Table S2 IC_{50} values of **50–125** against cancer and normal cell lines, at different incubation time, mechanism of action, target and cell cycle arrest.

Complex Number	Cell line/IC_{50} (μM) [1,2]						Mechanism of action	Cell Cycle arrest	Target	Ref.
3.2.4.1. N^N (2,2'-bipyridine, 1,10-phenanthroline and aliphatic diamine)										
50a	A2780 (SRB)	> 100						n.d	n.d	24, 176
50b		15.86 ± 1.49								24, 28
50c	A549	14.7 ± 0.4					**1A**	n.d	Mitochondria	24, 28, 179
50d		12.5 ± 0.2					NADH			28, 207
50e		16.2 ± 0.5								28
50f		11.3 ± 1.0								
50g		12.0 ± 0.9					**1A**	S-phase and G_2/M	Mitochondria	
50h		> 100					NADH/MMP	S-phase	Mitochondria	
50i		> 100					NADH	n.d		
50j [T]	A549	30.7 ± 1.4	BEAS-2B [N]	70.3 ± 1.9	16HBE [N]	74.6 ± 0.6	NADH/ROS	G_1	Doesn't target the DNA	116
50k [T]		35.2 ± 1.4		28.1 ± 3.1		19.6 ± 1.4		n.d		
50l [T]		14.9 ± 0.3		14.7 ± 1.3		26.6 ± 1.2				
50m [T]		14.3 ± 1.2		14.3 ± 1.3		16.7 ± 1.7				
50n [T]		11.3 ± 0.9		5.0 ± 0.4		3.9 ± 0.1				22, 116
50o [T]		7.3 ± 1.2		21.7 ± 2.3		43.0 ± 3.7		sub-G_1 & G_2/M and		
50p	MCF-7	22.9 ± 2.0	HT-29	10.5 ± 0.7				n.d		22
50q		> 250		> 250						
50r		2.3 ± 0.3		2.0 ± 0.4						
50s		> 250		> 250						
50t		184.5 ± 16.0		> 250						
50u		> 250		> 250						
51a	A2780 (SRB)	> 100						n.d	DNA	24, 176
51b		6.70 ± 0.62								24

51c [T]	A2780 (SRB); 0.22 ± 0.03 A2780cisR (SRB); 0.42 ± 0.03 CHO-K1 [(N)] (SRB); 12.0 ± 0.3			MCF-7 (SRB); 0.84 ± 0.08 HL-60 (SRB); 0.28 ± 0.05 HSF [(N)] (SRB); 5.48 ± 0.37			**1A or 2A** DNA Damage	G_0/G_1	DNA/ Mitochondria	24, 29, 205
51d [T]	MCF-7 (crystal violet)	63.2	HT-29 (crystal violet)	56.0	HEK-293T [(N)] (crystal violet)	50.7		n.d		204
51e [T]		33.9		19.0		51.6				
51f [T]		29.9		28.5		15.7				
51g	A549	> 100		BEAS-2B [(N)]	n.d			n.d		29
51h		> 100			n.d					
51i		> 100			n.d					
51j		> 100			n.d.					
51k		16.9 ± 0.2			n.d.					
51l		25.3 ± 0.1			n.d.					
51m [T]		4.4 ± 1.2			6.3 ± 0.8		**1B**	No effect	Lysosome	
51n [*]	A2780; 15.8 ± 1.8		A2780cisR; 13.0 ± 1.4	MRC-5 [(N)]; 124.1 ± 16.7			MMP\ROS HDAC inhibition	S-phase	Mitochondria	206
52	A2780 (MTS); 1.83 ± 0.04 A2780cisR (MTS); 1.35 ± 0.08			OVCAR-3 (MTS); 1.92 ± 0.03 SKOV-3 (MTS); 5.41 ± 0.22			DNA damage/Apoptosis	n.d	Late endosomes and lysosomes DNA	207
53a	A2780 (SRB)	49.5					n.d	n.d	No interaction with nucleobases.	208
53b		48.4								
53c		0.98					Convert GSH into GSSG.			
53d		0.61								
54a [*]	HeLa (48h)	11.60 ± 1.6	Caco-2 (72h)	4.43 ± 0.52	HEK-293T [(N)]	> 100	n.d	n.d	Mitochondria	209
54b [*]		30.61 ± 1.5		11.52 ± 0.54		> 100				
54c [*]		27.57 ± 2.0		6.05 ± 0.77		> 100	Mitochondrial damage		Mitochondria\ DNA	
54d [*]		12.72 ± 1.01		7.28 ± 0.37		> 100	n.d			
54e [*]		2.47 ± 0.68		9.85 ± 0.44		> 100	Mitochondrial damage		Mitochondria\ DNA	
54f [*]		1.70 ± 0.49		4.72 ± 0.95		> 100	n.d			
54g [*]		113.22 ± 2.30		4.28 ± 0.32		> 100				
54o	HCT-116; 4.14 ± 1.2			HEK-293T [(N)]; > 100			**2A** / inhibitor of	G_0/G_1	Mitochondria\	210

