

Electronic Supplementary Information

Targeting cancer cell metabolism with mitochondria-immobilized phosphorescent cyclometalated iridium(III) complexes

Jian-Jun Cao,^a Cai-Ping Tan,^{*a} Mu-He Chen,^a Na Wu,^a De-Yang Yao,^b Xing-Guo Liu,^b Liang-Nian Ji^a and Zong-Wan Mao^{*a}

^a MOE Key Laboratory of Bioinorganic and Synthetic Chemistry, School of Chemistry and Chemical Engineering, Sun Yat-Sen University, Guangzhou 510275 (P. R. China). E-mail: tancaip@mail.sysu.edu.cn; cesmzw@mail.sysu.edu.cn

^b Key Laboratory of Regenerative Biology, Guangdong Provincial Key Laboratory of Stem Cell and Regenerative Medicine, South China Institute for Stem Cell Biology and Regenerative Medicine, Guangzhou Institutes of Biomedicine and Health, Chinese Academy of Sciences, Guangzhou, People's Republic of China.

Table of Contents

Experimental section

Materials and measurements.....	S5
Synthesis and characterization.....	S5
Crystallographic structure determination.....	S7
Stability studies of complex 2	S7
Cell lines and culture conditions.....	S8
Cytotoxicity assay.....	S8
Co-culture of A549 cells and LO2 cells.....	S8
Lipophilicity.....	S8
ICP-MS measurement	S9
Cellular localization assay.....	S9
Cellular uptake mechanism studies.....	S10
Sensitivity of emission intensity against cell fixation and permeabilization.....	S10
Protein isolation and electrophoresis.....	S10
Fluorescence quenching of BSA by Ir(III) complexes.....	S11
Analysis of MMP.....	S11
Intracellular quantification.....	ATP S11
Mitochondrial bioenergetics analysis.....	S12
Real-time tracking of mitochondrial morphology.....	S12
Intracellular ROS detection.....	S12
Cell cycle analysis.....	S13
Transmission electron microscopy.....	S13
Hoechst 33342 staining.....	S13
Caspase-3/7 activity assay.....	S13
Annexin V/PI double staining assay.....	S13
Microarray gene chip analysis.....	S14
Quantitative real-time PCR.....	S14
Statistical analysis.....	S15

Supplementary figures and tables

Fig. S1 ¹ H NMR spectrum of complex 1	S16
Fig. S2 ¹ H NMR spectrum of complex 2	S16
Fig. S3 ¹ H NMR spectrum of complex 3	S17
Fig. S4 ¹ H NMR spectrum of complex 4	S17
Fig. S5 UV/Vis spectra of complexes 1–4	S18
Fig. S6 Emission spectra of complexes 1–4	S18
Fig. S7 ¹ H NMR spectral study of the stability of complex 2	S19
Fig. S8 Selective 2 -induction of apoptosis by a coculture cell model.....	S20
Fig. S9 Intracellular cellular localization of 1–4	S20
Fig. S10 Colocalization of 2 and 4 with MTDR by confocal microscopy with Airyscan.....	S21
Fig. S11 Intracellular colocalization of 1–4 with LTDR	S21
Fig. S12 Distribution of complexes 1–4 in cellular compartments.....	S22
Fig. S13 Cellular uptake mechanisms of complex 1	S22
Fig. S14 Cellular uptake mechanisms of complex 2	S23
Fig. S15 Cellular uptake mechanisms of complex 3	S23
Fig. S16 Cellular uptake mechanisms of complex 4	S24
Fig. S17 SDS-PAGE analysis of total cellular lysates.....	S24
Fig. S18 SDS-PAGE analysis of Ir(III)-treated BSA.....	S25
Fig. S19 Emission spectra of BSA quenched by complexes 1–4	S25
Fig. S20 Emission spectra of complexes 1–4 upon reaction with BSA.....	S26
Fig. S21 Effects of 2 and 4 on MMP analyzed by confocal microscopy.....	S27
Fig. S22 Intracellular ROS production caused by Ir(III) treatment.....	S28
Fig. S23 Impact of NAC on Ir(III)-induced cell death.....	S28
Fig. S24 Characterization of apoptosis induced by Ir(III) by Hoechst 33342 staining.....	S29
Fig. S25 Activation of caspases-3/7 by Ir(III) treatment.....	S30
Fig. S26 Impact of z-VAD-fmk on Ir(III)-induced cell death.....	S30
Fig. S27 Annexin V/PI double staining analyzed by flow cytometry.....	S31
Fig. S28 Annexin V/PI double staining analyzed by confocal microscopy.....	S32

Fig. S29 Cluster analysis of the microarray data.....	S32
Fig. S30 Heat Map of the 2 -induced expression profile.....	S33
Fig. S31 The fold changes of gene expression determined by RT-PCR.....	S33
Fig. S32 Proposed mechanisms of action of complex 2	S34
Table S1 Crystallographic data of 1 , 3 and 4	S35
Table S2 Selected bond lengths and bond angles of 1 , 3 and 4	S36
Table S3 Photophysical data of complexes 1–4	S37
Table S4 Lipophilicity and cellular uptake efficiency of complexes 1–4	S37
Table S5 Treatment information and the number of differentially expressed genes.....	S38
Table S6 List of differentially regulated genes induced by 2	S38
Table S7 Top 10 pharmaceutical perturbagens displaying positive correlation with 2	S91
Table S8 Top 25 GO terms enriched with differentially expressed genes.....	S92
Table S9 Kyoto encyclopedia of Genes and Genomes (KEGG) pathways.....	S93
Table S10 Primers and sequences of the selected genes.....	S95
Table S11 Functions of the selected genes studied in RT-PCR.....	S97
Supplementary references	S102

Experimental section

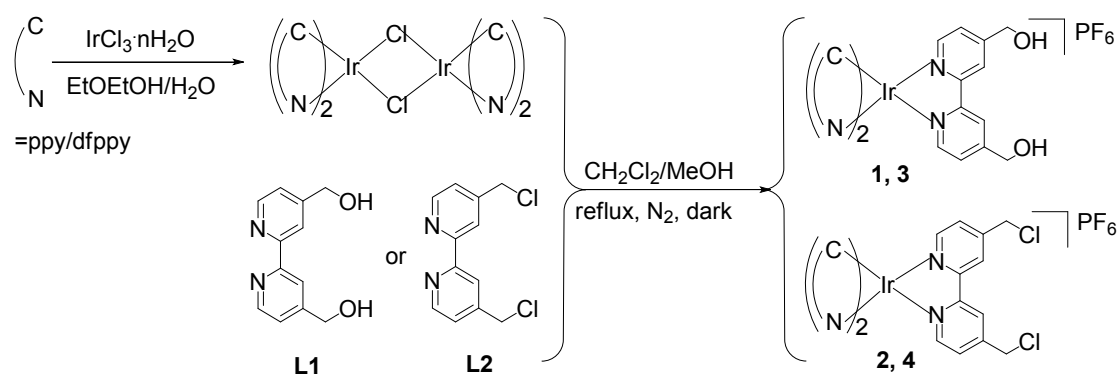
Materials and measurements

Iridium chloride hydrate (Alfa Aesar), ppy (2-phenylpyridine, Aladdin), dfppy (2-(2,4-difluorophenyl)pyridine, Aladdin), (2,2'-bipyridine)-4,4'-diyldimethanol (**L1**, J&K Scientific Ltd.), 4,4'-bis(chloromethyl)-2,2'-bipyridine (**L2**, TCI (Shanghai) Development Co., Ltd.), cisplatin (Alfa Aesar), FCCP (carbonyl cyanide 4-(trifluoromethoxy)phenylhydrazone, Sigma Aldrich), Chloroquine (Sigma Aldrich), MTT (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide, J&K Scientific Ltd.), DMSO (dimethyl sulfoxide, Sigma Aldrich), **MTDR** (MitoTracker Deep Red, Life Technologies), Rhodamine 123 (Sigma-Aldrich), **LTDR** (LysoTracker Deep Red, Life Technologies), PI (propidium iodide, Sigma Aldrich), BSA (bovine serum albumin, Sigma Aldrich), JC-1 (5,5',6,6'-tetrachloro-1,1',3,3'-tetraethylbenzimidazolylcarbocyanine iodide, Life Technologies), H₂DCFDA (2',7'-dichlorodihydrofluorescein diacetate, Sigma Aldrich) and Hoechst 33342 (2'-(4-ethoxyphenyl)-5-(4-methyl-1-piperazinyl)-1H,3'H-2,5'-bibenzimidazole, Sigma Aldrich) were used as received. Solvents were purified and degassed by standard procedures. Caspase-3/7 activity assay kit and cellular ATP quantification assay kit were purchased from Promega (USA). The tested compounds were dissolved in DMSO just before the experiments, and the final working concentration of DMSO was kept at 1% (v/v).

Electrospray ionization mass spectrometry (ESI-MS) was recorded on a Thermo Finnigan LCQ DECA XP spectrometer (USA). The quoted m/z values represented the major peaks in the isotopic distribution. Nuclear magnetic resonance (NMR) spectra were recorded on a Bruker Avance III 400 MHz spectrometer (Germany). Shifts were referenced relative to the internal solvent signals. Microanalysis of elements (C, H, and N) was carried out using an Elemental Vario EL CHNS analyzer (Germany). UV/Vis spectra were recorded on a Varian Cary 300 spectrophotometer (USA). Steady-state emission spectra and lifetime measurements were conducted on a combined

fluorescence lifetime and steady state spectrometer FLS 980 (Edinburgh Instruments Ltd, England). Quantum yields of luminescence at room temperature were calculated according to literature procedures using $[\text{Ru}(\text{bpy})_3](\text{PF}_6)_2$ as the reference.¹ Cell imaging experiments were carried out on a confocal microscope (LSM 800 with Airyscan, ZEISS, Germany). Flow cytometric analysis was done using a BD FACS Calibur™ flow cytometer (Becton Dickinson, USA).

Synthesis and characterization



Scheme S1. Synthetic routes of complexes 1–4.

The cyclometalated iridium(III) chloro-bridged dimer $[\text{Ir}(\text{ppy})_2\text{Cl}]_2$ ² and $[\text{Ir}(\text{dfppy})_2\text{Cl}]_2$ ³ were prepared according to literature method.

General synthetic procedure of the complexes: A mixture of the cyclometalated iridium(III) chloro-bridged dimer (0.15 mmol, 1 equiv.) and L1/L2 (0.33 mmol, 2.2 equiv.) in $\text{CH}_2\text{Cl}_2/\text{CH}_3\text{OH}$ (1:1, v/v) was heated to 60 °C and refluxed 6 h under nitrogen atmosphere in the dark. The solution was cooled to room temperature and evaporated to dryness under reduced pressure. The oil-like substance was dissolved in CH_2Cl_2 and purified by column chromatography on silica gel eluted with $\text{CH}_2\text{Cl}_2/\text{CH}_3\text{OH}$. Isolated solution was added a 4-fold excess of NH_4PF_6 and stirred for 1 h. The mixture was filtered and the filtrate was evaporated under reduced pressure to obtain dry powder. The crude product was washed with water to remove excess NH_4PF_6 . The desired product was further purified by recrystallization.

