

GO: Biological Process

ID	Name	Source	q-value Bonferroni	Hit Count in Query List	Hit Count in Genome
GO:0006937	regulation of muscle contraction	GO: Biological Process	1.01E-04	16	175
GO:0090257	regulation of muscle system process	GO: Biological Process	7.83E-04	17	229
GO:0044057	regulation of system process	GO: Biological Process	1.73E-03	26	526
GO:0006936	muscle contraction	GO: Biological Process	2.44E-03	20	337
GO:0048812	neuron projection morphogenesis	GO: Biological Process	3.83E-03	36	929
GO:0048667	cell morphogenesis involved in neuron differentiation	GO: Biological Process	4.36E-03	35	894
GO:0008016	regulation of heart contraction	GO: Biological Process	6.32E-03	14	182
GO:0007409	axonogenesis	GO: Biological Process	7.13E-03	32	794
GO:0007517	muscle organ development	GO: Biological Process	7.51E-03	21	395
GO:0003012	muscle system process	GO: Biological Process	1.63E-02	21	415
GO:0061564	axon development	GO: Biological Process	1.68E-02	32	827
GO:0031175	neuron projection development	GO: Biological Process	1.95E-02	41	1211
GO:0061061	muscle structure development	GO: Biological Process	2.37E-02	27	644
GO:0048858	cell projection morphogenesis	GO: Biological Process	2.95E-02	40	1188
GO:0032990	cell part morphogenesis	GO: Biological Process	4.36E-02	40	1208
GO:0060047	heart contraction	GO: Biological Process	4.40E-02	14	215
GO:1903522	regulation of blood circulation	GO: Biological Process	4.51E-02	16	276
GO:0003015	heart process	GO: Biological Process	4.89E-02	14	217
GO:0014070	response to organic cyclic compound	GO: Biological Process	5.80E-02	32	879
GO:0006935	chemotaxis	GO: Biological Process	7.43E-02	32	890
GO:0042330	taxis	GO: Biological Process	7.76E-02	32	892
GO:0043269	regulation of ion transport	GO: Biological Process	8.28E-02	26	651
GO:0022008	neurogenesis	GO: Biological Process	8.64E-02	53	1848
GO:0008015	blood circulation	GO: Biological Process	8.68E-02	22	500
GO:0003013	circulatory system process	GO: Biological Process	9.23E-02	22	502

Pathway

ID	Name	Source	q-value Bonferroni	Hit Count in Query List	Hit Count in Genome
477129	Developmental Biology	BioSystems: REACTOME	4.91E-03	22	419
105688	Axon guidance	BioSystems: REACTOME	1.79E-02	16	262
198906	Calcium Regulation in the Cardiac Cell	BioSystems: WikiPathways	7.69E-02	11	149
105689	NCAM signaling for neurite out-growth	BioSystems: REACTOME	1.42E-01	7	63
105698	Biological oxidations	BioSystems: REACTOME	1.47E-01	11	160
SMP00083	Acetylsalicylic Acid Pathway	SMPDB	2.40E-01	4	17
SMP00106	Meloxicam Pathway	SMPDB	4.68E-01	4	20
SMP00084	Etodolac Pathway	SMPDB	4.68E-01	4	20
SMP00096	Celecoxib Pathway	SMPDB	4.68E-01	4	20
SMP00116	Valdecoxib Pathway	SMPDB	4.68E-01	4	20
SMP00087	Rofecoxib Pathway	SMPDB	4.68E-01	4	20
M15394	Acute Myocardial Infarction	MSigDB C2: BioCarta	4.68E-01	4	20

Coexpression

ID	Name	Source	q-value Bonferroni	Hit Count in Query List	Hit Count in Genome
18498629-GeneList	Human Breast_Loi08_239genes	GeneSigDB	5.68E-10	21	178
M19391	Genes down-regulated in prostate cancer samples.	MSigDB C2: Broad Institute	2.12E-09	32	480
M8124	Genes up-regulated in basal subtype of breast cancer samples.	MSigDB C2: Broad Institute	2.77E-07	34	647
20421987-TableS1	Human Lung_Hou10_1067genes	GeneSigDB	3.38E-07	36	724
M1834	Genes up-regulated in freshly isolated CD31- [GeneID=5175] (stromal stem cells from adipose tissue) versus the CD31+ (non-stem) counterparts.	MSigDB C2: Broad Institute	5.59E-06	20	260
M17923	Genes up-regulated in cultured stromal stem cells from adipose tissue, compared to the freshly isolated cells.	MSigDB C2: Broad Institute	1.21E-05	25	425
16280042-GeneList	Human Breast_Pawitan05_64genes_prognosisGenes	GeneSigDB	1.21E-05	10	51
M2761	Top 100 probe sets contributing to the positive side of the 2nd principal component; associated with adipocytic differentiation.	MSigDB C2: Aristoteles Universit	2.02E-05	12	87