				autophagy for the eradication of cancer stem cells. BcL-2 increase /DNA damage		DNA	
54p [T]	MDA-MB-468	3.673	HaCaT [(N)]	11.42	MMP/ROS	Sub-G_1	Mitochondria	212
54q		20.35		n.d		n.d		
54r		20.27						
54s		5.202						
54t		4.412						
55a	A549	6.8 ± 0.5			NADH	n.d	DNA	213
55b		1.5 ± 0.1						
55c		3.6 ± 0.5			NADH/ROS/Apoptosis	sub-G_1, G_1 and S-phase		
55d		4.8 ± 2.1			NADH	n.d		
55e		1.7 ± 0.2						
55f		7.1 ± 0.8			NADH/ROS/Apoptosis	sub-G_1, G_2/M and S-phase		
56a	A549	36.3 ± 0.6			NADH	n.d		214
56b		> 100						
56c		> 100						
56d		3.5 ± 0.1						
56e		1.3 ± 0.1			ROS	Disrupt G_0/G_1 and G_2/M	Lysosome	
56f		3.7 ± 0.2			NADH	n.d		
56g		5.7 ± 0.2						
56h		1.2 ± 0.1			**1B**	G_2/M	Lysosome	
56i		1.8 ± 0.2			NADH	n.d		
57a	A549; 18.3 ± 0.8		HeLa; 20.1 ± 2.1			n.d		189
	16HBE [(N)]; n.d		BEAS-2B [(N)]; n.d					
57b [T]	A549; 4.3 ± 0.2		HeLa; 4.2 ± 0.2					
	16HBE [(N)]; 7.7 ± 0.1		BEAS-2B [(N)]; 7.2 ± 0.6					
57c [T]	A549; 3.8 ± 0.1		HeLa; 3.0 ± 0.5		MMP/LMP/Apoptosis	G_0/G_1	Lysosome / Mitochondria	
	16HBE [(N)]; 10.1 ± 0.2		BEAS-2B [(N)]; 4.4 ± 0.5					

								and Doesn't target the DNA	
57d [T]	A549; 12.1 ± 0.3			HeLa; 7.3 ± 1.4			n.d	Doesn't target the DNA	
	16HBE [(N)]; 11.6 ± 1.7			BEAS-2B [(N)]; 13.5 ± 1.7					
57e [*]	A549; 56.7 ± 8.6			HeLa; > 100			n.d	n.d		202
	HepG2; > 100			16HBE [(N)]; 35.4 ± 0.1					
	BEAS-2B [(N)]; > 100								
57f [T]	A549; 2.6 ± 0.3			HeLa; 3.6 ± 0.8			**1B**	No effect	Lysosome	
	HepG2; 5.5 ± 0.7			16HBE [(N)]; 2.6 ± 0.1					
	BEAS-2B [(N)]; 3.0 ± 0.2								
57g [T]	A549; 7.9 ± 0.2			HeLa; 6.7 ± 1.1			Apoptosis	n.d		
	HepG2; 9.7 ± 1.7			16HBE [(N)]; 5.0 ± 1.6						
	BEAS-2B [(N)]; 11.7 ± 1.3									
57h [T]	A549; 6.2 ± 0.3			HeLa; 5.6 ± 0.6						
	HepG2; 8.3 ± 0.1			16HBE [(N)]; 7.4 ± 1.1						
	BEAS-2B [(N)]; 9.2 ± 3.4									
58a [*]	A549; > 100			HeLa; > 100			n.d	n.d		203
	HepG2; > 100			BEAS-2B [(N)]; > 100						
58b [T]	A549; 15.6 ± 1.2			HeLa; 11.3 ± 0.1			**2A** /anti-metastasis	G_2/M and S-phase	Mitochondria	
	HepG2; 11.8 ± 3.6			BEAS-2B [(N)]; 14.0 ± 2.1						
58c [T]	A549; 17.0 ± 4.1			HeLa; 17.1 ± 3.6			**2A**	n.d	Lysosome	
	HepG2; 4.9 ± 0.7			BEAS-2B [(N)]; 16.4 ± 1.4						
59a [T]	A549	3.56 ± 0.5	16HBE [(N)]	6.61 ± 0.2	BEAS-2B [(N)]	6.31 ± 0.9	NADH/ROS/Apoptosis	Sub-G_1	DNA	215
59b [T]		17.27 ± 0.1		35.10 ± 0.7		20.52 ± 1.4	NADH/ROS	n.d		
60	A549; > 200			A2780; > 200				n.d		6
	A549R; > 200			HeLa; > 200						
	MCF-7; > 200			LO2; > 200						
61a	A2780; 2.49			A549; 22.9				n.d		216
	HCT-116; 19.1			MCF-7; 17.5						
	PC3; 9.02									
61b	A2780; 0.89			A549; 10.7						
	HCT-116; 49.5			MCF-7; 7.2						
	PC3; 5.77									
61c	A2780; 1.06			A549; 1.82						
	HCT-116; 2.22			MCF-7; 1.5						

	PC3; 9.23						
62a [T]	A2780; 2.8 ± 0.4		A2780cisR; 6.4 ± 0.5	COX/GST enzyme inhibition DNA metalation.	n.d	DNA and GST Enzyme	217
	MCF-7; 8.0 ± 0.9		HeLa; 17.1 ± 0.6				
	HEK-293T [(N)]; 10.3 ± 0.6						
62b [T]	A2780; 7.0 ± 0.8		A2780cisR; 8.5 ± 0.5				
	MCF-7; 9 ± 1		HeLa; 24 ± 5				
	HEK-293T [(N)]; 12.5 ± 0.8						
62c [*]	A2780; > 100		A2780cisR; 63 ± 6				
	MCF-7; 140 ± 30		HeLa; 190 ± 9				
	HEK-293T [(N)]; > 100						
63 [T]	A2780; 5.9 ± 0.2		HLF [(N)]; 11.9 ± 0.4	ROS/MMP/ Autophagy down regulation of MMP2/MMP9 proteins/Metastasis	G_2/M	Mitochondria	218
64a	A2780	> 100	MCF-7; > 500		n.d		24, 219
64b		16.97 ± 0.05					24
65a	MCF-7	> 500		NADH/ROS	n.d		219
65b		> 500					
65c		> 500					
65d		105.2 ± 1.4					
66a		394.6 ± 10.8					
67	No Cytotoxic activity could be obtained				n.d		220
68a	A2780 (SRB); 0.40 ± 0.03				S/G_2		140, 222
68b	A549 (SRB); 1.01 ± 0.08		CNE2 (SRB); 1.26 ± 0.04		n.d		223
	A2780 (SRB); 0.25 ± 0.02		A2780cisR (SRB); 0.049 ± 0.001				
68j	A549 (SRB); 1.5 ± 0.3		CNE2 (SRB); 2.3 ± 0.3				
	A2780 (SRB); 0.12 ± 0.04		A2780cisR (SRB); 0.114 ± 0.003				
3.2.4.2. Azo-, hydroxylamine and Schiff-base N,N-ligands							
69a	DI	366.2 ± 0.07	EAC	393.11 ± 0.06	Apoptosis	n.d		224
69b		1.52 ± 0.06		2.41 ± 0.09			
69c		9.58 ± 0.06		7.23 ± 0.09			

