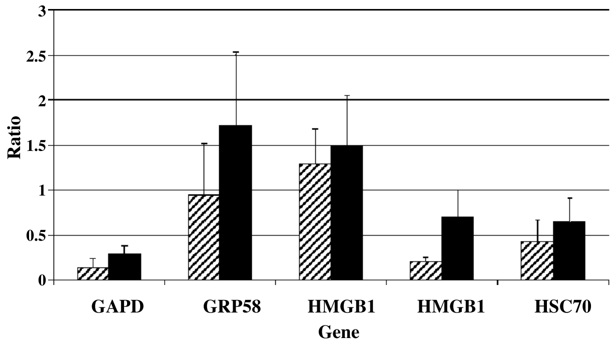

Figure W2. *Validation by real-time RT-PCR of members of the nuclear complex. Arithmetic means representing relative expressions of each gene in the resistant and sensitive groups are depicted with hashed (▨) and solid (■) bars, respectively. Expression levels were calibrated against Human Universal Reference. The error bars represent standard deviation.*

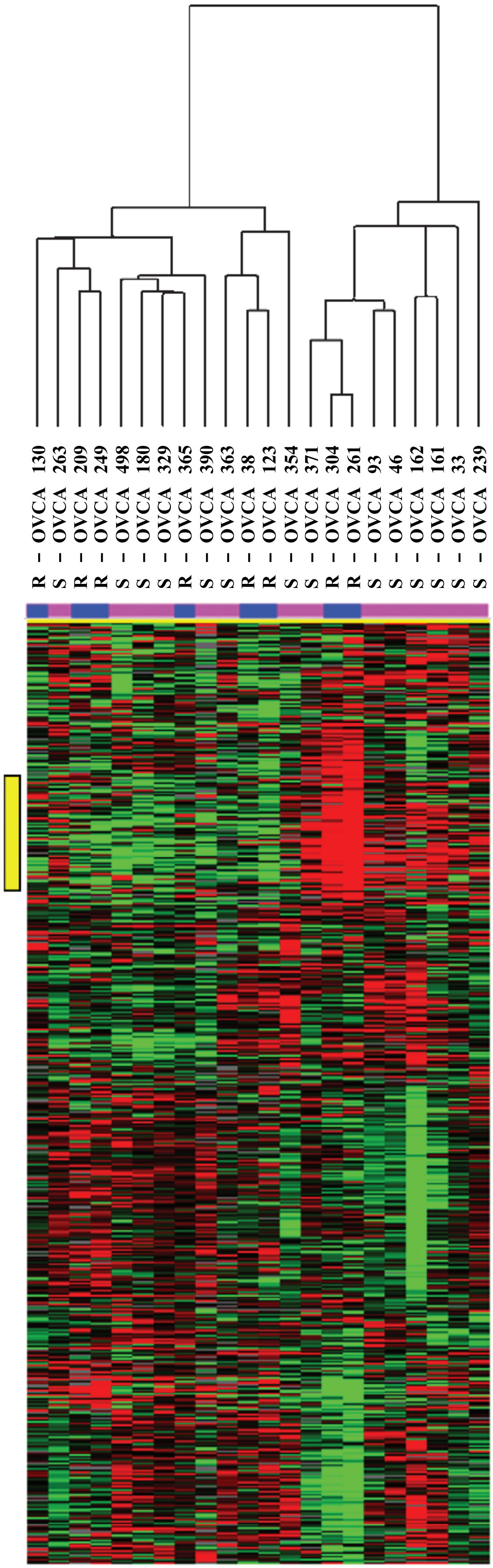

Figure W1. *Analysis of 22 samples using unsupervised hierarchical clustering. Sensitive (S; pink) and resistant (R; blue) samples are interspersed throughout the dendogram. Relative expression levels of genes are depicted in green (down), red (up), black (no change), or grey (data missing). The yellow vertical bar highlights a major gene cluster within which most genes identified as differentially expressed between the sensitive and resistant groups by SAM analysis were localized.*

Table W1. Genes Identified by SAM* Analysis that are Differentially Expressed between the Resistant and Sensitive Groups.

