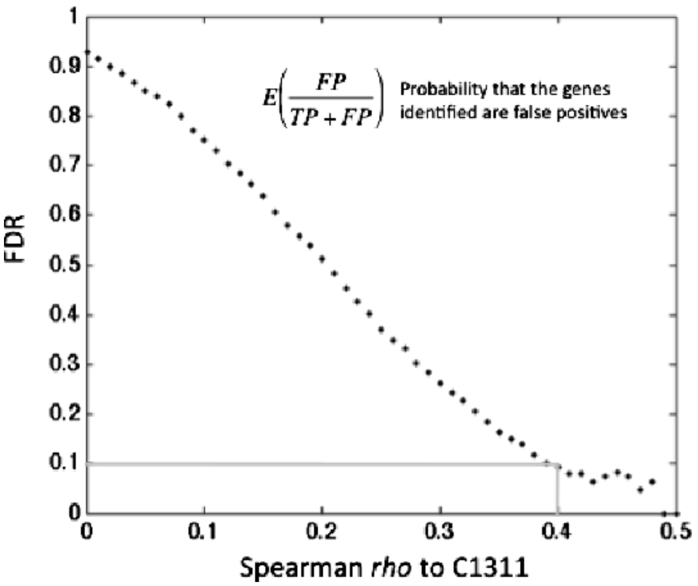
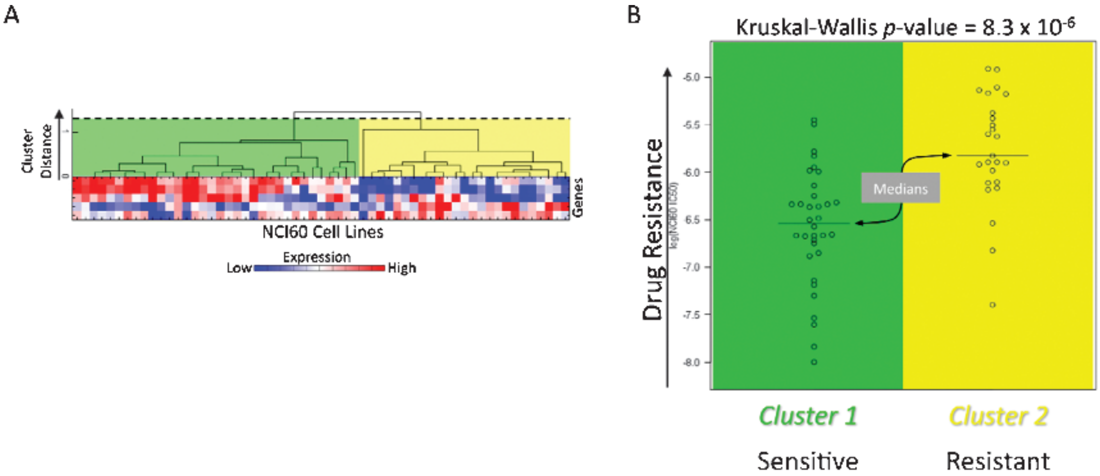
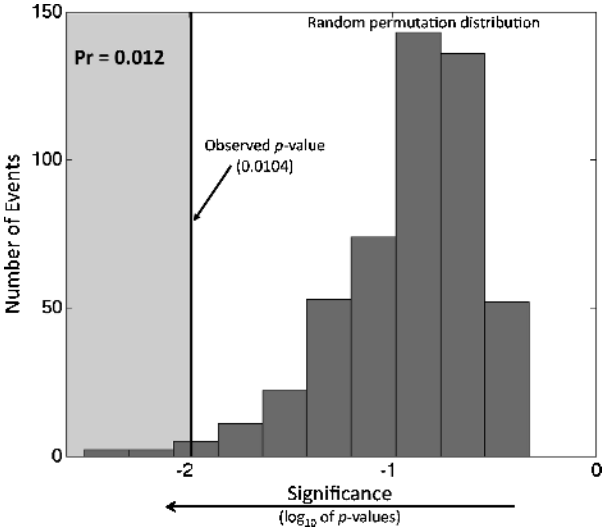

$E\left(\frac{FP}{TP+FP}\right)$
Probability that the genes identified are false positives
FDR
Spearman *rho* to C1311
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
0
0.1
0.2
0.3
0.4
0.5


A
Cluster Distance
0
Genes
NCI60 Cell Lines
Expression
Low
High
B
Kruskal-Wallis p-value = 8.3 x 10^-6
Drug Resistance
log(NCI60 IC50)
-5.0
-5.5
-6.0
-6.5
-7.0
-7.5
-8.0
Medians
Cluster 1
Cluster 2
Sensitive
Resistant


Random permutation distribution
Pr = 0.012
Observed p-value (0.0104)
Number of Events
150
100
50
0
-2
-1
0
Significance
($\log_{10}$ of p-values)

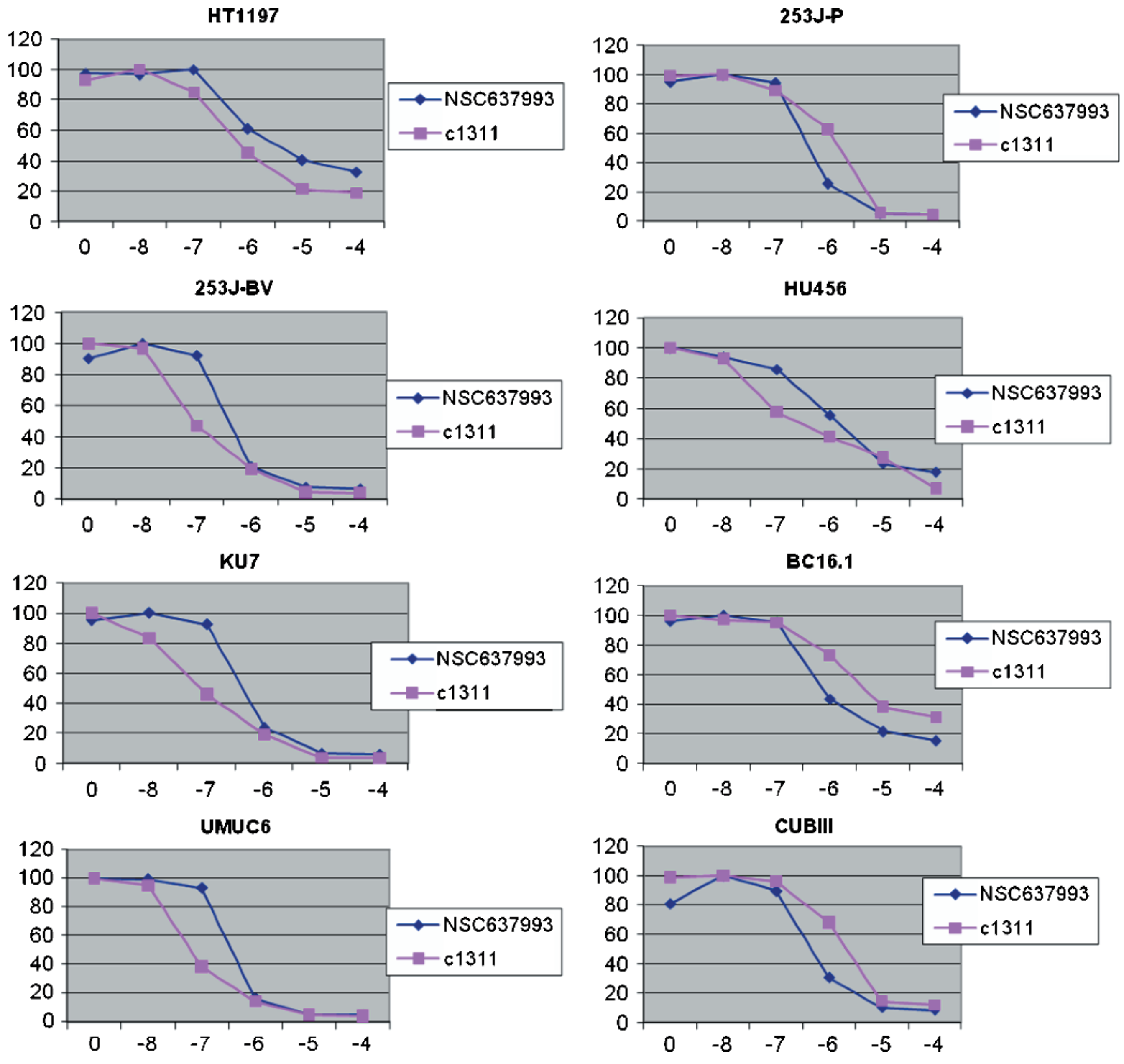


Figure W1. C1311 and NSC-637993 dose-response curves. Cells were exposed to RPMI 1640/10% FBS medium with diluted NSC-637993 or C1311 at concentrations of 0 (control), 0.01, 0.1, 1, 10, and 100 μM; after 72 hours of culture, cell counts were assayed. Each concentration of drug was tested on six replicate wells in more than 4 individual experiments. Data presented below for each of the cell lines show percent of maximal cell growth (*y* axis) per drug, averaged across the four replicates, plotted against the $\log_{10}$ treatment dose. These drug-response curves were used in Spline regression to estimate the IC_{50} values presented in Figure 1*A* and Table W1 as described in Materials and Methods.

