Figure W1. The MiPP algorithm. In Step 1, gene expression or phosphoproteomics data for the 11 sensitive and 16 resistant cell lines were split into multiple training and test sets and subjected to the development of prediction models for prediction by linear discriminant analysis. In Step 2, these models are then evaluated against a large number of random splits of the data into training and test sets so as to provide objective confidence intervals for prediction performance and average accuracy. Models may then be ranked by their MiPP score (the sum of the correct classification probabilities of correctly predicted samples minus the sum of incorrect classification probabilities of the incorrectly predicted samples) or the sMiPP (standardized MiPP score ranging to from −1 to 1). This second step thus allows candidate models to be ranked by their objective overall performance, selecting against models overfitting their training data. More detailed information (Soukup et al, *Bioinformatics* 2005;21 Suppl 1:i423–30) and code are available (www.bioconductor.org).
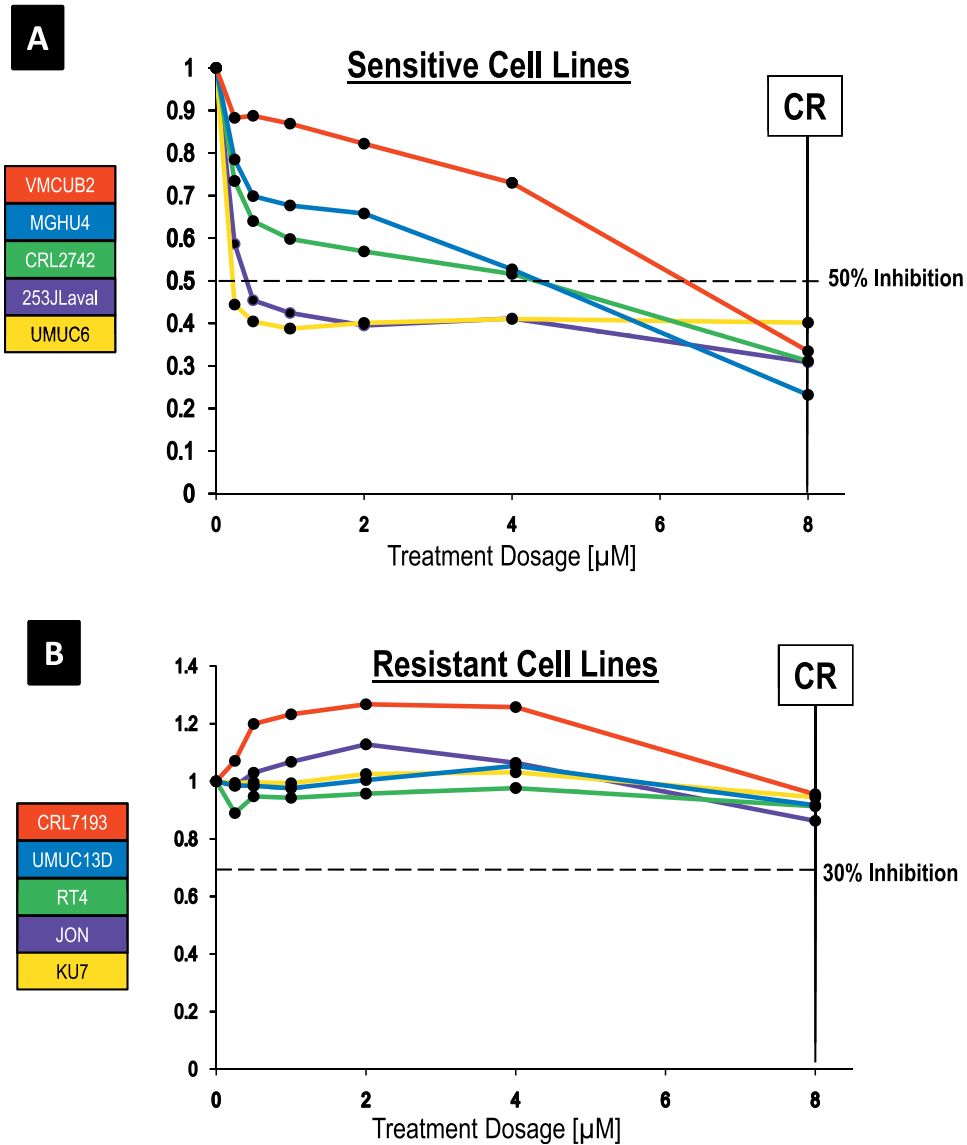
Figure W2. Examples of dose-response curves of (A) five sensitive and (B) five resistant bladder cancer cell lines. Sensitivity was defined as GI50 < 8 μM, whereas resistance was defined as GI30 > 8 μM. All cell lines were incubated with lapatinib for 72 hours in RPMI with 10% FBS to ensure internal consistency, with quantitation through the Alamar Blue assay. Cell counts were determined in at least three biologic replicates, normalized by the fraction of control growth for interassay comparison, and means were plotted for the indicated cell lines.