$[\text{Ir}(\text{ppy})_2(\text{L1})](\text{PF}_6)$ (1). Complex 1 was obtained as a red crystalline powder. Yield: 168.0 mg (65%). ¹H NMR (400 MHz, $[\text{D}_6]$ -Acetone): δ 8.78 (s, 2H), 8.24 (d, $J = 8.2$ Hz, 2H), 8.01 (d, $J = 5.6$ Hz, 2H), 7.99–7.93 (m, 2H), 7.90 (dd, $J = 7.8, 0.8$ Hz, 2H), 7.85 (d, $J = 5.8$ Hz, 2H), 7.66 (d, $J = 5.2$ Hz, 2H), 7.16 (ddd, $J = 7.3, 5.9, 1.3$ Hz, 2H), 7.03 (td, $J = 7.6, 1.1$ Hz, 2H), 6.91 (td, $J = 7.4, 1.3$ Hz, 2H), 6.36 (dd, $J = 7.5, 0.7$ Hz, 2H), 4.93 (s, 4H). ESI-MS (CH_3OH): m/z 717.4 $[\text{M}-\text{PF}_6]^+$. Elemental

analysis: calcd (%) for $C_{34}H_{28}F_6IrN_4O_2P$: C, 45.39; H, 3.27; N, 6.20; found: C, 45.69; H, 3.22; N, 6.11.

[Ir(ppy)₂(L2)](PF₆) (2). Complex **2** was obtained as an orange powder. Yield: 148.3 mg (55%). ¹H NMR (400 MHz, [D₆]-Acetone): δ 8.99 (s, 2H), 8.24 (d, *J* = 8.1 Hz, 2H), 8.11 (d, *J* = 5.7 Hz, 2H), 7.96 (td, *J* = 8.3, 1.5 Hz, 2H), 7.93–7.84 (m, 4H), 7.80 (dd, *J* = 5.7, 1.4 Hz, 2H), 7.15 (ddd, *J* = 7.3, 5.9, 1.3 Hz, 2H), 7.04 (td, *J* = 7.7, 1.2 Hz, 2H), 6.92 (td, *J* = 7.4, 1.3 Hz, 2H), 6.34 (dd, *J* = 7.6, 0.7 Hz, 2H), 4.96 (s, 4H). ESI-MS (CH₃OH): *m/z* 745.5 [M–PF₆]⁺. Elemental analysis calcd (%) for $C_{34}H_{26}Cl_2F_6IrN_4P \cdot 0.3H_2O$: C, 45.17; H, 2.97; N, 6.19; found: C, 44.89; H, 2.86; N, 6.09.

[Ir(dfppy)₂(L1)](PF₆) (3). Complex **3** was obtained as a bright yellow crystalline powder. Yield: 168.0 mg (60%). ¹H NMR (400 MHz, [D₆]-Acetone): δ 8.80 (s, 2H), 8.40 (d, *J* = 8.4 Hz, 2H), 8.13 (d, *J* = 5.7 Hz, 2H), 8.07 (t, *J* = 7.9 Hz, 2H), 7.94 (d, *J* = 5.8 Hz, 2H), 7.71 (d, *J* = 5.7 Hz, 2H), 7.30–7.21 (m, 2H), 6.83–6.70 (m, 2H), 5.81 (dd, *J* = 8.6, 2.3 Hz, 2H), 4.95 (s, 4H). ESI-MS (CH₃OH): *m/z* 789.3 [M–PF₆]⁺. Elemental analysis calcd (%) for $C_{34}H_{24}F_4IrN_4O_2F_6P \cdot CH_2Cl_2$: C, 41.26; H, 2.57; N, 5.50; found: C, 41.27; H, 2.55; N, 5.43.

[Ir(dfppy)₂(L2)](PF₆) (4). Complex **4** was obtained as a yellow powder. Yield: 145.6 mg (50%). ¹H NMR (400 MHz, [D₆]-Acetone): δ 9.00 (s, 2H), 8.40 (d, *J* = 8.4 Hz, 2H), 8.25 (d, *J* = 5.7 Hz, 2H), 8.07 (t, *J* = 8.0 Hz, 2H), 7.97 (d, *J* = 5.8 Hz, 2H), 7.84 (d, *J* = 5.7 Hz, 2H), 7.24 (ddd, *J* = 7.4, 5.9, 1.3 Hz, 2H), 6.84–6.72 (m, 2H), 5.79 (dd, *J* = 8.6, 2.4 Hz, 2H), 4.98 (s, 4H). ESI-MS (CH₃OH): *m/z* 825.3 [M–PF₆]⁺. Elemental analysis calcd (%) for $C_{34}H_{22}Cl_2F_4IrN_4F_6P \cdot 0.3C_3H_6O$: C, 42.42; H, 2.43; N, 5.67; found: C, 42.32; H, 2.39; N, 5.46.

Crystallographic structure determination

Single crystals of **1**, **3** and **4** qualified for X-ray analysis were obtained by diffusion of diethyl ether to the mixture solutions of CH₂Cl₂ and CH₃OH for **1**, CH₂Cl₂ and CH₃CH₂OH for **3**, and CH₂Cl₂ and CH₃COCH₃ for **4**. X-ray diffraction measurements were performed on a Bruker Smart 1000 CCD diffractometer with Mo and Cu K α radiation (λ = 0.71073 or 1.54178 Å) at 150(2), 250(2) and 293(2) K for **1**, **3** and **4**, respectively. The crystal structures of **1**, **3** and **4** were solved by direct methods with program SHELXS and refined using the full-matrix least-squares program SHELXL.⁴ Crystallographic data and details of data collection and structure refinements are listed in Table S1. Selected bond distances and angles are listed in Table S2. The structural plots were drawn using the xp package in SHELXL at a 30% thermal ellipsoids probability level.

Stability studies of complex 2

Complex **2** (10 mg/mL) was stored in DMSO-*d*₆/D₂O (v/v, 7/3) at 37 °C for 7 days. The ¹H NMR spectra were measured at different time intervals. The relative contents of intact form and the hydrolytic product of **2** at each time point were calculated from the integration value of peaks belonging to the methylene of 2, 2'-bipyridine ligands. The peaks of methylene in intact form and hydrolytic product of **2** locate at δ 4.82 ppm and δ 4.71 ppm, respectively.

Cell lines and culture conditions

HeLa, A549, A549R, MDB-MA-231, PC3, and LO2 cells were obtained from Experimental Animal Center of Sun Yat-Sen University (Guangzhou, China). Cells were routinely maintained in DMEM (Dulbecco's modified Eagle's medium, Gibco BRL) or RPMI 1640 (Roswell Park Memorial Institute 1640, Gibco BRL) medium containing 10% FBS (fetal bovine serum, Gibco BRL), 100 µg/mL streptomycin, and 100 U/mL penicillin (Gibco BRL). The cells were cultured in tissue culture flasks in a humidified incubator at 37 °C, in an atmosphere of 5% CO₂ and 95% air. Cisplatin-resistant A549R cells were cultured in RPMI 1640 with additional cisplatin to maintain the resistance. In each experiment, the cells treated with vehicle DMSO (1%, v/v) were used as the referent group.

Cytotoxicity assay

Cells cultured in 96-well plates were grown to confluence. The compounds were dissolved in DMSO (1%, v/v), and diluted with fresh media immediately. Then the cells were incubated with different concentrations of the tested compounds for 44 h at 37 °C. 20 µL of MTT solution was then added to each well, and the plates were incubated for an additional 4 h. The medium was carefully removed, and DMSO was added (150 µL per well). The plates were incubated for 10 min with shaking. The absorbance at 595 nm was measured using a microplate reader (Infinite M200 Pro, Tecan, Switzerland). IC₅₀ values (compound concentration that produces 50% of cell growth inhibition) were calculated from curves constructed by plotting cell survival (%) versus drug concentration (µM). When necessary, cells were pretreated with NAC (10 mM) for 1 h or z-VAD-fmk (50 µM) for 2 h before the addition of the tested compounds. Each experiment was repeated at least three times to gain the mean values.

Co-culture model of A549 cells and LO2 cells

The co-culture model of A549 cells and LO2 cells was established to detect the selectivity of complex **2** towards A549 cells over LO2 cells. Briefly, A549 cells were pre-incubated with Hoechst

33342 (2.0 $\mu\text{g}/\text{mL}$) for 15 min then washed with PBS. The Hoechst-labeled A549 cells were suspended in fresh medium with similar amount of LO2 cells. The mixed cells were seeded into 35 mm confocal dishes and cultured for 24 h. The co-cultured cells were incubated with **2** (10 μM) for 24 h and then stained with Annexin V and PI as described above, after which the cells were observed with a confocal microscope.

Lipophilicity

The lipophilicity of the complexes was measured by the determination of $\log P_{o/w}$, which was referred to as the n-octan-1-ol/water partition coefficient, following a reported procedure.⁵

ICP-MS measurement

The cellular uptake capacity of the complexes was measured by determination of intracellular iridium contents by a method reported in literature with slight modifications.⁶ Briefly, A549 cells were seeded in 100 mm tissue culture dishes and incubated for 24 h. The medium was removed and replaced with medium/DMSO (v/v, 99:1) containing **1–4** (10 μM). After 2 h incubation, the cells were trypsinised, collected in PBS (3 mL) and counted.

Mitochondria were isolated from Ir(III)-treated cells using the mitochondria isolation kit (89874, Thermo Scientific) according to the manufacturer's instructions. The centrifuged cell pellet was resuspended in reagent A (800 μL) and incubated on ice for 2 min. Then reagent B (10 μL) was added and the mixture was incubated on ice for 5 min. After the addition of reagent C (800 μL), the cell suspension was centrifuged at 700 g for 10 min at 4 $^{\circ}\text{C}$. The supernatant was transferred to another tube and further centrifuged at 12 000 g for 15 min at 4 $^{\circ}\text{C}$ to obtain the mitochondrial pellets and the cytosolic supernatant. The mitochondrial pellet was resuspended in reagent C (500 μL), and the resulting suspension was centrifuged at 12 000 g for 5 min to gain a purified mitochondrial fraction.

Nuclear fraction was extracted using a nucleoprotein extraction kit (C500009, Sangon Biotech, China) according to the manufacturer's instructions. The harvested cells were resuspended in the Hypotonic Buffer (600 μL) and incubated on ice for 10 min. After being vortexed for 10 s, the cell suspension was centrifuged at 800 g for 5 min at 4 $^{\circ}\text{C}$, and the supernatant was discarded. The resulting pellet was resuspended in Hypotonic Buffer (400 μL). The nuclei were pelleted by centrifugation at 2500 g for 5 minutes at 4 $^{\circ}\text{C}$.

