512	0.055596795	0.995	1,633	tags=38%, list=13%, signal=43%
ALONSO_METASTASIS_DN	22	0.5795752	1.6493391	0.016427105	0.05575049	0.995	491	tags=14%, list=4%, signal=14%
ZHOU_INFLAMMATORY_RESPONSE_LPS_UP	283	0.43913665	1.6485244	<0.0001	0.056035314	0.995	1,944	tags=26%, list=15%, signal=30%
AMUNDSON_GENOTOXIC_SIGNATURE	96	0.5067416	1.6475482	<0.0001	0.056397945	0.995	1,227	tags=26%, list=9%, signal=29%
GAVIN_FOXP3_TARGETS_CLUSTER_P2	60	0.52143157	1.6472422	0.002040816	0.05645659	0.995	1,507	tags=25%, list=12%, signal=28%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
MULLIGHAN_MLL_SIGNATURE_2_DN	253	0.4551741	1.6465214	0.003831418	0.056762077	0.995	1,787	tags=26%, list=14%, signal=30%
ZHANG_ANTIVIRAL_RESPONSE_TO_RIBAVIRIN_DN	48	0.593307	1.6460799	0.0056926	0.05688915	0.995	1,887	tags=44%, list=14%, signal=51%
CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_UP	25	0.84395176	1.6450266	0.003929273	0.0573078	0.995	541	tags=60%, list=4%, signal=62%
TENEDINI_MEGAKARYOCYTE_MARKERS	64	0.51243687	1.6446862	0.003984064	0.057410024	0.995	1,346	tags=25%, list=10%, signal=28%
TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_10D_DN	116	0.59737617	1.642377	0.005758158	0.058551338	0.995	1,723	tags=37%, list=13%, signal=42%
PID_AVB3_OPN_PATHWAY	30	0.6102073	1.6421901	0.015122874	0.058530834	0.995	735	tags=27%, list=6%, signal=28%
PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP	175	0.6655087	1.6410596	0.012987013	0.059069484	0.995	1,973	tags=48%, list=15%, signal=56%
SHAFFER_IRF4_MULTIPLE_MYELOMA_PROGRAM	34	0.58660334	1.6398387	0.003944773	0.0595433	0.995	903	tags=32%, list=7%, signal=35%
HAN_JNK_SINGALING_UP	29	0.68061644	1.6392883	0.006097561	0.059767954	0.995	819	tags=34%, list=6%, signal=37%
RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN	15	0.70805365	1.6390599	0.005825243	0.05975934	0.995	1,035	tags=53%, list=8%, signal=58%
DAZARD_UV_RESPONSE_CLUSTER_G28	20	0.75852495	1.6389083	0.011152417	0.05975101	0.996	1,366	tags=50%, list=10%, signal=56%
LI_INDUCED_T_TO_NATURAL_KILLER_DN	90	0.5211676	1.6388714	0.009765625	0.059657246	0.996	1,286	tags=24%, list=10%, signal=27%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
MARTORIATI_MDM4_TARGETS_NEUROEPITHELIUM_DN	117	0.52353173	1.6378243	<0.0001	0.060060665	0.996	1,729	tags=26%, list=13%, signal=30%
IIZUKA_LIVER_CANCER_PROGRESSION_L1_G1_UP	23	0.7660613	1.6377034	0.007858546	0.060014892	0.996	838	tags=43%, list=6%, signal=46%
MIKKELSEN_IPS_LCP_WITH_H3K4ME3	103	0.50412977	1.6371543	0.007874016	0.06018186	0.996	1,984	tags=36%, list=15%, signal=42%
CHAUHAN_RESPONSE_TO_METHOXYESTRADIOL_DN	92	0.48464516	1.6362228	0.023809524	0.06061323	0.996	1,278	tags=21%, list=10%, signal=23%
KORKOLA_EMBRYONAL_CARCCINOMA_UP	34	0.6113267	1.6357328	0.020283977	0.060828432	0.996	2,302	tags=53%, list=18%, signal=64%
PODAR_RESPONSE_TO_ADAPHOSTIN_UP	134	0.5498013	1.6355135	0.003795066	0.060842767	0.996	1,366	tags=33%, list=10%, signal=36%
VART_KSHV_INFECTION_ANGIOGENIC_MARKERS_UP	148	0.5848897	1.6348939	0.009505703	0.06111981	0.996	1,638	tags=36%, list=13%, signal=41%
PID_INTEGRIN_CS_PATHWAY	23	0.603422	1.6347647	0.027881041	0.061057087	0.996	767	tags=26%, list=6%, signal=28%
KEEN_RESPONSE_TO_ROSIGLITAZONE_DN	94	0.6362991	1.634687	0.005703422	0.060986497	0.996	1,572	tags=38%, list=12%, signal=43%
DAVIES_MULTIPLE_MYELOMA_VS_MGUS_DN	26	0.6977676	1.6343584	0.01192843	0.061047774	0.996	1,607	tags=46%, list=12%, signal=53%
AMIT_EGF_RESPONSE_60_MCF10A	37	0.71516305	1.6339698	0.01119403	0.061155684	0.996	1,700	tags=51%, list=13%, signal=59%
JOHNSTONE_PARVB_TARGETS_2_UP	121	0.53624064	1.6332096	0.005597015	0.06146872	0.996	1,388	tags=28%, list=11%, signal=31%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
UROSEVIC_RESPONSE_TO_IMIQIMOD	22	0.85112053	1.6331555	0.009784736	0.06137624	0.996	1,331	tags=82%, list=10%, signal=91%
MOSERLE_IFNA_RESPONSE	25	0.8876933	1.6330993	0.007905139	0.061298337	0.996	663	tags=76%, list=5%, signal=80%
PID_SHP2_PATHWAY	54	0.48277485	1.6330891	0.015873017	0.06118935	0.996	2,102	tags=28%, list=16%, signal=33%
REACTOME_MYPD88_MAL_CASCADE_INITIATED_ON_PLASMA_MEMBRANE	73	0.44127703	1.6324819	0.005617978	0.06144744	0.996	1,898	tags=26%, list=15%, signal=30%
PHONG_TNF_RESPONSE_NOT_VIA_P38	314	0.47144434	1.6307501	0.009487666	0.062232114	0.996	1,768	tags=31%, list=14%, signal=35%
WANG_TARGETS_OF_MLL_CBP_FUSION_UP	34	0.51638067	1.63039	0.001984127	0.062310103	0.996	1,482	tags=29%, list=11%, signal=33%
HOFFMANN_PRE_BI_TO_LARGE_PRE_BII_LYMPHOCYTE_DN	63	0.5199679	1.6293745	0.009578544	0.062794216	0.996	1,887	tags=35%, list=14%, signal=41%
REACTOME_SIGNALING_BY_RHO_GTPASES	84	0.44006768	1.6293296	0.003913894	0.06270749	0.996	2,393	tags=29%, list=18%, signal=35%
BROWNE_HCMV_INFECTION_4HR_UP	52	0.5275677	1.6288784	0.021825397	0.062903635	0.996	1,632	tags=31%, list=13%, signal=35%
GAVIN_FOXP3_TARGETS_CLUSTER_T4	74	0.5149975	1.6279975	0.007490637	0.063273795	0.996	1,950	tags=38%, list=15%, signal=44%
REACTOME_PLATELET_AGGREGATION_PLUG_FORMATION	35	0.46615312	1.627957	0.011881189	0.0631737	0.996	1,419	tags=20%, list=11%, signal=22%
KYNG_RESPONSE_TO_H2O2	62	0.519503	1.627589	0.003759399	0.06327116	0.996	2,418	tags=34%, list=19%, signal=41%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
XU_HGF_TARGETS_INDUCED_BY_AKT1_6HR	16	0.82179916	1.626878	0.005928854	0.06356747	0.996	1,288	tags=63%, list=10%, signal=69%
LANDIS_ERBB2_BREAST_PRENEOPLASTIC_DN	48	0.5699596	1.6260359	0.014925373	0.063970864	0.996	1,619	tags=31%, list=12%, signal=36%
RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_UP	316	0.47522378	1.6254435	0.007490637	0.064217046	0.996	2,041	tags=33%, list=16%, signal=38%
KIM_PTEN_TARGETS_UP	17	0.67807436	1.6253004	0.015209125	0.06417963	0.996	1,965	tags=41%, list=15%, signal=48%
REACTOME_INTEGRIN_ALPHAIIIB_BETA3_SIGNALING	26	0.5101204	1.6249979	0.025742574	0.06424534	0.996	1,419	tags=23%, list=11%, signal=26%
MANTOVANI_NFKB_TARGETS_UP	35	0.63715994	1.6244255	0.005813954	0.06451748	0.996	942	tags=31%, list=7%, signal=34%
ZHAN_MULTIPLE_MYELOMA_MF_UP	36	0.578467	1.6242628	0.009940358	0.06450378	0.996	658	tags=19%, list=5%, signal=20%
BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN	44	0.61672515	1.6239518	0.011257036	0.06456649	0.997	1,363	tags=34%, list=10%, signal=38%
HERNANDEZ_ABERRANT_MITOSIS_BY_DOCETACEL_2NM_DN	22	0.6896802	1.623513	0.011650485	0.064673714	0.997	1,637	tags=45%, list=13%, signal=52%
PETROVA_PROX1_TARGETS_DN	61	0.6731427	1.6227417	0.009596929	0.0649811	0.997	1,738	tags=51%, list=13%, signal=58%
NABA_ECM_AFFILIATED	109	0.5213947	1.6217935	0.002	0.06544246	0.998	1,566	tags=32%, list=12%, signal=36%
ZEMBUTSU_SENSITIVITY_TO_MITOMYCIN	15	0.6906633	1.6215801	0.007662835	0.06547572	0.998	1,332	tags=40%, list=10%, signal=45%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
JAZAG_TGFB1_SIGNALING_VIA_SMAD4_UP	93	0.40905762	1.6213069	<0.0001	0.06555358	0.998	1,056	tags=13%, list=8%, signal=14%
FERRANDO_TAL1_NEIGHBORS	19	0.80784523	1.6210111	0.005769231	0.06560279	0.998	513	tags=53%, list=4%, signal=55%
DURAND_STROMA_S_UP	221	0.4959501	1.6206188	0.007827789	0.0657092	0.998	1,623	tags=28%, list=12%, signal=32%
HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_DN	59	0.6461862	1.6204985	0.013861386	0.06567837	0.998	661	tags=36%, list=5%, signal=37%
HAHTOLA_MYCOSIS_FUNGOIDES_UP	18	0.7083852	1.6200924	0.001976285	0.065846875	0.998	1,287	tags=39%, list=10%, signal=43%
HOEBEKE_LYMPHOID_STEM_CELL_UP	84	0.5180315	1.620047	0.019011406	0.065761276	0.998	1,814	tags=32%, list=14%, signal=37%
REACTOME_LATENT_INFECTION_OF_HOMO_SAPIENS_WITH_MYCOBACTERIUM_TUBERCULOSIS	26	0.60921615	1.6195613	0.02173913	0.065902494	0.998	2,669	tags=46%, list=20%, signal=58%
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	102	0.4193099	1.619296	0.011516315	0.06596472	0.998	2,329	tags=27%, list=18%, signal=33%
LAIHO_COLORECTAL_CANCER_SERRATED_UP	106	0.53476876	1.6189247	0.03195489	0.06607053	0.998	2,061	tags=38%, list=16%, signal=44%
GAJATE_RESPONSE_TO TRABECTEDIN_UP	62	0.61925286	1.6185517	0.005780347	0.06617401	0.998	1,075	tags=35%, list=8%, signal=38%
ABE_VEGFA_TARGETS_30MIN	28	0.628677	1.6184393	0.007936508	0.06613215	0.998	1,341	tags=32%, list=10%, signal=36%
ZHANG_RESPONSE_TO_IKK_INHIBITOR_AND_TNF_UP	170	0.5373758	1.6178086	0.012	0.06639694	0.998	2,501	tags=45%, list=19%, signal=55%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
YE_METASTATIC_LIVER_CANCER	26	0.60710174	1.6176083	0.007984032	0.06639298	0.998	2,249	tags=50%, list=17%, signal=60%
XU_AKT1_TARGETS_6HR	24	0.6865686	1.6173135	0.02008032	0.06645013	0.998	485	tags=38%, list=4%, signal=39%
BIOCARTA_ERYTH_PATHWAY	15	0.6292304	1.6165882	0.024904214	0.06682818	0.998	1,275	tags=20%, list=10%, signal=22%
LANG_MYB_FAMILY_TARGETS	25	0.573162	1.6151409	0.030241935	0.06748711	0.998	476	tags=16%, list=4%, signal=17%
HORIUCHI_WTAP_TARGETS_UP	225	0.53910154	1.6144627	0.003868472	0.067719504	0.998	2,016	tags=38%, list=15%, signal=44%
VALK_AML_CLUSTER_4	26	0.60407186	1.6122143	0.017475728	0.06900385	0.999	1,341	tags=38%, list=10%, signal=43%
SAFFORD_T_LYMPHOCYTE_ANERGY	76	0.4595614	1.6121708	0.003838772	0.06891066	0.999	1,698	tags=29%, list=13%, signal=33%
CHIARETTI_ACUTE_LYMPHOBLASTIC_LEUKEMIA_ZAP70	62	0.48745024	1.6118891	0.001908397	0.068978764	0.999	1,198	tags=19%, list=9%, signal=21%
CHEN_LVAD_SUPPORT_OF_FAILING_HEART_UP	97	0.5833035	1.6114646	0.01183432	0.0691135	0.999	2,172	tags=42%, list=17%, signal=50%
GROSS_HYPOXIA_VIA_ELK3_DN	133	0.56292444	1.6098047	0.015122874	0.06998311	0.999	1,534	tags=32%, list=12%, signal=35%
OISHI_CHOLANGIOMA_STEM_CELL_LIKE_DN	268	0.5671361	1.6091334	0.015414258	0.0702545	0.999	1,357	tags=32%, list=10%, signal=35%
GAUSSMANN_MLL_AF4_FUSION_TARGETS_F_UP	140	0.5351771	1.6090425	0.005681818	0.07016716	0.999	1,985	list=15%, signal=45%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
SESTO_RESPONSE_TO_UV_C1	65	0.51542413	1.6082546	0.024253732	0.07055076	0.999	2,033	tags=31%, list=16%, signal=36%
CHANG_IMMORTALIZED_BY_HP31_DN	61	0.58527625	1.6079823	0.00996016	0.07060228	0.999	663	tags=30%, list=5%, signal=31%
TOOKER_GEMCITABINE_RESISTANCE_UP	73	0.4644721	1.6075599	0.006012024	0.070731685	0.999	1,111	tags=22%, list=9%, signal=24%
NOJIMA_SFRP2_TARGETS_DN	24	0.7072828	1.6064883	0.019267824	0.07135616	0.999	424	tags=29%, list=3%, signal=30%
VILIMAS_NOTCH1_TARGETS_DN	18	0.62459326	1.6049612	0.025490196	0.07223364	0.999	1,651	tags=39%, list=13%, signal=44%
REACTOME_RAP1_SIGNALING	15	0.56068707	1.6047016	0.034351144	0.07223132	0.999	1,419	tags=27%, list=11%, signal=30%
DORN_ADENOVIRUS_INFECTION_12HR_UP	26	0.6805683	1.6036955	0.01178782	0.07275765	0.999	1,312	tags=46%, list=10%, signal=51%
HASLINGER_B_CLL_WITH_11Q23_DELETION	21	0.5633267	1.6033523	0.028688524	0.07281303	0.999	2,440	tags=43%, list=19%, signal=53%
BOGNI_TREATMENT_RELATED_MYELOID_LEUKEMIA_DN	30	0.5106717	1.6033515	0.013972056	0.07268898	0.999	135	tags=10%, list=1%, signal=10%
HIRSCH_CELLULAR_TRANSFORMATION_SIGNATURE_UP	220	0.5061073	1.6032388	0.005870841	0.072626345	0.999	1,743	tags=31%, list=13%, signal=36%
SCHOEN_NFKB_SIGNALING	31	0.7665673	1.6029105	0.005617978	0.07270002	0.999	1,037	tags=48%, list=8%, signal=52%
GARY_CD5_TARGETS_UP	365	0.40661073	1.6024038	0.005802708	0.07290969	0.999	1,938	tags=23%, list=15%, signal=27%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
ROZANOV_MMP14_TARGETS_UP	195	0.539585	1.6014274	0.003846154	0.07340241	0.999	1,482	tags=31%, list=11%, signal=35%
SA_B_CELL_RECEPTOR_COMPLEXES	24	0.5538855	1.6007191	0.031007752	0.07372772	0.999	968	tags=21%, list=7%, signal=22%
AZARE_NEOPLASTIC_TRANSFORMATION_BY_STAT3_UP	112	0.54765725	1.6005515	0.003816794	0.07370071	0.999	1,489	tags=32%, list=11%, signal=36%
PID_IL6_7_PATHWAY	46	0.5597877	1.6004981	0.024253732	0.07361119	0.999	1,646	tags=33%, list=13%, signal=37%
LIANG_SILENCED_BY_METHYLATION_2	50	0.69583994	1.5996355	0.009784736	0.07404083	0.999	1,230	tags=42%, list=9%, signal=46%
KAYO_AGING_MUSCLE_UP	219	0.37124452	1.5993917	0.001934236	0.074056216	0.999	2,000	tags=20%, list=15%, signal=23%
VANASSE_BCL2_TARGETS_DN	56	0.49851707	1.5988955	0.003898636	0.07423252	0.999	1,253	tags=25%, list=10%, signal=28%
BOYVAULT_LIVER_CANCER_SUBCLASS_G1_DN	38	0.77746636	1.5986185	0.014056225	0.07427296	0.999	2,113	tags=74%, list=16%, signal=88%
UZONYI_RESPONSE_TO_LEUKOTRIENE_AND_THROMBIN	34	0.76476187	1.5983146	0.014897579	0.07431933	0.999	1,202	tags=62%, list=9%, signal=68%
ST_DIFFERENTIATION_PATHWAY_IN_PC12_CELLS	42	0.45463535	1.5982931	0.028790787	0.07420049	0.999	797	tags=14%, list=6%, signal=15%
PID_CD40_PATHWAY	29	0.5189542	1.5982208	0.027829314	0.074125506	0.999	1,415	tags=21%, list=11%, signal=23%
HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_UP	157	0.4730649	1.5976104	0.019157087	0.074255005	0.999	1,426	tags=24%, list=11%, signal=27%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
AMIT_SERUM_RESPONSE_40_MCF10A	28	0.75624114	1.5967696	0.020484172	0.07462623	0.999	1,977	tags=68%, list=15%, signal=80%
BECKER_TAMOXIFEN_RESISTANCE_UP	49	0.60323924	1.5960467	0.013487476	0.0749245	0.999	1,078	tags=33%, list=8%, signal=35%
CHEOK_RESPONSE_TO_MERCAPTOPURINE_DN	21	0.61918247	1.5960052	0.011695907	0.07482578	0.999	494	tags=24%, list=4%, signal=25%
PETROVA_ENDOTHELIIUM_LYMPHATIC_VS_BLOOD_DN	153	0.62079984	1.5939002	0.018691588	0.076095946	0.999	1,738	tags=41%, list=13%, signal=46%
TING_SILENCED_BY_DICER	22	0.70582163	1.5931709	0.015473888	0.07647222	0.999	2,349	tags=73%, list=18%, signal=89%
REACTOME_CA_DEPENDENT_EVENTS	27	0.48369884	1.5925307	0.029411765	0.076809056	0.999	955	tags=19%, list=7%, signal=20%
OKUMURA_INFLAMMATORY_RESPONSE_LPS	164	0.44723842	1.5920246	0.001855288	0.07705271	0.999	1,861	tags=27%, list=14%, signal=32%
GRANDVAUX_IRF3_TARGETS_UP	15	0.8183733	1.59147	0.012170386	0.07728588	1	1,241	tags=67%, list=10%, signal=74%
BURTON_ADIPOGENESIS_1	30	0.6828338	1.5912704	0.02330097	0.077283576	1	1,136	tags=50%, list=9%, signal=55%
BOWIE_RESPONSE_TO_TAMOXIFEN	17	0.9067015	1.5906627	0.003891051	0.07754428	1	1,230	tags=100%, list=9%, signal=110%
NAM_FXYD5_TARGETS_DN	16	0.5927851	1.590592	0.021484375	0.07746536	1	2,499	tags=50%, list=19%, signal=62%
RAGHAVACHARI_PLATELET_SPECIFIC_GENES	67	0.51719666	1.5902321	0.007648184	0.07755017	1	1,973	tags=28%, list=15%, signal=33%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
KEGG_MAPK_SIGNALING_PATHWAY	242	0.3572063	1.5901303	0.00189394	0.077483326	1	1,933	tags=22%, list=15%, signal=25%
WANG_IMMORTALIZED_BY_HOXA9_AND_MEIS1_UP	27	0.56878024	1.5901242	0.007905139	0.07735917	1	2,054	tags=41%, list=16%, signal=48%
KATSANOU_ELAVL1_TARGETS_UP	124	0.5140875	1.5900917	0.003809524	0.07726529	1	1,147	tags=23%, list=9%, signal=25%
RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_DN	227	0.45322058	1.5897913	0.005703422	0.07733919	1	2,041	tags=33%, list=16%, signal=38%
MCBRYAN_PUBERTAL_BREAST_4_5WK_DN	158	0.43722486	1.5895933	0.007736944	0.07734357	1	2,090	tags=31%, list=16%, signal=36%
SANA_TNF_SIGNALING_DN	72	0.59085196	1.5888144	0.020754717	0.07774265	1	1,359	tags=32%, list=10%, signal=35%
YAGI_AML_WITH_T_9_11_TRANSLOCATION	122	0.38780674	1.5887332	0.003976143	0.07768638	1	2,084	tags=25%, list=16%, signal=30%
REACTOME_SEMAPHORIN_INTERACTIONS	60	0.5078731	1.586045	0.024291499	0.07927835	1	1,937	tags=32%, list=15%, signal=37%
WEST_ADRENOCORTICAL_TUMOR_DN	494	0.50082535	1.5850505	0.011342155	0.079848096	1	2,469	list=19%, signal=44%
HOSHIDA_LIVER_CANCER_LATE_RECURRENCE_UP	55	0.6493291	1.5846491	0.016	0.0800292	1	1,250	tags=35%, list=10%, signal=38%
GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_UP	22	0.7807653	1.5845226	0.007692308	0.07996485	1	1,244	tags=50%, list=10%, signal=55%
SARRIO_EPITHELIAL_MESENCHYMAL_TRANSITION_DN	134	0.5047884	1.5844492	0.003831418	0.07987213	1	1,272	tags=25%, list=10%, signal=28%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
YAGI_AML_WITH_11Q23_REARRANGED	330	0.3762629	1.5843519	0.001964637	0.07980258	1	2,093	tags=27%, list=16%, signal=31%
BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX	17	0.90670145	1.5841798	0.005769231	0.07978627	1	1,230	tags=100%, list=9%, signal=110%
WANG_METASTASIS_OF_BREAST_CANCER_ESR1_DN	25	0.55187106	1.5840883	0.032258064	0.07971184	1	1,793	tags=32%, list=14%, signal=37%
HUMMERICH_SKIN_CANCER_PROGRESSION_UP	80	0.6133715	1.5839742	0.011363637	0.07964306	1	998	tags=29%, list=8%, signal=31%
BOYLAN_MULTIPLE_MYELOMA_C_CLUSTER_DN	27	0.6371262	1.583863	0.013232514	0.07958534	1	2,273	tags=59%, list=17%, signal=72%
TCGA_GLIOMASTOMA_COPY_NUMBER_DN	23	0.5659183	1.5837847	0.030947777	0.079495065	1	2,478	tags=43%, list=19%, signal=54%
BIOCARTA_PML_PATHWAY	16	0.54535943	1.5836201	0.037109375	0.07946105	1	2,738	tags=50%, list=21%, signal=63%
KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	64	0.40119407	1.5833514	0.01	0.079510696	1	1,786	tags=20%, list=14%, signal=23%
KRIEG_KDM3A_TARGETS_NOT_HYPOXIA	135	0.44937593	1.5833242	0.005870841	0.079395875	1	2,012	list=15%, signal=30%, tags=61%, list=8%, signal=66%
MAHADEVAN_RESPONSE_TO_MP470_DN	18	0.8216179	1.58299	0.007677543	0.07950164	1	1,057	tags=39%, list=17%, signal=47%
GAVIN_FOXP3_TARGETS_CLUSTER_P7	62	0.5154791	1.5829586	0.015686275	0.07941106	1	2,266	tags=29%, list=15%, signal=34%
REACTOME_GROWTH_HORMONE_RECEPTOR_SIGNALING	24	0.5314	1.5827549	0.033755273	0.07937534	1	1,914	

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
OSMAN_BLADDER_CANCER_DN	288	0.33500552	1.582595	0.023952097	0.07934968	1	1,509	tags=15%, list=12%, signal=16%
ZHAN_V1_LATE_DIFFERENTIATION_GENES_UP	32	0.6001004	1.5804613	0.01178782	0.08062009	1	2,448	tags=47%, list=19%, signal=58%
BAELDE_DIABETIC_NEPHROPATHY_DN	396	0.4461378	1.5804533	0.007797271	0.08049939	1	1,646	tags=24%, list=13%, signal=27%
GENTLES_LEUKEMIC_STEM_CELL_UP	21	0.7037761	1.5804439	0.00952381	0.08038339	1	1,814	tags=62%, list=14%, signal=72%
PHONG_TNF_TARGETS_UP	60	0.66273516	1.580187	0.028735632	0.080440946	1	1,703	tags=48%, list=13%, signal=55%
MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP	187	0.44744736	1.5792452	0.009451796	0.08092941	1	1,693	tags=27%, list=13%, signal=30%
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_UP	169	0.52994007	1.5791802	0.009380863	0.08086279	1	1,626	tags=34%, list=12%, signal=39%
NIELSEN_GIST_VS_SYNOVIAL_SARCOMA_DN	17	0.7203268	1.5787519	0.009861933	0.08105021	1	1,497	tags=59%, list=11%, signal=66%
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYTE_UP	180	0.48550978	1.5778124	0.001972387	0.08158257	1	1,455	tags=26%, list=11%, signal=29%
CHENG_RESPONSE_TO_NICKEL_ACETATE	36	0.44135153	1.5766674	0.030592734	0.08229455	1	420	tags=11%, list=3%, signal=11%
MARZEC_IL2_SIGNALING_DN	27	0.5699529	1.5764775	0.020746889	0.08229556	1	609	tags=19%, list=5%, signal=19%
SCIAN_INVERSED_TARGETS_OF_TP53_AND_TP73_DN	26	0.5255726	1.5762185	0.03522505	0.082351156	1	2,807	tags=46%, list=22%, signal=59%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
TSUNODA_CISPLATIN_RESISTANCE_DN	45	0.59547955	1.5756949	0.009765625	0.08255063	1	1,968	tags=40%, list=15%, signal=47%
SWEET_LUNG_CANCER_KRAS_DN	373	0.51465017	1.575301	0.011560693	0.08269188	1	2,117	tags=37%, list=16%, signal=43%
GHANDHI_DIRECT_IRRADIATION_UP	86	0.5842733	1.5748379	0.009746589	0.08286858	1	2,323	tags=47%, list=18%, signal=56%
MCMURRAY_TP53_HRAS_COOPERATION_RESPONSE_UP	22	0.6569387	1.5736172	0.013944224	0.08356264	1	1,399	tags=36%, list=11%, signal=41%
REACTOME_SYNTHESIS_OF_PA	19	0.58762974	1.5732291	0.021072797	0.083675876	1	1,472	tags=32%, list=11%, signal=36%
LANDIS_BREAST_CANCER_PROGRESSION_DN	65	0.63657886	1.5731001	0.018382354	0.08363911	1	1,886	tags=45%, list=14%, signal=52%
AMIT_DELAYED_EARLY_GENES	17	0.72332776	1.5728182	0.033932135	0.08369634	1	1,459	tags=53%, list=11%, signal=60%
MADAN_DPPA4_TARGETS	28	0.56612235	1.5727719	0.023465704	0.08360591	1	304	tags=14%, list=2%, signal=15%
LIU_NASOPHARYNGEAL_CARCINOMA	62	0.39408135	1.5726702	0.009881423	0.08353713	1	1,225	tags=15%, list=9%, signal=16%
SHEPARD_CRUSH_AND_BURN_MUTANT_UP	153	0.44030163	1.5722282	0.003787879	0.08374174	1	2,848	tags=39%, list=22%, signal=50%
PETRETTO_HEART_MASS_QTL_CIS_DN	18	0.58213806	1.5715556	0.019120459	0.08409592	1	60	tags=11%, list=0%, signal=11%
RHEIN_ALL_GLUCOCORTICOID_THERAPY_UP	70	0.5765492	1.5711837	0.009578544	0.08425171	1	2,006	tags=47%, list=15%, signal=55%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_DN	98	0.42005652	1.5704359	0.02443609	0.08457306	1	2,408	tags=29%, list=18%, signal=35%