Table S1

Analysis of the 346 prostate transcripts differentially regulated by vitamin D3 supplementation in African Americans that overlap with those differentially expressed between African Americans and European Americans

GO: Biological Process						
ID	Name	Source	q-value Bonferroni	Hit Count in Query List	Hit Count in Genome	
GO:0045236	CXCR chemokine receptor binding	GO: Molecular Function	4.66E-05	7	17	
GO:0008092	cytoskeletal protein binding	GO: Molecular Function	5.41E-04	44	874	
GO:0008009	chemokine activity	GO: Molecular Function	9.07E-04	9	47	
GO:0042379	chemokine receptor binding	GO: Molecular Function	6.59E-03	9	59	
GO:0032403	protein complex binding	GO: Molecular Function	5.97E-02	44	1053	
GO:0015631	tubulin binding	GO: Molecular Function	1.08E-01	18	289	
GO:0001664	G-protein coupled receptor binding	GO: Molecular Function	1.47E-01	17	270	
GO:0008017	microtubule binding	GO: Molecular Function	2.86E-01	14	208	
GO:0005126	cytokine receptor binding	GO: Molecular Function	3.03E-01	17	287	
GO:0003012	muscle system process	GO: Biological Process	9.57E-05	30	415	
GO:0006936	muscle contraction	GO: Biological Process	9.17E-04	25	337	
GO:0051270	regulation of cellular component movement	GO: Biological Process	1.56E-03	43	830	
GO:0019932	second-messenger-mediated signaling	GO: Biological Process	1.06E-02	19	242	
GO:0051345	positive regulation of hydrolase activity	GO: Biological Process	1.65E-02	41	849	
GO:0002690	positive regulation of leukocyte chemotaxis	GO: Biological Process	1.67E-02	11	86	
GO:0090257	regulation of muscle system process	GO: Biological Process	2.16E-02	18	229	
GO:0002688	regulation of leukocyte chemotaxis	GO: Biological Process	2.21E-02	12	106	
GO:0050921	positive regulation of chemotaxis	GO: Biological Process	3.28E-02	13	129	
GO:0086064	cell communication by electrical coupling involved in cardiac conduction	GO: Biological Process	3.30E-02	6	22	
GO:0061337	cardiac conduction	GO: Biological Process	3.97E-02	9	61	
GO:0002027	regulation of heart rate	GO: Biological Process	4.44E-02	11	95	
GO:0070098	chemokine-mediated signaling pathway	GO: Biological Process	5.11E-02	10	79	
GO:0055001	muscle cell development	GO: Biological Process	5.16E-02	15	176	
GO:0051353	positive regulation of oxidoreductase activity	GO: Biological Process	5.88E-02	8	49	
GO:0043085	positive regulation of catalytic activity	GO: Biological Process	7.87E-02	61	1570	
GO:2000145	regulation of cell motility	GO: Biological Process	7.88E-02	36	751	
GO:0014866	skeletal myofibril assembly	GO: Biological Process	7.94E-02	4	8	
GO:1902622	regulation of neutrophil migration	GO: Biological Process	9.16E-02	7	38	
GO:0040011	locomotion	GO: Biological Process	9.47E-02	71	1932	
GO:0002687	positive regulation of leukocyte migration	GO: Biological Process	1.31E-01	12	126	
GO:0048870	cell motility	GO: Biological Process	1.34E-01	55	1391	
GO:0051674	localization of cell	GO: Biological Process	1.34E-01	55	1391	
GO:0019722	calcium-mediated signaling	GO: Biological Process	1.45E-01	13	148	
GO:0010644	cell communication by electrical coupling	GO: Biological Process	1.49E-01	6	28	
GO:0002685	regulation of leukocyte migration	GO: Biological Process	1.69E-01	14	172	
Pathway						
ID	Name	Source	q-value Bonferroni	Hit Count in Query List	Hit Count in Genome	
161025	Smooth Muscle Contraction	BioSystems: REACTOME	3.75E-05	8	24	
83050	Calcium signaling pathway	BioSystems: KEGG	6.49E-04	17	181	
106359	Chemokine receptors bind chemokines	BioSystems: REACTOME	4.52E-03	9	56	
M13494	Bioactive Peptide Induced Signaling Pathway	MSigDB C2: BioCarta	5.16E-03	8	43	
SMP00368	Labetalol Pathway	SMPDB	6.26E-03	6	21	
SMP00367	Carvedilol Pathway	SMPDB	6.26E-03	6	21	
P00031	Inflammation mediated by chemokine and cytokine signaling pathway	PantherDB	6.47E-03	16	191	
154409	Gastric acid secretion	BioSystems: KEGG	7.33E-03	10	75	
96530	Vascular smooth muscle contraction	BioSystems: KEGG	1.92E-02	12	121	
106261	Muscle contraction	BioSystems: REACTOME	1.95E-02	8	51	
99051	Chemokine signaling pathway	BioSystems: KEGG	2.48E-02	15	189	
119550	G alpha (i) signalling events	BioSystems: REACTOME	2.72E-02	17	238	
908257	Adrenergic signaling in cardiomyocytes	BioSystems: KEGG	3.37E-02	13	149	
SMP00375	Verapamil Pathway	SMPDB	4.52E-02	8	57	
SMP00359	Diltiazem Pathway	SMPDB	4.52E-02	8	57	
M16518	Wnt/Ca2+/cyclic GMP signaling.	MSigDB C2: Signaling Transduction KE	8.40E-02	5	20	
83110	Glioma	BioSystems: KEGG	1.19E-01	8	65	
105679	Caspase-mediated cleavage of cytoskeletal proteins	BioSystems: REACTOME	1.42E-01	4	12	
Coexpression						
ID	Name	Source	q-value Bonferroni	Hit Count in Query List	Hit Count in Genome	
17297478-SuppTable5	Human Intestine_Vecchi07_1024genes	GeneSigDB	9.13E-11	52	781	
M18855	Up-regulated genes distinguishing between early gastric cancer (EGC) and normal tissue samples.	MSigDB C2: Broad Institute	3.78E-08	34	428	
18318837-TableS1	Human MesenchymalStemCells_Yamamoto08_1252genes	GeneSigDB	4.08E-07	48	853	
19204204-SupplementaryTable5	Human Breast_Parker09_1918genes_IntrinsicGenes_Compilation	GeneSigDB	4.34E-06	71	1681	
11823860-SuppTable3	Human Breast_van'tVeer02_2460genes_Ergenes	GeneSigDB	6.09E-06	77	1910	
19658189-TableS3	Human EmbryonicStemCell_Xu09_1311genes	GeneSigDB	9.56E-06	49	969	