69d		7.98 ± 0.06		13.22 ± 0.04				
70a	MCF-7; 5				Apoptosis	S-phase	DNA, Protein and RNA	225
70b	A549	5.1 ± 0.3	HeLa	6.5 ± 0.6	**1A**	n.d	Nucleus	226
70c		25.7 ± 2.5		28.7 ± 1.2				
71a	HT-29	5.82 ± 2.41	MIA-PaCa-2	2.87 ± 0.26		n.d		227
71b		7.92 ± 1.00		8.35 ± 0.29				
71c		10.54 ± 4.73		9.65 ± 1.68				
71d	A549	75.9 ± 0.7					n.d	228
71e		14.4 ± 0.8						
71f		11.8 ± 0.3			Interact with nucleobases. NADH/ROS / apoptosis	G_2/M and S-phases		
71g		> 100						
71h		16.9 ± 0.8						
71i		2.7 ± 0.1			NADH/ROS/ apoptosis	G_1-phase		
72a	A549; 16.3 ± 2.2		HeLa; >100			n.d	DNA does not appear to be the major target.	117
	16HBE (N); n.d		BEAS-2B (N); n.d					
72b	A549; 28.8 ± 0.6		HeLa; 13.9 ± 0.1					
	16HBE (N); n.d		BEAS-2B (N); n.d					
72c T	A549; 1.4 ± 0.2		HeLa; 1.3 ± 0.1		NADH/ROS/Apoptosis	S-phase		
	16HBE (N); 2.6 ± 0.1		BEAS-2B (N); 1.7 ± 0.1					
72d	A549; 26.3 ± 1.0		HeLa; 38.6 ± 1.6		NADH	n.d		
	16HBE (N); n.d		BEAS-2B (N); n.d					
72e	A549; 4.1 ± 0.6		HeLa; n.d					
	16HBE (N); n.d		BEAS-2B (N); n.d					
72f	A549; 15.4 ± 0.1		HeLa; 6.7 ± 0.7					
	16HBE (N); n,d		BEAS-2B (N); n.d					
72g T	A549; 1.1 ± 0.1		HeLa; 1.4 ± 0.1		NADH/ROS/Apoptosis	G_2/M		
	16HBE (N); 1.1 ± 0.1		BEAS-2B (N); 0.7 ± 0.1					
73a		11.4 ± 1.8		21.7 ± 1.2		n.d		229
73b		3.5 ± 0.1		2.2 ± 0.7				
73c		1.2 ± 0.2		1.5 ± 0.4	NADH/LMP/MMP/	No effect	Lysosome	

	A549		HeLa		Apoptosis			
73d		2.6 ± 1.3		4.3 ± 0.1		n.d		
73e		2.3 ± 0.1		2.8 ± 0.3				
73f		1.5 ± 0.2		1.4 ± 0.2				
74a	A549; 167.0 ± 2.7		HepG2; 183.2 ± 2.1		NADH	n.d	Lysosome	230
	HeLa; 164.0 ± 3.0		BEAS-2B (N); n.d					
74b	A549; 182.5 ± 3.1		HepG2; 175.0 ± 2.8		NADH/ROS/Apoptosis	No effect		
	HeLa; 177.5 ± 3.5		BEAS-2B (N); n.d					
74c	A549; 193.4 ± 2.5		HepG2; 179.3 ± 3.2		NADH	n.d		
	HeLa; 173.5 ± 2.7		BEAS-2B (N); n.d					
74d T	A549; 38.6 ± 0.5		HepG2; 34.6 ± 1.1		**1B**	G_1		
	HeLa; 35.6 ± 1.8		BEAS-2B (N); 58.8 ± 1.7					
74e T	A549; 50.5 ± 0.7		HepG2; 35.7 ± 0.9		NADH	n.d		
	HeLa; 32.6 ± 1.4		BEAS-2B (N); 82.1 ± 2.0					
74f T	A549; 50.3 ± 1.2		HepG2; 46.9 ± 1.3					
	HeLa; 41.1 ± 1.7		BEAS-2B (N); 82.6 ± 1.5					
74g T	A549; 51.0 ± 0.8		HepG2; 34.8 ± 0.9					
	HeLa; 33.1 ± 1.0		BEAS-2B (N); 57.8 ± 0.9					
74h	A549; > 100		HepG2; > 100		Slight loss in MMP ROS not the major MoA	No effect	Mitochondria	231
	HeLa; > 100		BEAS-2B (N); n.d					
74i	A549; > 100		HepG2; > 100			n.d		
	HeLa; > 100		BEAS-2B (N); n.d					
74j	A549; > 100		HepG2; > 100					
	HeLa; > 100		BEAS-2B (N); n.d					
74k	A549; > 100		HepG2; > 100					
	HeLa; > 100		BEAS-2B (N); n.d					
74l T	A549; 20.5 ± 0.4		HepG2; 12.5 ± 2.8		MMP/Apoptosis ROS not the major MoA	Sub-G_1 & S	Mitochondria	
	HeLa; 6.9 ± 0.7		BEAS-2B (N); 6.9 ± 0.7					
74m T	A549; 5.4 ± 1.4		HepG2; 23.0 ± 0.7			n.d		
	HeLa; 3.4 ± 0.1		BEAS-2B (N); 1.9 ± 0.7					
75a		32.4 ± 3.5		12.3 ± 1.8	35.3 ± 0.2		n.d	Lysosome	232
75b		11.7 ± 0.1		9.1 ± 0.5	14.8 ± 0.4				
75c		7.6 ± 0.4		7.5 ± 0.2	9.2 ± 0.2				