These fractions were lysed in radio immunoprecipitation assay (RIPA) Buffer. The protein concentration of each fraction was measured using the bicinchoninic acid (BCA) assay. HNO_3 (65%, 1 mL) was added to the lysates of the whole cell and different cellular compartments (mitochondrial,

cytosolic and nuclear fractions) and the mixture was incubated at room temperature for 24 h to digest entirely. The solution was then diluted to a final volume of 10 mL with Milli-Q water (containing 10 ppb indium as internal standard). The concentration of iridium was measured using the XSERIES 2 ICP-MS.⁷

Cellular localization assay

A549 cells were seeded into 35 mm dishes (Greiner, Germany) for confocal microscopy. After cultured overnight, the cells were incubated with complexes **1–4** at 10 μ M for 1 h. The treated cells were observed immediately under a confocal microscope with excitation at 405 nm. For colocalization studies, the cells were incubated with complexes **1–4** (10 μ M) for 1 h. Subsequently, the medium was replaced with staining medium containing **MTDR/LDTR** (100 nM) and stained for another 30 min. The cells were washed twice with PBS, and then viewed immediately under a confocal microscope.

Cellular uptake mechanism studies

A549 cells were seeded in 35 mm dishes and cultured for 24 h. After the cells were pre-treated with chloroquine (50 μ M), the cells were incubated with complexes **1–4** (10 μ M) for 1 h. For metabolic inhibition, cells were incubated in glucose-free modified HBSS buffer (containing Ca^{2+} and Mg^{2+}) supplemented with glutamine (2 mM) as the sole metabolic substrate for 2 hours at 37 °C to deplete the endogenous metabolic substrates. Then the cells were incubated in glucose-free modified HBSS buffer containing oligomycin (3 μ M) and 2-deoxyglucose (10 mM) for 30 min to deplete ATP rapidly. The cells were then incubated with complexes **1–4** (10 μ M) for 1 h. To investigate the impact of temperature on cellular uptake, the cells were incubated at 4 °C or 37 °C for 1 h. In each case, the cells were washed three times with PBS and visualized by confocal microscopy immediately.

Sensitivity of emission intensity against cell fixation and permeabilization

A549 cells were seeded in 35 mm dishes and cultured for 24 h. After incubated with **1–4** (10 μ M) for 2 h, the stained cells were fixed with paraformaldehyde and then rinsed in pre-warmed PBS containing 10% DMSO. The emission intensity of **1–4** in A549 cells was monitored by confocal microscopy after each step.

Protein isolation and electrophoresis

A549 cells were seeded into 60 mm dishes and cultured for 24 h. After treated with vehicle

DMSO (1%, v/v) or complexes **1–4** (10 μ M), the cells were detached with trypsin-EDTA and washed with PBS. The cell lysates were prepared by RIPA Lysis Buffer supplemented with protease inhibitors (Roche Diagnostics GmbH, Mannheim, Germany) and sodium orthovanadate (a phosphatase inhibitor, Sigma Aldrich, USA) and collected by centrifugation. After determination of protein concentration by the BCA assay (Novagen Inc, USA), equal amounts of cellular total proteins or bovine serum albumin (BSA) were denatured by boiling in sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) sample loading buffer for 10 min. The denatured protein was loaded and separated on SDS-PAGE (5% stacking gel, 12% resolving gel). After electrophoresis, the gel was scanned by transmissive ultraviolet (365 nm) using a FluorChem M imaging station and analyzed manually with AlphaView software (ProteinSimple, CA, USA). The same gel was also stained with colloidal CBB (Coomassie Brilliant Blue G-250 Dye, Thermo Scientific) and imaged.

Fluorescence quenching of BSA by Ir(III) complexes

A mixture of BSA (1.5 μ M) and different concentrations of Ir(III) complexes (0, 1.5, 3, 6, 12 or 24 μ M) in PBS buffer was incubated at 37 °C for 6 h. The emission spectra in the range of 305–480 nm were measured with excitation wavelength at 296 nm. The binding constants (K_{SV}) were calculated by Stern–Volmer equation.⁸

Analysis of MMP

Flow cytometry. A549 cells were seeded into 6 well plates and cultured for 24 h. After treated with complexes **1–4** at the indicated concentrations for 6 h, the cells were harvested and resuspended in pre-warmed staining buffer containing 5 μ g/mL JC-1 (1 mL) and incubated at 37 °C for 20 min. Subsequently, the cells were washed twice with blank buffer and immediately measured by flow cytometry at an excitation at 488 nm and dual emission at 530 nm (FITC, Green) and 585 nm (PE, Red). Mean fluorescence intensity (MFI) was analyzed using FlowJo 7.6.1 software (Tree Star, OR, USA). 10, 000 cells were acquired for each sample.

Confocal microscopy. A549 cells were seeded into 35 mm dishes and treated with **1–4** at the indicated concentrations for 6 h. After stained with JC-1, the cells were visualized by a confocal microscope with excitation at 488 nm. Fluorescence was monitored by measuring both the monomer (530 ± 20 nm; green) and the aggregate (590 ± 20 nm; red) forms of JC-1.

Intracellular ATP quantification

Cellular ATP quantification was measured using CellTiter-Glo® Luminescent Cell Viability

Assay kit (G7570, Promega, USA) according to the manufacturer's instructions. A549 cells were seeded at a density of 1.4×10^5 cells per mL in 96 well plates and incubated for 24 h. Cells were treated with the vehicle DMSO (1%, v/v) or Ir(III) at the indicated concentrations for 6 h at 37 °C. The culture medium was replaced by PBS then equilibrated at room temperature for 30 min. Then CellTiter-Glo reagent was added to each well, and then the plate was shaken for 2 min and incubated for 10 min at room temperature. The luminescence was recorded using a microplate reader (Infinite M200 Pro, Tecan, Switzerland). ATP concentration was calculated by interpolation to values (triplicates) determined with known concentrations of ATP (standard curve) in the same assay.

Mitochondrial bioenergetics analysis

The key parameters of mitochondrial function were assessed using the XF Cell Mito Stress Test Kit with the Seahorse XFe24 analyzer (Seahorse Bioscience, Billerica, USA) by directly measuring the oxygen consumption rate (OCR) according to the manufacturer's instructions. A series of preliminary experiments were performed to determine the optimal seeding density of A549 cells and the appropriate concentrations of the compounds including oligomycin (0.75 μ M), FCCP (0.6 μ M) and a mixture of antimycin A (0.5 μ M) and rotenone (0.5 μ M).

A549 cells were seeded in Seahorse 24-well XF Cell Culture Microplates at a density of 3×10^4 cells per well (0.275 cm²). Then A549 cells were treated with complexes **2** and **4** at the indicated doses for 5 h at 37 °C under a 5% CO₂ atmosphere. The cell culture growth medium was removed and replaced with assay medium. The plates were placed into a 37 °C non-CO₂ incubator to equilibrate for 1 h. During the equilibration, the tested compounds diluted to optimal concentration were loaded into the XF sensor cartridges. After baseline measurement, the tested compounds targeting components of the electron transport chain (ETC) were injected consecutively to reveal key metabolic parameters in mitochondria.

Real-time tracking of mitochondrial morphology

A549 cells were seeded in 35 mm dishes and incubated with **2** or **4** (10 μ M) in a humidified incubator linked to the confocal microscope, which provided an atmosphere of 5% CO₂ and 95% air at 37 °C. Cell imaging was carried out at different time intervals.

Intracellular ROS detection

Flow cytometry. After treated with complexes **2** or **4** at the indicated concentrations for 6 h, the cells were harvested and incubated with 10 μ M H₂DCFDA for 15 min at 37 °C in the dark. The cells were collected by centrifugation and washed twice with serum-free medium to remove the excess staining

Dye. The fluorescence intensity of cells was measured immediately by flow cytometry with excitation at 488 nm and emission at 530 ± 30 nm. The MFI was analyzed using FlowJo 7.6 software (Tree Star, OR, USA). 10,000 cells were acquired for each sample.

Confocal microscopy. A549 cells were seeded into 35 mm dishes and treated with **2** or **4** at the indicated concentrations for 6 h. After stained with 10 μ M H₂DCFDA and washed with twice with serum-free medium, the cells were observed immediately by confocal microscopy with excitation at 488 nm and emission at 530 ± 20 nm.

Cell cycle analysis

Cells were cultured in 6-well tissue culture plates (Corning) and incubated with cisplatin, **2** or **4** for 24 h. The cells were collected and fixed in 2 mL of 70% ethanol. After storage at -20 °C overnight, cells were centrifuged and washed twice with cold PBS, and then resuspended in 500 μ L PBS containing PI (50 μ g/mL) and DNase-free RNase (100 μ g/mL). The samples were analyzed by a flow cytometry and the data were processed using the ModFit LT 2.0 software (Verity Software House, USA).

Transmission electron microscopy

A549 cells were cultured in 60 mm dishes (Corning) and incubated with **2** and **4** at indicated concentrations for 24 h. The cells were harvested and fixed overnight at 4 °C in phosphate buffer (pH 7.4) containing 2.5% glutaraldehyde. After treated with osmium tetroxide as post fixative, the cells stained with uranyl acetate and lead citrate was observed under a transmission electron microscope (JEM 100 CX, JEOL, Tokyo, Japan). Images were photographed using the Eversmart Jazz program (Scitex).

Hoechst 33342 staining

A549 cells were seeded into 35 mm dishes and incubated for 24 h and then treated with **2** (10 μ M) or **4** (10 μ M) for 24 h. The cells were then washed once with cold PBS and fixed with 4% paraformaldehyde at room temperature for 10 min. After washed with cold PBS, the cells were labeled with Hoechst 33342 (5 μ g/mL in PBS) for 15 min. The cells were analyzed immediately by confocal microscopy with excitation at 405 nm and emission at 460 ± 20 nm.

Caspase-3/7 activity assay

Caspase-3/7 activity was measured using the Caspase-Glo® Assay kit (Promega, Madison, USA) according to the manufacturer's instructions. Briefly, cells were cultured in white-walled 96-well plates and treated with cisplatin, **2** or **4** at the indicated concentrations for 12 h. Caspase-Glo®

3/7 reagent (100 μ L) was added in each well. The mixture was incubated at room temperature for 1 h and the luminescence was measured using a microplate reader (Infinite M200 Pro, Tecan, Switzerland).

Annexin V/PI double staining assay

Flow cytometry. Translocation of phosphatidylserine (PS) was measured by flow cytometry using the Annexin V-FITC apoptosis detection kit (Sigma-Aldrich, USA) according to the manufacturer's instructions. A549 cells cultured in 6-well plates were exposed to the cisplatin, **2** and **4** at the indicated concentrations for 24 h. The cell suspension was stained with 5 μ L Annexin V-FITC and 10 μ L/mL PI at room temperature for 10 min in the dark. The samples were analyzed immediately by flow cytometry with FITC filters (Green, excitation at 488 nm and emission at 530 ± 30 nm) and PI filters (Red, excitation at 488 nm and emission at 630 ± 30 nm). For the inhibition of ROS, cells were pretreated with NAC (10 mM) for 1 h before the addition of the tested compounds. Data were analyzed using FlowJo 7.6.1 software (Tree Star, OR, USA). 10, 000 cells were acquired for each sample.

