Supplementary Information for:

Exploring the cytotoxicity, uptake, cellular response, and proteomics of mono- and dinuclear DNA light-switch complexes.

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Contents

Experimental

Syntheses

Ru(tpphz) was prepared by methods described by Bolger, *et al.*[1]

Ru(taptp) $[Ru(phen)_2Cl_2]$ (0.26 g, 0.5 mmol) and taptp[2] (0.191 g, 0.5 mmol) in ethylene glycol (100 mL) were heated to 150 °C under N_2 for 6 hours. After cooling to room temperature an equal volume of aqueous NH_4PF_6 solution was added. The resulting brown precipitate was collected by centrifugation, washed with water, ethanol and diethyl ether using the same technique and dried *in vacuo* to give a brown solid (0.362 g, 0.32 mmol, 63.8 %). ^{1}H NMR (400 MHz, CD_3CN) δ 9.90 (dd, *J* = 1.2, 8.2 Hz, 2H), 9.64 (dd, *J* = 1.3, 7.9 Hz, 2H), 8.83 (d, *J* = 7.9 Hz, 2H), 8.65 (d, *J* = 8.3 Hz, 4H), 8.31 (s, 4H), 8.26 (dd, *J* = 1.2, 5.3 Hz, 2H), 8.19 (dd, *J* = 1.2, 5.3 Hz, 2H), 8.08 (dd, *J* = 1.2, 5.2 Hz, 2H), 7.99 (t, *J* = 6.8, 2H), 7.94 (t, *J* = 7.1 Hz, 2H), 7.86 (d, *J* = 8.4 Hz, 1H), 7.85 (d, *J* = 8.3 Hz, 1H), 7.70 (t, *J* = 5.3 Hz, 2H), 7.68 (t, *J* = 5.3 Hz, 2H). MS; m/z (%): 989 (50) $[M](PF_6)^+$, 422 (100) $[M]^{2+}$.

RuRe $[Ru(phen)_2(tpphz)](PF_6)_2$ (0.40 g, 0.35 mmol) and $Re(CO)_5Cl$ (0.14 g, 0.39 mmol) were mixed in acetonitrile (100 mL, dry) and heated to reflux under N_2 for 16 hours. After cooling to room temperature the volume of acetonitrile was decreased under reduced pressure and the complex was precipitated by addition of diethyl ether. The precipitate was collected by centrifugation, washed

with diethyl ether and dried *in vacuo* to give an orange solid (0.28 g, 0.19 mmol, 55.0 %). ^{1}H NMR (400 MHz, CD_3CN): δ 10.12 (t, *J* = 7.5 Hz, 2H), 9.93 (d, *J* = 10.0 Hz, 2H), 9.60 (d, *J* = 5.0 Hz, 2H), 8.67 (d, *J* = 10.0 Hz, 4H), 8.34-8.17 (m, 10H), 8.08 (t, *J* = 5.0 Hz, 2H), 7.94-7.88 (m, 2H), 7.74-7.63 (m, 4H). MS; m/z: 1297 $[M](PF_6)^+$. Accurate Mass: Calc. for $RuReC_{51}H_{28}N_{10}O_3F_6PCl$ $[M](PF_6)^+$: 1297.0277, Observed: 1297.0260. Elemental Analysis: Calc. for $RuReC_{51}H_{28}N_{10}O_3ClP_2F_{12}$: C 42.50; H 1.96; N 9.72. Observed: C 42.75; H 1.61; N 9.83.

RuPt $[Ru(phen)_2(tpphz)](PF_6)_2$ (0.040 g, 0.035 mmol) and $K_2[PtCl_4]$ (0.0146 g, 0.035 mmol) were mixed in methanol:water (1:1, 20 mL, N_2 purged) and heated to reflux under N_2 for 12 hours. After cooling to room temperature the methanol was removed under reduced pressure, the precipitate collected by filtration, washed with ethanol, methanol and hexanes. The collected precipitate was dissolved in acetonitrile and re-precipitated by addition of diethyl ether, collected by filtration, washed with ether and dried *in vacuo* to give a brown solid (0.029 g, 0.024 mmol, 69.1 %). ^{1}H NMR (400 MHz, CD_3CN) δ 9.84 (d, *J* = 7.7 Hz, 2H), 9.58 (d, *J* = 8.7 Hz, 2H), 9.49 (s, 2H), 8.66 (t, *J* = 8.4 Hz, 6H), 8.52 (s, 2H), 8.32 (t, *J* = 5.6Hz, 8H), 8.21 (t, *J* = 7.8 Hz, 2H), 8.08 (d, *J* = 5.0 Hz, 2H), 7.97 (dd, *J* = 5.5, 8.0 Hz, 2H), 7.69 (dd, *J* = 5.2, 8.4 Hz, 6H). MS; m/z (%): 1257 (100) $[M](PF_6)^+$, 556 (100) $[M]^{2+}$.

Anion metathesis All complexes were converted to water soluble chloride salts by anion metathesis prior to DNA and cell studies.

