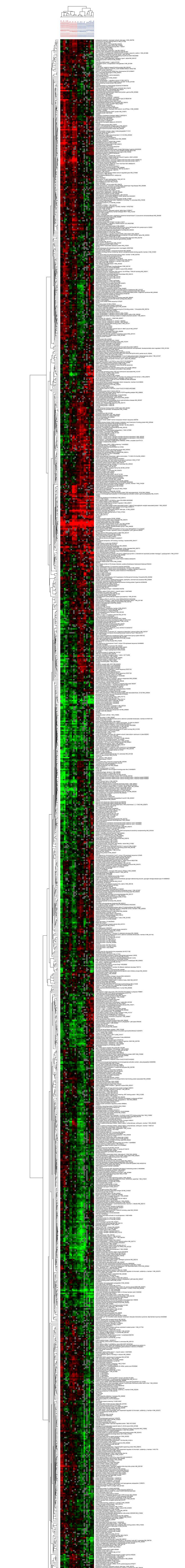


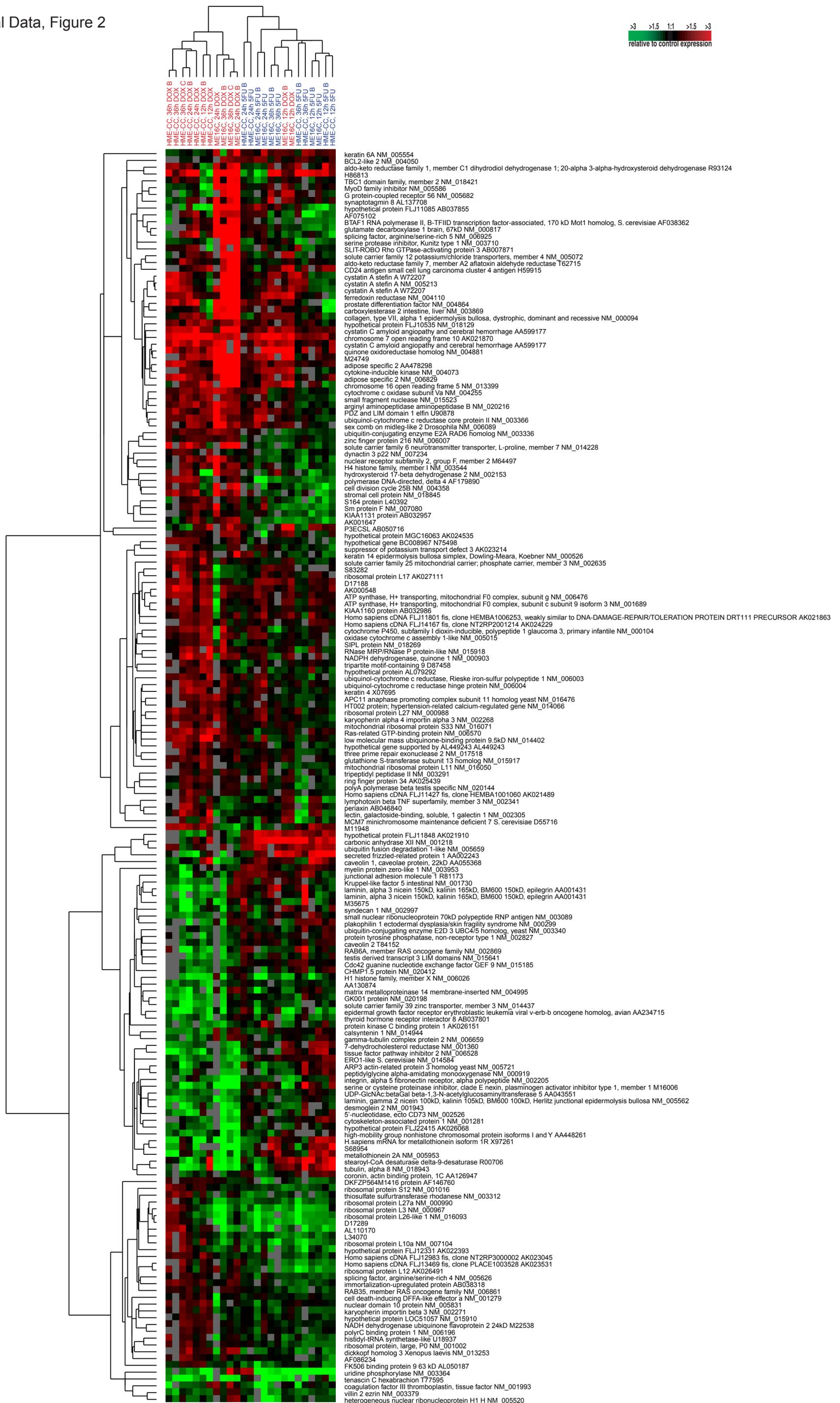
Supplemental Data, Figure 1. The complete hierarchical cluster diagram for the toxicant-specific gene expression patterns of luminal epithelium derived cell lines (MCF-7 and ZR-75-1).