Table W1. Thirty-three Probes Associated with Sensitivity*.

Probe Set[†]	Name	Symbol	Fold[‡]
200951_s_at	Cyclin D2	CCND2	−5.94
200953_s_at	Cyclin D2	CCND2	−3.97
217767_at	Complement component 3	C3	−3.13
202219_at	Solute carrier family 6 (neurotransmitter transporter, creatine), member 8	SLC6A8	−2.70
212599_at	Autism susceptibility candidate 2	AUTS2	−2.70
213843_x_at	Solute carrier family 6 (neurotransmitter transporter, creatine), member 8	SLC6A8	−2.70
213506_at	Coagulation factor II (thrombin) receptor-like 1	F2RL1	−2.57
212399_s_at	Vestigial like 4 (*Drosophila*)	VGLL4	−2.02
210910_s_at	POM (POM121 homolog, rat) and ZP3 fusion	POMZP3	−1.74
218055_s_at	WD repeat domain 41	WDR41	−1.53
203066_at	B-cell RAG associated protein	GALNAC4S-6ST	−1.41
202653_s_at	Membrane-associated ring finger (C3HC4) 7	MARCH7	−1.33
212150_at	EFR3 homolog A (*S. cerevisiae*)	EFR3A	−1.07
206110_at	—	—	1.21
203765_at	Grancalcin, EF-hand calcium binding protein	GCA	1.24
219603_s_at	Zinc finger protein 226	ZNF226	1.24
218538_s_at	MRS2 magnesium homeostasis factor homolog (*S. cerevisiae*)	MRS2	1.25
214099_s_at	Phosphodiesterase 4D interacting protein	PDE4DIP	1.27
210102_at	von Willebrand factor A domain containing 5A	VWA5A	1.29
200733_s_at	Protein tyrosine phosphatase type IVA, member 1	PTP4A1	1.30
210054_at	HAUS augmin-like complex, subunit 3	HAUS3	1.39
219474_at	Chromosome 3 open reading frame 52	C3orf52	1.49
218000_s_at	Pleckstrin homology-like domain, family A, member 1	PHLDA1	1.53
203865_s_at	Adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)	ADARB1	1.56
219676_at	Zinc finger and SCAN domain containing 16	ZSCAN16	1.65
207655_s_at	B-cell linker	BLNK	1.70
221304_at	UDP glucuronosyltransferase 1 family, polypeptide A10	UGT1A10	1.93
205428_s_at	Calbindin 2	CALB2	2.06
204035_at	Secretogranin II (chromogranin C)	SCG2	2.14
205402_x_at	Protease, serine, 2 (trypsin 2)	PRSS2	2.28
210105_s_at	FYN oncogene related to SRC, FGR, YES	FYN	2.35
209942_x_at	Melanoma antigen family A, 3	MAGEA3	2.41
210467_x_at	Melanoma antigen family A, 12	MAGEA12	5.67

*Using SAM analysis (see Materials and Methods) for differential expression between 11 sensitive cell lines compared with 16 resistant cell lines.
[†]Probeset ID from the Affymetrix HG-U133A oligonucleotide microarray platform.
[‡]Fold change comparing resistant cell lines to sensitive ones.