75d	A549 (24h)	25.8 ± 2.0	A549 (48h)	10.2 ± 0.9	HeLa (24h)	28.3 ± 1.5				
75e		10.0 ± 0.9		8.9 ± 0.4		13.7 ± 0.6				
75f		6.6 ± 0.3		3.7 ± 0.2		9.4 ± 0.4				
75g		14.1 ± 0.1		12.1 ± 0.5		18.4 ± 0.5	NADH			
75h		5.6 ± 0.5		5.0 ± 0.1		9.1 ± 0.47				
75i [T]	A549 (24h); 3.4 ± 0.2			A549 (48h); 2.9 ± 0.2			**1B**	G_1	Lysosome	
	HeLa (24h); 6.7 ± 0.1			BEAS-2B [(N)]; 3.8 ± 0.5						
75j	A549 (24h)	20.7 ±1.9	A549 (48h)	13.2 ± 0.7	HeLa (24h)	23.3 ±0.6		n.d		
75k		10.7 ± 0.6		7.8 ± 0.5		13.5 ± 0.3				
75l		3.4 ± 0.1		3.0 ± 0.4		6.7 ± 0.2				
75m		21.5 ± 0.9		15.4 ± 0.2		25.4 ± 0.8				
75n		12.9 ± 0.6		12.6 ± 0.3		14.2 ± 0.3				
75o		3.6 ± 0.2		3.5 ± 0.3		6.2 ± 0.2				
76 [*]	HCT-116; 31.33 ± 12.92		MIA-PaCa-2; 82.09 ± 2.55		ARPE-19 [(N)]; > 100		n.d	n.d		165
77a	HepG2 (SRB); 11 ± 2		NCI-H460 (SRB); 0.9 ± 0.01				Strong inhibitor of kinesin spindle protein.	n.d		233
	SW620 (SRB); 0.86		SW480 (SRB); 2.9 ± 0.3							
	HCT-116 (SRB); 0.41 ± 0.05		SiHa (SRB); 3.1 ± 0.2							
77b	HepG2; 110 ± 77		NCI-H460; 29 ± 3							
	SW620; 39		SW480; 40 ± 2							
	HCT-116; 14 ± 2		SiHa;26 ± 1							
77c	SiHa;6.14						Apoptosis\necrosis	n.d	CT-DNA binding	235
3.2.4.3 Heterocyclic based N^N-ligands										
78	A2780; > 300		A2780cisR; > 300					n.d		237
79 [*]	DI; 30-40						DNA intercalative/ electrostatic interactions Apoptosis	n.d	DNA	238
80	n.d						DNA binding Apoptosis	n.d	DNA	239
81a	n.d						Cross-linked DNA binding	n.d	DNA	240
81b	n.d							n.d	DNA	
81c [*]	A549 (MTS); > 500	Hela (MTS); > 500	MT4 (MTS); 67 ± 6	HEK-293 [(N)] (MTS); > 500				n.d	DNA	10
	BHK21 [(N)]; 55 ± 1									

81d *	A549 (MTS); > 500		Hela (MTS); 2.5 ± 1		MT4 (MTS); 111 ± 7		HEK-293 (N) (MTS); > 500							n.d		
	BHK21 (N) (MTS); n.d															
82	arterial thrombosis or the bidirectional crosstalk between platelets and tumor cells; 6µM													n.d		241
83 *	MV-4-11; 81.5 ± 9.4			MCF-7; > 100			BALB/3T3 (N); > 100						DNA electrostatic interactions	n.d	Endoplasmic reticulum and Mitochondria.	242
	HL-60; 30.86 ± 0.75			LoVo; 61 ± 0												
84a T	A2780; 22.0 ± 2.5			A2780cisR; 32.7 ± 1.7			PNT2 (N); 32.1 ± 3.9						NADH/ROS	n.d		113
84b	DU-145; 8.6 ± 0.8			A375; 6.5 ± 0.6			HepG2; 8.7 ± 0.8						NADH	n.d		138
	A549; 3.7 ± 0.4			MCF-7; 12.6 ± 1.3												
84c	DU-145; 11.0 ± 1.0			A375; 12.0 ± 0.9			HepG2; 10.0 ± 0.5									
	A549; 10.1 ± 0.7			MCF-7; 13.1 ± 0.9												
85	A549; > 200		SW480; > 200		HepG2; 130 ± 9		A2780; 162 ± 12		IMR-90; > 200				DNA binding	n.d	DNA	124
86a	A2780		> 100											n.d		243
86b			76.9 ± 11.4													
86c			23.5 ± 1.1													
86d			70.6 ± 2.6													
86e			87.1 ± 5.3													
86f			83.0 ± 4.1													
87a	A2780 (SRB)	n.d	ID8 (SRB)	n.d	Cap-an2 (SRB)	n.d	Sasos (SRB)	n.d	L428 (SRB)	n.d	Fibro-Blast (N) (SRB)	n.d		n.d		244
87b		n.d		n.d		n.d		n.d		n.d		n.d				
87c		n.d		n.d		n.d		n.d		n.d		n.d				
87d		n.d		n.d		n.d		n.d		n.d		n.d				
87e		n.d		n.d		n.d		n.d		n.d		n.d				
87f		1.64		0.98		4.15		n.d		n.d		n.d	ROS/ Activates cytostatic activity			
87g		n.d		n.d		n.d		n.d		n.d		n.d				
87h		n.d		n.d		n.d		n.d		n.d		n.d				
87i		n.d		n.d		n.d		n.d		n.d		n.d				
87j		n.d		n.d		n.d		n.d		n.d		n.d				
87k		n.d		n.d		n.d		n.d		n.d		n.d				
87l		n.d		n.d		n.d		n.d		n.d		n.d				
87m	A2780 (SRB); 0.891			ID8 (SRB); 0.799			L428 (SRB); n.d			Fibroblast (N) (SRB);n.d			ROS	n.d		245
	Capan2 (SRB); 1.93			Sasos (SRB); 1.58			A2780cis (SRB); 1.535									