Supplemental Data, Figure 2. The complete hierarchical cluster diagram for the toxicant-specific gene expression patterns of basal-like cell lines (ME16C and HME-CC).

Supplemental Data, Figure 3. The complete hierarchical cluster diagram for 100 genes selected using a k-nearest neighbors metric to classify samples by treatment. All four cell lines and three treatments (5FU, DOX, and ETOP) are represented.

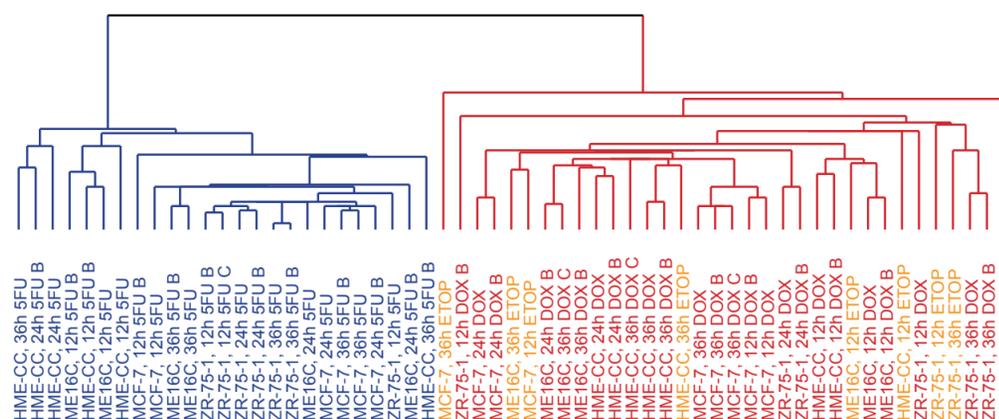


Supplemental Data, Figure 2

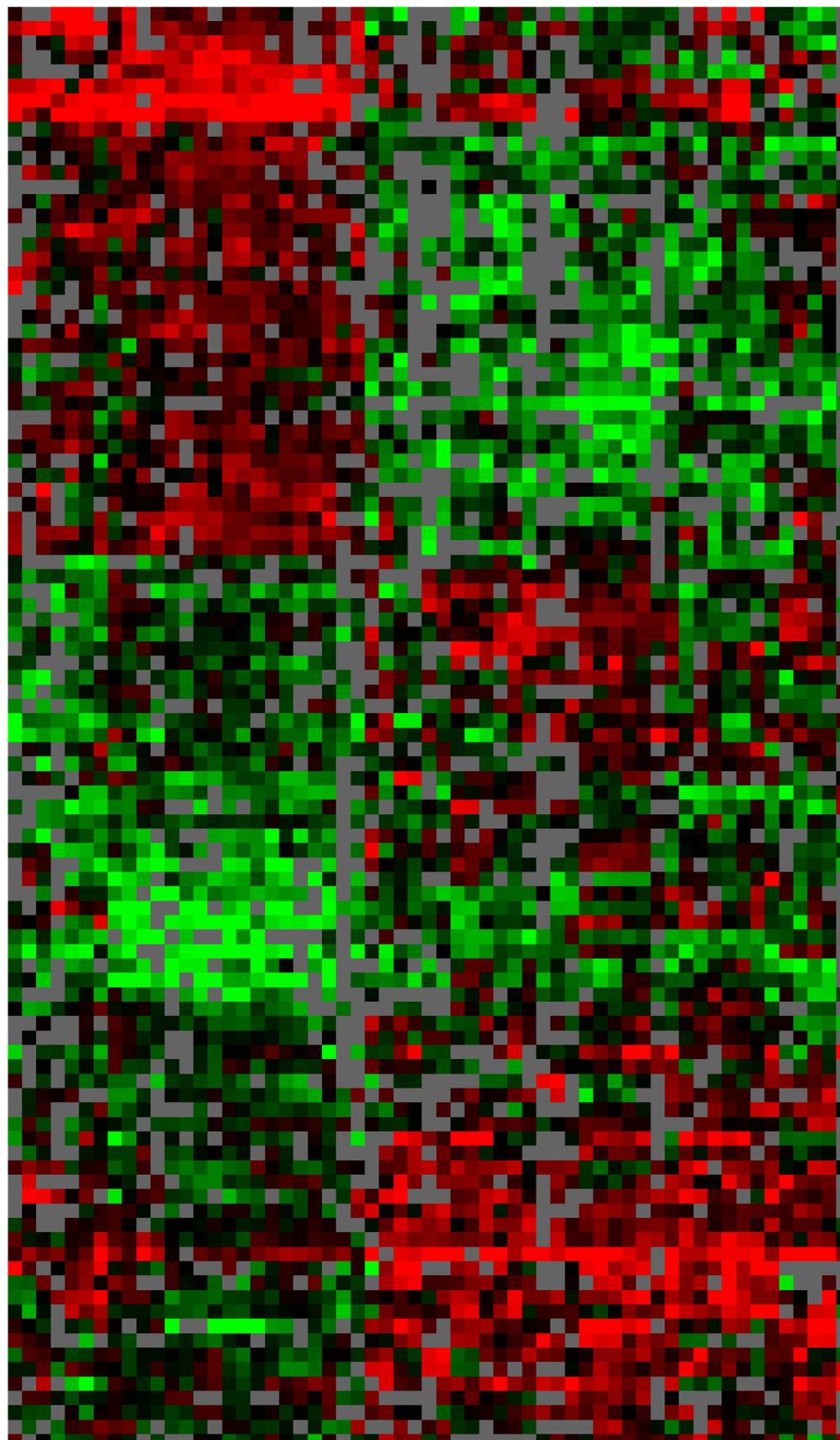
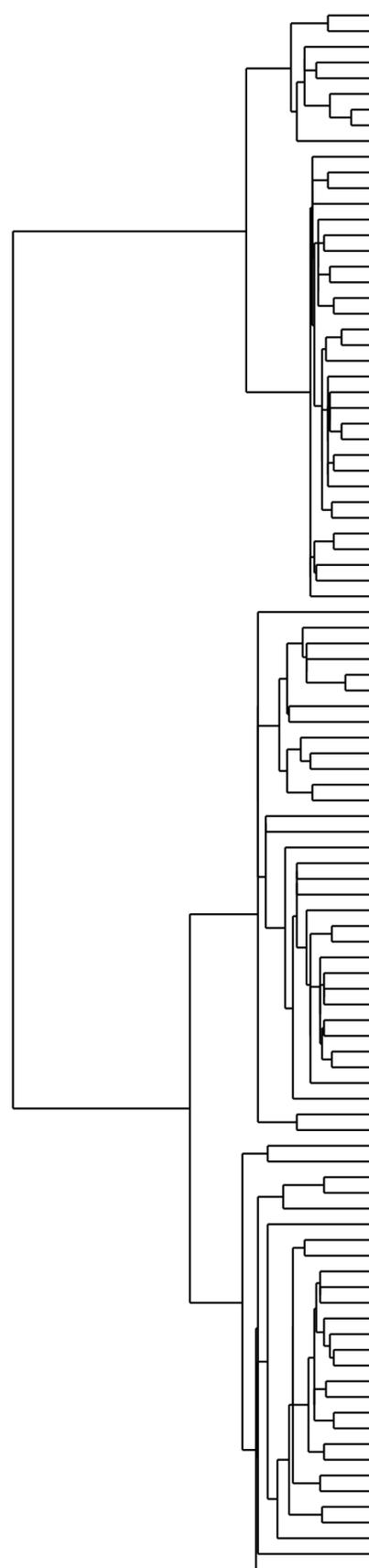


