CellR4 2017; 5 (5): e2439

Cancer microarray data weighted gene co-expression network analysis identifies a gene module and hub genes shared across nine types of solid cancer

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Keywords: Hub Gene, Gene Module, Gene Co-Expression Network, Microarra, Breast cancer, Glioblastoma, Meduloblastoma, Ependymoma, Astrocytoma, Colon cancer, Gastric cancer, Liver cancer, Lung cancer, Pancreatic cancer, Renal cancer, Prostate cancer.

ABSTRACT

Objective: **Microarray and next-generation sequencing techniques have revealed a series of somatic mutations and differentially expressed genes associated with multiple cancers. The objective of this research was to identify networks of overexpressed genes for nine common solid cancers using a novel combination of systematic genomic analysis and published cancer microarray databases.**

Materials and Methods: **A total of twelve gene expression microarray datasets containing nine types of common solid cancers were obtained from the Gene Expression Omnibus, which included 104 breast, 117 brain, 32 colon, 108 gastric, 95 liver, 60 lung, 72 pancreatic, 72 renal, 26 prostate, and a total of 330 matching non-cancerous control tissue samples. Differentially expressed genes (DEG) were analyzed between each cancer sample and its matching controls. Weighted gene co-expression network analysis (WGCNA) was used to construct pairwise correlated co-expressed gene networks and to detect overexpressed gene modules for each cancer.**

Results: **WGCNA of a total of 1,016 cancer genes identified specific hub genes and gene modules for each type of cancer. Gene co-expression networks were constructed. Overexpressed module genes were compared to their matching non-tumor controls. This revealed significantly overexpressed proliferative cell-cycle related gene modules. These gene modules included BIRC5, TPX2, CDK1, and MKI67, which have previously been shown to be associated with cancers.**

Conclusions: **Genomic analysis revealed overexpressed gene modules in nine different types of solid cancers and a shared network of overexpressed genes common to all types. These shared, overexpressed genes involve cell and proliferation, supporting the idea that different cancers have a shared core molecular pathway. Elucidation of various networks of gene modules among different types of cancers may provide better understanding of molecular mechanisms for different cancers.**

INTRODUCTION

Tremendous progress has been made in genomic sequencing of cancer in the last decade. Microarray and next-generation sequencing have previously been used to identify somatic mutations and differentially expressed genes associated with multiple cancers[1-4]. This massive amount of genomic data has yet to significantly impact clinical care and overall survival. A new approach to identify common actionable genes for targeted therapy is needed.

Previous approaches to construct shared gene networks among cancer types have identified essential functional pathways of cancer biology. The Weighted Gene Co-expression Network Analysis (WGCNA) has been utilized to study whole-genome expression profiles of microarray and RNA-Seq data[5-8]. WGCNA has the capability to define biologically relevant gene modules, hub genes, and enriched signaling pathways by utilizing pairwise Pearson's correlation among gene expression values.

We performed WGCNA on the gene expression profiles of nine types of solid cancer to detect highly interconnected gene modules. This approach will help to identify universal actionable genes for targeted therapy and biomarkers to assess cancer progression.

MATERIALS AND METHODS

GENE EXPRESSION MICROARRAY

Twelve gene-expression microarray datasets were selected which contain nine types of solid cancer using Affymetrix Human Genome U133 Plus 2.0 Array platform (GPL570) from the Gene Expression Omnibus (GEO) Database. These twelve microarray datasets were generated at multiple cancer centers worldwide from 2005 to 2014 (Table 1). The datasets contained nine types of solid cancers – these include 104 breast cancers[9], 117 brain cancers[10], 32 colon cancers[11], 108 gastric cancers[12,13], 95 liver cancers, 60 lung cancers[14], 72 pancreatic cancers[15,16], 72 renal cancers[17], 26 prostate cancers[18,19], and a total of 330 matching non-cancerous control tissue samples.

WGCNA ANALYSIS

The WGCNA was used for scale-free network topology analysis of the microarray expression data. WGCNA R package was used to cluster highly correlated genes and detect clusters whose expression was correlated with the traits examined. WGCNA was carried out on data from all 12 gene-expression microarray datasets for a total number of 1016 tumors and 330 matched non-cancerous control samples[9,10,20]. An adjacency matrix based on expression correlation was created using a soft threshold procedure to allow a scale free topology. Clusters created by WGCNA are defined as modules, and the minimum number of genes in a module was set to 30. Standard WGCNA parameters were used for analysis, with the exceptions of soft-thresholding power and deep split. A soft-thresholding power of 9 was used for all samples. Modules were validated by bioinformatics analysis for over-represented biological functions.

We restricted the analysis to the 12,576 genes with average gene-expression value higher than 5 in the Affymetrix Human Genome U133 Plus 2.0 microarray analysis. First, the differential gene-expression values between each individual tumor specimen *vs.* the average of gene-expression values of matching non-tumor control specimens were calculated and used to construct networks using WGCNA. The value of the Pearson correlation between all pairs

Table 1. 12 microarray datasets are whole genome gene expression profiles of human tumor specimens and matching non-tumor control samples, including 104 breast, 117 brain, 32 colon, 108 gastric, 95 liver, 60 lung, 72 pancreatic, 72 renal, and 26 prostate cancer specimens along with 330 matching non-tumor control tissue samples.

Cancer type	Subtypes	Microarray plattaform	Year published	Tumor samples	Control samples	Author	DataID
Breast Cancer	ER positive ER negative	GPL570	2013	67 34	17	Colin Clarke	GSE42568
Brain Cancer	Gliobastoma Medulioblastoma Ependymoma Pilocytic astrocytoma	GPL570	2013	20 22 46 15	13	Andrew M, Donson	GSE50161
Colon Cancer		GPL570	2007	32	32	Sabates-Bellver J	GSE8671
Gastric Cancer		GPL570	2012	70	0	Zhengdeng Lei	GSE35809
Gastric Cancer		GPL570	2008	38	31	Via Pontina	GSE13911
Liver Cancer		GPL570	2014	95	39	Jul-Yu Hsleh	GSE45436
Lung Cancer		GPL570	2011	60	60	Tzu-Pin Lu	GSE19804
Pancreatic Cancer		GPL570	2009	36	36	Liviu Badea	GSE15471
Pancreatic Cancer		GPL570	2009	36	16	Huadong Pei	GSE16515
Renal Cancer		GPL570	2014	72	72	Christina A von Roemeling	GSE53757
Prostate Cancer		GPL570	2005	13	6	Jianjun Yu	GSE3325
Prostate Cancer		GPL570	2014	13	8	Arredouani MS	GSE55945

of values was calculated and then used to measure the connection strengths between the gene and all the other genes in the network. Hierarchical average linkage clustering was used to determine co-expression modules. DAVID Gene Ontology analysis was used to assess the biological function of the genes within the co-expression modules.

Gene Ontology Term Enrichment Analysis

Throughout the analysis, the functional annotation tool DAVID Bioinformatics Resources 6.7 was used to determine gene ontology terms enriched by a list of genes. DAVID analyses were performed on lists of genes corresponding to significant WGCNA modules. WGCNA modules were considered significant for a certain trait when the nominal p-value of the correlation between the ME and the trait of interest was less than 0.10.

Immunoflorescent staining

Anti-CDK1 (abcam ab193829), anti- BIRC5 (abcam ab175809), and anti-TPX2 (ab32795) antibodies were applied to fixed slides of human pancreatic cancer specimens with 1:100 dilution and followed by overnight incubation at 4°C. Slides were incubated with FITC-conjugated anti-rabbit or mouse secondary antibody depending on derivation of primary antibodies for one hour, and mounted with cover slides. To visualize the nuclei, VECTASHIELD® Mounting Medium with DAPI was used (10 ul per slide).

Results

The use of microarray datasets to analyze gene expression differences in nine types of solid cancer

Two data sets were combined on the Affymetrix HG-U133 Plus 2.0 platform to analyze differentially expressed genes (DEGs) between colon cancer *vs.* its control samples. The combined dataset was processed for GSE8671 colon cancer and 32 control tissue gene expression profiles. A list of 2,722 probes, which reflect a total of 1,914 unique genes with at least two-fold change and a $p < 1.0E\text{-}6$, were revealed to be significantly differential expressed. The identified DEGs consist of 968 unique, up-regulated genes (1,311 probes) and 946 unique, down-regulated genes (1,411 probes) in colon cancer. Using the same strategy, we further identified DEGs between cancer *vs.* non-cancerous control samples of breast cancer, gastric cancer, brain cancer, liver cancer, lung cancer, pancreatic cancer, renal cancer, and prostate cancer, respectively. Figure 1 shows the heat-maps and hierarchical clustering of the 100 most significantly up-regulated or down-regulated genes between each type of cancer *vs.* their matching non-cancerous nor-

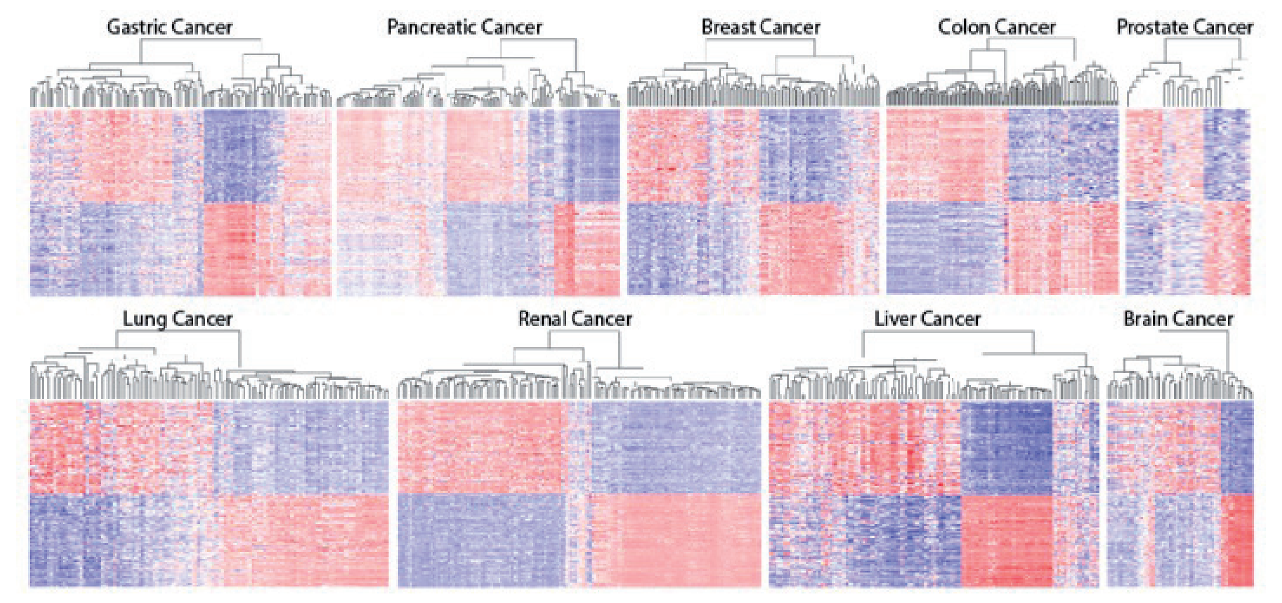


Figure 1. The Heatmap of a total of 209 overlapped differentially expressed genes (DEGs) from the comparison between tumor and non-tumor samples for all 9 cancers.

mal tissues. These DEGs distinguish differential gene expression patterns between each type of cancer and their matching non-cancerous tissue Figure 1. These results suggest that analysis of gene-expression microarray datasets of individual cancer samples may reveal cancer specific DEGs that distinguish cancer from non-cancerous tissues. A complete list of the 100 most up-regulated genes and 100 most down-regulated genes for each of the 9 cancers is provided as supplemental Table 2.

Table 2. 100 most over-expressed and 100 most under-expressed genes for pancreatic cancer. Positive difference value indicates over-expression and negative difference value indicates under-expression. Colon cancer.

Probe_id	Gene_ symbol	Difference	*p*_value	Probe_id	Gene_ symbol	Difference	*p*_value
227475_at	FOXQ1	5,331724867	5,962E-104	228955_at	LRP8	2,801700061	8,71662E-39
212942_s_at	KIAA1199	5,122171348	1,8491E-82	203798_s_at	VSNL1	2,789806847	2,52831E-53
227140_at	INHBA	4,503910371	6,40002E-88	223381_at	NUF2	2,776825084	2,81307E-46
238021_s_at	CRNDE	4,383930436	4,6274E-79	212686_at	PPM1H	2,742163885	2,9387E-61
222549_at	CLDN1	4,369394865	5,5928E-111	213680_at	KRT6B	2,728835388	2,43405E-34
205983_at	DPEP1	4,047031135	1,44088E-43	211207_s_at	ACSL6	2,72194424	2,04645E-42
204259_at	MMP7	3,947382081	4,99037E-67	205815_at	REG3A	2,712386522	9,28709E-23
239579_at	EPHX4	3,916884855	1,67736E-86	205472_s_at	DACH1	2,685902961	1,58274E-40
203256_at	CDH3	3,894250258	1,78587E-35	205295_at	CKMT2	2,682736469	5,2278E-34
202859_x_at	IL8	3,85869484	2,12228E-34	204286_s_at	PMAIP1	2,673086537	3,31296E-54
37892_at	COL11A1	3,8073942	8,16495E-59	229221_at	CD44	2,664476613	1,61901E-55
213880_at	LGR5	3,69057921	5,82454E-34	204146_at	RAD51AP1	2,658573221	1,60696E-41
205828_at	MMP3	3,687805924	1,5939E-56	228033_at	E2F7	2,655628158	5,58447E-42
205421_at	SLC22A3	3,681610009	9,5795E-58	203797_at	VSNL1	2,650178024	1,77049E-64
218963_s_at	KRT23	3,658448357	1,38836E-54	222740_at	ATAD2	2,645965877	1,96397E-43
204475_at	MMP1	3,606007443	2,89132E-42	222696_at	AXIN2	2,639938946	3,34093E-74
229215_at	ASCL2	3,490944516	7,89761E-60	201111_at	CSE1L	2,638826616	3,63658E-50
228754_at	SLC6A6	3,469452598	1,98739E-75	203961_at	NEBL	2,63689562	4,33821E-47
225806_at	AJUBA	3,431113591	1,23217E-49	204470_at	CXCL1	2,62169189	2,10385E-40
202286_s_at	TACSTD2	3,373014897	7,06354E-44	225842_at	PHLDA1	2,615073033	6,11229E-43
241031_at	C2CD4A	3,30071336	5,17278E-41	211122_s_at	CXCL11	2,60234628	6,58344E-34
229725_at	ACSL6	3,18764289	2,9112E-45	204702_s_at	NFE2L3	2,598462302	3,57783E-57
222608_s_at	ANLN	3,18069654	6,87475E-38	1553970_s_at	CEL	2,59186291	8,36713E-22
207457_s_at	LY6G6D	3,144177369	3,93685E-42	210511_s_at	INHBA	2,589257077	3,88424E-43
206354_at	SLCO1B3	3,133234893	1,19081E-41	225295_at	SLC39A10	2,573182396	6,15989E-61
201506_at	LOC100652886	3,129557479	2,88382E-61	205499_at	SRPX2	2,565804101	4,30398E-47
210445_at	FABP6	3,099116486	1,5518E-54	244407_at	CYP39A1	2,563991248	1,01501E-50
225681_at	CTHRC1	3,089770338	5,83148E-47	1554020_at	BICD1	2,55958718	1,93953E-54
231341_at	SLC35D3	3,063416108	1,05868E-37	203438_at	STC2	2,540479309	1,27393E-38
205513_at	TCN1	3,061238668	1,44483E-32	209792_s_at	KLK10	2,536838689	9,24443E-31
230030_at	HS6ST2	3,058164884	2,22663E-32	232238_at	ASPM	2,529849181	3,6406E-57
223949_at	TMPRSS3	3,04811581	8,04258E-65	238898_at	LOC100505730	2,522892173	1,54981E-47
230875_s_at	ATP11A	3,036355905	6,91583E-60	1552619_a_at	ANLN	2,519623312	7,57373E-35
210163_at	CXCL11	3,004679102	1,18321E-37	207165_at	HMMR	2,508180544	4,42976E-34
219494_at	FSBP	2,949385701	4,53612E-73	226670_s_at	PABPC1L	2,501370466	8,26084E-22
1552767_a_at	HS6ST2	2,944305498	7,00519E-32	205282_at	LRP8	2,498971932	1,02091E-45
207850_at	CXCL3	2,928384739	1,30781E-40	206286_s_at	TDGF1	2,488158868	7,63358E-50
223062_s_at	PSAT1	2,909399516	1,50669E-43	229802_at	WISP1	2,488144654	2,58575E-41
223509_at	CLDN2	2,88401912	5,5041E-45	204709_s_at	KIF23	2,481216805	1,11102E-33
204320_at	COL11A1	2,879792746	1,85188E-49	1555920_at	CBX3	2,455805491	5,93189E-45
228915_at	DACH1	2,873716195	2,37491E-51	219787_s_at	ECT2	2,452933681	1,40598E-44
225438_at	NUDCD1	2,873445614	2,62119E-46	225520_at	MTHFD1L	2,449205867	1,05669E-38
236471_at	NFE2L3	2,857925314	2,9562E-65	229899_s_at	ZNFX1-AS1	2,441819166	1,19379E-53
209309_at	AZGP1	2,841605558	2,55339E-43	227174_at	WDR72	2,435271492	2,37523E-24
203213_at	CDK1	2,804594638	2,59362E-33	209395_at	CHI3L1	2,433165526	4,8254E-45

Table 2 *(continued)*. Colon cancer.