Luminescence titrations

Calf thymus DNA (CT-DNA) was dissolved in aqueous buffer (25 mM NaCl, 5 mM Tris, pH 7.4) and broken into an average of 150-200 base pair fragments by sonication (2 × 15 minutes). The purity of the sample was determined by UV-vis spectroscopy, with $A^{260nm}/A^{290nm} > 1.9$ indicating a protein-free sample. The concentration of CT-DNA was determined by UV-vis spectroscopy (ε280nm = 13200 M^{-1} cm^{-1}). A solution of the complex (concentration stated) was dissolved in aqueous buffer (25 mM NaCl, 5 mM Tris, pH 7.4) and loaded into a quartz cuvette. This was allowed to equilibrate at 25 °C for 30 minutes and the emission spectra recorded. 2 µL of a concentrated stock CT-DNA solution in aqueous buffer (typically 200 µM) was added and the solution mixed by pipette. The emission spectrum was recorded and whilst showing an enhancement in emission this procedure was continued until the emission became constant. The maxima of each emission spectrum were then carried forward to calculate the fraction bound. This could then be plotted against the concentration of DNA divided by the concentration of complex to generate a binding curve. A Scatchard plot[3] could be generated using the McGhee and Von Hippel (MVH) model to account for non-linear deviation associated with the complex overlapping binding site system of DNA base pairs. Data points between

a bound ligand fraction of 0.3 and 0.9 were used as the model is inaccurate at high and low concentrations, and the following MVH equation was used in SigmaPlot 12.0 software:

$$\frac{r}{C_f} = K \cdot (1 - nr)\left(\frac{1 - nr}{1 - (n-1)r}\right)^{n-1}$$

Isosbestic Point Determination

CT-DNA dissolved in aqueous buffer (25 mM NaCl, 5 mM Tris, pH 7.4) was prepared using the method as described in the luminescence titration. A solution of RuPt as the chloride salt (15 μM) was dissolved in aqueous buffer (25 mM NaCl, 5 mM Tris, pH 7.4) and loaded into a quartz cuvette. Absorption spectra were then collected on a Cary 50 Probe UV-vis spectrophotometer and Cary Win UV software. A concentrated CT-DNA stock solution in aqueous buffer (40 mM) was added in 5 μL increments and the solution mixed by pipette. The sample was allowed to equilibrate for 5 minutes before the spectrum was recorded. This was repeated until a clear isosbestic point was visualised at 300 nm.

Equilibrium dialysis

Calf thymus DNA, dissolved in 5 mM Tris, pH 7.4, was exhaustively dialysed to remove small fragments. Each DNA (0.5 ml, 10 μM base-pairs) sample was introduced into a pre-rinsed dialysis bag with a molecular weight cut off of 15,000 Da. The samples were dialysed against a range (0.2 μM – 10 μM) of RuPt concentrations dissolved in either 5 mM Tris, pH 7.4, or 5 mM Tris, pH 7.4 containing 150 mM NaCl. Dialysis was performed for a minimum of 15 hours at 22°C. To measure the concentrations of RuPt within the dialysis bag, the absorbance of each solution was determined at 300 nm, and the RuPt concentration determined using ε_{300} = 33694 M^{-1} cm^{-1}. The free RuPt concentration was determined using ICP-MS, as described below.

Viscosity

Viscosity measurements were obtained using a Cannon-Manning semi-micro viscometer (size 50) immersed in a temperature controlled water bath at 27 °C. CT-DNA was prepared as for luminescence titrations, and used at a concentration of 0.5 mM (base pairs). Experimental samples were generated by adding an increasing concentration of ligand to the DNA solution to give a series of ligand/bp ratios. Each sample was allowed to equilibrate for 20 minutes, measured three times and the average used in calculations.

Cell culture

A2780 and A2780cis cell lines were cultured in RPMI-1640 medium. HEK293, MRC5, MCF7 and T24 cells were cultured in DMEM medium. All growth medium was supplemented by 10% v/v fetal bovine serum (FBS), 2 mM L-Glutamine, 100 IU mL^{-1} penicillin and 100 µg mL^{-1} streptomycin. Cultures were grown at 37 °C with 5% CO_2, routinely subcultured using trypsin (0.1% v/v in PBS) at 80 – 90% confluence and used between passage numbers 5 – 50.

Complex preparation

Complex stock solutions were made up in one part phosphate buffered saline (PBS) to one part high purity milli-Q® water with vortex agitation and gentle heating (60 ºC max) to aid dissolution at a high concentration, followed by sterile filtration with a 0.22 µm filter.

Cytotoxicity (MTT assay)

Cells were seeded in 48 well plates at 4 $x10^4$ cells/well and incubated for 24 h before treatment with 0 – 500 µM complex (maintaining 10% PBS/H_2O: 90% medium throughout all solutions) in triplicate for 48 h. Solutions were removed and cells incubated with MTT (0.5 mg mL^{-1} in serum free medium) for 30 – 40 minutes. The MTT was removed and formazan product eluted using 110 µl/well acidified isopropanol, 100 µl/well of which was transferred to a 96 well plate and absorbance quantified by spectrophotometer (595 nm). An average absorbance for each complex concentration treatment was calculated and cell viability determined as a percentage of the untreated negative control wells (10% PBS/H_2O: 90% medium, average of triplicate). Data were plotted in a percentage viability curve from which the IC_{50} value could be calculated by interpolation. IC_{50} values reported are an average ± S.D. of at least 2 independent experiments.

Microscopy

Live cell samples were prepared by first pre-coating 35 mm glass bottomed tissue culture dishes (ibidi µ-dish) with poly-l-lysine (10 minutes, PBS wash x5), which were seeded at 1.5 $x10^4$ cells/dish and incubated for 24 h. The medium was removed, cells washed with PBS and complex added (50 µM, 10% PBS/H_2O: 90% medium). Treated dishes were placed in a live cell microscopy chamber (37 °C, 5% CO_2) and immediately imaged using a 100X plan apochromat (1.4NA) objective lens on a Nikon Ti inverted microscope. Samples were illuminated at 405 nm using a Lumencor spectraX solid state light engine, and emission from the sample at 640–800 nm was collected using an Andor Zyla

sCMOS camera. All images were taken using the Nikon Elements software in a programmed cycle of a multiple coordinate set every 2 minutes for 3 hours to construct a time-lapse sequence. A control dish of cells seeded to the same density (10% PBS/H_2O: 90% medium) remained alongside each treated sample experiment in the live cell chamber and was imaged after 3 hours to ensure no change in cell morphology under the ambient experimental conditions. In addition, a control experiment was performed with a dish of cells seeded to the same density imaged using the same exposure cycle (multiple coordinate images every 2 minutes for 3 hours) to assess any background phototoxic effects; and these cells retained regular morphology.