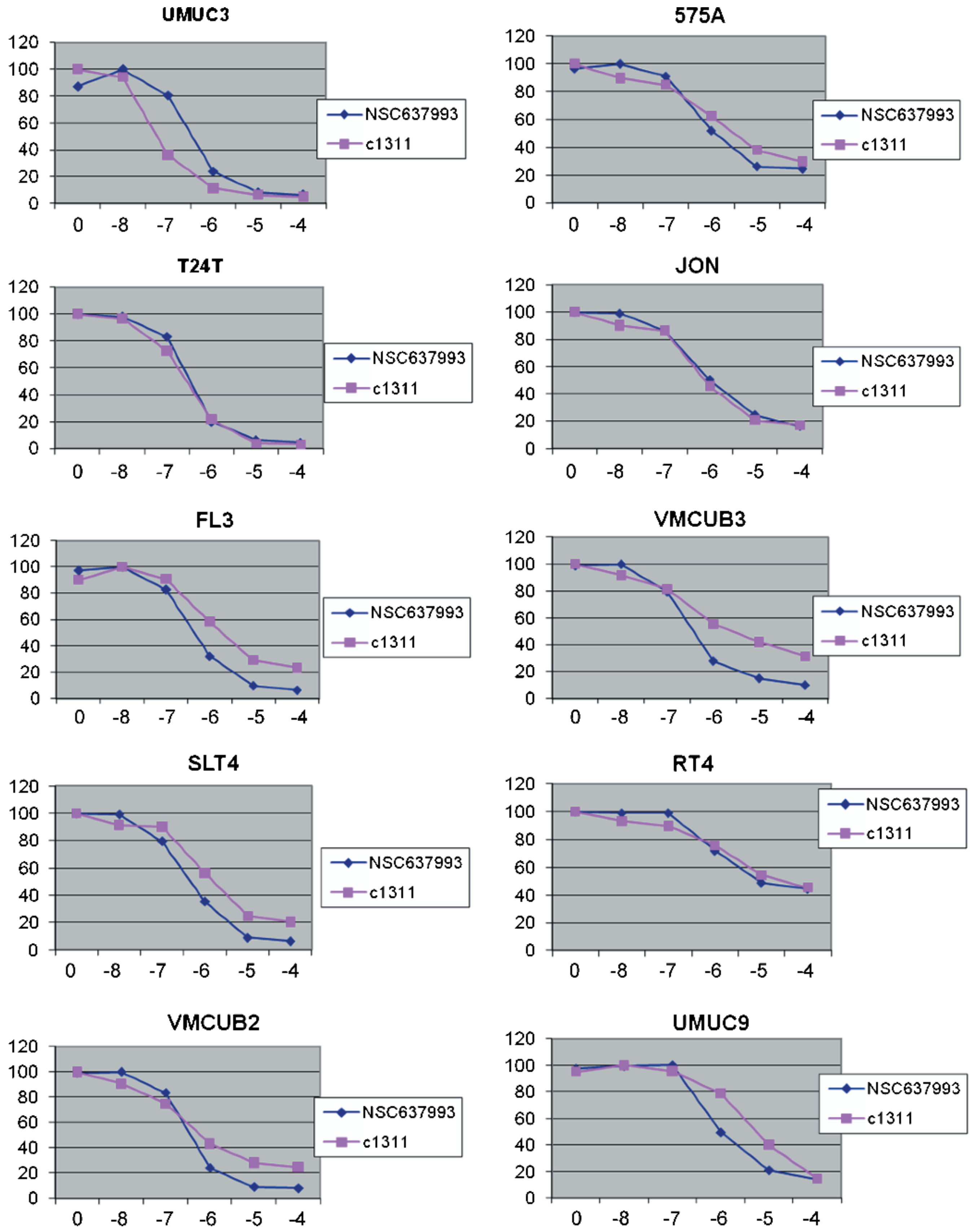


Figure W1. (*continued*).

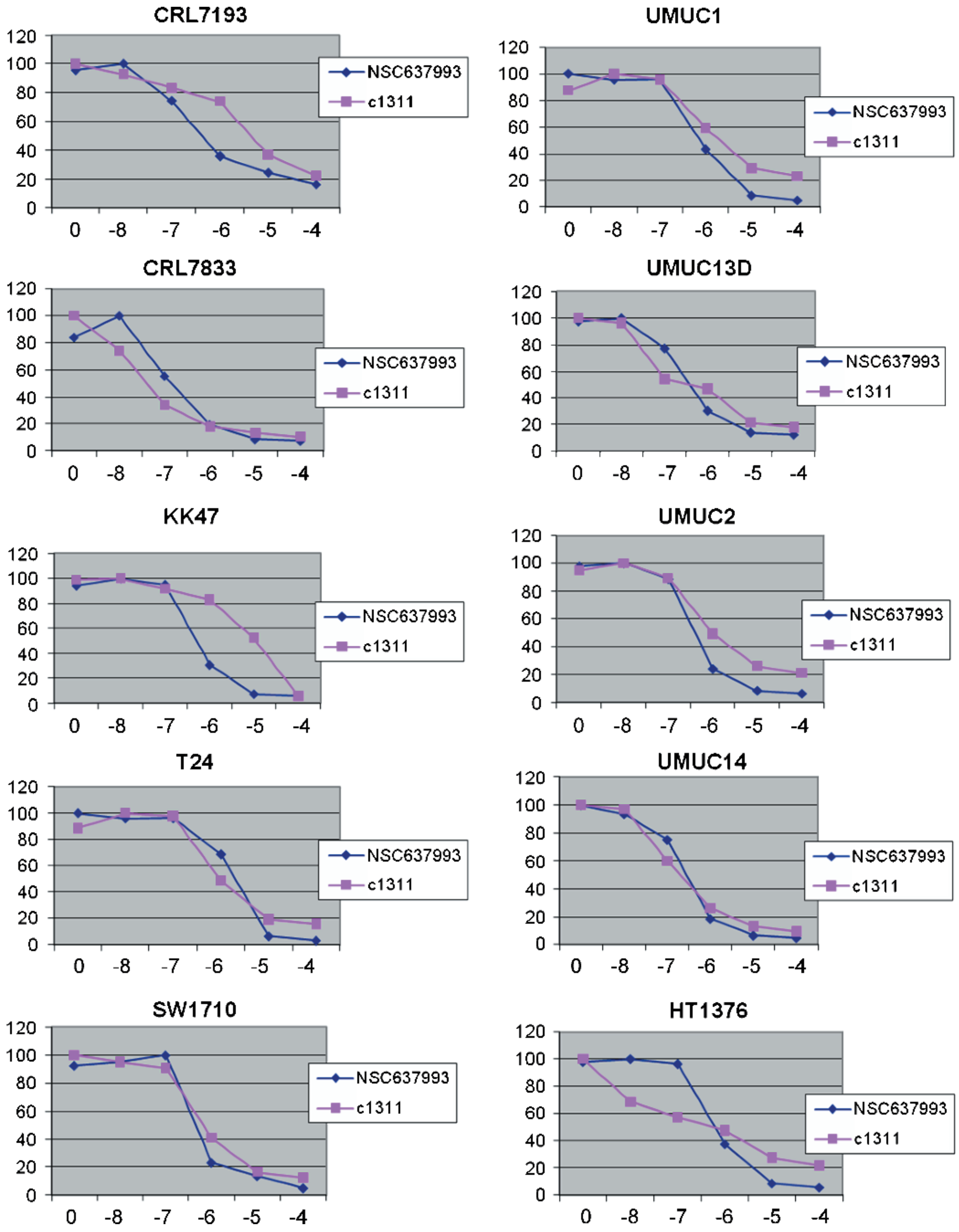


Figure W1. (*continued*).