Probe_id	Gene_ symbol	Difference	*p*_value	Probe_id	Gene_ symbol	Difference	*p*_value
227928_at	PARPBP	2,431448383	5,6786E-37	230788_at	GCNT2	-3,599249922	1,52501E-38
235391_at	FAM92A1	2,422849632	5,59058E-36	228232_s_at	VSIG2	-3,624009537	7,58808E-57
203362_s_at	MAD2L1	2,422843487	1,84509E-36	206710_s_at	EPB41L3	-3,678660168	2,21629E-82
214708_at	SNTB1	2,400355879	5,41098E-45	211494_s_at	SLC4A4	-3,688305061	1,10107E-49
234985_at	LDLRAD3	2,388684437	8,02499E-55	204673_at	MUC2	-3,70243539	1,43378E-37
235644_at	CCDC138	2,387041231	1,70141E-45	228195_at	C2orf88	-3,722195313	5,71361E-67
209774_x_at	CXCL2	2,386005769	2,53154E-27	219909_at	MMP28	-3,729989963	1,88885E-66
203083_at	THBS2	2,38329644	1,14867E-23	207245_at	UGT2B17	-3,752509543	5,73842E-08
223586_at	ARNTL2	2,382645487	5,45993E-41	213921_at	SST	-3,775671707	3,25973E-23
222830_at	GRHL1	2,375018265	1,59625E-63	219799_s_at	DHRS9	-3,786050874	7,07198E-36
1552365_at	SCIN	-3,07673464	3,99409E-40	1555963_x_at	B3GNT7	-3,790128751	5,63124E-49
1552367_a_at	SCIN	-3,080765789	1,49418E-48	222722_at	OGN	-3,798425513	1,29101E-37
210735_s_at	CA12	-3,090627538	1,90084E-42	222943_at	GBA3	-3,798707952	9,55853E-31
205861_at	SPIB	-3,097030309	2,71909E-54	229839_at	SCARA5	-3,842734114	8,93352E-76
240389_at	TRPM6	-3,102427454	5,62352E-36	231120_x_at	PKIB	-3,871358547	2,26385E-41
205757_at	ENTPD5	-3,115697515	1,82711E-57	220075_s_at	CDHR5	-3,919913822	1,87844E-35
203913_s_at	HPGD	-3,116921484	1,24273E-46	209687_at	CXCL12	-3,932450109	1,40135E-61
203963_at	CA12	-3,132092708	8,99038E-43	207080_s_at	PYY	-4,022741677	1,1349E-23
213764_s_at	MFAP5	-3,171896353	1,62721E-26	223597_at	ITLN1	-4,030225797	2,17195E-20
215100_at	ADTRP	-3,17346622	7,65599E-47	204719_at	ABCA8	-4,031823347	1,79101E-45
205242_at	CXCL13	-3,175494136	2,1047E-22	238143_at	LOC646627	-4,063966979	1,526E-43
229070_at	ADTRP	-3,184192354	8,70236E-33	205464_at	SCNN1B	-4,070583427	1,80269E-58
228885_at	MAMDC2	-3,195584851	3,12344E-29	223551_at	PKIB	-4,090827567	8,36398E-46
226654_at	MUC12	-3,199696367	1,96784E-26	210107_at	CLCA1	-4,094379997	5,58362E-23
220421_at	BTNL8	-3,212279706	2,31765E-23	206100_at	CPM	-4,143877899	6,16147E-64
227048_at	LAMA1	-3,215333701	6,06171E-38	202888_s_at	ANPEP	-4,14787938	3,01529E-36
1554522_at	CNNM2	-3,2154546	3,43646E-37	1552296_at	BEST4	-4,154709722	1,71829E-39
208450_at	LGALS2	-3,242893459	1,99173E-39	221091_at	INSL5	-4,266089118	6,11874E-24
206561_s_at	AKR1B10	-3,258099851	4,98932E-36	220435_at	SLC30A10	-4,285081961	1,27654E-44
235019_at	CPM	-3,283101405	4,09699E-56	223952_x_at	DHRS9	-4,303641305	1,0781E-46
230830_at	OSTBETA	-3,31351057	1,97856E-43	204697_s_at	CHGA	-4,308338135	3,24723E-51
210739_x_at	SLC4A4	-3,330832902	1,42163E-73	236313_at	CDKN2B	-4,405012434	6,62916E-48
209114_at	TSPAN1	-3,336003253	7,19579E-34	224009_x_at	DHRS9	-4,438783875	4,45934E-49
239272_at	MMP28	-3,346480464	1,27229E-70	224412_s_at	TRPM6	-4,535623787	1,76359E-40
205593_s_at	PDE9A	-3,353960425	2,52337E-48	206664_at	SI	-4,588704808	6,34617E-38
235706_at	CPM	-3,366072166	8,37447E-66	211848_s_at	CEACAM7	-4,676101323	2,13574E-37
212681_at	EPB41L3	-3,390923315	1,24544E-76	209735_at	ABCG2	-4,678712834	1,29073E-43
219014_at	PLAC8	-3,40290675	5,13529E-37	219669_at	CD177	-4,697471719	2,28143E-34
220724_at	CWH43	-3,412600147	9,1096E-39	217546_at	MT1M	-4,858627726	1,53325E-51
228706_s_at	CLDN23	-3,425461314	4,30499E-41	209612_s_at	ADH1B	-5,030587441	4,3403E-56
203240_at	FCGBP	-3,447262936	1,57471E-34	209613_s_at	ADH1B	-5,173311625	1,58917E-56
1555962_at	B3GNT7	-3,454711907	9,91617E-50	209301_at	CA2	-5,17644153	3,62129E-62
206143_at	SLC26A3	-3,460635554	7,36172E-34	207003_at	GUCA2A	-5,215287344	2,4967E-53
209373_at	MALL	-3,467985767	1,46107E-52	206208_at	CA4	-5,43457	3,10951E-63
220266_s_at	KLF4	-3,483514495	1,02481E-67	206422_at	GCG	-5,508536737	6,5561E-30
206199_at	CEACAM7	-3,491996167	4,56299E-40	203908_at	SLC4A4	-5,55720749	1,6445E-75
205945_at	IL6R	-3,492956783	1,19019E-91	207502_at	GUCA2B	-5,58326799	3,10547E-55
223754_at	C2orf88	-3,505680019	1,09535E-58	206198_s_at	CEACAM7	-5,839335454	3,38481E-38
239273_s_at	MMP28	-3,523689999	6,53694E-75	214142_at	ZG16	-5,96693273	1,0323E-57
205185_at	SPINK5	-3,524314397	4,22931E-36	206209_s_at	CA4	-6,026805064	1,46133E-62
226492_at	SEMA6D	-3,529234818	2,61215E-66	205950_s_at	CA1	-6,225412654	1,59674E-61
206149_at	CHP2	-3,546689083	5,67516E-45	206784_at	AQP8	-6,345682696	5,75273E-43
242601_at	HEPACAM2	-3,580571742	1,3975E-25	214598_at	CLDN8	-6,357399979	2,2592E-49
206262_at	ADH1C	-3,59431901	6,51516E-43	220834_at	MS4A12	-6,408803751	9,03065E-61
204818_at	HSD17B2	-3,594484097	2,43844E-37	220026_at	CLCA4	-7,242562624	2,52611E-70

Table 2. Pancreatic cancer.

Probe_id	Gene_ symbol	Difference	*p*_value
227140_at	INHBA	3,228614581	5,11115E-12
210809_s_at	POSTN	3,172591125	2,69688E-11
1555778_a_at	POSTN	3,159072878	5,81736E-12
204351_at	S100P	2,978494316	4,68703E-09
217428_s_at	COL10A1	2,924380599	2,26746E-09
212354_at	SULF1	2,914310725	1,00292E-13
212353_at	SULF1	2,912165747	4,23164E-12
205941_s_at	COL10A1	2,832500584	1,11677E-11
226237_at	COL8A1	2,821409613	5,30273E-11
37892_at	COL11A1	2,820967603	3,25263E-08
210511_s_at	INHBA	2,810210847	7,44641E-14
227566_at	LOC100653217	2,777668921	4,26696E-14
212488_at	COL5A1	2,744707142	1,46931E-17
225681_at	CTHRC1	2,712261917	3,33157E-11
209955_s_at	FAP	2,663916547	1,85889E-16
203083_at	THBS2	2,611611274	2,01903E-14
211571_s_at	VCAN	2,567808162	5,50484E-13
215646_s_at	VCAN	2,566829191	6,81974E-12
205713_s_at	COMP	2,562104581	2,84861E-10
229802_at	WISP1	2,54794863	3,92626E-12
212344_at	SULF1	2,524560785	1,00561E-13
232458_at	COL3A1	2,433447111	4,17654E-16
201650_at	KRT19	2,430108796	3,49668E-08
203108_at	GPRC5A	2,414129826	7,45106E-11
202310_s_at	COL1A1	2,403560011	1,24971E-13
204619_s_at	VCAN	2,376891432	1,92444E-10
202267_at	LAMC2	2,341877791	6,40419E-11
214927_at	ITGBL1	2,333709902	4,61729E-12
221730_at	COL5A2	2,319750251	1,43175E-10
212489_at	COL5A1	2,307639812	1,07822E-11
204463_s_at	EDNRA	2,300946699	5,42379E-13
207173_x_at	CDH11	2,291235606	2,21194E-10
221872_at	RARRES1	2,275606714	1,70529E-11
204620_s_at	VCAN	2,253278481	3,72771E-14
221731_x_at	VCAN	2,246111168	2,30778E-13
202311_s_at	COL1A1	2,216374813	1,63627E-07
221558_s_at	LEF1	2,211181954	3,34048E-11
210095_s_at	IGFBP3	2,206631467	1,64636E-13
232231_at	RUNX2	2,130240838	5,63098E-11
229218_at	COL1A2	2,129937267	1,7476E-11
211597_s_at	HOPX	2,126342799	2,08771E-10
213125_at	OLFML2B	2,10709192	7,74148E-12
219773_at	NOX4	2,096006066	8,78903E-12
204464_s_at	EDNRA	2,088415664	3,23779E-13
226311_at	ADAMTS2	2,080620281	2,20909E-13
202404_s_at	COL1A2	2,076952517	1,74809E-09
202859_x_at	IL8	2,075162294	2,36407E-07
204051_s_at	SFRP4	2,072335962	4,42425E-08
206392_s_at	RARRES1	2,071040094	2,13171E-10
221729_at	COL5A2	2,045599626	6,55728E-11
213680_at	KRT6B	2,045001667	9,31676E-07
215446_s_at	LOX	2,037647024	5,58617E-10
205422_s_at	ITGBL1	2,025147893	1,55285E-07
211430_s_at	IGHG1	2,005882198	5,79043E-07
204052_s_at	SFRP4	1,999557657	1,86298E-07
231766_s_at	COL12A1	1,995462441	1,08971E-08
212444_at	GPRC5A	1,990383993	1,01026E-08
205927_s_at	CTSE	1,984411666	7,03635E-07
33323_r_at	SFN	1,981259541	1,91557E-07
216442_x_at	FN1	1,980434782	1,07824E-13
1558034_s_at	CP	1,966833353	1,95476E-07
226535_at	ITGB6	1,957770222	5,34282E-07
203789_s_at	SEMA3C	1,952402701	2,49285E-09
212464_s_at	FN1	1,935953238	1,3449E-11
209758_s_at	MFAP5	1,930008114	2,54052E-09
219179_at	DACT1	1,929982092	2,12028E-14
211719_x_at	FN1	1,926026965	5,44408E-12
205890_s_at	GABBR1	1,922675225	3,56018E-09
207191_s_at	ISLR	1,917415992	7,85388E-13
219463_at	LAMP5	1,886199194	2,76725E-09
206391_at	RARRES1	1,886099266	1,22781E-11
210495_x_at	FN1	1,878218243	1,21526E-12
217764_s_at	RAB31	1,874718359	3,14975E-12
226997_at	ADAMTS12	1,866530499	7,8494E-13
201792_at	AEBP1	1,854157461	1,86857E-14
209201_x_at	CXCR4	1,838427403	1,61238E-08
203021_at	SLPI	1,836771599	2,12643E-09
226930_at	FNDC1	1,831985373	2,55801E-08
203726_s_at	LAMA3	1,828793377	7,36182E-08
212143_s_at	IGFBP3	1,811281942	4,59623E-10
202450_s_at	CTSK	1,806899278	7,21162E-13
209708_at	MOXD1	1,804236685	1,28185E-09
204846_at	CP	1,800920145	6,27397E-07
218804_at	ANO1	1,7877655	1,00732E-07
1557080_s_at	ITGBL1	1,78679787	1,70972E-07
202765_s_at	FBN1	1,78260087	2,04867E-11
217762_s_at	RAB31	1,781422617	1,6816E-10
224694_at	ANTXR1	1,756226583	1,48562E-10
212992_at	AHNAK2	1,750256908	2,09654E-07
226695_at	PRRX1	1,74886748	8,0908E-11
238617_at	KIF26B	1,747530643	3,47102E-08
217763_s_at	RAB31	1,739811545	2,11262E-10
202202_s_at	LAMA4	1,719038454	2,07477E-10
228904_at	HOXB3	1,717545339	1,76734E-13
212236_x_at	JUP	1,709850881	1,18075E-07
202411_at	IFI27	1,709751014	7,97165E-10
211919_s_at	CXCR4	1,706819976	6,64156E-08
231240_at	DIO2	1,697592686	2,99016E-11
209360_s_at	LOC100506403	1,69636782	2,74968E-14
228640_at	PCDH7	1,69616522	3,3912E-07

Table 2 *(continued)*. Pancreatic cancer.

Probe_id	Gene_ symbol	Difference	*p*_value
1556473_at	FLJ38379	-1,034361357	3,42999E-08
1559633_a_at	CHRM3	-1,037553958	9,40929E-08
225820_at	PHF17	-1,038945188	8,02439E-07
215058_at	DENND5B	-1,038989162	7,43348E-08
35974_at	LRMP	-1,039122382	7,77655E-10
1569257_at	FMNL1	-1,039658117	2,57664E-07
227771_at	LIFR	-1,040117069	2,89698E-07
233953_at	GUCA1C	-1,041359947	5,57081E-10
1555450_a_at	NAA16	-1,042906685	2,14754E-10
1553645_at	CCDC141	-1,04873965	2,10805E-09
201625_s_at	INSIG1	-1,052086846	8,91073E-09
210705_s_at	TRIM5	-1,054114304	5,60943E-07
1564315_at	C8orf49	-1,056033512	2,74871E-08
225570_at	SLC41A1	-1,05954432	1,46998E-07
220038_at	C8orf44-SGK3	-1,065035567	2,95042E-10
201627_s_at	INSIG1	-1,076396859	5,11607E-10
1560720_at	MKNK1	-1,081464912	1,82514E-10
211909_x_at	PTGER3	-1,088590884	1,09922E-07
213705_at	GGCX	-1,089737304	6,86437E-09
222317_at	PDE3B	-1,090936048	1,30085E-07
1554489_a_at	CEP70	-1,09445039	2,10346E-08
1553493_a_at	TDH	-1,095183074	7,9605E-11
213792_s_at	INSR	-1,097059217	9,88976E-07
225066_at	PPP2R2D	-1,099478435	7,37276E-08
1555151_s_at	TDH	-1,100607351	4,07662E-08
214837_at	ALB	-1,102626402	2,05513E-08
230479_at	EIF3F	-1,103438193	7,26949E-07
210683_at	NRTN	-1,106904057	4,15144E-08
202731_at	MIR4680	-1,110751928	9,4416E-07
228993_s_at	BBIP1	-1,111342966	5,55381E-11
231050_at	HRASLS5	-1,113695451	2,9456E-10
202730_s_at	MIR4680	-1,120389093	1,3847E-08
211682_x_at	UGT2B28	-1,129718477	1,41738E-08
213650_at	GOLGA8A	-1,130992951	1,59528E-09
219976_at	HOOK1	-1,131029596	1,24207E-07
214033_at	ABCC6	-1,139993154	5,36928E-08
236207_at	SSFA2	-1,143113297	3,28435E-07
239533_at	GPR155	-1,151219687	2,54067E-07
211419_s_at	CHN2	-1,158648171	2,34721E-13
1554755_a_at	MTUS2	-1,162720739	8,51546E-10
1554182_at	TRIM73	-1,1643876	2,07402E-10
205355_at	ACADSB	-1,165860154	2,74157E-13
220144_s_at	ANKRD5	-1,181695183	5,5231E-10
206209_s_at	CA4	-1,201255589	4,3593E-07
224151_s_at	AK3	-1,208623327	5,45144E-07
203642_s_at	COBLL1	-1,213356553	1,10438E-10
241833_at	PEX5L	-1,214110704	4,50196E-10
231667_at	SLC39A5	-1,215170768	9,55953E-07
202843_at	DNAJB9	-1,215861068	3,57416E-08
219298_at	ECHDC3	-1,217118006	1,42169E-08
1569592_a_at	F11	-1,218253128	3,87623E-07
214058_at	MYCL1	-1,222416653	1,78702E-08
209522_s_at	CRAT	-1,225663684	1,05936E-08
1569591_at	F11	-1,230964591	3,23159E-07
226811_at	FAM46C	-1,236320816	8,50625E-08
229299_at	NADKD1	-1,239766273	1,15627E-09
234110_at	LOC283075	-1,247462051	6,45758E-07
219118_at	FKBP11	-1,251779406	3,54688E-09
239303_at	PIWIL2	-1,268046473	1,52179E-07
239517_at	ITGB6	-1,270099924	1,26554E-09
238763_at	RBM20	-1,270609183	1,16095E-08
214711_at	GATC	-1,282468645	2,64765E-12
205352_at	SERPINI1	-1,304619236	8,45427E-08
226596_x_at	LOC729852	-1,324179139	3,5364E-11
203675_at	NUCB2	-1,32813987	2,7842E-08
205111_s_at	PLCE1	-1,351511748	7,81377E-08
1559870_at	LOC100129129	-1,360738237	3,68643E-09
1552910_at	SIGLEC11	-1,368407256	2,5551E-09
205848_at	GAS2	-1,374856402	2,88028E-07
205420_at	PEX7	-1,388821827	1,55085E-10
225571_at	LIFR	-1,390124033	2,72817E-08
214156_at	MYRIP	-1,40307691	4,87877E-10
210472_at	MT1G	-1,415704839	1,55922E-09
238778_at	MPP7	-1,418458598	2,43968E-09
236219_at	SLC35G1	-1,424409689	1,20485E-08
212594_at	MIR4680	-1,427989614	5,02664E-10
244276_at	KLB	-1,461844312	4,58945E-11
224321_at	TMEFF2	-1,466127108	1,37322E-07
212886_at	CCDC69	-1,467326267	7,81097E-13
217127_at	CTH	-1,467838394	3,7724E-08
230900_at	CCDC110	-1,473721592	2,51603E-07
219970_at	GIPC2	-1,48144763	4,54463E-09
231202_at	ALDH1L2	-1,494685089	3,59657E-07
231192_at	LPAR3	-1,506390778	2,40555E-09
205517_at	GATA4	-1,540637612	1,29409E-08
209459_s_at	ABAT	-1,548987234	7,25599E-07
1553102_a_at	CCDC69	-1,592679791	1,43505E-15
227629_at	PRLR	-1,59534275	4,63374E-11
1554242_a_at	COCH	-1,649186482	8,09543E-08
1563498_s_at	SLC25A45	-1,655572191	5,04451E-11
205500_at	C5	-1,664133341	1,11965E-08
1562321_at	PDK4	-1,757345836	4,43351E-08
222939_s_at	SLC16A10	-1,797739104	2,44153E-08
228598_at	DPP10	-1,843219661	2,5202E-09
219915_s_at	SLC16A10	-1,845458772	2,79082E-08
1553494_at	TDH	-1,914639125	3,27513E-10
230467_at	TMEM52	-1,926090673	2,44486E-08
219937_at	TRHDE	-2,04372461	6,74521E-10
234296_s_at	TEX11	-2,683293758	4,08197E-08
229778_at	C12orf39	-2,739462568	1,2077E-08

Table 2. Lung cancer.

