Supplementary Material

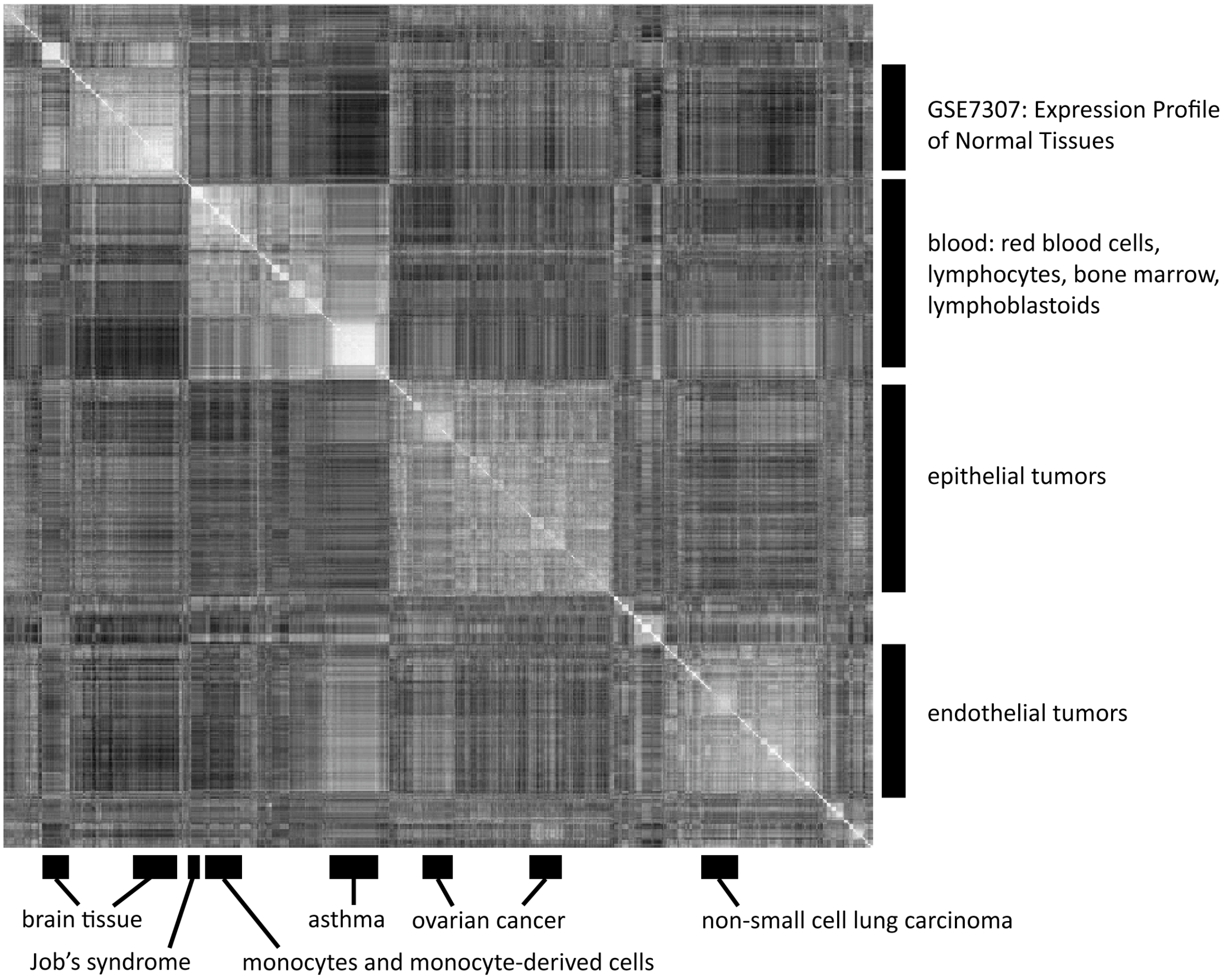
Independent component analysis: mining microarray data for fundamental human gene expression modules

Jesse M. Engreitz[1], Bernie J. Daigle, Jr.[2], Jonathan J. Marshall[1], Russ B. Altman[1,2,*]

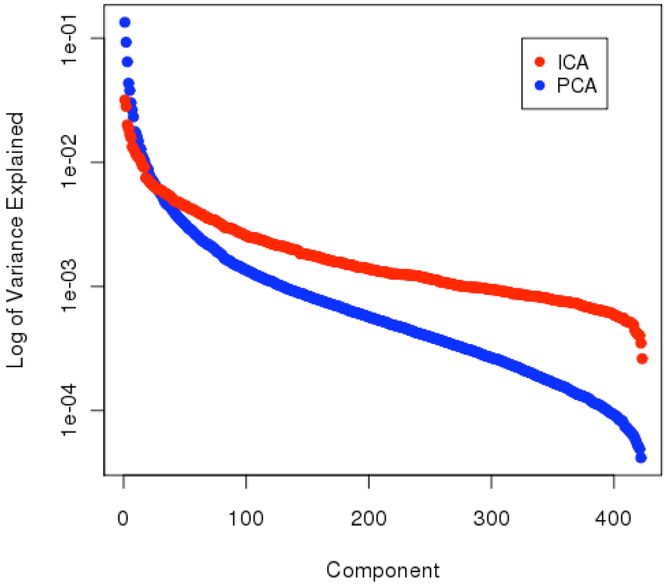
1 Department of Bioengineering, Stanford University, Stanford, CA 94305, USA