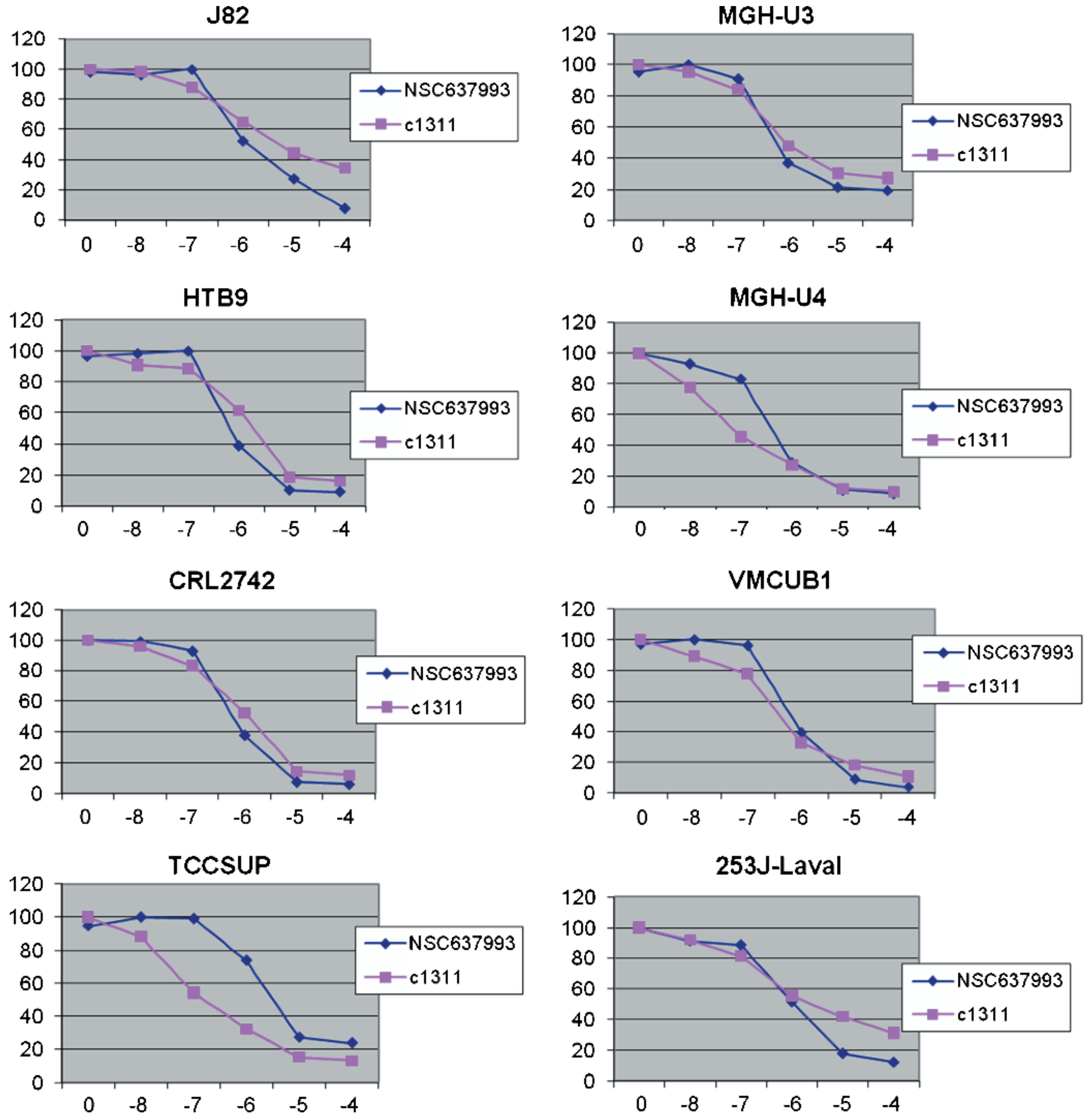


Figure W1. (*continued*).

Table W1. Log$_{10}$ IC$_{50}$ Values for the BLA-40 Cell Line Panel.

Cell Line[*]	C1311	NSC-637993[†]
CRL7833	–7.173	–6.574
KU7	–6.954	–6.378
UMUC3	–6.951	–6.337
UMUC6	–6.923	–6.281
MGH-U4	–6.874	–6.187
253J-BV	–6.836	–6.342
TCCSUP	–6.682	–5.193
SCaBER	–6.671	[‡]
UMUC14	–6.651	–6.641
T24T	–6.622	–6.604
HU456	–6.476	–5.675
UMUC3-E	–6.454	[‡]
VMCUB1	–6.383	–6.071
UMUC13D	–6.353	–6.361
VMCUB2	–6.197	–6.433
HT1376	–6.137	–5.959
CRL2169	–6.107	[‡]
SW1710	–6.101	–6.238
JON	–5.972	–5.926
MGH-U3	–5.965	–6.033
HT1197	–5.949	–5.245
CRL2742	–5.893	–6.135
UMUC2	–5.781	–6.425
253J-P	–5.727	–6.320
SLT4	–5.676	–6.273
T24	–5.656	–5.610
HTB9	–5.645	–5.946
253JLaval	–5.597	–5.722
VMCUB3	–5.597	–6.269
CUBIII	–5.565	–6.075
FL3	–5.448	–6.404
575A	–5.418	–5.634
UMUC1	–5.351	–6.009
CRL7193	–5.327	–6.327
J82	–5.269	–5.648
PSI	–5.266	[‡]
BC16.1	–5.231	–5.930
UMUC9	–5.180	–5.751
KK47	–4.841	–6.203
RT4	–4.722	–4.672

[*] The BLA-40 cell line panel has been reported before [15].

[†] Reported IC$_{50}$ values for NSC-637993 [15] were recalculated using Spline regression and listed here for comparison between the related imidazoacridinones.

[‡] Four of the BLA-40 cell lines were not tested for NSC-637993 in the prior report.

Table W2. HFA Results for NSC-637993 (A) and NSC and Paclitaxel (B).

(A)

Tx	Cell Line	NSC Log$_{10}$ IC$_{50}$	SC[*]	P[†]	IP[‡]	P[†]	Overall[§]	Overall P[†]
NSC Alone	T24T	–6.60	62.7	.005	71.6	.0006	61.3	<.0001
	FL3	–6.40	66.0	.0002	56.6	<.0001	67.2	<.0001
	UMUC1	–6.00	88.9	.2	54.9	<.0001	71.9	.0115
	KK47	–6.20	118.0	.04	107.8	.0002	112.8	.0018

(B)

Tx	Cell Line	NSC Log$_{10}$ IC$_{50}$	Paclitaxel Log$_{10}$ IC$_{50}$[¶]	SQ[*]	P[†]	IP[‡]	P[†]	Overall	Overall P[†]
NSC + Paclitaxel	UMUC6	–6.28	–8.99	12.5	<.0001	27.0	<.0001	19.8	<.0001
	HTB9	–5.94	–8.93	20.6	<.0001	8.1	<.0001	14.4	.0006
	T24	–5.61	–7.36	62.8	<.0001	28.3	<.0001	45.6	<.0001
	KK47	–6.20	>–7	94.3	.04	37.1	<.0001	65.7	.02

[*] Average percentage of control growth across four replicates at the subcutaneous implantation site.

[†] Two-tailed P value for single-sample t test against the hypothesis that the inhibition was 0%.

[‡] Average percentage of control growth across four replicates at the intraperitoneal implantation site.

[§] Average percentage of control growth across all replicates and sites.

[¶] We have reported *in vitro* sensitivities to paclitaxel across the BLA-40 panel before [16].

Table W3. Union of Yeast Strains with Reduced Fitness in C1311 (A) and Benomyl (B) Treatment.