Clone ID	Fold Change[†]	Name	Gene Symbol	Cytoband
UP[‡]				
296275	15.43	H19, imprinted maternally expressed untranslated mRNA	LOC283120	11p15.5
109357	4.73	placenta-specific 4	PLAC4	21q22.3
53087	3.65	hypothetical protein LOC283922	LOC283922	16q22.3
158123	3.32	ATPase, H+ transporting, lysosomal 56/58kDa	ATP6V1B1	2p13.3
470393	3.29	matrix metalloproteinase 7	MMP7	11q22.2
5301677	2.85	retinol binding protein 1, cellular	RBP1	3q23
148914	2.76	Homo sapiens mRNA; cDNA DKFZp564B076	N/A	6p21.1
29988	2.42	pre-B-cell leukemia transcription factor 1	PBX1	2q23.1
149421	2.09	dual specificity phosphatase 1	DUSP1	5q35.1
2262605	2.07	Homo sapiens EMX2OS mRNA, complete sequence	N/A	10q26.11
501985	2.02	sphingosine-1-phosphate lyase 1	SGPL1	10q22.1
DOWN[§]				
162892	10.39	Homo sapiens cDNA FLJ26905 fis	N/A	22q11.22
146669	6.73	immunoglobulin lambda joining 3	IGLJ3	22q11.22
308924	6.47	hemoglobin, epsilon 1	HBE1	11p15.4
293298	5.62	Homo sapiens IGL mRNA for immunoglobulin lambda light chain	N/A	22q11.22
4701351	4.94	ferritin, light polypeptide	FTL	19q13.33
5922013	4.84	tubulin, beta polypeptide	TUBB	6p25.2
33203	4.77	tubulin, alpha 3	TUBA3	12q13.12
5784795	4.57	metallothionein 2A	MT2A	16q12.2
163221	4.56	Homo sapiens clone P2-114 anti-oxidized LDL immunoglobulin light chain	N/A	22q11.22
110243	4.47	Homo sapiens cDNA FLJ26905 fis, clone RCT01427, highly similar to	N/A	22q11.22
300017	4.18	apolipoprotein B	APOB	2p24.1
5923231	4.10	RAN, member RAS oncogene family	RAN	12q24.33
4876644	4.08	tubulin, beta, 5	TUBB5	19p13.3
261822	3.79	Homo sapiens, clone IMAGE:5728597	N/A	22q11.23
503601	3.74	glyceraldehyde-3-phosphate dehydrogenase	WT1	11p13
184151	3.72	tubulin, beta, 4	TUBB4	16q24.3
33204	3.72	tubulin, beta polypeptide paralog	MGC8685	6p25.2
303100	3.68	fibronectin 1	FN1	2q35
5762339	3.65	membrane targeting (tandem) C2 domain containing 1	MTAC2D1	14q32.12
198960	3.42	hemoglobin, gamma G	HBG2	11p15.4
470628	3.39	Homo sapiens cDNA clone IMAGE:5288757	N/A	1p32.2
5926230	3.36	peroxiredoxin 1	PRDX1	1p34.1
229610	3.35	Homo sapiens transcribed sequence	N/A	11p15.4
5749861	3.34	immunoglobulin lambda locus	IGL@	22q11.22
5422775	3.32	ribosomal protein S5	RPS5	19q13.43
208059	3.27	heat shock 70kDa protein 8	HSC70	11q24.1
5740157	3.26	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation pro	YWHAQ	2p25.1
5421424	3.19	enolase 1	ENO1	1p36.23
5454961	2.88	Homo sapiens transcribed sequence	N/A	15q25.1
120559	2.87	metallothionein 1F	MT1F	16q12.2
5406583	2.82	H2A histone family, member Z	H2AFZ	4q23
5806641	2.81	histone H2A.F/Z variant	H2AV	15q26.1
212856	2.79	hemoglobin, zeta	HBZ	16p13.3
5925346	2.77	chromosome 7 open reading frame 17	LOC51142	7p11.2
504180	2.75	Homo sapiens, clone IMAGE:5742072	N/A	6p22.3
267145	2.74	high-mobility group box 2	HMGB2	4q34.1
154975	2.69	Homo sapiens transcribed sequence	N/A	22q11.22
471144	2.64	electron-transfer-flavoprotein, beta polypeptide	ETFB	19q13.41
307027	2.59	heterogeneous nuclear ribonucleoprotein A2/B1	HNRPA2B1	7p15.2
27920	2.57	mitogen-activated protein kinase kinase kinase 7 interacting protein 1	MAP3K7IP1	22q13.1
297215	2.55	annexin A5	ANXA5	4q27
145972	2.54	KIAA0101 gene product	KIAA0101	15q22.31
5111837	2.52	cofilin 1	CFL1	11q13.1
5934101	2.50	pyruvate kinase, muscle	PKM2	15q23
4734377	2.49	ubiquitin B	UBB	17p11.2
270551	2.48	CD44 antigen	CD44	11p13
155222	2.48	glutathione peroxidase 4	GPX4	19p13.3
3546201	2.45	ribosomal protein L10	RPL10	Xq28
5494320	2.45	heat shock 90kDa protein 1, alpha	HSPCA	14q32.32
488225	2.44	ribosomal protein S19	RPS19	19q13.2
139590	2.43	RAN binding protein 1	RANBP1	22q11.21
29774	2.43	eukaryotic translation initiation factor 2	EIF2S2	2q31.1
341798	2.34	ubiquinol-cytochrome c reductase hinge protein	UQCRH	1p36.13
5809010	2.31	putative translation initiation factor	SUI1	17q21.2
5533075	2.30	small nuclear ribonucleoprotein polypeptides B and B1	SNRPB	20p13
490368	2.29	ribosomal protein S16	RPS16	19q13.2
489898	2.27	nuclease sensitive element binding protein 1	NSEP1	1p34.2
300041	2.26	non-metastatic cells 1	NME1	17q21.33