Table S2
Analysis of the 471 prostate transcripts differentially regulated by vitamin D3 supplementation in African Americans that do not overlap with transcripts differentially expressed between African Americans and European Americans

Table S3

ID	Name	q-value Bonferroni	Hit Count in Query List	Hit Count in Genome
GO:0002684	positive regulation of immune system process	6.54E-17	172	732
GO:0006955	immune response	4.60E-16	276	1416
GO:0045321	leukocyte activation	2.20E-15	162	695
GO:0001775	cell activation	1.87E-14	195	916
GO:0002682	regulation of immune system process	4.74E-14	239	1212
GO:0046649	lymphocyte activation	1.04E-11	135	589
GO:0050776	regulation of immune response	9.61E-11	166	801
GO:0042110	T cell activation	4.22E-10	104	428
GO:0050865	regulation of cell activation	6.94E-10	105	437
GO:0050778	positive regulation of immune response	1.06E-09	119	524
GO:0002694	regulation of leukocyte activation	3.00E-09	98	405
GO:0048584	positive regulation of response to stimulus	4.40E-09	274	1584

GO:0050870	positive regulation of T cell activation	9.61E-09	59	195
GO:0050867	positive regulation of cell activation	1.10E-08	75	281
GO:0051249	regulation of lymphocyte activation	1.64E-08	88	357
GO:0006952	defense response	2.71E-08	261	1515
GO:0002253	activation of immune response	3.48E-08	100	433
GO:0002696	positive regulation of leukocyte activation	3.92E-08	72	271
GO:0002252	immune effector process	4.28E-08	131	628
GO:0070661	leukocyte proliferation	9.29E-08	71	270
GO:0032943	mononuclear cell proliferation	1.15E-07	69	260
GO:0050900	leukocyte migration	1.66E-07	78	313
GO:0046651	lymphocyte proliferation	2.26E-07	68	258
GO:0050863	regulation of T cell activation	2.62E-07	70	270
GO:0002429	immune response-activating cell surface receptor signaling pathway	4.58E-07	63	234