88a [T]	A2780 (MTT)	n.d	A2780 (SRB)	1.69	Fibrob last [(N)]	n.d	Fibro blast [(N)] (SRB)	14.14	Induced cytostasis	n.d		246
88b		11.64		6.20		n.d		n.d				
88c		n.d		n.d		n.d		n.d				
88d		n.d		n.d		n.d		n.d				
88e		n.d		n.d		n.d		n.d				
88f		n.d		n.d		n.d		n.d				
89a	Dl				n.d					n.d		247
89b					26							
90a	A549			245 ± 4.23					DNA binding	n.d	DNA & G–C rich region.	248, 249
90b				89 ± 0.79								
90c				198.71 ± 4.23								
90d				88.12 ± 1.29								
91a				96 ± 1.72								
91b				74 ± 2.78								
91c				76.28 ± 2.45								
91d				63.56 ± 1.57								
92a				163 ± 0.43								
92b				116 ± 3.49								
92c				122.66 ± 2.58								
92d				93.34 ± 4.87								
3.2.4.4 N^N-picolinamide ligands												
93a	HT-29; 34.1 ± 0.7			MCF-7; 39 ± 2			A2780; 19.7 ± 0.6		Trx-R inhibition.	n.d		251
93b	HT-29; 81 ± 1			MCF-7; 149 ± 1			A2780; 27 ± 2					159
93c	A2780				66 ± 2							
93d					25 ± 3							
93e					33 ± 1							
93f					18.6 ± 0.4							
93g					23 ± 1							
94	HT-29; n.d			A2780; 52.5 ± 0.8			A2780cis; n.d		n.d	n.d	n.d	157
95	Dl; 690											252
96a		17.2 ± 0.7			14.2 ± 2.8			n.d				110
96b		12.0 ± 2.1			14.5 ± 2.8			17.5 ± 0.6				

96c [T]	A549	30.1 ± 2.1	HeLa	20.5 ± 4.3	BEAS-2B [(N)]	35.1 ± 0.7				
96d		22.5 ± 8.5		10.5 ± 1.4		n.d				
96e [T]		13.5 ± 2.9		4.9 ± 2.1		10.0 ± 0.7	**2B**	Influence the A549 cell cycle	Lysosome	
96f [T]		7.9 ± 2.1		4.9 ± 1.0		2.3 ± 0.5				
96g [T]		14.8 ± 2.1		11.4 ± 1.6		n.d				
96h [T]		34.6 ± 1.9		27.7 ± 5.3		n.d				
96i [T]		14.5 ± 2.7		6.9 ± 0.6		n.d				
96j [T]		9.3 ± 1.5		5.8 ± 0.2		n.d				

3.2.5. N^O ligands

97a	SK-Mel; 0.8	SNB-19; 9.8	C-32; 4.9	SH-4; 100						253
97b	MDA-MB-231; 18.76 ± 0.11	MCF-7; 13.95 ± 0.12	A549; 100 ± 0.22					n.d		254
	HeLa; 24.39 ± 0.20	HepG2; 26.37 ± 0.25								
97c	MDA-MB-231; 14.33 ± 0.09	MCF-7; 5.82 ± 0.08	A549; 8.13 ± 0.06							
	HeLa; 5.64 ± 0.10	HepG2; 23.66 ± 0.22								
97d	MDA-MB-231; 41.3 ± 0.17	MCF-7; 22.30 ± 0.28	A549; 20.18 ± 0.18							
	HeLa; 19.40 ± 0.19	HepG2; 51.87 ± 0.24								
98a [T]	HeLa (24hr);3.7 ± 3.6	HeLa (48hr); 2.2 ± 1.1	HL60 (24hr); 1.8 ± 0.2	HL60 (48hr); 2 ± 0.34	HUVEC [(N)] (24hr); 1 ± 0.16	HUVEC [(N)] (48hr); 5 ± 1.2		n.d		255
98b	n.d									
98c										
99a	A2780 (SRB)	> 100						n.d		24
99b		> 100								
99c		16.30 ± 0.32								
	A549	31.3 ± 0.9					**2AB**	Disrupt G_0/G_1 + G_2/M	Mitochondria \ Lysosome.	7
99d		5.6 ± 0.4								
99e		4. 9 ± 0.4								
99f		> 100								
99g		15.7 ± 1.0								
99h		4.4 ± 0.4					**2AB**	G_0/G_1 +	Mitochondria\	