SARTIPY_NORMAL_AT_INSULIN_RESISTANCE_UP	27	0.6504285	1.5702051	0.017408123	0.08460384	1	496	tags=26%, list=4%, signal=27%
FALVELLA_SMOKERS_WITH_LUNG_CANCER	64	0.47548616	1.5700492	0.025974026	0.08459575	1	1,758	list=13%, signal=31%, tags=10%, signal=35%
VANHARANTA_UTERINE_FIBROID_DN	61	0.60253745	1.5698718	0.009746589	0.08457698	1	1,352	tags=50%, list=16%, signal=60%
GUENTHER_GROWTH_SPHERICAL_VS_ADHERENT_DN	26	0.63123983	1.5696769	0.030018762	0.0845769	1	2,108	tags=42%, list=19%, signal=51%
ZHANG_TARGETS_OF_EWSR1_FLI1_FUSION	79	0.49610823	1.5690241	0.009174312	0.08492067	1	2,422	tags=33%, list=6%, signal=35%
WINNEPENINCKX_MELANOMA_METASTASIS_DN	33	0.62880105	1.5688217	0.016064256	0.08492329	1	750	tags=33%, list=13%, signal=38%
NUTT_GBM_VS_AO_GLIOMA_UP	45	0.55817324	1.5685893	0.03508772	0.08496467	1	1,696	tags=31%, list=7%, signal=44%
MAGRANGEAS_MULTIPLE_MYELOMA_IGG_VS_IGA_UP	18	0.59633183	1.5680447	0.038314175	0.08510287	1	1,225	tags=19%, list=3%, signal=19%
RASHI_NFKB1_TARGETS	17	0.75672376	1.5679754	0.033771105	0.08503409	1	898	tags=40%, list=14%, signal=46%
GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_GREY_DN	42	0.5496275	1.5677218	0.010121457	0.08509459	1	330	
GYORFFY_DOXORUBICIN_RESISTANCE	40	0.5258909	1.5671935	0.014028057	0.085332006	1	1,767	

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
MATTIOLI_MULTIPLE_MYELOMA_WITH_14Q32_TRANSLOCATIONS	35	0.56989497	1.567085	0.02819549	0.085285224	1	1,301	tags=37%, list=10%, signal=41%
ZHENG_RESPONSE_TO_ARSENITE_UP	16	0.8234502	1.566448	0.014256619	0.08561624	1	743	tags=56%, list=6%, signal=60%
RIGGI_EWING_SARCOMA_PROGENITOR_UP	314	0.47598982	1.5662904	<0.0001	0.08558875	1	1,647	tags=28%, list=13%, signal=32%
MOREIRA_RESPONSE_TO_TSA_DN	18	0.6226141	1.5662019	0.025490196	0.08552375	1	785	tags=28%, list=6%, signal=30%
SA_CASPASE_CASCADE	18	0.5865809	1.5656261	0.026970955	0.0857681	1	609	tags=22%, list=5%, signal=23%
CROONQUIST_IL6_DEPRIVATION_UP	19	0.6723723	1.5655483	0.023210831	0.08570118	1	1,589	tags=53%, list=12%, signal=60%
BIOCARTA_CXCR4_PATHWAY	22	0.5281876	1.5653213	0.044176705	0.08573782	1	693	tags=14%, list=5%, signal=14%
NIKOLSKY_OVERCONNECTED_IN_BREAST_CANCER	18	0.5669154	1.5642023	0.020833334	0.08635559	1	814	tags=28%, list=6%, signal=30%
IGLESIAS_E2F_TARGETS_UP	140	0.57759005	1.5638301	0.026871402	0.0864944	1	1,339	tags=31%, list=10%, signal=34%
NATSUME_RESPONSE_TO_INTERFERON_BETA_UP	66	0.4969918	1.5635132	0.003921569	0.08655327	1	1,194	tags=23%, list=9%, signal=25%
XU_HGF_TARGETS_REPRESSED_BY_AKT1_DN	84	0.4345485	1.5633465	0.007984032	0.086541876	1	1,199	tags=13%, list=9%, signal=14%
KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_4NQO_IN_WS	35	0.51801646	1.5612773	0.030181086	0.087954834	1	1,014	tags=14%, list=8%, signal=15%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
ZHAN_EARLY_DIFFERENTIATION_GENES_DN	41	0.5523429	1.5609946	0.02739726	0.08800944	1	1,409	tags=32%, list=11%, signal=35%
BIOCARTA_TPO_PATHWAY	23	0.50196916	1.5606676	0.03219697	0.088082895	1	1,639	tags=26%, list=13%, signal=30%
HOLLEMAN_ASPARAGINASE_RESISTANCE_ALL_UP	20	0.50395083	1.5606254	0.024096385	0.08797332	1	2,217	tags=20%, list=17%, signal=24%
MISSIAGLIA_REGULATED_BY_METHYLATION_UP	112	0.57154715	1.5604208	0.022727273	0.08794511	1	1,951	tags=46%, list=15%, signal=53%
MULLIGHAN_NPM1_MUTATED_SIGNATURE_2_DN	69	0.39796743	1.5592811	0.021400778	0.088611685	1	2,367	tags=26%, list=18%, signal=32%
MARTINEZ_RESPONSE_TO_TRABECTEDIN_UP	64	0.46283418	1.55918	0.015503876	0.08855261	1	1,950	tags=30%, list=15%, signal=35%
FLECHNER_PBL_KIDNEY_TRANSPLANT_OK_VS_DONOR_UP	142	0.35554004	1.5590962	0.020120725	0.08847735	1	2,451	tags=25%, list=19%, signal=30%
HAHTOLA_MYCOSIS_FUNGOIDES_CD4_UP	63	0.6236821	1.5581676	0.024299065	0.08899696	1	1,754	tags=44%, list=13%, signal=51%
PID_INTEGRIN5_PATHWAY	17	0.6379856	1.5575721	0.04868914	0.0892992	1	1,395	tags=41%, list=11%, signal=46%
PIEPOLI_LGI1_TARGETS_UP	15	0.71875036	1.5560375	0.013806706	0.09015919	1	972	tags=40%, list=7%, signal=43%
JACKSON_DNMT1_TARGETS_UP	74	0.55007386	1.5554827	0.01724138	0.09041202	1	2,061	tags=42%, list=16%, signal=49%
AMIT_EGF_RESPONSE_60_HELA	40	0.6357069	1.5554436	0.025490196	0.090315975	1	1,363	tags=40%, list=10%, signal=45%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
ZHENG_FOXP3_TARGETS_IN_THYMUS_UP	150	0.4280685	1.5549457	0.018292682	0.09051942	1	2,781	tags=33%, list=21%, signal=42%
ROSS_AML_WITH_AML1_ETO_FUSION	71	0.4464424	1.5533602	0.00610998	0.09148277	1	1,825	tags=23%, list=14%, signal=26%
SWEET_LUNG_CANCER_KRAS_UP	419	0.42029297	1.5523412	0.009505703	0.09222049	1	1,157	tags=17%, list=9%, signal=18%
PLASARI_TGFB1_SIGNALING_VIA_NFIC_1HR_UP	28	0.598064	1.55137	0.014227643	0.09278932	1	1,251	tags=39%, list=10%, signal=43%
ZHAN_MULTIPLE_MYELOMA_LB_UP	27	0.58040947	1.5507755	0.017475728	0.09303372	1	1,901	tags=33%, list=15%, signal=39%
DORSAM_HOXA9_TARGETS_DN	31	0.503032	1.5507058	0.007936508	0.09295176	1	1,310	tags=26%, list=10%, signal=29%
HERNANDEZ_ABERRANT_MITOSIS_BY_DOCETACEL_4NM_UP	19	0.6966637	1.5503155	0.006012024	0.09312443	1	1,428	tags=47%, list=11%, signal=53%
CROONQUIST_STROMAL_STIMULATION_UP	57	0.7036496	1.5502524	0.020637898	0.09301834	1	1,240	tags=44%, list=10%, signal=48%
HELLER_SILENCED_BY_METHYLATION_DN	95	0.519901	1.5497826	0.005802708	0.09323596	1	966	tags=21%, list=7%, signal=23%
BIOCARTA_TOLL_PATHWAY	32	0.51955724	1.5488219	0.0317757	0.0938414	1	1,868	tags=34%, list=14%, signal=40%
SABATES_COLORECTAL_ADENOMA_DN	216	0.50222015	1.5485955	0.010141988	0.0938789	1	1,333	tags=27%, list=10%, signal=29%
DITTMER_PTHLH_TARGETS_DN	70	0.42077512	1.548505	0.015655577	0.09380312	1	1,951	tags=21%, list=15%, signal=25%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
RIZKI_TUMOR_INVASIVENESS_2D_DN	61	0.41093263	1.5481576	0.013307985	0.09392288	1	1,820	tags=26%, list=14%, signal=30%
HOOI_ST7_TARGETS_UP	60	0.5447935	1.5481377	0.013779528	0.09380661	1	645	tags=25%, list=5%, signal=26%
WATANABE_COLON_CANCER_MSL_VS_MSS_UP	20	0.6530896	1.547626	0.031558186	0.09404267	1	1,038	tags=35%, list=8%, signal=38%
CHEN_LVAD_SUPPORT_OF_FAILING_HEART_DN	41	0.59551626	1.5474318	0.005940594	0.09404338	1	1,723	tags=49%, list=13%, signal=56%
WESTON_VEGFA_TARGETS_3HR	69	0.545515	1.5471797	0.016333938	0.09409526	1	1,534	tags=35%, list=12%, signal=39%
KLEIN_PRIMARY_EFFUSION_LYMPHOMA_UP	51	0.46404123	1.5460212	0.018	0.094772086	1	1,698	tags=22%, list=13%, signal=25%
BIOCARTA_PPARA_PATHWAY	51	0.4754807	1.5460048	0.014373717	0.09466495	1	1,639	tags=25%, list=13%, signal=29%
HOWLIN_PUBERTAL_MAMMARY_GLAND	61	0.5504815	1.5459793	0.009416196	0.09454031	1	1,723	tags=41%, list=13%, signal=47%
LIU_SMARCA4_TARGETS	48	0.64961314	1.545779	0.02389706	0.09457013	1	1,057	tags=38%, list=8%, signal=41%
MIKKELSEN_IPS_ICP_WITH_H3K27ME3	33	0.50065875	1.545337	0.02357564	0.094725505	1	742	tags=18%, list=6%, signal=19%
TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_ERYTHROCYTE_UP	147	0.5538133	1.5445478	0.013282732	0.09518536	1	1,333	tags=31%, list=10%, signal=34%
SMIRNOV_RESPONSE_TO_IR_6HR_DN	105	0.5537849	1.5444461	0.023166023	0.09513908	1	797	tags=29%, list=6%, signal=30%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
SATO_SILENCED_BY_METHYLATION_IN_PANCREATIC_CANCER_1	392	0.4208659	1.5427349	0.003802281	0.09626025	1	1,312	tags=19%, list=10%, signal=20%
LINDGREN_BLADDER_CANCER_HIGH_RECURRENCE	41	0.67354774	1.5403314	0.02534113	0.09791578	1	1,202	tags=44%, list=9%, signal=48%
STEARMAN_TUMOR_FIELD_EFFECT_UP	30	0.6901328	1.540246	0.035984848	0.097852655	1	564	tags=30%, list=4%, signal=31%
FIGUEROA_AML_METHYLATION_CLUSTER_1_DN	32	0.48372874	1.5391092	0.04761905	0.09855396	1	1,227	tags=22%, list=9%, signal=24%
KUNINGER_IGF1_VS_PDGF_TARGETS_DN	34	0.6429701	1.5389076	0.021153847	0.09853408	1	1,651	tags=47%, list=13%, signal=54%
VECCHI_GASTRIC_CANCER_EARLY_DN	268	0.53240067	1.5377734	0.010060363	0.09932816	1	1,662	tags=30%, list=13%, signal=34%
PID_IL4_2PATHWAY	59	0.43727806	1.5376103	0.015533981	0.09930875	1	2,154	tags=17%, signal=40%
SCHAEFFER_PROSTATE_DEVELOPMENT_6HR_UP	134	0.4365538	1.5373785	0.009451796	0.099360384	1	1,803	tags=27%, list=14%, signal=31%
SESTO_RESPONSE_TO_UV_C3	20	0.6631599	1.5371425	0.039697543	0.09943197	1	2,310	tags=65%, list=18%, signal=79%
REACTOME_SIGNALING_BY_SCF_KIT	65	0.38838276	1.5362531	0.016460905	0.099972	1	1,202	tags=17%, list=9%, signal=19%
KENNY_CTNNB1_TARGETS_DN	42	0.46845356	1.5357451	0.012448133	0.100230604	1	1,798	tags=26%, list=14%, signal=30%
BROWNE_HCMV_INFECTION_2HR_UP	34	0.6635702	1.5350589	0.029354207	0.10060819	1	1,802	tags=50%, list=14%, signal=58%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
VISALA_AGING_LYMPHOCYTE_DN	15	0.6435901	1.5348192	0.029962547	0.10068781	1	869	tags=27%, list=7%, signal=29%
LIANG_HEMATOPOIESIS_STEM_CELL_NUMBER_SMALL_VS_HUGE_DN	26	0.5629011	1.5346625	0.027888447	0.10068332	1	1,887	tags=38%, list=14%, signal=45%
MIKKELSEN_MCV6_LCP_WITH_H3K27ME3	15	0.59262186	1.5340413	0.04509804	0.101066515	1	772	tags=20%, list=6%, signal=21%
BROWNE_HCMV_INFECTION_30MIN_DN	135	0.37086204	1.5328243	0.003937008	0.101876505	1	1,362	tags=17%, list=10%, signal=19%
MANTOVANI_VIRAL_GPCR_SIGNALING_UP	63	0.52073926	1.5322708	0.011472276	0.102177635	1	942	tags=22%, list=7%, signal=24%
RODWELL_AGING_KIDNEY_NO_BLOOD_UP	167	0.57321817	1.5321717	0.039252337	0.10211068	1	1,301	tags=29%, list=10%, signal=32%
FLORIO_NEOCORTEX_BASAL_RADIAL_GLIA_UP	193	0.4163689	1.5314977	0.009784736	0.1025035	1	1,638	tags=21%, list=13%, signal=23%
VANHARANTA_UTERINE_FIBROID_WITH_7Q_DELETION_DN	34	0.4941139	1.5314856	0.046511628	0.10237808	1	1,977	tags=32%, list=15%, signal=38%
GENTILE_UV_RESPONSE_CLUSTER_D6	32	0.5499398	1.5309867	0.024489796	0.10257513	1	2,423	tags=34%, list=19%, signal=42%
MIKKELSEN_MCV6_ICP_WITH_H3K27ME3	46	0.41764465	1.5308682	0.037401576	0.102535404	1	339	tags=7%, list=3%, signal=7%
KYNG_DNA_DAMAGE_BY_4NQO_OR_UV	59	0.42030227	1.5307441	0.007936508	0.10248896	1	1,356	tags=24%, list=10%, signal=26%
GAL_LEUKEMIC_STEM_CELL_DN	220	0.48960826	1.529584	0.04255319	0.10324523	1	1,218	tags=24%, list=9%, signal=26%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
PLASARL_TGFB1_SIGNALING_VIA_NFIC_10HR_UP	38	0.568239	1.5292895	0.014	0.10319479	1	749	tags=29%, list=6%, signal=31%
ZHOU_TNF_SIGNALING_4HR	48	0.51826316	1.528737	0.040515654	0.103450276	1	401	tags=15%, list=3%, signal=15%
BIOCARTA_ETS_PATHWAY	15	0.5728216	1.5285555	0.043137256	0.103447795	1	174	tags=13%, list=1%, signal=13%
PID_SYNDECAN_4_PATHWAY	31	0.57250386	1.5281607	0.02385686	0.10360993	1	422	tags=16%, list=3%, signal=17%
NAKAMURA_METASTASIS_MODEL_UP	33	0.5234173	1.5281287	0.031067962	0.10350194	1	300	tags=12%, list=2%, signal=12%
GERHOLD_ADIPOGENESIS_UP	47	0.5485046	1.5278196	0.046242774	0.10361399	1	965	tags=26%, list=7%, signal=27%
PID_KIT_PATHWAY	49	0.3970149	1.527787	0.03508772	0.103495546	1	939	tags=16%, list=7%, signal=18%
SHIN_B_CELL_LYMPHOMA_CLUSTER_2	25	0.544073	1.5277368	0.019417476	0.103394724	1	1,887	tags=44%, list=14%, signal=51%
AMIT_EGF_RESPONSE_40_HELA	39	0.62223244	1.525781	0.038986355	0.10478815	1	1,703	tags=44%, list=13%, signal=50%
BURTON_ADIPOGENESIS_PEAK_AT_0HR	57	0.6089985	1.5257504	0.019193858	0.10467483	1	1,470	tags=37%, list=11%, signal=41%
DARWICHE_PAPILLOMA_RISK_HIGH_VS_LOW_DN	24	0.52684045	1.525686	0.042307694	0.104573175	1	491	tags=21%, list=4%, signal=22%
REACTOME_CD28_DEPENDENT_PI3K_AKT_SIGNALING	17	0.5396712	1.525346	0.035433073	0.104717195	1	504	tags=24%, list=4%, signal=24%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
KEGG_APOPTOSIS	80	0.38885808	1.5253223	0.024	0.1045938	1	2,917	tags=33%, list=22%, signal=42%
MIDORIKAWA_AMPLIFIED_IN_LIVER_CANCER	31	0.45513698	1.5251312	0.03137255	0.10461445	1	2,484	tags=35%, list=19%, signal=44%
KEGG_NICOTINATE_AND_NICOTINAMIDE_METABOLISM	15	0.6740765	1.524715	0.021359224	0.10476499	1	2,163	tags=47%, list=17%, signal=56%
GESERICK_TERT_TARGETS_DN	18	0.7352972	1.5243721	0.041666668	0.10490491	1	1,459	tags=72%, list=11%, signal=81%
BRACHAT_RESPONSE_TO_CISPLATIN	17	0.5889444	1.5238107	0.036363635	0.10523848	1	3,338	tags=59%, list=26%, signal=79%
BASSO_HAIRY_CELL_LEUKEMIA_UP	77	0.5179754	1.5232214	0.024952015	0.10557908	1	2,212	tags=39%, list=17%, signal=47%
REACTOME_SIGNALING_BY_FGFR1_MUTANTS	25	0.46304238	1.5230659	0.040860213	0.10555332	1	2,909	tags=44%, list=22%, signal=57%
HU_GENOTOXIC_DAMAGE_24HR	32	0.5550911	1.5228903	0.032945737	0.10553779	1	303	tags=16%, list=2%, signal=16%
LINDSTEDT_DENDRITIC_CELL_MATURATION_C	63	0.5426353	1.5214593	0.019305019	0.106514506	1	1,932	tags=33%, list=15%, signal=39%
SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP	150	0.5121086	1.5206728	0.01532567	0.106955916	1	2,015	tags=38%, list=15%, signal=44%
AMIT_SERUM_RESPONSE_120_MCF10A	59	0.5506422	1.5199288	0.020325202	0.107393354	1	1,676	tags=32%, list=13%, signal=37%
KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	184	0.3742286	1.5197892	0.02918288	0.10737138	1	1,639	tags=18%, list=13%, signal=21%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GROSS_ELK3_TARGETS_DN	27	0.6428716	1.5187135	0.020833334	0.10811636	1	907	tags=37%, list=7%, signal=40%
MCDOWELL_ACUTE_LUNG_INJURY_DN	42	0.5256252	1.5180423	0.019193858	0.10854088	1	678	tags=24%, list=5%, signal=25%
KAN_RESPONSE_TO_ARSENIC_TRIOXIDE	115	0.56756175	1.5168624	0.02226345	0.109391585	1	1,240	tags=35%, list=10%, signal=38%
KEGG_ENDOCYTOSIS	148	0.36198357	1.5168335	0.022	0.10927643	1	1,759	tags=18%, list=14%, signal=21%
RODRIGUES_NTN1_AND_DCC_TARGETS	30	0.62334347	1.5167555	0.034816246	0.10921232	1	1,363	tags=30%, list=10%, signal=33%
REACTOME_ERK_MAPK_TARGETS	21	0.5002299	1.5162326	0.029296875	0.10951309	1	2,097	tags=29%, list=16%, signal=34%
BROWNE_HCMV_INFECTION_10HR_UP	96	0.44962782	1.5159377	0.016359918	0.109629765	1	924	tags=14%, list=7%, signal=14%
SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_2FC_DN	19	0.680736	1.5141659	0.036821704	0.11092958	1	1,322	tags=53%, list=10%, signal=58%
REACTOME_NUCLEOTIDE_BINDING_DOMAIN_LEUCINE_RICH_REPEAT_CONTAINING_RECEPTOR_NLR_SIGNALING_PATHWAYS	39	0.5036941	1.5133569	0.03422053	0.111454606	1	1,951	tags=38%, list=15%, signal=45%
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_8	42	0.53189206	1.5128635	0.017821781	0.111760534	1	2,694	tags=45%, list=21%, signal=57%
FONTAINE_FOLLICULAR_THYROID_ADENOMA_DN	57	0.487217	1.5123707	0.02173913	0.11205338	1	1,571	tags=32%, list=12%, signal=36%
HERNANDEZ_ABERRANT_MITOSIS_BY_DOCETACEL_2NM_UP	69	0.54061	1.5116342	0.019157087	0.112499505	1	1,417	tags=30%, list=11%, signal=34%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
REACTOME_PKA_MEDIATED_PHOSPHORYLATION_OF_CREB	15	0.5118938	1.5115176	0.04950495	0.11245224	1	323	tags=13%, list=2%, signal=14%
KASLER_HDAC7_TARGETS_1_UP	145	0.36394048	1.511345	0.013487476	0.1124459	1	1,735	tags=25%, list=13%, signal=28%
PID_TCPTP_PATHWAY	41	0.42615768	1.5111811	0.0498008	0.11247776	1	2,932	tags=32%, list=23%, signal=41%
VALK_AML_CLUSTER_1	26	0.6137054	1.5110735	0.03420523	0.112448536	1	1,887	tags=38%, list=14%, signal=45%
CEBALLOS_TARGETS_OF_TP53_AND_MYC_UP	20	0.6443111	1.5101455	0.013592233	0.11310998	1	1,877	tags=50%, list=14%, signal=58%
ADDYA_ERYTHROID_DIFFERENTIATION_BY_HEMIN	70	0.51590955	1.5098808	0.02661597	0.11316502	1	1,401	tags=36%, list=11%, signal=40%
GAUSSMANN_MLL_AF4_FUSION_TARGETS_E_UP	75	0.5448859	1.5084155	0.013232514	0.114215374	1	1,521	tags=35%, list=12%, signal=39%
SARTIPY_BLUNTED_BY_INSULIN_RESISTANCE_UP	16	0.6849045	1.5083005	0.02745098	0.11418405	1	879	tags=38%, list=7%, signal=40%
VALK_AML_WITH_CEBPA	33	0.57196724	1.5067058	0.018	0.11523548	1	1,402	tags=30%, list=11%, signal=34%
PARK_TRETINOIN_RESPONSE_AND_RARA_PLZF_FUSION	22	0.64293176	1.5064814	0.04109589	0.11528482	1	1,545	tags=45%, list=12%, signal=51%
VART_KSHV_INFECTION_ANGIOGENIC_MARKERS_DN	123	0.4765337	1.5060401	0.02079395	0.11539513	1	1,339	tags=26%, list=10%, signal=29%
BYSTRYKH_HEMATOPOIESIS_STEM_CELL_QTL_CIS	97	0.39799887	1.5058446	0.011472276	0.11540237	1	1,704	tags=26%, list=13%, signal=29%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GILDEA_METASTASIS	28	0.7135339	1.5053821	0.030947777	0.1156454	1	1,038	tags=39%, list=8%, signal=43%
PID_PDGFRA_PATHWAY	21	0.5461459	1.5031191	0.027944112	0.11741857	1	1,640	tags=33%, list=13%, signal=38%
BIOCARTA_VIP_PATHWAY	25	0.509971	1.5030193	0.04517454	0.11735334	1	915	tags=20%, list=7%, signal=21%
HUANG_FOXA2_TARGETS_DN	36	0.6190245	1.5026233	0.036968578	0.11751704	1	2,021	tags=36%, list=16%, signal=43%
HAHTOLA_SEZARY_SYNDROM_UP	91	0.4972618	1.5014955	0.029296875	0.11816361	1	1,341	tags=26%, list=10%, signal=29%
NIELSEN_GIST	73	0.47683707	1.5009152	0.016917294	0.11856955	1	2,745	tags=37%, list=21%, signal=47%
BOQUEST_STEM_CELL_CULTURED_VS_FRESH_UP	393	0.50475425	1.5008234	0.0056926	0.11852037	1	1,748	tags=33%, list=13%, signal=37%
DARWICHE_PAPILLOMA_RISK_LOW_DN	113	0.35954028	1.4999081	0.011904762	0.11922111	1	2,030	tags=21%, list=16%, signal=25%
BIOCARTA_TNFR2_PATHWAY	18	0.53291494	1.499689	0.044401545	0.11930209	1	2,215	tags=39%, list=17%, signal=47%
REACTOME_GLUCAGON_SIGNALING_IN_METABOLIC_REGULATION	28	0.43826646	1.4996425	0.036363635	0.119183764	1	705	tags=14%, list=5%, signal=15%
HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_DN	61	0.5113886	1.4996167	0.022181146	0.11907047	1	2,083	tags=28%, list=16%, signal=33%
EPPERT_CE_HSC_LSC	38	0.52573615	1.49932	0.014373717	0.119148694	1	1,396	tags=42%, list=11%, signal=47%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
LEE_AGING_MUSCLE_UP	41	0.5012394	1.4992208	0.031657357	0.119108625	1	1,366	tags=20%, list=10%, signal=22%
KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION	61	0.42783338	1.49899	0.03508772	0.11918104	1	2,091	tags=28%, list=16%, signal=33%
ZHANG_TLX_TARGETS_60HR_UP	239	0.42946887	1.4981469	0.013257576	0.1196467	1	2,448	tags=33%, list=19%, signal=40%
AMIT_EGF_RESPONSE_120_HELA	64	0.5341006	1.4965867	0.04597701	0.12054667	1	2,395	tags=42%, list=18%, signal=51%
RODRIGUES_DCC_TARGETS_DN	104	0.42302266	1.4962133	0.017928287	0.12077255	1	1,806	tags=26%, list=14%, signal=30%
WANG_MLL_TARGETS	208	0.45222896	1.4955007	0.003831418	0.12108056	1	1,702	tags=30%, list=13%, signal=34%
GUILLAUMOND_KLF10_TARGETS_UP	42	0.5450009	1.493683	0.016917294	0.12252773	1	1,811	tags=33%, list=14%, signal=39%
VALK_AML_CLUSTER_9	31	0.5985653	1.4933399	0.039923955	0.12267728	1	2,498	tags=52%, list=19%, signal=64%
DOUGLAS_BMI1_TARGETS_DN	216	0.38614985	1.4929339	0.005736138	0.12287897	1	2,286	tags=28%, list=18%, signal=33%
KERLEY_RESPONSE_TO_CISPLATIN_UP	41	0.61589396	1.492705	0.042990655	0.12294611	1	2,433	tags=51%, list=19%, signal=63%
OSADA_ASCL1_TARGETS_DN	22	0.6815529	1.4922976	0.047709923	0.12306874	1	1,388	tags=45%, list=11%, signal=51%
REACTOME_IRON_UPTAKE_AND_TRANSPORT	29	0.54133177	1.4915416	0.04389313	0.12345151	1	2,438	tags=38%, list=19%, signal=47%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
BIOCARTA_BAD_PATHWAY	26	0.48675543	1.4907657	0.049079753	0.123989515	1	968	tags=15%, list=7%,
GREGORY_SYNTHETIC_LETHAL_WITH_IMATINIB	123	0.3706431	1.4906349	0.011764706	0.123948395	1	2,324	signal=17% tags=30%, list=18%,
ZHENG_IL22_SIGNALING_UP	42	0.5852147	1.4905437	0.015904572	0.12387737	1	2,054	signal=36% tags=43%, list=16%,
GRADE_COLON_VS_RECTAL_CANCER_DN	44	0.43593767	1.4903748	0.015065913	0.12387173	1	464	signal=51% tags=11%, list=4%,
PID_ENDOTHELIN_PATHWAY	59	0.43572944	1.4901549	0.044401545	0.12390059	1	884	signal=12% tags=17%, list=7%,
IVANOVA_HEMATOPOIESIS_LATE_PROGENITOR	366	0.37778735	1.4901456	0.017441861	0.123756215	1	1,927	signal=18% tags=24%, list=15%,
TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_NORMAL_DN	53	0.58981645	1.4890672	0.033834588	0.12428359	1	2,249	signal=27% tags=53%, list=17%,
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_9	62	0.5327164	1.4881581	0.036511157	0.124934845	1	1,328	signal=64% tags=29%, list=10%,
LEE_NEURAL_CREST_STEM_CELL_UP	138	0.50025237	1.4871187	0.041984733	0.12561698	1	1,709	signal=32% tags=30%, list=13%,
KAMIKUBO_MYELOID_CEBPA_NETWORK	27	0.63359797	1.4864947	0.039033458	0.12600513	1	1,141	signal=35% tags=37%, list=9%,
WANG_CISPLATIN_RESPONSE_AND_XPC_DN	201	0.37702072	1.4847583	0.009560229	0.127301	1	2,932	signal=41% tags=36%, list=23%,
SYED ESTRADIOL_RESPONSE	18	0.5460066	1.4844708	0.043564357	0.12742084	1	83	signal=46% tags=11%, list=1%, signal=11%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