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Supplemental Data, Figure 3



HME-CC, 36h 5FU B
 HME-CC, 24h 5FU B
 HME-CC, 24h 5FU B
 ME16C, 12h 5FU B
 HME-CC, 12h 5FU B
 HME-CC, 12h 5FU B
 HME-CC, 12h 5FU B
 MCF-7, 12h 5FU B
 MCF-7, 12h 5FU B
 ME16C, 36h 5FU B
 ME16C, 36h 5FU B
 ZR-75-1, 12h 9FU B
 ZR-75-1, 12h 9FU C
 ZR-75-1, 24h 5FU B
 ZR-75-1, 24h 5FU B
 ZR-75-1, 36h 5FU B
 ME16C, 24h 5FU B
 MCF-7, 24h 5FU B
 MCF-7, 36h 5FU B
 MCF-7, 36h 5FU B
 MCF-7, 24h 5FU B
 ZR-75-1, 12h 5FU B
 ME16C, 24h 5FU B
 HME-CC, 36h 5FU B
 MCF-7, 36h ETOP
 ZR-75-1, 12h DOX B
 MCF-7, 24h DOX B
 MCF-7, 24h DOX B
 ME16C, 36h ETOP
 MCF-7, 12h ETOP
 ME16C, 24h DOX B
 ME16C, 36h DOX C
 ME16C, 36h DOX B
 HME-CC, 24h DOX B
 HME-CC, 24h DOX C
 HME-CC, 36h DOX C
 HME-CC, 36h DOX B
 HME-CC, 36h ETOP
 MCF-7, 36h DOX
 MCF-7, 36h DOX B
 MCF-7, 36h DOX C
 MCF-7, 12h DOX B
 MCF-7, 12h DOX
 ZR-75-1, 24h DOX
 HME-CC, 12h DOX B
 HME-CC, 12h DOX
 ME16C, 12h DOX
 ME16C, 12h DOX
 HME-CC, 12h DOX B
 HME-CC, 12h ETOP
 ZR-75-1, 12h DOX
 ZR-75-1, 12h ETOP
 ZR-75-1, 36h ETOP
 ZR-75-1, 36h DOX
 ME16C, 24h DOX B



PTD011 protein NM_014051
 ubiquitin fusion degradation 1-like NM_005659
 tyrosine kinase, non-receptor, 1 NM_003985
 carnitine palmitoyltransferase I, muscle NM_004377
 retinoblastoma binding protein 6 NM_006910
 seven transmembrane protein TM7SF3 NM_016551
 D28449
 inhibitor of DNA binding 3, domit negative helix-loop-helix protein AA482119
 KIAA0339 gene product AB002337
 cysteine-rich protein 2 NM_001312
 ATP-binding cassette, sub-family F GCN20, member 1 AF027302
 protein phosphatase 2 formerly 2A, regulatory subunit B PR 52, alpha isoform NM_002717
 sialic acid binding Ig-like lectin 9 AF227924
 mucopolipin-3 NM_018298
 hypothetical protein FLJ10774 AK022241
 microfibrillar-associated protein 1 NM_005926
 DnaJ Hsp40 homolog, subfamily C, member 5 AK024508
 mitogen-activated protein kinase 6 AA603152
 testis derived transcript 3 LIM domains NM_015641
 hypothetical protein FLJ20039 NM_017635
 AK025859
 KIAA0697 protein AB014597
 phosphatase and tensin homolog mutated in multiple advanced cancers 1 NM_000314
 AK024752
 phosphofructokinase, muscle NM_000289
 hypothetical protein FLJ20552 NM_017876
 isocitrate dehydrogenase 3 NAD+ gamma NM_004135
 palladin NM_016081
 CCCTC-binding factor zinc finger protein NM_006565
 splicing factor 30, survival of motor neuron-related NM_005871
 RAB10, member RAS oncogene family NM_016131
 jumonji homolog mouse NM_004973
 protein kinase C binding protein 1 AK026151
 protein phosphatase 1, regulatory subunit 10 NM_002714
 tousled-like kinase 2 AF162667
 KIAA1025 protein AL133033
 Yes-associated protein 1, 65 kD NM_006106
 nuclear receptor co-repressor/HDAC3 complex subunit AK022956
 acetyl-Coenzyme A transporter NM_004733
 D17216
 glutathione transferase zeta 1 maleylacetoacetate isomerase NM_001513
 AF076617
 Homo sapiens cDNA: FLJ22572 fis, clone HSI02313 AK026225
 polymerase DNA-directed, delta 4 AF179890
 chromosome 20 open reading frame 81 AL442086
 SH3-domain GRB2-like endophilin B2 NM_020145
 thiosulfate sulfurtransferase rhodanese NM_003312
 low density lipoprotein receptor-related protein 5 NM_002335
 hypothetical protein FLJ21044 similar to Rbig1 AK024697
 ribosomal protein L12 AK026491
 ribosomal protein L10a NM_007104
 phospholipase C, beta 4 NM_000933
 cerebral cell adhesion molecule NM_016174
 brain acyl-CoA hydrolase NM_007274
 AF275804
 cell division cycle 25B NM_004358
 histone deacetylase 6 NM_006044
 tumor protein p53 Li-Fraumeni syndrome NM_000546
 tumor protein p53 Li-Fraumeni syndrome NM_000546
 tumor protein p53 Li-Fraumeni syndrome NM_000546
 transformer-2 alpha htra-2 alpha NM_013293
 actin related protein 2/3 complex, subunit 4 20 kD NM_005718
 catenin cadherin-associated protein, beta 1 88kD NM_001904
 nuclear transport factor 2 NM_005796
 integral membrane protein 1 NM_002219
 coat protein gamma-cop AF100756
 kinesin family member 1B AB011163
 heterogeneous nuclear ribonucleoprotein H1 H NM_005520
 U5 snRNP-specific 40 kDa protein hPrp8-binding NM_004814
 NM_016259
 chromosome 2 open reading frame 6 NM_018221
 CGI-90 protein NM_016033
 galactose-4-epimerase, UDP- NM_000403
 transmembrane protein 4 NM_014255
 TAF12 RNA polymerase II, TATA box binding protein TBP-associated factor, 20 kD NM_005644
 leukotriene A4 hydrolase NM_000895
 beclin 1 coiled-coil, myosin-like BCL2 interacting protein NM_003766
 NAD kinase AK023114
 Homo sapiens mRNA; cDNA DKFZp434A1422 from clone DKFZp434A1422 AL137705
 F-box and leucine-rich repeat protein 6 AK026541
 hypothetical protein FLJ10535 NM_018129
 F-box only protein 22 AK024048
 annexin A4 NM_001153
 Homo sapiens clone CDABP0028 mRNA sequence AY007126
 NADH dehydrogenase ubiquinone 1 alpha subcomplex, 7 14.5kD, B14.5a NM_005001
 polymerase RNA II DNA directed polypeptide H U37689
 cystatin C amyloid angiopathy and cerebral hemorrhage AA599177
 cathepsin L NM_001912
 egl nine homolog 3 C. elegans R00226
 D17222
 transketolase Wernicke-Korsakoff syndrome NM_001064
 hypothetical protein MGC16063 AK024535
 Homo sapiens clone CDABP0071 mRNA sequence AY007143
 solute carrier family 25 mitochondrial carrier, phosphate carrier, member 3 NM_002635
 FK506 binding protein 3 25kD NM_002013
 stromal cell protein NM_018845
 D17082
 leucine carboxyl methyltransferase NM_016015
 protein tyrosine phosphatase, receptor type, G NM_002841
 UMP-CMP kinase NM_016308