							G_2/M	Lysosome.	
99i		15.4 ± 0.1							
99j		43.8 ± 4.9							
100a	HT-29; 5.1 ± 0.3	MCF-7; 11.0 ± 0.40	A2780; 5.70 ± 0.10	A2780cis; 5.80 ± 0.50	ARPE-19 (N); n.d	Trx-R inhibition. Apoptosis/ Single strand DNA breakage.		DNA	158, 251, 256
100b	HT-29; 83.00 ± 3.00	MCF-7; n.d	A2780; n.d	A2780cis; n.d	ARPE-19 (N); n.d				
100c T	HCT-116 p53+/+; 80 ± 1	HCT-116 p53-/-; 47 ± 2	MIA-PaCa-2; > 100				n.d		
	A549; > 100	PNT2 (N); 55 ± 2	ARPE-19 (N); > 100						
100d T	HCT-116 p53+/+; 19 ± 1	HCT-116 p53-/-; 17.6 ± 0.3	MIA-PaCa-2; 37 ± 1						
	A549; >100	PNT2 (N); 10.8 ± 0.3	ARPE-19 (N); > 100						
100e T	HCT-116 p53+/+; 75 ± 2	HCT-116 p53-/-; 2.8 ± 0.2	MIA-PaCa-2; > 100						
	A549; > 100	PNT2 (N); 40 ± 4	ARPE-19 (N); > 100						
100f T	HCT-116 p53+/+; 75 ± 4	HCT-116 p53-/-; 23 ± 2	MIA-PaCa-2; > 100						
	A549; > 100	PNT2 (N); 44 ± 2	ARPE-19 (N); > 100						
100g *	HCT-116 p53+/+; 33 ± 1	HCT-116 p53-/-; 6.6 ± 0.9	MIA-PaCa-2; > 100						
	A549; 43 ± 1	PNT2 (N); 20 ± 1	ARPE-19 (N); 71 ± 2						
100h T	HCT-116 p53+/+; > 100	HCT-116 p53-/-; 67 ± 2	MIA-PaCa-2; > 100						
	A549; > 100	PNT2 (N); > 100	ARPE-19 (N); > 100						
100i T	HCT-116 p53+/+; 20.7 ± 0.2	HCT-116 p53-/-; 17 ± 1	MIA-PaCa-2; 31.5 ± 0.7						
	A549; > 100	PNT2 (N); > 100	ARPE-19 (N); > 100						
100j T	HCT-116 p53+/+; 24 ± 2	HCT-116 p53-/-; 4.9 ± 0.6	MIA-PaCa-2; 35 ± 1						
	A549; 52 ± 2	PNT2 (N); 20 ± 1	ARPE-19 (N); > 100						
100k T	HCT-116 p53+/+; 42 ± 2	HCT-116 p53-/-; 37 ± 2	MIA-PaCa-2; 66 ± 2						
	A549; > 100	PNT2 (N); 41 ± 2	ARPE-19 (N); > 100						
101a	A549	30.9 ± 1.6	HeLa	36.0 ± 10.4			n.d		257
101b		12.0 ± 0.1		9.9 ± 0.1		**1B** /Metastasis	n.d	Lysosome	
101c		13.1 ± 0.8		10.8 ± 0.1			n.d		
101d		39.6 ± 1.0		40.7 ± 12.9					
101e		24.2 ± 4.2		22.1 ± 0.5		**1B** /Metastasis	n.d	Lysosome	
101f		33.4 ± 0.7		39.2 ± 2.5			n.d		
102a	MDA-MB-231 (WST-8)	157 ± 1.41	Caco-2 (WST-8)	29.0 ± 0.36			n.d		258
102b		67 ± 0.01		32 ± 0.18					
103a T		24.4 ± 5.2		19.5 ± 2.0		72.14 ± 2.24		n.d		144

103b	A549	> 100	HeLa	> 100	BEAS-2B (N)	n.d		n.d		
103c T		18.2 ± 1.3		14.9 ± 2.6		73.72 ± 0.38	**1B** /Metastasis	G_0/G_1, S, and G_2/M	Lysosome	
103d		> 100		> 100		n.d		n.d		
103e		> 100		> 100		n.d		n.d		
104	HeLa; Negligible toxicity for cell imaging at a concentration of 5 µM							n.d	Mitochondria	259
105a	n.d							n.d		260
105b T	MCF-7; 21 ± 1.3			CHO (N); 96 ± 6.0						
105c	n.d									
3.2.6. N^P ligands										
106a	A549			6.5 ± 1.0			NADH	n.d		93
106b				7.2 ± 2.0						
106c				6.9 ± 0.6			**1B** /Necrosis			
106d				25.3 ± 0.1			NADH			
106e				6.3 ± 0.1						
106f				7.9 ± 0.9			Necrosis			
106g				5.8 ± 0.2						
106h				4.7 ± 1.5						
107a T	A549	14.7 ± 0.4	HeLa	9.1 ± 0.2	BEAS-2B (N)	25.3 ± 0.6	ROS/Apoptosis	n.d	Lysosome	262
107b T		15.6 ± 0.1		8.0 ± 0.1		27.6 ± 0.1				
107c T		15.2 ± 0.1		8.5 ± 0.4		25.6 ± 0.2				
107d T		16.1 ± 0.2		7.2 ± 0.7		29.3 ± 0.3				
3.2.7. N^S ligands										
108a T	A549	39.4 ± 1.3	DU-145	49.0 ± 2.8	HeLa	41.6 ± 2.3	MCF-7	51.4 ± 2.4	HEK-293T (N)	90.6 ± 2.7		n.d		263
108b T		21.4 ± 1.5		38.0 ± 1.9		26.3 ± 1.6		39.7 ± 1.7		134.4 ± 3.5				
108c T		18.1 ± 1.1		31.6 ± 1.9		23.4 ± 1.7		37.4 ± 1.4		110.3 ± 3.3				
109a	PC3 (light) (WST-8); 5.5		SKOV-3(dark) (WST-8); 20.5		SKOV-3(light) (WST-8); 2.7						ROS	n.d		264
109b	PC3 (light) (WST-8); 5.7		SKOV-3(dark) (WST-8); 12.1		SKOV-3(light) (WST-8); 2.3									
110	HCT-116 (SRB);		NCI-H460 (SRB);		SiHa (SRB);		SW480 (SRB); 24 ± 6					n.d		266

