Supplemental Materials and Methods

Description of human and murine tumor expression data. Forty-two gene expression CEL files of human and murine xenograft tumors were analyzed. CEL files were generated from Affymetrix U133A2.0 gene array chips. Of the 42 CEL files, un-prefixed CEL files (CRC###.CEL, where ### is the tumor ID number) are original fresh frozen human tumors; CEL files prefixed with "PDCCE_" are the fresh frozen mouse xenografts derived from their respective human tumors; and CEL files prefixed with "PDCCE_FFPE_" are the formalin-fixed paraffin-embedded mouse xenografts derived from their human tumors.

Description of NCI-60 cell line expression data. Fifty-nine NCI-60 cell line CEL files were obtained from the NCI-60 CellMiner repository (http://discover.nci.nih.gov/cellminer/home.do). We used the "RNA: Affymetrix HG-U133 44K probeset microarray" data set (Shankavaram et al., 2007) which contains CEL files generated from Affymetrix U133A and Affymetrix U133B gene array chips; however, only the U133A CEL files were relevant to our study.

Preprocess of expression data. RMA-estimated expression values are calculated using the bioconductor R package with the justRMA() function. The following pre-normalized expression matrices and descriptor text files are available as supplemental files:

- **Human_Tumor_RMA.txt** – CRC###.CEL files, RMA-normalized
- **PDCCE_freshfrozen_RMA.txt** – PDCCE_CRC###.CEL files, RMA-normalized
- **PDCCE_ FFPE_RMA.txt** – PDCCE_FFPE _CRC###.CEL files, RMA-normalized
- **PDCCE_ FFPE _remCRC057_RMA.txt** – PDCCE_FFPE _CRC###.CEL files with PDCCE_FFPE _CRC0057.CEL removed for QC reasons, RMA-normalized
- **HT_PDCCE_FF_RMA.txt** – CRC###.CEL files and PDCCE_CRC###.CEL, RMA-normalized expression data, file merged and formatted for ComBat
- **RMA_Batch_Info.txt** – Batch information descriptor file for ComBat analysis
- **Adjusted_HT_PDCCE_FF_RMA.txt** – CRC###.CEL files and PDCCE_CRC###.CEL, RMA-normalized expression data, ComBat normalized
- **Filtered_Adjusted_HT_PDCCE_FF_RMA.txt** – CRC###.CEL files and PDCCE_CRC###.CEL, RMA-normalized expression data, ComBat normalized and CV filtered
- **NCI60_oxaliplatin_sensitive.txt** – Oxaliplatin-sensitive training set consisting of expression data from 8 oxaliplatin-sensitive NCI-60 cell lines, RMA-normalized
- **NCI60_oxaliplatin_resistant.txt** – Oxaliplatin-resistant training set consisting of expression data from 8 oxaliplatin-resistant NCI-60 cell lines, RMA-normalized

The following R scripts are also available as supplemental files:

- **ComBat.R** is the unaltered ComBat batch normalization algorithm as downloaded from http://jlab.byu.edu/ComBat/Download.html. Detailed instructions on its usage are described on the main ComBat webpage. All ComBat analysis should be performed using default parameters.

- **AllScripts.R** contains scripts for gene filtering (FilterData function), unsupervised hierarchical clustering (HCluster function), and application of the R package "pvclust" (pvcluster function). Specific comments on their usage are described in commented sections in the script prior to each function.

Scripts must be sourced in R prior to usage and may have specific external R library dependencies as described in their comments.

Generating heatmaps and dendrograms. To generate **Figure 2b and 2c**, we first performed ComBat on RMA-normalized human tumor samples file merged (http://filemerger.genome.duke.edu/) with fresh frozen PDCCE samples. File merging was used to align samples according to their Affymetrix probe IDs. Pre-normalized and merged expression values are provided as described above. Human samples are designated as batch 1, and PDCCE samples are designated as batch 2 in the batch info file. To perform ComBat, the following command can be executed in R using the provided ComBat script and tumor expression data:

```
> ComBat('HT_PDCCE_FF_RMA.txt', 'RMA_Batch_Info.txt', skip=1)
```

After ComBat has finished, the ComBat outputted expression matrix can be formatted for further analysis. The top label row requires being shifted to the right one cell, and the subsequent first column containing only ascending numbers should be deleted (this is a minor issue with the ComBat script). Affymetrix housekeeping probes should be removed prior to filtering probes. From here, the file can be saved as a tab-delimited text file and proceeded to filter probes based on coefficient of variation. Coefficient of variation (CV) filtering filters out the least variable probes according to the formula CV = (standard deviation) / (mean). We chose to filter out 80% of the least variable probes as determined by their CV values, such that CV > 0.8 for each probe. The following command "FilterData" for CV filtering can be executed in R using the provided AllScripts script:

```
> FilterData('Adjusted_HT_PDCCE_FF_RMA.txt')
```

After filtering the ComBat expression data, we then proceeded to perform an unsupervised hierarchical cluster analysis to generate the heatmap in **Figure 2b** using pearson correlations and complete linkage. The following command "HCluster" for clustering and heatmap generation can be executed in R using the provided AllScripts script:

```
> HCluster('Filtered_Adjusted_HT_PDCCE_FF_RMA.txt')
```

To generate the dendrogram in **Figure 2c** and to calculate pvclust cluster AU and BP probabilities at 10,000 iterations, we used the following command "pvcluster" to calculate dendrogram cluster probabilities in R using the same pearson correlation and complete linkage as in the previously generated heatmap with the provided AllScripts script (Note: this is a resource-intensive process that may take several hours depending on your computing power):

```
> pvcluster('Filtered_Adjusted_HT_PDCCE_FF_RMA.txt')
```

Generating Oxaliplatin signature. To generate the Oxaliplatin Sensitivity signature, NCI-60 cell line expression data must be generated. U133A CEL files for NCI-60 cell lines along with RMA-normalized NCI-60 gene expression data can be downloaded from CellMiner (http://discover.nci.nih.gov/cellminer/loadDownload.do). We chose to RMA-normalize the U133A CEL files for analysis.