2 Department of Genetics, Stanford University School of Medicine, Stanford, CA 94305, USA

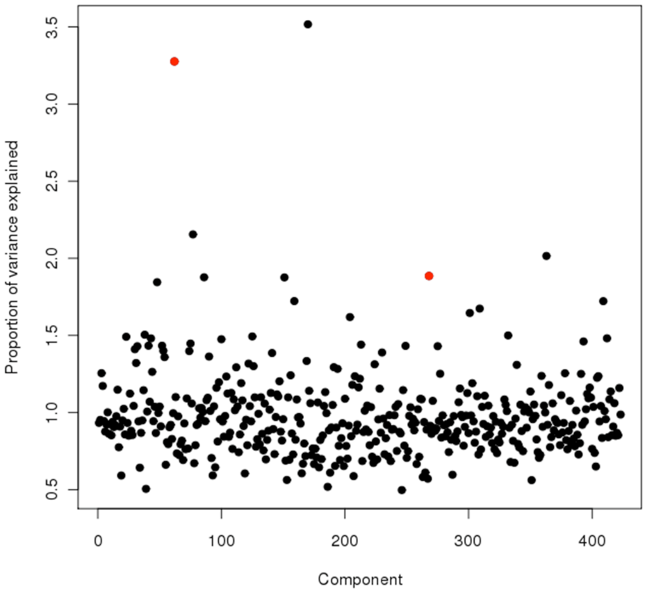
* E-mail: russ.altman@stanford.edu



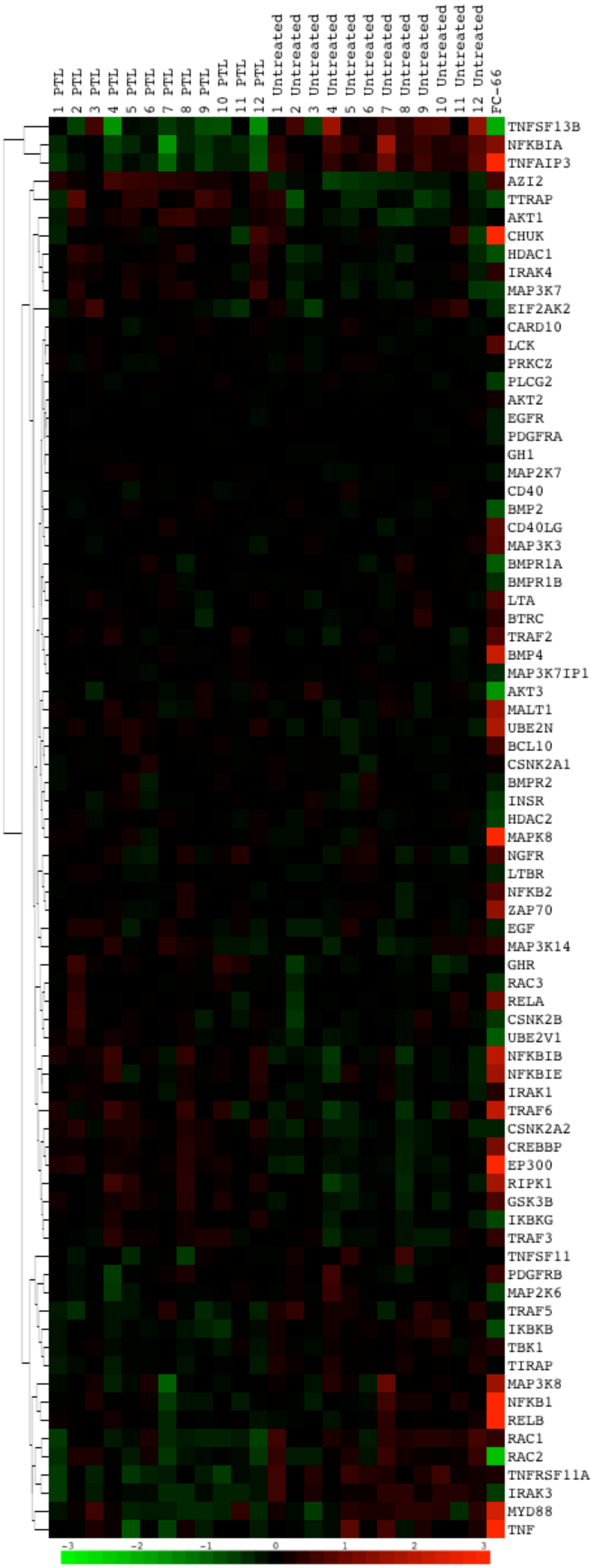
Supplementary Figure 1. Similarity matrix for 9,395-array compendium. The initial compendium contains large contributions from specific datasets, conditions, and cell types. A similarity metric based on Spearman's rank correlation shows large blocks of arrays that have similar signals (bright). These over-represented conditions may bias our module analysis, inflating the weights for components that describe these data sets.



Supplementary Figure 2. Variance explained by independent and principal components. We applied ICA and PCA to the meta-compendium to find the maximum number of components possible (423). Components were ordered based on percentage variance of the meta-compendium explained. We plotted the variance of the meta-compendium explained by each component on a log scale to show the difference in the tails of the distribution. Principal component 1 explains 13.4% of the variance of the meta-compendium, while independent component 1 explains 3.2% of the variance.



Supplementary Figure 3. Ratio of variance explained in the original compendium to variance explained in the meta-compendium for 423 fundamental components. A ratio greater than one indicates that a component explains more variance in the original than in the meta-compendium. Red dots represent fundamental components 62 and 268 (see Results 3.1).



Supplementary Figure 4. Differential expression of genes in the NF-κB pathway in parthenolide-treated and untreated AML CD34$^+$ cells. We used the original data from GSE7538, applied RMA and *bias* normalizations as described in the text, and visualized the pair-centered expression of genes in the Ingenuity Canonical Pathway “NF-κB Signaling.” The right-most column shows the expression of each of these genes in fundamental component 66 (FC-66).

Supplementary Table 1

Enriched GO categories for the ten fundamental components that explain the most variance in the meta-compendium.

Component	GO Category	Bonferroni p-value
1	immune response	<1E-30
	inflammatory response	2.71E-06
	cellular defense response	6.89E-05
	intracellular signaling cascade	1.23E-04
	hemopoietic or lymphoid organ development	2.26E-04
	elevation of cytosolic calcium ion concentration	6.89E-04
	chemotaxis	1.13E-03
	apoptosis	1.48E-03
	T cell proliferation	1.97E-03
	defense response	3.74E-03
	cell surface receptor linked signal transduction	4.73E-03
	signal transduction	1.33E-02
	hemopoiesis	2.36E-02
	response to other organism	4.38E-02
2	cell division	<1E-30
	mitosis	<1E-30
	DNA replication	5.91E-20
	response to endogenous stimulus	4.77E-13
	DNA replication initiation	4.92E-13
	DNA repair	4.92E-13
	regulation of mitosis	3.30E-12
	spindle organization	4.43E-10
	interphase of mitotic cell cycle	1.33E-08
	cell cycle process	1.48E-08
	mitotic sister chromatid segregation	2.71E-08
	mitotic chromosome condensation	1.57E-07
	regulation of cell cycle	2.07E-07
	microtubule-based movement	1.38E-06
	regulation of cyclin-dependent protein kinase activity	3.64E-06
	cell cycle	4.48E-06
	mitotic spindle organization	9.35E-06
	establishment of chromosome localization	2.41E-05
	phosphoinositide-mediated signaling	3.10E-05
	DNA integrity checkpoint	5.91E-05
	positive regulation of mitosis	4.87E-04
	cell proliferation	5.41E-04
	chromosome segregation	5.91E-04
	cytokinesis	6.40E-04
	meiotic cell cycle	2.66E-03
	DNA unwinding during replication	2.95E-03
	regulation of DNA metabolic process	4.87E-03
	DNA recombination	5.41E-03
	mitotic cell cycle checkpoint	5.91E-03
	mitotic cell cycle spindle assembly checkpoint	8.86E-03
	traversing start control point of mitotic cell cycle	8.86E-03
	cell cycle checkpoint	2.36E-02