Symbol	Description
(A)	
ACB1	Acyl-CoA-binding protein, transports newly synthesized acyl-CoA esters from fatty acid synthetase (Fas1p-Fas2p) to acyl-CoA-consuming processes
ACE2	Transcription factor that activates expression of early G_1-specific genes, localizes to daughter cell nuclei after cytokinesis and delays G_1 progression in daughters, localization is regulated by phosphorylation; potential Cdc28p substrate
ADO1	Adenosine kinase, required for the utilization of *S*-adenosylmethionine (AdoMet); may be involved in recycling adenosine produced through the methyl cycle
AIM22	Putative lipoate-protein ligase, required along with Lip2 and Lip5 for lipoylation of Lat1p and Kgd2p; similar to *E. coli* LplA; null mutant displays reduced frequency of mitochondrial genome loss
AKR1	Palmitoyl transferase involved in protein palmitoylation; acts as a negative regulator of pheromone response pathway; required for endocytosis of pheromone receptors; involved in cell shape control; contains ankyrin repeats
ALG13	Catalytic component of UDP-GlcNAc transferase, required for the second step of dolichyl-linked oligosaccharide synthesis; anchored to the ER membrane through interaction with Alg14p; similar to bacterial and human glycosyltransferases
ARC15	Subunit of the ARP2/3 complex, which is required for the motility and integrity of cortical actin patches
ARO1	Pentafunctional arom protein, catalyzes steps 2 through 6 in the biosynthesis of chorismate, which is a precursor to aromatic amino acids
ARO2	Bifunctional chorismate synthase and flavin reductase, catalyzes the conversion of 5-enolpyruvylshikimate 3-phosphate (EPSP) to form chorismate, which is a precursor to aromatic amino acids
BEM2	Rho GTPase activating protein (RhoGAP) involved in the control of cytoskeleton organization and cellular morphogenesis; required for bud emergence
BEM4	Protein involved in establishment of cell polarity and bud emergence; interacts with the Rho1p small GTP–binding protein and with the Rho-type GTPase Cdc42p; involved in maintenance of proper telomere length
BIM1	Microtubule-binding protein that together with Kar9p makes up the cortical microtubule capture site and delays the exit from mitosis when the spindle is oriented abnormally
BUD20	Protein involved in bud site selection; diploid mutants display a random budding pattern instead of the wild-type bipolar pattern
COY1	Golgi membrane protein with similarity to mammalian CASP; genetic interactions with GOS1 (encoding a Golgi snare protein) suggest a role in Golgi function
CPA1	Small subunit of carbamoyl phosphate synthetase, which catalyzes a step in the synthesis of citrulline, an arginine precursor; translationally regulated by an attenuator peptide encoded by YOR302W within the CPA1 mRNA 5′-leader
CSR1	Phosphatidylinositol transfer protein with a potential role in regulating lipid and fatty acid metabolism under heme-depleted conditions; interacts specifically with thioredoxin peroxidase; may have a role in oxidative stress resistance
CTF4	Chromatin-associated protein, required for sister chromatid cohesion; interacts with DNA polymerase α (Pol1p) and may link DNA synthesis to sister chromatid cohesion
CYB5	Cytochrome b5, involved in the sterol and lipid biosynthesis pathways; acts as an electron donor to support sterol C5-6 desaturation
DYN1	Cytoplasmic heavy chain dynein, microtubule motor protein, required for anaphase spindle elongation; involved in spindle assembly, chromosome movement, and spindle orientation during cell division, targeted to microtubule tips by Pac1p
ERG2	C-8 sterol isomerase, catalyzes the isomerization of the delta-8 double bond to the delta-7 position at an intermediate step in ergosterol biosynthesis
ERG25	C-4 methyl sterol oxidase, catalyzes the first of three steps required to remove two C-4 methyl groups from an intermediate in ergosterol biosynthesis; mutants accumulate the sterol intermediate 4,4-dimethylzymosterol
ERG28	Endoplasmic reticulum membrane protein, may facilitate protein-protein interactions between the Erg26p dehydrogenase and the Erg27p 3-ketoreductase and/or tether these enzymes to the ER, also interacts with Erg6p
ERG3	C-5 sterol desaturase, catalyzes the introduction of a C-5(6) double bond into episterol, a precursor in ergosterol biosynthesis; mutants are viable, but cannot grow on nonfermentable carbon sources
ERG6	Delta(24)-sterol C-methyltransferase, converts zymosterol to fecosterol in the ergosterol biosynthetic pathway by methylating position C-24; localized to both lipid particles and mitochondrial outer membrane
FEN2	Plasma membrane H^+-pantothenate symporter; confers sensitivity to the antifungal agent fenpropimorph
GCR2	Transcriptional activator of genes involved in glycolysis; interacts and functions with the DNA-binding protein Gcr1p
GET2	Subunit of the GET complex; involved in insertion of proteins into the ER membrane; required for the retrieval of HDEL proteins from the Golgi to the ER in an ERD2 dependent fashion and for meiotic nuclear division
GLO4	Mitochondrial glyoxalase II, catalyzes the hydrolysis of *S*-D-lactoylglutathione into glutathione and D-lactate
GTR2	Putative GTP binding protein that negatively regulates Ran/Tc4 GTPase cycle; activates transcription; subunit of EGO and GSE complexes; required for sorting of Gap1p; localizes to cytoplasm and to chromatin; homolog of human RagC and RagD
ISC1	Mitochondrial membrane localized inositol phosphosphingolipid phospholipase C, hydrolyzes complex sphingolipids to produce ceramide; activated by phosphatidylserine, cardiolipin, and phosphatidylglycerol; mediates Na^+ and Li^+ halotolerance
MGA2	ER membrane protein involved in regulation of OLE1 transcription, acts with homolog Spt23p; inactive ER form dimerizes and one subunit is then activated by ubiquitin/proteasome–dependent processing followed by nuclear targeting
MGM1	Mitochondrial GTPase related to dynamin, present in a complex containing Ugo1p and Fzo1p; required for normal morphology of cristae and for stability of Tim11p; homolog of human OPA1 involved in autosomal dominant optic atrophy
MNN11	Subunit of a Golgi mannosyltransferase complex that also contains Anp1p, Mnn9p, Mnn10p, and Hoc1p, and mediates elongation of the polysaccharide mannan backbone; has homology to Mnn10p
MNN9	Subunit of Golgi mannosyltransferase complex also containing Anp1p, Mnn10p, Mnn11p, and Hoc1p that mediates elongation of the polysaccharide mannan backbone; forms a separate complex with Van1p that is also involved in backbone elongation
MRPL16	Mitochondrial ribosomal protein of the large subunit
MSF1	Mitochondrial phenylalanyl-tRNA synthetase, active as a monomer, unlike the cytoplasmic subunit which is active as a dimer complexed to a β-subunit dimer; similar to the α subunit of *E. coli* phenylalanyl-tRNA synthetase
NPT1	Nicotinate phosphoribosyltransferase, acts in the salvage pathway of NAD^+ biosynthesis; required for silencing at rDNA and telomeres and has a role in silencing at mating-type loci; localized to the nucleus
PDX3	Pyridoxine (pyridoxamine) phosphate oxidase, has homologs in *E. coli* and *Myxococcus xanthus*; transcription is under the general control of nitrogen metabolism
PER1	Protein of the endoplasmic reticulum, required for GPI-phospholipase A2 activity that remodels the GPI anchor as a prerequisite for association of GPI-anchored proteins with lipid rafts; functionally complemented by human ortholog PERLD1
PFY1	Profilin, actin- and phosphatidylinositol 4,5-bisphosphate-binding protein, involved in cytoskeleton organization, required for normal timing of actin polymerization in response to thermal stress; localizes to plasma membrane and cytosol
PGA1	Essential component of GPI-mannosyltransferase II, responsible for second mannose addition to GPI precursors as a partner of Gpi18p; required for maturation of Gas1p and Pho8p; has synthetic genetic interactions with secretory pathway genes
PIB2	Protein binding phosphatidylinositol 3-phosphate, involved in telomere-proximal repression of gene expression; similar to Fab1 and Vps27
PPM1	Carboxyl methyltransferase, methylates the C-terminus of the protein phosphatase 2A catalytic subunit (Pph21p or Pph22p), which is important for complex formation with regulatory subunits
PRO1	γ-Glutamyl kinase, catalyzes the first step in proline biosynthesis
RAD51	Strand exchange protein, forms a helical filament with DNA that searches for homology; involved in the recombinational repair of double-strand breaks in DNA during vegetative growth and meiosis; homolog of Dmc1p and bacterial RecA protein

Table W3. (*continued*)