Confocal microscopy. A549 cells were seeded into 35 mm dishes for confocal microscopy and treated with **2** or **4** at 10 μ M for 24 h. After the same staining process as described for flow cytometry, the cells were observed under a confocal microscope with excitation at 488 nm and dual emission at 525 ± 20 nm (FITC) and 620 ± 20 nm (PI).

Microarray gene chip analysis

Human genome-wide gene expression profiles of **2**-treated cells were determined by Affymetrix human U133 plus 2.0 microarray analysis in triplicate. A549 cells (1×10^6) were treated with vehicle control (1% DMSO) or complex **2** (3 μ M) for 24 h then total RNA was extracted using TRIZOL Reagent (Life technologies, USA). The Trizol-isolated RNA was checked by an Agilent Bioanalyzer 2100 (Agilent technologies, Santa Clara, CA, US) and purified with RNeasy micro kit (Cat#74004, QIAGEN, GmbH, Germany) and RNase-Free DNase Set (Cat#79254, QIAGEN, GmbH, Germany). The cRNA was synthesized and biotin labeled using GeneChip 3' IVT PLUS Reagent Kit (Cat#902416, Affymetrix, Santa Clara, CA, US). Array hybridization and wash was performed using GeneChip® Hybridization, Wash and Stain Kit (Cat#900720, Affymetrix, Santa Clara, CA, US) in Hybridization Oven 645 (Cat#00-0331-220V, Affymetrix, Santa Clara, CA, US) and Fluidics Station 450 (Cat#00-0079, Affymetrix, Santa Clara, CA, US). The Microarray were scanned with GeneChip® Scanner 3000 (Cat#00-00212, Affymetrix, Santa Clara, CA, US) and Command Console Software 4.0 (Affymetrix, Santa Clara, CA, US). Raw data were normalized by MAS 5.0

algorithm, Gene Spring Software12.6.1 (Agilent technologies, Santa Clara, CA, US). Regulated genes with 2-fold or more differences in expression between groups were listed in Table S5. The genome-wide transcriptional expression data were enriched into Gene Ontology (GO) database, Kyoto encyclopedia of Genes and Genomes (KEGG) Pathway Maps and analyzed with the Connectivity Map resources.

Quantitative real-time PCR

To validate the microarray results of 2-treated cells, RT-PCR was performed using ABI Power SYBR Green PCR Master Mix (ABI, USA) in 7900 HT Sequence Detection System (ABI, USA). The samples were obtained under the same experimental conditions as described for microarray analysis. Total RNA from A549 cells was isolated using TRIzol (Life technologies, USA) according to the manufacturer's instructions. The cDNA was synthesized using iScript cDNA synthesis kit (BIO-RAD, USA). The resulting 5 ng cDNA was mixed with 0.5 μ M of each primer for final concentration, SYBR Green PCR buffer and ddH₂O into 25 μ L of volume. The reaction mixtures were incubated at 50 °C for 2 min and the following cycling conditions: denature 95 °C for 10 min, followed by 40 cycles of 95 °C for 15 s, 60 °C for 1 min, The GAPDH gene was used as a normalizing control. The primer sequences are listed in Table S9.

Statistical analysis

All biological experiments were performed at least twice with triplicates in each experiment. Representative results were depicted in this report and data were presented as means \pm standard deviations (SD).

Supporting figures and tables

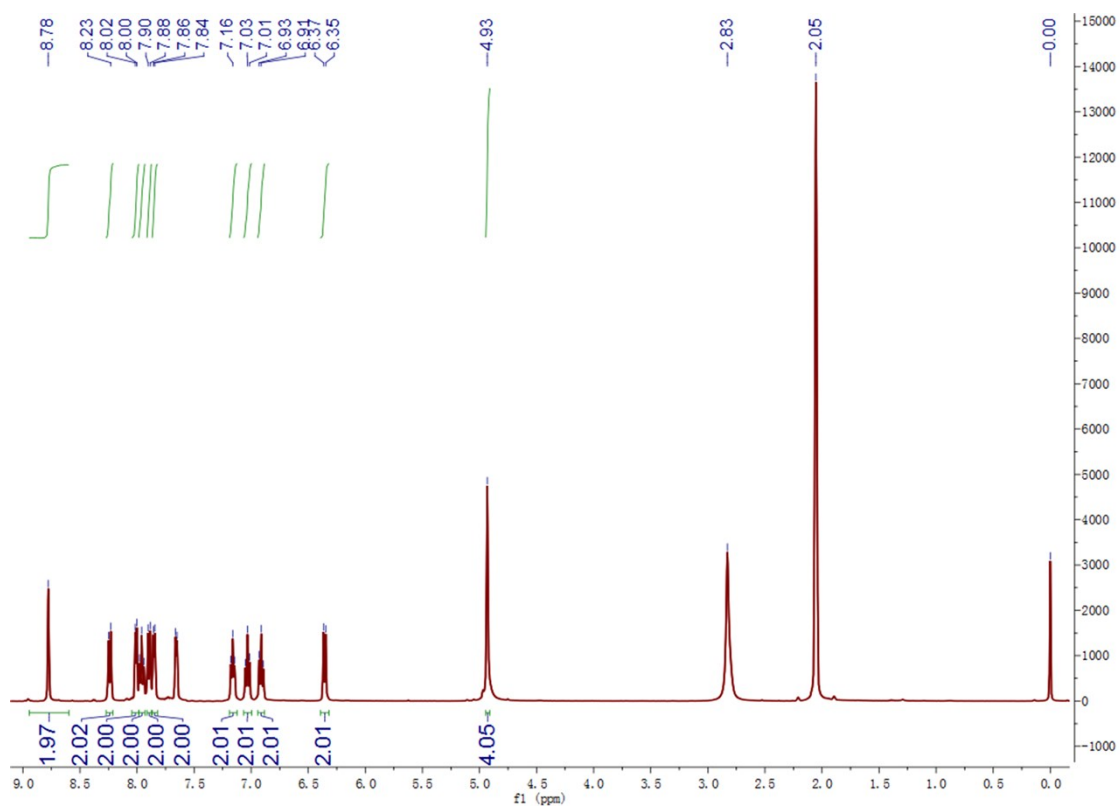


Fig. S1 ^1H NMR spectrum of complex **1** measured in acetone- d_6 .

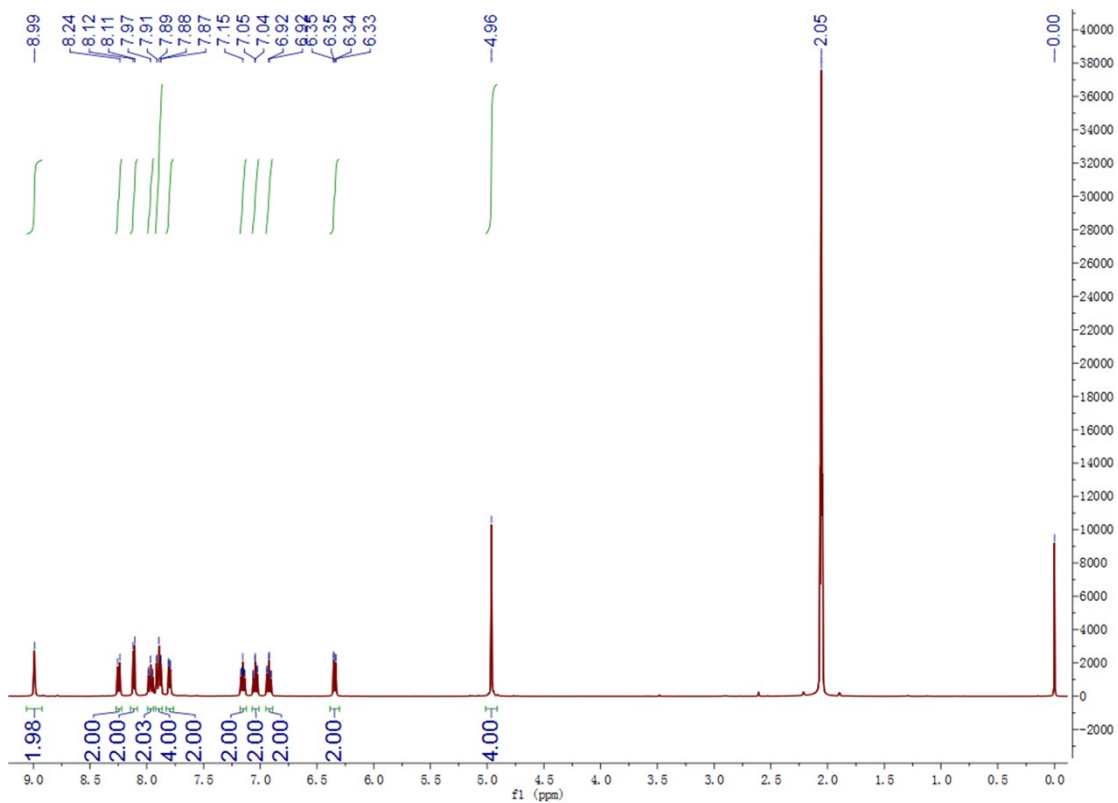


Fig. S2 ^1H NMR spectrum of complex **2** measured in acetone- d_6 .

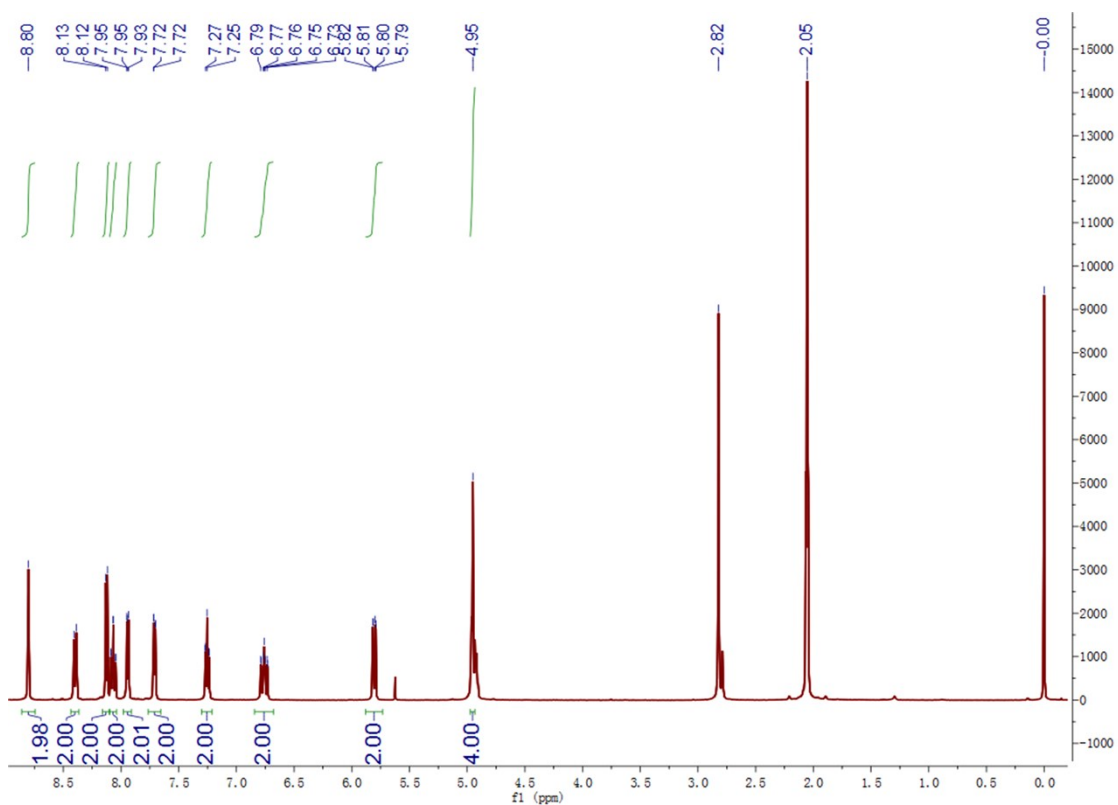


Fig. S3 ^1H NMR spectrum of complex **3** measured in acetone- d_6 .