GO:0009611	response to wounding	5.60E-07	219	1255
GO:0051251	positive regulation of lymphocyte activation	1.16E-06	65	250
GO:0006954	inflammatory response	1.18E-06	122	599
GO:0002757	immune response-activating signal transduction	3.79E-06	86	381
GO:0002274	myeloid leukocyte activation	4.59E-06	46	154
GO:0070663	regulation of leukocyte proliferation	4.63E-06	53	191
GO:0002768	immune response-regulating cell surface receptor signaling pathway	8.14E-06	81	356
GO:0050851	antigen receptor-mediated signaling pathway	1.01E-05	44	147
GO:0002764	immune response-regulating signaling pathway	1.14E-05	102	490
GO:0002250	adaptive immune response	1.40E-05	67	276
GO:0032944	regulation of mononuclear cell proliferation	1.53E-05	51	186

GO:0016477	cell migration	1.74E-05	187	1073
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Table 3

Category	ID	Name	Source	q-value Bonferroni	Hit Count in Query List	Hit Count in Genome
GO: Molecular Function	GO:0008092	cytoskeletal protein binding		5.46E-04	60	792
GO: Molecular Function	GO:0032403	protein complex binding		1.16E-03	66	924
GO: Molecular Function	GO:0008009	chemokine activity		1.31E-03	11	46
GO: Molecular Function	GO:0015631	tubulin binding		6.18E-03	26	251
GO: Molecular Function	GO:0042379	chemokine receptor binding		1.24E-02	11	57
GO: Molecular Function	GO:0008017	microtubule binding		3.82E-02	20	184
GO: Molecular Function	GO:0001664	G-protein coupled receptor binding		1.94E-01	22	239
GO: Biological Process	GO:0006928	movement of cell or subcellular component		3.65E-09	125	1703
GO: Biological Process	GO:0006936	muscle contraction		2.02E-08	40	295

GO: Biological Process	GO:0003012	muscle system process		3.86E-07	42	352
GO: Biological Process	GO:0040011	locomotion		1.19E-05	105	1522
GO: Biological Process	GO:0016477	cell migration		2.01E-05	81	1073
GO: Biological Process	GO:0006937	regulation of muscle contraction		2.61E-05	23	142
GO: Biological Process	GO:0090257	regulation of muscle system process		3.22E-05	26	180
GO: Biological Process	GO:0007155	cell adhesion		3.45E-05	80	1067
GO: Biological Process	GO:0022610	biological adhesion		5.22E-05	80	1077
GO: Biological Process	GO:0044057	regulation of system process		9.65E-05	43	438
GO: Biological Process	GO:0051674	localization of cell		1.02E-04	84	1170
GO: Biological Process	GO:0048870	cell motility		1.02E-04	84	1170
GO: Biological Process	GO:0006935	chemotaxis		1.35E-04	56	661

GO: Biological Process	GO:0042330	taxis		1.42E- 04	56	662
GO: Biological Process	GO:0051049	regulation of transport		3.03E- 04	100	1517
GO: Biological Process	GO:0022008	neurogenesis		6.81E- 04	95	1441
GO: Biological Process	GO:0007267	cell-cell signaling		6.84E- 04	87	1281
GO: Biological Process	GO:0008016	regulation of heart contraction		8.18E- 04	22	157
GO: Biological Process	GO:0060047	heart contraction		8.94E- 04	24	184
GO: Biological Process	GO:0003015	heart process		9.90E- 04	24	185
Pathway	83050	Calcium signaling pathway	Bio- Systems: KEGG	1.26E- 05	26	181
Pathway	198906	Calcium Regulation in the Cardiac Cell	Bio- Systems: Wiki- Pathways	2.40E- 05	23	149
Pathway	P00031	Inflammation mediated by chemokine and cytokine signaling pathway	PantherD B	3.96E- 05	26	191
Pathway	154409	Gastric acid secretion	Bio- Systems: KEGG	1.70E- 03	14	75