NAKAMURA_ADIPOGENESIS_EARLY_UP	56	0.53827864	1.4843843	0.046277665	0.12734234	1	1,146	tags=29%, list=9%, signal=31%
GALLUZZI_PERMEABILIZE_MITOCHONDRIA	41	0.4868199	1.4841574	0.042168673	0.12740357	1	2,249	tags=32%, list=17%, signal=38%
KEGG_VEGF_SIGNALING_PATHWAY	68	0.38173437	1.4836711	0.03125	0.12767369	1	780	tags=13%, list=6%, signal=14%
HILLION_HMGA1_TARGETS	86	0.3924324	1.4836423	0.04715128	0.12755008	1	1,067	tags=13%, list=8%, signal=14%
PLASARI_TGFB1_SIGNALING_VIA_NFIC_10HR_DN	25	0.5722927	1.4828714	0.025948104	0.12789266	1	1,476	tags=44%, list=11%, signal=50%
SCHAEFFER_PROSTATE_DEVELOPMENT_12HR_UP	93	0.4997829	1.4825416	0.025540275	0.12804979	1	1,976	tags=33%, list=15%, signal=39%
PEDRIOLI_MIR31_TARGETS_DN	289	0.4058703	1.4820138	0.010968922	0.12835631	1	1,978	tags=30%, list=15%, signal=34%
DELYS_THYROID_CANCER_DN	221	0.5103933	1.4819496	0.021194605	0.12827606	1	1,871	tags=36%, list=14%, signal=41%
BROWNE_HCMV_INFECTION_18HR_DN	162	0.43481958	1.4804163	0.046242774	0.12935798	1	1,924	tags=30%, list=15%, signal=34%
PENG_LEUCINE_DEPRIVATION_UP	129	0.37639153	1.4772727	0.015238095	0.13202244	1	2,006	tags=26%, list=15%, signal=30%
BARIS_THYROID_CANCER_DN	54	0.48703712	1.4769042	0.04789272	0.13219653	1	2,289	tags=35%, list=18%, signal=43%
VALK_AML_WITH_EVII	24	0.55428	1.4758679	0.046468403	0.13287485	1	1,301	tags=29%, list=10%, signal=32%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
DORSEY_GAB2_TARGETS	31	0.63286823	1.4751465	0.035580523	0.13334541	1	1,057	tags=35%, list=8%, signal=39%
GRABARCZYK_BCL11B_TARGETS_DN	44	0.44578886	1.4740517	0.035580523	0.13384402	1	1,217	tags=20%, list=9%, signal=22%
WAMUNYOKOLI_OVARIAN_CANCER_LMP_DN	143	0.5092425	1.473214	0.03875969	0.13449836	1	1,867	tags=34%, list=14%, signal=39%
BHATI_G2M_ARREST_BY_2METHOXYESTRADIOL_DN	91	0.40410712	1.4730129	0.006134969	0.1345325	1	1,983	tags=23%, list=15%, signal=27%
HU_ANGIOGENESIS_UP	20	0.5977447	1.4717542	0.04054054	0.13538872	1	2,911	tags=55%, list=22%, signal=71%
BIOCARTA_LAIR_PATHWAY	16	0.7081902	1.4716896	0.049603175	0.13529558	1	1,906	tags=63%, list=15%, signal=73%
BOYLAN_MULTIPLE_MYELOMA_D_UP	60	0.4677594	1.4706668	0.011299435	0.13605924	1	1,807	tags=32%, list=14%, signal=37%
WATANABE_RECTAL_CANCER_RADIOOTHERAPY_RESPONSIVE_DN	86	0.5195596	1.4705552	0.046421662	0.13600725	1	1,591	tags=33%, list=12%, signal=37%
FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_DN	48	0.37637144	1.4704726	0.0498008	0.13577797	1	3,284	tags=40%, list=25%, signal=53%
REACTOME_G_ALPHA_Z_SIGNALLING_EVENTS	38	0.40719232	1.4702573	0.031311154	0.13582143	1	1,035	tags=18%, list=8%, signal=20%
DANG_REGULATED_BY_MYC_DN	236	0.46828985	1.4666976	0.027985075	0.13876855	1	1,812	tags=32%, list=14%, signal=37%
MULLIGHAN_NPM1_SIGNATURE_3_DN	148	0.36950818	1.4656197	0.022857143	0.13959134	1	2,397	tags=24%, list=18%, signal=29%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
VALK_AML_CLUSTER_10	32	0.5313338	1.4650542	0.04868914	0.13998815	1	1,297	tags=22%, list=10%, signal=24%
PLASARI_TGFB1_TARGETS_10HR_DN	192	0.4538672	1.4644083	0.017821781	0.1401422	1	1,230	tags=24%, list=9%, signal=26%
REACTOME_G_ALPHA_Q_SIGNALLING_EVENTS	142	0.34453836	1.4631246	0.02970297	0.14122428	1	1,109	tags=13%, list=9%, signal=14%
ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_UP	184	0.4448713	1.4627508	0.045889102	0.1414151	1	1,755	tags=26%, list=13%, signal=30%
BURTON_ADIPOGENESIS_9	78	0.5643645	1.461515	0.03119266	0.14214231	1	918	tags=28%, list=7%, signal=30%
FIGUEROA_AML_METHYLATION_CLUSTER_4_UP	76	0.39488727	1.4579061	0.020992367	0.14488736	1	2,114	tags=26%, list=16%, signal=31%
DARWICHE_PAPILLOMA_RISK_HIGH_DN	126	0.33530518	1.4572877	0.015209125	0.14504918	1	2,030	tags=22%, list=16%, signal=26%
ST_ERK1_ERK2_MAPK_PATHWAY	30	0.46613416	1.4554799	0.046277665	0.14635064	1	2,097	tags=37%, list=16%, signal=44%
VALK_AML_CLUSTER_13	28	0.5125003	1.4509742	0.038229376	0.14997321	1	619	tags=18%, list=5%, signal=19%
GROSS_HYPOXIA_VIA_ELK3_AND_HIF1A_UP	115	0.46832874	1.4465508	0.040618956	0.1538002	1	2,103	tags=37%, list=16%, signal=44%
JI_RESPONSE_TO_FSH_UP	68	0.4608245	1.4437954	0.032323234	0.1559807	1	865	tags=22%, list=7%, signal=24%
KIM_MYC_AMPLIFICATION_TARGETS_UP	150	0.38151455	1.4422119	0.01934236	0.15712129	1	2,170	tags=24%, list=17%, signal=28%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
LABBE_TARGETS_OF_TGFB1_AND_WNT3A_UP	99	0.4303481	1.4421691	0.022900764	0.15699908	1	1,018	tags=18%, list=8%, signal=20%
PID_CMYB_PATHWAY	77	0.3945357	1.4388443	0.015873017	0.15975183	1	1,777	tags=26%, list=14%, signal=30%
SHAFFER_IRF4_TARGETS_IN_MYELOMA_VS_MATURE_B_LYMPHOCYTE	97	0.4052338	1.4348716	0.038610037	0.16265757	1	1,509	tags=24%, list=12%, signal=27%
DELPUECH_FOXO3_TARGETS_UP	66	0.5221545	1.4346229	0.045454547	0.16278343	1	1,738	tags=35%, list=13%, signal=40%
SHEPARD_BMYB_MORPHOLINO_UP	158	0.35851297	1.4328942	0.011650485	0.16405897	1	1,643	tags=21%, list=13%, signal=24%
NING_CHRONIC_OBSTRUCTIVE_PULMONARY_DISEASE_UP	137	0.4107554	1.432851	0.04681648	0.16394696	1	1,637	tags=22%, list=13%, signal=25%
BOYLAN_MULTIPLE_MYELOMA_PCA3_UP	56	0.48515564	1.431819	0.025390625	0.16429238	1	943	tags=23%, list=7%, signal=25%
MIKKELSEN_ES_LCP_WITH_H3K4ME3	78	0.43651253	1.4311271	0.044487428	0.16470604	1	2,242	tags=36%, list=17%, signal=43%
JECHLINGER_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_DN	62	0.5405841	1.4308509	0.04990403	0.16485423	1	2,435	tags=52%, list=19%, signal=63%
KANG_IMMORTALIZED_BY_TERT_DN	101	0.45536047	1.4306453	0.034068137	0.16490084	1	1,638	tags=28%, list=13%, signal=31%
WESTON_VEGFA_TARGETS	100	0.527144	1.4266479	0.04797048	0.16806744	1	1,812	tags=38%, list=14%, signal=44%
RUIZ_TNC_TARGETS_UP	143	0.4828883	1.4237156	0.033834588	0.16979091	1	1,637	tags=31%, list=13%, signal=35%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
JOHNSTONE_PARVB_TARGETS_3_UP	338	0.41171038	1.4234331	0.03787879	0.16974267	1	1,395	tags=20%, list=11%, signal=21%
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_12	69	0.41451156	1.422417	0.037328094	0.17030874	1	1,729	tags=22%, list=13%, signal=25%
PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_4	78	0.4735653	1.421268	0.02745098	0.17123756	1	1,650	tags=27%, list=13%, signal=31%
HAN_JNK_SINGALING_DN	32	0.6008008	1.4209716	0.046468403	0.17137697	1	1,300	tags=41%, list=10%, signal=45%
ENK_UV_RESPONSE_EPIDERMIS_DN	479	0.38922223	1.4182391	0.013257576	0.17358384	1	1,968	tags=27%, list=15%, signal=31%
KIM_TIAL1_TARGETS	29	0.49503475	1.417346	0.047817048	0.17439745	1	1,371	tags=24%, list=11%, signal=27%
REACTOME_GASTRIN_CREB_SIGNALLING_PATHWAY_VIA_PKC_AND_MAPK	162	0.32196754	1.4168117	0.041420117	0.17482384	1	2,136	tags=20%, list=16%, signal=23%
LINDGREN_BLADDER_CANCER_CLUSTER_3_DN	178	0.39105526	1.4153258	0.034136545	0.176071	1	2,163	tags=25%, list=17%, signal=29%
KYNG_WERNER_SYNDROM_AND_NORMAL_AGING_DN	184	0.3284936	1.4145347	0.009615385	0.17672874	1	876	tags=11%, list=7%, signal=12%
ROPERO_HDAC2_TARGETS	101	0.3481622	1.4132788	0.04527559	0.1780114	1	2,355	tags=24%, list=18%, signal=29%
ZWANG_CLASS_1_TRANSIENTLY_INDUCED_BY_EGF	344	0.37637767	1.4107168	0.039848197	0.17952591	1	2,165	tags=27%, list=17%, signal=32%
BROWNE_HCMV_INFECTION_48HR_DN	459	0.34689012	1.4053817	0.015503876	0.1840157	1	1,758	tags=19%, list=13%, signal=21%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
WINZEN_DEGRADED_VIA_KHSRP	86	0.5232226	1.4050013	0.03929273	0.18423022	1	1,468	tags=31%, list=11%, signal=35%
SAMOLS_TARGETS_OF_KHSV_MIRNAS_DN	50	0.5161026	1.3990104	0.04	0.19011717	1	2,028	tags=32%, list=16%, signal=38%
PURBEY_TARGETS_OF_CTBPI_NOT_SATBI_DN	359	0.31170243	1.3974525	0.002070393	0.19125193	1	2,004	tags=21%, list=15%, signal=24%
YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_2	67	0.39689782	1.395296	0.036893204	0.19160834	1	1,848	tags=22%, list=14%, signal=26%
COATES_MACROPHAGE_M1_VS_M2_DN	54	0.4690434	1.3905205	0.048169557	0.19489697	1	131	tags=9%, list=1%, signal=9%
FIRESTEIN_PROLIFERATION	135	0.3054892	1.390459	0.022267206	0.19477326	1	1,831	tags=20%, list=14%, signal=23%
MONNIER_POSTRADIATION_TUMOR_ESCAPE_DN	243	0.36905575	1.3854549	0.02739726	0.19854178	1	1,821	tags=25%, list=14%, signal=28%
SCHAEFFER_PROSTATE_DEVELOPMENT_48HR_DN	294	0.37729502	1.3823403	0.049335863	0.20134641	1	1,940	tags=22%, list=15%, signal=25%
SENESE_HDAC1_AND_HDAC2_TARGETS_UP	181	0.39959285	1.3801848	0.04863813	0.2031785	1	2,144	tags=30%, list=16%, signal=35%
HUTTMANN_B_CLL_POOR_SURVIVAL_UP	250	0.37101266	1.3778374	0.042471044	0.2050489	1	1,370	tags=17%, list=11%, signal=19%
ZHOU_INFLAMMATORY_RESPONSE_FIMA_DN	168	0.31612828	1.3762621	0.016632017	0.20635581	1	1,848	tags=21%, list=14%, signal=25%
YAGI_AML_WITH_INV_16_TRANSLOCATION	385	0.28121084	1.3754027	0.017374517	0.20684537	1	1,387	tags=14%, list=11%, signal=15%

Table SII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
KOYAMA_SEMA3B_TARGETS_UP	204	0.38284165	1.3736221	0.037453182	0.20842563	1	1,398	tags=19%, list=11%, signal=21%
KYNG_DNA_DAMAGE_BY_4NQO	37	0.47545567	1.3710425	0.03875969	0.21067968	1	2,391	tags=41%, list=18%, signal=50%
BRUINS_UVC_RESPONSE_VIA_TP53_GROUP_D	199	0.3231931	1.370087	0.007874016	0.21162772	1	1,301	tags=13%, list=10%, signal=14%
BROWNE_HCMV_INFECTION_4HR_DN	228	0.28793198	1.3576678	0.015904572	0.21982193	1	2,105	tags=19%, list=16%, signal=23%
ALFANO_MYC_TARGETS	216	0.36945048	1.3546107	0.0415879	0.22242124	1	2,017	tags=25%, list=15%, signal=29%
KUMAR_PATHOGEN_LOAD_BY_MACROPHAGES	154	0.30049476	1.3491969	0.017892644	0.22616953	1	2,303	tags=23%, list=18%, signal=28%
MOOTHA_PGC	397	0.33743763	1.3472906	0.049056605	0.22748534	1	2,661	tags=28%, list=20%, signal=34%
YAGI_AML_FAB_MARKERS	177	0.38418537	1.3446417	0.04780115	0.22985311	1	1,106	tags=18%, list=8%, signal=19%
MIKKELSEN_NPC_ICP_WITH_H3K4ME3	290	0.3195419	1.332369	0.017274473	0.24007116	1	2,365	tags=26%, list=18%, signal=31%
HELLER_HDAC_TARGETS_SILENCED_BY_METHYLATION_UP	417	0.37581608	1.3278017	0.027944112	0.24418488	1	1,250	tags=18%, list=10%, signal=19%

ES, enrichment score; FDR q-val, false discovery rate q-value; FWER p-val, familywise-error rate P-value; NES, normalized enrichment score; NOM p-val, nominal P-value.

Table SIII. Gene set enrichment analysis results of c5-reference gene sets for groups with high cystatin 7 expression.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_FC_RECEPTOR_SIGNALING_PATHWAY	172	0.56581265	2.2980094	<0.0001	3.53x10 ⁻⁴	0.001	1,067	tags=20%, list=8%, signal=21%
GO_FC_EPSILON_RECEPTOR_SIGNALING_PATHWAY	117	0.5498332	2.2428753	<0.0001	0.001277946	0.005	1,067	tags=17%, list=8%, signal=18%
GO_REGULATION_OF_CALCINIUM_MEDIATED_SIGNALING	64	0.6994756	2.2110283	<0.0001	0.003115448	0.01	1,461	tags=38%, list=11%, signal=42%
GO_LEUKOCYTE_DIFFERENTIATION	256	0.58493257	2.2095234	<0.0001	0.002670384	0.01	1,702	tags=31%, list=13%, signal=35%
GO_THYMOCYTE_AGGREGATION	41	0.6770469	2.206718	<0.0001	0.002336586	0.01	622	tags=27%, list=5%, signal=28%
GO_FC_GAMMA_RECEPTOR_SIGNALING_PATHWAY	70	0.6633983	2.2013485	<0.0001	0.002451154	0.012	639	tags=27%, list=5%, signal=28%
GO_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	59	0.6961177	2.1987367	<0.0001	0.002347331	0.012	1,702	tags=47%, list=13%, signal=54%
GO_ACTIVATION_OF_IMMUNE_RESPONSE	344	0.65827435	2.193581	<0.0001	0.002574659	0.014	1,750	tags=40%, list=13%, signal=45%
GO_SIDE_OF_MEMBRANE	348	0.6105121	2.1927373	<0.0001	0.002360104	0.014	1,157	tags=29%, list=9%, signal=31%
GO_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	107	0.6341802	2.1851163	<0.0001	0.00235914	0.015	1,110	tags=31%, list=9%, signal=33%
GO_T_CELL_DIFFERENTIATION	109	0.6744169	2.1815274	<0.0001	0.00219063	0.015	1,702	tags=39%, list=13%, signal=44%
GO_POSITIVE_REGULATION_OF_IMMUNE_RESPONSE	454	0.6309283	2.1792326	<0.0001	0.002141474	0.016	1,812	tags=38%, list=14%, signal=42%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_ADAPTIVE_IMMUNE_RESPONSE	213	0.7007977	2.1779242	<0.0001	0.002007632	0.016	1,762	tags=49%, list=14%, signal=56%
GO_LYMPHOCYTE_DIFFERENTIATION	184	0.58563673	2.177086	<0.0001	0.001889536	0.016	1,702	tags=31%, list=13%, signal=35%
GO_REGULATION_OF_HOMOTYPIC_CELL_CELL_ADHESION	253	0.6653556	2.175576	<0.0001	0.001867254	0.017	1,134	tags=33%, list=9%, signal=36%
GO_LEUKOCYTE_ACTIVATION	355	0.61491066	2.175465	<0.0001	0.001768978	0.017	1,777	tags=36%, list=14%, signal=41%
GO_LYMPHOCYTE_ACTIVATION	294	0.60230273	2.1661541	<0.0001	0.001752678	0.017	1,803	tags=36%, list=14%, signal=41%
GO_REGULATION_OF_CELL_ACTIVATION	384	0.6317943	2.1647186	<0.0001	0.001669218	0.017	1,134	tags=30%, list=9%, signal=32%
GO_REGULATION_OF_INNATE_IMMUNE_RESPONSE	298	0.56654346	2.1598532	<0.0001	0.001863707	0.018	1,914	tags=34%, list=15%, signal=39%
GO_LEUKOCYTE_CELL_CELL_ADHESION	226	0.64131075	2.1586907	<0.0001	0.001846815	0.019	1,713	tags=37%, list=13%, signal=42%
GO_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	189	0.608194	2.1563818	<0.0001	0.001816563	0.019	1,702	tags=34%, list=13%, signal=38%
GO_REGULATION_OF_LEUKOCYTE_PROLIFERATION	173	0.6635326	2.1518457	<0.0001	0.001867595	0.02	1,275	tags=35%, list=10%, signal=39%
GO_PROTEIN_KINASE_C_SIGNALING	16	0.7912366	2.1515355	<0.0001	0.001795764	0.02	168	tags=19%, list=1%, signal=19%
GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	69	0.70109475	2.1420588	<0.0001	0.002006884	0.022	992	tags=41%, list=8%, signal=44%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	136	0.60451424	2.139998	<0.0001	0.00197286	0.023	1,803	tags=37%, list=14%,
GO_CELL_ACTIVATION	490	0.5802118	2.1348493	<0.0001	0.002298772	0.029	1,777	signal=42% tags=33%, list=14%,
GO_IMMUNE_SYSTEM_DEVELOPMENT	479	0.5004895	2.1303637	<0.0001	0.002356711	0.03	1,392	signal=37% tags=22%, list=11%,
GO_CYTOKINE_MEDIATED_SIGNALING_PATHWAY	393	0.64146954	2.126149	<0.0001	0.002373424	0.031	1,342	signal=24% tags=30%, list=10%,
GO_REGULATION_OF_CELL_KILLING	54	0.7072368	2.1227002	<0.0001	0.002530623	0.034	904	signal=32% tags=33%, list=7%,
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_ANTIGEN	155	0.63728356	2.1225007	<0.0001	0.002453937	0.034	1,124	signal=36% tags=28%, list=9%,
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I	85	0.6512454	2.1214302	0.001988072	0.002419163	0.035	1,124	signal=30% tags=31%, list=9%,
GO_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	186	0.52763015	2.120269	<0.0001	0.002404766	0.036	1,997	signal=33% tags=33%, list=15%,
GO_DENDRITIC_CELL_DIFFERENTIATION	30	0.7795703	2.1167967	<0.0001	0.002469846	0.037	1,275	signal=39% tags=53%, list=10%,
GO_NEGATIVE_REGULATION_OF_HOMEOSTATIC_PROCESS	110	0.6017659	2.116316	<0.0001	0.002403094	0.037	1,275	signal=59% tags=29%, list=10%,
GO_POSITIVE_REGULATION_OF_CELL_ACTIVATION	251	0.67941827	2.113673	<0.0001	0.002469152	0.038	1,029	signal=32% tags=34%, list=8%, signal=36%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	111	0.6535658	2.113188	<0.0001	0.002441054	0.039	1,363	tags=36%, list=10%, signal=40%
GO_IMMUNE_EFFECTOR_PROCESS	380	0.6538271	2.1124148	<0.0001	0.002406435	0.039	1,362	tags=34%, list=10%, signal=37%
GO_REGULATION_OF_T_CELL_PROLIFERATION	123	0.6805994	2.1090238	<0.0001	0.00257945	0.043	1,275	tags=38%, list=10%, signal=42%
GO_REGULATION_OF_CELL_CELL_ADHESION	313	0.6155728	2.1088266	<0.0001	0.002518035	0.043	1,134	tags=29%, list=9%, signal=31%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_PROLIFERATION	114	0.67064583	2.1066945	<0.0001	0.002459476	0.043	1,246	tags=33%, list=10%, signal=37%
GO_REGULATION_OF_INTERLEUKIN_4_PRODUCTION	25	0.7373535	2.0997336	<0.0001	0.002738173	0.049	2,129	tags=60%, list=16%, signal=72%
GO_CELLULAR_DEFENSE_RESPONSE	55	0.76385665	2.0981932	<0.0001	0.002835134	0.051	857	tags=38%, list=7%, signal=41%
GO_NEGATIVE_REGULATION_OF_CELL_ACTIVATION	127	0.6052236	2.0969899	<0.0001	0.002831596	0.053	1,738	tags=36%, list=13%, signal=41%
GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	45	0.7186255	2.094623	<0.0001	0.002943629	0.056	1,214	tags=44%, list=9%, signal=49%
GO_RESPONSE_TO_VIRUS	206	0.6566426	2.0926623	<0.0001	0.002951641	0.056	1,333	tags=31%, list=10%, signal=34%
GO_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	114	0.60895663	2.090784	<0.0001	0.002919709	0.057	1,702	tags=36%, list=13%, signal=41%
GO_LEUKOCYTE_MIGRATION	234	0.65834934	2.0894344	<0.0001	0.002886386	0.058	998	tags=30%, list=8%, signal=32%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_INNATE_IMMUNE_RESPONSE	466	0.6559909	2.0886405	<0.0001	0.002874115	0.06	1,713	tags=39%, list=13%, signal=43%
GO_EXTERNAL_SIDE_OF_PLASMA_MEMBRANE	188	0.6601501	2.084015	<0.0001	0.0030667	0.064	1,157	tags=34%, list=9%, signal=36%
GO_REGULATION_OF_T_CELL_DIFFERENTIATION	87	0.62129647	2.0832417	<0.0001	0.003040185	0.065	1,702	tags=34%, list=13%, signal=39%
GO_POSITIVE_REGULATION_OF_CELL_CELL_ADHESION	209	0.66727906	2.0823765	<0.0001	0.003005463	0.066	1,124	tags=34%, list=9%, signal=37%
GO_REGULATION_OF_HEMOPOIESIS	249	0.5510617	2.0789227	<0.0001	0.003012559	0.069	1,702	tags=29%, list=13%, signal=33%
GO_ANTIGEN_PROCESSING_AND_PRESENTATION	183	0.61086196	2.0758998	<0.0001	0.003098615	0.073	1,124	tags=25%, list=9%, signal=27%
GO_T_CELL_SELECTION	32	0.7826215	2.0752883	<0.0001	0.003122906	0.074	613	tags=41%, list=5%, signal=43%
GO_POSITIVE_REGULATION_OF_DEFENSE_RESPONSE	306	0.58536804	2.0747094	<0.0001	0.003129821	0.076	1,673	tags=33%, list=13%, signal=37%
GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_VIRUS	26	0.7401749	2.0717707	<0.0001	0.00322024	0.078	1,124	tags=42%, list=9%, signal=46%
GO_MYELOID_CELL_DIFFERENTIATION	161	0.5108317	2.071705	<0.0001	0.00316657	0.078	1,511	tags=25%, list=12%, signal=28%
GO_TUMOR_NECROSIS_FACTOR_MEDIATED_SIGNALING_PATHWAY	105	0.5574837	2.0716078	<0.0001	0.003114659	0.078	1,830	tags=27%, list=14%, signal=31%
GO_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	50	0.6653229	2.0683548	<0.0001	0.00322822	0.083	904	tags=30%, list=7%, signal=32%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_PHAGOCYTOSIS	148	0.6212763	2.0680087	<0.0001	0.003176978	0.083	998	tags=28%, list=8%, signal=30%
GO_POSITIVE_REGULATION_OF_HEMOPOIESIS	135	0.60470515	2.067895	<0.0001	0.003127338	0.083	1,363	tags=31%, list=10%, signal=34%
GO_REGULATION_OF_NATURAL_KILLER_CELL_ACTIVATION	20	0.74367446	2.065299	<0.0001	0.003181496	0.085	851	tags=40%, list=7%, signal=43%
GO_REGULATION_OF_HOMEOSTATIC_PROCESS	364	0.48957655	2.0609856	<0.0001	0.003376457	0.092	1,280	tags=21%, list=10%, signal=23%
GO_REGULATION_OF_SEQUESTERING_OF_CALCIIUM_ION	93	0.6495815	2.0598795	<0.0001	0.003387403	0.095	1,275	tags=27%, list=10%, signal=30%
GO_NEGATIVE_REGULATION_OF_IMMUNE_RESPONSE	105	0.6234489	2.0597687	<0.0001	0.003337589	0.095	1,313	tags=30%, list=10%, signal=34%
GO_POSITIVE_REGULATION_OF_INNATE_IMMUNE_RESPONSE	206	0.58305866	2.057353	<0.0001	0.003430647	0.098	1,786	tags=34%, list=14%, signal=39%
GO_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION	311	0.56307393	2.0569003	<0.0001	0.003381638	0.098	1,702	tags=32%, list=13%, signal=36%
GO_ACTIVATION_OF_INNATE_IMMUNE_RESPONSE	173	0.5805074	2.056477	<0.0001	0.003361201	0.099	1,786	tags=34%, list=14%, signal=39%
GO_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	99	0.5733579	2.0564165	<0.0001	0.003314518	0.099	1,124	tags=25%, list=9%, signal=27%
GO_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	29	0.7639744	2.0557768	<0.0001	0.003269114	0.099	1,124	tags=48%, list=9%, signal=53%
GO_NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	302	0.56666094	2.0551813	<0.0001	0.00324111	0.1	1,738	tags=31%, list=13%, signal=35%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	350	0.53809416	2.0549061	<0.0001	0.003197895	0.1	1,930	tags=33%, list=15%, signal=37%
GO_REGULATION_OF_TYPE_I_INTERFERON_PRODUCTION	91	0.56637156	2.0536106	<0.0001	0.003214347	0.102	1,764	tags=34%, list=14%, signal=39%
GO_POSITIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	135	0.58310795	2.053024	<0.0001	0.003191717	0.103	1,803	tags=38%, list=14%, signal=43%
GO_LEUKOCYTE_CHEMOTAXIS	104	0.73886037	2.0509038	<0.0001	0.003217871	0.104	992	tags=38%, list=8%, signal=40%
GO_POSITIVE_REGULATION_OF_CALCIIUM_MEDIATED_SIGNALING	35	0.7207691	2.050604	<0.0001	0.003177138	0.104	1,426	tags=43%, list=11%, signal=48%
GO_MYELOID_LEUKOCYTE_ACTIVATION	84	0.685148	2.050072	<0.0001	0.003178608	0.105	1,333	tags=39%, list=10%, signal=43%
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	43	0.712102	2.0482202	<0.0001	0.003246121	0.107	858	tags=37%, list=7%, signal=40%