Intracellular metal content (ICP-MS)

Cell cultures were grown on 60 mm dishes at a seeding density of 5 x10^5 cells per dish and incubated for 24 h. Cells were then treated with the complex (solubilised in and maintained at 10% PBS/H_2O: 90% medium throughout all solutions) at the stated concentration and incubated for 24 h. All complex solution (or control medium) was removed, cells washed with PBS and 1 mL of both serum-free medium and trypsin solution added. Dishes were incubated for 3 min and shaken to remove cells (plus scraped to detach any remaining cells) which were transferred to microcentrifuge tubes and centrifuged (4000 rpm, 3 min). The supernatant was removed, pellet resuspended in 500 µL serum-free medium and cells counted. Each sample was transferred to a glass sample tube, 2 mL concentrated HNO_3 added, heated to 60°C overnight and then diluted to 10 mL total volume with ultrapure Milli-Q H_2O before analysis of ruthenium content by inductively coupled plasma mass spectrometry (ICP-MS). Using the obtained ruthenium concentration, the sample volume, number of cells per sample and the assumption of a cell volume of 2 x10^{-12} L an estimate of intracellular concentration (mol L^{-1}) could be deducted.

Mitochondrial membrane potential ($\Delta\Psi m$) assay

The mitochondrial membrane potential was measured using the TMRE-Mitochondrial Membrane Potential Assay Kit (Abcam ab113852). A2780 or A2780cis cells were seeded in 96 well plates (10^4 cells/well) and incubated for 24 h (37°C, 5% CO_2) in regular RPMI culture medium (RPMI 1640 supplemented with 10% FBS, 2mM glutamine and penicillin/streptomycin). All media was removed before complex Ru(tpphz) or Ru(taptp) (IC_{50} concentration; made from 2 mM stock in PBS, diluted in regular RPMI culture medium, 10% PBS maintained throughout all solutions) or control media was added in triplicate for 24 h. 10 min prior to TMRE addition, additional wells were treated with complex solutions (either IC_{50} concentration or 50 µM) or the positive control 20 µM FCCP in regular

RPMI media (carbonyl cyanide-*p*-trifluoromethoxyphenylhydrazone; a known mitochondrial oxidative phosphorylation uncoupler), before cells were incubated with 500 nM TMRE (11X stock overlaid for resultant 1X) for a further 20 mins. Cells were washed once with PBS, before a volume of PBS was added to each well and the fluorescence measured using a BMG LABTECH FLUOstar OPTIMA plate reader with excitation/emission 544/590 nm.

Proteomics

Sample preparation for mass spectrometry

An A2780CIS cell line culture was established in regular RPMI 1640 medium (10% v/v dialysed FBS [Dundee Cell Products SILAC dialysed calf serum, cat no. DS1002], 2 mM L-glutamine, 100 IU mL-1 penicillin and 100 µg mL-1 streptomycin) and split into two parallel cultures which were identically sub-cultured but with contrasting regular RPMI medium and SILAC RPMI medium containing labelled amino acids ([Dundee Cell Products SILAC RPMI 1640 R10K8, cat no. LM021] supplemented with 10% v/v dialysed FBS [Dundee Cell Products SILAC dialysed calf serum, cat no. DS1002], 2 mM L-glutamine, 100 IU mL-1 penicillin and 100 µg mL-1). Labelled SILAC media was used for 6 passages to ensure heavy amino acid incorporation (exceeding the recommended 10-12 cell cycles) and was a heavy combination with amino acid isotopes R10 (L-arginine-13C6,15N4 hydrochloride) and K8 (L-lysine-13C6,15N2 hydrochloride). Cells were seeded in 100 mm dishes at 106 cells/dish, incubated for 24 h and either remained as control samples or were treated with complex at the 48 h IC50 concentration but for 24 h to ensure sufficient intact cells. The complex solution was removed, samples washed with 4 °C PBS x3, treated with IP lysis buffer (e.g. ThermoFisher no. 87787) and subjected to a freeze/thaw cycle x3. The soluble protein fraction was separated from the insoluble fraction by 4 °C centrifugation and a Bradford assay with BSA standard curve used to determine protein concentration. Proteins were separated by SDS-PAGE and subjected to an in-gel digest (excision, de-stain, reduction, alkylation, trypsin digestion and peptide extraction) of whole gel lanes cut into ten fractions for mass spectrometry analysis.