	15 ± 2		18 ± 4		46 ± 6						
111	BE; 36.29 ± 8.68		HT-29; 49.55 ± 2.97		MIA-Pa-Ca2; 17.12 ± 4.58		ARPE-19 (N); 59.71 ± 1.75		Partial intercalators or bind to DNA through electrostatic interactions.	n.d	DNA	267
112a T	HCT-116	1.37 ± 0.09	Mia-PaCa-2	14.33± 0.79	HT-29	4.89 ± 0.56	ARPE-19 (N)	18.26 ± 0.58		n.d		268
112b T		5.18 ± 0.12		4.48 ± 0.18		6.99 ± 0.51		9.79 ± 0.05				
112c T		5.50 ± 1.86		6.22 ± 0.07		8.09 ± 1.06		18.25 ± 0.48				
113a	n.d									n.d		269
113b												
3.2.8. O^O, O^P and O^S ligands												
114	HT-29; 20 ± 1				MCF-7;13.2 ± 0.2					n.d		251
115 *	HT-29; 93.00 ± 7		MCF-7; 51.00 ± 4		A2780; 35.00 ± 1		A2780cis; 51.00 ± 1	ARPE-19 (N); > 100	Trx-R Inhibition / very low levels of apoptosis/necrosis.	n.d		158
116a T	A2780; 23.2 ± 0.8			A2780cisR; 14.1 ± 2.5			HEK-293T (N); 16.3 ± 0.7			n.d		270
116b T	A2780; 20.7 ± 5.6			A2780cisR; 23.6 ± 2.3			HEK-293T (N); 26.1 ± 2.9					270, 272
	HepG2; 37.9 ± 2.2			HeLa; 59.6 ± 0.7			HEK-293T (N); 67.8 ± 3.8					
116c T	A2780	23.2 ± 2.3	A2780cisR		39.4 ± 9.4		HEK-293T (N)	29.4 ± 3.9				270
116d T		21.0 ± 1.0			33.3 ± 3.6			15.6 ± 1.4				
116e T		94.4 ± 4.1			89.2 ± 5.2			89.1 ± 3.3				271
116f T		11.1 ± 1.1			17.0 ± 0.5			11.6 ± 3.1				
116g T		26.9 ± 0.7			22.4 ± 2.3			15.0 ± 2.6				
116h T		37.6 ± 2.1			34.7 ± 0.9			21.0 ± 0.1				
116i T		24.0 ± 1.2			43.0 ± 3.7			24.3 ± 0.3				
116j T		16.9 ± 2.4			24.6 ± 2.1			10.0 ± 6.7				
117a T	HepG2	49.2 ± 2.4	HeLa		30.1 ± 2.1		HEK-293T (N)	63.3 ± 3.9				272
117b T		44.3 ± 3.1			25.1 ± 0.2			79.2 ± 5.2				
117c *		> 100			>100			> 100				

117d [T]		90.1 ± 6.3		>100		60.0 ± 5.7				
117e [T]		42.9 ± 3.3		34.8 ± 2.7		75.1 ± 6.5				
117f [*]		54.7 ± 0.3		43.7 ± 3.4		> 100				
118a	SW480		51.9 ± 1.6	A549		> 200		n.d		273
118b			119.8 ± 1.1			> 200				
118c			> 200			36.8 ± 1.2				
118d			15.9 ± 1.3			18.9 ± 1.1	ROS /Necrosis /DNA binding.	G_0/G_1	DNA	
119a [T]	HeLa	1.2 ± 0.1	A549	4.9 ± 1.2	BEAS-2B [(N)]	1.3 ± 0.2	16HBE [(N)]	1.9 ± 0.2	**1B**	S-phase + G_2/ M	Lysosome\ Mitochondria.	274
119b [T]		3.8 ± 0.2		4.4 ± 0.4		3.5 ± 0.1		4.5 ± 0.2	NADH	n.d		
119c [T]		1.6 ± 0.3		7.5 ± 1.1		2.8 ± 0.4		3.0 ± 0.1				
120a [T]	HeLa	7.9 ± 0.2	A549	23.2 ± 1.4	16HBE [(N)]	26.7 ± 0.6	NADH	n.d		106
120b [T]		5.9 ± 0.3		6.5 ± 0.4		11.9 ± 0.9				
120c [T]		3.6 ± 0.3		20.8 ± 2.5		7.0 ± 0.3		S-phase	Lysosome	
120d		17.8 ± 0.6		34.4 ± 0.3		n.d	NADH	n.d		
120e		10.9 ± 0.1		12.5 ± 0.5		n.d				
120f		32.4 ± 0.2		25.8 ± 0.2		n.d				
120g		n.d		n.d		n.d				
121a	A549	14 ± 6	SW480	6.0 ± 0.7	CH1/PA-1	14 ± 2		n.d		275
121b		1.2 ± 0.1		0.33 ± 0.04		0.46 ± 0.02				
122a		63 ± 6		4.2 ± 0.2		7.0 ± 1.6		n.d	-	276
122b		2.2 ± 0.8		0.59 ± 0.08		0.82 ± 0.05				
122c		1.1 ± 0.2		0.54 ± 0.07		0.57 ± 0.05		Disturb the cell cycle at G_1		
122d		2.0 ± 0.4		0.80 ± 0.15		0.68 ± 0.02		n.d		
3.2.9. P^P and S^S based complexes										
123a [T]	A549	4.6 ± 0.1	HeLa	3.4 ± 0.5	16HBE [(N)]	2.4 ± 0.1	BEAS-2B [(N)]	2.8 ± 0.1	NADH /ROS /Apoptosis		DNA is not the main target.	277
123b		8.0 ± 0.1		6.2 ± 0.3		n.d		n.d	NADH	n.d		