GO_REGULATION_OF_ION_HOMEOSTASIS	175	0.5516555	2.0473838	<0.0001	0.00321841	0.107	1,280	tags=23%, list=10%, signal=26%
GO_NEGATIVE_REGULATION_OF_TYPE_I_INTERFERON_PRODUCTION	31	0.69180894	2.0472035	<0.0001	0.003179634	0.107	1,750	tags=39%, list=13%, signal=45%
GO_CALCIIUM_ION_TRANSPORT	170	0.51520944	2.0469112	<0.0001	0.003163648	0.108	1,312	tags=20%, list=10%, signal=22%
GO_ANTIGEN_PROCESSING_AND_PRESENTATION _OF_EXOGENOUS_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I	63	0.6842062	2.0434687	<0.0001	0.003314278	0.118	1,431	tags=37%, list=11%, signal=41%
GO_POSITIVE_REGULATION_OF_CELL_ADHESION	323	0.60099137	2.0428643	<0.0001	0.003303619	0.118	1,275	tags=29%, list=10%, signal=31%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_REGULATION_OF_INFLAMMATORY_RESPONSE_TO_ANTIGENIC_STIMULUS	15	0.7537894	2.0428543	<0.0001	0.003265646	0.118	572	tags=20%, list=4%,
GO_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	75	0.6791391	2.0408008	<0.0001	0.003360445	0.122	1,702	signal=21% tags=47%, list=13%,
GO_REGULATION_OF_INTERLEUKIN_2_BIOSYNTHETIC_PROCESS	15	0.790258	2.0405688	<0.0001	0.003322687	0.122	1,698	signal=53% tags=53%, list=13%,
GO_LYMPHOCYTE_COSTIMULATION	64	0.7722536	2.0385737	<0.0001	0.003394613	0.122	690	signal=61% tags=41%, list=5%,
GO_REGULATION_OF_B_CELL_ACTIVATION	88	0.6326809	2.036255	<0.0001	0.003474437	0.127	927	signal=43% tags=27%, list=7%,
GO_REGULATION_OF_CYTOKINE_PRODUCTION	466	0.5426902	2.0356293	<0.0001	0.00346255	0.129	1,764	signal=29% tags=32%, list=14%,
GO_REGULATION_OF_CAMP_MEDIATED_SIGNALING	22	0.7442944	2.0329158	<0.0001	0.003547981	0.135	528	signal=36% tags=18%, list=4%,
GO_ENDOCYTIC_VESICLE_MEMBRANE	126	0.61860746	2.032176	<0.0001	0.003536082	0.137	1,176	signal=19% tags=29%, list=9%,
GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_ACTIVATION	15	0.8219168	2.0293486	<0.0001	0.003665178	0.142	851	signal=32% tags=53%, list=7%,
GO_DEFENSE_RESPONSE_TO_VIRUS	131	0.6955836	2.0284607	<0.0001	0.003672626	0.145	1,333	signal=57% tags=37%, list=10%,
GO_RESPONSE_TO_TUMOR_NECROSIS_FACTOR	203	0.5545329	2.0258026	<0.0001	0.003757323	0.148	1,830	signal=41% tags=29%, list=14%,
GO_CELLULAR_RESPONSE_TO_BIOTIC_STIMULUS	143	0.5961847	2.0254965	<0.0001	0.003745029	0.149	1,689	signal=33% tags=36%, list=13%, signal=41%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATION	39	0.6703684	2.024547	<0.0001	0.003757533	0.15	1,702	tags=41%, list=13%, signal=47%
GO_MYELOID_DENDRITIC_CELL_ACTIVATION	22	0.7714285	2.0243144	<0.0001	0.003719958	0.15	1,275	tags=55%, list=10%, signal=60%
GO_REGULATION_OF_LEUKOCYTE_MEDIATED_CYTOTOXICITY	44	0.735336	2.0220778	<0.0001	0.003956082	0.158	851	tags=36%, list=7%, signal=39%
GO_ALPHA_BETA_T_CELL_ACTIVATION	47	0.68558294	2.0220628	<0.0001	0.003917297	0.158	1,702	tags=49%, list=13%, signal=56%
GO_ANTIGEN_BINDING	77	0.75801176	2.0207741	<0.0001	0.003910181	0.161	943	tags=44%, list=7%, signal=47%
GO_MHC_PROTEIN_BINDING	24	0.8447889	2.014059	<0.0001	0.004268575	0.178	1,055	tags=63%, list=8%, signal=68%
GO_NEGATIVE_REGULATION_OF_MULTI_ORGANISM_PROCESS	123	0.6230714	2.0136077	<0.0001	0.004242058	0.178	1,678	tags=36%, list=13%, signal=41%
GO_MYELOID_CELL_HOMEOSTASIS	79	0.5286014	2.0127528	<0.0001	0.004249324	0.179	1,511	tags=25%, list=12%, signal=28%
GO_ALPHA_BETA_T_CELL_DIFFERENTIATION	39	0.68796676	2.0110776	<0.0001	0.004316183	0.183	1,702	tags=49%, list=13%, signal=56%
GO_REGULATION_OF_B_CELL_PROLIFERATION	44	0.6610926	2.0093403	<0.0001	0.00445442	0.186	927	tags=25%, list=7%, signal=27%
GO_INNATE_IMMUNE_RESPONSE_ACTIVATING_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY	95	0.5316563	2.0079582	0.004106776	0.004508586	0.191	1,431	tags=21%, list=11%, signal=23%
GO_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	89	0.5861538	2.0073059	<0.0001	0.004492685	0.193	1,511	tags=29%, list=12%, signal=33%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_POSITIVE_REGULATION_OF_T_CELL_PROLIFERATION	81	0.7039921	2.0066168	<0.0001	0.00450136	0.195	1,246	tags=41%, list=10%, signal=45%
GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	17	0.80573094	2.0065787	<0.0001	0.004471442	0.196	851	tags=47%, list=7%, signal=50%
GO_RESPONSE_TO_INTERFERON_GAMMA	125	0.7517855	2.0048778	<0.0001	0.004554186	0.202	1,484	tags=49%, list=11%, signal=55%
GO_REGULATION_OF_TRANSCRIPTION_FACTOR_IMPORT_INTO_NUCLEUS	83	0.57199776	2.0036812	<0.0001	0.004580345	0.205	1,870	tags=33%, list=14%, signal=38%
GO_POSITIVE_REGULATION_OF_CELL_KILLING	33	0.693003	2.0033884	<0.0001	0.004549389	0.205	1,124	tags=39%, list=9%, signal=43%
GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS	147	0.48893782	2.002949	<0.0001	0.004522624	0.206	1,997	tags=30%, list=15%, signal=35%
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_EXTERNAL_STIMULUS	259	0.5953112	2.0025218	<0.0001	0.004500198	0.206	1,652	tags=31%, list=13%, signal=34%
GO_CALCIIUM_ION_TRANSMEMBRANE_TRANSPORT	120	0.48057497	2.001931	<0.0001	0.00449819	0.208	1,312	tags=18%, list=10%, signal=20%
GO_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	107	0.5603616	1.9991853	<0.0001	0.004701268	0.217	1,803	tags=33%, list=14%, signal=38%
GO_CELL_CHEMOTAXIS	144	0.70795596	1.9988527	<0.0001	0.00466209	0.217	992	tags=35%, list=8%, signal=37%
GO_POSITIVE_REGULATION_OF_B_CELL_ACTIVATION	59	0.6405143	1.99758	<0.0001	0.004708874	0.223	904	tags=27%, list=7%, signal=29%
GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATION	32	0.7098949	1.996988	<0.0001	0.004704415	0.224	904	tags=38%, list=7%, signal=40%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_MULTI_ORGANISM_MEMBRANE_ORGANIZATION	21	0.7096719	1.9960191	<0.0001	0.004699792	0.226	1,429	tags=33%, list=11%, signal=37%
GO_POSITIVE_REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_SIGNALING	150	0.5933491	1.9951591	<0.0001	0.004712347	0.229	1,922	tags=37%, list=15%, signal=43%
GO_REGULATION_OF_MULTI_ORGANISM_PROCESS	381	0.4824367	1.9947453	<0.0001	0.004689132	0.229	1,706	tags=27%, list=13%, signal=30%
GO_THYMIC_T_CELL_SELECTION	18	0.84024805	1.9946179	<0.0001	0.004689027	0.233	609	tags=44%, list=5%, signal=47%
GO_POSITIVE_REGULATION_OF_B_CELL_PROLIFERATION	28	0.70278573	1.9945697	<0.0001	0.004661672	0.233	338	tags=18%, list=3%, signal=18%
GO_REGULATION_OF_LEUKOCYTE_APOPTOTIC_PROCESS	63	0.7015334	1.992951	<0.0001	0.004721851	0.239	1,240	tags=38%, list=10%, signal=42%
GO_MHC_CLASS_I_PROTEIN_BINDING	17	0.8388978	1.9917265	<0.0001	0.004828132	0.245	795	tags=53%, list=6%, signal=56%
GO_NEGATIVE_REGULATION_OF_HOMOTYPIC_CELL_CELL_ADHESION	78	0.58847654	1.9913096	<0.0001	0.00481837	0.246	2,148	tags=38%, list=16%, signal=46%
GO_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION	166	0.53953606	1.9905859	<0.0001	0.004817037	0.247	1,750	tags=33%, list=13%, signal=37%
GO_CELLULAR_RESPONSE_TO_INTERFERON_GAMMA	108	0.7624107	1.9879847	<0.0001	0.004925966	0.254	1,124	tags=46%, list=9%, signal=50%
GO_REGULATION_OF_INTERLEUKIN_12_PRODUCTION	45	0.6495759	1.9876931	<0.0001	0.004914526	0.254	1,311	tags=38%, list=10%, signal=42%
GO_REGULATION_OF_INTERLEUKIN_2_PRODUCTION	38	0.6687488	1.9839149	<0.0001	0.005215059	0.268	1,702	tags=47%, list=13%, signal=54%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_ER_TO_GOLGI_TRANSPORT_VESICLE_MEMBRANE	47	0.7062944	1.982555	0.00204918	0.005264888	0.273	1,124	tags=34%, list=9%, signal=37%
GO_DEFENSE_RESPONSE_TO_OTHER_ORGANISM	359	0.55629706	1.9812028	<0.0001	0.005324303	0.278	1,333	tags=26%, list=10%, signal=29%
GO_CELLULAR_RESPONSE_TO_INTERLEUKIN_1	78	0.65022373	1.980406	<0.0001	0.005298601	0.278	788	tags=23%, list=6%, signal=24%
GO_SINGLE_ORGANISM_CELL_ADHESION	393	0.5283219	1.978686	<0.0001	0.005363714	0.281	1,812	tags=30%, list=14%, signal=34%
GO_RESPONSE_TO_INTERLEUKIN_1	103	0.62285995	1.9783677	<0.0001	0.005355664	0.282	788	tags=21%, list=6%, signal=23%
GO_REGULATION_OF_B_CELL_DIFFERENTIATION	18	0.7445963	1.9777734	<0.0001	0.005382205	0.282	897	tags=44%, list=7%, signal=48%
GO_POSITIVE_REGULATION_OF_CYTOKINE_SECRETION	82	0.66207844	1.9775655	<0.0001	0.005376583	0.284	1,313	tags=37%, list=10%, signal=40%
GO_ENDOCYTOSIS	404	0.5201574	1.9767257	<0.0001	0.005383869	0.285	1,735	tags=28%, list=13%, signal=32%
GO_PEPTIDYL_TYROSINE_AUTOPHOSPHORYLATION	38	0.614008	1.9753113	<0.0001	0.005488152	0.291	947	list=7%, signal=34%
GO_B_CELL_PROLIFERATION	35	0.5795052	1.9751853	0.001945525	0.005469509	0.291	1,322	tags=26%, list=10%, signal=29%
GO_CALCIIUM_IION_IMPORT_INTO_CYTOSOL	41	0.6842881	1.9745598	<0.0001	0.005512497	0.298	1,155	tags=32%, list=9%, signal=35%
GO_B_CELL_RECEPTOR_SIGNALING_PATHWAY	34	0.8153505	1.9714403	<0.0001	0.00574521	0.309	897	list=7%, signal=57%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_NATURAL_KILLER_CELL_ACTIVATION	45	0.6797517	1.9714079	<0.0001	0.005706127	0.309	1,305	tags=33%, list=10%, signal=37%
GO_PLATELET_ACTIVATION	129	0.57979304	1.9706175	<0.0001	0.005720825	0.31	1,014	tags=27%, list=8%, signal=29%
GO_REGULATION_OF_TUMOR_NECROSIS _FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION	90	0.66194624	1.9704756	<0.0001	0.00568243	0.31	1,689	tags=42%, list=13%, signal=48%
GO_MYELOID_LEUKOCYTE_MIGRATION	89	0.6794416	1.968563	<0.0001	0.005739971	0.316	992	tags=31%, list=8%, signal=34%
GO_CYTOSOLIC_CALCIIUM_ION_TRANSPORT	49	0.6533139	1.966163	<0.0001	0.005940233	0.327	1,155	tags=29%, list=9%, signal=31%
GO_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	29	0.7786217	1.9650677	<0.0001	0.005976756	0.328	1,251	tags=45%, list=10%, signal=49%
GO_REGULATION_OF_CALCIIUM_ION_TRANSPORT	179	0.5279947	1.9635807	<0.0001	0.006049526	0.334	1,812	tags=26%, list=14%, signal=29%
GO_MYELOID_LEUKOCYTE_DIFFERENTIATION	81	0.5724093	1.9633615	<0.0001	0.006017468	0.335	1,322	tags=30%, list=10%, signal=33%
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_PROLIFERATION	58	0.65305674	1.9624791	<0.0001	0.006075181	0.338	2,148	tags=52%, list=16%, signal=62%
GO_PLASMA_MEMBRANE_PROTEIN_COMPLEX	426	0.43724555	1.9598335	<0.0001	0.006217632	0.348	1,269	tags=16%, list=10%, signal=17%
GO_PHOSPHOLIPASE_C_ACTIVITY	24	0.6946257	1.9584188	<0.0001	0.00631529	0.35	552	tags=21%, list=4%, signal=22%
GO_RESPONSE_TO_MOLECULE_OF_BACTERIAL_ORIGIN	285	0.56875956	1.9574594	<0.0001	0.006351756	0.351	1,922	tags=36%, list=15%, signal=41%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_RESPONSE_TO_BACTERIUM	404	0.5532219	1.957211	<0.0001	0.006343393	0.354	1,922	tags=35%, list=15%, signal=39%
GO_INTEGRIN_MEDIATED_SIGNALING_PATHWAY	73	0.67838794	1.9556173	<0.0001	0.006490969	0.361	785	tags=29%, list=6%, signal=30%
GO_CLATHRIN_COATED_ENDOCYTIC_VESICLE	54	0.6618109	1.9538537	<0.0001	0.006580683	0.365	851	tags=26%, list=7%, signal=28%
GO_DEATH_RECEPTOR_ACTIVITY	20	0.7314523	1.9524262	<0.0001	0.006706404	0.372	1,830	tags=45%, list=14%, signal=52%
GO_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIIUM _ION_INTO_CYTOSOL	62	0.6145229	1.9520648	<0.0001	0.006700545	0.376	1,812	tags=29%, list=14%, signal=34%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	74	0.56035227	1.9511713	<0.0001	0.006731167	0.381	1,803	tags=35%, list=14%, signal=41%
GO GRANULOCYTE MIGRATION	65	0.7212005	1.9509364	<0.0001	0.006724718	0.382	992	tags=34%, list=8%, signal=36%
GO_PLASMA_MEMBRANE_RECEPTOR_COMPLEX	144	0.4678688	1.9507816	<0.0001	0.006694242	0.383	767	tags=17%, list=6%, signal=18%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_12_PRODUCTION	29	0.68939006	1.9495062	<0.0001	0.006706044	0.385	965	tags=38%, list=7%, signal=41%
GO_LEUKOCYTE_PROLIFERATION	78	0.56384456	1.9474046	0.001926782	0.006846233	0.394	1,771	tags=35%, list=14%, signal=40%
GO_REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_SIGNALING	196	0.55542874	1.9473698	<0.0001	0.006812807	0.394	1,865	tags=33%, list=14%, signal=38%
GO_INFLAMMATORY_RESPONSE	378	0.6148516	1.9470748	<0.0001	0.00681272	0.397	1,280	tags=29%, list=10%, signal=32%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_MYELOID_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	35	0.75064707	1.9462788	<0.0001	0.006843587	0.4	1,029	tags=43%, list=8%, signal=46%
GO_ER_TO_GOLGI_TRANSPORT_VESICLE	61	0.6436248	1.9461784	0.002074689	0.006803799	0.4	1,124	tags=30%, list=9%, signal=32%
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_APOPTOTIC_PROCESS	36	0.76452154	1.9453843	<0.0001	0.006847265	0.403	701	tags=39%, list=5%, signal=41%
GO_MODIFICATION_OF_MORPHOLOGY_OR_PHYSIOLOGY_OF_OTHER_ORGANISM	87	0.54379946	1.9452155	<0.0001	0.006813514	0.403	1,713	tags=31%, list=13%, signal=35%
GO_G_PROTEIN_COUPLED_PURINERGIC_RECEPTOR_SIGNALING_PATHWAY	16	0.7182099	1.9444289	<0.0001	0.006807975	0.404	2,539	tags=63%, list=19%, signal=78%
GO_REGULATION_OF_SYNCYTIUM_FORMATION_BY_PLASMA_MEMBRANE_FUSION	22	0.76478285	1.9442277	<0.0001	0.006775739	0.404	1,419	tags=36%, list=11%, signal=41%
GO_G_PROTEIN_COUPLED_RECEPTOR_BINDING	210	0.5155527	1.9425635	<0.0001	0.006904386	0.409	1,641	tags=22%, list=13%, signal=25%
GO_REGULATION_OF_SYMBIOSIS_ENCOMPASSING_MUTUALISM_THROUGH_PARASITISM	177	0.5251345	1.9400969	<0.0001	0.00713814	0.424	1,706	tags=29%, list=13%, signal=33%
GO_POSITIVE_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	51	0.67800486	1.9376565	<0.0001	0.007232143	0.427	1,333	tags=41%, list=10%, signal=46%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_4_PRODUCTION	19	0.6809292	1.9371245	0.001976285	0.007229905	0.429	2,129	tags=53%, list=16%, signal=63%
GO_CALCIIUM_ION_IMPORT	59	0.58096904	1.9358398	0.00204918	0.007328745	0.435	924	tags=20%, list=7%, signal=22%
GO_REGULATION_OF_PHAGOCYTOSIS	62	0.65151674	1.9356151	<0.0001	0.007288478	0.435	1,607	tags=34%, list=12%, signal=38%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_CHEMOKINE_MEDIATED_SIGNALING_PATHWAY	64	0.7863392	1.9349004	<0.0001	0.007289772	0.438	662	tags=38%, list=5%, signal=39%
GO_REGULATION_OF_CYTOSOLIC_CALCIIUM_ION_CONCENTRATION	179	0.49729255	1.9347975	<0.0001	0.007264704	0.44	1,205	tags=20%, list=9%, signal=22%
GO_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	148	0.50816333	1.9334857	<0.0001	0.00739922	0.446	1,428	tags=24%, list=11%, signal=26%
GO_ACTIN_FILAMENT	59	0.5990163	1.9333314	<0.0001	0.007368736	0.446	937	tags=22%, list=7%, signal=24%
GO_CLATHRIN_COATED_VESICLE_MEMBRANE	66	0.6395277	1.9330423	<0.0001	0.007358291	0.446	851	tags=24%, list=7%, signal=26%
GO_REGULATION_OF_LEUKOCYTE_DEGRANULATION	38	0.6901312	1.930693	<0.0001	0.007552699	0.456	1,783	tags=47%, list=14%, signal=55%
GO_POSITIVE_REGULATION_OF_ACUTE_INFLAMMATORY_RESPONSE	26	0.7355855	1.9304286	<0.0001	0.007543281	0.456	1,639	tags=38%, list=13%, signal=44%
GO_REGULATION_OF_NF_KAPPAB_IMPORT_INTO_NUCLEUS	45	0.6558915	1.9299477	<0.0001	0.007547895	0.459	1,678	tags=38%, list=13%, signal=43%
GO_REGULATION_OF_CYTOKINE_SECRETION	123	0.62932205	1.9291354	<0.0001	0.007612724	0.462	1,391	tags=37%, list=11%, signal=41%
GO_REGULATION_OF_MITOCHONDRIAL_MEMBRANE_POTENTIAL	45	0.60472304	1.9286207	<0.0001	0.007596967	0.463	1,923	tags=36%, list=15%, signal=42%
GO_NEGATIVE_REGULATION_OF_VIRAL_PROCESS	76	0.6640228	1.9258605	<0.0001	0.007864483	0.472	1,410	tags=37%, list=11%, signal=41%
GO_T_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	51	0.5535609	1.9250009	0.001934236	0.007891243	0.472	1,702	tags=33%, list=13%, signal=38%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_REGULATION_OF_CALCIIUM_ION_TRANSPORT_INTO_CYTOSOL	79	0.5702564	1.9242228	<0.0001	0.007920402	0.473	1,812	tags=28%, list=14%, signal=32%
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_WOUNDING	142	0.6069115	1.922433	<0.0001	0.008009761	0.478	1,650	tags=33%, list=13%, signal=37%
GO_REGULATION_OF_CHEMOTAXIS	167	0.64286107	1.9210947	<0.0001	0.008031742	0.478	1,311	tags=30%, list=10%, signal=33%
GO_POSITIVE_REGULATION_OF_INFLAMMATORY_RESPONSE	98	0.6298024	1.921027	<0.0001	0.008001544	0.478	1,650	tags=35%, list=13%, signal=39%
GO_RUFFLE_ORGANIZATION	16	0.77570236	1.9182009	<0.0001	0.008271126	0.485	563	tags=38%, list=4%, signal=32%
GO_REGULATION_OF_LEUKOCYTE_MIGRATION	137	0.7054689	1.9171325	<0.0001	0.008320252	0.488	707	list=5%, signal=34%
GO_POSITIVE_REGULATION_OF_CAMP_METABOLIC_PROCESS	82	0.48831075	1.9162993	<0.0001	0.008317976	0.491	1,751	tags=21%, list=13%, signal=24%
GO_NEGATIVE_REGULATION_OF_VIRAL_TRANSCRIPTION	22	0.71277946	1.915467	<0.0001	0.008346927	0.494	90	tags=14%, list=1%, signal=14%
GO_POSITIVE_REGULATION_OF_CHEMOTAXIS	114	0.68501294	1.9152979	<0.0001	0.00833098	0.494	1,311	tags=34%, list=10%, signal=38%
GO_MONOCYTE_CHEMOTAXIS	36	0.7985726	1.9138159	<0.0001	0.008438333	0.495	574	tags=33%, list=4%, signal=35%
GO_NEGATIVE_REGULATION_OF_INNATE_IMMUNE_RESPONSE	33	0.6503414	1.9132514	<0.0001	0.008438786	0.495	1,179	tags=33%, list=9%, signal=37%
GO_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY	46	0.54025	1.9127492	<0.0001	0.008432774	0.496	1,124	tags=24%, list=9%, signal=26%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_INTERFERON_GAMMA_MEDIATED_SIGNALING_PATHWAY	65	0.7902312	1.9105042	<0.0001	0.008642716	0.5	1,825	tags=71%, list=14%, signal=82%
GO_REGULATION_OF_CALCIIUM_ION_IMPORT	88	0.5788171	1.9097571	<0.0001	0.00869883	0.505	1,275	tags=20%, list=10%, signal=23%
GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	32	0.69672364	1.9094182	<0.0001	0.008682575	0.505	1,124	tags=34%, list=9%, signal=38%
GO_REGULATION_OF_ERK1_AND_ERK2_CASCADE	200	0.5620821	1.9067312	<0.0001	0.008911381	0.512	1,689	tags=30%, list=13%, signal=34%
GO_REGULATION_OF_T_CELL_RECEPTOR_SIGNALING_PATHWAY	24	0.71621007	1.9058672	<0.0001	0.008975505	0.516	1,812	tags=46%, list=14%, signal=53%
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	32	0.6142876	1.9054639	<0.0001	0.008978818	0.518	1,750	tags=38%, list=13%, signal=43%
GO_REGULATION_OF_MAST_CELL_ACTIVATION	36	0.6962953	1.9043225	<0.0001	0.009047891	0.52	1,783	tags=50%, list=14%, signal=58%
GO_RESPONSE_TO_ISOQUINOLINE_ALKALOID	28	0.5644478	1.9020323	0.001890359	0.009313975	0.53	349	tags=11%, list=3%, signal=11%
GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	61	0.53856057	1.9018148	<0.0001	0.009294577	0.531	1,803	tags=33%, list=14%, signal=38%
GO_PROTEIN_PHOSPHORYLATED_AMINO_ACID_BINDING	21	0.6646142	1.9016271	0.003913894	0.009271739	0.532	755	tags=24%, list=6%, signal=25%
GO_STAT_CASCADE	46	0.59014565	1.8996722	<0.0001	0.009482765	0.542	939	tags=24%, list=7%, signal=26%
GO_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	91	0.7445726	1.8987274	<0.0001	0.009516399	0.545	627	tags=35%, list=5%, signal=37%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_POSITIVE_T_CELL_SELECTION	18	0.783261	1.8969444	<0.0001	0.00973589	0.554	533	tags=39%, list=4%,
GO_IMMUNOGLOBULIN_BINDING	21	0.88075703	1.8965491	<0.0001	0.00972438	0.556	392	signal=40% tags=48%, list=3%,
GO_MEMBRANE_INVAGINATION	30	0.7040507	1.8927594	<0.0001	0.010115725	0.568	703	signal=49% tags=30%, list=5%,
GO_IMMUNOGLOBULIN_PRODUCTION	36	0.6228976	1.8925767	<0.0001	0.010104869	0.568	656	signal=32% tags=25%, list=5%,
GO_RESPONSE_TO_TYPE_I_INTERFERON	62	0.77980214	1.8925425	<0.0001	0.010066113	0.569	1,230	signal=26% tags=52%, list=9%,
GO_THREONINE_TYPE_PEPTIDASE_ACTIVITY	18	0.76895267	1.8907229	<0.0001	0.010230502	0.575	144	signal=57% tags=17%, list=1%,
GO_CLATHRIN_COATED_ENDOCYTIC_VESICLE_MEMBRANE	39	0.73263574	1.8906723	<0.0001	0.010191587	0.575	851	signal=17% tags=36%, list=7%,
GO_LYMPHOCYTE_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	79	0.5059888	1.8904368	<0.0001	0.010182861	0.576	1,702	signal=38% tags=29%, list=13%,
GO_NEGATIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	90	0.5637233	1.8903108	<0.0001	0.010153378	0.578	1,880	signal=33% tags=33%, list=14%,
GO_CELLULAR_EXTRAVASATION	23	0.7386299	1.8901025	<0.0001	0.010124743	0.579	998	signal=39% tags=39%, list=8%,
GO_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	51	0.56473553	1.8898118	<0.0001	0.010107778	0.579	858	signal=42% tags=24%, list=7%,
GO_REGULATION_OF_INTERLEUKIN_17_PRODUCTION	19	0.6871498	1.8887444	<0.0001	0.010203951	0.585	1,673	signal=25% tags=47%, list=13%, signal=54%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_DIVALENT_INORGANIC_CATION_TRANSPORT	196	0.45208657	1.8873373	<0.0001	0.010378767	0.591	1,312	tags=18%, list=10%, signal=20%
GO_POSITIVE_REGULATION_OF_HOMEOSTATIC_PROCESS	178	0.4562018	1.887116	<0.0001	0.010371798	0.592	1,275	tags=19%, list=10%, signal=20%
GO_NEGATIVE_REGULATION_OF_CALCIIUM_MEDIATED_SIGNALING	18	0.72771204	1.8848398	0.002066116	0.010591705	0.596	1,461	tags=39%, list=11%, signal=20%