(*continued on next page*)

Table W1. (*continued*).

Clone ID	Fold Change[†]	Name	Gene Symbol	Cytoband
343295	2.25	lectin, galactoside-binding, soluble, 1 (galectin 1)	LGALS1	22q13.1
138280	2.23	DKFZp564J157 protein	DKFZP564J157	12q13.13
3916469	2.23	NHP2 non-histone chromosome protein 2-like 1	NHP2L1	22q13.2
5540049	2.22	Homo sapiens transcribed sequence	HCP15	7p15.3
5475005	2.22	Homo sapiens similar to ribosomal protein L18a	RPL18A	19p13.11
4126974	2.22	malate dehydrogenase 2, NAD	MDH2	7q11.23
230534	2.22	hemoglobin, alpha 2	HBA1	16p13.3
5785893	2.21	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c	ATP5G3	2q31.1
5431259	2.21	glyceraldehyde-3-phosphate dehydrogenase	GAPD	12p13.31
278772	2.21	stearoyl-CoA desaturase	SCD	10q24.31
5770525	2.21	activating transcription factor 4	ATF4	22q13.1
5932330	2.20	SH3 domain binding glutamic acid-rich protein like 3	SH3BGRL3	1p36.11
5704441	2.20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	DDX5	17q24.1
5528790	2.19	excision repair cross-complementing rodent repair deficiency, comp	ERCC1	19q13.32
4762963	2.19	ribosomal protein S13	RPS13	11p15.1
505381	2.19	syndecan 2	SDC2	8q22.1
4702445	2.19	ferritin, heavy polypeptide 1	FTH1	11q12.3
5806598	2.18	keratin 8	KRT8	12q13.13
5927927	2.17	ribosomal protein L10a	RPL10A	6p21.31
200573	2.16	CDC28 protein kinase regulatory subunit 1B	CKS1B	1q22
346784	2.15	alpha-2-HS-glycoprotein	AHSG	3q27.3
209207	2.15	superoxide dismutase 1	SOD1	21q22.11
295004	2.14	hepatoma-derived growth factor	HDGF	1q23.1
137317	2.13	chromosome 6 open reading frame 49	C6orf49	6p21.1
186682	2.13	trefoil factor 1	TFF1	21q22.3
5788140	2.13	ras homolog gene family, member A	ARHA	3p21.31
5420166	2.12	actin, alpha 2, smooth muscle, aorta	ACTA2	10q23.31
4772211	2.12	calmodulin 2	CALM2	2p21
4347418	2.10	high-mobility group nucleosome binding domain 1	HMGN1	21q22.2
5455241	2.09	solute carrier family 25	SLC25A5	Xq24
471551	2.09	Homo sapiens transcribed sequence	N/A	8q13.2
505115	2.09	chaperonin containing TCP1, subunit 8 (theta)	CCT8	21q21.3
5927445	2.08	peroxiredoxin 6	PRDX6	1q25.1
200190	2.07	nascent-polypeptide-associated complex alpha polypeptide	CA	12q13.3
151473	2.06	G1 to S phase transition 1	GSPT1	16p13.13
221318	2.05	CDC28 protein kinase regulatory subunit 2	CKS2	9q22.2
5926362	2.04	solute carrier family 25 (mitochondrial carrier; phosphate carrier	SLC25A3	12q23.1
4304010	2.04	stathmin 1/oncoprotein 18	STMN1	1p36.11
5270796	2.03	syndecan binding protein	SDCBP	8q12.1
504916	2.03	hypothetical protein MGC10812	MGC10812	19p13.11
4279563	2.02	tissue factor pathway inhibitor 2	TFPI2	7q21.3
172079	2.01	triosephosphate isomerase 1	TPI1	12p13.31
503300	2.01	hypothetical protein LOC51315	LOC51315	1p36.33
200586	2.00	metallothionein 1B	MT1B	16q12.2
23904	2.00	ELOVL family member 5, elongation of long chain fatty acids	ELOVL5	6p12.1