Mass spectrometry analysis

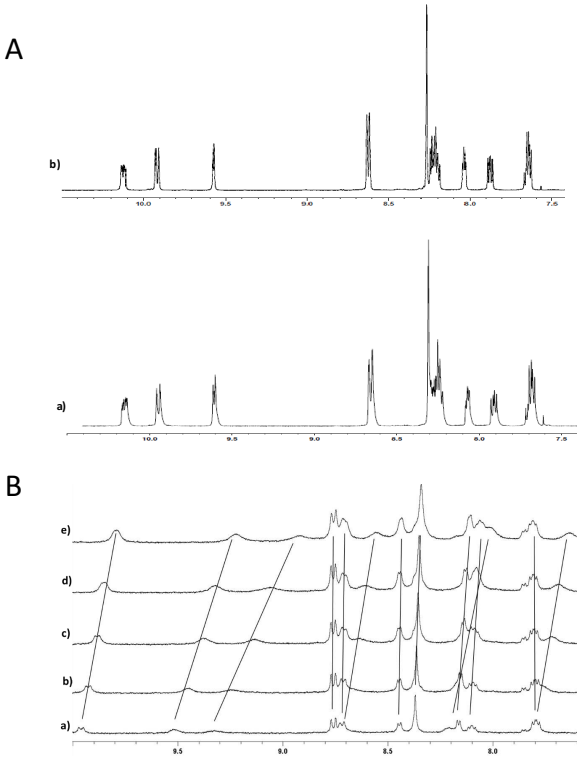
Extracted peptides were re-suspended in 0.5% formic acid and analysed by nano-liquid chromatography tandem mass spectrometry (LC-MS/MS) on an Orbitrap Elite (Thermo Fisher) hybrid mass spectrometer equipped with a nanospray source, coupled with an Ultimate RSLCnano LC System (Dionex). The system was controlled by Xcalibur 2.1 (Thermo Fisher) and DCMSLink 2.08 (Dionex). Peptides were desalted on-line using a micro-Precolumn cartridge (C18 Pepmap 100, LC Packings) and then separated using a 90 min reversed phase gradient (4-32% acetonitrile/0.1%

formic acid) on a PepMap C18 column, 15 cm x 50 µm ID, 2 µm particles, 100 Å pore size (Thermo). The Orbitrap Elite was operated with a cycle of one MS (in the Orbitrap) acquired at a resolution of 60,000 at m/z 400, with the top 20 most abundant multiply-charged (2+ and higher) ions in a given chromatographic window subjected to MS/MS fragmentation in the linear ion trap. A Fourier-transform mass-spectrometry (FTMS) target value of 1E6 and an ion trap MSn target value of 1E4 was used and with the lock mass (445.120025) enabled. Maximum FTMS scan accumulation time of 500 ms and maximum ion trap MSn scan accumulation time of 100 ms were used. Dynamic exclusion was enabled with a repeat duration of 45 s with an exclusion list of 500 and exclusion duration of 30 s.

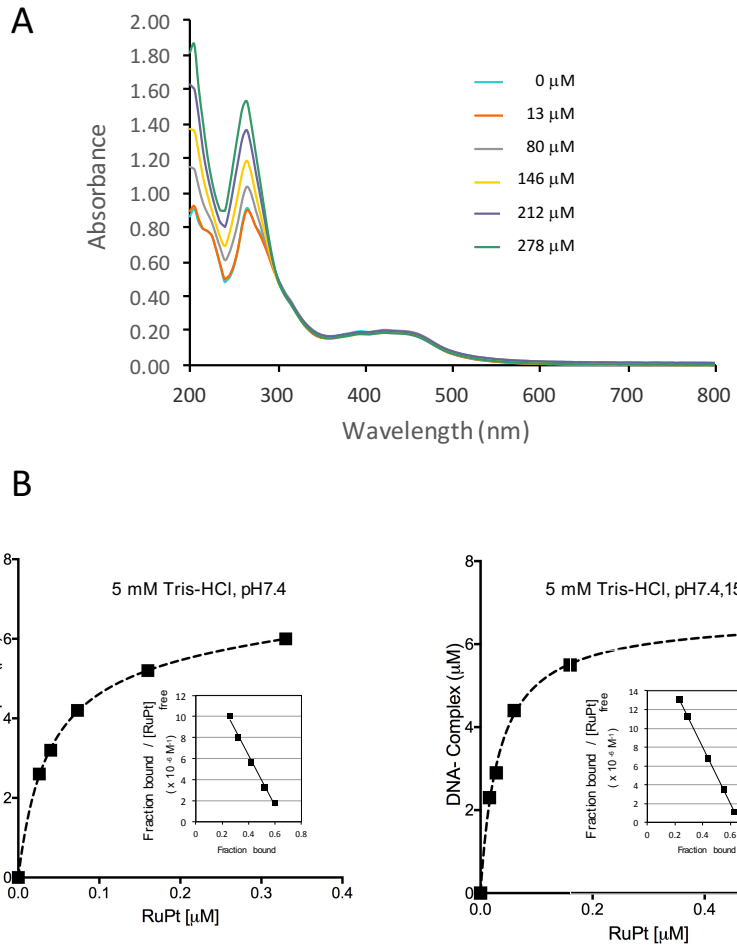
Proteomic data analysis

MS data were analysed using MaxQuant version 1.5.5.1. [4] Data was searched against a human UniProt sequence database (downloaded June 2015) using the following search parameters: trypsin with a maximum of 2 missed cleavages, 7 ppm for MS mass tolerance, 0.5 Da for MS/MS mass tolerance, with acetyl (Protein N-term) and oxidation (M) set as variable modifications and carbamidomethylation (C) set as a fixed modification. A protein false discovery rate (FDR) of 0.01 and a peptide FDR of 0.01 were used for identification level cut offs. SILAC-based quantification was performed using MaxQuant with matching between runs (with a 2-minute retention time window) enabled and a minimum ratio count of 2 (Cox et al., 2014). Protein ratios are calculated as the median of all SILAC peptide ratios and an outlier significance score for normalised log protein ratios "Significance A" was calculated in Perseus [5] with a Benjamini-Hochberg FDR threshold of 0.05.