GO_REGULATION_OF_PLATELET_AGGREGATION	15	0.7090066	1.8836067	<0.0001	0.010747288	0.603	701	signal=44%, tags=40%, list=5%, signal=42%
GO_REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_STAT_PROTEIN	60	0.5859757	1.8833725	<0.0001	0.010746238	0.604	602	tags=18%, list=5%, signal=19%
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_OR_POLYSACCHARIDE_ANTIGEN_VIA_MHC_CLASS_II	78	0.6440164	1.8830533	0.002	0.010767714	0.606	864	tags=23%, list=7%, signal=25%
GO_ENDOCYTIC_VESICLE	215	0.5170008	1.8828225	<0.0001	0.010763192	0.607	1,176	tags=23%, list=9%, signal=25%
GO_CYTOKINE_RECEPTOR_ACTIVITY	78	0.58435196	1.8799329	<0.0001	0.011097902	0.625	1,373	signal=31%, list=11%, signal=34%
GO_RESPONSE_TO_AUDITORY_STIMULUS	17	0.66709167	1.8798082	0.002066116	0.011072743	0.626	293	tags=12%, list=2%, signal=12%
GO_SIGNAL_TRANSDUCTION_BY_PROTEIN_PHOSPHORYLATION	359	0.39707118	1.8793949	<0.0001	0.011081105	0.628	1,881	tags=19%, list=14%, signal=22%
GO_ERYTHROCYTE_HOMEOSTASIS	66	0.47530407	1.8786165	<0.0001	0.011145129	0.631	1,702	tags=23%, list=13%, signal=26%
GO_CELL_CELL_ADHESION	483	0.47651958	1.8773025	<0.0001	0.011332736	0.634	1,812	tags=26%, list=14%, signal=29%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_LEUKOCYTE_MEDIATED_IMMUNITY	133	0.6446642	1.8754989	<0.0001	0.011495595	0.641	1,213	tags=33%, list=9%,
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MIGRATION	104	0.7156184	1.875192	<0.0001	0.011476394	0.641	690	signal=36% tags=32%, list=5%,
GO_HOMEOSTASIS_OF_NUMBER_OF_CELLS	145	0.47136715	1.8751153	<0.0001	0.011450096	0.642	1,511	signal=33% tags=23%, list=12%,
GO_REGULATION_OF_CAMP_METABOLIC_PROCESS	119	0.4592346	1.8749629	<0.0001	0.011428988	0.643	1,751	signal=25% tags=20%, list=13%,
GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_MIGRATION	28	0.7027585	1.8747205	<0.0001	0.011414822	0.644	1,638	signal=23% tags=39%, list=13%,
GO_POSITIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION	52	0.6989706	1.8735706	<0.0001	0.011532665	0.648	1,218	signal=45% tags=40%, list=9%,
GO_HUMORAL_IMMUNE_RESPONSE	142	0.6151812	1.8735675	<0.0001	0.011486349	0.648	1,492	signal=44% tags=32%, list=11%,
GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_FACTOR_IMPORT_INTO_NUCLEUS	44	0.65880203	1.8708872	<0.0001	0.01183947	0.658	1,777	signal=36% tags=43%, list=14%,
GO_LYMPHOCYTE_MIGRATION	40	0.810758	1.8698395	<0.0001	0.011983582	0.666	857	signal=50% tags=48%, list=7%,
GO_PHOSPHATIDYLINOSITOL_3_KINASE_BINDING	24	0.63227856	1.8695643	<0.0001	0.011966731	0.666	1,022	signal=51% tags=25%, list=8%,
GO_NEGATIVE_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	26	0.67248493	1.8687434	0.001934236	0.012042031	0.671	2,148	signal=27% tags=58%, list=16%,
GO_NEGATIVE_REGULATION_OF_OXIDOREDUCTASE_ACTIVITY	23	0.6030526	1.8683968	<0.0001	0.012027939	0.673	1,227	signal=69% tags=17%, list=9%, signal=19%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_ADAPTIVE_IMMUNE_RESPONSE_BASED_ON_SOMATIC_RECOMBINATION_OF_IMMUNE_RECEPTORS_BUILT_FROM_IMMUNOGLOBULIN_SUPERFAMILY_DOMAINS	109	0.6703	1.8676218	<0.0001	0.01211005	0.679	1,743	tags=46%, list=13%, signal=53%
GO_ENDOSOMAL_PART	314	0.4310355	1.8668375	<0.0001	0.012201698	0.681	1,815	tags=22%, list=14%, signal=25%
GO_RESPONSE_TO_INTERFERON_BETA	16	0.8582177	1.8660419	<0.0001	0.012231049	0.683	716	tags=44%, list=5%, signal=46%
GO_TAXIS	388	0.5151704	1.8651237	<0.0001	0.012277531	0.687	1,351	tags=23%, list=10%, signal=25%
GO_TRANS_GOLGI_NETWORK_MEMBRANE	56	0.5832592	1.8639867	<0.0001	0.012404915	0.693	980	tags=23%, list=8%, signal=38%
GO_REGULATION_OF_MAST_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	29	0.703749	1.8628522	<0.0001	0.012581475	0.698	826	list=6%, signal=40%
GO_RECEPTOR_MEDIATED_ENDOCYTOSIS	179	0.54084945	1.862616	<0.0001	0.012607917	0.698	1,759	tags=30%, list=14%, signal=34%
GO_G_PROTEIN_COUPLED_CHEMOATTRACTANT_RECEPTOR_ACTIVITY	22	0.6758685	1.8617487	0.001876173	0.01268736	0.701	1,330	tags=45%, list=10%, signal=51%
GO_NEGATIVE_REGULATION_OF_T_CELL_PROLIFERATION	41	0.5839942	1.8593832	<0.0001	0.01301415	0.716	2,148	tags=44%, list=16%, signal=52%
GO_REGULATION_OF_MYELOID_CELL_APOPTOTIC_PROCESS	22	0.7005164	1.8582745	<0.0001	0.013131331	0.716	533	tags=23%, list=4%, signal=24%
GO_NEGATIVE_REGULATION_OF_CELL_CELL_ADHESION	107	0.5284096	1.8581636	<0.0001	0.013090736	0.717	1,738	tags=29%, list=13%, signal=33%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_T_CELL_RECEPTOR_COMPLEX	18	0.8533599	1.8548825	<0.0001	0.013656028	0.734	726	tags=61%, list=6%,
GO_MYELOID_DENDRITIC_CELL_DIFFERENTIATION	17	0.7087046	1.8544393	<0.0001	0.013662132	0.736	1,698	signal=65% tags=53%, list=13%,
GO_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	124	0.49571356	1.8541992	<0.0001	0.013653819	0.737	1,914	signal=61% tags=27%, list=15%,
GO_NEGATIVE_REGULATION_OF_CELL_KILLING	17	0.82446283	1.8541762	<0.0001	0.013603061	0.737	606	signal=31% tags=47%, list=5%,
GO_INTERACTION_WITH_SYMBIONT	45	0.5718174	1.8525741	<0.0001	0.013817741	0.745	1,678	signal=49% tags=27%, list=13%,
GO_POSITIVE_REGULATION_OF_PROTEIN_SECRETION	178	0.504666	1.8523949	<0.0001	0.013806382	0.746	2,061	signal=31% tags=31%, list=16%,
GO_CELLULAR_RESPONSE_TO_LIPID	390	0.42885336	1.8523698	<0.0001	0.013764359	0.746	1,694	signal=37% tags=23%, list=13%,
GO_NON_MEMBRANE_SPANNING_PROTEIN_TYROSINE_KINASE_ACTIVITY	41	0.5645196	1.8516805	0.005928854	0.013823787	0.746	1,652	signal=26% tags=34%, list=13%,
GO_COATED_VESICLE_MEMBRANE	115	0.5293219	1.851514	0.002141328	0.013809778	0.746	929	signal=39% tags=20%, list=7%,
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	66	0.5242237	1.8497944	0.001937985	0.013998752	0.75	801	signal=21% tags=20%, list=6%,
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	78	0.7467521	1.8497343	<0.0001	0.013974756	0.75	627	signal=21% tags=36%, list=5%,
GO_REGULATION_OF_CALCIIUM_ION_TRANSMEMBRANE_TRANSPORT	98	0.5065265	1.8469626	<0.0001	0.014449638	0.759	1,984	signal=37% tags=28%, list=15%, signal=32%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_PATTERN_RECOGNITION_RECEPTOR_SIGNALING_PATHWAY	91	0.5633605	1.8455825	0.004048583	0.014616857	0.765	1,898	tags=42%, list=15%, signal=49%
GO_POSITIVE_REGULATION_OF_CALCIIUM_ION_TRANSPORT	92	0.56904376	1.8450861	<0.0001	0.014669673	0.766	956	tags=21%, list=7%, signal=22%
GO_POSITIVE_REGULATION_OF_ERK1_AND_ERK2_CASCADE	148	0.55716103	1.8449488	<0.0001	0.014640183	0.766	1,689	tags=30%, list=13%, signal=34%
GO_T_HELPER_1_TYPE_IMMUNE_RESPONSE	18	0.6985052	1.8446215	<0.0001	0.014645611	0.766	2,154	tags=56%, list=17%, signal=66%
GO_LYMPHOCYTE_MEDIATED_IMMUNITY	97	0.67824644	1.8408768	<0.0001	0.015368531	0.779	1,213	tags=38%, list=9%, signal=42%
GO_NEGATIVE_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	16	0.7337612	1.8395611	<0.0001	0.015562893	0.783	1,812	tags=44%, list=14%, signal=51%
GO_T_CELL_DIFFERENTIATION_INVOLVED_IN_IMMUNE_RESPONSE	23	0.6379616	1.8391519	0.003984064	0.015559671	0.783	1,702	tags=48%, list=13%, signal=55%
GO_POSITIVE_REGULATION_OF_PHAGOCYTOSIS	40	0.686613	1.8337504	0.001964637	0.016398925	0.795	992	tags=30%, list=8%, signal=32%
GO_PHAGOCYTOSIS_ENGULFMENT	22	0.7743591	1.8325043	0.001926782	0.016580617	0.8	703	tags=41%, list=5%, signal=43%
GO_CYTOKINE_PRODUCTION	100	0.54564476	1.8300667	<0.0001	0.017043665	0.806	1,877	tags=36%, list=14%, signal=42%
GO_REGULATION_OF_METAL_ION_TRANSPORT	274	0.45346656	1.8299872	<0.0001	0.016997324	0.806	2,125	tags=25%, list=16%, signal=29%
GO_REGULATION_OF_T_CELL_MEDIATED_CYTOTOXICITY	21	0.6516613	1.8275015	<0.0001	0.017335976	0.809	1,124	tags=29%, list=9%, signal=31%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_EXTRINSIC_COMPONENT_OF_CYTOPLASMIC_SIDE_OF_PLASMA_MEMBRANE	84	0.49313635	1.827341	0.001992032	0.017304098	0.809	1,035	tags=23%, list=8%, signal=24%
GO_LUMENAL_SIDE_OF_MEMBRANE	25	0.85262924	1.8271781	<0.0001	0.01727456	0.809	811	tags=60%, list=6%, signal=64%
GO_CHEMOKINE_ACTIVITY	41	0.8410555	1.823542	<0.0001	0.01789045	0.819	627	tags=44%, list=5%, signal=46%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_2_PRODUCTION	27	0.6381744	1.8228655	0.005847953	0.017969059	0.821	1,698	tags=44%, list=13%, signal=51%
GO_REGULATION_OF_ANTIGEN_PROCESSING_AND_PRESENTATION	21	0.8283572	1.8228302	<0.0001	0.017912962	0.821	1,229	tags=67%, list=9%, signal=73%
GO_PHOSPHATIDYLSERINE_METABOLIC_PROCESS	18	0.6961055	1.8213617	<0.0001	0.018171385	0.827	1,011	tags=39%, list=8%, signal=42%
GO_MACROPHAGE_ACTIVATION	29	0.5998262	1.820702	0.001869159	0.01826656	0.827	1,333	tags=31%, list=10%, signal=34%
GO_POSITIVE_REGULATION_OF_CYTOKINE_BIOSYNTHETIC_PROCESS	50	0.57970345	1.8202906	0.001930502	0.018312134	0.827	1,924	tags=40%, list=15%, signal=47%
GO_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	53	0.55711854	1.8184714	<0.0001	0.018690191	0.832	1,803	tags=36%, list=14%, signal=41%
GO_CYTOKINE_ACTIVITY	173	0.5461626	1.8183359	<0.0001	0.018672753	0.833	1,313	tags=20%, list=10%, signal=22%
GO_LYMPHOCYTE_CHEMOTAXIS	32	0.8382278	1.818115	<0.0001	0.018706918	0.834	574	tags=47%, list=4%, signal=49%
GO_LIPOPOLYSACCHARIDE_MEDIATED_SIGNALING_PATHWAY	30	0.72819823	1.8179581	<0.0001	0.01868135	0.835	1,689	tags=50%, list=13%, signal=57%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_REGULATION_OF_INTERLEUKIN_10_PRODUCTION	35	0.64547205	1.8178835	<0.0001	0.018647052	0.835	2,148	tags=40%, list=16%, signal=48% tags=18%, list=10%, signal=20% tags=50%, list=13%, signal=58% tags=29%, list=13%, signal=33% tags=21%, list=11%, signal=23% tags=32%, list=12%, signal=36% tags=19%, list=13%, signal=22% tags=31%, list=5%, signal=33% tags=43%, list=7%, signal=46% tags=24%, list=12%, signal=27% tags=38%, list=8%, signal=41% tags=15%, list=5%, signal=16%
GO_LATE_ENDOSOME_MEMBRANE	67	0.50691164	1.8175124	0.002028398	0.018692425	0.837	1,282	
GO_REGULATION_OF_INTERFERON_ALPHA_PRODUCTION	16	0.6973979	1.8166219	0.003868472	0.018859126	0.838	1,750	
GO_REGULATION_OF_INFLAMMATORY_RESPONSE	248	0.53818387	1.8154697	<0.0001	0.019056274	0.844	1,722	
GO_B_CELL_ACTIVATION	114	0.4482957	1.8152355	<0.0001	0.019044293	0.845	1,391	
GO_POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	41	0.60005176	1.8142288	0.003846154	0.019138787	0.845	1,511	
GO_POSITIVE_REGULATION_OF_CYCLIC_NUCLEOTIDE_METABOLIC_PROCESS	98	0.4403168	1.813148	<0.0001	0.019351378	0.848	1,751	
GO_REGULATION_OF_PLATELET_ACTIVATION	29	0.6663025	1.8128124	0.003773585	0.019364197	0.85	701	
GO_CCR_CHEMOKINE_RECEPTOR_BINDING	30	0.8047258	1.8109041	<0.0001	0.019801348	0.853	857	
GO_CYTOPLASMIC_SIDE_OF_MEMBRANE	142	0.45222637	1.8105779	<0.0001	0.019779243	0.854	1,512	
GO_ALDITOL_PHOSPHATE_METABOLIC_PROCESS	24	0.67341477	1.8104733	0.001992032	0.019737922	0.854	1,011	
GO_MONOAMINE_TRANSPORT	20	0.6061756	1.8099898	0.002004008	0.019779949	0.854	613	

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	34	0.65876496	1.8084037	<0.0001	0.020072266	0.854	781	tags=21%, list=6%,
GO_ACTIN_MONOMER_BINDING	21	0.59447235	1.806945	0.002008032	0.020325301	0.858	2,470	signal=22% tags=43%, list=19%,
GO_PROTEIN_TRIMERIZATION	30	0.649419	1.8052413	0.001941748	0.02069976	0.864	1,614	signal=53% tags=40%, list=12%,
GO_REGULATION_OF_INTERLEUKIN_1_PRODUCTION	49	0.71636254	1.8044909	<0.0001	0.020820163	0.865	1,107	signal=46% tags=41%, list=8%,
GO_CYTOKINE_BINDING	78	0.587371	1.8039384	0.001945525	0.020895224	0.868	1,638	signal=44% tags=38%, list=13%,
GO_REGULATION_OF_PROTEIN_SECRETION	329	0.43945536	1.8034264	<0.0001	0.020940037	0.871	2,167	signal=44% tags=29%, list=17%,
GO_REGULATION_OF_MYOBLAST_FUSION	17	0.7802362	1.8018696	<0.0001	0.021261547	0.874	1,039	signal=34% tags=29%, list=8%,
GO_POSITIVE_REGULATION_OF_AUTOPHAGY	59	0.48592228	1.8014505	0.006012024	0.02126319	0.874	2,419	signal=32% tags=34%, list=19%,
GO_LATE_ENDOSOME	148	0.46177807	1.8008902	<0.0001	0.02131405	0.876	1,386	signal=41% tags=17%, list=11%,
GO_HEMOSTASIS	276	0.47528017	1.7987424	<0.0001	0.021723777	0.878	1,971	signal=19% tags=29%, list=15%,
GO_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_ACTIVITY	33	0.62675464	1.7980697	0.001897533	0.021832416	0.88	2,917	signal=34% tags=52%, list=22%,
GO_REGULATION_OF_MYOTUBE_DIFFERENTIATION	42	0.5563607	1.79656	0.001926782	0.022113742	0.882	1,039	signal=66% tags=14%, list=8%, signal=15%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_IMMUNOLOGICAL_SYNAPSE	28	0.7319311	1.7954584	<0.0001	0.022269605	0.884	785	tags=36%, list=6%,
GO_PURINERGIC_RECEPTOR_SIGNALING_PATHWAY	22	0.60191923	1.792808	0.002118644	0.022909032	0.892	2,539	signal=38% tags=50%, list=19%,
GO_NEGATIVE_REGULATION_OF_MUSCLE_CELL_APOPTOTIC_PROCESS	28	0.56568414	1.7906879	0.003853565	0.023327138	0.899	1,931	signal=62% tags=36%, list=15%,
GO_REGULATION_OF_LYMPHOCYTE_MIGRATION	32	0.8279751	1.7896152	<0.0001	0.023611085	0.899	857	signal=42% tags=56%, list=7%,
GO_REGULATION_OF_LIPID_KINASE_ACTIVITY	40	0.5910831	1.7870078	0.001960784	0.024281777	0.908	2,917	signal=60% tags=50%, list=22%,
GO_NEGATIVE_REGULATION_OF_CYTOKINE_SECRETION	36	0.61591595	1.7868776	<0.0001	0.024245394	0.908	1,738	signal=64% tags=42%, list=13%,
GO_LEUKOCYTE_HOMEOSTASIS	46	0.58955085	1.785185	<0.0001	0.024712231	0.914	1,275	signal=48% tags=33%, list=10%,
GO_REGULATION_OF_NEUTROPHIL_MIGRATION	31	0.777509	1.7848808	0.001964637	0.024705503	0.915	1,235	signal=36% tags=48%, list=9%,
GO_NEGATIVE_REGULATION_OF_B_CELL_ACTIVATION	27	0.6533316	1.7822087	0.004	0.025370436	0.92	2,051	signal=53% tags=44%, list=16%,
GO_POSITIVE_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	56	0.61007464	1.7808273	0.001890359	0.025672227	0.924	1,237	signal=53% tags=29%, list=9%,
GO_CELLULAR_RESPONSE_TO_VIRUS	20	0.67922753	1.7800436	0.003968254	0.025869448	0.926	485	signal=31% tags=25%, list=4%,
GO_NEGATIVE_REGULATION_OF_EXOCYTOSIS	26	0.6429737	1.7792343	0.002066116	0.026023524	0.927	1,438	signal=26% tags=38%, list=11%, signal=43%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_PEPTIDE_ANTIGEN_BINDING	26	0.7961733	1.7778559	0.00204918	0.02634807	0.928	894	tags=54%, list=7%, signal=58%
GO_REGULATION_OF_INTERLEUKIN_1_BETA_PRODUCTION	40	0.7099092	1.7776984	<0.0001	0.026304768	0.928	2,011	tags=52%, list=15%, signal=62%
GO_NEGATIVE_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	21	0.6272876	1.7776933	0.007936508	0.026227402	0.928	801	tags=33%, list=6%, signal=35%
GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_6_PRODUCTION	28	0.5747053	1.7774639	0.006085193	0.026211843	0.928	1,880	tags=43%, list=14%, signal=50%
GO_REGULATION_OF_PHOSPHOLIPASE_ACTIVITY	58	0.58025056	1.7772278	0.00591716	0.026212683	0.929	1,964	tags=28%, list=15%, signal=32%
GO_REGULATION_OF_RYANODINE_SENSITIVE_CALCIIUM_RELEASE_CHANNEL_ACTIVITY	23	0.5897472	1.7768034	0.008196721	0.026243595	0.931	1,984	tags=30%, list=15%, signal=36%
GO_POSITIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	67	0.5281822	1.7766201	0.003875969	0.026218124	0.931	1,511	tags=25%, list=12%, signal=29%
GO_PHAGOCYTIC_VESICLE	70	0.59064806	1.7758168	0.004024145	0.026349831	0.931	2,068	tags=44%, list=16%, signal=52%
GO GRANULOCYTE_ACTIVATION	16	0.8388103	1.7742324	<0.0001	0.026669988	0.933	627	tags=44%, list=5%, signal=46%
GO_MODULATION_OF_TRANSCRIPTION_IN_OTHER_ORGANISM_INVOLVED_IN_SYMBIOTIC_INTERACTION	21	0.67090356	1.7742136	0.001886793	0.026596794	0.933	90	tags=14%, list=1%, signal=14%
GO_REGULATION_OF_CYCLIC_NUCLEOTIDE_METABOLIC_PROCESS	141	0.41767743	1.7736619	0.001984127	0.02666809	0.935	1,751	tags=19%, list=13%, signal=22%
GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_PROLIFERATION	53	0.5843188	1.7724451	0.001934236	0.027006162	0.939	1,228	tags=26%, list=9%, signal=29%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	122	0.5028118	1.7722933	<0.0001	0.026975898	0.94	1,263	tags=22%, list=10%, signal=24%, tags=41%, list=15%, signal=48%
GO_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	71	0.5619948	1.7719647	0.006302521	0.027003976	0.941	1,898	tags=20%, list=5%, signal=21%, tags=38%, list=14%, signal=44%
GO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	69	0.5237757	1.7719636	<0.0001	0.026927259	0.941	671	tags=27%, list=6%, signal=29%, tags=40%, list=17%, signal=49%
GO_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	32	0.64183474	1.7718425	<0.0001	0.02688023	0.941	1,877	tags=53%, list=5%, signal=56%, tags=38%, list=5%, signal=40%
GO_REGULATION_OF_POSITIVE_CHEMOTAXIS	22	0.6892905	1.7714562	<0.0001	0.026928987	0.941	749	tags=44%, list=8%, signal=48%, tags=29%, list=13%, signal=33%
GO_MODIFICATION_BY_SYMBIONT_OF_HOST_MORPHOLOGY_OR_PHYSIOLOGY	42	0.5010243	1.76929	<0.0001	0.027518786	0.943	2,204	tags=33%, list=7%, signal=36%, tags=14%, list=7%, signal=15%
GO_POSITIVE_REGULATION_OF_CELL_ADHESION_MEDIATED_BY_INTEGRIN	15	0.83977646	1.7685311	<0.0001	0.027684882	0.943	613	
GO_CHEMOKINE_RECEPTOR_BINDING	50	0.764399	1.7677121	<0.0001	0.027832866	0.944	627	
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_1_BETA_PRODUCTION	27	0.74907154	1.7676187	<0.0001	0.027795015	0.944	1,107	
GO_REGULATION_OF_RESPONSE_TO_WOUNDING	352	0.5102874	1.7674828	0.001930502	0.027769538	0.944	1,722	
GO_POSITIVE_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	18	0.71326065	1.7672404	0.007707129	0.027772084	0.944	904	
GO_CLATHRIN_COATED_VESICLE	128	0.4556876	1.7670499	<0.0001	0.027754795	0.944	851	

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_LEUKOCYTE_DEGRANULATION	24	0.7162586	1.7660999	0.00390625	0.027951304	0.945	1,029	tags=33%, list=8%, signal=36%
GO_REGULATION_OF_MUSCLE_CELL_APOPTOTIC_PROCESS	40	0.49402148	1.764435	0.007722008	0.028440485	0.947	1,931	tags=30%, list=15%, signal=35%
GO_REGULATION_OF_INTERLEUKIN_1_SECRETION	28	0.7489847	1.7638924	0.001960784	0.028548004	0.948	1,107	tags=50%, list=8%, signal=55%
GO_MHC_PROTEIN_COMPLEX_BINDING	18	0.84224415	1.7628956	<0.0001	0.028802339	0.951	849	tags=50%, list=7%, signal=53%
GO_CYTOKINE_RECEPTOR_BINDING	231	0.46680793	1.7625198	<0.0001	0.028898498	0.951	1,933	tags=24%, list=15%, signal=27%
GO_REGULATION_OF_LIPOPOLYSACCHARIDE_MEDIATED_SIGNALING_PATHWAY	17	0.7376409	1.7620667	0.006369427	0.028962633	0.951	1,341	tags=59%, list=10%, signal=65%
GO_POSITIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	65	0.49931717	1.7594956	<0.0001	0.029740231	0.955	1,803	tags=32%, list=14%, signal=37%
GO_PHOSPHORIC_DIESTER_HYDROLASE_ACTIVITY	68	0.4492382	1.7593913	0.001949318	0.029690653	0.956	1,545	tags=16%, list=12%, signal=18%
GO_REGULATION_OF_NEUTROPHIL_CHEMOTAXIS	26	0.80189884	1.7592345	<0.0001	0.029663464	0.956	1,235	tags=54%, list=9%, signal=59%
GO_ERK1_AND_ERK2_CASCADE	19	0.6712929	1.7582357	0.001883239	0.029918103	0.957	474	tags=26%, list=4%, signal=27%
GO_POSITIVE_REGULATION_OF_ION_TRANSPORT	203	0.44166738	1.7560912	<0.0001	0.030534266	0.958	2,136	tags=26%, list=16%, signal=31%
GO_REGULATION_OF_CELL_SHAPE	108	0.5190137	1.7553321	<0.0001	0.03070805	0.96	1,074	tags=20%, list=8%, signal=22%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_AMMONIUM_ION_BINDING	62	0.5154778	1.755314	0.001904762	0.030631972	0.96	522	tags=11%, list=4%,
GO_REGULATION_OF_INTERFERON_BETA_PRODUCTION	38	0.58018243	1.7548633	0.002136752	0.03067386	0.961	1,750	signal=12% tags=37%, list=13%,
GO_REGULATION_OF_GRANULOCYTE_CHEMOTAXIS	38	0.75175667	1.7547239	<0.0001	0.030621516	0.961	1,311	signal=42% tags=47%, list=10%,
GO_REGULATION_OF_MITOCHONDRIAL_DEPOLARIZATION	15	0.7212038	1.7541286	0.002083333	0.030728888	0.962	1,280	signal=53% tags=47%, list=10%,
GO_MODULATION_BY_SYMBIONT_OF_HOST_CELLULAR_PROCESS	26	0.53779066	1.752783	0.007797271	0.031033104	0.965	2,204	signal=52% tags=42%, list=17%,
GO_NEGATIVE_REGULATION_OF_DEFENSE_RESPONSE	122	0.4787067	1.752577	<0.0001	0.030996168	0.965	1,880	signal=51% tags=28%, list=14%,
GO_POSITIVE_REGULATION_OF_TYPE_I_INTERFERON_PRODUCTION	59	0.49349123	1.7524191	0.002066116	0.030961439	0.965	1,764	signal=32% tags=31%, list=14%,
GO_CYTOKINE_SECRETION	31	0.6464973	1.75185	0.002012072	0.03106565	0.967	1,113	signal=35% tags=35%, list=9%,
GO_POSITIVE_REGULATION_OF_NEUTROPHIL_MIGRATION	26	0.7902688	1.7515824	<0.0001	0.031080961	0.968	1,213	signal=39% tags=50%, list=9%,
GO_CELL_KILLING	41	0.6239075	1.750887	<0.0001	0.031244205	0.968	857	signal=55% tags=29%, list=7%,
GO_CAMP_METABOLIC_PROCESS	28	0.5575043	1.7505983	0.013833992	0.031232225	0.968	2,378	signal=31% tags=39%, list=18%,
GO_NEGATIVE_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	37	0.5513491	1.7504314	0.003891051	0.031224636	0.968	801	signal=48% tags=24%, list=6%, signal=26%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_CORECEPTOR_ACTIVITY	34	0.6226392	1.7501369	0.004040404	0.031253047	0.968	726	tags=32%, list=6%, signal=34%