	meiosis	2.51E-02
	M phase of meiotic cell cycle	2.51E-02
	DNA-dependent DNA replication	4.23E-02
3	cell adhesion	2.36E-23
	phosphate transport	3.99E-16
	skeletal system development	3.59E-06
	cell surface receptor linked signal transduction	4.63E-05
	organ development	1.92E-04
	extracellular matrix organization	1.43E-03
	response to wounding	1.48E-03
	organ morphogenesis	3.54E-03
	bioluminescence	2.02E-02
	enzyme linked receptor protein signaling pathway	2.22E-02
	transmembrane receptor protein tyrosine kinase activity	2.31E-02
	blood vessel development	4.33E-02
	vasculature development	4.92E-02
4	epidermis development	5.42E-07
	cell adhesion	1.92E-05
5	immune response	5.91E-27
	inflammatory response	9.35E-19
	antigen processing and presentation of peptide antigen	3.59E-10
	multicellular organismal process	1.82E-05
	detection of biotic stimulus	2.02E-05
	antimicrobial humoral response	4.09E-05
	regulation of cytokine production	8.37E-05
	signal transduction	3.00E-04
	response to other organism	5.91E-04
	innate immune response	1.08E-03
	cellular defense response	3.54E-03
	regulation of response to stimulus	4.23E-03
	positive regulation of immune system process	8.37E-03
	leukocyte activation	1.18E-02
	regulation of immune response	1.33E-02
	response to bacterium	1.72E-02
	Toll signaling pathway	3.15E-02
	interleukin-1 secretion	3.84E-02
	interleukin-1 beta secretion	3.84E-02
	cytokine secretion	3.94E-02
	cell activation	4.28E-02
6	cell differentiation	1.18E-04
	regulation of cell proliferation	1.92E-04
	regulation of biological quality	2.61E-04
	anatomical structure morphogenesis	4.33E-04
	cell adhesion	2.02E-03
	wound healing	3.54E-03
	negative regulation of biological process	3.59E-03
	blood vessel morphogenesis	4.92E-03

	blood coagulation	1.77E-02
	system development	1.92E-02
	coagulation	2.41E-02
	regulation of body fluid levels	2.46E-02
	hemostasis	2.95E-02
	angiogenesis	4.09E-02
	negative regulation of cellular process	4.38E-02
7	multicellular organismal process	1.28E-04
	anatomical structure development	9.85E-03
	fat cell differentiation	2.07E-02
	system development	4.53E-02
8	immune response	6.40E-09
	antimicrobial humoral response	7.38E-06
	positive regulation of translation	3.50E-05
	regulation of lymphocyte proliferation	5.42E-04
	adaptive immune response based on somatic recombination of immune rec…	7.38E-04
	alpha-beta T cell activation	8.86E-04
	B cell proliferation	1.28E-03
	positive regulation of cytokine biosynthesis	1.48E-03
	positive regulation of T cell activation	2.17E-03
	defense response	3.00E-03
	regulation of T cell differentiation	3.64E-03
	regulation of B cell activation	8.86E-03
	T-helper cell differentiation	1.13E-02
	T cell differentiation during immune response	1.13E-02
	alpha-beta T cell differentiation during immune response	1.13E-02
	CD4-positive, alpha-beta T cell differentiation	1.13E-02
	cell activation during immune response	1.13E-02
	lymphocyte activation during immune response	1.13E-02
	T cell activation during immune response	1.13E-02
	leukocyte activation during immune response	1.13E-02
	regulation of interferon-gamma biosynthesis	1.38E-02
	interferon-gamma biosynthetic process	1.97E-02
	regulation of interferon-gamma production	1.97E-02
	CD4-positive, alpha beta T cell differentiation during immune response	2.17E-02
	regulation of immune response	2.61E-02
	interferon-gamma production	2.76E-02
	regulation of apoptosis	3.20E-02
	regulation of programmed cell death	3.89E-02
	regulation of protein localization	4.09E-02
	regulation of protein transport	4.09E-02
	regulation of establishment of protein localization	4.09E-02
	cell communication	4.92E-02
9	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1.97E-02
10	macromolecule metabolic process	1.18E-02
	primary metabolic process	3.45E-02

Supplementary Table 2.

Enriched Ingenuity Canonical Pathways and GO categories for differentially expressed genes between PTL-treated and untreated AML CD34$^+$ cells.*

Annotation	P-Value
Ingenuity Canonical Pathways (up-regulated)	
Protein Ubiquitination Pathway	7.94E-14
NRF2-mediated Oxidative Stress Response	5.37E-10
Hypoxia Signaling in the Cardiovascular System	3.02E-08
Polyamine Regulation in Colon Cancer	3.02E-08
Glucocorticoid Receptor Signaling	2.45E-03
Huntington's Disease Signaling	2.69E-03
Endoplasmic Reticulum Stress Pathway	2.69E-03
Death Receptor Signaling	1.23E-02
RAN Signaling	1.23E-02
Oxidative Phosphorylation	1.23E-02
Glutamate Metabolism	1.55E-02
Prostate Cancer Signaling	1.55E-02
Molecular Mechanisms of Cancer	1.86E-02
GO Categories (up-regulated)	
organ development	4.87E-15
multicellular organismal process	3.94E-09
cell-cell signaling	1.18E-07
system process	3.00E-07
signal transduction	1.38E-05
immune response	1.87E-05
transmembrane receptor protein tyrosine kinase signaling pathway	3.15E-05
cell proliferation	3.30E-05
multicellular organismal development	1.97E-04
cell development	4.92E-04
generation of precursor metabolites and energy	1.43E-03
positive regulation of cell proliferation	3.05E-03
inflammatory response	3.40E-03
behavior	7.38E-03
response to chemical stimulus	1.28E-02
phosphorylation	1.38E-02
cell cycle process	1.62E-02
cell surface receptor linked signal transduction	1.62E-02
regulation of cell cycle	2.12E-02
pattern specification process	2.36E-02
hormone biosynthetic process	2.41E-02
blood circulation	2.56E-02
circulatory system process	2.56E-02
skeletal system development	2.71E-02
biological adhesion	3.40E-02
cell adhesion	3.40E-02
Ingenuity Canonical Pathways (down-regulated)	
none	
GO Categories (down-regulated)	
generation of precursor metabolites and energy	1.87E-10
cell surface receptor linked signal transduction	6.89E-09

blood circulation	2.51E-08
regulation of multicellular organismal process	1.33E-07
positive regulation of biological process	3.59E-07
cellular calcium ion homeostasis	3.69E-05
organ morphogenesis	1.53E-04
cellular alcohol metabolic process	3.50E-04
organ development	4.92E-04
regulation of immune system process	5.91E-04
multicellular organismal process	6.40E-04
behavior	6.40E-04
nucleotide biosynthetic process	6.40E-04
cell proliferation	6.89E-04
cofactor metabolic process	1.13E-03
regulation of biological quality	1.67E-03
blood coagulation	3.59E-03
myeloid cell differentiation	4.53E-03
inflammatory response	4.73E-03
humoral immune response	4.87E-03
synaptic transmission	5.91E-03
activation of adenylate cyclase activity	9.85E-03
carboxylic acid metabolic process	1.33E-02
positive regulation of cellular process	1.33E-02
negative regulation of biological process	1.43E-02
organic acid metabolic process	1.58E-02
vascular process in circulatory system	1.92E-02
G-protein coupled receptor protein signaling	2.02E-02
acute inflammatory response	2.12E-02
second-messenger-mediated signaling	2.17E-02
regulation of blood pressure	2.17E-02
response to stimulus	2.22E-02
regulation of developmental process	2.26E-02
reproductive process in a multicellular organism	2.90E-02
multicellular organism reproduction	2.90E-02
regulation of cell proliferation	3.00E-02
monohydric alcohol metabolic process	3.15E-02
ethanol metabolic process	3.15E-02
ethanol oxidation	3.15E-02
skeletal system development	3.50E-02
positive regulation of multicellular organismal process	3.79E-02
negative regulation of multicellular organismal process	4.43E-02

* P-values for Ingenuity Canonical Pathways have Benjamini-Hochberg correction applied. P-values for GO categories have Bonferroni correction applied.