After RMA-normalization, we performed quality assessment of the samples using 3D principle components (3DPCA) analysis in Matlab. Using 3DPCA, it was found that one sample, MCF-7, appeared to be an outlier as shown in **Supplementary Figure 1**. This sample was removed from subsequent analysis.

To determine phenotypes of oxaliplatin sensitivity, we obtained cancer screening dose response data from DTP (http://dtp.nci.nih.gov/) for oxaliplatin (NSC 266046). As described in the manuscript, phenotypes were determined as the 8 most sensitive and 8 most resistant NCI-60 cell lines according to GI50. Expression values of oxaliplatin response phenotypes used as training sets for the oxaliplatin sensitivity signature are provided as "nci60_oxaliplatin_sensitive.txt" and "nci60_oxaliplatin_resistant.txt".

To generate the gene list for the signature, we uploaded the resistant (for "train0") and sensitive (for "train1") training sets to the CreateSignature module of the Duke GenePattern instance server (https://genepattern.genome.duke.edu/gp/pages/login.jsf), which is a Duke-written module to automate running the BinReg script in the GenePattern environment. Before running, relevant parameters were set as follows:

- version: 2
- num_metagenes: 2
- apply_quantile_normalization: Yes
- apply_shiftscale_normalization: Yes
- burnin: 2000
- niter: 5000
- skips: 3

To determine the optimal number of genes for the signature (num_genes), we ran the simulation from 50-200 genes in increments of 10 as described in the manuscript and compared leave-one-out performance for phenotype stability. Data from **Figure 1** was generated using 120 genes.

Oxaliplatin signature validation. To validate the Oxaliplatin Sensitivity signature on fresh frozen PDCCE and formalin-fixed paraffin-embedded PDCCE samples, we generated RMA-normalized data from each xenograft RNA extraction environment (PDCCE and PDCCE_FFPE) separately. Pre-normalized expression values are provided as described above.

Because of the tendency of FFPE RNA to degrade during the fixation process, quality assessment of FFPE samples was performed by using 3DPCA as before. Using 3DPCA, it was found that one PDCCE FFPE sample, PDCCE_FFPE_CRC057.CEL, appeared to be an outlier as shown in **Supplementary Figure 2**. A box and whisker plot of the PDCCE FFPE samples supported this observation. This sample was removed from subsequent analysis, and the other PDCCE FFPE samples were RMA-normalized without this sample. These renormalized expression values are provided as described above.

To validate the oxaliplatin sensitivity signature on the fresh frozen PDCCE and formalin-fixed paraffin-embedded PDCCE samples, we uploaded the resistant NCI-60 oxaliplatin training set (for “train0”), the sensitive NCI-60 oxaliplatin training set (for “train1”), and both validation sets separately (PDCCE or PDCCE_FFPE, for “test”) to the CreateSignature module of the Duke GenePattern instance server (https://genepattern.genome.duke.edu/gp/pages/login.jsf) in order to generate predicted probabilities for the validation samples. Before running, relevant parameters were set as follows:

- version: 2
- num_genes: 120
- num_metagenes: 2
- apply_quantile_normalization: Yes
- apply_shiftscale_normalization: Yes
- burnin: 2000
- niter: 5000
- skips: 3

Predicted probabilities of validation data sets were generated as XY scatter plot of predicted probability versus metagene score (predictions.png) and numerically as predicted probabilities (probabilities.txt). Pearson correlations of mouse TGI versus predicted probability of oxaliplatin sensitivity were calculated in Graphpad Prism using Correlation analysis. **Figure 3b** was generated using BinReg probabilities from the PDCCE validation data set. **Figure 3c** was generated using BinReg probabilities the PDCCE_FFPE validation data set with CRC057 removed.

The following table summarizes the components of the BinReg model in terms of Affymetrix probesets, gene annotation, and posterior means of the Bayesian probit regression model, as determined by the MCMC parameters described above.