GO_T_CELL_PROLIFERATION	30	0.63500106	1.7494174	0.001996008	0.03148087	0.969	1,639	tags=50%, list=13%, signal=57%
GO_POSITIVE_REGULATION_OF_STAT_CASCADE	66	0.5515172	1.74938	<0.0001	0.03140801	0.969	904	tags=20%, list=7%, signal=21%
GO_INTERACTION_WITH_HOST	126	0.47090015	1.7489833	0.001923077	0.031478886	0.969	2,204	tags=35%, list=17%, signal=42%
GO_REGULATION_OF_INTERLEUKIN_6_PRODUCTION	86	0.5351674	1.7484177	<0.0001	0.031563878	0.969	1,880	list=14%, signal=49%, tags=29%, list=14%, signal=33%
GO_CELL_RECOGNITION	97	0.50552136	1.7474774	0.001941748	0.03178851	0.97	1,780	tags=21%, list=7%, signal=22%
GO_PHOSPHOLIPASE_ACTIVITY	68	0.54198885	1.7462428	0.001956947	0.032142334	0.972	920	tags=29%, list=7%, signal=31%
GO_NEGATIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION	38	0.6018998	1.7451367	0.015904572	0.03240187	0.972	956	tags=37%, list=8%, signal=40%
GO_MAST_CELL_ACTIVATION	19	0.72167844	1.7442006	<0.0001	0.032655302	0.974	1,029	tags=21%, list=7%, signal=23%
GO_POSITIVE_REGULATION_OF_CALCIIUM_ION_IMPORT	47	0.60578406	1.7439994	0.001960784	0.03266002	0.974	915	tags=35%, list=16%, signal=41%
GO_POSITIVE_REGULATION_OF_CALCIIUM_ION_TRANSPORT_INTO_CYTOSOL	46	0.55909425	1.7411062	0.004149378	0.03357668	0.975	2,125	list=4%, signal=24%, list=4%, signal=24%
GO_RESPONSE_TO_OXYGEN_RADICAL	17	0.67554754	1.7406478	0.006237006	0.033714823	0.976	522	

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_B_CELL_MEDIATED_IMMUNITY	64	0.6824676	1.7386832	0.005825243	0.03433041	0.979	1,213	tags=41%, list=9%,
GO_LEUKOCYTE_MEDIATED_CYTOTOXICITY	24	0.6601555	1.7382634	0.003921569	0.034433052	0.979	554	signal=45% tags=25%, list=4%,
GO_RETINA_HOMEOSTASIS	47	0.5053131	1.7349317	0.002118644	0.035591252	0.981	1,842	signal=26% tags=19%, list=14%,
GO_POSITIVE_REGULATION_OF_LOCOMOTION	371	0.49981356	1.7345837	0.001908397	0.035608288	0.981	1,345	signal=22% tags=23%, list=10%,
GO_POSITIVE_REGULATION_OF_VASCULATURE_DEVELOPMENT	118	0.5375452	1.7340171	0.00189394	0.0356975	0.981	1,737	signal=25% tags=33%, list=13%,
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_APOPTOTIC_PROCESS	21	0.69055897	1.7339588	0.001960784	0.035637412	0.981	1,029	signal=38% tags=33%, list=8%,
GO_POSITIVE_REGULATION_OF_NF_KAPPAB_IMPORT_INTO_NUCLEUS	25	0.7236723	1.7322909	<0.0001	0.03617872	0.981	1,468	signal=36% tags=52%, list=11%,
GO_NEGATIVE_REGULATION_OF_PEPTIDE_SECRETION	41	0.49103704	1.7318846	0.002	0.036256917	0.981	1,855	signal=58% tags=29%, list=14%,
GO_NEGATIVE_REGULATION_OF_G_PROTEIN_COUPLED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	39	0.59601766	1.7289724	0.004040404	0.03723968	0.983	1,380	signal=34% tags=26%, list=11%,
GO_REGULATION_OF_CATION_TRANSMEMBRANE_TRANSPORT	174	0.44540688	1.7284188	0.00204499	0.037380643	0.985	2,125	signal=29% tags=26%, list=16%,
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_1_PRODUCTION	32	0.70937485	1.7282617	<0.0001	0.03735493	0.985	1,107	signal=31% tags=41%, list=8%,
GO_NEGATIVE_REGULATION_OF_HEMOPOIESIS	103	0.45283553	1.7276381	<0.0001	0.037496347	0.985	801	signal=44% tags=17%, list=6%, signal=17%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_POSITIVE_REGULATION_OF_MAPK_CASCADE	400	0.42910516	1.7275227	<0.0001	0.037461516	0.985	1,936	tags=25%, list=15%, signal=29%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_10_PRODUCTION	23	0.65672547	1.7273457	0.004032258	0.037440285	0.985	354	tags=22%, list=3%, signal=22%
GO_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	29	0.5698986	1.7259735	0.009708738	0.037870884	0.985	2,154	signal=22% tags=48%, list=17%, signal=58%
GO_MUSCLE_ADAPTATION	26	0.59920233	1.7258973	0.003861004	0.037808586	0.985	992	tags=27%, list=8%, signal=29%
GO_REGULATION_OF_ALPHA_BETA_T_CELL_PROLIFERATION	21	0.7079277	1.7253886	0.005964215	0.03795797	0.985	2,125	tags=71%, list=16%, signal=85%
GO_CELLULAR_RESPONSE_TO_DRUG	58	0.5143793	1.7239339	<0.0001	0.038422085	0.986	1,852	tags=33%, list=14%, signal=38%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_1_SECRETION	21	0.7723581	1.7236658	0.003898636	0.038411025	0.986	1,107	tags=52%, list=8%, signal=57%
GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_MIGRATION	24	0.8260401	1.7234873	<0.0001	0.03839714	0.986	857	tags=54%, list=7%, signal=58%
GO_POSITIVE_REGULATION_OF_PROTEIN_KINASE_B_SIGNALING	72	0.53211045	1.7233918	0.003898636	0.03834189	0.986	2,166	tags=36%, list=17%, signal=43%
GO_REGULATION_OF_PEPIDYL_TYROSINE_PHOSPHORYLATION	186	0.4671589	1.7221525	<0.0001	0.03865438	0.986	1,933	tags=27%, list=15%, signal=31%
GO_NEGATIVE_REGULATION_OF_PROTEIN_SECRETION	87	0.47187728	1.7216474	<0.0001	0.038775224	0.986	1,855	tags=32%, list=14%, signal=37%
GO_NEGATIVE_REGULATION_OF_VIRAL_GENOME_REPLICATION	39	0.7157666	1.7215452	0.004024145	0.038699824	0.986	1,192	tags=46%, list=9%, signal=51%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_POSITIVE_REGULATION_OF_ALPHA_BETA_T_CELL_PROLIFERATION	18	0.7252045	1.7204026	0.003976143	0.03907675	0.987	2,125	tags=72%, list=16%, signal=86%
GO_RENAL_SYSTEM_PROCESS	90	0.4916161	1.7189918	0.001897533	0.039545413	0.988	1,095	tags=20%, list=8%, signal=22%
GO_PHOSPHOPROTEIN_BINDING	51	0.46871978	1.718659	0.004048583	0.03961413	0.988	1,750	tags=25%, list=13%, signal=29%
GO_POSITIVE_REGULATION_OF_MAST_CELL_ACTIVATION	15	0.698499	1.7185397	0.007968128	0.03955995	0.988	1,650	tags=47%, list=13%, signal=53%
GO_REGULATION_OF_CYTOKINE_BIOSYNTHETIC_PROCESS	81	0.4930263	1.7183707	0.007604563	0.039524462	0.988	2,006	tags=36%, list=15%, signal=42%
GO_RESPONSE_TO_INTERLEUKIN_4	29	0.5906991	1.7180754	0.005747126	0.039550666	0.988	2,413	tags=48%, list=19%, signal=59%
GO_MHC_PROTEIN_COMPLEX	23	0.89456546	1.7163448	<0.0001	0.04009018	0.989	736	tags=70%, list=6%, signal=74%
GO_NEGATIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	32	0.6092885	1.7154894	0.003875969	0.040335044	0.989	858	tags=19%, list=7%, signal=20%
GO_MHC_CLASS_II_PROTEIN_COMPLEX_BINDING	16	0.8460932	1.7143055	<0.0001	0.040681884	0.989	680	tags=44%, list=5%, signal=46%
GO_POSITIVE_REGULATION_OF_MYOTUBE_DIFFERENTIATION	24	0.6291054	1.714152	0.007707129	0.0406283	0.989	1,039	tags=17%, list=8%, signal=18%
GO_RESPONSE_TO_PROTOZOAN	19	0.6579047	1.7137913	0.009652509	0.040671404	0.989	1,698	tags=32%, list=13%, signal=36%
GO_DENDRITIC_CELL_MIGRATION	15	0.8489057	1.7135756	<0.0001	0.04065374	0.99	857	tags=60%, list=7%, signal=64%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_REGULATION_OF_GTPASE_ACTIVITY	484	0.38836253	1.7133865	<0.0001	0.040630758	0.99	1,652	tags=19%, list=13%, signal=21%
GO_POSITIVE_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	24	0.6919546	1.7131908	0.006060606	0.040608767	0.99	904	tags=33%, list=7%, signal=36%
GO_REGULATION_OF_LYMPHOCYTE_APOPTOTIC_PROCESS	40	0.5693412	1.7130693	0.001988072	0.040548455	0.99	897	tags=23%, list=7%, signal=24%
GO_REGULATION_OF_ION_TRANSPORT	484	0.37443087	1.7121652	<0.0001	0.040809523	0.99	2,136	tags=20%, list=16%, signal=23%
GO_NEGATIVE_REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYLATION	32	0.5888769	1.7119789	0.007692308	0.040801585	0.99	689	tags=25%, list=5%, signal=26%
GO_DIVALENT_INORGANIC_CATION_HOMEOSTASIS	292	0.41130772	1.7109592	<0.0001	0.041107226	0.99	1,205	tags=15%, list=9%, signal=16%
GO_REGULATION_OF_RNA_STABILITY	116	0.37696254	1.7068299	0.013833992	0.042745013	0.99	1,886	tags=18%, list=14%, signal=21%
GO_REGULATION_OF_VIRAL_GENOME_REPLICATION	64	0.5837243	1.7066398	0.014028057	0.042696003	0.99	1,706	tags=36%, list=13%, signal=41%
GO_REGULATION_OF_TYPE_2_IMMUNE_RESPONSE	23	0.6593105	1.7045233	0.011881189	0.043431737	0.99	2,307	tags=48%, list=18%, signal=58%
GO_PHAGOCYTIC_VESICLE_MEMBRANE	45	0.6106065	1.704519	0.014	0.043333698	0.99	1,176	tags=33%, list=9%, signal=37%
GO_REGULATION_OF_SMOOTH_MUSCLE_CELL_PROLIFERATION	92	0.5128374	1.7038559	0.003861004	0.043554336	0.99	1,686	tags=25%, list=13%, signal=29%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_DEGRANULATION	17	0.6914683	1.7029865	0.003937008	0.043882094	0.99	1,686	tags=41%, list=13%, signal=47%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_PROTEIN_SECRETION	88	0.46626243	1.7028526	0.002016129	0.043864977	0.991	1,121	tags=18%, list=9%, signal=20%
GO_NEGATIVE_REGULATION_OF_T_CELL_DIFFERENTIATION	25	0.584564	1.7020695	0.007619048	0.044134635	0.991	1,617	tags=24%, list=12%, signal=27%
GO_POSITIVE_REGULATION_OF_PHOSPHOLIPASE_ACTIVITY	47	0.5383247	1.7013012	0.009803922	0.044344958	0.991	2,243	tags=28%, list=17%, signal=33%
GO_REGULATION_OF_NITRIC_OXIDE_SYNTHASE_BIOSYNTHETIC_PROCESS	16	0.72484285	1.7006935	0.004115226	0.04448494	0.991	692	tags=38%, list=5%, signal=40%
GO_EXTRINSIC_COMPONENT_OF_PLASMA_MEMBRANE	116	0.4305448	1.7001531	0.003952569	0.044686537	0.991	1,512	tags=21%, list=12%, signal=23%
GO_INFLAMMATORY_RESPONSE_TO_ANTIGENIC_STIMULUS	20	0.662298	1.6997823	0.013645224	0.044721518	0.991	2,808	tags=60%, list=22%, signal=76%
GO_POSITIVE_REGULATION_OF_GLYCOPROTEIN_METABOLIC_PROCESS	18	0.6661368	1.6995796	0.003960396	0.04472392	0.991	326	tags=28%, list=3%, signal=28%
GO_POSITIVE_REGULATION_OF_STRESS_ACTIVATED_PROTEIN_KINASE_SIGNALING_CASCADE	119	0.4405813	1.6980499	<0.0001	0.045318075	0.991	1,841	tags=28%, list=14%, signal=32%
GO_PHAGOCYTOSIS_RECOGNITION	16	0.7887393	1.6974385	0.001984127	0.04549758	0.991	1,492	tags=63%, list=11%, signal=70%
GO_REGULATION_OF_PHOSPHOLIPASE_C_ACTIVITY	34	0.5518536	1.6971331	0.007952286	0.04552687	0.991	2,583	tags=38%, list=20%, signal=48%
GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_APOPTOTIC_PROCESS	21	0.620148	1.6970999	0.00407332	0.04543287	0.991	701	tags=19%, list=5%, signal=20%
GO_PROSTANOID_METABOLIC_PROCESS	21	0.67924565	1.6949985	0.004081633	0.04615291	0.992	1,830	tags=38%, list=14%, signal=44%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_APOPTOTIC_CELL_CLEARANCE	24	0.6037777	1.6948177	0.009803922	0.046127006	0.992	1,924	tags=42%, list=15%, signal=49%
GO_POSITIVE_CHEMOTAXIS	33	0.6478908	1.6934813	0.002028398	0.046698637	0.992	413	tags=15%, list=3%, signal=16%
GO_RESPONSE_TO_INTERFERON_ALPHA	20	0.735804	1.6932168	0.004065041	0.046677716	0.992	548	tags=40%, list=4%, signal=42%
GO_PURINERGIC_NUCLEOTIDE_RECEPTOR_SIGNALING_PATHWAY	17	0.6098168	1.693195	0.017964073	0.046584014	0.992	1,109	tags=29%, list=9%, signal=32%
GO_NEGATIVE_REGULATION_OF_LYASE_ACTIVITY	26	0.50422597	1.6931634	0.012072435	0.046497792	0.992	2,514	tags=35%, list=19%, signal=43%
GO_PROTEIN_KINASE_B_SIGNALING	31	0.5996633	1.692913	0.003787879	0.046495676	0.992	1,275	tags=32%, list=10%, signal=36%
GO_MEMBRANE_MICRODOMAIN	251	0.4393348	1.692394	0.005791506	0.04664503	0.993	2,177	tags=30%, list=17%, signal=36%
GO_PROTEIN_COMPLEX_INVOLVED_IN_CELL_ADHESION	26	0.61954904	1.6921184	0.019646365	0.046637032	0.993	767	tags=27%, list=6%, signal=29%
GO_EMBRYONIC_HEMOPOIESIS	18	0.5675768	1.6906922	0.01923077	0.047188908	0.993	2,617	tags=44%, list=20%, signal=56%
GO_REGULATION_OF_LIPASE_ACTIVITY	73	0.51269907	1.6870124	0.001937985	0.04882752	0.993	1,686	tags=21%, list=13%, signal=23%
GO_POSITIVE_REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYLATION	142	0.44961143	1.6850901	<0.0001	0.049718138	0.993	1,933	tags=27%, list=15%, signal=31%
GO_RESPONSE_TO_VITAMIN_D	32	0.6031821	1.6842252	0.005836576	0.05005602	0.993	1,401	tags=34%, list=11%, signal=38%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_REGULATION_OF_ERYTHROCYTE_DIFFERENTIATION	28	0.53962976	1.6833166	0.007843138	0.050365683	0.993	779	tags=25%, list=6%, signal=27%
GO_ACTIN_POLYMERIZATION_OR_DEPOLYMERIZATION	33	0.5510305	1.6812793	0.003787879	0.05128354	0.994	714	tags=24%, list=5%, signal=26%
GO_DEFENSE_RESPONSE_TO_BACTERIUM	149	0.5156749	1.6812707	0.001915709	0.051174887	0.994	2,006	tags=36%, list=15%, signal=42%
GO_REGULATION_OF_T_CELL_MIGRATION	21	0.8098312	1.6804435	0.002016129	0.05145071	0.994	857	tags=52%, list=7%, signal=56%
GO_CELL_CELL_RECOGNITION	41	0.5245067	1.6801103	0.003960396	0.051519234	0.994	326	tags=15%, list=3%, signal=15%
GO_POSITIVE_REGULATION_OF_WOUND_HEALING	43	0.61657333	1.6800473	0.001901141	0.051436365	0.994	965	tags=30%, list=7%, signal=33%
GO_NEGATIVE_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	20	0.62751234	1.6788567	0.012474013	0.05187594	0.994	1,438	tags=45%, list=11%, signal=51%
GO_CHEMOKINE_BINDING	19	0.6739428	1.6778512	0.017509727	0.05225219	0.995	1,637	tags=58%, list=13%, signal=66%
GO_INTRINSIC_COMPONENT_OF_ENDOPLASMIC_RETICULUM_MEMBRANE	94	0.49455816	1.6774647	0.00204499	0.05231441	0.995	1,242	tags=23%, list=10%, signal=26%
GO_NEGATIVE_REGULATION_OF_CELL_ADHESION	184	0.47135058	1.6772134	0.005769231	0.052339967	0.995	1,346	tags=22%, list=10%, signal=24%
GO_REGULATION_OF_MACROPHAGE_CHEMOTAXIS	15	0.756752	1.676961	0.003838772	0.05234555	0.995	491	tags=33%, list=4%, signal=35%
GO_LIPASE_ACTIVITY	82	0.498321	1.6748518	0.003891051	0.05323888	0.995	920	tags=18%, list=7%, signal=20%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_PODOSOME	16	0.71842396	1.6740463	0.013645224	0.053582188	0.995	836	tags=44%, list=6%, signal=47%
GO_REGULATION_OF_NUCLEASE_ACTIVITY	21	0.59528714	1.6738061	0.009881423	0.053603686	0.995	482	tags=14%, list=4%, signal=15%
GO_POSITIVE_REGULATION_OF_NF_KAPPAB_TRANSCRIPTION_FACTOR_ACTIVITY	116	0.44419417	1.6737623	0.007952286	0.05352827	0.995	1,675	tags=22%, list=13%, signal=25%
GO_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	21	0.6095065	1.6734543	0.019762846	0.053594723	0.995	3,160	tags=52%, list=24%, signal=69%
GO_POSITIVE_REGULATION_OF_SECRETION	315	0.40215108	1.6733084	<0.0001	0.053550158	0.995	2,019	tags=24%, list=15%, signal=28%
GO_REGULATION_OF_ACTIN_CYTOSKELETON_REORGANIZATION	29	0.58845127	1.6717042	0.008080808	0.054176316	0.995	174	tags=17%, list=1%, signal=17%
GO_REGULATION_OF_MONOCYTE_CHEMOTAXIS	19	0.81784075	1.6698437	0.005836576	0.05503222	0.995	857	tags=53%, list=7%, signal=56%
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_MIGRATION	28	0.69106454	1.6693434	0.00591716	0.05516261	0.995	619	tags=32%, list=5%, signal=34%
GO_POSITIVE_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIIUM_IION_INTO_CYTOSOL	33	0.57768655	1.6688395	0.009727626	0.05532485	0.995	2,125	tags=36%, list=16%, signal=43%
GO_NEURONAL_CELL_BODY_MEMBRANE	15	0.54601926	1.6680969	0.007874016	0.055594597	0.995	2,243	tags=33%, list=17%, signal=40%
GO_LYTIC_VACUOLE	394	0.43830115	1.6678655	0.002066116	0.055630323	0.995	1,737	tags=22%, list=13%, signal=24%
GO_NEGATIVE_REGULATION_OF_BEHAVIOR	15	0.4978872	1.6670024	0.030800821	0.05597134	0.996	187	tags=7%, list=1%, signal=7%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_REGULATION_OF_CYSSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY	183	0.46807796	1.6667646	<0.0001	0.055999085	0.996	1,322	tags=21%, list=10%, signal=23%
GO_POSITIVE_REGULATION_OF_MUSCLE_CELL_DIFFERENTIATION	67	0.44632638	1.6661528	0.001890359	0.05621736	0.996	1,675	tags=19%, list=13%, signal=22%
GO_REGULATION_OF_ENDOCYTOSIS	173	0.4310654	1.6661099	0.001968504	0.0561278	0.996	1,661	tags=20%, list=13%, signal=23%
GO_FATTY_ACID_DERIVATIVE_BIOSYNTHETIC_PROCESS	33	0.59479517	1.6660037	0.016129032	0.056079432	0.996	1,641	tags=39%, list=13%, signal=45%
GO_POSITIVE_REGULATION_OF_STRIATED_MUSCLE_CELL_DIFFERENTIATION	39	0.52498645	1.6650743	0.011560693	0.056441057	0.996	3,070	tags=46%, list=24%, signal=60%
GO_WOUND_HEALING	410	0.43785834	1.6641076	0.003717472	0.056859415	0.996	1,310	tags=22%, list=10%, signal=23%
GO_RESPONSE_TO_TEMPERATURE_STIMULUS	129	0.46067154	1.6626776	<0.0001	0.057553455	0.996	1,924	tags=15%, signal=31%, tags=31%, list=4%, signal=32%
GO_REGULATION_OF_MONONUCLEAR_CELL_MIGRATION	16	0.7773211	1.6625817	0.011857707	0.057495896	0.996	491	tags=31%, list=4%, signal=32%
GO_POSITIVE_REGULATION_OF_ENDOCYTOSIS	96	0.5143921	1.6624179	0.007827789	0.057463013	0.996	1,933	tags=31%, list=15%, signal=36%
GO_NEGATIVE_REGULATION_OF_SECRETION	171	0.4086896	1.6611387	0.001848429	0.05801641	0.996	1,855	tags=26%, list=14%, signal=30%
GO_RESPONSE_TO_EXOGENOUS_DSRNA	37	0.4793092	1.6610442	0.017175572	0.057939034	0.996	1,609	tags=22%, list=12%, signal=25%
GO_REGULATION_OF_BONE_RESORPTION	28	0.59013915	1.660557	0.008492569	0.058153924	0.996	1,150	tags=36%, list=9%, signal=39%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_REGULATION_OF_CELLULAR_AMINO_ACID_METABOLIC_PROCESS	60	0.4705263	1.6589645	0.038934425	0.05890962	0.997	1,702	tags=18%, list=13%, signal=21%
GO_POSITIVE_REGULATION_OF_LIPID_KINASE_ACTIVITY	28	0.6318595	1.6574925	0.011811024	0.059654377	0.997	2,340	tags=43%, list=18%, signal=52%
GO_COATED_VESICLE	193	0.4018852	1.6557094	0.004123712	0.06045135	0.997	1,035	tags=15%, list=8%, signal=16%
GO_POSITIVE_REGULATION_OF_TRANSMEMBRANE_TRANSPORT	110	0.46212065	1.6549575	0.001964637	0.06078703	0.997	2,125	tags=27%, list=16%, signal=32%
GO_GLYCOSAMINOGLYCAN_BINDING	166	0.5700713	1.653691	0.005736138	0.06146447	0.997	1,638	tags=33%, list=13%, signal=24%
GO_RESPONSE_TO_WOUNDING	493	0.4314735	1.6536663	0.001838235	0.061361298	0.997	1,645	tags=24%, list=13%, signal=26%
GO_POSITIVE_REGULATION_OF_LIPASE_ACTIVITY	56	0.49611095	1.6524596	0.007782101	0.0619012	0.997	1,205	tags=16%, list=9%, signal=18%
GO_REGULATION_OF_MYOBlast_DIFFERENTIATION	39	0.56578183	1.6510456	0.007984032	0.062561154	0.997	808	tags=18%, list=6%, signal=19%
GO_NEGATIVE_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	20	0.5854017	1.6497446	0.015779093	0.06316219	0.997	690	tags=25%, list=5%, signal=26%
GO_RESPIRATORY_GASEOUS_EXCHANGE	43	0.47522587	1.6485827	0.004115226	0.063703835	0.997	1,641	tags=21%, list=13%, signal=24%
GO_REGULATION_OF_LYMPHOCYTE_CHEMOTAXIS	18	0.8365054	1.6484256	<0.0001	0.06365371	0.997	333	tags=44%, list=3%, signal=46%
GO_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	91	0.44227648	1.647313	<0.0001	0.0642078	0.997	1,803	tags=27%, list=14%, signal=32%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_SH2_DOMAIN_BINDING	26	0.5083324	1.6471581	0.00996016	0.06417494	0.997	665	tags=23%, list=5%, signal=24%
GO_CARBOHYDRATE_BINDING	195	0.46877322	1.6469892	<0.0001	0.064155184	0.997	1,713	tags=26%, list=13%, signal=30%
GO_RESPONSE_TO_HEAT	78	0.47371614	1.6460786	0.001953125	0.06456932	0.997	1,591	tags=26%, list=12%, signal=29%
GO_VACUOLAR_MEMBRANE	418	0.38154572	1.6438872	<0.0001	0.065663666	0.998	1,527	tags=17%, list=12%, signal=19%
GO_POSITIVE_REGULATION_OF_NUCLEOTIDE_METABOLIC_PROCESS	120	0.39775303	1.6437685	0.001996008	0.06561043	0.998	1,425	tags=16%, list=11%, signal=18%
GO_POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	15	0.6816081	1.6437383	0.015533981	0.065511994	0.998	1,686	tags=40%, list=13%, signal=46%
GO_REGULATION_OF_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	36	0.6168438	1.6432487	0.02004008	0.06564188	0.998	1,880	tags=47%, list=14%, signal=55%
GO_MAST_CELL_GRANULE	17	0.68839246	1.6427972	0.010162601	0.065832764	0.998	1,029	tags=41%, list=8%, signal=45%
GO_RESPONSE_TO_AMMONIUM_ION	41	0.51495653	1.6420949	0.011538462	0.06615705	0.998	414	tags=15%, list=3%, signal=15%
GO_LYTIC_VACUOLE_MEMBRANE	192	0.44220704	1.6420468	0.012578616	0.06605077	0.998	905	tags=14%, list=7%, signal=15%
GO_QUATERNARY_AMMONIUM_GROUP_BINDING	41	0.549468	1.6416852	0.00733945	0.066144675	0.998	522	tags=12%, list=4%, signal=13%
GO_POSITIVE_REGULATION_OF_SEQUESTERING_OF_CALCIIUM_ION	15	0.6283605	1.6415176	0.01443299	0.06613593	0.998	1,984	tags=40%, list=15%, signal=47%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_POSITIVE_REGULATION_OF_PHOSPHOLIPID_METABOLIC_PROCESS	38	0.58154684	1.6374198	0.00952381	0.068494804	0.998	1,275	tags=26%, list=10%, signal=29%
GO_REGULATION_OF_PEPTIDE_TRANSPORT	221	0.3763373	1.6368446	<0.0001	0.06870789	0.998	1,777	tags=20%, list=14%, signal=23%
GO_NEGATIVE_REGULATION_OF_ERK1_AND_ERK2_CASCADE	41	0.559067	1.6362346	0.020120725	0.0689411	0.998	1,302	tags=29%, list=10%, signal=32%
GO_REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_STAT5_PROTEIN	18	0.6317847	1.6352926	0.007326007	0.069378175	0.998	602	tags=22%, list=5%, signal=23%
GO_PEPTIDYL_TYROSINE_MODIFICATION	168	0.39073545	1.634941	0.009363296	0.069455616	0.998	1,652	tags=20%, list=13%, signal=22%
GO_RECEPTOR_COMPLEX	268	0.37122625	1.6347965	0.005758158	0.069407634	0.998	2,027	list=16%, signal=26%
GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	31	0.531752	1.6345485	0.011516315	0.069419906	0.998	139	tags=10%, list=1%, signal=10%