Supplementary Table 3. Enriched Ingenuity Canonical Pathways and GO categories for the single differentially expressed experiment-specific component.*

Annotation	P-Value
Ingenuity Canonical Pathways (up-regulated)	
NRF2-mediated Oxidative Stress Response	2.95E-09
Protein Ubiquitination Pathway	7.59E-03
Hypoxia Signaling in the Cardiovascular System	7.59E-03
Inositol Metabolism	1.10E-02
Polyamine Regulation in Colon Cancer	1.91E-02
Glucocorticoid Receptor Signaling	2.09E-02
GO Categories (up-regulated)	
response to unfolded protein	1.77E-12
protein folding	4.63E-09

* P-values for Ingenuity Canonical Pathways have Benjamini-Hochberg correction applied. P-values for GO categories have Bonferroni correction applied.

Supplementary Table 4.

Annotations for nineteen DE fundamental components between PTL-treated and untreated AML CD34$^+$ cells.

Component (Δexpr)	**Annotation**	**P-Value**
66	***Ingenuity Canonical Pathways***	
(+3.11)	NF-κB Signaling	8.51E-03
	T Cell Receptor Signaling	8.51E-03
	Type I Diabetes Mellitus Signaling	8.51E-03
	IL-6 Signaling	1.51E-02
	Glucocorticoid Receptor Signaling	1.51E-02
	HMGB1 Signaling	1.62E-02
	Prolactin Signaling	1.62E-02
	LPS-stimulated MAPK Signaling	1.62E-02
	Role of NFAT in Regulation of the Immune Response	1.62E-02
	IL-12 Signaling and Production in Macrophages	2.04E-02
	CD28 Signaling in T Helper Cells	2.04E-02
	Lymphotoxin β Receptor Signaling	2.04E-02
	Type II Diabetes Mellitus Signaling	2.04E-02
	EIF2 Signaling	2.04E-02
	PPAR Signaling	2.04E-02
	Apoptosis Signaling	2.14E-02
	Gα12/13 Signaling	2.19E-02
	PAK Signaling	2.29E-02
	PTEN Signaling	2.45E-02
	JAK/Stat Signaling	2.45E-02
	Neurotrophin/TRK Signaling	2.51E-02
	Role of PKR in Interferon Induction and Antiviral Response	3.02E-02
	Agrin Interactions at Neuromuscular Junction	3.02E-02
	iCOS-iCOSL Signaling in T Helper Cells	3.02E-02
	Cholecystokinin/Gastrin-mediated Signaling	3.02E-02
	Acute Phase Response Signaling	3.16E-02
	Rac Signaling	3.47E-02
	14-3-3-mediated Signaling	3.98E-02
	Estrogen Receptor Signaling	4.07E-02
	B Cell Receptor Signaling	4.07E-02
	TGF-β Signaling	4.07E-02
	Ceramide Signaling	4.27E-02
	Germ Cell-Sertoli Cell Junction Signaling	4.27E-02
	Androgen Signaling	4.27E-02
	CD27 Signaling in Lymphocytes	4.47E-02
	PPARα/RXRα Activation	4.68E-02
	IL-2 Signaling	4.90E-02
	GO Categories	
	regulation of transcription, DNA-dependent	2.76E-06
	negative regulation of biological process	4.23E-02
	GEO experiments with high expression of this component	
GSE10609	the recurrent SET-NUP214 fusion as a new HOXA activation mechanism in pediatric T-ALL	
GSE7440	Early Response and Outcome in High-Risk Childhood Acute Lymphoblastic Leukemia: A Children's Oncology Group Study	
GSE10358	Discovery and validation of expression data for the Genomics of Acute Myeloid Leukemia Program at Washington University.	
GSE10792	Genome wide genotyping and gene expression data of childhood B-cell precursor ALL without known genetic aberrations	
GSE7757	Robustness of gene expression signatures in leukemia: comparison of three distinct total RNA preparation procedures.	

GSE11190	Interferon signaling and treatment outcome in chronic hepatitis C	
362	***Ingenuity Canonical Pathways***	
(+2.34)	NRF2-mediated Oxidative Stress Response	1.05E-04
	Complement System	1.23E-02
	Aryl Hydrocarbon Receptor Signaling	1.23E-02
	Glucocorticoid Receptor Signaling	2.40E-02
	Role of Pattern Recognition Receptors in Recognition of Bacteria and Viruses	2.40E-02
	GO Categories	
	response to unfolded protein	1.67E-15
	protein folding	2.86E-15
	organ development	4.48E-02
	GEO experiments with high expression of this component	
GSE7307	Human body index - transcriptional profiling	
GSE7621	Expression data of substantia nigra from postmortem human brain of Parkinson's disease patients (PD)	
GSE10315	Multipotent mesenchymal stromal cells: identification of pathways common to TGFβ3/BMP2-induced chondrogenesis	
GSE8977	Bone-marrow-derived mesenchymal stem cells promote breast cancer metastasis	
GSE2816	cMyb and vMyb in human monocytes	
GSE7904	Expression data from human breast tissue	
GSE3325	Integrative Genomic and Proteomic Analysis of Prostate Cancer Reveals Signatures of Metastatic Progression	
GSE2109	Expression Project for Oncology (expO)	
GSE9916	The genomic-level expression patterns of human mononuclear cells subjected heat shock or lipopolysaccharide stress	
GSE5281	Alzheimer's disease and the normal aged brain (steph-affy-human-433773)	
GSE9089	Reanalysis of GSE8884 Samples with Endothelial Samples from GSE3998.	
GSE8586	Expression profiles of extremely low gestational age newborns as predictors of BPD	
GSE3526	Comparison of gene expression profiles across the normal human body	
84	***Ingenuity Canonical Pathways***	
(+1.53)	N-Glycan Biosynthesis	3.38E-10
	Endoplasmic Reticulum Stress Pathway	1.23E-04
	NRF2-mediated Oxidative Stress Response	1.23E-02
	Antigen Presentation Pathway	1.72E-02
	Lipid Antigen Presentation by CD1	3.03E-02
	Aminosugars Metabolism	3.16E-02
	Starch and Sucrose Metabolism	4.88E-02
	GO Categories	
	protein folding	4.92E-10
	protein amino acid N-linked glycosylation	2.46E-07
	secretion	6.40E-05
	intracellular protein transport	2.26E-04
	cell redox homeostasis	2.90E-04
	ER to Golgi vesicle-mediated transport	4.92E-04
	protein retention in ER lumen	3.64E-03
	signal peptide processing	8.37E-03
	response to endoplasmic reticulum stress	9.85E-03
	ER-nuclear signaling pathway	4.73E-02
	GEO experiments with high expression of this component	
GSE10315	Multipotent mesenchymal stromal cells: identification of pathways common to TGFβ3/BMP2-induced chondrogenesis	
GSE6283	Specific transcriptional changes in human fetus with autosomal trisomies	
GSE6400	Cultured A549 lung cancer cells treated with actinomycin D and sapphyrin PCI-2050	
GSE6241	The effects of Serum Amyloid A on gene expression profile in HUVECs	
GSE7846	Differentially expressed genes in HEECs of eutopic endometrium of patients with endometriosis compared with control	
GSE10444	gene expression levels in long-term cultures of human dental pulp stem cells	