Symbol	Description
RAD55	Protein that stimulates strand exchange by stabilizing the binding of Rad51p to single-stranded DNA; involved in the recombinational repair of double-strand breaks in DNA during vegetative growth and meiosis; forms heterodimer with Rad57p
RAX2	N-glycosylated protein involved in the maintenance of bud site selection during bipolar budding; localization requires Rax1p; RAX2 mRNA stability is regulated by Mpt5p
RET2	Delta subunit of the coatomer complex (COPI), which coats Golgi-derived transport vesicles; involved in retrograde transport between Golgi and ER
RIM2	Mitochondrial pyrimidine nucleotide transporter; imports pyrimidine nucleoside triphosphates and exports pyrimidine nucleoside monophosphates; member of the mitochondrial carrier family
RML2	Mitochondrial ribosomal protein of the large subunit, has similarity to *E. coli* L2 ribosomal protein; fat21 mutant allele causes inability to use oleate and may interfere with activity of the Adr1p transcription factor
RPA135	RNA polymerase I subunit A135
RPB4	RNA polymerase II subunit B32; forms two subunit dissociable complex with Rpb7p; involved recruitment of 3′-end processing factors to transcribing RNA polymerase II complex and in export of mRNA to cytoplasm under stress conditions
RPD3	Histone deacetylase; regulates transcription and silencing; plays a role in regulating Ty1 transposition
RPL13B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl13Ap; not essential for viability; has similarity to rat L13 ribosomal protein
RPL1A	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl1Bp and has similarity to *E. coli* L1 and rat L10a ribosomal proteins; rpl1a rpl1b double null mutation is lethal /// N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl1Ap and has similarity to *E. coli* L1 and rat L10a ribosomal proteins; rpl1a rpl1b double null mutation is lethal
RPL2B	Protein component of the large (60S) ribosomal subunit, identical to Rpl2Ap and has similarity to *E. coli* L2 and rat L8 ribosomal proteins; expression is upregulated at low temperatures
RPL35A	Protein component of the large (60S) ribosomal subunit, identical to Rpl35Bp and has similarity to rat L35 ribosomal protein /// Protein component of the large (60S) ribosomal subunit, identical to Rpl35Ap and has similarity to rat L35 ribosomal protein
RPL39	Protein component of the large (60S) ribosomal subunit, has similarity to rat L39 ribosomal protein; required for ribosome biogenesis; loss of both Rpl31p and Rpl39p confers lethality; also exhibits genetic interactions with SIS1 and PAB1
RPS14A	Ribosomal protein 59 of the small subunit, required for ribosome assembly and 20S pre-rRNA processing; mutations confer cryptopleurine resistance; nearly identical to Rps14Bp and similar to *E. coli* S11 and rat S14 ribosomal proteins
RPS1B	Ribosomal protein 10 (rp10) of the small (40S) subunit; nearly identical to Rps1Ap and has similarity to rat S3a ribosomal protein
RPS25A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps25Bp and has similarity to rat S25 ribosomal protein
RSB1	Suppressor of sphingoid long chain base (LCB) sensitivity of an LCB-lyase mutation; putative integral membrane transporter or flippase that may transport LCBs from the cytoplasmic side toward the extracytoplasmic side of the membrane
SAC1	Phosphatidylinositol phosphate (PtdInsP) phosphatase involved in hydrolysis of PtdIns[4]P; transmembrane protein localizes to ER and Golgi; involved in protein trafficking and processing, secretion, and cell wall maintenance
SEC59	Dolichol kinase, catalyzes the terminal step in dolichyl monophosphate (Dol-P) biosynthesis; required for viability and for normal rates of lipid intermediate synthesis and protein N-glycosylation
SGO1	Component of the spindle checkpoint, involved in sensing lack of tension on mitotic chromosomes; protects centromeric Rec8p at meiosis I; required for accurate chromosomal segregation at meiosis II and for mitotic chromosome stability
SGS1	Nucleolar DNA helicase of the RecQ family involved in genome integrity maintenance; regulates chromosome synapsis and meiotic joint molecule/crossover formation; similar to human BLM and WRN proteins implicated in Bloom and Werner syndromes
SMC3	Subunit of the multiprotein cohesin complex required for sister chromatid cohesion in mitotic cells; also required, with Rec8p, for cohesion and recombination during meiosis; phylogenetically conserved SMC chromosomal ATPase family member
SNF1	AMP-activated serine/threonine protein kinase found in a complex containing Snf4p and members of the Sip1p/Sip2p/Gal83p family; required for transcription of glucose-repressed genes, thermotolerance, sporulation, and peroxisome biogenesis
SOK2	Nuclear protein that plays a regulatory role in the cyclic AMP (cAMP)–dependent protein kinase (PKA) signal transduction pathway; negatively regulates pseudohyphal differentiation; homologous to several transcription factors
SOV1	Mitochondrial protein of unknown function
SPO7	Putative regulatory subunit of Nem1p-Spo7p phosphatase holoenzyme, regulates nuclear growth by controlling phospholipid biosynthesis, required for normal nuclear envelope morphology, premeiotic replication, and sporulation
SPT14	UDP-GlcNAc-binding and catalytic subunit of the enzyme that mediates the first step in glycosylphosphatidylinositol (GPI) biosynthesis, mutations cause defects in transcription and in biogenesis of cell wall proteins
SSQ1	Mitochondrial hsp70-type molecular chaperone, required for assembly of iron/sulfur clusters into proteins at a step after cluster synthesis, and for maturation of Yfh1p, which is a homolog of human frataxin implicated in Friedreich’s ataxia
SUR4	Elongase, involved in fatty acid and sphingolipid biosynthesis; synthesizes very long chain 20-26-carbon fatty acids from C18-CoA primers; involved in regulation of sphingolipid biosynthesis
TBF1	Telobox-containing general regulatory factor; binds to TTAGGG repeats within subtelomeric anti–silencing regions (STARs) and possibly throughout the genome and mediates their insulating capacity by blocking silent chromatin propagation
TIP20	Peripheral membrane protein required for fusion of COPI vesicles with the ER, prohibits back fusion of COPII vesicles with the ER, may act as a sensor for vesicles at the ER membrane; interacts with Sec20p
TMA23	Nucleolar protein of unknown function implicated in ribosome biogenesis; TMA23 may be a fungal-specific gene as no homologs have been yet identified in higher eukaryotes
TRP3	Bifunctional enzyme exhibiting both indole-3-glycerol-phosphate synthase and anthranilate synthase activities, forms multifunctional hetero-oligomeric anthranilate synthase:indole-3-glycerol phosphate synthase enzyme complex with Trp2p
VAC7	Integral vacuolar membrane protein involved in vacuole inheritance and morphology; activates Fab1p kinase activity under basal conditions and also after hyperosmotic shock
VPS65	Protein coding
VPS8	Membrane-associated protein that interacts with Vps21p to facilitate soluble vacuolar protein localization; component of the CORVET complex; required for localization and trafficking of the CPY sorting receptor; contains RING finger motif
YIP1	Integral membrane protein required for the biogenesis of ER-derived COPII transport vesicles; interacts with Yif1p and Yos1p; localizes to the Golgi, the ER, and COPII vesicles
YML012C-A	Hypothetical ORF
YMR290W-A	Protein required for cell viability
YOR199W	Hypothetical ORF
YPL080C	Hypothetical ORF
YIL014C-A	Putative protein of unknown function
YBR056W	Putative cytoplasmic protein of unknown function
YBR221W-A	Putative protein of unknown function; identified by expression profiling and mass spectrometry
YDL118W	Nonessential protein of unconfirmed function; mutants are defective in telomere maintenance, and are synthetically sick or lethal with α-synuclein
YDL119C	Putative mitochondrial transport protein; GFP fusion protein is induced in response to the DNA-damaging agent MMS; the authentic, nontagged protein is detected in purified mitochondria

Table W3. (*continued*)

Symbol	Description
(B)	
ABD1	Methyltransferase, catalyzes the transfer of a methyl group from *S*-adenosylmethionine to the GpppN terminus of capped mRNA
AKR1	Palmitoyl transferase involved in protein palmitoylation; acts as a negative regulator of pheromone response pathway; required for endocytosis of pheromone receptors; involved in cell shape control; contains ankyrin repeats
ARP6	Actin-related protein that binds nucleosomes; a component of the SWR1 complex, which exchanges histone variant H2AZ (Htz1p) for chromatin-bound histone H2A
BLM10	Proteasome activator subunit; found in association with core particles, with and without the 19S regulatory particle; required for resistance to bleomycin, may be involved in protecting against oxidative damage; similar to mammalian PA200
BUB3	Kinetochore checkpoint WD40 repeat protein that localizes to kinetochores during prophase and metaphase, delays anaphase in the presence of unattached kinetochores; forms complexes with Mad1p-Bub1p and with Cdc20p, binds Mad2p and Mad3p
CIN1	Tubulin folding factor D involved in β-tubulin (Tub2p) folding; isolated as mutant with increased chromosome loss and sensitivity to benomyl
CIN2	GTPase-activating protein (GAP) for Cin4p; tubulin folding factor C involved in β-tubulin (Tub2p) folding; mutants display increased chromosome loss and benomyl sensitivity; deletion complemented by human GAP, retinitis pigmentosa 2
CIN4	GTP-binding protein involved in β-tubulin (Tub2p) folding; isolated as mutant with increased chromosome loss and sensitivity to benomyl; regulated by the GTPase-activating protein, Cin2p, the human retinitis pigmentosa 2 (RP2) homolog
CMC1	Evolutionarily conserved copper-binding protein of the mitochondrial intermembrane space, may be involved in delivering copper from the matrix to the cytochrome *c* oxidase complex; contains a twin CX9C motif
DAL82	Positive regulator of allophanate-inducible genes; binds a dodecanucleotide sequence upstream of all genes that are induced by allophanate; contains an UISALL DNA-binding, a transcriptional activation, and a coiled-coil domain
ECM23	Nonessential protein of unconfirmed function; affects pre-rRNA processing, may act as a negative regulator of the transcription of genes involved in pseudohyphal growth; homologous to Srd1p
ERG2	C-8 sterol isomerase, catalyzes the isomerization of the delta-8 double bond to the delta-7 position at an intermediate step in ergosterol biosynthesis
GIM3	Subunit of the heterohexameric cochaperone prefoldin complex which binds specifically to cytosolic chaperonin and transfers target proteins to it
GIM4	Subunit of the heterohexameric cochaperone prefoldin complex which binds specifically to cytosolic chaperonin and transfers target proteins to it
GND1	6-Phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in the pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress
MGR3	Subunit of the mitochondrial (mt) i-AAA protease supercomplex, which degrades misfolded mitochondrial proteins; forms a subcomplex with Mgr1p that binds to substrates to facilitate proteolysis; required for growth of cells lacking mtDNA
MTQ2	*S*-adenosylmethionine-dependent methyltransferase of the seven β-strand family; subunit of complex with Trm112p that methylates translation release factor Sup45p (eRF1) in the ternary complex eRF1-eRF3-GTP; similar to *E. coli* PrmC
PAC10	Part of the heteromeric co-chaperone GimC/prefoldin complex, which promotes efficient protein folding
PAC2	Microtubule effector required for tubulin heterodimer formation, binds α-tubulin, required for normal microtubule function, null mutant exhibits cold-sensitive microtubules and sensitivity to benomyl
PFD1	Subunit of heterohexameric prefoldin, which binds cytosolic chaperonin and transfers target proteins to it; involved in the biogenesis of actin and of α- and γ-tubulin
RVS161	Amphiphysin-like lipid raft protein; interacts with Rvs167p and regulates polarization of the actin cytoskeleton, endocytosis, cell polarity, cell fusion and viability following starvation or osmotic stress
SET6	SET domain protein of unknown function; deletion heterozygote is sensitive to compounds that target ergosterol biosynthesis, may be involved in compound availability
STB5	Transcription factor, involved in regulating multidrug resistance and oxidative stress response; forms a heterodimer with Pdr1p; contains a Zn(II)2Cys6 zinc finger domain that interacts with a pleiotropic drug resistance element *in vitro*
SWR1	Swi2/Snf2–related ATPase that is the structural component of the SWR1 complex, which exchanges histone variant H2AZ (Htz1p) for chromatin-bound histone H2A
TIF1	translation initiation factor eIF4E, 4F complex subunit (PMID 8955119)
TUB3	Alpha-tubulin; associates with β-tubulin (Tub2p) to form tubulin dimer, which polymerizes to form microtubules; expressed at lower level than Tub1p
UGO1	Protein of unknown function; outer membrane component of the mitochondrial fusion machinery; Ugo1p bind directly to Fzo1p and Mgm1p and thereby link these two GTPases during mitochondrial fusion
VPS53	Component of the GARP (Golgi-associated retrograde protein) complex, Vps51p-Vps52p-Vps53p-Vps54p, which is required for the recycling of proteins from endosomes to the late Golgi; required for vacuolar protein sorting
VPS71	Nucleosome-binding component of the SWR1 complex, which exchanges histone variant H2AZ (Htz1p) for chromatin-bound histone H2A; required for vacuolar protein sorting
VPS72	Htz1p-binding component of the SWR1 complex, which exchanges histone variant H2AZ (Htz1p) for chromatin-bound histone H2A; required for vacuolar protein sorting
YAF9	Subunit of both the NuA4 histone H4 acetyltransferase complex and the SWR1 complex, may function to antagonize silencing near telomeres; interacts directly with Swc4p, has homology to human leukemogenic protein AF9, contains a YEATS domain
YKE2	Subunit of the heterohexameric Gim/prefoldin protein complex involved in the folding of α-tubulin, β-tubulin, and actin
YLR269C	Hypothetical ORF
YML094C-A	Hypothetical ORF