GO_REGULATION_OF_CELL_ADHESION_MEDIATED_BY_INTEGRIN	34	0.6399531	1.634022	0.013011153	0.06957873	0.998	613	tags=29%, list=5%, signal=31%
GO_ACTIVATION_OF_PHOSPHOLIPASE_C_ACTIVITY	22	0.55139333	1.6334804	0.012096774	0.06975509	0.998	2,583	tags=41%, list=20%, signal=51%
GO_RESPONSE_TO_VITAMIN	97	0.5084193	1.6318773	0.003861004	0.0705805	0.999	1,437	tags=27%, list=11%, signal=30%
GO_RESPONSE_TO_ATP	26	0.57034755	1.6311241	0.022857143	0.07093846	1	1,242	tags=27%, list=10%, signal=30%
GO_NATURAL_KILLER_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	20	0.5158592	1.6304823	0.032818533	0.07124633	1	795	tags=10%, list=6%, signal=11%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_HYDROGEN_PEROXIDE_METABOLIC_PROCESS	26	0.65050497	1.6282947	0.015594542	0.0724298	1	764	tags=31%, list=6%, signal=33%
GO_REGULATION_OF_VASCULATURE_DEVELOPMENT	208	0.49029812	1.6278462	0.007434944	0.07257382	1	2,153	tags=34%, list=17%, signal=40%
GO_REGULATION_OF_JNK_CASCADE	135	0.41237795	1.6273332	0.007590133	0.07272968	1	1,841	tags=26%, list=14%, signal=30%
GO_RESPONSE_TO_COPPER_ION	27	0.6072811	1.6265616	0.007782101	0.073034324	1	1,932	tags=37%, list=15%, signal=43%
GO_REGULATION_OF_VASOCONSTRICTION	61	0.46238223	1.6251533	0.019569471	0.073857635	1	2,979	tags=39%, list=23%, signal=51%
GO_NEGATIVE_REGULATION_OF_SIGNAL_TRANSDUCTION_IN_ABSENCE_OF_LIGAND	27	0.5336353	1.6249008	0.013207547	0.073871605	1	992	tags=19%, list=8%, signal=20%
GO_RECEPTOR_METABOLIC_PROCESS	70	0.49931595	1.6248444	0.011976048	0.07376011	1	2,066	tags=31%, list=16%, signal=37%
GO_RESPONSE_TO_COLD	37	0.5727713	1.622818	0.013752456	0.074841194	1	1,771	tags=27%, list=14%, signal=31%
GO_AGING	236	0.41214135	1.6226403	<0.0001	0.074791886	1	1,136	tags=17%, list=9%, signal=18%
GO_REGULATION_OF_ACUTE_INFLAMMATORY_RESPONSE	69	0.58681303	1.6208405	0.029354207	0.07579995	1	1,722	tags=33%, list=13%, signal=38%
GO_POSITIVE_REGULATION_OF_CATION_TRANSMEMBRANE_TRANSPORT	81	0.46252343	1.6207762	0.003984064	0.07570439	1	2,125	tags=28%, list=16%, signal=34%
GO_G_PROTEIN_ALPHA_SUBUNIT_BINDING	20	0.66085917	1.6205537	0.015810277	0.075685486	1	1,035	tags=35%, list=8%, signal=38%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_REGULATION_OF_RESPONSE_TO_INTERFERON_GAMMA	19	0.5683653	1.6203823	0.022267206	0.07565565	1	1,914	tags=32%, list=15%, signal=37%
GO_AMIDE_BINDING	233	0.4064042	1.6201241	0.003937008	0.07567735	1	2,152	tags=25%, list=17%, signal=30%
GO_EARLY_ENDOSOME_MEMBRANE	81	0.4063196	1.619373	0.01026694	0.07605624	1	1,527	tags=21%, list=12%, signal=24%
GO_REGULATION_OF_INTERLEUKIN_5_PRODUCTION	18	0.516418	1.6184427	0.030991735	0.07658821	1	2,117	tags=33%, list=16%, signal=40%
GO_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	178	0.46018672	1.6182923	0.005905512	0.07656341	1	1,233	tags=22%, list=9%, signal=24%
GO_CYTOLYSIS	23	0.7442266	1.6182748	<0.0001	0.076444544	1	661	tags=39%, list=5%, signal=41%
GO_PEPTIDE_RECEPTOR_ACTIVITY	102	0.4188236	1.6180683	0.02303263	0.07643392	1	1,330	tags=17%, list=10%, signal=18%
GO_NEGATIVE_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	27	0.5547977	1.6176138	0.01754386	0.07660388	1	1,313	tags=26%, list=10%, signal=29%
GO_SH3_DOMAIN_BINDING	91	0.4461407	1.6168742	0.015779093	0.076888435	1	1,886	tags=30%, list=14%, signal=34%
GO_RESPONSE_TO_IMMOBILIZATION_STRESS	19	0.6766947	1.616021	0.011627907	0.07729871	1	426	tags=26%, list=3%, signal=27%
GO_HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_BUT_NOT_PEPTIDE_BONDS_IN_CYCLIC_AMIDINES	25	0.56361735	1.6157919	0.017928287	0.07731517	1	1,885	tags=36%, list=14%, signal=42%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_EXTRINSIC_COMPONENT_OF_MEMBRANE	204	0.36614722	1.6151824	0.003944773	0.07755418	1	1,678	tags=20%, list=13%, signal=22%
GO_CELLULAR_CHEMICAL_HOMEOSTASIS	476	0.37752402	1.6147146	<0.0001	0.07777504	1	2,033	tags=22%, list=16%, signal=26%
GO_REGULATION_OF_VESICLE_MEDIATED_TRANSPORT	364	0.37182406	1.6143713	0.003952569	0.077858694	1	1,803	tags=20%, list=14%, signal=23%
GO_REGULATION_OF_GLYCOPROTEIN_METABOLIC_PROCESS	37	0.5299447	1.6138818	0.008163265	0.078032814	1	905	tags=22%, list=7%, signal=23%
GO_POSITIVE_REGULATION_OF_PEPTIDASE_ACTIVITY	133	0.44513747	1.6115044	0.005555556	0.079610266	1	1,417	tags=21%, list=11%, signal=26%
GO_REGULATION_OF_PROTEIN_IMPORT	155	0.42717382	1.6111833	0.005964215	0.07967744	1	1,777	tags=14%, signal=30%
GO_NEGATIVE_REGULATION_OF_VIRAL_ENTRY_INTO_HOST_CELL	18	0.6478269	1.6109498	0.024048096	0.07968459	1	1,298	tags=28%, list=10%, signal=31%
GO_NEGATIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	71	0.44421846	1.6106853	0.003984064	0.07972274	1	801	tags=18%, list=6%, signal=19%
GO_NEGATIVE_REGULATION_OF_MUSCLE_CONTRACTION	22	0.6257531	1.6106497	0.02631579	0.07961466	1	1,678	tags=45%, list=13%, signal=52%
GO_RESPONSE_TO_PROSTAGLANDIN_E	24	0.6179022	1.6105227	0.013752456	0.079573765	1	326	tags=21%, list=3%, signal=21%
GO_POSITIVE_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	30	0.5718105	1.6097096	0.020833334	0.080006234	1	1,280	tags=23%, list=10%, signal=26%
GO_REGULATION_OF_BODY_FLUID_LEVELS	440	0.3986867	1.6088496	0.001824818	0.08044537	1	2,066	tags=26%, list=16%, signal=30%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_REGULATION_OF_CYTOPLASMIC_TRANSPORT	385	0.36882934	1.607118	<0.0001	0.08152557	1	1,875	tags=21%, list=14%, signal=23%
GO_EARLY_ENDOSOME	231	0.35334077	1.6069337	<0.0001	0.08150465	1	1,848	tags=20%, list=14%, signal=23%
GO_ACTIVATION_OF_PROTEIN_KINASE_A_ACTIVITY	15	0.549266	1.6058896	0.03206413	0.082134776	1	323	tags=13%, list=2%, signal=14%
GO_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	133	0.46699125	1.6051867	0.007827789	0.08247016	1	1,678	tags=27%, list=13%, signal=31%
GO_PHOSPHATIDYLCHOLINE_BINDING	16	0.7486771	1.6047784	0.007380074	0.08263372	1	522	tags=31%, list=4%, signal=33%
GO_ENDOPEPTIDASE_ACTIVITY	311	0.41902053	1.6025649	0.001930502	0.08414562	1	1,767	tags=21%, list=14%, signal=24%
GO_CELLULAR_RESPONSE_TO_HEAT	30	0.56308794	1.6022106	0.013888889	0.084240414	1	348	tags=17%, list=3%, signal=17%
GO_PROSTANOID_BIOSYNTHETIC_PROCESS	15	0.67827386	1.601997	0.016096579	0.08424953	1	1,641	tags=40%, list=13%, signal=46%
GO_POSITIVE_REGULATION_OF_CALCIIUM_ION_TRANSMEMBRANE_TRANSPORT	50	0.50207436	1.6016357	0.010060363	0.084351756	1	2,125	tags=32%, list=16%, signal=38%
GO_POSITIVE_REGULATION_OF_CYTOPLASMIC_TRANSPORT	221	0.40352935	1.6014302	0.002028398	0.0843505	1	1,875	tags=24%, list=14%, signal=28%
GO_POSITIVE_REGULATION_OF_INTRACELLULAR_TRANSPORT	295	0.3844743	1.6010702	0.003921569	0.08446372	1	1,831	tags=22%, list=14%, signal=25%
GO_POSITIVE_REGULATION_OF_PROTEIN_COMPLEX_ASSEMBLY	157	0.42255938	1.5995139	0.001968504	0.08530157	1	1,692	tags=20%, list=13%, signal=23%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_MOVEMENT_IN_ENVIRONMENT_OF_OTHER_ORGANISM_INVOLVED_IN_SYMBIOTIC_INTERACTION	82	0.46533743	1.5988591	0.003831418	0.08559607	1	1,723	tags=29%, list=13%, signal=34%
GO_REGULATION_OF_CARDIAC_MUSCLE_CONTRACTION_BY_REGULATION_OF_THE_RELEASE_OF_SEQUESTERED_CALCIIUM_ION	19	0.5675399	1.5986755	0.037656903	0.085587025	1	1,984	tags=26%, list=15%, signal=31%
GO_POSITIVE_REGULATION_OF_MYOBLAST_DIFFERENTIATION	19	0.5856352	1.5985917	0.015841585	0.08550437	1	808	tags=16%, list=6%, signal=17%
GO_CHEMOATTRACTANT_ACTIVITY	24	0.66283524	1.5985628	0.00408998	0.08538139	1	413	tags=17%, list=3%, signal=17%
GO_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_BIOSYNTHETIC_PROCESS	59	0.5183318	1.5973943	0.01778656	0.08603993	1	1,824	tags=34%, list=14%, signal=39%
GO_NEGATIVE_REGULATION_OF_SMOOTH_MUSCLE_CONTRACTION	15	0.6996116	1.5970716	0.028806584	0.08613654	1	1,650	tags=53%, list=13%, signal=61%
GO_POSITIVE_REGULATION_OF_PROTEOLYSIS	302	0.37027892	1.5963862	<0.0001	0.08655412	1	1,675	tags=19%, list=13%, signal=22%
GO_REGULATION_OF_VIRAL_ENTRY_INTO_HOST_CELL	26	0.592323	1.5954287	0.025742574	0.087090306	1	1,471	tags=31%, list=11%, signal=35%
GO_ENZYME_ACTIVATOR_ACTIVITY	336	0.36121917	1.5944977	0.003992016	0.08759516	1	1,637	tags=18%, list=13%, signal=20%
GO_POSITIVE_REGULATION_OF_KINASE_ACTIVITY	407	0.3670306	1.594292	<0.0001	0.087598324	1	1,936	tags=22%, list=15%, signal=25%
GO_RESPONSE_TO_DRUG	393	0.42127782	1.5932866	0.001862197	0.08819739	1	1,437	tags=20%, list=11%, signal=22%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	96	0.42133406	1.593167	0.010162601	0.08813351	1	1,783	tags=25%, list=14%, signal=29%
GO_POSITIVE_REGULATION_OF_INTERFERON_BETA_PRODUCTION	26	0.5439814	1.5924957	0.020283977	0.088441275	1	2,103	tags=38%, list=16%, signal=46%
GO_CELLULAR_RESPONSE_TO_INTERLEUKIN_4	24	0.5942298	1.5923799	0.01953125	0.08839475	1	2,364	tags=46%, list=18%, signal=56%
GO_REGULATION_OF_T_HELPER_CELL_DIFFERENTIATION	22	0.57716715	1.5907526	0.023166023	0.08936153	1	306	tags=14%, list=2%, signal=14%
GO_REGULATION_OF_STAT_CASCADE	121	0.42983338	1.5902407	0.020754717	0.08960042	1	963	tags=15%, list=7%, signal=16%
GO_RESPONSE_TO_TRANSITION_METAL_NANOPARTICLE	130	0.52599704	1.5902002	0.003795066	0.08947369	1	1,092	tags=24%, list=8%, signal=26%
GO_REGULATION_OF_ACTIN_FILAMENT_LENGTH	118	0.44284996	1.5900828	0.013592233	0.08940962	1	650	tags=14%, list=5%, signal=14%
GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_NUCLEUS	184	0.39811233	1.5898719	0.007952286	0.0893899	1	1,777	tags=23%, list=14%, signal=26%
GO_NEGATIVE_REGULATION_OF_BIOMINERAL_TISSUE_DEVELOPMENT	16	0.69006467	1.5891459	0.017716536	0.08979904	1	2,061	tags=63%, list=16%, signal=74%
GO_CALCIIUM_MEDIATED_SIGNALING	76	0.44902647	1.587518	0.011976048	0.090871684	1	994	tags=17%, list=8%, signal=18%
GO_TRANSITION_METAL_ION_HOMEOSTASIS	82	0.47446078	1.5870253	0.007707129	0.091118686	1	1,803	tags=30%, list=14%, signal=35%
GO_RECEPTOR_INTERNALIZATION	47	0.549609	1.5869439	0.018480493	0.091031305	1	1,228	tags=26%, list=9%, signal=28%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_ACTIVATION_OF_GTPASE_ACTIVITY	50	0.47707304	1.5869141	0.011952192	0.09091259	1	1,933	tags=30%, list=15%, signal=35%
GO_POSITIVE_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION	410	0.37452075	1.5863159	<0.0001	0.09118065	1	1,884	tags=23%, list=14%, signal=27%
GO_INACTIVATION_OF_MAPK_ACTIVITY	23	0.5758043	1.5859618	0.010288066	0.09127138	1	1,038	tags=30%, list=8%, signal=33%
GO_REGULATION_OF_AUTOPHAGY	194	0.3707718	1.5858507	0.002087683	0.09120092	1	2,445	tags=28%, list=19%, signal=34%
GO_REGULATION_OF_VIRAL_TRANSCRIPTION	58	0.4308992	1.584255	0.01192843	0.09221609	1	1,410	tags=14%, list=11%, signal=15%
GO_REGULATION_OF_NUCLEOTIDE_METABOLIC_PROCESS	191	0.37335977	1.5830222	0.004115226	0.09297471	1	1,751	tags=18%, list=13%, signal=20%
GO_CELLULAR_RESPONSE_TO_AMINO_ACID_STARVATION	18	0.56387824	1.5829109	0.022916667	0.09292113	1	1,692	tags=28%, list=13%, signal=32%
GO_CELLULAR_RESPONSE_TO_OXIDATIVE_STRESS	155	0.43070754	1.5828198	<0.0001	0.09283431	1	1,280	tags=21%, list=10%, signal=23%
GO_CELLULAR_RESPONSE_TO_ACID_CHEMICAL	152	0.44707972	1.5824952	0.003838772	0.09293288	1	1,686	tags=24%, list=13%, signal=28%
GO_BLOOD_MICROPARTICLE	103	0.6062135	1.5822635	0.04174573	0.09295068	1	1,763	tags=34%, list=14%, signal=39%
GO_DETECTION_OF_BIOTIC_STIMULUS	20	0.6493365	1.5821697	0.02886598	0.09288049	1	1,841	tags=55%, list=14%, signal=64%
GO_NEGATIVE_REGULATION_OF_RECEPTOR_ACTIVITY	23	0.57186043	1.581836	0.02970297	0.09301716	1	1,984	tags=39%, list=15%, signal=46%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_MODULATION_BY_VIRUS_OF_HOST_MORPHOLOGY_OR_PHYSIOLOGY	35	0.3950923	1.5816705	0.013539651	0.0930114	1	2,204	tags=34%, list=17%, signal=41%
GO_MYD88_INDEPENDENT_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	29	0.536574	1.5812528	0.04347826	0.09318458	1	1,786	tags=31%, list=14%, signal=36%
GO_C21_STEROID_HORMONE_METABOLIC_PROCESS	24	0.6354846	1.5794928	0.01980198	0.09446306	1	2,058	tags=46%, list=16%, signal=54%
GO_IMMUNOGLOBULIN_PRODUCTION_INVOLVED_IN _IMMUNOGLOBULIN_MEDIATED_IMMUNE_RESPONSE	18	0.6174812	1.5785809	0.028282829	0.095020354	1	621	tags=28%, list=5%, signal=29%
GO_REGULATION_OF_PROTEIN_AUTOPHOSPHORYLATION	32	0.5492554	1.5779927	0.031007752	0.0952971	1	1,468	tags=28%, list=11%, signal=32%
GO_MAST_CELL_MEDIATED_IMMUNITY	16	0.613695	1.5776978	0.035051547	0.09536977	1	1,029	tags=38%, list=8%, signal=41%
GO_ION_HOMEOSTASIS	481	0.36480296	1.5764912	<0.0001	0.096138686	1	2,090	tags=21%, list=16%, signal=25%
GO_OVULATION	16	0.6834791	1.5763439	0.01734104	0.0960869	1	992	tags=38%, list=8%, signal=41%
GO_PEPTIDASE_ACTIVITY	438	0.38251337	1.5760585	0.003861004	0.09611979	1	1,820	tags=22%, list=14%, signal=25%
GO_RESPONSE_TO_OXIDATIVE_STRESS	308	0.40930682	1.5756147	0.005905512	0.09632467	1	1,301	tags=20%, list=10%, signal=22%
GO_CELLULAR_RESPONSE_TO_FLUID_SHEAR_STRESS	19	0.6262779	1.5746142	0.04008016	0.0970002	1	1,659	tags=42%, list=13%, signal=48%
GO_REGULATION_OF_CELLULAR_EXTRAVASATION	20	0.7011876	1.573882	0.019305019	0.097404666	1	1,906	tags=55%, list=15%, signal=64%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_CELLULAR_RESPONSE_TO_ALKALOID	31	0.51790226	1.571339	0.02385686	0.099194616	1	280	tags=10%, list=2%, signal=10%
GO_MANNOSE_BINDING	17	0.608629	1.5713043	0.023166023	0.09906045	1	1,832	tags=47%, list=14%, signal=55%
GO_REGULATION_OF_WOUND_HEALING	112	0.5116885	1.5705945	0.009469697	0.09945906	1	1,288	tags=29%, list=10%, signal=32%
GO_REGULATION_OF_STRESS_ACTIVATED_PROTEIN_KINASE_SIGNALING_CASCADE	170	0.38573074	1.5701944	0.005576208	0.099609695	1	1,841	tags=25%, list=14%, signal=28%
GO_RESPONSE_TO_LIPOPROTEIN_PARTICLE	19	0.70537186	1.5683478	0.017475728	0.10085251	1	965	tags=37%, list=7%, signal=40%
GO_POSITIVE_REGULATION_OF_PHOSPHATASE_ACTIVITY	22	0.5273975	1.5682348	0.023529412	0.10080242	1	915	tags=27%, list=7%, signal=29%
GO_POSITIVE_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_BIOSYNTHETIC_PROCESS	45	0.5154954	1.5679824	0.013592233	0.10080912	1	992	tags=24%, list=8%, signal=26%
GO_SUPEROXIDE_METABOLIC_PROCESS	26	0.5741343	1.5671799	0.026530612	0.10131439	1	612	tags=23%, list=5%, signal=24%
GO_SECOND_MESSENGER_MEDIATED_SIGNALING	139	0.39431605	1.5652554	0.008016032	0.10268211	1	1,419	tags=17%, list=11%, signal=19%
GO_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	16	0.6637055	1.5652145	0.017964073	0.10255099	1	849	tags=31%, list=7%, signal=33%
GO_VASCULAR_PROCESS_IN_CIRCULATORY_SYSTEM	148	0.41731265	1.5647718	0.008064516	0.10273381	1	2,136	tags=28%, list=16%, signal=33%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_REGULATION_OF_PROTEIN_KINASE_B_SIGNALING	105	0.44400927	1.5642767	0.015625	0.10300312	1	2,166	tags=29%, list=17%, signal=34%
GO_POSITIVE_REGULATION_OF_PEPTIDYL_SERINE_PHOSPHORYLATION	76	0.396907	1.5638247	0.01183432	0.10318572	1	1,936	tags=26%, list=15%, signal=31%
GO_BONE_RESORPTION	18	0.5591434	1.563735	0.047904193	0.10311407	1	389	tags=11%, list=3%, signal=11%
GO_REGULATION_OF_INTERLEUKIN_8_SECRETION	17	0.7439021	1.5631915	0.042510122	0.10330101	1	1,689	tags=47%, list=13%, signal=54%
GO_PHAGOSOME_MATURATION	29	0.589179	1.5610179	0.03292181	0.10485202	1	2,286	tags=38%, list=18%, signal=46%
GO_POSITIVE_REGULATION_OF_T_HELPER_CELL_DIFFERENTIATION	16	0.64994365	1.5604873	0.040384617	0.10511876	1	306	tags=19%, list=2%, signal=19%
GO_IRON_ION_HOMEOSTASIS	54	0.50910836	1.5594608	0.01734104	0.10573858	1	1,803	tags=35%, list=14%, signal=41%
GO_HEMATOPOIETIC_PROGENITOR_CELL_DIFFERENTIATION	69	0.42455992	1.5581723	0.00984252	0.106597446	1	1,718	tags=22%, list=13%, signal=25%
GO_LYMPHOCYTE_HOMEOSTASIS	38	0.5157216	1.5580672	0.025157232	0.10653597	1	1,275	tags=26%, list=10%, signal=29%
GO_SIGNALING_PATTERN_RECOGNITION_RECEPTOR_ACTIVITY	15	0.7071069	1.5563309	0.026530612	0.10757307	1	1,686	tags=67%, list=13%, signal=76%
GO_REGULATION_OF_STRIATED_MUSCLE_CELL_DIFFERENTIATION	64	0.45284316	1.5556002	0.00591716	0.108008154	1	1,675	tags=19%, list=13%, signal=21%
GO_REGULATION_OF_SMOOTH_MUSCLE_CELL_MIGRATION	47	0.5394554	1.555568	0.023622047	0.10786912	1	1,638	tags=26%, list=13%, signal=29%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_CELLULAR_RESPONSE_TO_INORGANIC_SUBSTANCE	140	0.45221394	1.5550238	0.017110266	0.108211316	1	1,106	tags=19%, list=8%,
GO_NEGATIVE_REGULATION_OF_KIDNEY_DEVELOPMENT	15	0.59625274	1.5535334	0.038539555	0.109305345	1	2,873	signal=20% tags=47%, list=22%,
GO_REGULATION_OF_MUSCLE_CELL_DIFFERENTIATION	119	0.40780565	1.5533344	0.004008016	0.109293446	1	1,675	signal=60% tags=18%, list=13%,
GO_REGULATION_OF_ANATOMICAL_STRUCTURE_SIZE	388	0.35306945	1.5530814	0.00390625	0.10935427	1	1,652	signal=21% tags=19%, list=13%,
GO_REGULATION_OF_TRANSMEMBRANE_TRANSPORT	342	0.3508361	1.5510957	0.008179959	0.1108562	1	2,125	signal=21% tags=19%, list=16%,
GO_REGULATION_OF_SEQUENCE_SPECIFIC_DNA_BINDING _TRANSCRIPTION_FACTOR_ACTIVITY	301	0.34442586	1.5504049	0.001980198	0.111258	1	1,678	signal=22% tags=19%, list=13%,
GO_PROTEIN_OLIGOMERIZATION	342	0.38594437	1.5503868	0.001988072	0.11111473	1	1,888	signal=22% tags=22%, list=14%,
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_6_PRODUCTION	57	0.5182606	1.549875	0.02366864	0.111399636	1	1,841	signal=25% tags=40%, list=14%,
GO_REGULATION_OF_NITRIC_OXIDE_BIOSYNTHETIC_PROCESS	50	0.52676415	1.5491182	0.03420523	0.11184498	1	1,824	signal=47% tags=36%, list=14%,
GO_POSITIVE_REGULATION_OF_NUCLEOCYTOPLASMIC_TRANSPORT	101	0.43922034	1.5488102	0.003976143	0.11197523	1	1,777	signal=42% tags=29%, list=14%,
GO_GAS_TRANSPORT	15	0.73603135	1.5476182	0.026515152	0.1129165	1	1,310	signal=33% tags=53%, list=10%,
GO_WIDE_PORE_CHANNEL_ACTIVITY	15	0.57973534	1.5469253	0.037383176	0.113340646	1	76	signal=59% tags=7%, list=1%, signal=7%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_T_CELL_MEDIATED_IMMUNITY	22	0.65033275	1.5465237	0.032	0.11354017	1	2,002	tags=50%, list=15%, signal=59%
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	25	0.53944254	1.5461192	0.018108651	0.11370027	1	1,591	tags=36%, list=12%, signal=41%
GO_COMPLEMENT_ACTIVATION	46	0.7079065	1.5450634	0.037254903	0.114464246	1	1,492	tags=54%, list=11%, signal=61%
GO_SECRETION_BY_CELL	382	0.3874144	1.5444571	0.007889546	0.11475576	1	1,159	tags=15%, list=9%, signal=16%
GO_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_PRODUCTION	27	0.5996082	1.5430696	0.040462427	0.115810566	1	1,662	tags=44%, list=13%, signal=51%
GO_POSITIVE_REGULATION_OF_TISSUE_REMODELING	24	0.53412414	1.542928	0.029795159	0.11576283	1	1,150	tags=25%, list=9%, signal=27%
GO_HETEROTYPIC_CELL_CELL_ADHESION	24	0.6030784	1.5425117	0.034	0.1159549	1	658	tags=29%, list=5%, signal=31%
GO_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIIUM_ION_INTO_CYTOSOL_BY_SARCOPLASMIC_RETICULUM	24	0.5002362	1.541674	0.04743083	0.116519116	1	1,984	tags=25%, list=15%, signal=29%
GO_CELL_MATRIX_ADHESION	99	0.44371217	1.541116	0.019305019	0.11677645	1	820	tags=15%, list=6%, signal=16%
GO_HUMORAL_IMMUNE_RESPONSE_MEDIATED_BY_CIRCULATING_IMMUNOGLOBULIN	39	0.7172501	1.5407512	0.027559055	0.116922185	1	1,450	tags=51%, list=11%, signal=58%
GO_CELLULAR_RESPONSE_TO_KETONE	62	0.49742532	1.5399926	0.006289308	0.1173778	1	1,275	tags=24%, list=10%, signal=27%
GO_REGULATION_OF_MEMBRANE_DEPOLARIZATION	37	0.50171673	1.5399234	0.024439918	0.11727007	1	2,083	tags=32%, list=16%, signal=38%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_HOST	99	0.37218446	1.5395386	0.001934236	0.11741179	1	1,997	tags=25%, list=15%, signal=30%
GO_REGULATION_OF_THYMOCYTE_AGGREGATION	23	0.5310654	1.5378321	0.025096525	0.11871615	1	1,110	tags=26%, list=9%, signal=28%
GO_COLLAGEN_TRIMER	62	0.63304424	1.5376947	0.03047619	0.118684575	1	1,492	tags=37%, list=11%, signal=42%
GO_SUBSTRATE_DEPENDENT_CELL_MIGRATION	24	0.56091845	1.5357456	0.036750484	0.12021741	1	3,121	tags=46%, list=24%, signal=60%
GO_POSITIVE_REGULATION_OF_BEHAVIOR	21	0.51307976	1.5353978	0.043052837	0.120360225	1	1,095	tags=19%, list=8%, signal=21%
GO_REGULATION_OF_T_CELL_APOPTOTIC_PROCESS	22	0.5784549	1.5326495	0.028806584	0.122663446	1	701	tags=18%, list=5%, signal=19%
GO_NEGATIVE_REGULATION_OF_MAP_KINASE_ACTIVITY	64	0.45764694	1.5321429	0.016096579	0.12294392	1	1,297	tags=25%, list=10%, signal=28%
GO_REGULATION_OF_SMOOTH_MUSCLE_CONTRACTION	53	0.4694039	1.5313711	0.037328094	0.123260364	1	2,008	tags=28%, list=15%, signal=33%
GO_RESPONSE_TO_FATTY_ACID	78	0.47129846	1.5309086	0.011560693	0.12353686	1	1,686	tags=27%, list=13%, signal=31%
GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION	130	0.45609483	1.5303888	0.01509434	0.12385467	1	1,275	tags=22%, list=10%, signal=24%
GO_CELLULAR_RESPONSE_TO_VITAMIN	26	0.605489	1.529289	0.03125	0.12453689	1	1,437	tags=38%, list=11%, signal=43%
GO_INTRINSIC_COMPONENT_OF_ORGANELLE_MEMBRANE	188	0.3752655	1.5271127	0.01778656	0.12632437	1	1,242	tags=15%, list=10%, signal=17%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_RESPONSE_TO_ANTIBIOTIC	43	0.50800484	1.5251237	0.015686275	0.1280277	1	1,932	tags=33%, list=15%, signal=38%
GO_CELLULAR_TRANSITION_METAL_ION_HOMEOSTASIS	59	0.4853048	1.5246171	0.019762846	0.12832715	1	1,795	tags=32%, list=14%, signal=37%
GO_POSITIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION _GLUTAMATERGIC	15	0.57700557	1.5240827	0.046558704	0.1286524	1	2,008	tags=40%, list=15%, signal=47%
GO_REGULATION_OF_CHEMOKINE_PRODUCTION	56	0.5304214	1.5240614	0.040983606	0.12848377	1	1,675	tags=32%, list=13%, signal=37%
GO_COPPER_ION_TRANSPORT	16	0.63343203	1.523515	0.037475344	0.12877528	1	3,106	tags=56%, list=24%, signal=74%
GO_PURINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	118	0.37336484	1.5233054	0.002053388	0.12882654	1	2,779	tags=33%, list=21%, signal=42%
GO_REGULATION_OF_ACTIN_FILAMENT_BASED_PROCESS	248	0.39862016	1.5227982	0.015384615	0.12914044	1	1,652	tags=22%, list=13%, signal=25%
GO_POSITIVE_REGULATION_OF_CHEMOKINE_PRODUCTION	43	0.54696465	1.5221595	0.047916666	0.12954535	1	1,675	tags=35%, list=13%, signal=40%
GO_REGULATION_OF_ACTIN_NUCLEATION	22	0.5303984	1.520895	0.036121674	0.13036966	1	980	tags=27%, list=8%, signal=29%
GO_TISSUE_HOMEOSTASIS	129	0.40300474	1.519467	0.012170386	0.13129447	1	812	tags=12%, list=6%, signal=12%
GO_POSITIVE_REGULATION_OF_PROTEIN_IMPORT	85	0.45264605	1.5194582	0.015748031	0.13112547	1	1,777	tags=32%, list=14%, signal=37%
GO_RESPONSE_TO_PEPTIDE	356	0.3772798	1.5188938	0.001934236	0.131541	1	2,102	tags=24%, list=16%, signal=27%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_POSITIVE_REGULATION_OF_FILOPODIUM_ASSEMBLY	20	0.55643296	1.5183564	0.046747968	0.13184182	1	865	tags=30%, list=7%,
GO_CELLULAR_RESPONSE_TO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_STIMULUS	27	0.5492612	1.5173907	0.03937008	0.13252167	1	1,693	signal=32% tags=33%, list=13%,
GO_NEGATIVE_REGULATION_OF_CALCIIUM_ION_IMPORT	23	0.49829355	1.5173028	0.038934425	0.13241282	1	1,984	signal=38% tags=30%, list=15%,
GO_PORPHYRIN_CONTAINING_COMPOUND_METABOLIC_PROCESS	31	0.6001088	1.5172534	0.044265594	0.1322872	1	1,215	signal=36% tags=32%, list=9%,
GO_NEGATIVE_REGULATION_OF_CATION_CHANNEL_ACTIVITY	31	0.49007824	1.5156865	0.03373016	0.13337357	1	915	signal=35% tags=19%, list=7%,
GO_NEGATIVE_REGULATION_OF_CHEMOTAXIS	45	0.54013354	1.5153335	0.0234375	0.13357662	1	1,638	signal=21% tags=24%, list=13%,
GO_PHOSPHOLIPID_TRANSPORTER_ACTIVITY	33	0.48925284	1.5144522	0.02264151	0.13430342	1	2,121	signal=28% tags=30%, list=16%,
GO_PHOSPHATIDYLCHOLINE_ACYL_CHAIN_REMODELING	15	0.5874581	1.5137063	0.012448133	0.13485676	1	780	signal=36% tags=20%, list=6%,
GO_REGULATION_OF_NUCLEOCYTOPLASMIC_TRANSPORT	188	0.38901523	1.5113056	0.008097166	0.13684304	1	1,777	signal=21% tags=23%, list=14%,
GO_HEPARIN_BINDING	131	0.5335326	1.5112964	0.020952381	0.13666178	1	1,932	signal=26% tags=32%, list=15%,
GO_PROTEIN_SELF_ASSOCIATION	35	0.48416743	1.510482	0.02631579	0.13731071	1	1,723	signal=37% tags=23%, list=13%,
GO_SKELETAL_MUSCLE_TISSUE_REGENERATION	23	0.5388064	1.5102493	0.04528302	0.1373382	1	1,395	signal=26% tags=22%, list=11%, signal=24%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_RESPONSE_TO_IRON_ION	33	0.5319163	1.5090501	0.02471483	0.1383782	1	876	tags=18%, list=7%, signal=19%
GO_REGULATION_OF_COAGULATION	80	0.5274973	1.508983	0.03364486	0.13826488	1	1,924	tags=36%, list=15%, signal=42%
GO_CELLULAR_RESPONSE_TO_ORGANIC_CYCLIC_COMPOUND	396	0.35076982	1.5070734	0	0.1400647	1	1,419	tags=17%, list=11%, signal=18%
GO_CXCR_CHEMOKINE_RECEPTOR_BINDING	16	0.8173812	1.5064744	0.017374517	0.14047644	1	979	tags=50%, list=8%, signal=54%
GO_NEGATIVE_REGULATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY	75	0.4709753	1.505347	0.022177419	0.14141597	1	1,322	tags=24%, list=10%, signal=27%
GO_REGULATION_OF_PROTEIN_TARGETING	240	0.36358616	1.5048256	0.004016064	0.14178206	1	1,875	tags=23%, list=14%, signal=26%
GO_VIRAL_LIFE_CYCLE	254	0.32613626	1.5047556	0.034412954	0.14165568	1	1,723	tags=15%, list=13%, signal=17%
GO_RESPONSE_TO_NUTRIENT	182	0.4242265	1.5038079	0.011560693	0.14212193	1	1,437	tags=21%, list=11%, signal=21%
GO_POSITIVE_REGULATION_OF_MULTI_ORGANISM_PROCESS	135	0.3398525	1.5026395	0.011152417	0.14314975	1	1,750	tags=21%, list=13%, signal=25%
GO_POSITIVE_REGULATION_OF_G1_S_TRANSITION_OF_MITOTIC_CELL_CYCLE	16	0.56514925	1.5023055	0.036511157	0.1432957	1	426	tags=19%, list=3%, signal=19%
GO_RESPONSE_TO_PROSTAGLANDIN	33	0.52687556	1.5022652	0.029469548	0.1431407	1	1,183	tags=24%, list=9%, signal=27%
GO_RAS_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	182	0.35376778	1.5020255	0.030360531	0.14313918	1	1,540	tags=16%, list=12%, signal=18%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_REGULATION_OF_CYSSTEINE_TYPE_ENDOPEPTIDASE ACTIVITY_INVOLVED_IN_APOPTOTIC_SIGNALING_PATHWAY	20	0.55696476	1.501794	0.045454547	0.14319146	1	1,288	tags=30%, list=10%, signal=33%
GO_POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_NUCLEUS	108	0.41785964	1.5013784	0.013916501	0.14322558	1	1,777	tags=27%, list=14%, signal=31%
GO_MULTI_MULTICELLULAR_ORGANISM_PROCESS	192	0.40234926	1.5009897	0.019762846	0.14340115	1	1,751	tags=24%, list=13%, signal=27%
GO_CELL_SUBSTRATE_ADHESION	136	0.4307554	1.5009122	0.027985075	0.1432711	1	1,369	tags=20%, list=11%, signal=22%
GO_CELLULAR_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	94	0.43642104	1.5000151	0.015904572	0.14390977	1	1,233	tags=21%, list=9%, signal=23%
GO_NEGATIVE_REGULATION_OF_LOCOMOTION	226	0.4227894	1.499806	0.02952756	0.14391786	1	2,153	tags=26%, list=17%, signal=30%
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_PHOSPHATASE_ACTIVITY	17	0.5794964	1.498473	0.03846154	0.14512146	1	497	tags=18%, list=4%, signal=18%
GO_RESPONSE_TO_CADMIUM_ION	37	0.6288055	1.4981304	0.041257367	0.14527667	1	1,092	tags=30%, list=8%, signal=32%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_8_PRODUCTION	39	0.55136716	1.4973713	0.041152265	0.14586449	1	1,333	tags=33%, list=10%, signal=37%
GO_TRANSPORT_VESICLE_MEMBRANE	118	0.4194555	1.4968891	0.031914894	0.14614832	1	929	tags=13%, list=7%, signal=14%
GO_LIPID_BINDING	468	0.37053275	1.4968635	0	0.14597465	1	1,960	tags=23%, list=15%, signal=26%
GO_PHOSPHATIDIC_ACID_METABOLIC_PROCESS	23	0.5329348	1.4958187	0.031558186	0.14684862	1	1,573	tags=35%, list=12%, signal=39%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_NEGATIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_PROLIFERATION	35	0.5456917	1.4950316	0.030549899	0.14750053	1	2,964	tags=49%, list=23%, signal=63%
GO_POSITIVE_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	78	0.472112	1.4942807	0.027027028	0.1480786	1	1,678	tags=29%, list=13%, signal=34%
GO_INOSITOL_LIPID_MEDIATED_SIGNALING	102	0.37781316	1.4941721	0.033333335	0.1479961	1	2,860	tags=34%, list=22%, signal=44%
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_SIGNALING_PATHWAY	437	0.33883813	1.4937195	0.015625	0.148239	1	1,652	tags=17%, list=13%, signal=19%
GO_ORGAN_REGENERATION	78	0.48645228	1.4917383	0.015655577	0.15000401	1	1,419	tags=27%, list=11%, signal=30%
GO_RESPONSE_TO_ACID_CHEMICAL	281	0.4079453	1.4911907	0.005628518	0.15037532	1	1,686	tags=22%, list=13%, signal=25%
GO_POSITIVE_REGULATION_OF_FATTY_ACID_BIOSYNTHETIC_PROCESS	15	0.6139067	1.4900732	0.033210333	0.15134469	1	780	tags=27%, list=6%, signal=28%
GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_SIGNAL_TRANSDUCTION	353	0.3512192	1.4871253	0.012	0.15407985	1	2,294	tags=24%, list=18%, signal=28%
GO_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION	241	0.4019533	1.4865398	0.016759777	0.15445565	1	2,296	tags=30%, list=18%, signal=36%
GO_POSITIVE_REGULATION_OF_DEPHOSPHORYLATION	37	0.44052276	1.4857982	0.042	0.15504564	1	1,275	tags=24%, list=10%, signal=27%
GO_PLASMA_MEMBRANE_RAFT	79	0.40796423	1.4840635	0.040697675	0.15665486	1	882	tags=15%, list=7%, signal=16%
GO_RESPONSE_TO_GAMMA_RADIATION	46	0.50871605	1.4829546	0.03992016	0.15734705	1	1,702	tags=26%, list=13%, signal=30%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_METAL_ION_TRANSPORT	430	0.32063654	1.4814228	0.005825243	0.15876754	1	1,251	tags=12%, list=10%, signal=12%
GO_I_KAPPAB_KINASE_NF_KAPPAB_SIGNALING	58	0.4244044	1.4805896	0.049484536	0.15945956	1	1,830	tags=26%, list=14%, signal=30%
GO_REGULATION_OF_OXIDOREDUCTASE_ACTIVITY	81	0.36791807	1.4804258	0.030075189	0.15942195	1	2,504	tags=19%, signal=36%
GO_RESPONSE_TO_AMINO_ACID	95	0.4901138	1.4802696	0.01934236	0.15918213	1	1,238	tags=23%, list=10%, signal=25%
GO_REGULATION_OF_CATION_CHANNEL_ACTIVITY	74	0.38962126	1.478737	0.030927835	0.16025819	1	2,435	tags=19%, signal=33%
GO_CELLULAR_IRON_ION_HOMEOSTASIS	35	0.52212644	1.4782248	0.04527559	0.16020547	1	1,731	tags=37%, list=13%, signal=43%
GO_PROTEIN_TYROSINE_KINASE_ACTIVITY	159	0.3523181	1.4768662	0.026217228	0.16098449	1	1,652	tags=19%, list=13%, signal=22%
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_EXTERNAL_STIMULUS	232	0.39336875	1.4763253	0.014925373	0.16137868	1	1,702	tags=23%, list=13%, signal=26%
GO_SCAVENGER_RECEPTOR_ACTIVITY	28	0.5580616	1.4763112	0.041257367	0.16119188	1	1,521	tags=46%, list=12%, signal=52%
GO_CARGO_RECEPTOR_ACTIVITY	47	0.5039759	1.4761832	0.031128405	0.16113174	1	1,521	tags=34%, list=12%, signal=38%
GO_CELLULAR_RESPONSE_TO_EXTERNAL_STIMULUS	224	0.39365965	1.4757183	0.011583012	0.1614185	1	2,065	tags=27%, list=16%, signal=32%
GO_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	36	0.5028022	1.4749098	0.042168673	0.16202915	1	1,639	tags=25%, list=13%, signal=29%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_CELLULAR_RESPONSE_TO_AMINO_ACID_STIMULUS	41	0.5737625	1.4738063	0.041420117	0.16281424	1	1,419	tags=32%, list=11%, signal=35%
GO_SECRETION	469	0.3600846	1.4724423	0.007736944	0.16404152	1	1,159	tags=14%, list=9%, signal=15%
GO_NEGATIVE_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_DNA_DAMAGE	22	0.5159709	1.4722761	0.032323234	0.16399643	1	424	tags=14%, list=3%, signal=14%
GO_PHOSPHOLIPID_BINDING	249	0.35777566	1.4692982	0.003883495	0.16676876	1	1,960	tags=22%, list=15%, signal=26%
GO_REGULATION_OF_PHOSPHOLIPID_METABOLIC_PROCESS	52	0.468691	1.4692473	0.044061303	0.16661519	1	2,403	tags=33%, list=18%, signal=40%
GO_RECEPTOR_REGULATOR_ACTIVITY	33	0.49962622	1.4684329	0.03353057	0.16702746	1	1,468	tags=18%, list=11%, signal=20%
GO_VIRUS_RECEPTOR_ACTIVITY	66	0.43020836	1.467808	0.024390243	0.16747418	1	1,032	tags=21%, list=8%, signal=23%
GO_RESPONSE_TO_FIBROBLAST_GROWTH_FACTOR	97	0.38986284	1.4676801	0.0332681	0.16740188	1	2,331	tags=24%, list=18%, signal=29%
GO_POSITIVE_REGULATION_OF_CYTOSKELETON_ORGANIZATION	140	0.3836641	1.4672495	0.02952756	0.1677052	1	1,652	tags=21%, list=13%, signal=24%
GO_CELLULAR_RESPONSE_TO_MECHANICAL_STIMULUS	75	0.4534645	1.4670087	0.024761904	0.16781169	1	1,830	tags=28%, list=14%, signal=32%
GO_NEGATIVE_REGULATION_OF_OSSIFICATION	54	0.43773013	1.4659921	0.02631579	0.16870452	1	2,861	tags=41%, list=22%, signal=52%
GO_RESPONSE_TO_HYDROGEN_PEROXIDE	102	0.43652144	1.4641279	0.04117647	0.17052634	1	1,233	tags=23%, list=9%, signal=25%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_POSITIVE_REGULATION_OF_CELLULAR_COMPONENT_BIOGENESIS	319	0.34690192	1.4638295	0.015444015	0.17065486	1	2,423	tags=26%, list=19%, signal=31%
GO_SERINE_HYDROLASE_ACTIVITY	159	0.477076	1.4618814	0.03529412	0.17198639	1	1,743	tags=29%, list=13%, signal=33%
GO_CYTOPLASMIC_VESICLE_PART	473	0.36086717	1.4614195	0.015904572	0.1720834	1	1,176	tags=15%, list=9%, signal=16%
GO_PHOSPHOLIPASE_A2_ACTIVITY	21	0.5571201	1.459016	0.036960986	0.17467009	1	835	tags=29%, list=6%, signal=30%
GO_CYSSTEINE_TYPE_ENDOPEPTIDASE_REGULATOR_ACTIVITY_INVOLVED_IN_APOPTOTIC_PROCESS	38	0.4942759	1.4589833	0.049079753	0.17450279	1	1,546	tags=29%, list=12%, signal=33%
GO_NEGATIVE_REGULATION_OF_TRANSPORT	381	0.33300975	1.4589564	0.011583012	0.17431583	1	2,165	tags=23%, list=17%, signal=26%
GO_NEGATIVE_REGULATION_OF_TRANSFERASE_ACTIVITY	283	0.33338642	1.4587625	0.009578544	0.17432058	1	1,914	tags=20%, list=15%, signal=23%
GO_POSITIVE_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	58	0.4192853	1.4585148	0.04288499	0.1743805	1	1,803	list=14%, signal=34%, tags=28%, list=20%, signal=34%
GO_REGULATION_OF_ADENYLATE_CYCLASE_ACTIVITY	65	0.3608492	1.4581522	0.030947777	0.17456813	1	2,583	tags=16%, list=13%, signal=18%, tags=18%, list=13%, signal=21%
GO_REGULATION_OF_PROTEIN_COMPLEX_ASSEMBLY	297	0.33807042	1.4573257	0.013671875	0.17533584	1	1,692	
GO_NEGATIVE_REGULATION_OF_NEURON_DEATH	146	0.3459474	1.4564104	0.016427105	0.17573348	1	1,661	

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_REGENERATION	147	0.42593473	1.4561228	0.013333334	0.17585734	1	1,419	tags=24%, list=11%, signal=26%
GO_EXOCYTOSIS	238	0.39742038	1.4560078	0.02385686	0.17582029	1	1,029	tags=14%, list=8%, signal=15%
GO_POSITIVE_REGULATION_OF_LIPID_METABOLIC_PROCESS	112	0.42208755	1.4553177	0.03018868	0.17632033	1	1,275	tags=21%, list=10%, signal=23%
GO_NEGATIVE_REGULATION_OF_APOPTOTIC_SIGNALING_PATHWAY	170	0.3649669	1.4542836	0.021484375	0.17706558	1	992	tags=14%, list=8%, signal=15%
GO_REGULATION_OF_G_PROTEIN_COUPLED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	109	0.3723458	1.4541986	0.020618556	0.17693594	1	915	tags=11%, list=7%, signal=12%
GO_NEGATIVE_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION	167	0.35191354	1.452818	0.01764706	0.17803824	1	1,777	tags=22%, list=14%, signal=25%
GO_POSITIVE_REGULATION_OF_SEQUENCE_SPECIFIC_DNA_BINDING_TRANSCRIPTION_FACTOR_ACTIVITY	197	0.3306818	1.4520743	0.011695907	0.17873618	1	1,786	tags=19%, list=14%, signal=22%
GO_NEGATIVE_REGULATION_OF_VASCULATURE_DEVELOPMENT	72	0.471144	1.4510063	0.043392505	0.17954138	1	2,153	tags=32%, list=17%, signal=38%
GO_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	82	0.46992216	1.4500319	0.039179105	0.18044163	1	1,806	tags=26%, list=14%, signal=30%
GO_REGULATION_OF_LYASE_ACTIVITY	76	0.34678495	1.4484202	0.032786883	0.18210194	1	2,583	tags=28%, list=20%, signal=34%
GO_ACTIN_FILAMENT_POLYMERIZATION	21	0.52010125	1.4433842	0.046728972	0.18762125	1	650	tags=24%, list=5%, signal=25%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_ABSENCE_OF_LIGAND	41	0.43800017	1.4426028	0.048964217	0.18811335	1	992	tags=17%, list=8%, signal=18%
GO_REGULATION_OF_PEPTIDYL_SERINE_PHOSPHORYLATION	101	0.37040147	1.4414964	0.01984127	0.18922816	1	1,936	tags=23%, list=15%, signal=27%
GO_RESPONSE_TO_INORGANIC_SUBSTANCE	440	0.37798688	1.4412341	0.009578544	0.18935212	1	1,332	tags=18%, list=10%, signal=19%
GO_CYSTEINE_TYPE_ENDOPEPTIDASE_INHIBITOR_ACTIVITY_INVOLVED_IN_APOPTOTIC_PROCESS	20	0.5373485	1.4412112	0.042510122	0.18914653	1	1,322	tags=35%, list=10%, signal=39%
GO_POSITIVE_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	28	0.50611156	1.4400038	0.046653144	0.18987359	1	1,803	tags=36%, list=14%, signal=41%
GO_NEGATIVE_REGULATION_OF_GROWTH	204	0.36432397	1.439779	0.009784736	0.18993501	1	1,185	tags=15%, list=9%, signal=16%
GO_VESICLE_MEMBRANE	392	0.35138837	1.4396437	0.023305085	0.18986599	1	1,176	tags=14%, list=9%, signal=15%
GO_SULFUR_COMPOUND_BINDING	195	0.46571887	1.438379	0.028355388	0.19112724	1	1,638	tags=26%, list=13%, signal=29%
GO_NUCLEOSIDE_TRIPHOSPHATASE_REGULATOR_ACTIVITY	216	0.34084398	1.4381291	0.026369167	0.19120787	1	1,539	tags=18%, list=12%, signal=20%
GO_RESPONSE_TO_KETONE	159	0.42661333	1.4341649	0.017142856	0.19504394	1	1,275	tags=23%, list=10%, signal=25%
GO_CIRCULATORY_SYSTEM_PROCESS	327	0.35079634	1.4333962	0.022222223	0.19553922	1	1,693	tags=18%, list=13%, signal=20%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_REGULATION_OF_MAP_KINASE_ACTIVITY	273	0.3399671	1.4327209	0.017857144	0.19588248	1	1,936	tags=23%, list=15%, signal=26%
GO_REGULATION_OF_EXOCYTOSIS	142	0.34726194	1.4299978	0.04489796	0.19776858	1	1,783	tags=20%, list=14%, signal=23%
GO_RESPONSE_TO_ALCOHOL	332	0.3741064	1.4277166	0.013358778	0.19988416	1	1,275	tags=17%, list=10%, signal=19%
GO_POSITIVE_REGULATION_OF_PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY	243	0.336072	1.4261763	0.028680688	0.2011275	1	1,936	tags=23%, list=15%, signal=26%
GO_PHOSPHATIDYLGLYCEROL_METABOLIC_PROCESS	20	0.47380027	1.4255941	0.0480167	0.201634	1	780	tags=15%, list=6%, signal=16%
GO_CELLULAR_RESPONSE_TO_NITROGEN_COMPOUND	430	0.33405533	1.4208012	0.017142856	0.20612279	1	2,177	tags=22%, list=17%, signal=25%
GO_REGULATED_EXOCYTOSIS	179	0.4160914	1.4205269	0.04563492	0.2062208	1	1,029	tags=17%, list=8%, signal=18%
GO_ACTIVATION_OF_PROTEIN_KINASE_ACTIVITY	236	0.32008862	1.4190782	0.021032505	0.20762669	1	2,149	tags=22%, list=16%, signal=26%
GO_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	234	0.31603006	1.4164007	0.033864543	0.20990326	1	1,584	tags=16%, list=12%, signal=18%
GO_REGULATION_OF_RECEPTOR_ACTIVITY	96	0.3589329	1.4151804	0.046332046	0.21058868	1	1,809	tags=20%, list=14%, signal=23%
GO_REGULATION_OF_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHONDRIA	38	0.45330286	1.4139031	0.04296875	0.21141934	1	2,200	tags=26%, list=17%, signal=32%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_CELLULAR_RESPONSE_TO_HYDROGEN_PEROXIDE	56	0.4441347	1.4130274	0.046511628	0.21181794	1	1,233	tags=25%, list=9%, signal=27%
GO_NEGATIVE_REGULATION_OF_MAPK_CASCADE	120	0.3773913	1.4115964	0.041666668	0.2130977	1	1,302	tags=19%, list=10%, signal=21%
GO_BINDING_BRIDGING	151	0.3545231	1.4107823	0.040462427	0.21366574	1	1,115	tags=13%, list=9%, signal=14%
GO_RESPONSE_TO_AMINE	42	0.41657698	1.4066978	0.042424243	0.21709134	1	2,565	tags=29%, list=20%, signal=35%
GO_DEFENSE_RESPONSE_TO_GRAM_POSITIVE_BACTERIUM	57	0.47466397	1.4055549	0.043737575	0.21829616	1	1,803	tags=32%, list=14%, signal=36%
GO_ALCOHOL_BINDING	80	0.41352034	1.4043206	0.03773585	0.21964732	1	997	tags=14%, list=8%, signal=15%
GO_POSITIVE_REGULATION_OF_INTRACELLULAR_PROTEIN_TRANSPORT	198	0.33998263	1.401764	0.027290449	0.22168624	1	1,875	tags=23%, list=14%, signal=27%
GO_RESPONSE_TO_ALKALOID	131	0.33825675	1.401729	0.031135531	0.22149861	1	997	tags=10%, list=8%, signal=11%
GO_RESPONSE_TO_ETHANOL	126	0.35677284	1.3997452	0.034358047	0.22281316	1	1,723	tags=17%, list=13%, signal=19%
GO_RESPONSE_TO_CORTICOSTEROID	159	0.42160693	1.3997197	0.021032505	0.2226151	1	997	tags=19%, list=8%, signal=20%
GO_REGULATION_OF_DNA_BINDING	78	0.41080192	1.3989154	0.035363458	0.22317134	1	1,702	tags=21%, list=13%, signal=23%
GO_RESPONSE_TO_MECHANICAL_STIMULUS	181	0.39030796	1.3962585	0.039697543	0.22562183	1	1,366	tags=19%, list=10%, signal=21%

Table SIII. Continued.

Name	Size	ES	NES	NOM p-val	FDR q-val	FWER p-val	Rank at max	Leading edge
GO_NEGATIVE_REGULATION_OF_NEURON_APOPTOTIC_PROCESS	115	0.34747386	1.3944168	0.035123967	0.22636287	1	2,433	tags=30%, list=19%, signal=36%
GO_ESTABLISHMENT_OR_MAINTENANCE_OF_CELL_POLARITY	116	0.37254634	1.3935785	0.03285421	0.2272163	1	1,550	tags=19%, list=12%, signal=21%
GO_REGULATION_OF_INTRACELLULAR_PROTEIN_TRANSPORT	299	0.32539654	1.3921765	0.011976048	0.22836453	1	1,875	tags=17%, list=13%, signal=19%
GO_REGULATION_OF_CELLULAR_COMPONENT_SIZE	269	0.3253315	1.3906995	0.037181996	0.22995389	1	1,652	tags=21%, list=14%, signal=24%
GO_RESPONSE_TO_TOXIC_SUBSTANCE	209	0.3966675	1.3860373	0.03076923	0.23364393	1	1,572	tags=17%, list=13%, signal=19%
GO_CELLULAR_RESPONSE_TO_ABIOTIC_STIMULUS	234	0.34277016	1.3855764	0.024621213	0.23400179	1	1,881	tags=21%, list=12%, signal=24%
GO_REGULATION_OF_APOPTOTIC_SIGNALING_PATHWAY	306	0.3237121	1.3848054	0.015151516	0.2342514	1	1,056	tags=14%, list=14%, signal=24%
GO_CELLULAR_RESPONSE_TO_EXTRACELLULAR_STIMULUS	153	0.379503	1.3848041	0.018	0.23400575	1	2,065	tags=13%, list=8%, signal=14%
GO_CELLULAR_RESPONSE_TO_ALCOHOL	100	0.39167717	1.3795019	0.03250478	0.23856978	1	1,401	tags=27%, list=16%, signal=31%
GO_CYSSTEINE_TYPE_PEPTIDASE_ACTIVITY	119	0.32996073	1.3721744	0.04227941	0.2457907	1	1,820	tags=19%, list=11%, signal=21%
								tags=21%, list=14%, signal=24%

ES, enrichment score; FDR q-val, false discovery rate q-value; FWER p-val, familywise-error rate P-value; NES, normalized enrichment score; NOM p-val, nominal P-value.