Probe_id	Gene_ symbol	Difference	*p*_value	Probe_id	Gene_ symbol	Difference	*p*_value
209875_s_at	SPP1	4,822808881	2,01912E-28	217771_at	GOLM1	2,228002571	9,0589E-32
217428_s_at	COL10A1	4,541640879	5,6483E-24	227725_at	ST6GALNAC1	2,203049007	5,84256E-16
37892_at	COL11A1	4,272078584	1,8653E-16	238439_at	ANKRD22	2,173624808	2,29485E-16
205941_s_at	COL10A1	4,110612063	5,54097E-28	203256_at	CDH3	2,138685121	5,23446E-21
1552767_a_at	HS6ST2	3,674026757	7,27409E-21	209773_s_at	RRM2	2,109538327	1,6333E-15
230030_at	HS6ST2	3,631421048	8,67795E-20	226777_at	ADAM12	2,10680679	1,67651E-11
206239_s_at	SPINK1	3,582037603	9,48459E-12	206102_at	GINS1	2,091111133	4,67958E-16
204320_at	COL11A1	3,527991018	8,55541E-16	211161_s_at	COL3A1	2,087870358	7,20307E-20
214774_x_at	TOX3	3,439939242	1,86409E-21	218976_at	DNAJC12	2,08762581	5,63758E-12
225681_at	CTHRC1	3,41195572	3,00421E-26	220622_at	LRRC31	2,080269589	6,40608E-12
204580_at	MMP12	3,390948142	5,78729E-16	209529_at	PPAP2C	2,068982345	1,77951E-21
216623_x_at	TOX3	3,348381144	5,76853E-21	228933_at	NHS	2,065161992	7,57588E-19
204475_at	MMP1	3,246386275	1,65798E-11	201890_at	RRM2	2,052860191	5,70649E-14
202311_s_at	COL1A1	3,236645324	2,96102E-20	210608_s_at	FUT2	2,052512926	1,0312E-23
218469_at	GREM1	3,227398383	1,72593E-13	206010_at	HABP2	2,048862466	1,50114E-14
206224_at	CST1	3,172711554	1,48587E-17	208650_s_at	CD24	2,040164895	1,94101E-12
215108_x_at	TOX3	2,976568023	4,17817E-20	207165_at	HMMR	2,038480363	8,07041E-16
218468_s_at	GREM1	2,937721293	3,68577E-12	1558508_a_at	C1orf53	2,028474118	1,10618E-18
201292_at	TOP2A	2,86461372	4,86273E-21	225655_at	UHRF1	2,026568369	9,97505E-16
1552797_s_at	PROM2	2,82100175	4,93994E-25	204675_at	SRD5A1	2,024398582	9,9439E-20
201884_at	CEACAM5	2,778299275	3,36096E-10	203764_at	DLGAP5	2,014366258	1,12834E-13
223278_at	GJB2	2,733209972	9,87147E-15	220334_at	RGS17	2,003889413	5,00839E-13
223779_at	AFAP1-AS1	2,692209094	1,32758E-17	218326_s_at	LGR4	1,990141358	2,02391E-16
219508_at	GCNT3	2,688965162	1,50117E-20	203744_at	HMGB3	1,984235175	5,45553E-18
222608_s_at	ANLN	2,659652863	2,45056E-16	202404_s_at	COL1A2	1,966501604	3,47606E-16
222484_s_at	CXCL14	2,613194288	1,59217E-13	244780_at	SGPP2	1,964739904	3,0391E-10
224428_s_at	CDCA7	2,596822585	1,07348E-17	225601_at	HMGB3	1,952799268	3,86703E-14
218002_s_at	CXCL14	2,563548086	1,72663E-12	229936_at	GFRA3	1,943499098	4,05286E-11
227253_at	CP	2,552002834	8,87205E-12	205959_at	MMP13	1,941784829	2,92553E-10
204846_at	CP	2,549225472	3,4778E-11	202870_s_at	CDC20	1,940020808	2,17658E-15
218960_at	TMPRSS4	2,532302487	2,47088E-17	203820_s_at	IGF2BP3	1,93873978	3,64797E-09
202575_at	CRABP2	2,479561855	4,30696E-19	231941_s_at	MUC20	1,924726327	2,20224E-15
223062_s_at	PSAT1	2,471748677	2,43611E-20	212354_at	SULF1	1,924442723	2,54853E-14
203878_s_at	MMP11	2,466480904	1,0658E-15	226622_at	MUC20	1,922090495	8,86415E-18
228143_at	CP	2,427176089	9,0678E-13	203755_at	BUB1B	1,919446311	3,19558E-15
227452_at	LOC100499467	2,42468255	3,37955E-21	204026_s_at	ZWINT	1,916756931	2,71741E-19
1569886_a_at	GLB1L3	2,423321323	1,30586E-10	213909_at	LRRC15	1,916529873	3,22442E-12
202310_s_at	COL1A1	2,417288003	1,32345E-16	223229_at	UBE2T	1,908339973	6,21865E-18
241994_at	XDH	2,394434566	7,58344E-17	204653_at	TFAP2A	1,903446401	1,64462E-15
201291_s_at	TOP2A	2,379807047	1,62376E-15	229271_x_at	COL11A1	1,900429114	6,40628E-10
205713_s_at	COMP	2,378479616	1,65969E-16	209641_s_at	ABCC3	1,898445808	1,13272E-20
212353_at	SULF1	2,296488005	1,39782E-16	203240_at	FCGBP	1,895883405	2,24046E-14
220393_at	LGSN	2,294927424	4,643E-12	225314_at	OCIAD2	1,887496192	1,37677E-25
205242_at	CXCL13	2,289449958	1,43278E-07	203889_at	SCG5	1,88187683	8,59046E-13
208161_s_at	ABCC3	2,28939051	4,85271E-23	201852_x_at	COL3A1	1,874986169	1,21991E-14
203083_at	THBS2	2,28560386	1,12155E-17	228956_at	UGT8	1,874614257	9,87159E-11
238617_at	KIF26B	2,270292767	1,09434E-18	214710_s_at	CCNB1	1,864861262	2,45239E-14
202503_s_at	KIAA0101	2,238995126	1,36884E-21	204641_at	NEK2	1,856733851	1,40852E-12
228347_at	SIX1	2,237599648	1,38854E-12	230193_at	WDR66	1,845107191	1,10418E-07
1558034_s_at	CP	2,232254405	3,74365E-09	210519_s_at	NQO1	1,844871092	5,28342E-14

Table 2 ***(continued).*** Lung cancer.

Probe_id	Gene_symbol	Difference	*p*_value	Probe_id	Gene_symbol	Difference	*p*_value
217414_x_at	HBA1	-2,58170257	4,469E-18	221132_at	CLDN18	-2,946144891	1,10467E-14
203434_s_at	MME	-2,581803171	5,83606E-20	228698_at	SOX7	-2,962023697	2,1381E-20
227197_at	ARHGEF26	-2,589448612	1,7699E-23	204271_s_at	EDNRB	-2,965491724	1,11001E-27
214146_s_at	PPBP	-2,605637214	1,96605E-12	206651_s_at	CPB2	-3,011421808	2,31175E-13
1556325_at	FILIP1	-2,625954294	2,94785E-22	206658_at	UPK3B	-3,014160128	7,72507E-19
204018_x_at	HBA1	-2,632164607	3,33773E-18	204719_at	ABCA8	-3,027500507	5,53513E-17
202524_s_at	SPOCK2	-2,63856631	2,21508E-33	205200_at	CLEC3B	-3,04590053	1,98934E-29
224013_s_at	SOX7	-2,641769227	1,64237E-18	207526_s_at	IL1RL1	-3,063921333	1,23173E-12
211745_x_at	HBA1	-2,653732703	5,28029E-18	1556579_s_at	IGSF10	-3,072672475	2,19629E-29
214505_s_at	FHL1	-2,655277157	4,82534E-18	205207_at	IL6	-3,073790451	1,44543E-13
241811_x_at	SLC6A4	-2,663621289	7,32505E-17	206742_at	FIGF	-3,080157247	4,26799E-21
205433_at	BCHE	-2,665056762	1,3298E-13	222717_at	SDPR	-3,089882481	7,11694E-22
210298_x_at	FHL1	-2,666853992	2,05644E-17	221133_s_at	CLDN18	-3,131162057	7,64135E-17
201539_s_at	FHL1	-2,675992245	5,22168E-17	227874_at	EMCN	-3,150461281	1,70734E-26
209458_x_at	HBA1	-2,678606175	1,55696E-17	228434_at	BTNL9	-3,155502679	1,52795E-26
223836_at	FGFBP2	-2,689585613	2,14796E-18	210299_s_at	FHL1	-3,169519634	1,44853E-19
228268_at	FMO2	-2,690981422	1,4516E-23	206701_x_at	EDNRB	-3,172896865	1,50695E-24
224061_at	INMT	-2,691587655	1,98779E-18	226228_at	AQP4	-3,232572897	5,54391E-11
217232_x_at	HBB	-2,697692059	9,19505E-18	217546_at	MT1M	-3,341012278	8,73281E-17
204396_s_at	GRK5	-2,698952351	1,18753E-30	209904_at	TNNC1	-3,366463173	1,53168E-29
228885_at	MAMDC2	-2,698970534	8,35243E-14	239650_at	NCKAP5	-3,381705471	1,02886E-33
38691_s_at	SFTPC	-2,70739547	1,07715E-10	214135_at	CLDN18	-3,423682527	4,39889E-18
218711_s_at	SDPR	-2,708583152	2,63479E-16	223678_s_at	SFTPA1	-3,426490608	1,13673E-10
230250_at	PTPRB	-2,709488662	3,1608E-22	204273_at	EDNRB	-3,433265884	1,37106E-23
220037_s_at	LYVE1	-2,712215518	6,58335E-19	229309_at	ADRB1	-3,445273089	4,93996E-19
206208_at	CA4	-2,713985008	1,46982E-34	215454_x_at	SFTPC	-3,476574349	7,60354E-18
203571_s_at	C10orf116	-2,716548679	1,0258E-24	238222_at	GKN2	-3,4948663	1,44925E-17
238332_at	ANKRD29	-2,726188477	3,68767E-22	209613_s_at	ADH1B	-3,558824404	3,10493E-14
215918_s_at	SPTBN1	-2,746545406	1,16205E-39	209612_s_at	ADH1B	-3,569685566	2,62718E-15
211699_x_at	HBA1	-2,749988194	1,24518E-17	214387_x_at	SFTPC	-3,614593607	5,81246E-13
210066_s_at	AQP4	-2,750555383	2,37983E-12	228766_at	CD36	-3,618478137	2,45553E-21
210068_s_at	AQP4	-2,767648058	1,7469E-14	205725_at	SCGB1A1	-3,630920736	7,31968E-11
235228_at	CCDC85A	-2,768234076	6,99409E-29	213456_at	SOSTDC1	-3,636740921	1,11612E-19
203065_s_at	CAV1	-2,793903917	3,94864E-24	205866_at	FCN3	-3,647941822	3,82412E-22
238018_at	FAM150B	-2,805116169	2,08651E-18	205982_x_at	SFTPC	-3,67261854	2,19252E-13
207519_at	SLC6A4	-2,809169349	5,33641E-18	230469_at	RTKN2	-3,67854121	9,74528E-33
206702_at	TEK	-2,822373167	3,26874E-26	213317_at	CLIC5	-3,68730945	1,79574E-22
206488_s_at	CD36	-2,823128982	5,77483E-19	209074_s_at	FAM107A	-3,693308377	7,00363E-26
209116_x_at	HBB	-2,827778556	1,59797E-16	211735_x_at	SFTPC	-3,693981316	3,82996E-13
204931_at	TCF21	-2,834624975	2,36341E-22	217046_s_at	AGER	-3,741921536	6,481E-39
205863_at	S100A12	-2,839067284	2,61914E-12	219230_at	TMEM100	-3,810006797	1,3624E-19
207547_s_at	FAM107A	-2,84190655	2,88972E-28	242009_at	SLC6A4	-3,853191728	9,45502E-20
205952_at	KCNK3	-2,846093279	3,31288E-21	209469_at	GPM6A	-3,896073429	3,46282E-31
209555_s_at	CD36	-2,86257616	1,83097E-17	230560_at	STXBP6	-3,912549845	1,40276E-24
202768_at	FOSB	-2,863123805	9,41575E-14	203980_at	FABP4	-3,99925218	4,25804E-23
219866_at	CLIC5	-2,867068317	6,20513E-21	204712_at	WIF1	-4,025682558	5,83501E-15
235568_at	C19orf59	-2,897526693	7,34271E-20	206209_s_at	CA4	-4,165591611	1,62169E-34
225207_at	PDK4	-2,910343277	1,08022E-13	232578_at	CLDN18	-4,490835039	3,27734E-17
235670_at	STX11	-2,91485741	2,59596E-27	209470_s_at	GPM6A	-4,519540718	5,53011E-32
241672_at	SERTM1	-2,923623253	5,26636E-26	210081_at	AGER	-4,692791964	1,26272E-29

Table 2. Renal cancer.