Supplementary Figures



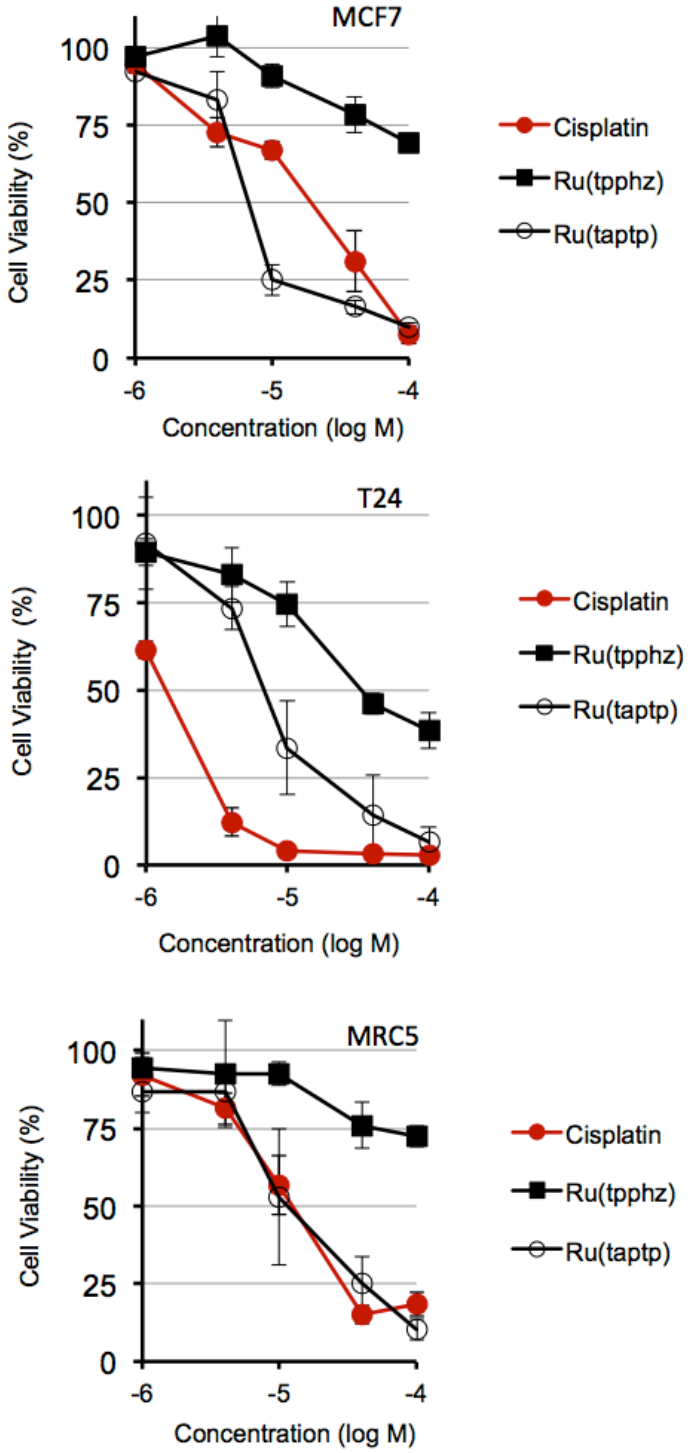
Supplementary Figure 1. ^{1}H-NMR spectra showing the effect of increasing concentration on (A) RuRe and (B) RuPt in MeOD at 298 K. (A) a) 1 mM, b) 6 mM RuRe. (B) a) 1 mM, b) 1.25 mM, c) 1.5 mM, d) 1.75 mM, e) 2 mM RuPt. The lines track the individual proton changes in chemical shift (ppm) upon increasing concentration. The upfield shift of the aromatic protons is due to the shielding influence of the ring current of neighbouring aromatic molecules. This is a strong indication of self-association through π-stacking.



C

	K_b (x 10^6 M^{-1}) (S.D.)	
	5 mM Tris-HCl, pH7.4	5 mM Tris-HCl, pH7.4,150 mM NaCl
RuPt	27.4 (1.9)	30.6 (5.3)

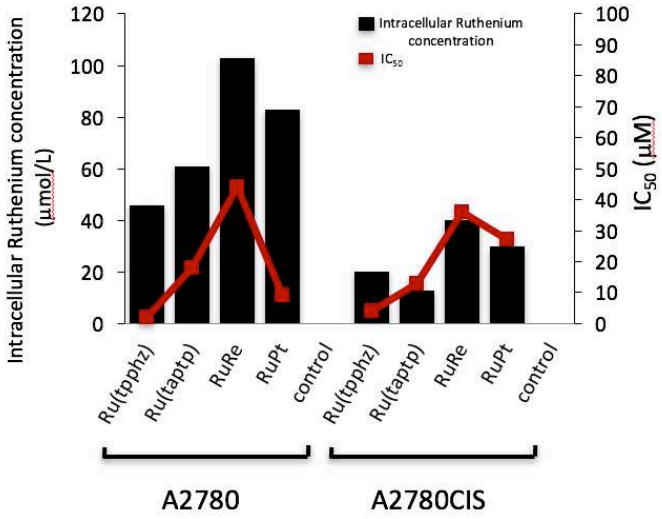
Supplementary Figure 2. Determination of RuPt binding affinity for DNA via equilibrium dialysis. (A) Isosbestic point determination. UV-VIS spectrogram of 15 mM RuPt in the presence of the indicated concentrations of added calf thymus DNA. (B) Binding curves derived from equilibrium dialysis of RuPt and DNA in the presence of indicated [NaCl]. Insets are data presented as Scatchard plots **(**C). Summary of DNA binding parameters for all complexes.