123c [T]	A549	3.0 ± 0.2	HeLa	5.2 ± 0.6	16HBE [(N)]	6.5 ± 0.7	**1B**	G_0/G_1	Lysosome	
123d		10.3 ± 0.6		12.9 ± 0.4		n.d				
123e		3.9 ± 0.4		8.5 ± 0.5		n.d		S-phase and Sub-G_1		261
123f		2.3 ± 0.1		4.3 ± 0.9		n.d				
123g		7.4 ± 0.7		10.2 ± 0.6		n.d	**1B**			105
124a [*]	HCT-116p53+/+; > 100		HCT-116p53-/-; > 100		PNT2 [(N)]; > 100			n.d		278
124b [*]	HCT-116p53+/+; > 100		HCT-116p53-/-; > 100		PNT2 [(N)]; > 100					
124c [*]	HCT-116p53+/+; > 100		HCT-116p53-/-; > 100		PNT2 [(N)]; > 100					
125a [T]	A549; 14.5 ± 1.5		HeLa; 12.3 ± 0.1		HepG2; 3.2 ± 0.2			n.d		279, 280
	BEAS-2B [(N)]; 11.9 ± 0.3		16HBE [(N)]; 13.7 ± 0.5							
125b [T]	A549; 5.1 ± 0.6		HeLa; 4.9 ± 0.9		HepG2; 3.6 ± 0.4					
	BEAS-2B [(N)]; 3.2 ± 0.01		16HBE [(N)]; 5.8 ± 0.4							
125c [T]	A549; 3.0 ± 0.1		HeLa; 4.2 ± 1.3		HepG2; 3.8 ± 0.4		**1AB** or **2AB**		Mitochondria\ Lysosome	
	BEAS-2B [(N)]; 3.4 ± 0.04		16HBE [(N)]; 4.7 ± 0.1							
125d [T]	A549; 4.5 ± 1.5		HeLa; 4.4 ± 0.4		HepG2; 3.2 ± 0.1					
	BEAS-2B [(N)]; 4.7 ± 0.9		16HBE [(N)]; 5.9 ± 0.6							
125e [T]	A549; 2.4 ± 0.1		HeLa; 2.2 ± 0.1		HepG2; 2.1 ± 0.1					
	BEAS-2B [(N)]; 1.9 ± 1.1		16HBE [(N)]; 3.0 ± 0.8							
125f [T]	A549; 5.6 ± 0.1		HeLa; 3.1 ± 0.01		HepG2; 5.8 ± 0.1					
	BEAS-2B [(N)]; 3.5 ± 1.0		16HBE [(N)]; 4.8 ± 0.4							
125g [T]	A549; 24.2 ± 1.4		HeLa; 13.5 ± 0.1		BEAS-2B [(N)]; 31.2 ± 0.9					

[1] IC_{50} is defined as the concentration of drug required to inhibit cell growth by 50% compared to the control. Each value represents the mean ± standard deviation from two or three independent experiments.

[2] Cell viability was determined by the MTT assay, other than this is mentioned.

[T]: The complex was examined against normal cell line; [*]: The complex was safe to the tested normal cell with IC_{50} > 100 µM; [N]: Normal cell line; n.d: not determined. Mechanism of action according to Fig. 3 (within the main text): **1A** pathway: NADH/ROS/MMP/Apoptosis. **1B** pathway: NADH/ROS/LMP/Apoptosis. **1AB** pathway: NADH/ROS/MMP/LMP/Apoptosis. **2A** pathway: ROS/MMP/Apoptosis.

Full names and Abbreviations of Cell lines: 16HBE, human bronchial epithelial cell lines; 518A2, human melanoma cell line; 5637, human bladder cancer cells; 8505C, human thyroid carcinoma; ARPE-19, human retinal epithelial cells; A253, human submandibular gland carcinoma; A2780, human ovarian carcinoma cell lines; A2780R/A2780cisR; Cisplatin resistant human ovarian; A427, human lung carcinoma cells; A549, Human lung carcinoma cell line; A549R, cisplatin resistant human lung

carcinoma cell line; BEAS-2B, human non-tumorigenic lung epithelial cell line; BEL-7402, human hepatoma cell line; BHK21, normal healthy kidney cells; Caco-2, human colon carcinoma cell lines; Capan2, pancreatic adenocarcinoma cell line; CH1/PA-1, ovarian teratocarcinoma cell lines; CHO, normal Chinese hamster ovarian cells; CHO-K1, Chinese Hamster Ovary-K1 Cells; CNS cancer, Central nervous system cancer; Colo-829, human, umbilical metastasis, melanoma; CRL-2115, human skin fibroblast adherent; CT26, mouse colon carcinoma; DL, Dalton's ascites lymphoma; DLD-1, human colorectal adenocarcinoma cells; DU-145, human prostatic carcinoma; EA.hy926, human umbilical vein endothelial cell line; HaCaT, human keratinocyte cell line; HCT-116, colon cancer cell line; HCT-116 p53-/-, colon cancer cell line depleted p53; HEK-293T, human embryonic kidney cell lines; HeLa, cervical cancer cell line; HepG2, human liver cancer cell line; HFF-1, human skin cell lines; HL-60, human leukaemia; HT29, human colorectal adenocarcinoma cells; KMST-6, human skin fibroblast cell line; LCLC-103H, human lung carcinoma cells; LoVo, colorectal adenoma; LO2, human normal liver; MCF-7, human breast cancer cell line; MCF-10, human breast cancer cell lines; MDA-MD-435S, human breast cancer cell lines; MDB-MA-231, human breast cancer cell line; MES-OV, ovarian cancer cells; MIA PaCa-2, pancreatic carcinoma cell lines; MRC-5, human fetal lung fibroblast cells; OVCAR-3, ovarian adenocarcinoma cell line; Panc-1, pancreatic ductular adenocarcinoma cell line; PC3, human prostatic carcinoma; PNT2, normal prostate cell line; Saos, osteosarcoma cell line; SiHa, cervical cancer cell line; SISO, human uterine cervical adenocarcinoma cells; SKOV-3, human ovarian cancer cell line; SW620, human colon cell lines; U87, human glioblastoma cell lines; WHCO1, esophageal cancer cell line; WI-38, human fetal lung fibroblast cells.