GSE2109	Expression Project for Oncology (expO)
GSE9452	Definition of an ulcerative colitis preinflammatory state
GSE9077	Expression profiles of immortal lung fibroblasts
GSE9647	Comparative transcriptomic profiling of unstimulated and inflamed HUVEC exposed to apple procyanidin oligomers
GSE9832	Reprogramming of human somatic cells to pluripotency with defined factors
GSE8742	The Induction of Senescence-Like Growth Arrest by Diterpene Esters in Solid Tumor Cells
GSE7307	Human body index - transcriptional profiling
GSE4183	Inflammation, adenoma and cancer: objective classification of colon biopsy specimens with gene expression signature
GSE6532	Definition of clinically distinct molecular subtypes in estrogen receptor positive breast carcinomas using genomic grade
GSE10575	Migratory chondrogenic progenitor cells from repair tissue during the later stages of human osteoarthritis
GSE7127	63 Melanoma cell lines
GSE8049	Expression analyses of glioblastoma derived neurosphere cultures
GSE8332	Death receptor O-glycosylation controls tumor-cell sensitivity to the proapoptotic ligand Apo2L/TRAIL

73	***Ingenuity Canonical Pathways***	
(+1.38)	Metabolism of Xenobiotics by Cytochrome P450	7.94E-13
	Xenobiotic Metabolism Signaling	3.98E-12
	NRF2-mediated Oxidative Stress Response	6.92E-10
	Glutathione Metabolism	5.75E-09
	Pentose and Glucuronate Interconversions	3.39E-08
	Arachidonic Acid Metabolism	3.02E-07
	LPS/IL-1 Mediated Inhibition of RXR Function	7.08E-06
	Starch and Sucrose Metabolism	1.45E-05
	PXR/RXR Activation	7.08E-05
	Bile Acid Biosynthesis	7.08E-05
	Aryl Hydrocarbon Receptor Signaling	9.12E-05
	Pyruvate Metabolism	1.00E-04
	Retinol Metabolism	1.45E-04
	Androgen and Estrogen Metabolism	6.76E-04
	Ascorbate and Aldarate Metabolism	6.92E-04
	Chondroitin Sulfate Biosynthesis	8.91E-04
	Cysteine Metabolism	9.33E-04
	Tryptophan Metabolism	1.58E-03
	Glycolysis/Gluconeogenesis	2.14E-03
	Pentose Phosphate Pathway	2.63E-03
	Glycerolipid Metabolism	2.63E-03
	Sulfur Metabolism	3.09E-03
	Fatty Acid Metabolism	3.89E-03
	C21-Steroid Hormone Metabolism	5.89E-03
	Keratan Sulfate Biosynthesis	7.59E-03
	Fructose and Mannose Metabolism	9.33E-03
	FXR/RXR Activation	1.07E-02
	Hepatic Cholestasis	1.10E-02
	Butanoate Metabolism	1.66E-02
	IL-10 Signaling	1.70E-02
	Eicosanoid Signaling	1.86E-02
	Propanoate Metabolism	2.00E-02
	Linoleic Acid Metabolism	2.19E-02
	MIF Regulation of Innate Immunity	2.82E-02
	Glutamate Metabolism	2.82E-02
	Altered T Cell and B Cell Signaling in Rheumatoid Arthritis	2.82E-02
	Arginine and Proline Metabolism	3.16E-02
	Ovarian Cancer Signaling	3.24E-02
	TR/RXR Activation	4.68E-02
	Galactose Metabolism	4.79E-02
	GO Categories	

	icosanoid metabolic process	9.35E-05
	pyridine nucleotide metabolic process	1.53E-03
	generation of precursor metabolites and energy	8.86E-03
	nicotinamide metabolic process	1.48E-02
	response to stimulus	2.46E-02
	steroid metabolic process	3.15E-02
	GEO experiments with high expression of this component	
GSE8961	Identification of human metapneumovirus-induced gene networks in airway epithelial cells by microarray analysis	
GSE3202	MK886 treatment of H720 non-small cell lung cancer cell line	
GSE6013	Gene expression in asbestos exposed lung cells	
GSE6960	Synthesis and Anticancer Properties of Water-Soluble Zinc Ionophores 1	
GSE6962	Synthesis and Anticancer Properties of Water-Soluble Zinc Ionophores 2	
GSE6400	Cultured A549 lung cancer cells treated with actinomycin D and sapphyrin PCI-2050	
GSE9008	Resveratrol action on A549 lung cancer cells	
GSE5816	A Genome-wide Screen for Hypermethylated Genes in Lung Cancer	
GSE2109	Expression Project for Oncology (expO)	
GSE7964	HDAC-42 modulates acid-induced gene expression in human SEG-1 esophageal adenocarcinoma cells	
GSE8527	Analysis of the in vitro transcriptional response of human pharyngeal epithelial cells to adherent pneumococci	
406	***Ingenuity Canonical Pathways***	
(+1.24)	Glucocorticoid Receptor Signaling	6.17E-03
	GO Categories	
	regulation of biological process	9.85E-03
	GEO experiments with high expression of this component	
GSE10358	Discovery and validation of expression data for the Genomics of Acute Myeloid Leukemia Program at Washington University.	
GSE10609	the recurrent SET-NUP214 fusion as a new HOXA activation mechanism in pediatric T-ALL	
GSE7440	Early Response and Outcome in High-Risk Childhood Acute Lymphoblastic Leukemia: A Children's Oncology Group Study	
GSE9089	Reanalysis of GSE8884 Samples with Endothelial Samples from GSE3998.	
GSE8565	Argyrin A is a p27 stabilizing drug with potent antiproliferative activity in vivo	
GSE8717	Expression data from Human MPNST cancer cells infected with G207 and oncolytic HSV	
GSE7757	Robustness of gene expression signatures in leukemia: comparison of three distinct total RNA preparation procedures.	
GSE9150	Primary nasal epithelium exposed to house dust mite extract shows activated expression in allergics	
GSE7845	Proinflammatory Responses of Human Airway Cells to Ricin Involve Stress-Activated Protein Kinases and NF-κB	
GSE9090	Reanalysis of GSE8884 Samples with Stromal Samples from GSE3998.	
GSE8977	Bone-marrow-derived mesenchymal stem cells promote breast cancer metastasis	
GSE6013	Gene expression in asbestos exposed lung cells	
GSE10792	Genome wide genotyping and gene expression data of childhood B-cell precursor ALL without known genetic aberrations	
GSE10021	mRNA expression profiles in human cell lines	
GSE6338	Gene expression analysis of Peripheral T-cell Lymphoma/Unspecified	
GSE7307	Human body index - transcriptional profiling	
GSE9091	Reanalysis of GSE8884 Samples with Leukocyte Samples from GSE3284.	
GSE8884	Expression data from human embryonic stem cells, early stage embryoid bodies, and hES-derived blast cells.	
GSE9086	Reanalysis of GSE8884 Samples with Breast Epithelial Samples from GSE3744.	
308	***Ingenuity Canonical Pathways***	
(+0.71)	Complement System	1.06E-02
	GO Categories	
	immune response	2.36E-04
	humoral immune response	1.48E-02
	response to external stimulus	2.95E-02
	response to stress	3.35E-02
	GEO experiments with high expression of this component	