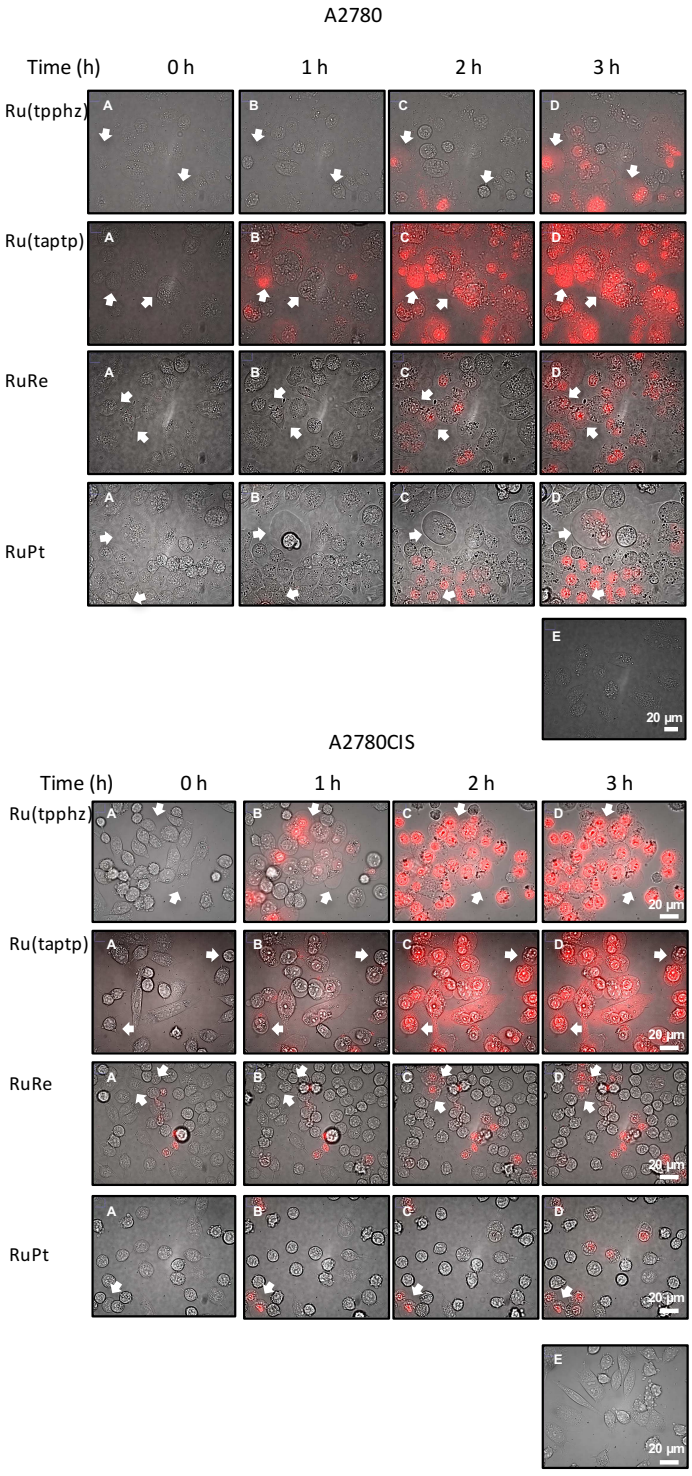
Supplementary Figure 3. Cell viability data for MCF7 breast carcinoma, T24 bladder carcinoma and MRC5 lung fibroblast cells treated with the indicated complexes and cisplatin, analysed by MTT assay (experiments performed in triplicate and data displayed as an average of at 3 independent experiments ± S.D.).

	IC50 values μM (S.D.)		
Cell Line	Cisplatin	Ru(tpphz)	Ru(taptp)
MCF7 Breast carcinoma	19.2 (5.6)	>100	7.2 (1.6)
T24 Bladder carcinoma	1.5 (0.3)	32.3 (5.5)	7.6 (2.0)
MRC5 Lung fibroblast	11.3 (2.2)	>100	15.8 (7.9)
HEK293 Embryonic kidney	-	>500	351