Pathway	908257	Adrenergic signaling in cardiomyocytes	Bio-Systems: KEGG	2.19E-03	20	149
Pathway	SMP00375	Verapamil Pathway	SMPDB	2.72E-03	12	57
Pathway	SMP00359	Diltiazem Pathway	SMPDB	2.72E-03	12	57
Pathway	161025	Smooth Muscle Contraction	Bio-Systems: REACTOME	3.89E-03	8	24
Pathway	698773	Circadian entrainment	Bio-Systems: KEGG	8.31E-03	15	97
Pathway	M12950	Angiotensin-converting enzyme 2 regulates heart function	MSigDB C2: BioCarta	8.56E-03	6	13
Pathway	217716	Cholinergic synapse	Bio-Systems: KEGG	1.30E-02	16	113
Pathway	106359	Chemokine receptors bind chemokines	Bio-Systems: REACTOME	1.53E-02	11	56
Pathway	SMP00368	Labetalol Pathway	SMPDB	1.74E-02	7	21
Pathway	SMP00367	Carvedilol Pathway	SMPDB	1.74E-02	7	21
Pathway	96530	Vascular smooth muscle contraction	Bio-Systems: KEGG	3.15E-02	16	121
Pathway	119550	G alpha (i) signalling events	Bio-Systems:	3.22E-02	24	238

			REACTOME			
Pathway	106261	Muscle contraction	Bio-Systems: REACTOME	4.03E-02	10	51
Pathway	M13494	Bioactive Peptide Induced Signaling Pathway	MSigDB C2: BioCarta	6.05E-02	9	43
Pathway	121494	Dilated cardiomyopathy	Bio-Systems: KEGG	7.64E-02	13	90
Pathway	121494	Dilated cardiomyopathy	Bio-Systems: KEGG	7.64E-02	13	90
Coexpression	17297478-SuppTable5	Human Intestine_Vecchi07_1024genes	GeneSigDB	2.50E-16	82	781
Coexpression	18498629-GeneList	Human Breast_Loi08_239genes	GeneSigDB	1.90E-14	36	178
Coexpression	M8124	Genes up-regulated in basal subtype of breast cancer samples.	MSigDB C2: Broad Institute	3.47E-14	70	647
Coexpression	20421987-TableS1	Human Lung_Hou10_1067genes	GeneSigDB	1.09E-12	72	724
Coexpression	M19391	Genes down-regulated in prostate cancer samples.	MSigDB C2: Broad Institute	1.32E-11	55	480
Coexpression	18318837-TableS1	Human MesenchymalStemCells_Yamamoto08_1252genes	GeneSigDB	1.91E-11	77	853

Coexpression	11823860-SuppTable3	Human Breast_van'tVeer02_2460genes_Ergenes	GeneSigDB	2.66E-11	130	1910
Coexpression	M18855	Up-regulated genes distinguishing between early gastric cancer (EGC) and normal tissue samples.	MSigDB C2: Broad Institute	2.99E-11	51	428
Coexpression	19014521-TableS6c	Human Breast_Reyal08_72genes	GeneSigDB	6.59E-11	20	63

Table S4

Category	ID	Name	Source	q-value Bonferroni	Hit Count in Query List	Hit Count in Genome
GO: Molecular Function	GO:0008092	cytoskeletal protein binding		5.46E-04	60	792
GO: Molecular Function	GO:0032403	protein complex binding		1.16E-03	66	924
GO: Molecular Function	GO:0008009	chemokine activity		1.31E-03	11	46
GO: Molecular Function	GO:0015631	tubulin binding		6.18E-03	26	251
GO: Molecular Function	GO:0042379	chemokine receptor binding		1.24E-02	11	57
GO: Molecular Function	GO:0008017	microtubule binding		3.82E-02	20	184
GO: Molecular Function	GO:0001664	G-protein coupled receptor binding		1.94E-01	22	239
GO: Biological Process	GO:0006928	movement of cell or subcellular component		3.65E-09	125	1703
GO: Biological Process	GO:0006936	muscle contraction		2.02E-08	40	295

GO: Biological Process	GO:0003012	muscle system process		3.86E-07	42	352
GO: Biological Process	GO:0040011	locomotion		1.19E-05	105	1522
GO: Biological Process	GO:0016477	cell migration		2.01E-05	81	1073
GO: Biological Process	GO:0006937	regulation of muscle contraction		2.61E-05	23	142
GO: Biological Process	GO:0090257	regulation of muscle system process		3.22E-05	26	180
GO: Biological Process	GO:0007155	cell adhesion		3.45E-05	80	1067
GO: Biological Process	GO:0022610	biological adhesion		5.22E-05	80	1077
GO: Biological Process	GO:0044057	regulation of system process		9.65E-05	43	438
GO: Biological Process	GO:0051674	localization of cell		1.02E-04	84	1170
GO: Biological Process	GO:0048870	cell motility		1.02E-04	84	1170
GO: Biological Process	GO:0006935	chemotaxis		1.35E-04	56	661