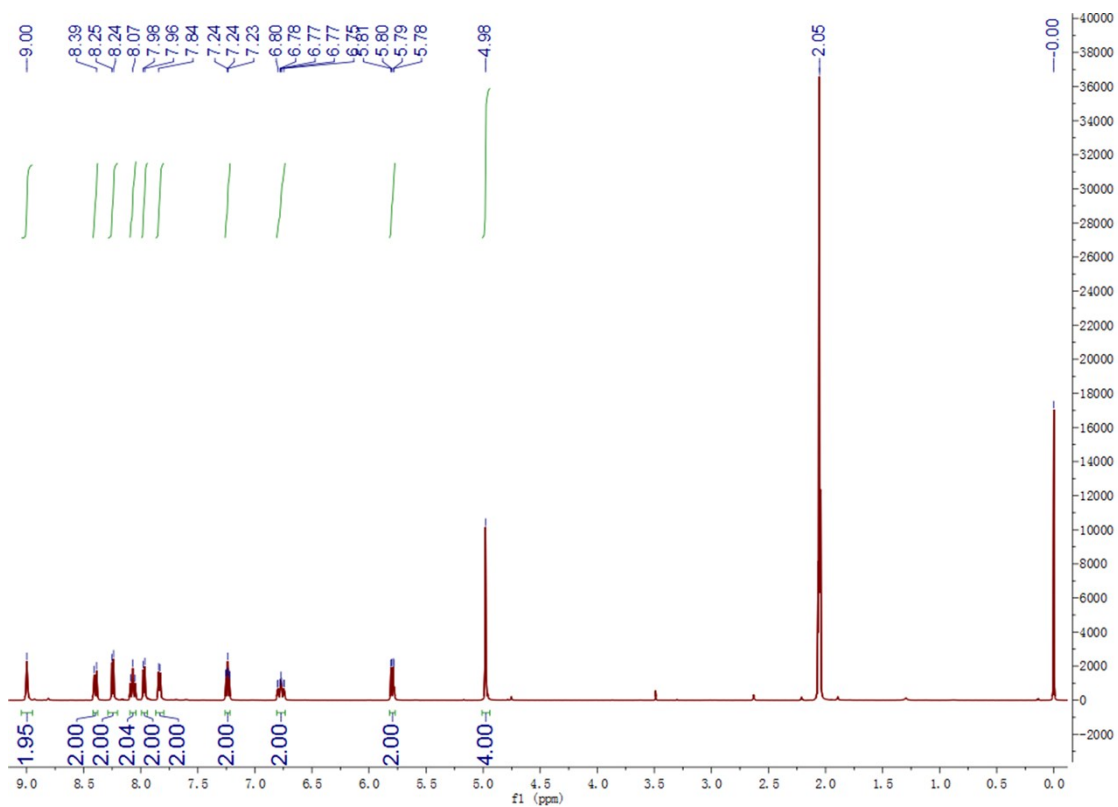


Fig. S4 ^1H NMR spectrum of complex **4** measured in acetone- d_6 .

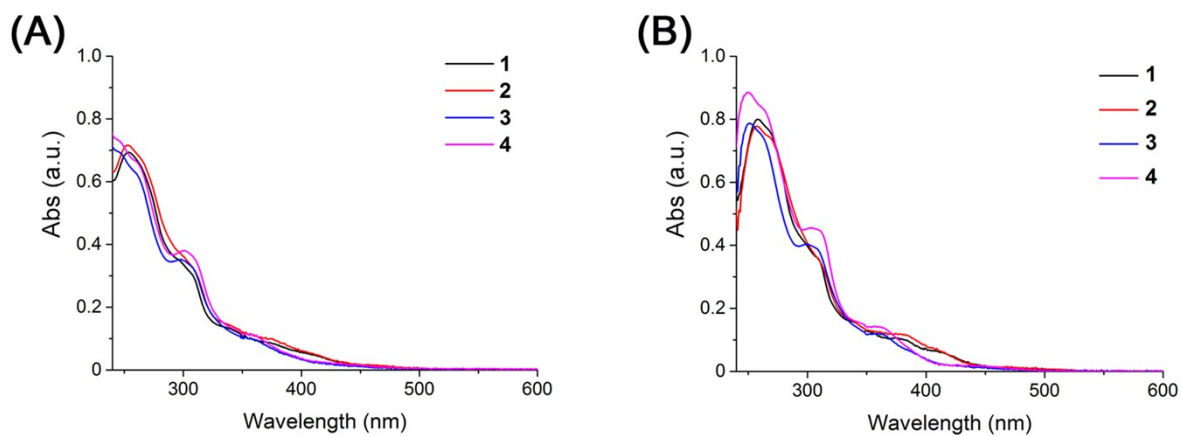


Fig. S5 UV/Vis spectra of complexes **1–4** measured in (A) PBS and (B) CH_2Cl_2 at 25 $^\circ\text{C}$.

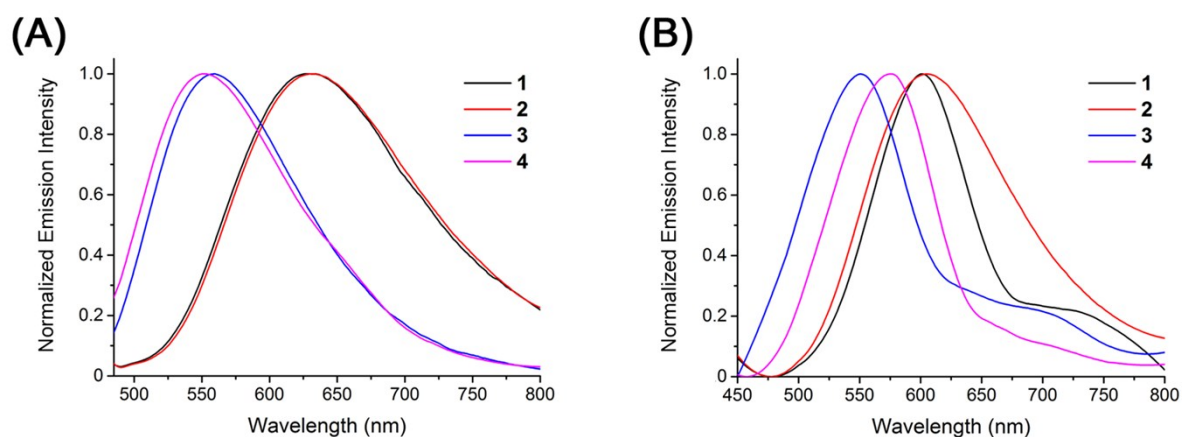


Fig. S6 Normalized emission spectra of complexes **1–4** measured in (A) PBS and (B) CH₂Cl₂ at 25 °C.

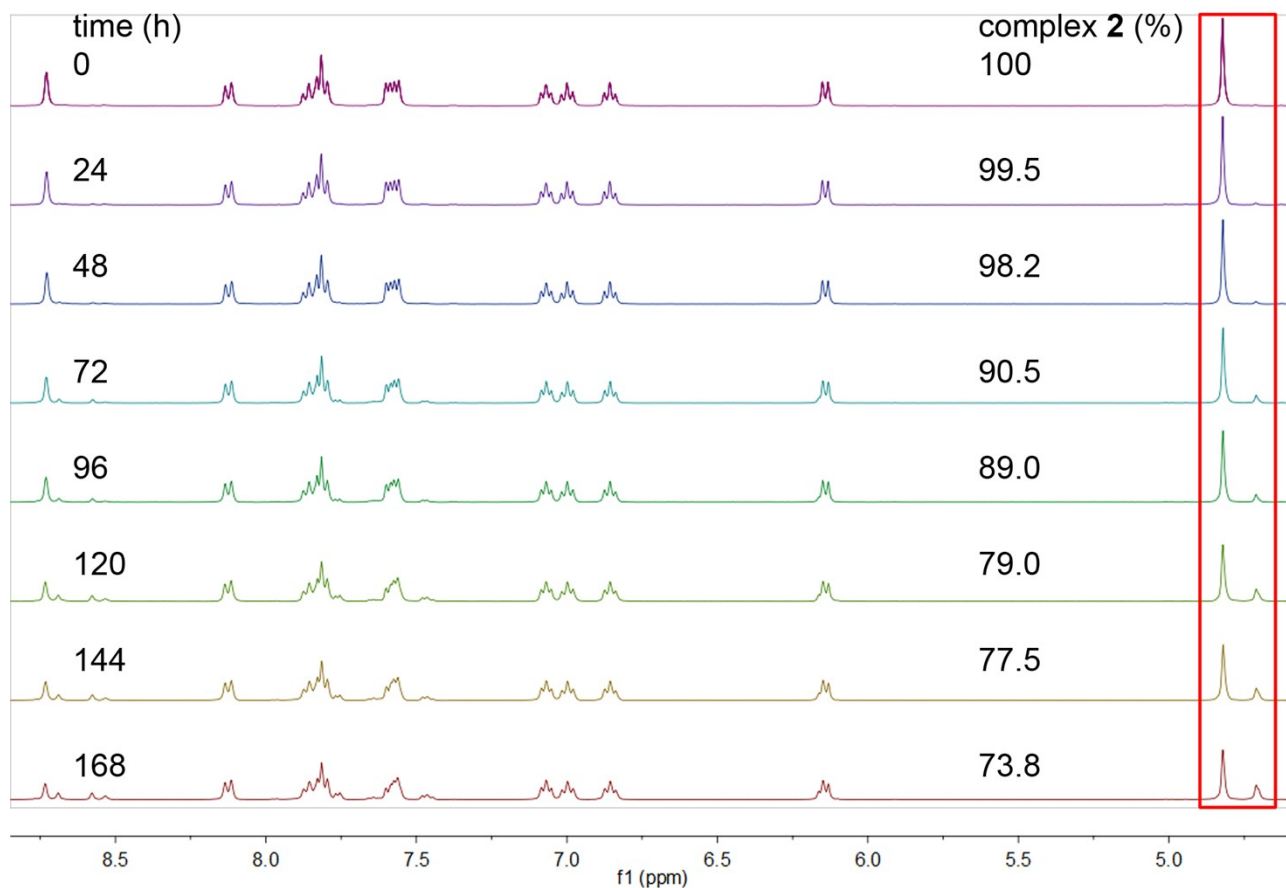


Fig. S7 ¹H NMR spectral study of the stability of complex **2** at a concentration of 10 mg/mL in 70% DMSO-*d*₆/30% D₂O (v/v) at 37 °C over time. The red box denotes the peaks that were integrated for analysis.