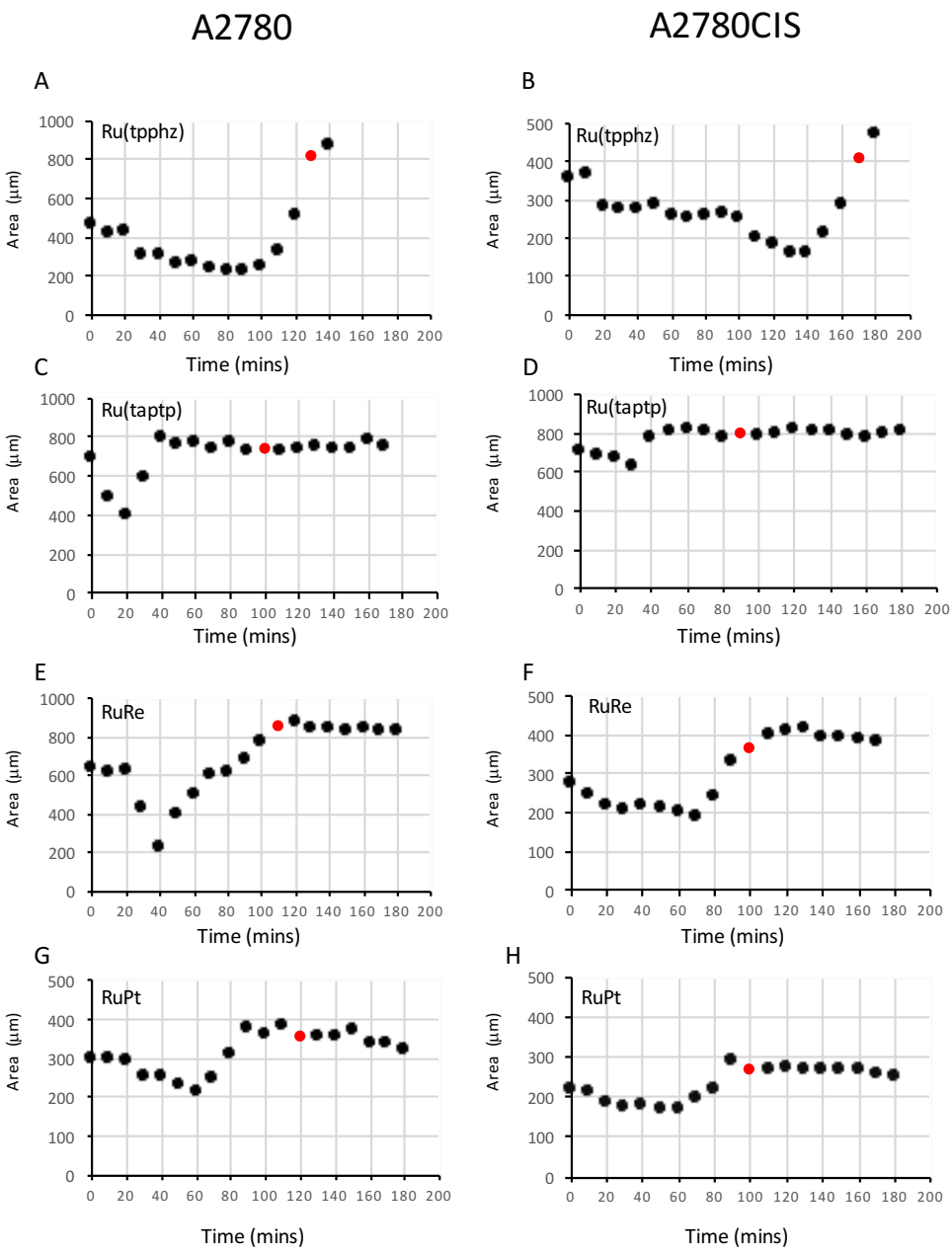
Supplementary Figure 4. Summary of IC_{50} (S.D.) values for indicated compounds for MCF7 breast carcinoma, T24 bladder carcinoma, MRC5 lung fibroblast and HEK human embryonic kidney cells.



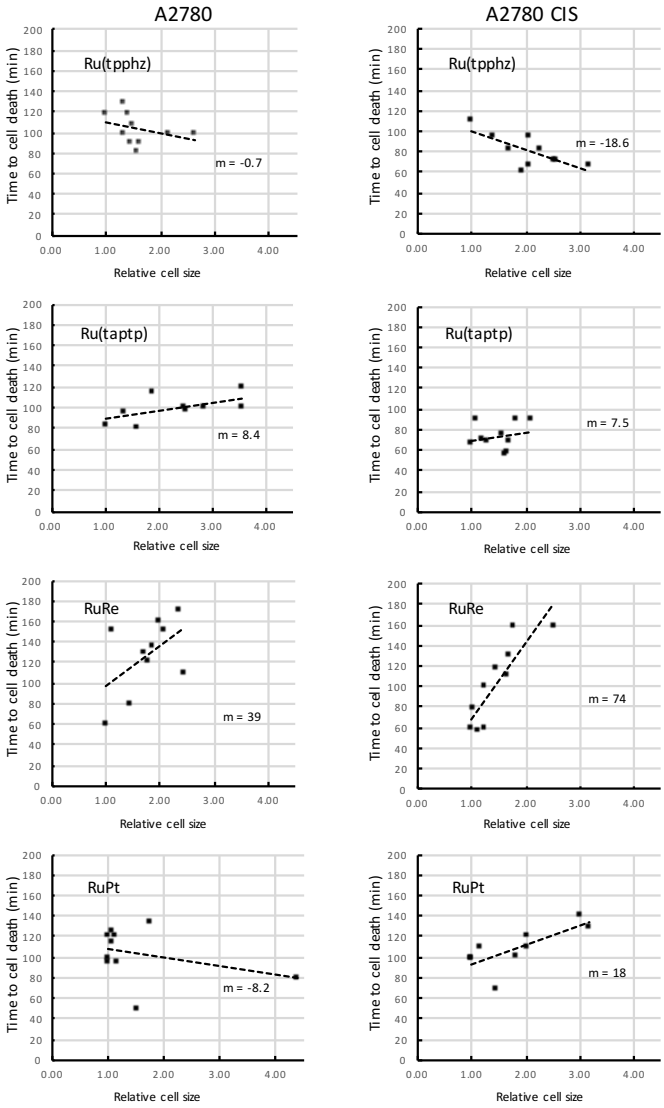
Supplementary Figure 5. Intracellular ruthenium concentration (µmol/L) of A2780 and A2780CIS cells after 1 treatment with equipotent (IC_{50}) concentrations of the four complexes **Ru(tpphz), Ru(taptp), RuRe** and **RuPt**; IC50 values for each compound (Table 2) are shown in red.



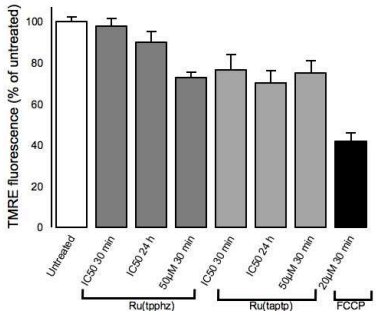
Supplementary Figure 6. Cellular uptake of the indicated compounds into (Upper panels) A2780 cells and (Lower panels) A2780CIS cells incubated with compound for 0h (A), 1h (B), 2h (C), 3h (D). Images show luminescence arising from MLCT superimposed on phase contrast micrographs. Arrows indicate examples of oncotic cell swelling. (E) Control cells imaged as in D without addition of any compound.