Table W4. C1311 IC$_{50}$-Correlated Microarray Probes.

Probe Set*	Rho†	Symbol	Gene Title	Entrez Gene ID	Cytoband
200661_at	0.4553	*CTSA*	cathepsin A	5476	20q13.1
200677_at	0.4239	*PTTG1IP*	pituitary tumor-transforming 1 interacting protein	754	21q22.3
200696_s_at	0.5067	*GSN*	gelsolin (amyloidosis, Finnish type)	2934	9q33
200827_at	0.4218	*PLOD1*	procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1	5351	1p36.22
201021_s_at	0.4644	*DSTN*	destrin (actin depolymerizing factor)	11034	20p12.1
201022_s_at	0.434	*DSTN*	destrin (actin depolymerizing factor)	11034	20p12.1
201032_at	0.4325	*BLCAP*	bladder cancer associated protein	10904	20q11.2-q12
201038_s_at	−0.4044	*ANP32A*	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	8125	15q22.3-q23
201051_at	−0.4105	*ANP32A*	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	8125	15q22.3-q23
201148_s_at	0.4094	*TIMP3*	TIMP metallopeptidase inhibitor 3	7078	22q12.1-q13.2|22q12.3
201204_s_at	0.4182	*RRBP1*	ribosome binding protein 1 homolog 180 kDa (dog)	6238	20p12
201305_x_at	−0.4189	*ANP32B*	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	10541	9q22.32
201481_s_at	0.405	*PYGB*	phosphorylase, glycogen; brain	5834	20p11.2-p11.1
201500_s_at	0.4222	*PPP1R11*	protein phosphatase 1, regulatory (inhibitor) subunit 11	6992	6p21.3
201525_at	0.475	*APOD*	apolipoprotein D	347	3q26.2-qter
201618_x_at	0.4073	*GPAA1*	glycosylphosphatidylinositol anchor attachment protein 1 homolog (yeast)	8733	8q24.3
201629_s_at	−0.4001	*ACP1*	acid phosphatase 1, soluble	52	2p25
201720_s_at	−0.4154	*LAPTM5*	lysosomal protein transmembrane 5	7805	1p34
201775_s_at	0.4114	*KIAA0494*	KIAA0494	9813	1pter-p22.1
201987_at	−0.4256	*MED13*	mediator complex subunit 13	9969	17q22-q23
202027_at	0.4175	*TMEM184B*	transmembrane protein 184B	25829	22q12
202058_s_at	0.4398	*KPNA1*	karyopherin α 1 (importin α 5)	3836	3q21
202066_at	0.4728	*PPFIA1*	PTPRF interacting protein, α 1	8500	11q13.3
202219_at	0.4223	*SLC6A8*	solute carrier family 6, member 8	6535	Xq28
202421_at	0.4328	*IGSF3*	immunoglobulin superfamily, member 3	3321	1p13
202478_at	0.4103	*TRIB2*	tribbles homolog 2 (*Drosophila*)	28951	2p24.3
202479_s_at	0.5655	*TRIB2*	tribbles homolog 2 (*Drosophila*)	28951	2p24.3
202503_s_at	−0.4017	*KIAA0101*	KIAA0101	9768	15q22.31
202609_at	0.4414	*EPS8*	epidermal growth factor receptor pathway substrate 8	2059	12q13
202629_at	−0.457	*APPBP2*	amyloid β-precursor protein (cytoplasmic tail) binding protein 2	10513	17q21-q23
202818_s_at	0.4258	*TCEB3*	transcription elongation factor B (SIII), polypeptide 3 (110 kDa, elongin A)	6924	1p36.1
202821_s_at	0.4163	*LPP*	LIM domain containing preferred translocation partner in lipoma	4026	3q28
202840_at	−0.5074	*TAF15*	TAF15 RNA polymerase II, TATA box binding protein (TBP)–associated factor	8148	17q11.1-q11.2
202853_s_at	0.4478	*RYK*	RYK receptor-like tyrosine kinase	6259	3q22
202894_at	0.4577	*EPHB4*	EPH receptor B4	2050	7q22
202943_s_at	0.4066	*NAGA*	N-acetylgalactosaminidase, α-	4668	22q13-qter|22q11
202946_s_at	0.4029	*BTBD3*	BTB (POZ) domain containing 3	22903	20p12.2
203054_s_at	0.5192	*TCTA*	T-cell leukemia translocation altered gene	6988	3p21
203137_at	−0.4221	*WTAP*	Wilms tumor 1 associated protein	9589	6q25-q27
203304_at	0.4496	*BAMBI*	BMP and activin membrane–bound inhibitor homolog (*Xenopus laevis*)	25805	10p12.3-p11.2
203455_s_at	0.4052	*SAT1*	spermidine/spermine N1-acetyltransferase 1	6303	Xp22.1
203488_at	0.4243	*LPHN1*	latrophilin 1	22859	19p13.2
203657_s_at	0.4297	*CTSF*	cathepsin F	8722	11q13
203832_at	−0.4357	*SNRPF*	small nuclear ribonucleoprotein polypeptide F	6636	12q23.1
204209_at	0.4157	*PCYT1A*	phosphate cytidylyltransferase 1, choline, α	5130	3q29
204233_s_at	0.4287	*CHKA*	choline kinase α	1119	11q13.2
204266_s_at	0.4633	*CHKA*	choline kinase α	1119	11q13.2
204301_at	−0.4881	*KBTBD11*	kelch repeat and BTB (POZ) domain containing 11	9920	8p23.3
204501_at	0.4265	*NOV*	nephroblastoma overexpressed gene	4856	8q24.1
204528_s_at	−0.4544	*NAP1L1*	nucleosome assembly protein 1-like 1	4673	12q21.2
204542_at	0.4563	*ST6GALNAC2*	ST6 -N-acetylgalactosaminide α-2,6-sialyltransferase 2	10610	17q25.1
204566_at	−0.4076	*PPM1D*	protein phosphatase 1D magnesium–dependent, delta isoform	8493	17q23.2
204626_s_at	0.4075	*ITGB3*	integrin, β_3 (platelet glycoprotein IIIa, antigen CD61)	3690	17q21.32
204638_at	0.4635	*ACP5*	acid phosphatase 5, tartrate resistant	54	19p13.3-p13.2
204653_at	0.4107	*TFAP2A*	transcription factor AP-2 α	7020	6p24
204654_s_at	0.4418	*TFAP2A*	transcription factor AP-2 α	7020	6p24
204783_at	0.4152	*MLF1*	myeloid leukemia factor 1	4291	3q25.1
204789_at	−0.5508	*FMNL1*	formin-like 1	752	17q21
204803_s_at	−0.4276	*RRAD*	Ras-related associated with diabetes	6236	16q22
205209_at	−0.4004	*ACVR1B*	activin A receptor, type IB	91	12q13
205334_at	0.4318	*S100A1*	S100 calcium binding protein A1	6271	1q21
205376_at	0.4913	*INPP4B*	inositol polyphosphate-4-phosphatase, type II, 105 kDa	8821	4q31.21
205441_at	0.4227	*OCEL1*	occludin/ELL domain containing 1	79629	19p13.11
205749_at	0.4594	*CYP1A1*	cytochrome P450, family 1, subfamily A, polypeptide 1	1543	15q24.1
206066_s_at	−0.4726	*RAD51C*	RAD51 homolog C (S. cerevisiae)	5889	17q22-q23
206077_at	0.4308	*KEL*	Kell blood group, metalloendopeptidase	3792	7q33
206305_s_at	−0.4283	*C8A*	complement component 8, α polypeptide	731	1p32
206523_at	0.4377	*CYTH3*	cytohesin 3	9265	7p22.1
206775_at	0.4011	*CUBN*	cubilin (intrinsic factor-cobalamin receptor)	8029	10p12.31
206994_at	0.4623	*CST4*	cystatin S	1472	20p11.21
207039_at	0.4992	*CDKN2A*	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	1029	9p21
207098_s_at	0.419	*MFN1*	mitofusin 1	55669	3q26.33
207714_s_at	0.4095	*SERPINH1*	serpin peptidase inhibitor, clade H, member 1	871	11q13.5
207833_s_at	0.4588	*HLCS*	holocarboxylase synthetase	3141	21q22.1|21q22.13