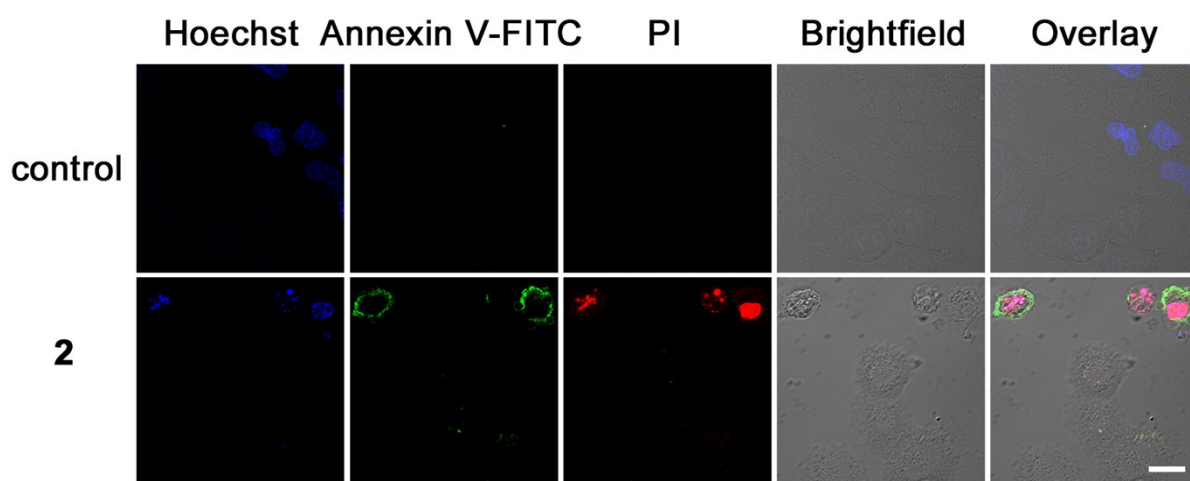


Fig. S8 Selective induction of cancer cell apoptosis by complex **2** (10 μ M, 24 h) in a A549/LO2 coculture cell model measured by annexin V/PI double staining. A549 cells were Hoechst-prelabeled (blue).

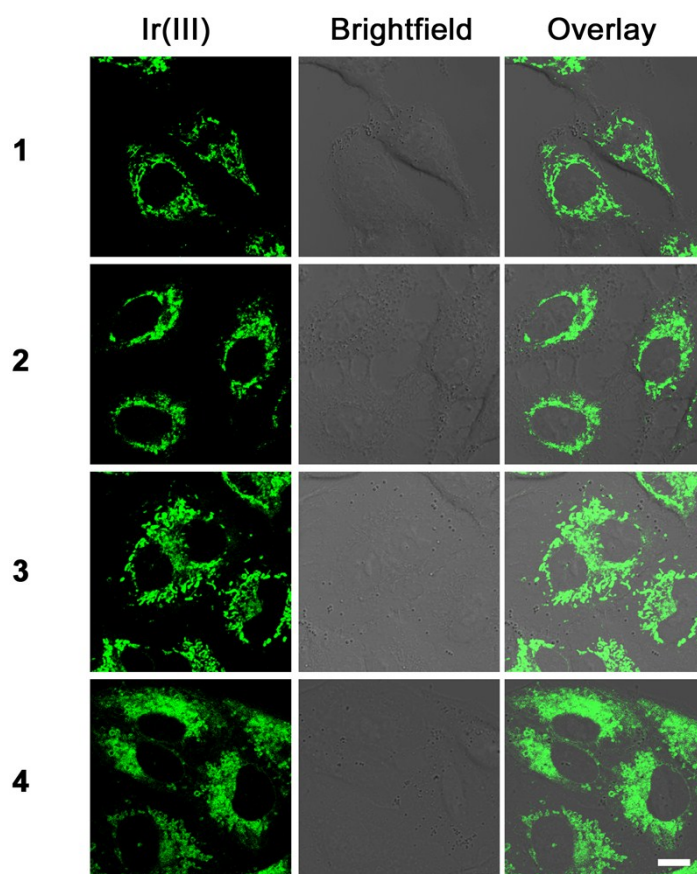


Fig. S9 Intracellular cellular localization of **1–4** observed by confocal microscopy. A549 cells were incubated with **1–4** (10 μ M, 1 h). **1** and **2**: $\lambda_{\text{ex}} = 405$ nm; $\lambda_{\text{em}} = 630 \pm 20$ nm. **3** and **4**: $\lambda_{\text{ex}} = 405$ nm; $\lambda_{\text{em}} = 560 \pm 20$ nm. Scale bar: 10 μ m.

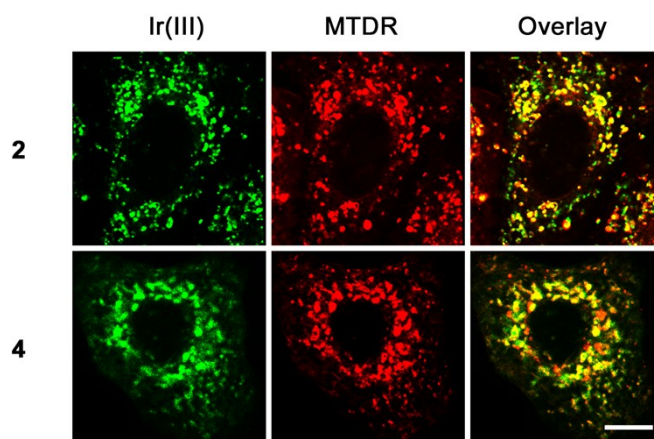


Fig. S10 Colocalization of **2** and **4** with **MTDR** by confocal microscopy with Airyscan. A549 cells were incubated with **2** and **4** (10 μ M, 1 h) and then stained with **MTDR** (100 nM, 30 min). **2**: $\lambda_{\text{ex}} = 405$ nm; $\lambda_{\text{em}} = 630 \pm 20$ nm. **4**: $\lambda_{\text{ex}} = 405$ nm; $\lambda_{\text{em}} = 560 \pm 20$ nm. **MTDR**: $\lambda_{\text{ex}} = 633$ nm, $\lambda_{\text{em}} = 655 \pm 20$ nm. Scale bar: 10 μ m.

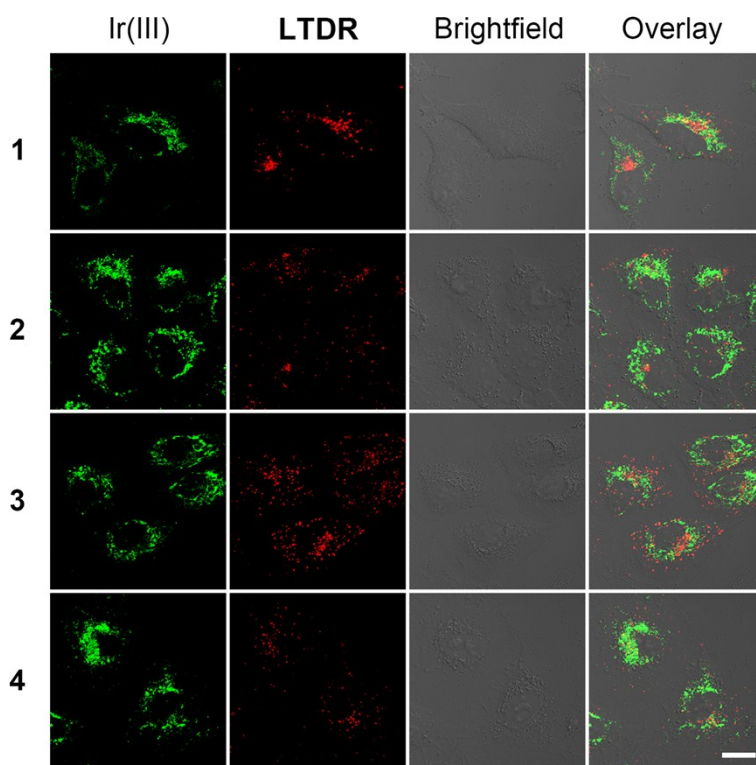


Fig. S11 Intracellular colocalization of **1–4** with **LTDR** observed by confocal microscopy. A549 cells were incubated with **1–4** (10 μ M, 1 h), and then stained with **LTDR** (100 nM, 30 mins). **1** and **2**:

$\lambda_{\text{ex}} = 405 \text{ nm}$; $\lambda_{\text{em}} = 630 \pm 20 \text{ nm}$. **3** and **4**: $\lambda_{\text{ex}} = 405 \text{ nm}$; $\lambda_{\text{em}} = 560 \pm 20 \text{ nm}$. LTDR: $\lambda_{\text{ex}} = 633 \text{ nm}$, $\lambda_{\text{em}} = 668 \pm 20 \text{ nm}$. Scale bar: $10 \mu\text{m}$.

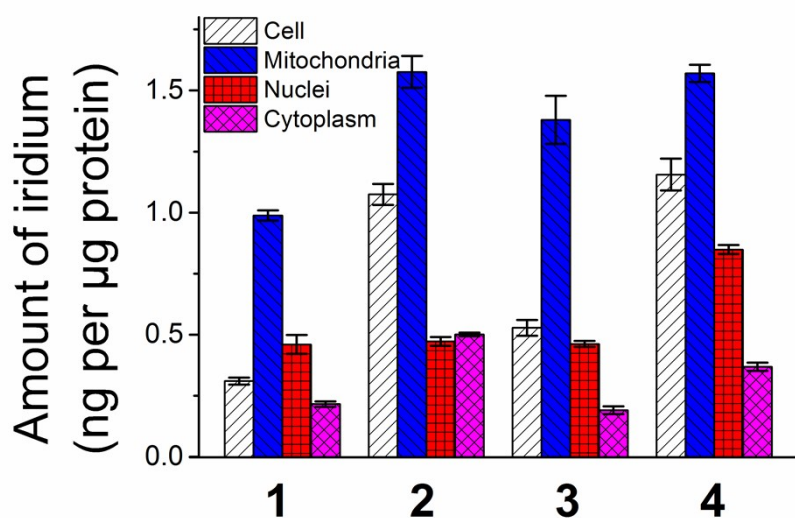


Fig. S12 Distribution of complexes **1–4** in cellular compartments of A549 cells measured by ICP-MS. Cells were treated with Ir(III) at a concentration of $10 \mu\text{M}$ for 2 h.