GSE8507	Neutrophil and PBMC gene expression data from Job's Syndrome	
GSE6338	Gene expression analysis of Peripheral T-cell Lymphoma/Unspecified	
GSE11190	Interferon signaling and treatment outcome in chronic hepatitis C	
GSE7874	Effects of EPO and EST on erythroid maturation	
GSE9894	Specific plasma membrane protein phenotype of culture-amplified and native human bone marrow mesenchymal stem cells	
GSE6269	Gene expression patterns in blood leukocytes discriminate patients with acute infections	
GSE10792	Genome wide genotyping and gene expression data of childhood B-cell precursor ALL without known genetic aberrations	
GSE10358	Discovery and validation of expression data for the Genomics of Acute Myeloid Leukemia Program at Washington University.	
GSE7757	Robustness of gene expression signatures in leukemia: comparison of three distinct total RNA preparation procedures.	
242	***Ingenuity Canonical Pathways***	
(+0.71)	Pentose Phosphate Pathway	8.14E-03
	GO Categories	
	spermatogenesis	8.37E-13
	single fertilization	1.28E-05
	spermatid development	2.81E-03
	GEO experiments with high expression of this component	
GSE6872	Spermatozoal RNA Profiles (U133 Plus 2.0 Array)	
GSE8507	Neutrophil and PBMC gene expression data from Job's Syndrome	
GSE5850	Microarray analysis of NL and PCOS oocytes	
GSE7307	Human body index - transcriptional profiling	
GSE5816	A Genome-wide Screen for Hypermethylated Genes in Lung Cancer	
GSE7364	Gene-resolution analysis of DNA copy number variation using oligonucleotide expression microarrays	
GSE2816	cMyb and vMyb in human monocytes	
GSE2109	Expression Project for Oncology (expO)	
GSE6728	Expression data for NMD inhibition in Mantle Cell Lymphoma	
GSE3526	Comparison of gene expression profiles across the normal human body	
GSE7451	Primary Sjogren's syndrome and control whole saliva	
GSE7808	Region specific gene expression profiling along the human epididymis	
GSE8658	PPARg regulated gene expression in human dendritic cells	
192	***Ingenuity Canonical Pathways***	
(+0.67)	none	
	GO Categories	
	serine family amino acid biosynthetic process	2.51E-02
	GEO experiments with high expression of this component	
GSE9819	Comparisons of Affymetrix Whole-Transcript Human Gene 1.0 ST array with standard 3' expression arrays	
GSE7708	Suppression of androgen receptor mediated gene expression by a sequence-specific DNA binding polyamide	
GSE8565	Argyrin A is a p27 stabilizing drug with potent antiproliferative activity in vivo	
GSE9890	Expression profile of 5 ovarian tumour samples (two different cell types from each sample profiles)	
GSE9264	Kaposi's Sarcoma-associated Herpesvirus Encodes an Ortholog of miR-155	
GSE7554	Identification of Cellular Genes Targeted by KSHV-Encoded MicroRNAs	
GSE8438	IP Staufen1	
GSE5816	A Genome-wide Screen for Hypermethylated Genes in Lung Cancer	
GSE7896	S1P mediates key targets associated with survival, proliferation and pluripotency in human embryonic stem cells	
GSE8640	TFAP2C regulates multiple pathways of estrogen signaling	
GSE8702	Longitudinal Analysis of Progression to Androgen Independence	
GSE7213	Comparative analysis of cellular mRNA incorporation into MLV and HIV1 virus-like particles	
GSE3202	MK886 treatment of H720 non-small cell lung cancer cell line	
GSE6629	Domain-Wide Regulation of Gene Expression in the Human Genome	
GSE8437	IP Staufen2	
GSE9089	Reanalysis of GSE8884 Samples with Endothelial Samples from GSE3998.	
151	***Ingenuity Canonical Pathways***	

(-0.54)	none	
	GO Categories	
	cell differentiation	2.76E-03
	epidermis development	4.23E-03
	epidermal cell differentiation	1.03E-02
	tissue morphogenesis	1.87E-02
	epidermis morphogenesis	2.02E-02
	GEO experiments with high expression of this component	
GSE10700	Time course of NHBE cells exposed to whole cigarette smoke	
GSE10718	Time course of NHBE cells exposed to whole cigarette smoke (full flavor)	
GSE9951	Transcriptome analyses in normal prostate epithelial cells following exposure to low-dose cadmium	
GSE6075	E6 in HOK/Bmi-1 cells	
GSE4824	Analysis of lung cancer cell lines	
GSE6283	Specific transcriptional changes in human fetus with autosomal trisomies	
GSE6885	Transformed Human Breast Epithelial Cell Types vs. Normal Cell-of-Origin	
79	***Ingenuity Canonical Pathways***	
(-0.61)	none	
	GO Categories	
	system development	7.88E-03
	organ development	1.72E-02
	GEO experiments with high expression of this component	
GSE7307	Human body index - transcriptional profiling	
GSE2109	Expression Project for Oncology (expO)	
GSE3526	Comparison of gene expression profiles across the normal human body	
GSE7808	Region specific gene expression profiling along the human epididymis	
GSE7305	Human endometriosis vs normal endometrium study - transcriptional profiling	
205	***Ingenuity Canonical Pathways***	
(-0.66)	none	
	GO Categories	
	none	
	GEO experiments with high expression of this component	
GSE10270	Bisphenol A induces a profile of tumor aggressiveness in high-risk cells of breast cancer patients	
GSE3678	PTC versus paired normal thyroid tissue	
GSE11166	Local regulation and clinical impact of complement gene expression in deceased and living donor kidney allografts	
GSE4217	Spheroid Formation and Recovery of Human Foreskin Fibroblasts at Ambient Temperature	
GSE9757	Response to estradiol-ERalpha	
GSE4218	Spheroid Formation and Recovery of Human T98G Glioma Cells at Ambient Temperature	
GSE9759	Response to estradiol-ERbeta and estradiol-ERbeta ERE binding defective mutant	
GSE6551	Expression data from intracranial arteries and intracranial aneurysms	
GSE7307	Human body index - transcriptional profiling	
GSE6369	Prostate Adenocarcinoma Progression	
GSE9890	Expression profile of 5 ovarian tumour samples (two different cell types from each sample profiles)	
GSE3526	Comparison of gene expression profiles across the normal human body	
GSE7538	Treatment of primary acute myelogenous leukemia (AML) specimens with parthenolide (PTL)	
314	***Ingenuity Canonical Pathways***	
(-0.70)	none	
	GO Categories	
	none	
	GEO experiments with high expression of this component	
GSE6791	Gene Expression Profiles of HPV-Positive and -Negative Head/Neck and Cervical Cancers	