Probeset	Posterior Mean to the Regression Parameter	Gene Symbol	Gene Description
200060_s_at	0.012701	RNPS1	RNA binding protein S1, serine-rich domain
200091_s_at	0.018285	RPS25	ribosomal protein S25
200615_s_at	-0.023449	AP2B1	adaptor-related protein complex 2, beta 1 subunit
200768_s_at	0.011861	MAT2A	methionine adenosyltransferase II, alpha
200787_s_at	-0.034132	PEA15	phosphoprotein enriched in astrocytes 15
200788_s_at	-0.036282	PEA15	phosphoprotein enriched in astrocytes 15
200859_x_at	-0.021852	FLNA	filamin A, alpha (actin binding protein 280)
200878_at	-0.035524	EPAS1	endothelial PAS domain protein 1
200885_at	-0.033432	RHOC	ras homolog gene family, member C
201038_s_at	0.018821	ANP32A	Acidic (leucine-rich) nuclear phosphoprotein 32 family
201051_at	0.014587	ANP32A	Acidic (leucine-rich) nuclear phosphoprotein 32 family
201108_s_at	-0.036206	THBS1	thrombospondin 1
201109_s_at	-0.05787	THBS1	thrombospondin 1
201110_s_at	-0.068315	THBS1	thrombospondin 1
201162_at	-0.038152	IGFBP7	insulin-like growth factor binding protein 7
201163_s_at	-0.063467	IGFBP7	insulin-like growth factor binding protein 7
201172_x_at	-0.011621	ATP6V0E	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e
201289_at	-0.085481	CYR61	cysteine-rich, angiogenic inducer, 61
201391_at	0.014042	TRAP1	TNF receptor-associated protein 1
201968_s_at	-0.019467	PGM1	phosphoglucomutase 1
201969_at	0.024789	NASP	nuclear autoantigenic sperm protein (histone-binding)
201984_s_at	-0.016938	EGFR	epidermal growth factor receptor
202107_s_at	0.014657	MCM2	MCM2 minichromosome maintenance deficient 2, mitotin
202246_s_at	0.008335	CDK4	cyclin-dependent kinase 4
202258_s_at	0.009999	PFAAP5	phosphonoformate immuno-associated protein 5

202377_at	-0.029127	---	---
202503_s_at	0.014223	KIAA0101	KIAA0101
202551_s_at	-0.048592	CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)
202552_s_at	-0.035816	CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)
202566_s_at	-0.014421	SVIL	supervillin
202607_at	-0.014346	NDST1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1
202679_at	-0.020945	NPC1	Niemann-Pick disease, type C1
202822_at	-0.027163	LPP	LIM domain containing preferred translocation partner in lipoma
203104_at	-0.007808	CSF1R	colony stimulating factor 1 receptor
203504_s_at	-0.025273	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1
203505_at	-0.021747	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1
204036_at	-0.026615	EDG2	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2
204425_at	0.028924	ARHGAP4	Rho GTPase activating protein 4
204489_s_at	-0.042092	CD44	CD44 molecule (Indian blood group)
204647_at	-0.029052	HOMER3	homer homolog 3 (Drosophila)
204676_at	0.010861	C16ORF51	chromosome 16 open reading frame 51
204688_at	-0.04282	SGCE	sarcoglycan, epsilon
204805_s_at	0.012989	H1FX	H1 histone family, member X
205129_at	0.013757	NPM3	nucleophosmin/nucleoplasmin, 3
205743_at	-0.012022	STAC	SH3 and cysteine rich domain
205811_at	0.007325	POLG2	polymerase (DNA directed), gamma 2, accessory subunit
206116_s_at	-0.040724	TPM1	tropomyosin 1 (alpha)
207357_s_at	-0.022075	GALNT10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10
208711_s_at	-0.027546	CCND1	cyclin D1
208773_s_at	0.009103	ANKHD1	ankyrin repeat and KH domain containing 1
208924_at	-0.02271	RNF11	ring finger protein 11
208944_at	-0.031149	TGFBR2	transforming growth factor, beta receptor II (70/80kDa)

208955_at	0.022795	DUT	dUTP pyrophosphatase
209143_s_at	0.012729	CLNS1A	chloride channel, nucleotide-sensitive, 1A
209214_s_at	0.012813	EWSR1	Ewing sarcoma breakpoint region 1
209528_s_at	0.00667	TELO2	TEL2, telomere maintenance 2, homolog (S. cerevisiae)
209834_at	-0.01502	CHST3	carbohydrate (chondroitin 6) sulfotransferase 3
209835_x_at	-0.048195	CD44	CD44 molecule (Indian blood group)
209897_s_at	-0.020236	SLIT2	slit homolog 2 (Drosophila)
209946_at	-0.035352	VEGFC	vascular endothelial growth factor C
210138_at	-0.037848	RGS20	regulator of G-protein signalling 20
210416_s_at	0.007938	CHEK2	CHK2 checkpoint homolog (S. pombe)
210445_at	0.011578	FABP6	fatty acid binding protein 6, ileal (gastrotropin)
210764_s_at	-0.072264	CYR61	cysteine-rich, angiogenic inducer, 61
210916_s_at	-0.03891	CD44	CD44 molecule (Indian blood group)
210986_s_at	-0.057149	TPM1	tropomyosin 1 (alpha)
210987_x_at	-0.041709	TPM1	tropomyosin 1 (alpha)
211510_s_at	-0.003763	CRHR2	corticotropin releasing hormone receptor 2
211612_s_at	-0.02027	IL13RA1	interleukin 13 receptor, alpha 1 /// interleukin 13 receptor, alpha 1
211668_s_at	-0.055531	PLAU	plasminogen activator, urokinase /// plasminogen activator, urokinase
211926_s_at	-0.025531	MYH9	myosin, heavy polypeptide 9, non-muscle
211971_s_at	0.009539	LRPPRC	leucine-rich PPR-motif containing
212014_x_at	-0.046877	CD44	CD44 molecule (Indian blood group)
212061_at	0.012315	SR140	U2-associated SR140 protein
212298_at	-0.047463	NRP1	neuropilin 1
212315_s_at	0.016992	NUP210	nucleoporin 210kDa
212316_at	0.02634	NUP210	nucleoporin 210kDa
212656_at	0.008187	TSFM	Ts translation elongation factor, mitochondrial
212714_at	0.010496	LARP4	La ribonucleoprotein domain family, member 4