GO: Biological Process	GO:0042330	taxis		1.42E- 04	56	662
GO: Biological Process	GO:0051049	regulation of transport		3.03E- 04	100	1517
GO: Biological Process	GO:0022008	neurogenesis		6.81E- 04	95	1441
GO: Biological Process	GO:0007267	cell-cell signaling		6.84E- 04	87	1281
GO: Biological Process	GO:0008016	regulation of heart contraction		8.18E- 04	22	157
GO: Biological Process	GO:0060047	heart contraction		8.94E- 04	24	184
GO: Biological Process	GO:0003015	heart process		9.90E- 04	24	185
Pathway	83050	Calcium signaling pathway	Bio- Systems: KEGG	1.26E- 05	26	181
Pathway	198906	Calcium Regulation in the Cardiac Cell	Bio- Systems: Wiki- Pathways	2.40E- 05	23	149
Pathway	P00031	Inflammation mediated by chemokine and cytokine signaling pathway	PantherD B	3.96E- 05	26	191
Pathway	154409	Gastric acid secretion	Bio- Systems: KEGG	1.70E- 03	14	75

Pathway	908257	Adrenergic signaling in cardiomyocytes	Bio-Systems: KEGG	2.19E-03	20	149
Pathway	SMP00375	Verapamil Pathway	SMPDB	2.72E-03	12	57
Pathway	SMP00359	Diltiazem Pathway	SMPDB	2.72E-03	12	57
Pathway	161025	Smooth Muscle Contraction	Bio-Systems: REACTOME	3.89E-03	8	24
Pathway	698773	Circadian entrainment	Bio-Systems: KEGG	8.31E-03	15	97
Pathway	M12950	Angiotensin-converting enzyme 2 regulates heart function	MSigDB C2: BioCarta	8.56E-03	6	13
Pathway	217716	Cholinergic synapse	Bio-Systems: KEGG	1.30E-02	16	113
Pathway	106359	Chemokine receptors bind chemokines	Bio-Systems: REACTOME	1.53E-02	11	56
Pathway	SMP00368	Labetalol Pathway	SMPDB	1.74E-02	7	21
Pathway	SMP00367	Carvedilol Pathway	SMPDB	1.74E-02	7	21
Pathway	96530	Vascular smooth muscle contraction	Bio-Systems: KEGG	3.15E-02	16	121
Pathway	119550	G alpha (i) signalling events	Bio-Systems:	3.22E-02	24	238

			REACTOME			
Pathway	106261	Muscle contraction	Bio-Systems: REACTOME	4.03E-02	10	51
Pathway	M13494	Bioactive Peptide Induced Signaling Pathway	MSigDB C2: BioCarta	6.05E-02	9	43
Pathway	121494	Dilated cardiomyopathy	Bio-Systems: KEGG	7.64E-02	13	90
Pathway	121494	Dilated cardiomyopathy	Bio-Systems: KEGG	7.64E-02	13	90
Coexpression	17297478-SuppTable5	Human Intestine_Vecchi07_1024genes	GeneSigDB	2.50E-16	82	781
Coexpression	18498629-GeneList	Human Breast_Loi08_239genes	GeneSigDB	1.90E-14	36	178
Coexpression	M8124	Genes up-regulated in basal subtype of breast cancer samples.	MSigDB C2: Broad Institute	3.47E-14	70	647
Coexpression	20421987-TableS1	Human Lung_Hou10_1067genes	GeneSigDB	1.09E-12	72	724
Coexpression	M19391	Genes down-regulated in prostate cancer samples.	MSigDB C2: Broad Institute	1.32E-11	55	480
Coexpression	18318837-TableS1	Human MesenchymalStemCells_Yamamoto08_1252genes	GeneSigDB	1.91E-11	77	853

Coexpression	11823860-SuppTable3	Human Breast_van'tVeer02_2460genes_Ergenes	GeneSigDB	2.66E-11	130	1910
Coexpression	M18855	Up-regulated genes distinguishing between early gastric cancer (EGC) and normal tissue samples.	MSigDB C2: Broad Institute	2.99E-11	51	428
Coexpression	19014521-TableS6c	Human Breast_Reyal08_72genes	GeneSigDB	6.59E-11	20	63