Table W4. (*continued*)

Probe Set*	Rho[†]	Symbol	Gene Title	Entrez Gene ID	Cytoband
207913_at	0.426	*CYP2F1*	cytochrome P450, family 2, subfamily F, polypeptide 1	1572	19q13.2
207938_at	0.4719	*PI15*	peptidase inhibitor 15	51050	8q21.11
207992_s_at	−0.407	*AMPD3*	adenosine monophosphate deaminase (isoform E)	272	11p15
208291_s_at	−0.4216	*TH*	tyrosine hydroxylase	7054	11p15.5
208356_x_at	−0.4035	*CSH1*	chorionic somatomammotropin hormone 1 (placental lactogen)	1442	17q24.2
208754_s_at	−0.455	*NAP1L1*	nucleosome assembly protein 1–like 1	4673	12q21.2
208776_at	−0.4355	*PSMD11*	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	5717	17q11.2
208949_s_at	0.5056	*LGALS3*	lectin, galactoside-binding, soluble, 3	3958	14q21-q22
208978_at	0.4147	*CRIP2*	cysteine-rich protein 2	1397	14q32.3
209054_s_at	−0.4028	*WHSC1*	Wolf-Hirschhorn syndrome candidate 1	7468	4p16.3
209280_at	−0.4334	*MRC2*	mannose receptor, C type 2	9902	17q23.2
209361_s_at	0.4418	*PCBP4*	poly(rC) binding protein 4	57060	3p21
209399_at	0.4037	*HLCS*	holocarboxylase synthetase	3141	21q22.1|21q22.13
209484_s_at	−0.4026	*NSL1*	NSL1, MIND kinetochore complex component, homolog (S. cerevisiae)	25936	1q41
209485_s_at	0.4055	*OSBPL1A*	oxysterol binding protein-like 1A	114876	18q11.1
209598_at	−0.4092	*PNMA2*	paraneoplastic antigen MA2	10687	8p21.2
209736_at	0.4124	*SOX13*	SRY (sex determining region Y)-box 13	9580	1q32
209744_x_at	0.4511	*ITCH*	itchy E3 ubiquitin protein ligase homolog (mouse)	83737	20q11.22-q11.23
209849_s_at	−0.4522	*RAD51C*	RAD51 homolog C (S. cerevisiae)	5889	17q22-q23
209945_s_at	0.4391	*GSK3B*	glycogen synthase kinase 3β	2932	3q13.3
210083_at	0.4181	*SEMA7A*	semaphorin 7A, GPI membrane anchor	8482	15q22.3-q23
210194_at	−0.5138	*PLA2R1*	phospholipase A2 receptor 1, 180 kDa	22925	2q23-q24
210235_s_at	0.4315	*PPFIA1*	PTPRF interacting protein, α 1	8500	11q13.3
210285_x_at	−0.4267	*WTAP*	Wilms tumor 1 associated protein	9589	6q25-q27
210740_s_at	0.411	*ITPK1*	inositol 1,3,4-triphosphate 5/6 kinase	3705	14q31
210854_x_at	0.4757	*SLC6A8*	solute carrier family 6, member 8	6535	Xq28
210980_s_at	0.4375	*ASAH1*	N-acylsphingosine amidohydrolase 1	427	8p22-p21.3
211381_x_at	0.403	*SPAG11B*	sperm associated antigen 11B	10407	8p23-p22
211870_s_at	0.4171	*PCDHA3*	protocadherin α 3	56145	5q31
211883_x_at*	0.4335	*CEACAM1*	carcinoembryonic antigen–related cell adhesion molecule 1	634	19q13.2
211988_at	−0.4108	*SMARCE1*	SWI/SNF related, matrix associated, subfamily e, member 1	6605	17q21.2
212007_at	−0.4351	*UBXN4*	UBX domain protein 4	23190	2q21.3
212056_at	−0.4018	*KIAA0182*	KIAA0182	23199	16q24.1
212086_x_at	0.4143	*LMNA*	lamin A/C	4000	1q21.2-q21.3
212089_at	0.4162	*LMNA*	lamin A/C	4000	1q21.2-q21.3
212226_s_at	0.4283	*PPAP2B*	phosphatidic acid phosphatase type 2B	8613	1pter-p22.1
212230_at	0.4355	*PPAP2B*	phosphatidic acid phosphatase type 2B	8613	1pter-p22.1
212252_at	−0.4583	*CAMKK2*	calcium/calmodulin–dependent protein kinase kinase 2, β	10645	12q24.2
212338_at	0.41	*MYO1D*	myosin ID	4642	17q11-q12
212375_at	−0.4327	*EP400*	E1A binding protein p400	57634	12q24.33
212631_at	0.4084	*STX7*	syntaxin 7	8417	6q23.1
212747_at	0.4647	*ANKS1A*	ankyrin repeat and sterile α motif domain containing 1A	23294	6p21.31
212807_s_at	0.5102	*SORT1*	sortilin 1	6272	1p21.3-p13.1|1p21.3-p13.1
212876_at	0.4171	*B4GALT4*	UDP-Gal:βGlcNAc β 1,4- galactosyltransferase, polypeptide 4	8702	3q13.3
212957_s_at	0.4444	*LOC92249*	hypothetical LOC92249	92249	Xq11.1
213236_at	0.4565	*SASH1*	SAM and SH3 domain containing 1	23328	6q24.3
213242_x_at	0.4868	*KIAA0284*	KIAA0284	283638	14q32.33
213293_s_at	−0.4534	*TRIM22*	tripartite motif–containing 22	10346	11p15
213294_at	−0.4017	—	—	—	—
213310_at	0.4496	*EIF2C2*	Eukaryotic translation initiation factor 2C, 2	27161	8q24
213343_s_at	0.604	*GDPD5*	glycerophosphodiester phosphodiesterase domain containing 5	81544	11q13.4-q13.5
213472_at	−0.4171	*HNRNPH1*	heterogeneous nuclear ribonucleoprotein H1 (H)	3187	5q35.3
213575_at	−0.4166	*TRA2A*	transformer 2 α homolog (*Drosophila*)	29896	7p15.3
213649_at	−0.4247	*SFRS7*	splicing factor, arginine/serine–rich 7, 35 kDa	6432	2p22.1
213672_at	−0.4654	*MARS*	methionyl-tRNA synthetase	4141	12q13.2
213702_x_at	0.4707	*ASAH1*	N-acylsphingosine amidohydrolase 1	427	8p22-p21.3
213843_x_at	0.4967	*SLC6A8*	solute carrier family 6, member 8	6535	Xq28
213864_s_at	−0.4207	*NAP1L1*	nucleosome assembly protein 1–like 1	4673	12q21.2
213902_at	0.4116	*ASAH1*	N-acylsphingosine amidohydrolase 1	427	8p22-p21.3
213921_at	0.4172	*SST*	somatostatin	6750	3q28
213954_at	−0.4715	*FAM169A*	family with sequence similarity 169, member A	26049	5q13.3
214152_at	0.4033	*CCPG1*	cell cycle progression 1	9236	15q21.1
214172_x_at	0.455	*RYK*	RYK receptor–like tyrosine kinase	6259	3q22
214180_at	0.4349	*MAN1C1*	mannosidase, α, class 1C, member 1	57134	1p35
214213_x_at	0.428	*LMNA*	Lamin A/C	4000	1q21.2-q21.3
214280_x_at	−0.4075	*HNRNPA1*	heterogeneous nuclear ribonucleoprotein A1	3178	12q13.1
214584_x_at	0.444	*ACACB*	acetyl-Coenzyme A carboxylase β	32	12q24.11
214635_at	0.4365	*CLDN9*	claudin 9	9080	16p13.3
214812_s_at	−0.5214	*MOBKL1B*	MOB1, Mps One Binder kinase activator–like 1B (yeast)	55233	2p13.1
214971_s_at	0.4022	*ST6GAL1*	ST6 β-galactosamide α-2,6-sialyltranferase 1	6480	3q27-q28
215017_s_at	0.4167	*FNBP1L*	formin binding protein 1-like	54874	1p22.1
215096_s_at	−0.4088	*ESD*	esterase D/formylglutathione hydrolase	2098	13q14.1-q14.2
215381_at	0.4365	*FRAP1*	FK506 binding protein 12-rapamycin associated protein 1	2475	1p36.2
215495_s_at	0.4115	*SAMD4A*	sterile α motif domain containing 4A	23034	14q22.2