212962_at	-0.007104	SYDE1	synapse defective 1, Rho GTPase, homolog 1 (C. elegans)
213798_s_at	-0.019111	CAP1	CAP, adenylate cyclase-associated protein 1 (yeast)
213947_s_at	0.019042	NUP210	nucleoporin 210kDa
214030_at	-0.004711	DKFZP667G2110	hypothetical protein DKFZp667G2110
214060_at	0.011862	SSBP1	single-stranded DNA binding protein 1
214752_x_at	-0.021732	FLNA	filamin A, alpha (actin binding protein 280)
214882_s_at	0.015475	SFRS2	splicing factor, arginine/serine-rich 2
215068_s_at	-0.014855	FBXL18	F-box and leucine-rich repeat protein 18
215489_x_at	-0.028232	HOMER3	homer homolog 3 (Drosophila)
215501_s_at	-0.013771	DUSP10	dual specificity phosphatase 10
216515_x_at	0.013513	PTMA	prothymosin, alpha (gene sequence 28)
216538_at	0.008553	EXOC4	Exocyst complex component 4
216580_at	0.005455	RPL7	ribosomal protein L7
216908_x_at	0.01551	LOC94431	RNA polymerase I transcription factor RRN3-like
217166_at	0.007509	---	---
217340_at	0.005821	LOC645452	similar to 60S ribosomal protein L21
217763_s_at	-0.045543	RAB31	RAB31, member RAS oncogene family
217863_at	0.007136	PIAS1	protein inhibitor of activated STAT, 1
217915_s_at	0.01845	C15ORF15	chromosome 15 open reading frame 15
217993_s_at	0.007667	MAT2B	methionine adenosyltransferase II, beta
218088_s_at	-0.013031	RRAGC	Ras-related GTP binding C
218456_at	-0.027693	C1QDC1	C1q domain containing 1
218656_s_at	-0.021668	LHFP	lipoma HMGIC fusion partner
218718_at	-0.075054	PDGFC	platelet derived growth factor C
218768_at	0.006653	NUP107	nucleoporin 107kDa
218880_at	-0.024006	FOSL2	FOS-like antigen 2
218980_at	-0.016303	FHOD3	formin homology 2 domain containing 3
219713_at	0.003583	CARKL	carbohydrate kinase-like
219733_s_at	0.018246	SLC27A5	solute carrier family 27 (fatty acid transporter), member 5

220296_at	-0.015467	GALNT10	UDP-N-acetyl-alpha-D-galactosamine
221224_s_at	0.004925	DCAKD	dephospho-CoA kinase domain containing
221534_at	-0.011424	C11ORF68	chromosome 11 open reading frame 68
221563_at	-0.022191	DUSP10	dual specificity phosphatase 10
221821_s_at	0.010827	C12ORF41	chromosome 12 open reading frame 41
221843_s_at	-0.02271	KIAA1609	KIAA1609
222036_s_at	0.013709	MCM4	MCM4 minichromosome maintenance deficient 4 (S. cerevisiae)
222040_at	0.016708	HNRPA1	heterogeneous nuclear ribonucleoprotein A1
222222_s_at	-0.016202	HOMER3	homer homolog 3 (Drosophila)
222297_x_at	0.005141	RPL18	Ribosomal protein L18
31874_at	-0.02167	GAS2L1	growth arrest-specific 2 like 1
32094_at	-0.010808	CHST3	carbohydrate (chondroitin 6) sulfotransferase 3

Software used for analysis. The R statistical software package is available at www.r-project.org. The Bioconductor R package is available at www.bioconductor.org. ComBat is available as an R script at http://jlab.byu.edu/ComBat/. Matlab is a product of Mathworks (Natick, MA, USA) and is available at www.mathworks.com/products/matlab/. Graphpad Prism is a product of Graphpad Software (La Jolla, CA, USA) and is available at www.graphpad.com/prism/prism.htm. GenePattern is a genomic analysis platform developed by the Broad Institute (Cambridge, MA, USA), and custom Duke University GenePattern modules for Bayesian Binary Regression are available for use at https://genepattern.genome.duke.edu/gp/pages/login.jsf. All expression data and algorithms used are available at https://www.cancer.duke.edu/caarray/home.action.

Supplementary Figure Legends

Supplementary Figure 1. Quality Control Omission of MCF7 in NCI-60 Oxaliplatin Sensitivity Signature