Probe_id	Gene_ symbol	Difference	*p*_value
218484_at	NDUFA4L2	6,490020323	9,22724E-52
223333_s_at	ANGPTL4	6,334067365	6,56994E-63
213479_at	NPTX2	5,863953266	4,1799E-36
221009_s_at	ANGPTL4	5,596124358	1,00533E-54
206025_s_at	TNFAIP6	5,563770699	1,23495E-52
206026_s_at	TNFAIP6	5,539349746	2,37677E-49
204416_x_at	APOC1	5,392463758	3,54931E-41
242517_at	KISS1R	5,354488316	2,8975E-33
202238_s_at	NNMT	5,120997008	1,43757E-45
205199_at	CA9	4,901610493	6,57835E-58
1554452_a_at	HILPDA	4,870905555	2,21402E-44
218507_at	HILPDA	4,800399598	1,93386E-52
202237_at	NNMT	4,620132174	2,1955E-41
227253_at	CP	4,602935109	1,42107E-27
201313_at	ENO2	4,517596438	2,3591E-57
221870_at	EHD2	4,461259033	1,63726E-49
205030_at	FABP7	4,439296744	1,95889E-16
202934_at	HK2	4,422891739	7,57042E-55
204846_at	CP	4,39734851	1,1483E-25
222847_s_at	EGLN3	4,354729046	8,36386E-65
1558034_s_at	CP	4,305258359	4,7193E-25
217767_at	C3	4,252064455	3,82662E-36
229168_at	COL23A1	4,198791991	1,33174E-40
212992_at	AHNAK2	4,119514893	3,26005E-45
225681_at	CTHRC1	4,099517555	2,07573E-33
202112_at	VWF	4,092011832	1,02394E-39
216834_at	RGS1	4,075608733	5,47029E-33
215446_s_at	LOX	4,06994737	1,61757E-38
210445_at	FABP6	4,009500772	4,68432E-27
206836_at	SLC6A3	3,953221744	8,63528E-31
213553_x_at	APOC1	3,942139763	2,98578E-37
1564485_at	LOC100131551	3,911512734	6,7345E-42
226661_at	CDCA2	3,910083426	8,23336E-39
219410_at	TMEM45A	3,890684247	1,44343E-31
219725_at	TREM2	3,856745293	7,2639E-43
212143_s_at	IGFBP3	3,852462536	1,41796E-53
221530_s_at	BHLHE41	3,830972324	8,80734E-52
205029_s_at	FABP7	3,744340512	4,71476E-14
219232_s_at	EGLN3	3,742385823	1,04923E-54
218888_s_at	NETO2	3,722555229	2,10386E-44
202856_s_at	SLC16A3	3,72202258	2,38567E-55
205258_at	INHBB	3,715602097	4,26303E-32
230836_at	ST8SIA4	3,631666494	3,1502E-51
204298_s_at	LOX	3,626368084	3,247E-32
202988_s_at	RGS1	3,599379316	1,4272E-36
215646_s_at	VCAN	3,589134086	1,06348E-29
229390_at	FAM26F	3,574057933	4,274E-33
219888_at	SPAG4	3,550689599	1,24259E-44
205572_at	ANGPT2	3,550316818	6,99781E-40
210095_s_at	IGFBP3	3,542797952	5,8404E-35
209652_s_at	PGF	3,528580537	1,56144E-26
1554195_a_at	C5orf46	3,504192648	4,63021E-20
219619_at	DIRAS2	3,491719906	9,06301E-37
211571_s_at	VCAN	3,49004408	2,37828E-31
213915_at	NKG7	3,483972629	1,30663E-35
204006_s_at	FCGR3A	3,477539957	5,23382E-43
223610_at	SEMA5B	3,469375852	1,05568E-52
201818_at	LPCAT1	3,465356448	8,49761E-53
205476_at	CCL20	3,459535408	7,50145E-19
236034_at	ANGPT2	3,431761411	2,73711E-40
202855_s_at	SLC16A3	3,426573309	2,35031E-51
202998_s_at	LOXL2	3,412706428	3,03842E-44
1558290_a_at	MIR1204	3,390827996	8,26373E-55
205073_at	CYP2J2	3,381795255	2,89511E-23
242943_at	ST8SIA4	3,366785796	3,32961E-53
202202_s_at	LAMA4	3,365714455	2,64898E-47
221731_x_at	VCAN	3,342316381	1,14124E-30
232693_s_at	FBXO16	3,31961889	2,15279E-45
1552256_a_at	SCARB1	3,302092561	6,09214E-38
222774_s_at	NETO2	3,300351717	6,6393E-44
204619_s_at	VCAN	3,275357447	4,09905E-30
217028_at	CXCR4	3,25291996	3,97928E-39
242662_at	PCSK6	3,244438946	2,3111E-31
236957_at	CDCA2	3,237169731	1,2049E-39
204914_s_at	SOX11	3,209521718	3,8438E-30
201506_at	LOC100652886	3,205796102	9,62424E-28
211756_at	PTHLH	3,195000152	8,25801E-16
32128_at	CCL18	3,189745909	3,0639E-21
211527_x_at	VEGFA	3,186309548	2,21897E-39
204620_s_at	VCAN	3,178062243	3,41491E-30
213349_at	TMCC1	3,176493188	3,15549E-47
217984_at	RNASET2	3,165822398	7,39176E-45
212097_at	CAV1	3,158961645	5,04364E-49
210029_at	IDO1	3,143126492	9,11133E-36
237261_at	ANGPT2	3,12799402	1,49472E-37
214978_s_at	PPFIA4	3,1260041	3,34304E-41
206488_s_at	CD36	3,122311095	5,60106E-29
206508_at	CD70	3,114511032	1,91995E-32
217983_s_at	RNASET2	3,102830221	3,23755E-39
230261_at	ST8SIA4	3,098266362	1,5861E-43
226452_at	PDK1	3,082841094	1,85816E-62
232737_s_at	ENPP3	3,080881487	8,36557E-25
228143_at	CP	3,071923455	5,77625E-21
232694_at	ZNF395	3,068270526	4,33541E-44
211148_s_at	ANGPT2	3,060197148	6,03997E-35
1405_i_at	CCL5	3,049667986	1,93924E-26
210538_s_at	BIRC3	3,025665417	7,4349E-31
203915_at	CXCL9	3,01958745	1,80787E-24
203438_at	STC2	3,015399941	1,13178E-27
204698_at	ISG20	3,006481068	2,87245E-33

Table 2 ***(continued).*** Renal cancer.

Probe_id	Gene_ symbol	Difference	*p*_value	Probe_id	Gene_ symbol	Difference	*p*_value
236225_at	GGT6	-4,229776096	9,16822E-54	1565228_s_at	ALB	-5,053360208	2,4389E-31
231021_at	SLC6A19	-4,238877845	1,10481E-31	206840_at	AFM	-5,058655486	2,37148E-43
1553153_at	ATP6V0D2	-4,253896054	3,41176E-46	202037_s_at	SFRP1	-5,077747034	2,54732E-42
237799_at	SLC22A12	-4,255004251	6,8037E-38	231398_at	SLC22A7	-5,097406235	2,5806E-40
209460_at	ABAT	-4,263195589	4,8172E-53	231376_at	UPP2	-5,112621608	1,6346E-47
205117_at	FGF1	-4,265302404	3,77763E-44	206952_at	G6PC	-5,126233434	3,74543E-36
233183_at	SLC4A9	-4,267368138	3,69536E-47	1554668_a_at	FAM151A	-5,136859028	9,54558E-37
219554_at	RHCG	-4,286696509	1,15958E-47	206226_at	HRG	-5,203337668	9,17061E-55
1553155_x_at	ATP6V0D2	-4,295569808	4,9245E-47	213967_at	RALYL	-5,220460249	6,07043E-57
223869_at	SOST	-4,300128707	6,74484E-50	220197_at	ATP6V0A4	-5,275954606	6,91688E-46
233604_at	FLJ22763	-4,326765917	2,65497E-42	231058_at	FXYD4	-5,342504576	4,35612E-49
207047_s_at	CLCNKA	-4,331035034	2,82184E-45	241436_at	SCNN1G	-5,430616378	2,55594E-37
226553_at	TMPRSS2	-4,337206752	8,48774E-49	210452_x_at	CYP4F2	-5,439209262	5,54883E-41
31835_at	HRG	-4,353072364	2,66551E-53	211357_s_at	ALDOB	-5,4649292	7,77894E-29
230565_at	ATP6V1G3	-4,355546302	1,3647E-46	231391_at	CTXN3	-5,488869631	3,38862E-43
223062_s_at	PSAT1	-4,362571402	1,21997E-29	205985_x_at	CLCNKB	-5,509298551	3,81893E-48
205336_at	PVALB	-4,408684371	1,44958E-40	209977_at	PLG	-5,551722671	3,33765E-31
236374_at	CTXN3	-4,444182763	2,20074E-45	209443_at	SERPINA5	-5,58664681	2,44742E-44
236652_at	LOC149703	-4,455247162	1,52215E-48	236646_at	C12orf59	-5,619223099	3,44688E-49
205751_at	SH3GL2	-4,462551325	1,7301E-46	205719_s_at	PAH	-5,661387741	4,21545E-34
214053_at	ERBB4	-4,485185688	4,73118E-45	217512_at	KNG1	-5,67956972	1,49816E-56
203453_at	SCNN1A	-4,487223719	1,90435E-27	239593_at	TMEM213	-5,694900715	5,02126E-46
205502_at	CYP17A1	-4,502730621	3,65452E-41	209978_s_at	LPA	-5,748432747	2,54843E-34
208354_s_at	SLC12A3	-4,528464715	2,61198E-43	238287_at	SLC7A13	-5,767271336	2,4295E-45
240320_at	C14orf164	-4,537539875	2,57337E-40	205983_at	DPEP1	-5,78387096	4,03259E-48
206254_at	EGF	-4,548105516	8,41384E-36	214598_at	CLDN8	-5,845577044	3,3956E-47
210343_s_at	SLC22A6	-4,551989595	1,02336E-32	216910_at	XPNPEP2	-5,869888482	5,38031E-48
206754_s_at	CYP2B6	-4,577798523	1,61979E-41	205243_at	SLC13A3	-5,958247114	1,42785E-46
205549_at	PCP4	-4,60006861	1,63804E-44	1554748_at	CLCNKB	-6,014912445	5,3423E-43
206515_at	CYP4F3	-4,600201594	2,04831E-37	210403_s_at	KCNJ1	-6,092791726	9,95087E-55
206404_at	FGF9	-4,613330119	6,91039E-46	204705_x_at	ALDOB	-6,114901086	3,78271E-33
228581_at	KCNJ10	-4,613678508	2,6734E-49	236630_at	AQP2	-6,177607514	2,16415E-54
225645_at	EHF	-4,651110313	1,23506E-33	240183_at	TMEM213	-6,343942596	2,93372E-47
223704_s_at	DMRT2	-4,67574443	2,65783E-47	206484_s_at	XPNPEP2	-6,424171093	2,28355E-53
230931_at	PLG	-4,679529803	1,24474E-38	220424_at	NPHS2	-6,508997123	4,30003E-51
214451_at	TFAP2B	-4,685269403	3,49018E-55	205244_s_at	SLC13A3	-6,534434367	1,53633E-47
227238_at	MUC15	-4,68747038	1,62435E-41	211298_s_at	ALB	-6,560949417	9,01759E-46
219732_at	LPPR1	-4,701418914	1,83343E-59	210402_at	KCNJ1	-6,569448092	3,72012E-53
231634_at	SLC12A3	-4,714711172	1,1306E-47	217238_s_at	ALDOB	-6,610702682	7,37974E-35
231068_at	SLC47A2	-4,74397905	8,93028E-51	206457_s_at	DIO1	-6,738716251	7,53458E-57
210199_at	CRYAA	-4,796523526	8,65595E-40	231352_at	SLC22A8	-6,763087573	3,19218E-51
239006_at	SLC26A7	-4,801479306	1,29652E-45	204704_s_at	ALDOB	-6,807492774	1,28244E-43
243562_at	KNG1	-4,814775106	2,01318E-52	206024_at	HPD	-7,036555362	8,36919E-44
216599_x_at	SLC22A6	-4,844634238	5,09753E-34	205892_s_at	FABP1	-7,076212776	1,6065E-45
227642_at	TFCP2L1	-4,898328833	1,75182E-37	221298_s_at	SLC22A8	-7,311839689	1,68384E-50
1552767_a_at	HS6ST2	-4,935341223	2,75356E-48	220281_at	SLC12A1	-7,664747945	1,19808E-48
230030_at	HS6ST2	-4,938473615	1,25812E-47	205625_s_at	CALB1	-7,67913435	6,9119E-55
202036_s_at	SFRP1	-4,978490648	6,59639E-42	205626_s_at	CALB1	-7,714125555	4,43843E-56
239805_at	SLC13A2	-4,980288004	2,75574E-53	206054_at	KNG1	-8,047830577	1,84841E-54
229916_at	ENPP6	-4,998127263	1,04327E-50	206716_at	UMOD	-8,448055168	2,89449E-47

Table 2. Gastric cancer.

Probe_id	Gene_ symbol	Difference	*p*_value	Probe_id	Gene_ symbol	Difference	*p*_value
227140_at	INHBA	4,8889124	1,22915E-31	212003_at	C1orf144	2,730177256	8,15549E-18
207714_s_at	SERPINH1	4,492491568	5,97848E-23	218029_at	FAM65A	2,729573296	6,2841E-26
210511_s_at	INHBA	3,982696503	4,41619E-39	219725_at	TREM2	2,705367883	2,74557E-22
203256_at	CDH3	3,887853499	6,17431E-25	218745_x_at	TMEM161A	2,694202682	3,19783E-27
226311_at	ADAMTS2	3,805295817	1,52608E-22	214507_s_at	EXOSC2	2,686743011	1,45794E-25
226237_at	COL8A1	3,797762018	4,24199E-24	205157_s_at	JUP	2,672983101	2,20375E-13
209955_s_at	FAP	3,693738781	1,02427E-50	203878_s_at	MMP11	2,667003346	7,99946E-20
37892_at	COL11A1	3,612084877	6,74104E-27	224396_s_at	ASPN	2,651368165	5,72759E-16
202465_at	PCOLCE	3,52562907	2,34219E-23	205941_s_at	COL10A1	2,650603696	7,31733E-18
206224_at	CST1	3,493220855	6,83423E-28	210495_x_at	FN1	2,64889057	1,25419E-21
224646_x_at	H19	3,396683848	7,00294E-14	211719_x_at	FN1	2,644037907	1,73793E-22
207172_s_at	CDH11	3,347507736	3,52036E-26	209901_x_at	AIF1	2,634389047	7,68533E-10
212942_s_at	KIAA1199	3,293207961	1,28934E-22	204281_at	TEAD4	2,627387846	7,84668E-30
226930_at	FNDC1	3,256805171	1,24259E-16	209680_s_at	KIFC1	2,623539662	1,58552E-20
203083_at	THBS2	3,18712675	1,44106E-20	216080_s_at	FADS3	2,616984693	1,79769E-22
209792_s_at	KLK10	3,173295589	1,91465E-24	209299_x_at	PPIL2	2,60895866	5,09693E-35
217818_s_at	ARPC4	3,17161663	2,99482E-20	202790_at	CLDN7	2,599417876	4,17204E-06
206392_s_at	RARRES1	3,143920339	5,71645E-11	225664_at	COL12A1	2,585386896	2,64171E-28
209875_s_at	SPP1	3,120638162	2,01792E-15	212464_s_at	FN1	2,583147086	5,24565E-24
202404_s_at	COL1A2	3,108846322	3,56806E-23	1552944_a_at	PANX2	2,580919217	1,26588E-29
219249_s_at	FKBP10	3,108796798	4,4461E-30	202580_x_at	FOXM1	2,580370022	1,88491E-12
212746_s_at	CEP170	3,099325939	5,5301E-20	210992_x_at	FCGR2C	2,570777559	2,16132E-17
212354_at	SULF1	3,083045406	2,86886E-26	212353_at	SULF1	2,566325108	4,44603E-21
217428_s_at	COL10A1	3,060255767	8,11761E-21	225329_at	FAM195B	2,566053283	6,72078E-21
221427_s_at	CCNL2	3,049313381	2,94863E-21	229802_at	WISP1	2,564212522	6,17952E-16
231766_s_at	COL12A1	3,029707887	3,81068E-21	214692_s_at	JRK	2,564194475	1,67591E-21
206391_at	RARRES1	3,026096414	6,34277E-15	230239_at	ROCK1	2,545958042	3,78086E-26
222760_at	ZNF703	3,022003214	5,34633E-13	212344_at	SULF1	2,545935733	2,50688E-24
204051_s_at	SFRP4	2,99917765	6,15823E-20	209294_x_at	TNFRSF10B	2,541747132	2,84373E-19
202145_at	LY6E	2,979830709	4,67994E-13	211506_s_at	IL8	2,539569273	1,80636E-13
212682_s_at	LMF2	2,957166935	6,5324E-29	202828_s_at	MMP14	2,535493174	1,59555E-17
218300_at	C16orf53	2,946267998	7,45256E-24	219261_at	C7orf26	2,527244729	3,65239E-12
201818_at	LPCAT1	2,938897827	1,11193E-16	204776_at	THBS4	2,527048108	2,60975E-12
212141_at	MCM4	2,910303434	6,50896E-19	208893_s_at	DUSP6	2,519502038	2,71351E-09
210132_at	EFNA3	2,902801201	4,80306E-31	221870_at	EHD2	2,518479822	8,24302E-13
201108_s_at	THBS1	2,891934948	3,28369E-18	219434_at	TREM1	2,518023608	1,21039E-19
203954_x_at	CLDN3	2,859530555	2,73439E-08	213147_at	HOXA10	2,514918947	1,06145E-17
216442_x_at	FN1	2,852455302	2,97358E-24	211709_s_at	CLEC11A	2,508930804	1,86614E-16
223121_s_at	SFRP2	2,840728931	3,50753E-08	204833_at	ATG12	2,50756557	3,66308E-15
215537_x_at	DDAH2	2,840055003	3,00224E-15	201564_s_at	FSCN1	2,502881351	1,83752E-21
209395_at	CHI3L1	2,834612271	3,81163E-09	226670_s_at	PABPC1L	2,502260053	1,02214E-11
203612_at	BYSL	2,820558711	1,13322E-22	224753_at	CDCA5	2,501946722	1,47492E-13
227477_at	ZMYND19	2,80227503	3,75723E-19	224790_at	ASAP1	2,501096317	1,07923E-19
222450_at	PMEPA1	2,783366119	6,68876E-16	226997_at	ADAMTS12	2,468958026	5,83597E-19
211981_at	COL4A1	2,77954004	2,20884E-14	204695_at	CDC25A	2,468781401	3,75562E-27
220633_s_at	HP1BP3	2,751982758	4,08268E-26	201109_s_at	THBS1	2,464989123	2,15111E-12
225681_at	CTHRC1	2,75128912	8,19208E-23	201428_at	CLDN4	2,453857445	1,9847E-08
203417_at	MFAP2	2,740699957	9,22411E-17	228302_x_at	CAMK2N1	2,44831858	8,37037E-08
211518_s_at	BMP4	2,737109069	4,2036E-31	210463_x_at	TRMT1	2,444117829	7,32357E-23
202859_x_at	IL8	2,734853455	4,22228E-10	209196_at	WDR46	2,443539246	1,58911E-16

Table 2 *(continued)*. Gastric cancer.