Table W4. (*continued*)

Probe Set*	Rho[†]	Symbol	Gene Title	Entrez Gene ID	Cytoband
215535_s_at	0.4043	*AGPAT1*	1-acylglycerol-3-phosphate O-acyltransferase 1	10554	6p21.3
215611_at	−0.4135	*TCF12*	transcription factor 12	6938	15q21
215693_x_at	0.4599	*DDX27*	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	55661	20q13.13
215731_s_at*	−0.4896	*MPHOSPH9*	M-phase phosphoprotein 9	10198	12q24.31
215749_s_at	0.4258	*GORASP1*	golgi reassembly stacking protein 1, 65 kDa	64689	3p22-p21.33
215812_s_at	0.5162	*LOC653562*	similar to solute carrier family 6 member 8	—	16p11.2 /// Xq28
216032_s_at	0.4316	*ERGIC3*	ERGIC and golgi 3	51614	20pter-q12
216060_s_at	0.4403	*DAAM1*	dishevelled associated activator of morphogenesis 1	23002	14q23.1
216086_at	0.4003	*SV2C*	synaptic vesicle glycoprotein 2C	22987	5q13.3
216560_x_at	0.4343	*IGL@*	immunoglobulin lambda locus	3535	22q11.1-q11.2
216629_at	0.4066	*SRRM2*	Serine/arginine repetitive matrix 2	23524	16p13.3
216751_at	−0.4111	—	—	—	—
216835_s_at	−0.4124	*DOK1*	docking protein 1, 62 kDa (downstream of tyrosine kinase 1)	1796	2p13
216874_at	0.489	*DKFZp686O1327*	Hypothetical gene supported by BC043549; BX648102	401014	2q22.3
216976_s_at	0.4007	*RYK*	RYK receptor–like tyrosine kinase	6259	3q22
217036_at	0.4367	*LOC100293679*	hypothetical protein LOC100293679	100293679	—
217094_s_at	0.4157	*ITCH*	itchy E3 ubiquitin protein ligase homolog (mouse)	83737	20q11.22–q11.23
217573_at	0.4175	*GRIN2C*	glutamate receptor, ionotropic, N–methyl D–aspartate 2C	2905	17q25
217606_at	0.4886	—	—	—	—
217613_at	−0.4542	*TMEM144*	transmembrane protein 144	55314	4q32.1
217730_at*	0.4432	*TMBIM1*	transmembrane BAX inhibitor motif containing 1	64114	2p24.3–p24.1
217749_at	0.4832	*COPG*	coatomer protein complex, subunit γ	22820	3q21.3
217925_s_at	0.4097	*C6orf106*	chromosome 6 open reading frame 106	64771	6p21.31
218099_at	0.4599	*TEX2*	testis expressed 2	55852	17q23.3
218299_at	0.4424	*C11orf24*	chromosome 11 open reading frame 24	53838	11q13
218509_at	0.5167	*LPPR2*	lipid phosphate phosphatase–related protein type 2	64748	19p13.2
218670_at	−0.4554	*PUS1*	pseudouridylate synthase 1	80324	12q24.33
218779_x_at	0.4243	*EPS8L1*	EPS8-like 1	54869	19q13.42
218936_s_at	−0.4272	*CCDC59*	coiled-coil domain containing 59	29080	12q21.31
218963_s_at	0.4383	*KRT23*	keratin 23 (histone deacetylase-inducible)	25984	17q21.2
218970_s_at	−0.4909	*CUTC*	cutC copper transporter homolog (*E. coli*)	51076	10q24.2
219011_at	0.4364	*PLEKHA4*	pleckstrin homology domain containing, family A member 4	57664	19q13.33
219046_s_at	0.4165	*PKNOX2*	PBX/knotted 1 homeobox 2	63876	—
219108_x_at	0.4345	*DDX27 /// SS18*	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	—	18q11.2 /// 20q13.13
219112_at	−0.4589	*RAPGEF6*	Rap guanine nucleotide exchange factor (GEF) 6	51735	5q31.1
219143_s_at	0.4134	*RPP25*	ribonuclease P/MRP 25 kDa subunit	54913	15q24.2
219278_at	0.4464	*MAP3K6*	mitogen-activated protein kinase kinase kinase 6	9064	1p36.11
219394_at	−0.4245	*PGS1*	phosphatidylglycerophosphate synthase 1	9489	17q25.3
219428_s_at	0.4054	*PXMP4*	peroxisomal membrane protein 4, 24 kDa	11264	20q11.22
219450_at	0.4348	*C4orf19*	chromosome 4 open reading frame 19	55286	4p14
219569_s_at	−0.4059	*TMEM22*	transmembrane protein 22	80723	3q22.3
219710_at	0.4466	*SH3TC2*	SH3 domain and tetratricopeptide repeats 2	79628	5q32
219873_at	0.4197	*COLEC11*	collectin subfamily member 11	78989	2p25.3
220038_at	0.4149	*C8orf44 /// SGK3*	chromosome 8 open reading frame 44	—	8q12.3-q13.1 /// 8q13.1
220499_at	0.443	*FNDC8*	fibronectin type III domain containing 8	54752	17q12
220559_at	0.4341	*EN1*	engrailed homeobox 1	2019	2q13-q21
220948_s_at	0.447	*ATP1A1*	ATPase, Na^+/K^+ transporting, α 1 polypeptide	476	1p21
220999_s_at	−0.4167	*CYFIP2*	cytoplasmic FMR1 interacting protein 2	26999	5q33.3
221017_s_at	0.409	*LRRC3*	leucine rich repeat containing 3	81543	21q22.3
221215_s_at	0.4981	*RIPK4*	receptor-interacting serine-threonine kinase 4	54101	21q22.3
221410_x_at	0.4631	*PCDHB3*	protocadherin β3	56132	5q31
221489_s_at	0.4378	*SPRY4*	sprouty homolog 4 (*Drosophila*)	81848	5q31.3
221616_s_at	−0.4113	*TAF9B*	TAF9B RNA polymerase II	51616	Xq13.1-q21.1
221681_s_at	−0.4101	*DSPP*	dentin sialophosphoprotein	1834	4q21.3
221683_s_at	−0.4697	*CEP290*	centrosomal protein 290 kDa	80184	12q21.32
221738_at	0.4105	*KIAA1219*	KIAA1219	57148	20q11.23
221816_s_at	−0.4902	*PHF11*	PHD finger protein 11	51131	13q14.2
221819_at	−0.4578	*RAB35*	RAB35, member RAS oncogene family	11021	12q24.31
221821_s_at*	−0.4137	*C12orf41*	chromosome 12 open reading frame 41	54934	12q13.11
221900_at	−0.4483	*COL8A2*	collagen, type VIII, α 2	1296	1p34.2
221919_at	−0.4026	*HNRNPA1*	heterogeneous nuclear ribonucleoprotein A1	3178	12q13.1
221965_at*	−0.5905	*MPHOSPH9*	M-phase phosphoprotein 9	10198	12q24.31
221986_s_at	0.4164	*KLHL24*	kelch-like 24 (*Drosophila*)	54800	3q27.1
222347_at	0.4183	*LOC644450*	hypothetical protein LOC644450	644450	1q12
32502_at	0.4446	*GDPD5*	glycerophosphodiester phosphodiesterase domain containing 5	81544	11q13.4-q13.5
36888_at	−0.4388	*HAUS5*	HAUS augmin–like complex, subunit 5	23354	19q13.12
38918_at	0.4097	*SOX13*	SRY (sex determining region Y)-box 13	9580	1q32
41644_at	0.4485	*SASH1*	SAM and SH3 domain containing 1	23328	6q24.3
52164_at	0.4047	*C11orf24*	chromosome 11 open reading frame 24	53838	11q13
52169_at	−0.4345	*STRADA*	STE20-related kinase adaptor α	92335	17q23.3
64899_at	0.4262	*LPPR2*	lipid phosphate phosphatase–related protein type 2	64748	19p13.2

*Probe set designation from the Affymetrix HG-U133A platform. The five probes exhibiting concordant expression across all three data sets are specifically asterisked.

[†] Correlation coefficient (ρ) for Spearman rank–based correlation of indicated probe expression in the NCI-60 cell line data set, *GSE5720*, to the C1311 IC_{50} values for each of the sixty cell lines. A cutoff of 0.4 was used for biomarker discovery.