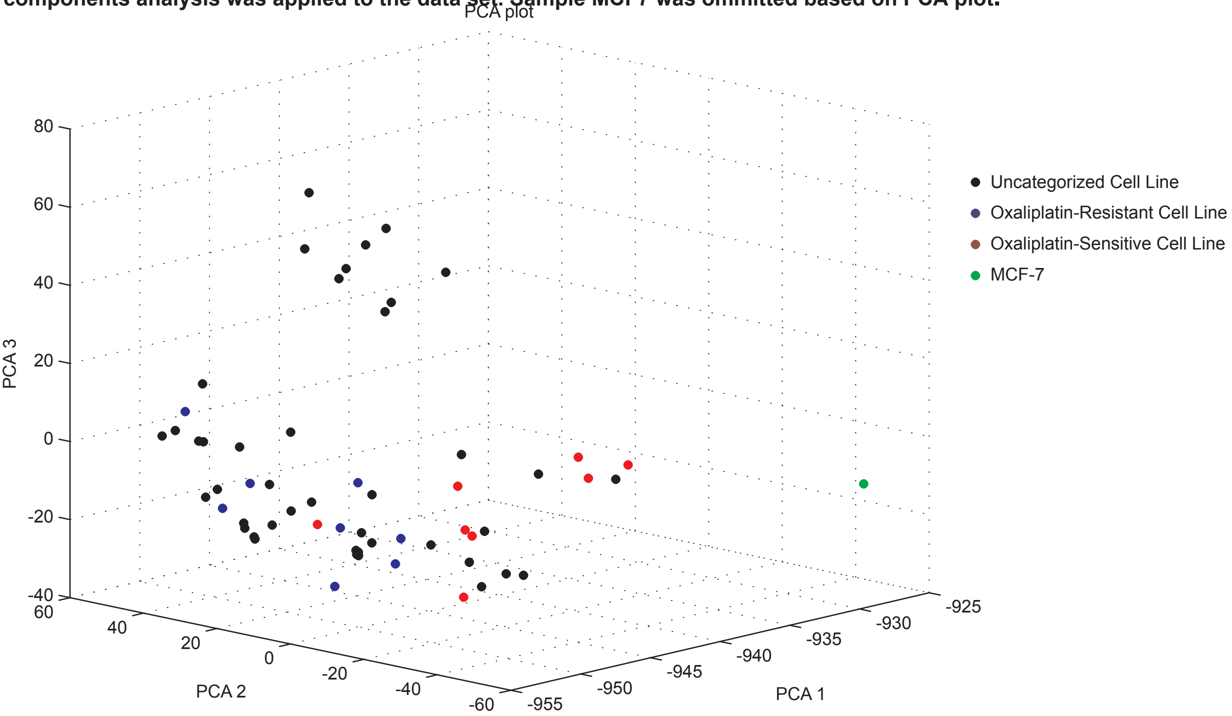
Fifty-nine samples from the NCI-60 cell panel were RMA normalized, and 3D principal components analysis was applied to the data set. The blue samples represent the resistant-classified cell lines in the oxaliplatin sensitivity signature. The red samples represent the sensitive-classified cell lines. The green sample represents MCF-7.

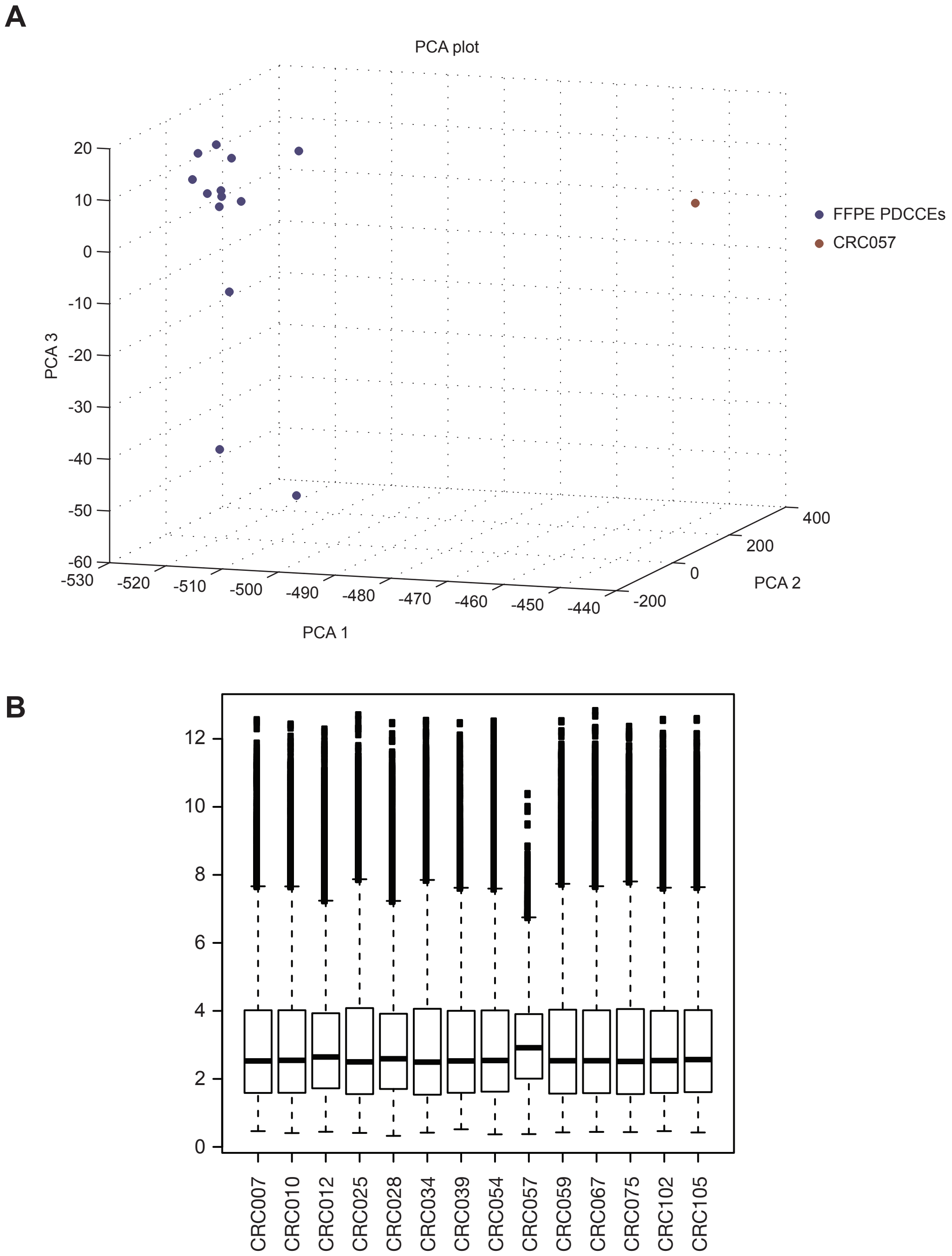
Supplementary Figure 2. Quality Control Omission of CRC057 in FFPE PDCCE Data Set

A. The 14 formalin-fixed paraffin-embedded PDCCEs were arrayed and RMA normalized, Affymetrix housekeeping probes were removed, and a 3D principal components analysis was applied to the data set. The red sample represents CRC057.

