



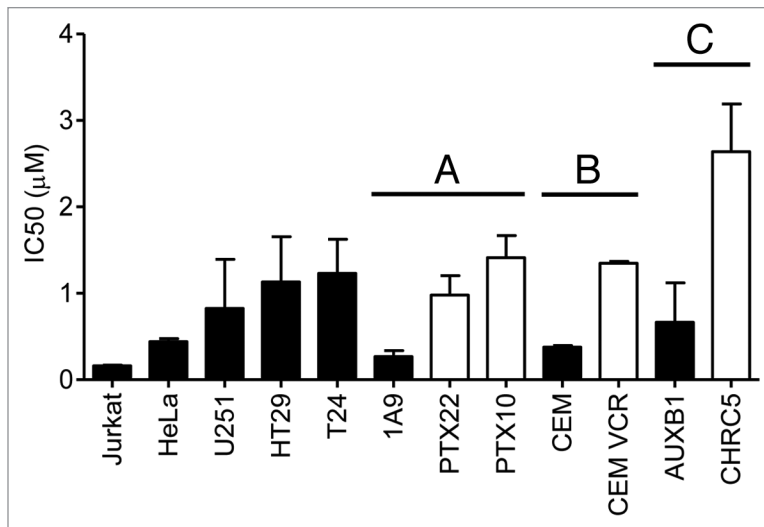
## **Supplemental Material to:**

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**A novel synthetic 1,3-phenyl bis-urea compound targets  
microtubule polymerization to cause cancer cell death**

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**Figure S1.** Half-maximal concentrations for cancer and drug-resistant cell lines treated with 41J. Cells were treated with 41J for 48 h and viability was determined by the resazurin assay. Non-linear least-squares regression was performed to determine the half-maximal concentration ( $IC_{50}$ ) for each drug. (A–C) Parental cell lines (black) are indicated with cell lines resistant to paclitaxel (A), vincristine (B), or colchicine (C) (white).

**Table S1.** Gene expression changes due to 41J treatment

Symbol	Accession ID	Gene title	Fold change <sup>a</sup>	P value <sup>b</sup>
<i>Upregulated genes</i>				
MAGT1	NM_032121.3	Magnesium transporter 1	2.02	0.0003
TROAP	NM_005480.2	Trophinin associated protein (tastin)	1.91	0.001
CCNB1	NM_031966.2	Cyclin B1	1.88	0.002
BORA	NM_024808.2	Bora, aurora kinase A activator	1.86	0.003
CKS2	NM_001827.1	CDC28 protein kinase regulatory subunit 2	1.81	0.003
CENPA	NM_001809.2	Centromere protein A, 17kDa	1.74	0.002
LOC643995	XM_934412.1	Predicted: similar to Importin alpha-2 subunit (Karyopherin alpha-2 subunit), transcript variant 4	1.74	2.7E-06
NEK2	NM_002497.2	NIMA (never in mitosis gene a)-related kinase 2	1.74	0.003
KIF14	NM_014875.1	Kinesin family member 14	1.72	0.004
AURKA	NM_198434.1	Aurora kinase A, transcript variant 3	1.72	0.0002
EPHA2	NM_004431.2	EPH receptor A2	1.70	0.009
CKAP2	NM_018204.2	Cytoskeleton associated protein 2	1.69	0.003
LOC649841	XM_938906.1	Predicted: similar to protein immuno-reactive with anti-PTH polyclonal antibodies	1.69	0.011
MCART1	NM_033412.1	Mitochondrial carrier triple repeat 1	1.68	0.009
TTK	NM_003318.3	TTK protein kinase	1.65	0.017
LOC100133840	XM_001714384.1	Predicted: similar to hCG1994151	1.65	0.017
KBTBD2	NM_015483.1	Kelch repeat and BTB (POZ) domain containing 2	1.63	0.001
LOC441087	NM_001013716.1	Hypothetical gene supported by AK125735	1.63	0.022
EGR1	NM_001964.2	Early growth response 1	1.63	0.018
HMMR	NM_012485.1	Hyaluronan-mediated motility receptor, transcript variant 2	1.62	0.002

<sup>a</sup>Fold change indicates expression levels for 41J treatment compared to DMSO; <sup>b</sup>P values are based on two-sample t test.

**Table S1.** Gene expression changes due to 41J treatment (continued)

Symbol	Accession ID	Gene title	Fold change <sup>a</sup>	P value <sup>b</sup>
<i>Downregulated genes</i>				
SOX18	NM_018419.2	SRY (sex determining region Y)-box 18	-1.78	0.003
FOXS1	NM_004118.3	Forkhead box S1	-1.77	0.009
MGC61598	XM_939432.1	Predicted: similar to ankyrin-repeat protein Nrarp	-1.66	0.001
TUBB3	NM_006086.2	Tubulin, beta 3	-1.58	0.002
LOC100132439	XM_001719283.1	Predicted: similar to Protein FAM27E3	-1.55	0.023
TUBA4A	NM_006000.1	Tubulin, alpha 4a	-1.52	0.021
PLEKHF1	NM_024310.2	Pleckstrin homology domain containing, family F (with FYVE domain) member 1	-1.50	0.006
MFSD5	NM_032889.2	Major facilitator superfamily domain containing 5	-1.49	0.005
HES2	NM_019089.3	Hairy and enhancer of split 2 (Drosophila)	-1.48	0.002
TUBB2A	NM_001069.2	Tubulin, beta 2A	-1.48	0.012
LOC255783	XR_001409.1	Predicted: hypothetical protein LOC255783, transcript variant 2, misc RNA	-1.45	0.016
EFNA1	NM_004428.2	Ephrin-A1, transcript variant 1	-1.45	0.012
FOXC1	NM_001453.1	Forkhead box C1	-1.45	0.014
LOC100134073	XM_001718050.1	Predicted: similar to LYPDC1 protein (LOC100134073)	-1.42	0.005
TUBB2B	NM_178012.3	Tubulin, beta 2B	-1.42	0.001
LOC92755	XR_016140.2	Predicted: miscRNA	-1.41	0.002
SOX9	NM_000346.2	SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	-1.41	0.009
SNORA24	NR_002963.1	Small nucleolar RNA, H/ACA box 24	-1.41	0.030
RGMA	NM_020211.1	RGM domain family, member A	-1.40	0.015
SOX13	NM_005686.2	SRY (sex determining region Y)-box 13	-1.40	0.013

<sup>a</sup>Fold change indicates expression levels for 41J treatment compared to DMSO; <sup>b</sup>P values are based on two-sample *t* test.