Probe_id	**Gene_ symbol**	**Difference**	***p*_value**	**Probe_id**	**Gene_ symbol**	**Difference**	***p*_value**
242271_at	SLC26A9	-2,66944082	2,64311E-12	235591_at	SSTR1	-3,157249267	1,52304E-13
209632_at	PPP2R3A	-2,676078191	3,94394E-13	226960_at	CXCL17	-3,169624106	3,5552E-13
210906_x_at	AQP4	-2,682243487	4,00079E-09	210505_at	ADH7	-3,174987251	3,89425E-25
216687_x_at	UGT2B15	-2,694255926	6,8124E-15	214385_s_at	MUC5AC	-3,179033374	6,60853E-19
217546_at	MT1M	-2,698330682	1,49289E-17	206212_at	CPA2	-3,183447977	2,00758E-10
236430_at	TMED6	-2,719734005	6,74277E-07	204777_s_at	MAL	-3,183558734	4,84494E-21
228232_s_at	VSIG2	-2,72836088	4,45427E-17	204697_s_at	CHGA	-3,192545338	2,03456E-14
206293_at	SULT2A1	-2,73097184	1,86424E-08	238862_at	MFSD4	-3,266526135	2,78914E-11
205623_at	ALDH3A1	-2,733534997	1,16128E-11	241436_at	SCNN1G	-3,275056064	2,28757E-10
210641_at	CAPN9	-2,744189173	1,20979E-26	1556097_at	HOMER2	-3,291420074	1,44636E-17
211470_s_at	SULT1C2	-2,745239559	1,33892E-19	1552910_at	SIGLEC11	-3,294474599	6,28583E-14
204704_s_at	ALDOB	-2,751923662	4,13807E-06	1555868_at	LOC100507477	-3,295093342	5,26997E-20
217238_s_at	ALDOB	-2,753451133	6,39597E-06	205979_at	SCGB2A1	-3,297810719	6,07427E-13
1554182_at	TRIM73	-2,755849382	1,42331E-11	223784_at	TMEM27	-3,307639475	2,66577E-24
211548_s_at	HPGD	-2,762983645	5,56362E-14	204469_at	PTPRZ1	-3,308622623	2,21159E-22
229070_at	ADTRP	-2,774662814	1,02049E-21	213921_at	SST	-3,315510798	4,44327E-13
205649_s_at	FGA	-2,788837232	5,01001E-08	215930_s_at	CTAGE5	-3,317331375	6,7249E-35
228262_at	MAP7D2	-2,795612446	1,71918E-13	214303_x_at	MUC5AC	-3,342618671	2,17498E-20
1556554_at	TRIM50	-2,801812787	4,86425E-09	220723_s_at	CWH43	-3,411965578	2,70989E-13
219727_at	DUOX2	-2,836946814	1,514E-12	205319_at	PSCA	-3,42838803	8,55377E-17
241137_at	DPCR1	-2,880461571	3,73646E-13	229254_at	MFSD4	-3,46583642	2,74704E-13
223862_at	GHRL	-2,880663334	6,61769E-11	231646_at	DPCR1	-3,495359344	2,36258E-16
242269_at	FLJ42875	-2,882004856	8,93613E-14	202018_s_at	LTF	-3,511467705	8,33731E-13
229177_at	C16orf89	-2,888076275	1,47958E-16	213265_at	PGA3	-3,526735958	6,84484E-15
242093_at	SYTL5	-2,895123095	7,11457E-17	243764_at	VSIG1	-3,533569073	5,42375E-23
227803_at	ENPP5	-2,895809017	6,49115E-11	213953_at	KRT20	-3,540825015	3,85144E-12
220351_at	CCRL1	-2,902203837	2,02234E-24	205815_at	REG3A	-3,545460838	9,18834E-10
205261_at	PGC	-2,906729774	2,01707E-14	230559_x_at	FGD4	-3,5508185	1,29049E-31
1552365_at	SCIN	-2,912290203	8,5639E-16	1569428_at	WIBG	-3,58231793	4,59803E-33
210143_at	ANXA10	-2,915648251	2,79258E-20	214601_at	TPH1	-3,582902896	9,45136E-20
230081_at	PLCXD3	-2,926245343	2,16665E-14	217187_at	MUC5AC	-3,583756641	1,19371E-13
205751_at	SH3GL2	-2,926851635	8,15181E-11	239533_at	GPR155	-3,634401083	6,5673E-13
210119_at	KCNJ15	-2,945489824	3,02174E-12	206334_at	LIPF	-3,638355412	1,01921E-15
242372_s_at	MFSD4	-2,953019366	3,10532E-07	1555236_a_at	PGC	-3,666002407	2,73287E-16
211357_s_at	ALDOB	-2,989889707	7,33832E-07	1565666_s_at	MUC6	-3,668542938	5,98222E-15
210375_at	PTGER3	-3,014183762	9,84673E-11	238383_at	C6orf58	-3,718123708	9,45129E-12
234709_at	CAPN13	-3,016962545	5,46779E-17	239006_at	SLC26A7	-3,756127678	1,03363E-13
209752_at	REG1A	-3,022992175	8,98147E-11	221095_s_at	KCNE2	-3,792350681	1,24433E-13
203924_at	GSTA1	-3,023785466	1,39504E-09	213456_at	SOSTDC1	-3,900848865	4,56592E-17
210381_s_at	CCKBR	-3,029564631	1,66049E-09	220191_at	GKN1	-3,947072632	6,398E-17
231978_at	TPCN2	-3,040997117	1,70745E-09	209966_x_at	ESRRG	-3,95172019	2,90961E-17
226281_at	DNER	-3,085602714	3,63112E-09	214046_at	FUT9	-4,005015595	1,37976E-23
214156_at	MYRIP	-3,09190143	7,56916E-15	204965_at	GC	-4,02078117	2,48235E-21
207185_at	SLC10A1	-3,093518366	5,3084E-19	219564_at	KCNJ16	-4,157101454	2,16012E-15
215118_s_at	IGHA1	-3,093882348	6,96357E-20	238222_at	GKN2	-4,563554991	6,95979E-22
1555854_at	AKR1C1	-3,09510848	1,54777E-19	207981_s_at	ESRRG	-4,90200127	1,53596E-15
228004_at	LINC00261	-3,099476434	1,88673E-14	207139_at	ATP4A	-5,015396407	2,24596E-14
203913_s_at	HPGD	-3,108192608	1,76535E-16	226228_at	AQP4	-5,090492628	1,3072E-11
221008_s_at	AGXT2L1	-3,126893339	2,42171E-08	207033_at	GIF	-5,323572263	4,51157E-18
206561_s_at	AKR1B10	-3,148363314	5,25329E-19	207546_at	ATP4B	-6,154351239	3,76789E-18

Table 2. Breast cancer.

Probe_id	**Gene_ symbol**	**Difference**	***p*_value**	**Probe_id**	**Gene_ symbol**	**Difference**	***p*_value**
205941_s_at	COL10A1	4,924777495	2,88019E-31	218355_at	KIF4A	1,996056179	9,43261E-16
37892_at	COL11A1	4,329633334	1,6289E-26	223229_at	UBE2T	1,958948024	3,62586E-17
204320_at	COL11A1	3,880423457	2,40269E-24	204826_at	CCNF	1,95712933	2,22619E-10
217428_s_at	COL10A1	3,558167133	5,69089E-32	202580_x_at	FOXM1	1,936638593	6,54284E-16
204351_at	S100P	3,33408717	4,84081E-15	218468_s_at	GREM1	1,919073317	1,14613E-07
203757_s_at	CEACAM6	3,155643412	4,95318E-09	203876_s_at	MMP11	1,918857311	3,80178E-18
205713_s_at	COMP	3,05320603	5,54592E-19	216442_x_at	FN1	1,916497101	1,1811E-12
203878_s_at	MMP11	2,993797943	2,50221E-27	222608_s_at	ANLN	1,907009048	5,1079E-16
204641_at	NEK2	2,83987696	3,97293E-14	206754_s_at	CYP2B6	1,901794745	2,29548E-05
209773_s_at	RRM2	2,788505108	4,81871E-12	208502_s_at	PITX1	1,899948816	3,64843E-18
227140_at	INHBA	2,759886784	2,33779E-23	1555203_s_at	SLC44A4	1,896338381	1,153E-09
210511_s_at	INHBA	2,703823192	1,61215E-27	210495_x_at	FN1	1,894551723	1,57416E-12
209642_at	BUB1	2,599854942	3,4132E-13	205597_at	SLC44A4	1,891668935	1,75858E-14
206364_at	KIF14	2,512739818	1,05798E-13	212344_at	SULF1	1,889996277	1,33338E-18
213909_at	LRRC15	2,442941732	1,42284E-16	226237_at	COL8A1	1,88635803	4,50024E-12
204475_at	MMP1	2,431727482	4,16726E-14	201884_at	CEACAM5	1,885912011	1,05228E-08
206110_at	HIST1H3H	2,428369056	7,97636E-12	219300_s_at	CNTNAP2	1,877381154	7,5398E-09
223278_at	GJB2	2,419506171	3,15232E-18	211122_s_at	CXCL11	1,874682526	3,24509E-11
206134_at	ADAMDEC1	2,39516106	3,43544E-09	212464_s_at	FN1	1,871631852	3,9373E-12
1562821_a_at	DSCAM-AS1	2,392304815	5,06639E-10	225687_at	FAM83D	1,868067897	9,69634E-18
205943_at	TDO2	2,350980087	1,41486E-12	220588_at	BCAS4	1,865667847	8,10847E-15
229802_at	WISP1	2,341057597	1,32426E-17	204033_at	TRIP13	1,837087313	1,72888E-09
229975_at	BMPR1B	2,262052115	2,61157E-05	218009_s_at	PRC1	1,827469921	3,12391E-17
205959_at	MMP13	2,253317255	4,63253E-11	225681_at	CTHRC1	1,827041696	7,96876E-11
201291_s_at	TOP2A	2,252354398	3,36333E-14	218039_at	NUSAP1	1,822330276	3,39869E-13
219918_s_at	ASPM	2,252036353	1,08619E-14	210056_at	RND1	1,822146265	1,22821E-10
210387_at	HIST1H2BC	2,251109143	8,33011E-15	211719_x_at	FN1	1,818748589	1,43724E-11
236044_at	PPAPDC1A	2,244385021	2,01678E-15	205483_s_at	ISG15	1,813473744	9,45422E-11
202095_s_at	BIRC5	2,230270207	1,52308E-13	236641_at	KIF14	1,808116298	3,35404E-14
226067_at	BPIFB1	2,220650132	7,68747E-10	228010_at	PPP2R2C	1,807147464	7,30829E-11
203108_at	GPRC5A	2,219845826	1,68584E-14	205306_x_at	KMO	1,791871749	6,72464E-05
212353_at	SULF1	2,21334287	9,94471E-24	214710_s_at	CCNB1	1,785446865	2,06862E-14
1555758_a_at	CDKN3	2,199554453	4,49472E-09	220651_s_at	MCM10	1,783252945	3,16386E-11
211657_at	CEACAM6	2,184583901	1,12581E-07	218585_s_at	DTL	1,777749195	7,61696E-12
204533_at	CXCL10	2,149492129	6,95915E-11	215145_s_at	CNTNAP2	1,777557745	6,23255E-10
209875_s_at	SPP1	2,142581182	1,23365E-09	205034_at	CCNE2	1,770262677	9,27919E-18
201890_at	RRM2	2,140060721	6,47029E-13	206796_at	WISP1	1,76193897	4,39027E-19
204913_s_at	SOX11	2,118758032	2,05084E-06	206224_at	CST1	1,758907563	1,25676E-09
210052_s_at	TPX2	2,094178911	3,27163E-17	226086_at	SYT13	1,752499795	3,23935E-08
214455_at	HIST1H2BC	2,077059507	1,07742E-11	208079_s_at	AURKA	1,747830096	8,22379E-16
212942_s_at	KIAA1199	2,048116007	1,32834E-10	219463_at	LAMP5	1,744715322	2,098E-10
219148_at	PBK	2,037724353	3,39338E-10	202856_s_at	SLC16A3	1,732933933	1,64095E-09
212354_at	SULF1	2,036514152	1,3187E-20	204415_at	IFI6	1,732654066	1,34866E-09
231766_s_at	COL12A1	2,02609761	2,18292E-15	203755_at	BUB1B	1,731277273	2,03076E-12
202954_at	UBE2C	2,018018115	3,88806E-17	236496_at	DEGS2	1,720755556	2,00276E-07
203214_x_at	CDK1	2,006608992	1,08204E-10	204962_s_at	C2orf18	1,71642151	9,34991E-14
202503_s_at	KIAA0101	2,002855803	8,47772E-13	216950_s_at	FCGR1A	1,715215212	1,92515E-07
203915_at	CXCL9	1,998782868	5,00754E-07	207828_s_at	CENPF	1,705315731	2,97985E-19
201292_at	TOP2A	1,99811998	1,1906E-15	218755_at	KIF20A	1,703042342	2,95361E-12
203936_s_at	MMP9	1,997527749	5,04513E-08	214290_s_at	HIST2H2AA3	1,702085748	7,79251E-13

Table 2 ***(continued).*** Breast cancer.

Probe_id	Gene_ symbol	Difference	*p*_value	Probe_id	Gene_ symbol	Difference	*p*_value
209894_at	LEPR	-2,217984791	2,38439E-16	203549_s_at	LPL	-2,575013703	1,31828E-14
205157_s_at	JUP	-2,225112511	3,93916E-11	228653_at	SAMD5	-2,580359759	6,50063E-18
228335_at	CLDN11	-2,239180865	1,83335E-22	219059_s_at	LYVE1	-2,605699427	1,4764E-17
226407_at	TPT1-AS1	-2,24155011	5,8157E-11	207175_at	ADIPOQ	-2,607162832	1,60851E-12
205392_s_at	CCL14	-2,258665442	1,26594E-15	205200_at	CLEC3B	-2,636814972	3,22337E-16
212236_x_at	JUP	-2,259694247	1,31121E-10	213451_x_at	TNXA	-2,640599518	2,63276E-20
209291_at	ID4	-2,275045415	5,67809E-17	238018_at	FAM150B	-2,652929544	6,41502E-14
230425_at	EPHB1	-2,282166914	9,57439E-16	203980_at	FABP4	-2,663230402	1,4017E-20
204731_at	TGFBR3	-2,289841956	6,85626E-18	201820_at	KRT5	-2,671600401	2,48838E-16
229302_at	TMEM178A	-2,297818507	1,44891E-13	203548_s_at	LPL	-2,679584625	9,57766E-12
229357_at	ADAMTS5	-2,298124898	1,10741E-24	214063_s_at	TF	-2,703541134	2,24626E-19
219564_at	KCNJ16	-2,300439624	5,46619E-09	205051_s_at	KIT	-2,716925194	7,76725E-17
206488_s_at	CD36	-2,306734157	6,49796E-11	216918_s_at	DST	-2,726875186	6,00489E-18
209842_at	SOX10	-2,311405967	4,43401E-16	204719_at	ABCA8	-2,7480831	2,47675E-22
208607_s_at	SAA1	-2,312930599	1,49976E-11	216333_x_at	TNXA	-2,753037157	8,26243E-20
228885_at	MAMDC2	-2,318251054	7,07753E-26	243140_at	ACTA2	-2,757873449	7,70834E-17
235355_at	CSRNP3	-2,319141906	6,25237E-12	206742_at	FIGF	-2,76348925	2,45565E-20
206262_at	ADH1C	-2,330959065	1,67477E-22	231535_x_at	ROPN1	-2,780242452	1,20514E-13
206453_s_at	NDRG2	-2,337539622	1,86426E-16	209774_x_at	CXCL2	-2,805890709	7,68737E-22
211726_s_at	FMO2	-2,342106268	7,72705E-18	213456_at	SOSTDC1	-2,816272526	3,1718E-14
202035_s_at	SFRP1	-2,348675451	2,74655E-11	209763_at	CHRDL1	-2,826022147	1,45822E-26
211737_x_at	LOC100287705	-2,368395928	5,48631E-12	238750_at	CCL28	-2,858873419	7,47209E-17
213844_at	HOXA5	-2,371567555	1,85103E-19	212768_s_at	OLFM4	-2,864030422	3,42845E-12
218730_s_at	OGN	-2,374341246	6,99659E-17	214680_at	NTRK2	-2,879170704	2,27717E-16
207092_at	LEP	-2,377553066	1,62505E-09	205363_at	BBOX1	-2,882849103	4,95127E-13
219795_at	SLC6A14	-2,397453526	1,93673E-10	205913_at	PLIN1	-2,895294612	6,32882E-12
209292_at	ID4	-2,398051087	4,79257E-19	224027_at	CCL28	-2,912886905	2,82905E-15
209560_s_at	DLK1	-2,402372437	3,3461E-07	204734_at	KRT15	-2,930081829	5,42243E-15
202018_s_at	LTF	-2,408423045	6,54605E-10	214598_at	CLDN8	-2,945193765	1,87705E-16
220037_s_at	LYVE1	-2,422516156	7,10837E-12	224191_x_at	ROPN1	-2,983293931	4,74072E-13
219935_at	ADAMTS5	-2,426656258	6,95808E-25	209686_at	S100B	-2,990610465	1,80994E-19
220624_s_at	ELF5	-2,441430583	1,54509E-07	220625_s_at	ELF5	-3,065690985	7,62804E-14
209283_at	CRYAB	-2,460133183	9,48275E-23	235849_at	SCARA5	-3,079023468	2,08808E-26
204712_at	WIF1	-2,460276231	1,51126E-08	203400_s_at	TF	-3,113478302	3,91645E-19
203881_s_at	DMD	-2,466618803	1,66381E-24	212730_at	SYNM	-3,148288897	4,85517E-20
228268_at	FMO2	-2,467600452	1,98296E-23	221795_at	NTRK2	-3,15172949	5,70236E-25
202768_at	FOSB	-2,468135916	1,13597E-11	209612_s_at	ADH1B	-3,197934581	5,73752E-21
206093_x_at	TNXA	-2,48220164	4,75308E-21	209613_s_at	ADH1B	-3,206365305	5,15731E-24
226625_at	TGFBR3	-2,501238083	2,91828E-22	221796_at	NTRK2	-3,209973936	5,18555E-21
1552848_a_at	PTCHD1	-2,502828915	1,87363E-12	209351_at	KRT14	-3,228881534	1,41525E-16
205382_s_at	CFD	-2,524541325	9,77015E-15	202036_s_at	SFRP1	-3,237863411	1,97932E-17
205030_at	FABP7	-2,529024595	3,79269E-11	223623_at	C2orf40	-3,245317139	7,51388E-24
222722_at	OGN	-2,529628699	8,74418E-18	202037_s_at	SFRP1	-3,293776038	6,66779E-19
208350_at	CSN1S1	-2,532354401	0,000265011	206825_at	OXTR	-3,329368596	1,27066E-18
203434_s_at	MME	-2,535153648	2,57193E-20	205044_at	GABRP	-3,42264444	1,55785E-18
201497_x_at	MYH11	-2,542673309	2,00643E-20	220425_x_at	ROPN1B	-3,454549443	2,93802E-14
202274_at	ACTG2	-2,545650001	9,13948E-19	226147_s_at	PIGR	-3,545733612	1,37271E-17
222717_at	SDPR	-2,546682497	4,08845E-30	204455_at	DST	-3,548971424	2,5025E-23
1552509_a_at	CD300LG	-2,553294761	1,74399E-24	229839_at	SCARA5	-3,648275765	1,33793E-28
228766_at	CD36	-2,561838915	1,2979E-15	230378_at	SCGB3A1	-3,970248307	1,06993E-14

Table 2. Brain tumor.