B. Box and whisker plot generated from the RMA normalized data.

Supplementary Figure 1 - Fifty-nine samples from the NCI-60 cell panel were RMA normalized and 3D principal components analysis was applied to the data set. Sample MCF7 was ommitted based on PCA plot.




A
PCA plot
PCA 3
20
10
0
-10
-20
-30
-40
-50
-60
-530
-520
-510
-500
-490
-480
-470
-460
-450
-440
PCA 1
-200
0
200
400
PCA 2
● FFPE PDCCEs
● CRC057
B
12
10
8
6
4
2
0
CRC007
CRC010
CRC012
CRC025
CRC028
CRC034
CRC039
CRC054
CRC057
CRC059
CRC067
CRC075
CRC102
CRC105

Supplementary Tables

Supplementary Table 1. Complete DTP NCI-60 Oxaliplatin Treatment Data

Cell Line[a]	Source	GI50 (μM)	TGI (μM)	LC50 (μM)
ADR-RES	Ovarian	0.03177	30.41	100
SW-620	Colon	0.04688	83.75	100
RPMI-8226	Leukemia	0.05272	91.20	100
MOLT-4	Leukemia	0.1365	15.63	100
HT29	Colon	0.1754	8.241	72.44
MCF7	Breast	0.2244	6.637	100
CCRF-CEM	Leukemia	0.3499	100	100
HCT-116	Colon	0.3784	100	100
NCI-H460	Non-Small Cell Lung	0.4355	38.28	100
MDA-MB-435	Melanoma	0.5768	18.62	48.19
A549	Non-Small Cell Lung	0.6152	84.14	100
HCC-2998	Colon	0.6180	10.02	61.24
HCT-15	Colon	0.6457	64.86	100
OVCAR-5	Ovarian	0.6714	21.23	100
SR	Leukemia	0.6966	92.68	100
786-0	Renal	0.7516	42.85	100
CAKI-1	Renal	0.7656	39.36	100
K-562	Leukemia	0.8551	95.28	100
LOX IMVI	Melanoma	1.127	100	100
SK-MEL-5	Melanoma	1.138	17.66	74.47
U251	Central Nervous System	1.832	27.04	63.24
IGROV1	Ovarian	1.849	35.89	100
ACHN	Renal	2.153	45.29	100
UACC-62	Melanoma	2.198	23.50	79.25

T-47D	Breast	2.213	100	100
NCI-H226	Non-Small Cell Lung	2.553	22.18	96.61
SN12C	Renal	2.564	100	100
SK-MEL-28	Melanoma	2.624	37.67	100
HL-60(TB)	Leukemia	2.831	100	100
MALME-3M	Melanoma	3.214	26.61	81.28
NCI-H522	Non-Small Cell Lung	3.926	32.36	100
OVCAR-4	Ovarian	4.093	83.75	100
SF-268	Central Nervous System	4.121	100	100
SF-295	Central Nervous System	4.710	100	100
A498	Renal	4.853	32.66	87.90
SK-MEL-2	Melanoma	5.152	52.84	100
OVCAR-3	Ovarian	5.702	41.69	100
OVCAR-8	Ovarian	5.998	100	100
DU-145	Prostate	6.166	100	100
M14	Melanoma	7.211	45.08	100
COLO 205	Colon	7.727	74.82	100
RXF 393	Renal	8.128	39.72	98.63
UO-31	Renal	8.472	43.65	92.47
SNB-19	Central Nervous System	9.840	100	100
SF-539	Central Nervous System	10.05	83.75	100
UACC-257	Melanoma	10.72	81.10	100
KM12	Colon	10.91	100	100
BT-549	Breast	12.33	100	100
PC-3	Prostate	17.86	100	100
SNB-75	Central Nervous System	18.45	100	100
TK-10	Renal	21.18	73.96	100

HOP-92	Non-Small Cell Lung	25.47	73.96	100
NCI-H322M	Non-Small Cell Lung	35.32	100	100
HOP-62	Non-Small Cell Lung	46.13	100	100
SK-OV-3	Ovarian	66.22	100	100
EKVX	Non-Small Cell Lung	88.72	100	100
MDA-MB-231	Breast	100	100	100
HS 578T	Breast	100	100	100

[a] There was no available data for the NCI-60 cell line MDA-N.