Supplementary Figure 7. Changes in individual cell circumference over time following treatment of either A2780 (A,C,E,G) or A2780CIS (B,D,F,H) cells with 50 µM (A,B) Ru(tpphz), (C,D) Ru(taptp), (E,F) RuRe, (G,H) RuPt. Data points in red indicate time of death as determined by rapid increase in nuclear luminescence.



Supplementary Figure 8. Dependency of time of individual cell death on initial cell size. In each dataset, 10 A2780 cells (left-hand panels) or A2780CIS cells (right-hand panels) incubated in the indicated compounds were monitored by live cell imaging, and the time of death determined as shown in Figure 5. For each cell, cell circumference at the start of each incubation was determined using Image J and cell sizes were normalised to the smallest cell in each experiment. In each case, the slope, m was calculated for the best fit line through all data points.



Supplementary Figure 9. Effect of Ru(tpphz) and Ru(taptp) on mitochondrial membrane potential. A2780CIS cells were exposed to IC_{50} concentrations of Ru(tpphz) or Ru(taptp) for 24 h or 30 min, prior to the mitochondrial membrane potential being measured by TMRE assay. The mitochondrial oxidative phosphorylation uncoupler FCCP (20 μM, 30 min) was included as a positive control and treatments were conducted in triplicate.

Ru(tpphz)

Log 2 (Light/Heavy)	Gene names (UniProt)	Protein names: Upregulated / Downregulated
6.19031	HBA1	Hemoglobin subunit alpha
3.34015	JUP	Junction plakoglobin
2.60621	MMS19	MMS19 nucleotide excision repair protein homolog
2.50022	C1QTNF3-AMACR	C1QTNF3-AMACR readthrough (NMD candidate)
2.11722	UBE2V2	Ubiquitin-conjugating enzyme E2 variant 2
1.90417	HMGA2	High mobility group protein HMGI-C
1.7502	HIST1H1D	Histone H1.3
1.73418	FN1	Fibronectin
1.60095	UCHL1	Ubiquitin carboxyl-terminal hydrolase isozyme L1
1.56738	TCOF1	Treacle protein
1.5135	ACAD9	Acyl-CoA dehydrogenase family member 9, mitochondrial
1.48843	ATN1	Atrophin-1
1.48072	NES	Nestin
1.43397	SLC25A15	Mitochondrial ornithine transporter 1
1.39396	HIST1H1E	Histone H1.4
1.38504	TMEM165	Transmembrane protein 165
1.36688	MMACHC	Methylmalonic aciduria and homocystinuria type C protein
1.32449	IGF2BP1	Insulin-like growth factor 2 mRNA-binding protein 1
1.2991	VPS28	Vacuolar protein sorting-associated protein 28 homolog
1.27834	METTL3	N6-adenosine-methyltransferase 70 kDa subunit
1.20058	USP19	Ubiquitin carboxyl-terminal hydrolase 19
1.19492	MRPS18B	28S ribosomal protein S18b, mitochondrial
1.18892	RELA	Transcription factor p65
1.1701	RPUSD2	RNA pseudouridylate synthase domain-containing protein 2
1.15701	ARHGEF1	Rho guanine nucleotide exchange factor 1
1.14839	WDR33	pre-mRNA 3' end processing protein WDR33
1.14035	HIST1H2AJ	Histone H2A type 1-J
1.13632	VTA1	Vacuolar protein sorting-associated protein VTA1 homolog
1.12419	MRPL45	39S ribosomal protein L45, mitochondrial
1.11597	VRK1	Serine/threonine-protein kinase VRK1
1.10107	SETD1A	Histone-lysine N-methyltransferase SETD1A
-0.733268	ALDH16A1	Aldehyde dehydrogenase family 16 member A1
-0.738552	GBP6	Guanylate-binding protein 6
-0.77484	GALM	Aldose 1-epimerase
-0.781654	COL18A1	Collagen alpha-1(XVIII) chain
-0.826762	TSC1	Hamartin
-0.948152	LAMC1	Laminin subunit gamma-1
-1.021551	HIP1R	Huntingtin-interacting protein 1-related protein
-1.052625	GYG1	Glycogenin-1
-1.225337	RPS6KA3	Ribosomal protein S6 kinase alpha-3
-1.463204	SEC62	Translocation protein SEC62

Ru(taptp)

Log (2) Light/Heavy	Gene names (UniProt)	Protein names: Upregulated / Downregulated
3.33379	EFTUD1	Elongation factor-like GTPase 1
3.24482	C1QTNF3-AMACR	C1QTNF3-AMACR readthrough (NMD candidate)
1.95696	UCHL1	Ubiquitin carboxyl-terminal hydrolase isozyme L1
1.39939	HIST1H1D	Histone H1.3
1.39021	PLIN2	Perilipin-2
1.31072	PPP2R4	Serine/threonine-protein phosphatase 2A activator
1.30747	PLD3	Phospholipase D3
1.29931	ACTBL2	Beta-actin-like protein 2
-1.283033	RPF2	Ribosome production factor 2 homolog
-1.329468	LRPPRC	Leucine-rich PPR motif-containing protein, mitochondrial
-1.373732	PGGT1B	Geranylgeranyl transferase type-1 subunit beta
-1.383552	MRPL37	39S ribosomal protein L37, mitochondrial
-1.538786	MKI67	Proliferation marker protein Ki-67
-1.66662	MRPL17	39S ribosomal protein L17, mitochondrial
-1.676042	KIAA0020	Pumilio homolog 3

Supplementary Figure 10. Identities of proteins up- and down-regulated following exposure to the indicated compound.

Supplementary References

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