Probe_id	Gene_ symbol	Difference	*p*_value	Probe_id	Gene_ symbol	Difference	*p*_value
201292_at	TOP2A	4,309558752	2,33726E-21	227462_at	ERAP2	2,757377769	1,51052E-16
201890_at	RRM2	4,151972295	1,14982E-19	211571_s_at	VCAN	2,75138539	2,06031E-14
210809_s_at	POSTN	3,997009044	2,99833E-09	204619_s_at	VCAN	2,738781323	1,67219E-09
219148_at	PBK	3,877040484	1,17136E-19	213258_at	TFPI	2,735165662	1,7759E-09
201291_s_at	TOP2A	3,769310892	2,19208E-18	201852_x_at	COL3A1	2,732029115	1,65805E-09
219918_s_at	ASPM	3,67741936	9,79653E-19	201860_s_at	PLAT	2,720561587	9,52207E-14
224588_at	XIST	3,566477479	6,38625E-09	203358_s_at	EZH2	2,700366935	3,42087E-14
225681_at	CTHRC1	3,524572501	2,59254E-19	202404_s_at	COL1A2	2,683399434	2,82615E-10
205347_s_at	TMSB15A	3,490152234	3,21196E-15	209395_at	CHI3L1	2,673222817	1,59698E-05
225655_at	UHRF1	3,463692783	5,66157E-13	209651_at	TGFB1I1	2,671600653	2,64134E-13
203854_at	CFI	3,437384018	2,48572E-12	202095_s_at	BIRC5	2,667993708	3,05965E-15
1569110_x_at	LOC728613	3,433895399	1,09252E-06	209309_at	AZGP1	2,663141674	9,40272E-11
1555564_a_at	CFI	3,380226366	6,0676E-15	227812_at	TNFRSF19	2,655694476	1,4879E-14
206157_at	PTX3	3,308730186	5,40691E-15	204444_at	KIF11	2,645036966	9,24229E-19
202503_s_at	KIAA0101	3,296831613	1,63166E-11	218755_at	KIF20A	2,634839229	2,18986E-14
203989_x_at	F2R	3,277767557	2,43572E-16	224428_s_at	CDCA7	2,626965054	2,00251E-13
221728_x_at	XIST	3,250429613	1,3851E-09	214297_at	CSPG4	2,625258344	4,39688E-17
224590_at	XIST	3,248717977	1,14044E-09	206785_s_at	KLRC1	2,624086411	2,48809E-07
215646_s_at	VCAN	3,224654225	1,42996E-13	209642_at	BUB1	2,6234951	2,00794E-14
212533_at	WEE1	3,18339259	7,40376E-10	228323_at	CASC5	2,615244286	2,33846E-17
217999_s_at	PHLDA1	3,166659834	3,13368E-15	219895_at	FAM70A	2,60788527	2,13724E-07
243483_at	TRPM8	3,162538042	1,03031E-12	225647_s_at	CTSC	2,599954781	7,33012E-11
218039_at	NUSAP1	3,149401276	1,45031E-16	242907_at	GBP2	2,599908587	1,74985E-10
211161_s_at	COL3A1	3,130066097	1,551E-08	213975_s_at	LYZ	2,595084675	1,47615E-10
219410_at	TMEM45A	3,116889935	4,26351E-11	205227_at	IL1RAP	2,594340233	2,29484E-19
238852_at	PRRX1	3,096802857	3,41287E-09	206432_at	HAS2	2,584899008	6,37492E-18
204162_at	NDC80	3,092003697	6,38812E-16	219010_at	C1orf106	2,574460037	4,03436E-10
203820_s_at	IGF2BP3	3,027750832	3,59286E-13	205499_at	SRPX2	2,571495372	1,76815E-15
203764_at	DLGAP5	3,02446715	6,90606E-17	228347_at	SIX1	2,567692146	6,98699E-13
223381_at	NUF2	3,018949636	2,58049E-16	213790_at	ADAM12	2,564878225	2,28622E-15
238021_s_at	CRNDE	2,996001805	0,000358944	222848_at	CENPK	2,55494462	2,68801E-12
236641_at	KIF14	2,969330367	1,44429E-15	218355_at	KIF4A	2,54245952	3,63328E-15
224997_x_at	H19	2,957398181	4,00387E-14	201666_at	TIMP1	2,541445737	5,05742E-08
209773_s_at	RRM2	2,954584867	8,55993E-14	209109_s_at	TSPAN6	2,541378036	1,09062E-10
230964_at	FREM2	2,937550981	2,64166E-11	224646_x_at	H19	2,536113947	1,61927E-08
203213_at	CDK1	2,930221351	2,15779E-15	209172_s_at	CENPF	2,528636603	1,60412E-13
218542_at	CEP55	2,915532817	2,16964E-14	204620_s_at	VCAN	2,52086059	6,72906E-12
227671_at	XIST	2,908753167	6,08132E-09	203755_at	BUB1B	2,519438948	4,56283E-15
1552365_at	SCIN	2,905261276	4,59608E-08	215076_s_at	COL3A1	2,516910028	2,72003E-08
1555778_a_at	POSTN	2,90491439	3,22314E-10	202705_at	CCNB2	2,516744047	4,27022E-16
218585_s_at	DTL	2,900995114	2,19583E-14	207828_s_at	CENPF	2,513739113	1,42917E-12
214218_s_at	XIST	2,886527253	5,92765E-09	206364_at	KIF14	2,507342634	5,38671E-16
230372_at	HAS2	2,861479305	2,73036E-12	202376_at	SERPINA3	2,502506123	0,000239913
202589_at	TYMS	2,844334955	1,9433E-11	203819_s_at	IGF2BP3	2,500013455	5,80402E-10
226777_at	ADAM12	2,816551429	8,63466E-15	204159_at	CDKN2C	2,493740421	2,76018E-08
221898_at	PDPN	2,815458672	4,63052E-12	224973_at	FAM46A	2,487332052	6,6525E-08
218883_s_at	MLF1IP	2,804024968	6,71664E-16	202718_at	IGFBP2	2,487035806	3,35135E-10
210559_s_at	CDK1	2,793564716	5,35662E-16	209396_s_at	CHI3L1	2,486314708	0,000101178
204822_at	TTK	2,781755309	2,18666E-16	222680_s_at	DTL	2,478336899	1,3988E-11
205114_s_at	CCL3	2,761052237	7,75343E-12	204825_at	MELK	2,475056733	1,61102E-15

Table 2 ***(continued).*** Brain cancer.

Probe_id	Gene_ symbol	Difference	*p*_value
230923_at	FAM19A1	-3,627857783	0,00064031
204722_at	SCN3B	-3,631378738	2,62201E-07
205814_at	GRM3	-3,637318614	1,91414E-16
1569969_a_at	UNC13C	-3,641507447	8,17755E-06
227702_at	CYP4X1	-3,649929982	7,92062E-15
206349_at	LGI1	-3,653230378	2,54059E-17
206731_at	CNKSR2	-3,666359144	9,12878E-06
37566_at	KIAA1045	-3,672385365	3,29907E-07
235225_at	SCN2B	-3,677372422	7,11709E-14
1557181_s_at	C11orf87	-3,6774567	1,02124E-06
214961_at	MTUS2	-3,69746316	1,99519E-10
214120_at	RFPL1-AS1	-3,707908549	1,29698E-09
230117_at	VSTM2A	-3,71082817	9,46678E-05
225792_at	HOOK1	-3,715950087	1,80326E-09
214230_at	CDC42	-3,71670448	1,72034E-13
229029_at	CAMK4	-3,727803904	1,53903E-07
228509_at	SPHKAP	-3,733840853	4,53755E-11
212732_at	MEG3	-3,735050866	1,19188E-10
236081_at	SNCA	-3,747361529	3,97331E-10
220030_at	STYK1	-3,754588424	6,26656E-05
205827_at	CCK	-3,79070334	0,000268738
242002_at	NKAIN2	-3,844437785	2,48692E-18
241833_at	PEX5L	-3,847103514	2,47174E-07
230698_at	CALN1	-3,858927394	1,7429E-14
203000_at	STMN2	-3,865192259	5,07669E-18
1554524_a_at	OLFM3	-3,874751539	1,7593E-12
206280_at	CDH18	-3,877538061	4,612E-17
204465_s_at	INA	-3,888236229	4,24867E-24
219671_at	HPCAL4	-3,895627713	1,00163E-12
243681_at	SHANK2	-3,916074512	7,36172E-10
220551_at	SLC17A6	-3,91710435	3,093E-05
229300_at	RAB3C	-3,922963894	7,38055E-19
205336_at	PVALB	-3,923812283	2,6456E-07
229039_at	SYN2	-3,933466955	5,26847E-11
244111_at	KRT222	-3,933700817	4,48096E-19
235781_at	CACNA1B	-3,947924733	1,38892E-19
229254_at	MFSD4	-3,95703133	2,21033E-09
239357_at	ATP2B2	-3,961263651	9,96095E-14
223654_s_at	CELF4	-3,968709521	5,46261E-23
233002_at	PPP4R4	-3,977311646	1,5201E-07
210675_s_at	PTPRR	-3,999013519	2,89592E-08
236308_at	VSTM2A	-4,008935928	3,62301E-05
233437_at	GABRA4	-4,021908113	5,00121E-06
207014_at	GABRA2	-4,027130762	1,46706E-09
213558_at	PCLO	-4,042076171	1,06158E-13
230765_at	KIAA1239	-4,088184451	1,03361E-05
229818_at	SVOP	-4,098378395	3,75728E-10
221217_s_at	RBFOX1	-4,110143446	1,07131E-13
214956_at	AAK1	-4,130313309	2,37032E-12
206084_at	PTPRR	-4,170783382	5,14915E-10
1556095_at	UNC13C	-4,182980615	1,05685E-06
223529_at	SYT4	-4,210865817	8,40363E-18
223500_at	CPLX1	-4,233495644	4,66986E-26
241805_at	GABRG1	-4,267434466	6,97471E-25
242286_at	GRIN2A	-4,278977859	4,54888E-08
221801_x_at	NEFL	-4,279538895	8,85252E-13
231220_at	CELF4	-4,280014029	6,04897E-26
203999_at	SYT1	-4,300275385	4,17234E-18
229294_at	JPH3	-4,302469419	6,92383E-16
1553864_at	GPR26	-4,307230435	4,90226E-06
226086_at	SYT13	-4,333136653	1,46699E-17
238966_at	CELF4	-4,357778876	2,31107E-20
220359_s_at	ARPP21	-4,375613946	3,50097E-05
206552_s_at	TAC1	-4,377588617	1,23496E-07
231384_at	GRIN2A	-4,377940912	2,78403E-09
232010_at	FSTL5	-4,399112335	6,34632E-11
1554526_at	OLFM3	-4,416626899	1,18566E-08
203001_s_at	STMN2	-4,418301994	3,24624E-20
229406_at	RBFOX3	-4,423876297	2,09799E-07
213921_at	SST	-4,452556098	3,36468E-05
233059_at	KCNJ3	-4,453981095	1,46867E-08
243998_at	KRT222	-4,460249699	1,08862E-13
206678_at	GABRA1	-4,501521862	5,23314E-09
1557122_s_at	GABRB2	-4,553500957	4,25253E-11
213920_at	CUX2	-4,558512967	5,89446E-08
203998_s_at	SYT1	-4,646522044	3,79006E-13
205113_at	NEFM	-4,649652208	1,4699E-19
228010_at	PPP2R2C	-4,71884079	7,54768E-18
207768_at	EGR4	-4,757448645	3,21742E-06
210016_at	MYT1L	-4,790033873	2,60774E-12
1556351_at	HCN1	-4,819910171	3,49359E-08
235066_at	MAP4	-4,833455102	1,65265E-20
205551_at	SV2B	-4,840499212	1,69966E-16
227053_at	PACSIN1	-4,863068777	1,31169E-17
221916_at	NEFL	-4,874330838	1,87425E-17
235468_at	RBFOX3	-4,895638512	7,77445E-09
203797_at	VSNL1	-4,944950118	8,91937E-22
224650_at	MAL2	-5,009125644	2,35924E-07
221008_s_at	AGXT2L1	-5,010853156	1,75767E-16
205625_s_at	CALB1	-5,029857338	4,59447E-18
210040_at	SLC12A5	-5,179351699	1,86964E-28
1556096_s_at	UNC13C	-5,200470357	7,67278E-14
242344_at	GABRB2	-5,211577365	9,65746E-10
230303_at	SYNPR	-5,418324833	1,37591E-23
205626_s_at	CALB1	-5,542360794	4,17939E-17
244118_at	GABRA1	-5,578879447	1,18766E-09
203798_s_at	VSNL1	-5,611641092	2,76492E-11
231771_at	GJB6	-5,616559419	1,56768E-18
221805_at	NEFL	-5,722790342	1,81959E-19
1568612_at	GABRG2	-5,809988311	2,82066E-22

Table 2. Prostate cancer.