Supplementary Table 2. Gene List of NCI60-Derived Oxaliplatin Sensitivity Signature

Probe Set ID	**Gene Symbol**	**Gene Title**
200060_s_at	RNPS1	RNA binding protein S1, serine-rich domain /// RNA binding protein S1, serine-rich domain
200091_s_at	RPS25	ribosomal protein S25 /// ribosomal protein S25
200615_s_at	AP2B1	adaptor-related protein complex 2, beta 1 subunit
200768_s_at	MAT2A	methionine adenosyltransferase II, alpha
200787_s_at	PEA15	phosphoprotein enriched in astrocytes 15
200788_s_at	PEA15	phosphoprotein enriched in astrocytes 15
200859_x_at	FLNA	filamin A, alpha (actin binding protein 280)
200878_at	EPAS1	endothelial PAS domain protein 1
200885_at	RHOC	ras homolog gene family, member C
201038_s_at	ANP32A	Acidic (leucine-rich) nuclear phosphoprotein 32 family, member A
201051_at	ANP32A	Acidic (leucine-rich) nuclear phosphoprotein 32 family, member A
201108_s_at	THBS1	thrombospondin 1
201109_s_at	THBS1	thrombospondin 1
201110_s_at	THBS1	thrombospondin 1
201162_at	IGFBP7	insulin-like growth factor binding protein 7
201163_s_at	IGFBP7	insulin-like growth factor binding protein 7
201172_x_at	ATP6V0E	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e
201289_at	CYR61	cysteine-rich, angiogenic inducer, 61
201391_at	TRAP1	TNF receptor-associated protein 1
201968_s_at	PGM1	phosphoglucomutase 1
201969_at	NASP	nuclear autoantigenic sperm protein (histone-binding)
201984_s_at	EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)
202107_s_at	MCM2	MCM2 minichromosome maintenance deficient 2, mitotin (S.

		cerevisiae)
202246_s_at	CDK4	cyclin-dependent kinase 4
202258_s_at	PFAAP5	phosphonoformate immuno-associated protein 5
202377_at	---	---
202503_s_at	KIAA0101	KIAA0101
202551_s_at	CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)
202552_s_at	CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)
202566_s_at	SVIL	supervillin
202607_at	NDST1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1
202679_at	NPC1	Niemann-Pick disease, type C1
202822_at	LPP	LIM domain containing preferred translocation partner in lipoma
203104_at	CSF1R	colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog /// colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog
203504_s_at	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1
203505_at	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1
204036_at	EDG2	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2
204425_at	ARHGAP4	Rho GTPase activating protein 4
204489_s_at	CD44	CD44 molecule (Indian blood group)
204647_at	HOMER3	homer homolog 3 (Drosophila)
204676_at	C16ORF51	chromosome 16 open reading frame 51
204688_at	SGCE	sarcoglycan, epsilon
204805_s_at	H1FX	H1 histone family, member X
205129_at	NPM3	nucleophosmin/nucleoplasmin, 3
205743_at	STAC	SH3 and cysteine rich domain

205811_at	POLG2	polymerase (DNA directed), gamma 2, accessory subunit
206116_s_at	TPM1	tropomyosin 1 (alpha)
207357_s_at	GALNT10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)
208711_s_at	CCND1	cyclin D1
208773_s_at	ANKHD1 /// MASK-BP3	ankyrin repeat and KH domain containing 1 /// MASK-4E-BP3 alternate reading frame gene
208924_at	RNF11	ring finger protein 11
208944_at	TGFBR2	transforming growth factor, beta receptor II (70/80kDa)
208955_at	DUT	dUTP pyrophosphatase
209143_s_at	CLNS1A /// CLDND1	chloride channel, nucleotide-sensitive, 1A /// claudin domain containing 1
209214_s_at	EWSR1	Ewing sarcoma breakpoint region 1
209528_s_at	TELO2	TEL2, telomere maintenance 2, homolog (S. cerevisiae)
209834_at	CHST3	carbohydrate (chondroitin 6) sulfotransferase 3
209835_x_at	CD44	CD44 molecule (Indian blood group)
209897_s_at	SLIT2	slit homolog 2 (Drosophila)
209946_at	VEGFC	vascular endothelial growth factor C
210138_at	RGS20	regulator of G-protein signalling 20
210416_s_at	CHEK2	CHK2 checkpoint homolog (S. pombe)
210445_at	FABP6	fatty acid binding protein 6, ileal (gastrotropin)
210764_s_at	CYR61	cysteine-rich, angiogenic inducer, 61
210916_s_at	CD44	CD44 molecule (Indian blood group)
210986_s_at	TPM1	tropomyosin 1 (alpha)
210987_x_at	TPM1	tropomyosin 1 (alpha)
211510_s_at	CRHR2	corticotropin releasing hormone receptor 2
211612_s_at	IL13RA1	interleukin 13 receptor, alpha 1 /// interleukin 13 receptor, alpha 1

211668_s_at	PLAU	plasminogen activator, urokinase /// plasminogen activator, urokinase
211926_s_at	MYH9	myosin, heavy polypeptide 9, non-muscle
211971_s_at	LRPPRC	leucine-rich PPR-motif containing
212014_x_at	CD44	CD44 molecule (Indian blood group)
212061_at	SR140	U2-associated SR140 protein
212298_at	NRP1	neuropilin 1
212315_s_at	NUP210	nucleoporin 210kDa
212316_at	NUP210	nucleoporin 210kDa
212656_at	TSFM	Ts translation elongation factor, mitochondrial
212714_at	LARP4	La ribonucleoprotein domain family, member 4
212962_at	SYDE1	synapse defective 1, Rho GTPase, homolog 1 (C. elegans)
213798_s_at	CAP1	CAP, adenylate cyclase-associated protein 1 (yeast)
213947_s_at	NUP210	nucleoporin 210kDa
214030_at	DKFZP667G2110	hypothetical protein DKFZp667G2110
214060_at	SSBP1	single-stranded DNA binding protein 1
214752_x_at	FLNA	filamin A, alpha (actin binding protein 280)
214882_s_at	SFRS2	splicing factor, arginine/serine-rich 2
215068_s_at	FBXL18	F-box and leucine-rich repeat protein 18
215489_x_at	HOMER3	homer homolog 3 (Drosophila)
215501_s_at	DUSP10	dual specificity phosphatase 10
216515_x_at	PTMA /// LOC643287	prothymosin, alpha (gene sequence 28) /// similar to prothymosin, alpha (gene sequence 28)
216538_at	EXOC4	Exocyst complex component 4
216580_at	RPL7 /// LOC389305 ///	ribosomal protein L7 /// similar to 60S ribosomal protein L7 /// similar to 60S ribosomal protein L7 /// similar to 60S ribosomal