GSE7392	Molecular Evidence of Injury and Inflammation in Normal and Fibrotic Renal Allografts One Year Post-Transplant	
GSE2328	Application of genome-wide expression analysis to human health & disease	
GSE7807	Leukotriene D4 induces gene expression in human monocytes through cysteinyl leukotriene type I receptor.	
GSE6573	Dysregulation of the circulating and tissue-based renin-angiotensin system in preeclampsia	
GSE7158	Genome Wide Gene Expression Study of Circulating Monocytes in human with extremely high vs. low bone mass	
GSE6092	IFN-gamma alters the response of Borrelia burgdorferi-activated endothelium to favor chronic inflammation	
GSE6791	Gene Expression Profiles of HPV-Positive and -Negative Head/Neck and Cervical Cancers	
GSE7392	Molecular Evidence of Injury and Inflammation in Normal and Fibrotic Renal Allografts One Year Post-Transplant	

163	***Ingenuity Canonical Pathways***	
(-0.81)	serine family amino acid biosynthetic process	4.63E-02
	GO Categories	
	none	
	GEO experiments with high expression of this component	
GSE7708	Suppression of androgen receptor mediated gene expression by a sequence-specific DNA binding polyamide	
GSE9819	Comparisons of Affymetrix Whole-Transcript Human Gene 1.0 ST array with standard 3' expression arrays	
GSE9361	Functional interaction between a PIP2 novel polyA polymerase and type 1 PIPKIalpha	
GSE8437	IP Staufen2	
GSE8438	IP Staufen1	
GSE10311	Systematic Assessment of Human Osteoblast Transcriptome in Resting and Induced Primary Cells	
GSE5486	Using GINI2 to identify novel mutations in candidate tumor suppressor genes in colon cancer cells	
GSE8596	Expression profiles of pediatric solid tumor cell lines	
GSE7213	Comparative analysis of cellular mRNA incorporation into MLV and HIV1 virus-like particles	
GSE8565	Argyrin A is a p27 stabilizing drug with potent antiproliferative activity in vivo	
GSE10946	Gene expression microarray profiles of cumulus cells in lean and overweight-obese polycystic ovary syndrome patients	
GSE6629	Domain-Wide Regulation of Gene Expression in the Human Genome	
GSE2555	HCaRG-9 vs NEO-1	
GSE5816	A Genome-wide Screen for Hypermethylated Genes in Lung Cancer	
GSE6890	Transcriptome maps of six different human cell lines	
GSE10021	mRNA expression profiles in human cell lines	
GSE8702	Longitudinal Analysis of Progression to Androgen Independence	
GSE6532	Definition of clinically distinct molecular subtypes in estrogen receptor positive breast carcinomas using genomic grade	
GSE9974	The effect of the HDAC inhibitor OSU-HDAC42 on gene expression in esophageal tissues and adenocarcinoma cells I	
GSE8066	Dickkopf-1 is down-regulated by MYCN and inhibits neuroblastoma cell proliferation	
GSE6013	Gene expression in asbestos exposed lung cells	

203	***Ingenuity Canonical Pathways***	
-0.84	Metabolism of Xenobiotics by Cytochrome P450	1.86E-06
	LPS/IL-1 Mediated Inhibition of RXR Function	7.59E-05
	Aryl Hydrocarbon Receptor Signaling	1.78E-03
	Glutathione Metabolism	1.78E-03
	Fatty Acid Metabolism	3.09E-03
	Arginine and Proline Metabolism	6.03E-03
	Ascorbate and Aldarate Metabolism	1.10E-02
	PXR/RXR Activation	2.40E-02
	NRF2-mediated Oxidative Stress Response	2.40E-02
	Xenobiotic Metabolism Signaling	3.09E-02
	Bladder Cancer Signaling	4.47E-02
	Bile Acid Biosynthesis	4.57E-02
	GO Categories	
	none	
	GEO experiments with high expression of this component	
GSE8671	Transcriptome profile of human colorectal adenomas.	