Probe_id	Gene_ symbol	Difference	*p*_value	Probe_id	Gene_ symbol	Difference	*p*_value
207802_at	CRISP3	4,468144042	9,3204E-08	236302_at	PPM1E	1,774344765	0,000608299
206858_s_at	HOXC6	3,777657931	2,74718E-11	242260_at	MATR3	1,767085189	2,89379E-08
209424_s_at	AMACR	3,705801513	9,33342E-10	214614_at	MNX1	1,761447976	1,02385E-06
209426_s_at	AMACR	3,601558906	7,55177E-11	229599_at	LOC440335	1,753634449	4,07066E-07
232575_at	PCA3	3,596309778	1,57413E-10	205505_at	GCNT1	1,720371	2,62504E-06
242138_at	DLX1	3,438457204	9,24016E-11	220541_at	MMP26	1,719410558	0,00018754
221424_s_at	OR51E2	3,29585253	0,000294557	1557207_s_at	LOC283177	1,718342585	4,52722E-06
209425_at	AMACR	3,176559324	3,23658E-10	204714_s_at	F5	1,696945951	2,52517E-05
232482_at	OR51E2	3,082011639	1,27764E-05	1552742_at	KCNH8	1,696799283	2,98201E-05
217111_at	AMACR	3,019148584	3,0264E-06	232572_at	PCA3	1,690434493	0,000309583
223642_at	ZIC2	2,940221311	1,20248E-05	204962_s_at	C2orf18	1,688040985	0,00011611
206502_s_at	INSM1	2,931013008	2,48387E-07	229302_at	TMEM178A	1,685812682	0,000166216
215432_at	ACSM1	2,740165231	1,54325E-06	226433_at	RNF157	1,68577808	1,46721E-09
233586_s_at	KLK12	2,70781492	1,98285E-05	204305_at	MIPEP	1,684964845	0,000556147
206307_s_at	FOXD1	2,681051534	1,50869E-09	207828_s_at	CENPF	1,67526192	0,000105937
224355_s_at	MS4A8B	2,664867234	7,3771E-08	222774_s_at	NETO2	1,67187489	2,76991E-07
214774_x_at	TOX3	2,561334759	2,8009E-06	36830_at	MIPEP	1,666456488	0,000889946
220782_x_at	KLK12	2,511372872	4,1136E-05	203358_s_at	EZH2	1,665329688	3,77802E-05
204623_at	TFF3	2,503847066	1,40418E-05	210108_at	CACNA1D	1,659407687	4,26551E-06
234316_x_at	KLK12	2,494082585	2,02646E-05	202095_s_at	BIRC5	1,657304313	4,27415E-05
215108_x_at	TOX3	2,469121219	1,98476E-06	202954_at	UBE2C	1,651630704	0,000363665
207147_at	DLX2	2,461539141	1,53304E-06	209714_s_at	CDKN3	1,6439399	1,20548E-05
206558_at	SIM2	2,461106461	0,000648876	203554_x_at	PTTG1	1,642325581	0,00020832
216623_x_at	TOX3	2,425916595	1,38063E-06	203213_at	CDK1	1,622429475	0,000301172
236365_at	AMACR	2,420325467	1,68124E-09	218834_s_at	TMEM132A	1,619740278	2,94975E-06
221577_x_at	GDF15	2,40293541	2,09998E-05	204825_at	MELK	1,616839969	0,000845736
201890_at	RRM2	2,363037762	8,63655E-07	201416_at	SOX4	1,612972653	2,12532E-05
204934_s_at	HPN	2,337938722	2,46476E-05	233477_at	KLK15	1,611901888	3,18359E-05
206194_at	HOXC4	2,301927962	2,76514E-11	1559276_at	LOC728606	1,588736012	0,000904552
1552897_a_at	KCNG3	2,227100868	5,412E-07	219773_at	NOX4	1,587798307	1,00768E-07
201291_s_at	TOP2A	2,196554107	0,000109538	221558_s_at	LEF1	1,585953113	3,22619E-06
232381_s_at	DNAH5	2,125199294	0,000350336	211626_x_at	ERG	1,576437755	4,27763E-05
218039_at	NUSAP1	2,109464221	2,92248E-05	205347_s_at	TMSB15A	1,575010767	8,35806E-06
218835_at	SFTPA1	2,105187456	1,03054E-06	219787_s_at	ECT2	1,569261262	6,12483E-05
201292_at	TOP2A	2,039013699	0,00020998	216803_at	PDLIM5	1,568190579	1,35843E-07
225681_at	CTHRC1	2,035312844	2,25279E-06	1557900_at	SIM2	1,562244129	0,000319203
213541_s_at	ERG	1,995330904	0,000209984	231558_at	INSM1	1,547230962	0,000801204
228260_at	ELAVL2	1,99028778	2,54284E-06	204713_s_at	F5	1,543535372	4,04569E-05
209773_s_at	RRM2	1,921827799	0,000204069	206951_at	HIST1H4A	1,53637025	3,21932E-06
207165_at	HMMR	1,888637607	5,33811E-05	215599_at	GUSBP3	1,532185872	0,00029401
225655_at	UHRF1	1,863465426	0,000172243	240303_at	TMC5	1,531336754	9,45284E-05
214596_at	CHRM3	1,851925701	1,47537E-06	1559633_a_at	CHRM3	1,528468203	1,75856E-05
213601_at	ARHGAP19	1,845884502	5,91433E-07	209875_s_at	SPP1	1,523668992	0,000711498
242488_at	CHRM3	1,841065997	1,25831E-05	201839_s_at	EPCAM	1,51834467	3,46102E-08
218888_s_at	NETO2	1,821177922	3,39885E-06	239911_at	ONECUT2	1,512494249	0,000435627
220245_at	SLC45A2	1,798897744	7,49399E-06	1553705_a_at	CHRM3	1,510970784	2,35632E-07
219659_at	ATP8A2	1,798800161	2,19923E-06	204942_s_at	ALDH3B2	1,500225746	1,55066E-05
219918_s_at	ASPM	1,780552646	9,80335E-05	244885_at	EBF2	1,491555524	3,7265E-06
213943_at	TWIST1	1,777559817	3,76618E-05	213622_at	COL9A2	1,488918387	0,000836857
218755_at	KIF20A	1,777521418	0,000130604	32128_at	CCL18	1,488597471	7,85116E-05

Table 2 *(continued)*. Prostate cancer.

Probe_id	Gene_ symbol	Difference	*p*_value	Probe_id	Gene_ symbol	Difference	*p*_value
1569956_at	MYLK	-1,772719701	8,02797E-06	211748_x_at	PTGDS	-2,101799411	0,000124724
203295_s_at	ATP1A2	-1,778269384	3,12432E-06	204083_s_at	TPM2	-2,113401635	0,0002614
205743_at	STAC	-1,783042868	7,95153E-05	203296_s_at	ATP1A2	-2,113577137	3,7709E-05
210471_s_at	KCNAB1	-1,791511963	1,3645E-05	212187_x_at	PTGDS	-2,12318245	0,000116317
219936_s_at	GPR87	-1,792722794	5,48627E-06	225721_at	SYNPO2	-2,127430582	1,4812E-05
238669_at	PTGS1	-1,796478015	0,000483262	206032_at	DSC3	-2,154355645	1,59864E-07
209948_at	KCNMB1	-1,802276592	0,000130207	204041_at	MAOB	-2,158290648	0,00012875
230378_at	SCGB3A1	-1,803457555	3,22754E-06	1566968_at	SPRY4-IT1	-2,162265354	6,85776E-06
228236_at	SLC52A3	-1,814765762	1,61571E-05	239237_at	LOC100506776	-2,168653586	0,000974358
227006_at	PPP1R14A	-1,818463429	2,36401E-05	205157_s_at	JUP	-2,180714152	0,000348749
213371_at	LDB3	-1,831257096	1,1367E-05	206434_at	SPOCK3	-2,185242817	0,000318126
227971_at	NRK	-1,831276349	4,40283E-05	236681_at	HOXD13	-2,187782432	4,15316E-08
205609_at	ANGPT1	-1,835701971	3,6697E-05	205132_at	ACTC1	-2,202219879	0,000926667
225720_at	SYNPO2	-1,835744235	0,000238619	203435_s_at	MME	-2,239990476	2,74116E-05
227909_at	LINC00086	-1,841268869	3,44058E-09	209616_s_at	CES1	-2,258720881	4,93007E-05
226755_at	MIR205HG	-1,843019715	0,00022432	204457_s_at	GAS1	-2,261104987	1,04928E-06
209863_s_at	TP63	-1,852007529	7,62973E-06	201495_x_at	MYH11	-2,283066285	0,00017974
227475_at	FOXQ1	-1,855615067	1,51468E-06	201497_x_at	MYH11	-2,2899044	0,000384514
229339_at	MYOCD	-1,860074638	2,19798E-05	205765_at	CYP3A5	-2,30081058	4,85864E-06
203065_s_at	CAV1	-1,865752637	1,04677E-08	242525_at	SLC2A5	-2,305520596	4,40477E-06
227742_at	CLIC6	-1,868072721	5,58745E-05	232332_at	KIAA1210	-2,311496403	2,29713E-06
228218_at	LSAMP	-1,868109462	2,59086E-05	203766_s_at	LMOD1	-2,345417636	0,000105228
219597_s_at	DUOX1	-1,876241614	5,58839E-06	219478_at	WFDC1	-2,349907622	8,28198E-05
243672_at	SALL3	-1,877153984	0,000224437	202888_s_at	ANPEP	-2,365985892	0,000646701
207397_s_at	HOXD13	-1,879537107	4,02273E-06	202504_at	TRIM29	-2,370699837	1,09307E-05
218963_s_at	KRT23	-1,883755215	0,000177073	214027_x_at	DES	-2,389330089	6,73497E-05
214235_at	CYP3A5	-1,887721228	1,74733E-06	205083_at	AOX1	-2,393937804	4,14961E-06
209541_at	IGF1	-1,887745836	0,000425299	235342_at	SPOCK3	-2,402253933	3,43935E-05
225895_at	SYNPO2	-1,893784446	0,000103634	223623_at	C2orf40	-2,408385729	6,61637E-06
228004_at	LINC00261	-1,895553348	0,00099653	205725_at	SCGB1A1	-2,411349196	9,74688E-05
208792_s_at	CLU	-1,9057372	1,34069E-05	202555_s_at	MYLK	-2,424961619	4,68547E-06
214234_s_at	CYP3A5	-1,907716427	3,94934E-06	218717_s_at	LEPREL1	-2,479352509	0,000114208
230238_at	SOWAHA	-1,918933309	4,9448E-06	201820_at	KRT5	-2,483944931	4,9381E-05
211562_s_at	LMOD1	-1,927078208	1,25099E-05	228133_s_at	MYH11	-2,494134258	7,04412E-05
208791_at	CLU	-1,935182737	4,7504E-06	204412_s_at	NEFH	-2,499300492	0,000381154
209540_at	IGF1	-1,944835551	0,00019593	202222_s_at	DES	-2,547021983	0,00025647
205827_at	CCK	-1,947832855	0,000432629	213791_at	PENK	-2,556190062	2,10068E-06
209570_s_at	D4S234E	-1,948051392	0,000223296	226303_at	PGM5	-2,561931539	3,31463E-05
1552511_a_at	CPA6	-1,982060178	9,98437E-07	207961_x_at	MYH11	-2,614153605	0,000319534
209763_at	CHRDL1	-1,984690234	0,00010699	201058_s_at	MYL9	-2,657509657	9,97478E-05
206116_s_at	TPM1	-1,987012436	3,22903E-07	230577_at	LOC100507008	-2,660205768	5,57175E-08
212236_x_at	JUP	-2,00152495	0,00071957	201496_x_at	MYH11	-2,721315368	5,84485E-05
225894_at	SYNPO2	-2,013628552	0,000411644	233059_at	KCNJ3	-2,722550431	0,000137854
203434_s_at	MME	-2,020340017	5,45648E-05	202274_at	ACTG2	-2,732641254	0,000432269
1568760_at	MYH11	-2,022302893	0,000226845	205856_at	SLC14A1	-2,776439023	9,27074E-07
243140_at	ACTA2	-2,03523556	0,000462116	203571_s_at	C10orf116	-2,790813531	2,21352E-05
204748_at	PTGS2	-2,042145273	0,000411948	230595_at	LOC100653336	-2,835824015	0,000130551
213992_at	COL4A6	-2,04988649	2,68417E-06	33767_at	NEFH	-3,082968256	0,000258118
206033_s_at	DSC3	-2,050780764	1,4972E-06	204430_s_at	SLC2A5	-3,131240595	3,12119E-06
205082_s_at	AOX1	-2,072728873	9,00496E-06	229151_at	SLC14A1	-3,29267308	4,19529E-06

Table 2. Liver cancer.

Probe_id	Gene_ symbol	Difference	*p*_value
209220_at	GPC3	5,078237186	1,19271E-33
212094_at	PEG10	4,55598478	3,05539E-24
201291_s_at	TOP2A	4,539458498	1,2769E-31
219918_s_at	ASPM	4,411495713	5,5262E-37
201292_at	TOP2A	4,050134515	8,47294E-36
204822_at	TTK	3,966737327	6,16711E-44
214710_s_at	CCNB1	3,833486562	4,67034E-44
222608_s_at	ANLN	3,826629551	4,0545E-36
201890_at	RRM2	3,811183118	9,18472E-24
206239_s_at	SPINK1	3,80180405	9,05978E-13
203213_at	CDK1	3,741080812	2,55489E-29
207165_at	HMMR	3,667927782	9,69977E-38
206102_at	GINS1	3,577221223	6,89129E-34
218585_s_at	DTL	3,518667424	1,63998E-27
218009_s_at	PRC1	3,51790688	8,83139E-35
209714_s_at	CDKN3	3,492603028	6,03862E-36
223381_at	NUF2	3,481466119	1,15729E-40
1555758_a_at	CDKN3	3,467445889	4,80559E-36
208079_s_at	AURKA	3,442999739	6,51534E-33
219787_s_at	ECT2	3,428545619	8,6602E-32
228273_at	PRR11	3,414401741	1,06531E-37
208650_s_at	CD24	3,371672061	1,73653E-16
238021_s_at	CRNDE	3,366351908	3,7396E-22
204162_at	NDC80	3,364322545	2,14506E-35
219148_at	PBK	3,297721269	2,07489E-33
222077_s_at	RACGAP1	3,289936526	1,74713E-31
202422_s_at	ACSL4	3,248170008	2,43991E-21
202095_s_at	BIRC5	3,134934458	5,45833E-34
218039_at	NUSAP1	3,118211844	1,3283E-23
225834_at	FAM72A	3,108417996	3,67356E-29
209773_s_at	RRM2	3,101233405	8,46836E-24
204641_at	NEK2	3,08076941	4,40856E-40
202870_s_at	CDC20	3,007683511	2,15834E-32
204026_s_at	ZWINT	2,981683072	1,67881E-22
211470_s_at	SULT1C2	2,968978121	1,37489E-18
203820_s_at	IGF2BP3	2,949206082	1,00087E-18
205034_at	CCNE2	2,947331095	1,77323E-31
202503_s_at	KIAA0101	2,944386484	3,30608E-25
205342_s_at	SULT1C2	2,917405333	1,42699E-20
218355_at	KIF4A	2,914950588	3,11844E-37
228729_at	CCNB1	2,898603395	4,85587E-40
205229_s_at	COCH	2,894346505	3,50619E-20
203477_at	COL15A1	2,889011084	3,92118E-22
232164_s_at	EPPK1	2,888527665	9,80866E-22
204092_s_at	AURKA	2,877011779	1,27318E-38
203764_at	DLGAP5	2,870804158	1,32764E-36
203967_at	CDC6	2,869424161	2,08871E-29
202705_at	CCNB2	2,864420107	1,3583E-36
205830_at	CLGN	2,858635786	5,77797E-17
218663_at	NCAPG	2,850718827	5,46408E-37
218662_s_at	NCAPG	2,848722512	8,03287E-34
225655_at	UHRF1	2,835251774	1,70183E-33
203362_s_at	MAD2L1	2,832501712	6,7195E-33
218883_s_at	MLF1IP	2,782297517	3,22384E-20
225612_s_at	B3GNT5	2,777824375	3,02521E-15
227350_at	HELLS	2,777366855	3,68304E-28
209642_at	BUB1	2,772606192	9,93788E-34
204444_at	KIF11	2,768766556	7,25979E-36
203755_at	BUB1B	2,745231855	1,56666E-32
204825_at	MELK	2,737138335	2,20686E-33
230165_at	SGOL2	2,732237451	2,35816E-37
204318_s_at	GTSE1	2,723847371	2,48212E-37
203819_s_at	IGF2BP3	2,689561002	3,98888E-17
219990_at	E2F8	2,674775281	7,00991E-32
225681_at	CTHRC1	2,653899631	2,71538E-15
207828_s_at	CENPF	2,650534109	5,45739E-38
224428_s_at	CDCA7	2,643233442	3,12112E-20
203358_s_at	EZH2	2,629085749	1,81728E-31
209035_at	MDK	2,622305615	1,20331E-30
202580_x_at	FOXM1	2,58804057	2,39511E-40
204709_s_at	KIF23	2,587103328	8,90013E-32
228338_at	C11orf93	2,586859426	1,11045E-28
225687_at	FAM83D	2,58317751	1,51264E-20
226936_at	CENPW	2,582018747	1,02721E-28
226980_at	DEPDC1B	2,577021452	1,58823E-31
209560_s_at	DLK1	2,569403371	1,71274E-07
204159_at	CDKN2C	2,563408991	2,6574E-21
212554_at	CAP2	2,558852951	1,27924E-30
232165_at	EPPK1	2,539678364	9,91276E-22
222848_at	CENPK	2,537033401	5,3094E-28
242881_x_at	LOC100506303	2,514690404	2,39718E-09
219978_s_at	NUSAP1	2,508978374	8,49311E-20
224367_at	BEX2	2,506374546	1,72619E-16
33323_r_at	SFN	2,503888108	1,5857E-17
223229_at	UBE2T	2,486754243	7,7387E-37
204962_s_at	C2orf18	2,483676559	4,29873E-33
204602_at	DKK1	2,45402368	1,47575E-10
232238_at	ASPM	2,452540489	1,70902E-26
228191_at	FLVCR1	2,449168086	9,40553E-30
236641_at	KIF14	2,444782851	1,49747E-33
205194_at	PSPH	2,438440525	7,37366E-31
218755_at	KIF20A	2,426445771	1,60284E-32
210052_s_at	TPX2	2,424459137	1,80819E-28
220085_at	HELLS	2,40848499	3,01504E-21
222906_at	FLVCR1	2,40512945	1,70309E-25
228494_at	PPP1R9A	2,393466262	4,62319E-19
203554_x_at	PTTG1	2,372991579	2,56428E-28
243243_at	GPC3	2,367251099	2,12773E-23
210559_s_at	CDK1	2,350434383	1,59139E-26
204146_at	RAD51AP1	2,34559161	7,97257E-31

Table 2 *(continued)*. Liver cancer.