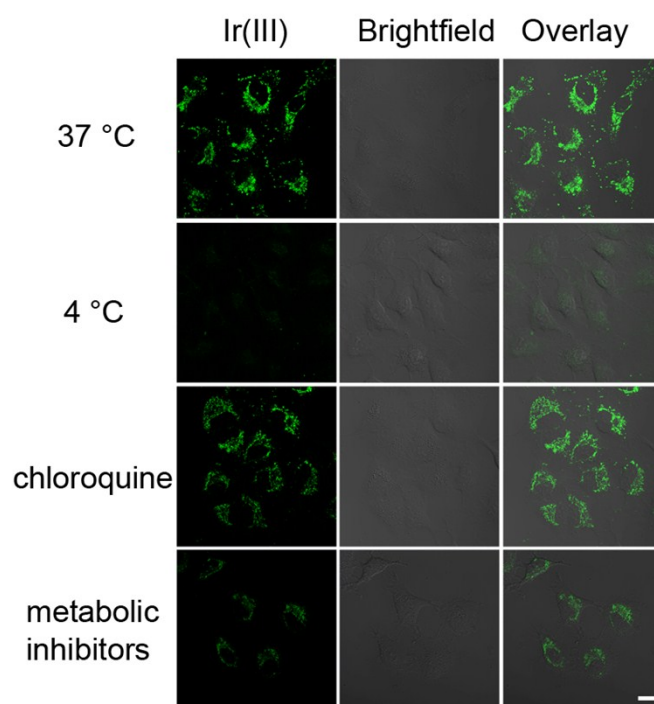


Fig. S13 Cellular uptake mechanisms of complex **1**. A549 cells were incubated with **1** ($10 \mu\text{M}$, 1 h) under different temperature, pretreated with chloroquine ($50 \mu\text{M}$) or metabolic inhibitors (2-deoxy-D-glucose (10 mM) and oligomycin ($3 \mu\text{M}$)). $\lambda_{\text{ex}} = 405 \text{ nm}$; $\lambda_{\text{em}} = 630 \pm 20 \text{ nm}$. Scale bar: $10 \mu\text{m}$.

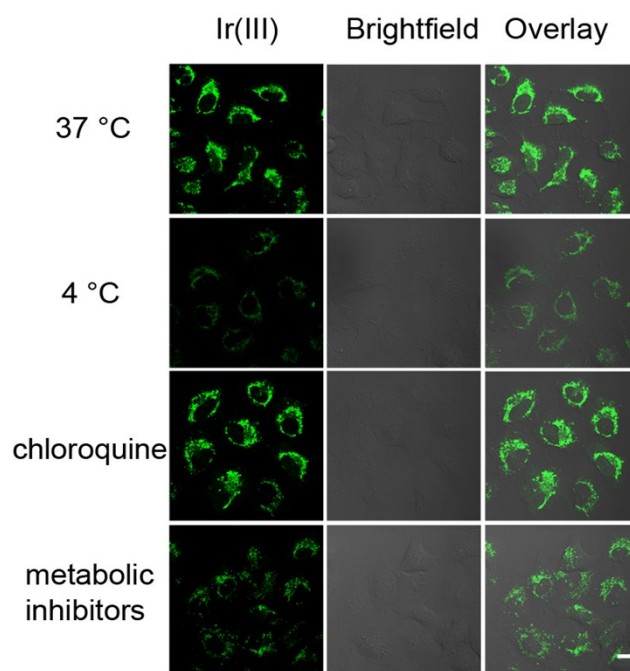


Fig. S14 Cellular uptake mechanisms of complex **2**. A549 cells were incubated with **2** (10 μ M, 1 h) under different temperature, pretreated with chloroquine (50 μ M) or metabolic inhibitors (2-deoxy-D-glucose (10 mM) and oligomycin (3 μ M)). $\lambda_{\text{ex}} = 405$ nm; $\lambda_{\text{em}} = 630 \pm 20$ nm. Scale bar: 10 μ m.

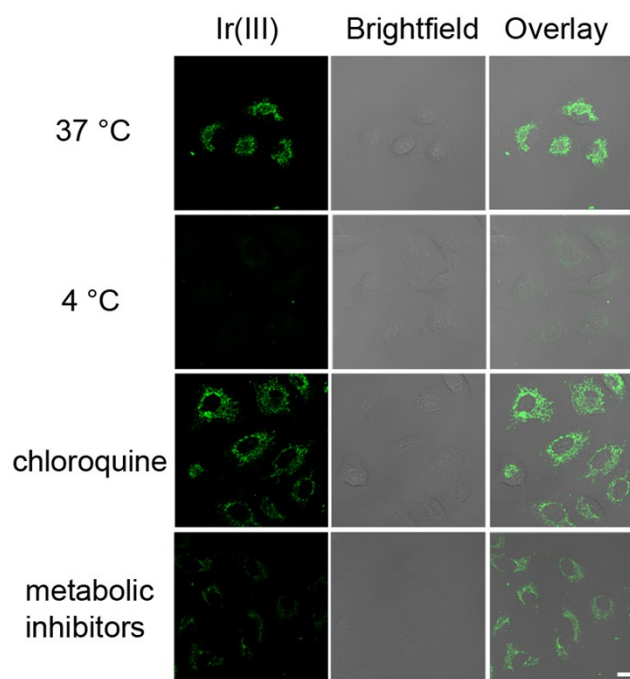


Fig. S15 Cellular uptake mechanisms of complex **3**. A549 cells were incubated with **3** (10 μ M, 1 h) under different temperature, pretreated with chloroquine (50 μ M) or metabolic inhibitors (2-deoxy-D-glucose (10 mM) and oligomycin (3 μ M)). $\lambda_{\text{ex}} = 405$ nm; $\lambda_{\text{em}} = 560 \pm 20$ nm. Scale bar: 10 μ m.

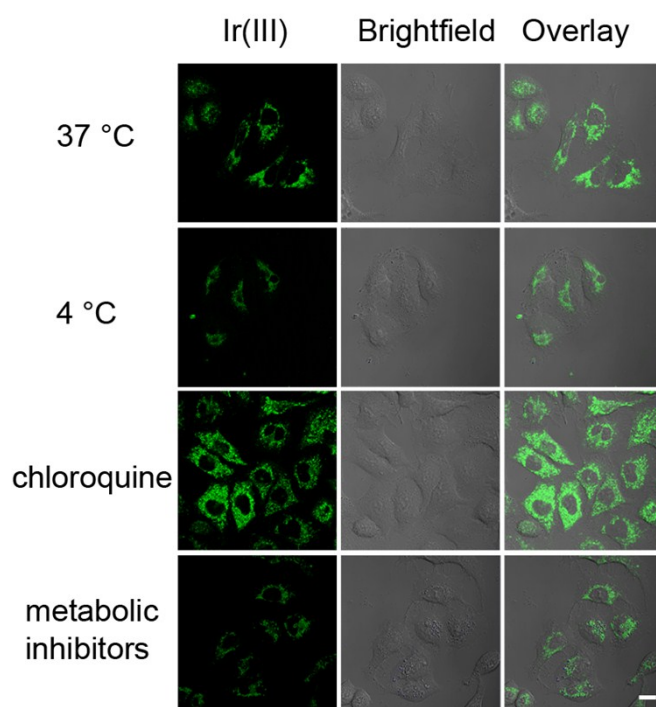


Fig. S16 Cellular uptake mechanisms of complex **4**. A549 cells were incubated with **4** (10 μ M, 1 h) under different temperature, pretreated with chloroquine (50 μ M) or metabolic inhibitors (2-deoxy-D-glucose (10 mM) and oligomycin (3 μ M)). $\lambda_{\text{ex}} = 405$ nm; $\lambda_{\text{em}} = 560 \pm 20$ nm. Scale bar: 10 μ m.

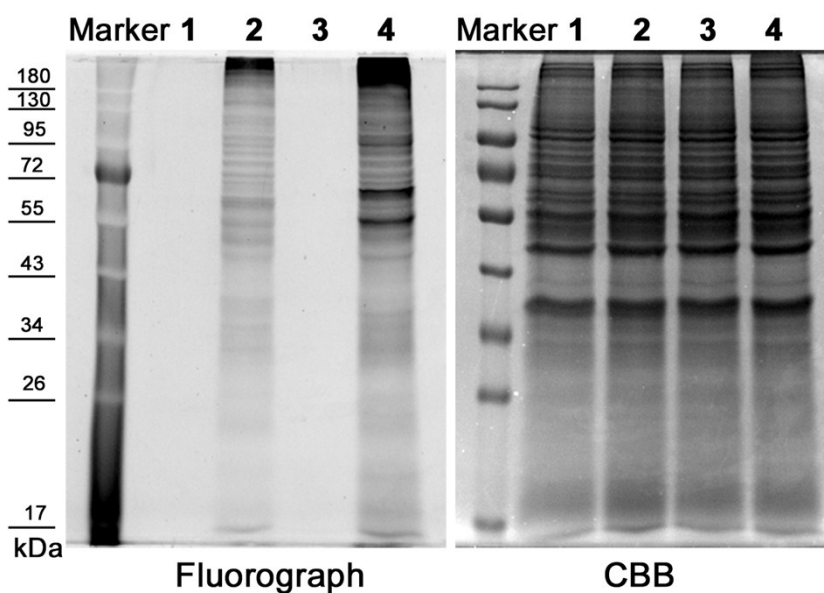


Fig. S17 SDS-PAGE analysis of proteins purified under denaturing conditions in lysed A549 cells. The cells were treated with **1–4** (10 μ M) for 2 h at 37 °C. The gel was scanned with transmissive ultraviolet ($\lambda_{\text{ex}} = 365$ nm, Left), and then stained with CBB (Right).

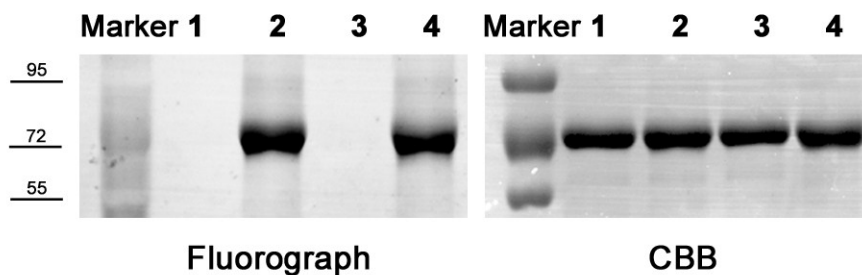


Fig. S18 SDS-PAGE analysis of Ir(III)-treated BSA under denaturing conditions. BSA was incubated with **1–4** (10 μM) for 2 h at 37 $^{\circ}\text{C}$. The gel was scanned with transmissive ultraviolet ($\lambda_{\text{ex}} = 365 \text{ nm}$, Left), and then stained with CBB (Right).