GSE2109	Expression Project for Oncology (expO)	
GSE6532	Definition of clinically distinct molecular subtypes in estrogen receptor positive breast carcinomas using genomic grade	
GSE7476	Analysis of clinical bladder cancer classification according to microarray expression profiles	
GSE9452	Definition of an ulcerative colitis preinflammatory state	
359	***Ingenuity Canonical Pathways***	
(-1.02)	none	
	GO Categories	
	immune response	6.40E-05
	GEO experiments with high expression of this component	
GSE10358	Discovery and validation of expression data for the Genomics of Acute Myeloid Leukemia Program at Washington University.	
GSE8023	AML1-ETO transduced human cord blood cells, CD34 selected, compared to normal cord blood cells, CD34 selected	
GSE7757	Robustness of gene expression signatures in leukemia: comparison of three distinct total RNA preparation procedures.	
43	***Ingenuity Canonical Pathways***	
(-1.19)	T Cell Receptor Signaling	1.26E-13
	iCOS-iCOSL Signaling in T Helper Cells	2.00E-12
	Calcium-induced T Lymphocyte Apoptosis	1.20E-09
	CCR5 Signaling in Macrophages	1.00E-08
	CD28 Signaling in T Helper Cells	1.38E-08
	CTLA4 Signaling in Cytotoxic T Lymphocytes	1.05E-07
	Role of NFAT in Regulation of the Immune Response	1.55E-07
	Primary Immunodeficiency Signaling	6.92E-07
	Systemic Lupus Erythematosus Signaling	3.89E-06
	Cytotoxic T Lymphocyte-mediated Apoptosis of Target Cells	4.37E-06
	Phospholipase C Signaling	6.03E-06
	Cdc42 Signaling	6.03E-05
	Communication between Innate and Adaptive Immune Cells	1.58E-04
	NF-κB Activation by Viruses	2.63E-04
	Natural Killer Cell Signaling	2.63E-04
	Type I Diabetes Mellitus Signaling	2.63E-04
	NF-κB Signaling	4.07E-04
	T Helper Cell Differentiation	5.25E-04
	Allograft Rejection Signaling	4.47E-03
	Autoimmune Thyroid Disease Signaling	5.50E-03
	Lipid Antigen Presentation by CD1	8.13E-03
	Melatonin Signaling	1.17E-02
	BMP signaling pathway	1.45E-02
	Altered T Cell and B Cell Signaling in Rheumatoid Arthritis	1.48E-02
	Molecular Mechanisms of Cancer	1.55E-02
	Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis	1.91E-02
	Factors Promoting Cardiogenesis in Vertebrates	2.09E-02
	β-Adrenergic Signaling	2.63E-02
	Crosstalk between Dendritic Cells and Natural Killer Cells	2.63E-02
	IL-15 Signaling	3.89E-02
	Cholecystokinin/Gastrin-mediated Signaling	3.98E-02
	Thrombin Signaling	4.17E-02
	Dendritic Cell Maturation	4.17E-02
	Synaptic Long Term Potentiation	4.37E-02
	Renin-Angiotensin Signaling	4.37E-02
	Thyroid Cancer Signaling	4.37E-02
	Glucocorticoid Receptor Signaling	4.37E-02
	IL-12 Signaling and Production in Macrophages	4.37E-02
	Prolactin Signaling	4.37E-02
	Corticotropin Releasing Hormone Signaling	4.37E-02

	Graft-versus-Host Disease Signaling	4.37E-02
	LPS-stimulated MAPK Signaling	4.37E-02
	FLT3 Signaling in Hematopoietic Progenitor Cells	4.37E-02
	CCR3 Signaling in Eosinophils	4.37E-02
	Acute Myeloid Leukemia Signaling	4.57E-02
	Chemokine Signaling	4.57E-02
	Androgen Signaling	4.57E-02
	Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis	4.90E-02
	GO Categories	
	immune response	1.62E-19
	cell surface receptor linked signal transduction	2.12E-08
	cellular defense response	4.14E-07
	multicellular organismal process	7.88E-05
	regulation of T cell activation	2.51E-04
	T cell differentiation	3.54E-04
	signal transduction	1.77E-03
	lymphocyte activation	2.81E-03
	positive regulation of T cell activation	6.40E-03
	regulation of multicellular organismal process	1.28E-02
	regulation of programmed cell death	4.48E-02
	GEO experiments with high expression of this component	
GSE6088	Imprints of atherosclerosis are present in circulating T cells of patients with Familial Hypercholesterolemia	
GSE9927	Chronic CD4+ T cell Activation & Depletion in HIV-1 Infection: Type I Interferon-Mediated Disruption of T Cell Dynamics	
GSE6338	Gene expression analysis of Peripheral T-cell Lymphoma/Unspecified	
GSE7345	Germline NRAS mutation causes a novel human autoimmune lymphoproliferative syndrome	
GSE6743	1,25 (OH)2 vitamin D3 induces expression of CCR10 and other genes	
GSE6269	Gene expression patterns in blood leukocytes discriminate patients with acute infections	
GSE6566	Strength of T cell stimulation	
GSE7307	Human body index - transcriptional profiling	
GSE10437	Dynamic regulation of nucleosome positioning in the human genome	
GSE11190	Interferon signaling and treatment outcome in chronic hepatitis C	
GSE8121	Pediatric septic shock	
GSE9692	Validation of Genome-wide Expression patterns in Pediatric Septic Shock	
GSE3077	Dillution series comparison of Affymetrix and Illumina Expression Platforms	
208	***Ingenuity Canonical Pathways***	
(-1.73)	none	
	GO Categories	
	none	
	GEO experiments with high expression of this component	
GSE2109	Expression Project for Oncology (expO)	
GSE10609	the recurrent SET-NUP214 fusion as a new HOXA activation mechanism in pediatric T-ALL	
GSE9891	Expression profile of 285 ovarian tumour samples	
GSE6532	Definition of clinically distinct molecular subtypes in estrogen receptor positive breast carcinomas using genomic grade	
GSE9151	Allergen induced gene expression of airway epithelial cells shows a possible role for TNF-α	
GSE7757	Robustness of gene expression signatures in leukemia: comparison of three distinct total RNA preparation procedures.	
GSE2677	Prednisolone treated childhood ALL samples	
GSE7307	Human body index - transcriptional profiling	
GSE3526	Comparison of gene expression profiles across the normal human body	
62	***Ingenuity Canonical Pathways***	
(-1.95)	EIF2 Signaling	1.91E-10
	Regulation of eIF4 and p70S6K Signaling	3.89E-08
	mTOR Signaling	3.72E-04
	GO Categories	

	translation	<1E-30
	translational elongation	3.99E-05
	regulation of translational initiation	4.18E-04
	ribonucleoprotein complex biogenesis	3.64E-03
	GEO experiments with high expression of this component	
GSE10358	Discovery and validation of expression data for the Genomics of Acute Myeloid Leukemia Program at Washington University.	
GSE10609	the recurrent SET-NUP214 fusion as a new HOXA activation mechanism in pediatric T-ALL	
GSE2109	Expression Project for Oncology (expO)	
GSE10792	Genome wide genotyping and gene expression data of childhood B-cell precursor ALL without known genetic aberrations	
GSE7307	Human body index - transcriptional profiling	
GSE6338	Gene expression analysis of Peripheral T-cell Lymphoma/Unspecified	
GSE9891	Expression profile of 285 ovarian tumour samples	
GSE9091	Reanalysis of GSE8884 Samples with Leukocyte Samples from GSE3284.	
GSE8884	Expression data from human embryonic stem cells, early stage embryoid bodies, and hES-derived blast cells.	
GSE9086	Reanalysis of GSE8884 Samples with Breast Epithelial Samples from GSE3744.	
GSE9090	Reanalysis of GSE8884 Samples with Stromal Samples from GSE3998.	
101	***Ingenuity Canonical Pathways***	
(-2.68)	none	
	GO Categories	
	defense response	2.22E-03
	icosanoid biosynthetic process	5.91E-03
	immune system process	8.37E-03
	GEO experiments with high expression of this component	
GSE10358	Discovery and validation of expression data for the Genomics of Acute Myeloid Leukemia Program at Washington University.	
GSE7757	Robustness of gene expression signatures in leukemia: comparison of three distinct total RNA preparation procedures.	
GSE8023	AML1-ETO transduced human cord blood cells, CD34 selected, compared to normal cord blood cells, CD34 selected	

* P-values for Ingenuity Canonical Pathways have Benjamini-Hochberg correction applied. P-values for GO categories have Bonferroni correction applied.