Probe_id	Gene_symbol	Difference	*p*_value	Probe_id	Gene_symbol	Difference	*p*_value
204428_s_at	LCAT	-3,346522639	8,45226E-45	202992_at	C7	-3,743697862	2,83279E-29
209612_s_at	ADH1B	-3,368071814	5,25625E-21	212592_at	IGJ	-3,748223594	2,17653E-21
203131_at	PDGFRA	-3,376332677	2,21738E-22	207102_at	AKR1D1	-3,751329055	1,9787E-26
205307_s_at	KMO	-3,394502191	6,55122E-31	223784_at	TMEM27	-3,767071635	5,67262E-33
201893_x_at	DCN	-3,407026237	1,10186E-34	220116_at	KCNN2	-3,771038761	8,85548E-16
1564706_s_at	GLS2	-3,411045622	2,10459E-21	1568638_a_at	IDO2	-3,799117453	2,55445E-25
227794_at	GLYATL1	-3,437654383	3,22717E-27	232449_at	BCO2	-3,839749902	1,89369E-44
225575_at	LIFR	-3,457225824	5,99296E-29	207218_at	F9	-3,845865222	7,15828E-23
204745_x_at	MT1G	-3,464520916	2,85571E-31	223781_x_at	ADH4	-3,849412503	3,73147E-30
231683_at	GLYAT	-3,466401126	1,21596E-36	213629_x_at	MT1F	-3,859625686	6,95785E-34
206754_s_at	CYP2B6	-3,492928651	2,27507E-28	208147_s_at	CYP2C8	-3,871724622	5,65764E-25
207407_x_at	CYP4A11	-3,497596643	5,55159E-27	209975_at	CYP2E1	-3,906285634	1,02943E-16
219014_at	PLAC8	-3,499276861	8,85136E-27	225571_at	LIFR	-3,913624464	4,963E-24
210521_s_at	FETUB	-3,501625451	4,91049E-23	209540_at	IGF1	-3,932371893	1,59087E-32
208607_s_at	SAA1	-3,507753349	3,33896E-16	219954_s_at	GBA3	-3,941364731	1,93984E-34
206262_at	ADH1C	-3,512885489	1,51721E-23	233604_at	FLJ22763	-3,949963941	3,78994E-35
209335_at	DCN	-3,524828122	1,87401E-32	206354_at	SLCO1B3	-4,089958735	4,23181E-20
209687_at	CXCL12	-3,526003605	1,2063E-31	209541_at	IGF1	-4,097091741	6,37805E-32
205404_at	HSD11B1	-3,528411025	9,79705E-18	211896_s_at	DCN	-4,123556131	1,31431E-38
203372_s_at	SOCS2	-3,538930897	2,8047E-17	230577_at	LOC100507008	-4,21741057	2,194E-23
207584_at	LPA	-3,562274176	9,27768E-31	230135_at	HHIP	-4,230968246	1,12979E-30
229777_at	CLRN3	-3,565459546	6,68067E-25	222943_at	GBA3	-4,258364706	6,96472E-31
206755_at	CYP2B6	-3,575311884	1,23855E-30	206024_at	HPD	-4,27246004	2,45726E-22
217165_x_at	MT1F	-3,585838351	3,90667E-33	237350_at	TTC36	-4,387766265	2,0274E-50
1494_f_at	CYP2A6	-3,60352559	4,21339E-25	207201_s_at	SLC22A1	-4,40142701	1,92995E-28
207874_s_at	CFHR4	-3,607231683	1,25539E-24	229477_at	THRSP	-4,412287553	1,8827E-36
210481_s_at	CLEC4M	-3,607572736	9,22424E-24	206797_at	NAT2	-4,443604656	1,82904E-47
204704_s_at	ALDOB	-3,609432095	1,12159E-22	1559065_a_at	CLEC4G	-4,457805585	6,34539E-25
211430_s_at	IGHG1	-3,616234431	1,35205E-15	205984_at	CRHBP	-4,470508583	9,29315E-23
232494_at	CYP8B1	-3,618475455	1,09642E-20	223699_at	CNDP1	-4,47866209	1,50395E-28
206938_at	SRD5A2	-3,620797775	1,28593E-30	207262_at	APOF	-4,537151361	2,3198E-38
207995_s_at	CLEC4M	-3,639855633	7,25042E-19	207609_s_at	CYP1A2	-4,580199558	6,09599E-24
217022_s_at	IGH@	-3,641733385	9,72918E-21	209614_at	ADH1B	-4,584793542	1,42065E-31
209960_at	HGF	-3,646115246	2,97981E-31	214621_at	GYS2	-4,647526675	3,17626E-27
217319_x_at	CYP4A22	-3,662650151	1,81327E-29	220432_s_at	CYP39A1	-4,708910396	2,58903E-36
231691_at	C3P1	-3,664188666	6,7585E-32	209976_s_at	CYP2E1	-4,759595721	8,27975E-21
205531_s_at	GLS2	-3,667611853	7,55493E-28	220496_at	CLEC1B	-4,783708236	6,21211E-27
208367_x_at	CYP3A4	-3,679396394	1,85371E-26	1431_at	CYP2E1	-4,869745077	2,39367E-20
211813_x_at	DCN	-3,68142055	1,81204E-42	218002_s_at	CXCL14	-4,878525778	2,23826E-32
206424_at	CYP26A1	-3,689932212	2,81426E-20	230478_at	OIT3	-4,895190573	7,0638E-29
205554_s_at	DNASE1L3	-3,691394851	3,32578E-28	222484_s_at	CXCL14	-4,954599627	1,65775E-31
209613_s_at	ADH1B	-3,699411796	1,44856E-20	207804_s_at	FCN2	-4,96298454	1,24443E-25
208383_s_at	PCK1	-3,70525053	2,90424E-19	207608_x_at	CYP1A2	-5,014901708	1,61481E-31
205225_at	ESR1	-3,711611121	1,43587E-26	205866_at	FCN3	-5,028207698	8,1531E-33
222083_at	GLYAT	-3,723538297	1,46906E-31	229476_s_at	THRSP	-5,117142443	2,41557E-33
237765_at	SLC25A47	-3,729548678	2,04256E-32	217546_at	MT1M	-5,185665089	2,71478E-30
220801_s_at	HAO2	-3,730198946	1,73402E-28	220491_at	HAMP	-5,270593896	4,42725E-22
1568765_at	SERPINE1	-3,736654861	4,04875E-20	1559573_at	LOC100506229	-5,494882246	1,04602E-38
202238_s_at	NNMT	-3,740817029	2,29563E-26	231678_s_at	ADH4	-5,537836229	6,66784E-26
205999_x_at	CYP3A4	-3,743570764	4,91956E-26	206727_at	C9	-5,943731237	1,24251E-31

WGCNA ANALYSIS IDENTIFIES A UNIQUE MODULE OF CO-EXPRESSED GENES SHARED ACROSS ALL NINE TYPES OF SOLID CANCER

WGCNA was able to create 10 unique gene co-expression modules based on the gene expression patterns across all cancer samples and each module was assigned a color label. Among these modules, one module (the red module) was shown to positively correlate with all nine types of cancers (Figure 2A).

The red module, which contains over 100 genes, was significantly enriched for cell cycle related biological functions (Figure 2B). Some of the big ‘‘hub genes’’ in the red module were BIRC5, TPX2, CDK1, and MKI67 (Figure 2C). To validate the over-expression of these hub genes in cancer cells, we performed immunofluorescence staining on human pancreatic cancer specimens. The staining of BIRC5, TPX2, and CDK1 hub genes on pancreatic cancer specimens showed a significant over-expression of all three genes in both pancreatic intraepithelial neoplasia (PanIN) and metastatic pancreatic cancer cells (Figure 2D).

DISCUSSION

Cancer pathogenesis involves complex genetic interplay among aberrant signaling pathways leading to unregulated cell proliferation, invasion, and metastasis to other parts of the human body. This study's main focus was to establish a network of co-expressed genes and identify overexpressed gene modules common to all types of cancer in order to better understand the oncogenic mechanism. We hypothesize that understanding the shared overexpressed genetic markers among multiple cancers will enable discovery of actionable genes.

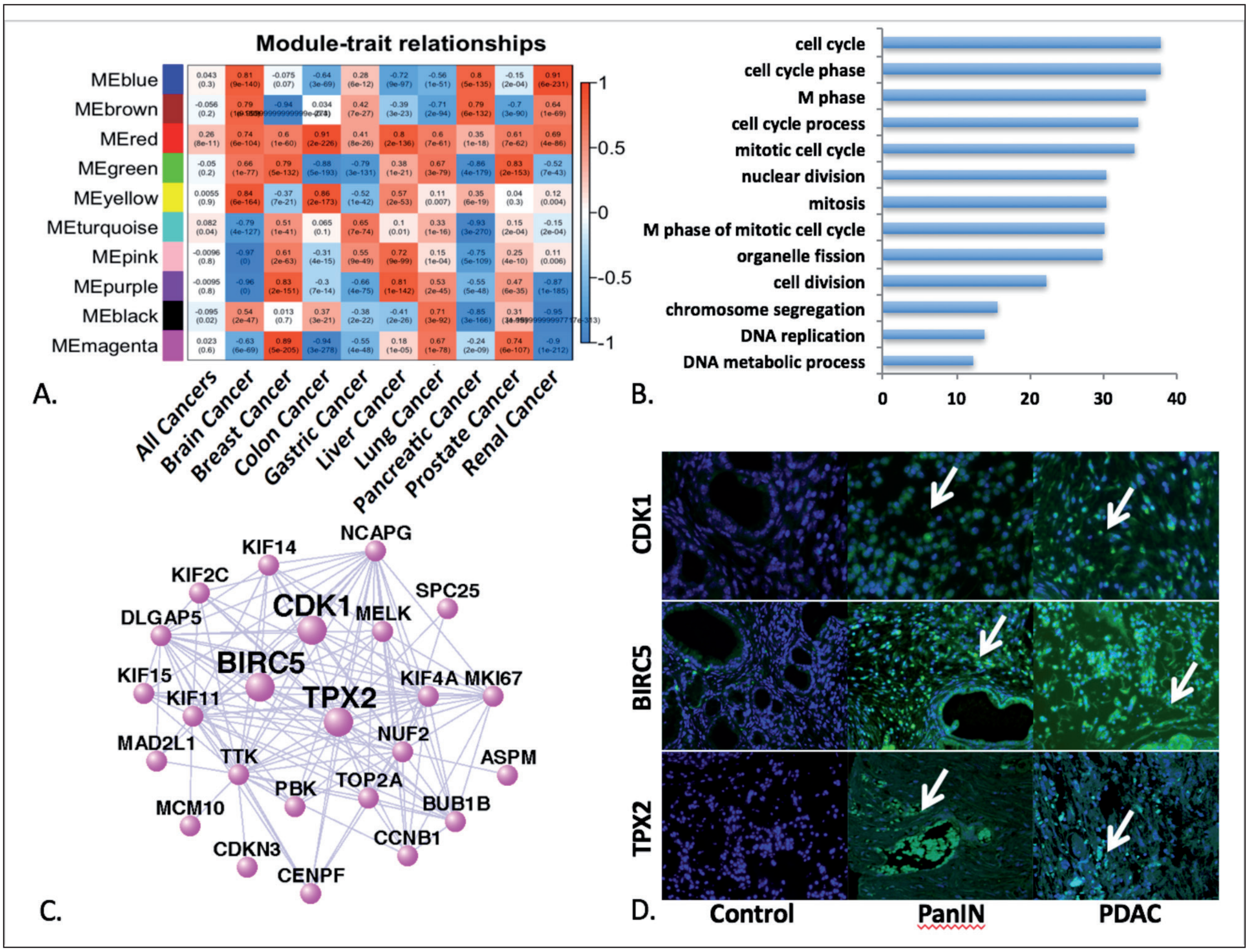
Conventional methods are capable of comparing gene expression profiles between cancer samples of a single type of cancer *vs.* its matching controls and identifying differentially expressed genes (DEGs), affected signaling pathways, and biological functions. However, these conventional methods have had-limited success in analyzing highly complicated large-scale data with multiple traits. Therefore, in this study, large-scale gene-expression microarray datasets were explored utilizing WGCNA since it has the ability to detect and study network topology of various shared modules and hub genes across microarray samples. This method has previously been used in other studies to detect and analyze gene modules and hub genes to establish a gene network within complex diseases[6].

Our study identified significantly overexpressed cell cycle related genes in all 9 types of cancer samples compared to their matching controls. The DEGs in the red module including BIRC5, TPX2, and CDK1 may be of great importance in all types of cancers, as they had high connectivity degrees within this module.

BIRC5, also known as Survivin, is a member of the inhibitor of apoptosis (IAP) gene family, which encodes negative regulatory proteins that prevent apoptotic cell death. It has been recognized to play dual roles in promoting cell proliferation and preventing apoptosis. It acts as an important regulator of the localization of the chromosome passage protein complex during mitosis and cytokinesis. Studies have demonstrated potential involvement of BIRC5 in multiple cancers. Furthermore, these studies have suggested that BIRC5 could potentially be utilized as a prognostic biomarker for both breast cancer[21] and pancreatic cancer[22], and inhibitors of BIRC5 have been studied as potential cancer treatments[23-27].

TPX2 is a microtubule-associated protein required for microtubule formation in human cells. Multiple studies have demonstrated that TPX2 is aberrantly overexpressed in multiple cancers, and it promotes tumor growth and metastasis potentially through activation and upregulation of different pathways, including the AKT pathway[28-30]. Furthermore, a strong correlation has been established between up-regulation of TPX2 and poor survival outcomes in different types of cancer, including gastric and pancreatic cancer[31,32]. It has been reported that treatment with TPX2-targeting small interfering RNAs effectively eliminated TPX2 overexpression and reduced cancer cell growth both *in vitro* and *in vivo*[33].

CDK1, which is encoded by the cdc2 gene, is a member of the protein kinase family, which plays a critical role in the control of the cell cycle by modulating the centrosome cycle as well as mitotic onset. It has been known to promote G2-M transition, regulate G1 progress, and promote G1-S transition via association with multiple interphase cyclins, and its overexpression has been demonstrated in multiple cancers. In fact, studies already have established CDK1 inhibitors, such as Purvalanol A, as potential adjuvant cancer treatment[34]. Furthermore, other members of the CDK family have also been shown to be involved in the oncogenesis of multiple cancers. Several other CDK inhibitors, including Abemaciclib and Ribociclib, are currently in clinical trials[35,36], and Palbociclib (CDK4 and 6 inhibitor) has already been approved for breast cancer treatment. In this study,



	All Cancers	Brain Cancer	Breast Cancer	Colon Cancer	Gastric Cancer	Liver Cancer	Lung Cancer	Pancreatic Cancer	Prostate Cancer	Renal Cancer
MEblue	0.043 (0.3)	0.81 (9e-140)	-0.075 (0.07)	-0.64 (3e-69)	0.28 (6e-12)	-0.72 (9e-97)	-0.56 (1e-51)	0.8 (5e-135)	-0.15 (2e-04)	0.91 (6e-231)
MEbrown	-0.056 (0.2)	0.79 [illegible]	-0.94 [illegible]	0.034 [illegible]	0.42 (7e-27)	-0.39 (3e-23)	-0.71 (2e-94)	0.79 (6e-132)	-0.7 (3e-90)	0.64 (1e-69)
MEred	0.26 (8e-11)	0.74 (6e-104)	0.6 (1e-60)	0.91 (2e-226)	0.41 (8e-26)	0.8 (2e-136)	0.6 (7e-61)	0.35 (1e-18)	0.61 (7e-62)	0.69 (4e-86)
MEgreen	-0.05 (0.2)	0.66 (1e-77)	0.79 (5e-132)	-0.88 (5e-193)	-0.79 (3e-131)	0.38 (1e-21)	0.67 (3e-79)	-0.86 (4e-179)	0.83 (2e-153)	-0.52 (7e-43)
MEyellow	0.0055 (0.9)	0.84 (6e-164)	-0.37 (7e-21)	0.86 (2e-173)	-0.52 (1e-42)	0.57 (2e-53)	0.11 (0.007)	0.35 (6e-19)	0.04 (0.3)	0.12 (0.004)
MEturquoise	0.082 (0.04)	-0.79 (4e-127)	0.51 (1e-41)	0.065 (0.1)	0.65 (7e-74)	0.1 (0.01)	0.33 (1e-16)	-0.93 (3e-270)	0.15 (2e-04)	-0.15 (2e-04)
MEpink	-0.0096 (0.8)	-0.97 (0)	0.61 (2e-63)	-0.31 (4e-15)	0.55 (9e-49)	0.72 (9e-99)	0.15 (1e-04)	-0.75 (5e-109)	0.25 (4e-10)	0.11 (0.006)
MEpurple	-0.0095 (0.8)	-0.96 (0)	0.83 (2e-151)	-0.3 (7e-14)	-0.66 (4e-75)	0.81 (1e-142)	0.53 (2e-45)	-0.55 (5e-48)	0.47 (6e-35)	-0.87 (1e-185)
MEblack	-0.095 (0.02)	0.54 (2e-47)	0.013 (0.7)	0.37 (3e-21)	-0.38 (2e-22)	-0.41 (2e-26)	0.71 (3e-92)	-0.85 (3e-166)	0.31 [illegible]	-0.95 [illegible]
MEmagenta	0.023 (0.6)	-0.63 (6e-69)	0.89 (5e-205)	-0.94 (3e-278)	-0.55 (4e-48)	0.18 (1e-05)	0.67 (1e-78)	-0.24 (2e-09)	0.74 (6e-107)	-0.9 (1e-212)

Figure 2. *A*, 10 unique gene co-expression modules. The Red module positively correlated with genes identified in all 9 studied cancers. *B,* The Red module contained over 100 genes related to cell cycle and function. *C,* BIRC5, CDK1, and TPX2 were identified as hub genes within the red module. *D,* Immunofluorescent staining of CDK1, BIRC5 and TPX2 show that hub genes were over-expressed in pancreatic cancer specimens.

we have confirmed the overexpression of the above cell cycle related genes (BIRC5, TPX2, and CDK1) using immunofluorescence staining on a panel of PanIN and metastatic pancreatic cancer cells. This result demonstrated a substantial overexpression of the above cell cycle related genes in both PanIN and metastatic pancreatic cancer cell specimens. Previous studies also demonstrate involvement of these cell-cycle related genes in pancreatic cancer, and they represent potential targets for therapy[37,38].

CONCLUSIONS

This study demonstrates the great potential of gene expression profiling with WGCNA to construct internal connective networks between genes and phenotypes in various type of cancers. Our systematic genomic analysis revealed overexpressed genes in nine different types of common solid cancers and a shared network of overexpressed gene modules common to all. This shared, overexpressed gene module involving BIRC5, TPX2, and CDK1 supports the idea that different types of cancers may have a shared core molecular pathway regarding their oncogenesis. Further elucidation of shared gene modules using WGCNA may identify biomarkers and universal actionable genes for targeted cancer therapy.

ACKNOWLEDGEMENTS:

The study was funded by the National Institutes of Health grants NIDDK R01-DK46441 and NCI R01-CA095731 and Ann and Jerry Moss Foundation (to F. C. B.).

CONFLICT OF INTERESTS:

All authors declare that there are no conflicts of interest regarding the publication of this paper..

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