Table 1. Results of Cross-Validation (CV) Analyses Using 2-Class PAM Method

Delta Value	Average No. of Genes	Average CV Accuracy (%)
4	1123.1	64
3.5	1928.3	76
3	2323.6	78
2.75	2460.4	80
2.5	2584.6	76
2.25	2706.8	76
2	2829.4	76
1.75	2948	76
1.5	3075	76
1.25	3213.9	76
1	3371.1	74
0.75	3543	70
0.5	3716.2	70
0.25	3902.5	70
0	4077	70

Table 2. Cross-Validation (CV) Accuracy (%) Using 2-Class KNN Method

Number of Genes	k=	1	3	5	7	9	11
10		58	72	72	66	66	64
30		84	92	90	92	94	94
50		74	80	90	96	94	92
70		80	86	92	92	90	92
100		80	82	94	94	96	98
200		74	76	86	88	88	90
4077		66	64	70	68	68	76

Table 3. Results of Cross-Validation (CV) Analyses Using 4-Class PAM Method

Delta Value	Average No. of Genes	Average CV Accuracy (%)
6	17.4	66
5	45.6	68
4	136.9	76
3.5	652	76
3	1830.7	50
2.75	2211.2	46
2.5	2510.9	42
2.25	2763.2	48
2	2975.5	48
1.75	3183.5	48
1.5	3379.4	48
1.25	3549.1	46
1	3693.8	46
0.75	3826.3	46
0.5	3944.6	46
0.25	4037.7	42
0	4077	38

Table 4. Cross-Validation (CV) Accuracy (%) Using 4-Class KNN Method

Number of Genes	k=	1	3	5	7	9	11
10		40	50	48	54	56	56
30		60	62	76	76	72	76
50		66	78	74	70	70	74
70		62	74	76	76	78	68
100		58	66	70	70	80	78
200		54	58	64	62	76	74
4077		48	48	48	46	48	52