Table S5

ID	Name	Source	q-value Bonferroni	q-value FDR B&H	Hit Count in Query List	Hit Count in Genoi
GO: Molecular Function						
GO:0004896	cytokine receptor activity		3.33E-03	3.33E-03	32	90
GO: Biological Process						
GO:0006955	immune response		8.87E-26	8.87E-26	438	1762
GO:0006954	inflammatory response		1.50E-19	7.51E-20	205	689
GO:0002682	regulation of immune system process		3.16E-19	1.05E-19	390	1626
GO:0070486	leukocyte aggregation		1.80E-16	4.49E-17	155	494
GO:0007159	leukocyte cell-cell adhesion		2.38E-16	4.76E-17	162	527
GO:0045321	leukocyte activation		3.17E-16	5.05E-17	222	813
GO:0002684	positive regulation of immune system process		3.53E-16	5.05E-17	259	998
GO:0006952	defense response		6.85E-16	8.57E-17	428	1901
GO:0071593	lymphocyte aggregation		1.97E-15	2.19E-16	151	487
GO:0070489	T cell aggregation		4.19E-15	3.81E-16	150	486
GO:0042110	T cell activation		4.19E-15	3.81E-16	150	486
GO:0034109	homotypic cell-cell adhesion		6.69E-15	5.58E-16	166	562
GO:0001816	cytokine production		2.82E-14	2.17E-15	191	689
GO:0001775	cell activation		3.63E-14	2.59E-15	264	1057
GO:0046649	lymphocyte activation		8.12E-13	5.41E-14	187	690
GO:0002252	immune effector process		1.35E-12	8.42E-14	216	838
GO:1903039	positive regulation of leukocyte cell-cell adhesion		1.84E-11	1.08E-12	82	225
GO:0050776	regulation of immune response		2.60E-11	1.44E-12	253	1052
GO:0050870	positive regulation of T cell activation		3.48E-11	1.83E-12	80	219
GO:0034112	positive regulation of homotypic cell-cell adhesion		4.55E-11	2.27E-12	81	224
GO:0002694	regulation of leukocyte activation		6.02E-11	2.87E-12	142	498
GO:0050865	regulation of cell activation		1.30E-10	5.92E-12	149	536
GO:0034110	regulation of homotypic cell-cell adhesion		1.97E-10	8.57E-12	105	333
GO:0050863	regulation of T cell activation		2.61E-10	1.05E-11	100	312
GO:0098602	single organism cell adhesion		2.62E-10	1.05E-11	208	836
GO:1903037	regulation of leukocyte cell-cell adhesion		3.35E-10	1.29E-11	102	322
GO:0001817	regulation of cytokine production		5.94E-10	2.20E-11	164	619
GO:0016337	single organismal cell-cell adhesion		7.17E-10	2.56E-11	196	782
GO:0022610	biological adhesion		7.60E-10	2.62E-11	333	1518
Pathway						
198862	TCR Signaling Pathway	BioSystems: WikiPathways	5.89E-04	2.96E-04	34	91
83078	Hematopoietic cell lineage	BioSystems: KEGG	8.02E-04	2.96E-04	33	88
83051	Cytokine-cytokine receptor interaction	BioSystems: KEGG	1.05E-03	2.96E-04	72	265
P00031	Inflammation mediated by chemokine and cytokine signaling pathway	PantherDB	1.51E-03	2.96E-04	56	191
198909	B Cell Receptor Signaling Pathway	BioSystems: WikiPathways	1.52E-03	2.96E-04	49	159
M9526	T Cell Signal Transduction	MSigDB C2: Signaling Transduction KE	1.78E-03	2.96E-04	21	45
160140	Signaling by Interleukins	BioSystems: REACTOME	4.02E-02	5.74E-03	36	116
83080	T cell receptor signaling pathway	BioSystems: KEGG	5.43E-02	6.42E-03	33	104
99051	Chemokine signaling pathway	BioSystems: KEGG	6.36E-02	6.42E-03	51	189
193147	Osteoclast differentiation	BioSystems: KEGG	6.42E-02	6.42E-03	39	132
83077	Jak-STAT signaling pathway	BioSystems: KEGG	7.11E-02	6.47E-03	44	156
198760	IL-4 signaling Pathway	BioSystems: WikiPathways	1.12E-01	9.31E-03	23	64
137998	TCR signaling in naive CD4+ T cells	BioSystems: Pathway Interaction Database	1.54E-01	1.18E-02	22	61
137922	IL12-mediated signaling events	BioSystems: Pathway Interaction Database	2.04E-01	1.46E-02	22	62
213306	Measles	BioSystems: KEGG	2.19E-01	1.46E-02	38	134
M1467	The Co-Stimulatory Signal During T-cell Activation	MSigDB C2: BioCarta	2.40E-01	1.50E-02	11	21
128760	Intestinal immune network for IgA production	BioSystems: KEGG	2.97E-01	1.70E-02	19	51
83081	B cell receptor signaling pathway	BioSystems: KEGG	3.06E-01	1.70E-02	24	72
Coexpression						
M10454	Genes up-regulated in pulpal tissue extracted from carious teeth.	MSigDB C2: University of Washington	2.44E-26	2.44E-26	110	252
M8513	Genes up-regulated in the normal-like subtype of breast cancer.	MSigDB C2: Broad Institute	3.84E-23	1.92E-23	159	476
M1278	Genes down-regulated in pulpal tissue extracted from carious teeth.	MSigDB C2: University of Washington	9.53E-22	3.18E-22	101	244
M5369	Genes up-regulated in atypical ductal hyperplastic tissues from patients with (ADHC) breast cancer vs those without the cancer (ADH).	MSigDB C2: Broad Institute	5.23E-20	1.31E-20	109	287
17174972-TableS1	Human Zola07_426genes_CellDifferentiationMarkers	GeneSigDB	6.15E-18	1.23E-18	119	345
M1920	Genes forming the macrophage-enriched metabolic network (MEMN) claimed to have a causal relationship with the metabolic syndrom traits.	MSigDB C2: Broad Institute	1.39E-16	2.31E-17	288	1210