N/A Not available.

*SAM analysis with FDR 0.07-0.8%, fold change 2.

[†] Relative fold change between the two classes (resistant/sensitive).

[‡] List of genes whose transcript levels are greater in the resistant compared to the sensitive group.

[§] List of genes whose transcript levels are less in the resistant compared to the sensitive group.

Table W2. Test of Agreement between Expression Changers and Discriminate Genomic Regions.

Expression Microarray	BAC CGH*			
	Cytoband Regions Gained	Cytoband Regions with No Change	Cytoband Regions Lost	
Number of Genes with Greater Transcript Levels[†]	2[‖][**]	10	0	12
Number of Genes with No Change	320	6194[‖]	175	6689
Number of Genes with Lower Transcript Levels[†]	7	95	8[‖][**]	110
TOTAL	329	6299	183	6811

Cohen's Kappa = 0.0230[‡]

Test of H_o: Kappa = 0: κ^* = 0.1316[§]

[*] Cytoband regions gained, lost, or with no change in the resistant compared to the sensitive group that were identified by the Fisher Exact test ($P < 0.05$).

[†] Genes whose transcript levels were determined to be significantly greater or lower in the resistant compared to the sensitive group by SAM analysis (FDR 0.7-0.08%, FC 2).

[‡] Slight agreement between the expression and BAC CGH data (0 < κ^* < 1).

[§] Agreement does not exceed chance (κ^* < 1.96).

[‖] Overall agreement between aCGH and expression data was 91%.

[**] 8.2% of SAM changers agree with changes in copy number.

Table W3. Overall Losses and Gains.

Loss	Gain
1p36.11-pter; 3p22.1-p21.31; 4p15.33-p16.1; 4p12-p14; 4q13.2-qter; 5q13.1-q23.3; 6q22.1-qter; 8p21.1-pter; 9p; 9q21.11-q33.1; 11p15.1-pter; 13q12.2-q21.1; 13q32.2-qter; 15q11.2-q15.1; 16q; 17p13.2-q11.2; 17q21.32-q21.33; 18q21.1-qter; 22	1q11-q25.3; 2p22.3-pter; 3q22.3-qter; 6p22.1-pter; 6p21.1-p21.31; 7q31.33-qter; 8q; 12p; 20p12.1-pter; 20q12-qter