	LOC641750 /// LOC643906 /// LOC645737 /// LOC648000 /// LOC649312 /// LOC653702 /// LOC653949	protein L7 /// 60S ribosomal protein L7-like /// similar to 60S ribosomal protein L7 /// similar to 60S ribosomal protein L7 /// similar to 60S ribosomal protein L7 /// similar to 60S ribosomal protein L7
216908_x_at	LOC94431	RNA polymerase I transcription factor RRN3-like
217166_at	---	---
217340_at	LOC645452 /// LOC650644	similar to 60S ribosomal protein L21 /// similar to 60S ribosomal protein L21
217763_s_at	RAB31	RAB31, member RAS oncogene family
217863_at	PIAS1	protein inhibitor of activated STAT, 1
217915_s_at	C15ORF15	chromosome 15 open reading frame 15
217993_s_at	MAT2B	methionine adenosyltransferase II, beta
218088_s_at	RRAGC	Ras-related GTP binding C
218456_at	C1QDC1	C1q domain containing 1
218656_s_at	LHFP	lipoma HMGIC fusion partner
218718_at	PDGFC	platelet derived growth factor C
218768_at	NUP107	nucleoporin 107kDa
218880_at	FOSL2	FOS-like antigen 2
218980_at	FHOD3	formin homology 2 domain containing 3
219713_at	CARKL	carbohydrate kinase-like
219733_s_at	SLC27A5	solute carrier family 27 (fatty acid transporter), member 5
220296_at	GALNT10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)
221224_s_at	DCAKD	dephospho-CoA kinase domain containing

221534_at	C11ORF68	chromosome 11 open reading frame 68
221563_at	DUSP10	dual specificity phosphatase 10
221821_s_at	C12ORF41	chromosome 12 open reading frame 41
221843_s_at	KIAA1609	KIAA1609
222036_s_at	MCM4	MCM4 minichromosome maintenance deficient 4 (S. cerevisiae)
222040_at	HNRPA1 /// LOC644245	heterogeneous nuclear ribonucleoprotein A1 /// hypothetical protein LOC644245
222222_s_at	HOMER3	homer homolog 3 (Drosophila)
222297_x_at	RPL18	Ribosomal protein L18
31874_at	GAS2L1	growth arrest-specific 2 like 1
32094_at	CHST3	carbohydrate (chondroitin 6) sulfotransferase 3

Supplementary Table 3. PDCCE Tumor Growth Inhibition Over Time

	Days				
Sample ID	**0**	**2**	**7**	**14**	**16**
CRC007	-0.142	0.183	0.820	0.916	0.907
CRC010	-0.260	0.035	0.483	0.858	0.875
CRC012	-0.689	0.049	-0.108	0.346	0.486
CRC025	-0.037	0.246	0.481	0.896	0.969
CRC028	-0.091	0.280	0.745	0.847	0.907
CRC034	0.035	-0.186	-0.053	0.391	0.559
CRC039	-0.059	0.128	0.542	0.397	0.159
CRC054	0.131	0.088	0.413	0.184	0.546
CRC057	-0.116	-0.519	0.544	0.944	0.943
CRC059	-0.070	-0.162	-0.101	0.150	0.214
CRC067	0.073	0.291	0.738	0.523	0.578
CRC075	-0.404	0.336	0.519	0.764	0.695
CRC102	-0.130	--	0.549	0.767	0.858
CRC105	0.152	0.378	0.509	0.619	0.611

Supplementary Table 4. List of FFPE PDCCEs with Corresponding Class and Predicted Response

Mouse Explant	**Tumor Growth Inhibition**	**Identified Classification**[a]	**Oxaliplatin Predicted Probability**	**Predicted Response**[b]
CRC007	0.907	Sensitive	0.761	Respond
CRC010	0.875	Sensitive	0.266	Non-respond
CRC012	0.486	Resistant	0.291	Non-respond
CRC025	0.969	Sensitive	0.553	Respond
CRC028	0.907	Sensitive	0.677	Respond
CRC034	0.559	Resistant	0.390	Non-respond
CRC039	0.159	Resistant	0.288	Non-respond
CRC054	0.546	Resistant	0.421	Non-respond
CRC057[c]	--	--	--	--
CRC059	0.214	Resistant	0.326	Non-respond
CRC067	0.578	Resistant	0.607	Respond
CRC075	0.694	Sensitive	0.697	Respond
CRC102	0.858	Sensitive	0.881	Respond
CRC105	0.611	Resistant	0.374	Non-respond

[a] Each sample was identified as either resistant or sensitive to oxaliplatin based on the TGI cutoff of 0.643.

[b] Predicted response to oxaliplatin was determined by the oxaliplatin predicted probability cutoff of 0.5.

[c] CRC057 was removed for quality control reasons as discussed in the manuscript.