Table S6

ID	Name	Source	q-value Bonferroni	q-value FDR B&H	Hit Count in Query List	Hit Count in Genome
GO: Molecular Function						
GO:0019899	enzyme binding		1.57E-05	1.57E-05	453	1851
GO:0032403	protein complex binding		1.92E-04	9.60E-05	272	1053
GO:0044877	macromolecular complex binding		9.95E-04	3.32E-04	382	1578
GO:0008092	cytoskeletal protein binding		2.37E-03	5.91E-04	226	874
GO:0004672	protein kinase activity		2.71E-02	5.42E-03	161	610
GO:0016773	phosphotransferase activity, alcohol group as acceptor		3.55E-02	5.91E-03	185	720
GO:0030554	adenyl nucleotide binding		5.98E-02	8.54E-03	357	1524
GO:0032559	adenyl ribonucleotide binding		8.60E-02	1.03E-02	354	1516
GO:0050840	extracellular matrix binding		9.27E-02	1.03E-02	24	55
GO:0005516	calmodulin binding		1.05E-01	1.05E-02	59	186
GO: Biological Process						
GO:0030030	cell projection organization		2.66E-12	2.66E-12	447	1642
GO:0022008	neurogenesis		5.57E-06	2.79E-06	459	1848
GO:0048699	generation of neurons		1.50E-05	4.71E-06	437	1759
GO:0048666	neuron development		2.50E-05	4.71E-06	349	1363
GO:0000902	cell morphogenesis		2.85E-05	4.71E-06	395	1574
GO:0030182	neuron differentiation		2.94E-05	4.71E-06	408	1634
GO:0007010	cytoskeleton organization		3.57E-05	4.71E-06	299	1142
GO:0048858	cell projection morphogenesis		4.02E-05	4.71E-06	309	1188
GO:0031175	neuron projection development		4.24E-05	4.71E-06	314	1211
GO:0032990	cell part morphogenesis		4.86E-05	4.86E-06	313	1208
GO:0032989	cellular component morphogenesis		1.11E-04	1.01E-05	410	1660
Pathway						
83067	Focal adhesion	BioSystems: KEGG	1.75E-04	1.02E-04	71	206
96530	Vascular smooth muscle contraction	BioSystems: KEGG	2.04E-04	1.02E-04	48	121
833810	Non-integrin membrane-ECM interactions	BioSystems: REACTOME	6.04E-04	2.01E-04	23	42
M5884	Ensemble of genes encoding core ECM	MSigDB C2: MIT	1.07E-03	2.69E-04	86	275
M3008	Genes encoding structural ECM glycoproteins	MSigDB C2: MIT	1.35E-03	2.70E-04	66	196
198906	Calcium Regulation in the Cardiac Cell	BioSystems: WikiPathways	1.58E-02	2.63E-03	51	149
698773	Circadian entrainment	BioSystems: KEGG	1.89E-02	2.70E-03	37	97
160966	Cell junction organization	BioSystems: REACTOME	2.85E-02	3.26E-03	33	84
105688	Axon guidance	BioSystems: REACTOME	2.94E-02	3.26E-03	78	262
477132	Cell-Cell communication	BioSystems: REACTOME	4.99E-02	4.69E-03	45	131
106496	PLC beta mediated events	BioSystems: REACTOME	5.64E-02	4.69E-03	21	45