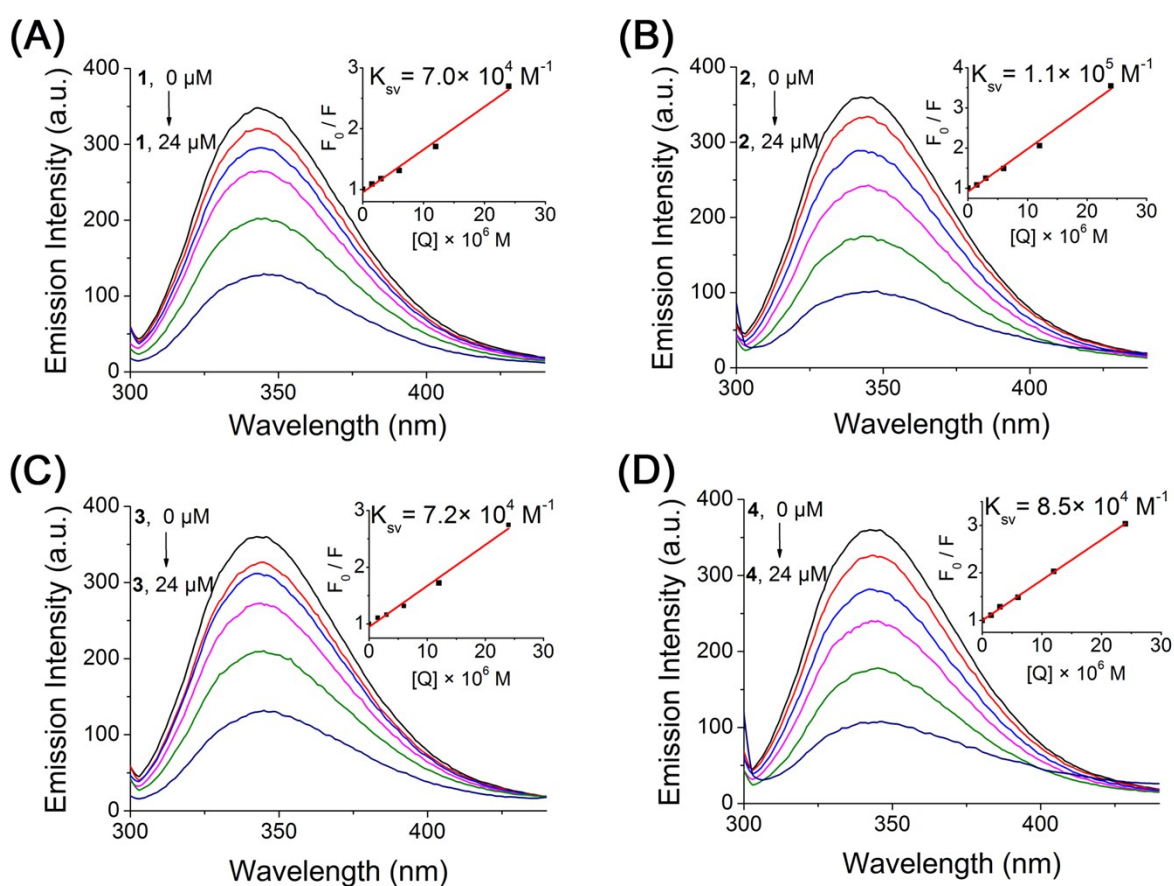


Fig. S19 Emission spectra of BSA quenched by complexes **1–4**. BSA (1.5 μM) was incubated with the Ir(III) complexes (0, 1.5, 3, 6, 12, 24 μM) at 37 $^{\circ}\text{C}$ for 24 h. $\lambda_{\text{ex}} = 296 \text{ nm}$.

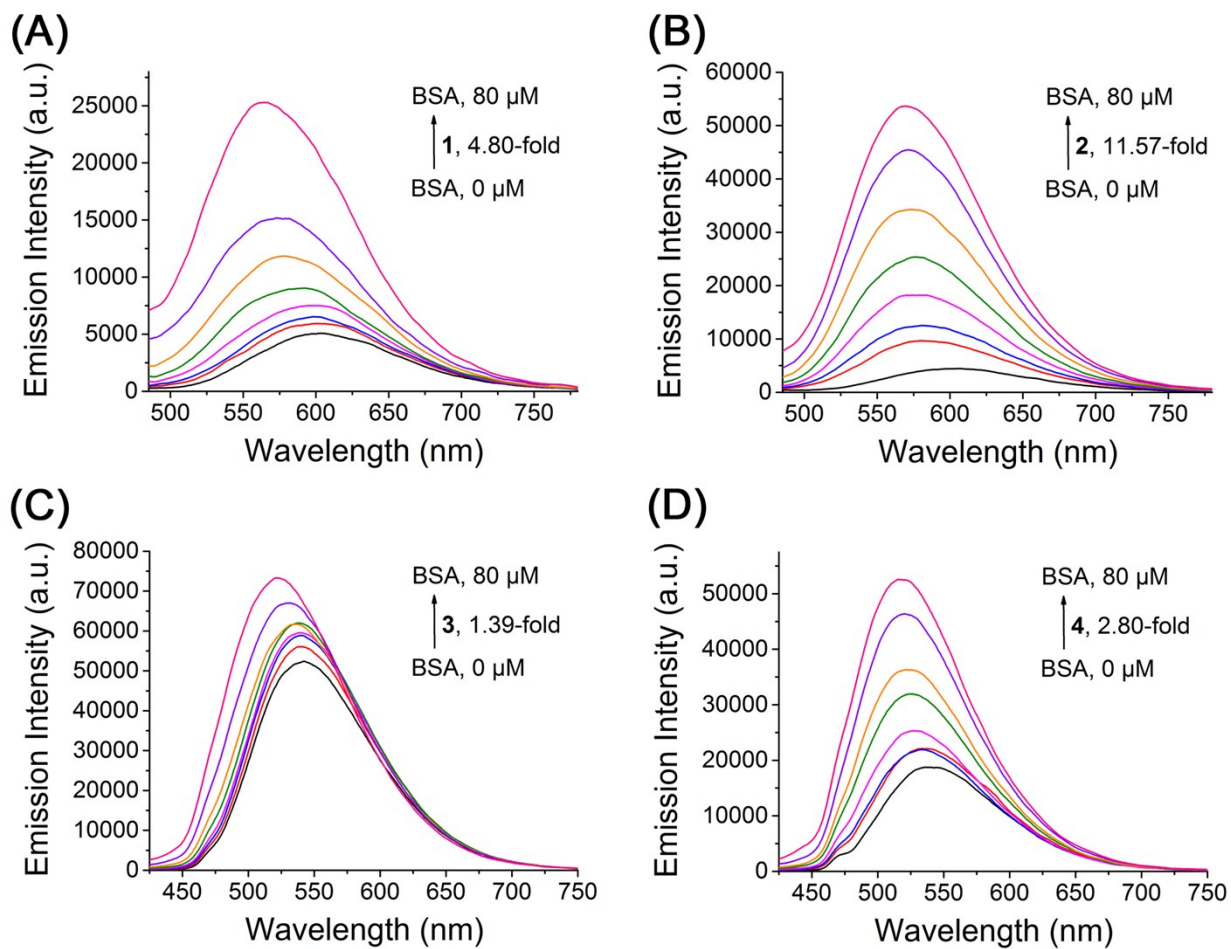


Fig. S20 Emission spectra of complexes 1–4 upon reaction with BSA. The Ir(III) complexes (10 μM) were incubated with BSA (0, 1.25, 2.5, 5, 10, 20, 40, 80 μM) at 37 $^{\circ}\text{C}$ for 24 h. $\lambda_{\text{ex}} = 405$ nm.

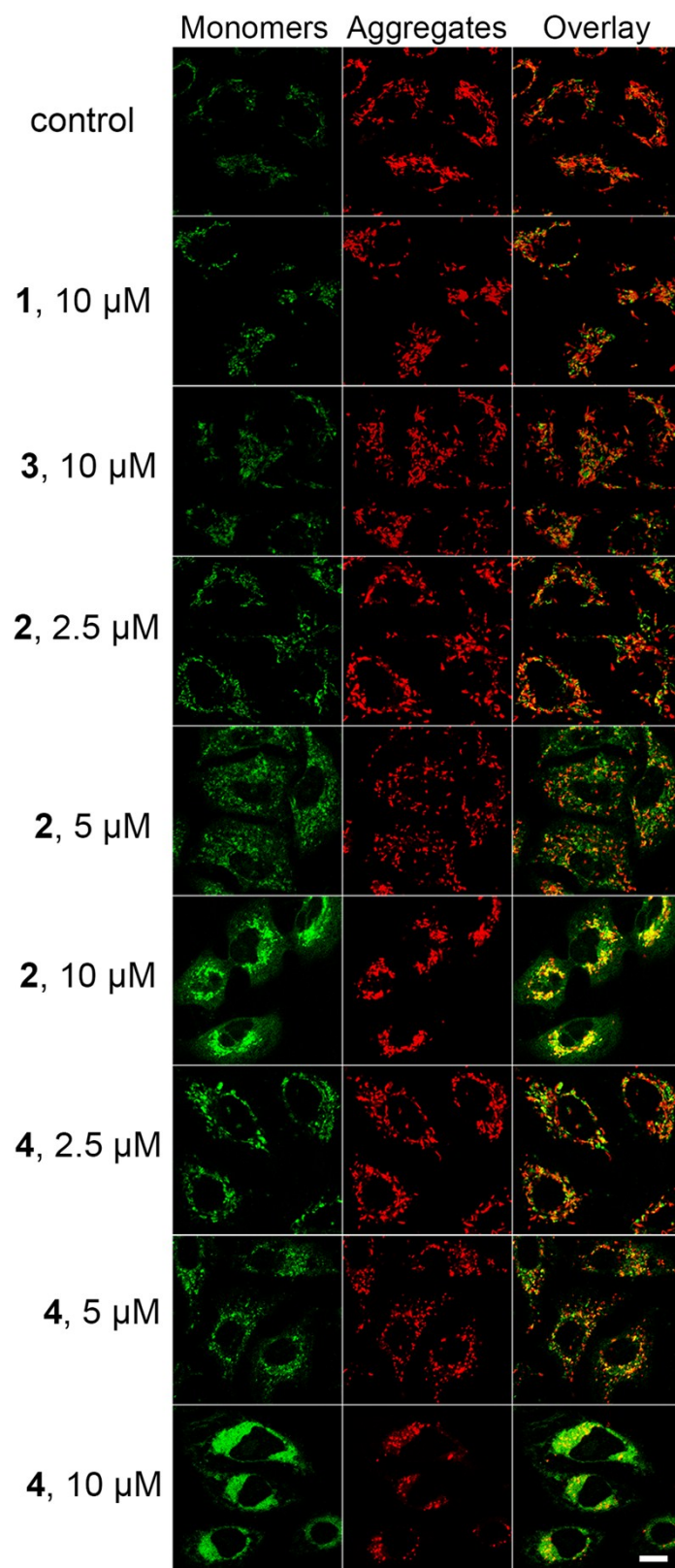


Fig. S21 Effects of **2** and **4** on MMP analyzed by confocal microscopy. Fluorescence imaging of A549 cells were treated with **1–4** at the indicated concentrations for 6 h, and then labeled with JC-1. $\lambda_{\text{ex}} = 488 \text{ nm}$. $\lambda_{\text{em}} = 530 \pm 20 \text{ nm}$ (Green) and $590 \pm 20 \text{ nm}$ (Red). Scale bar: 10 μm .

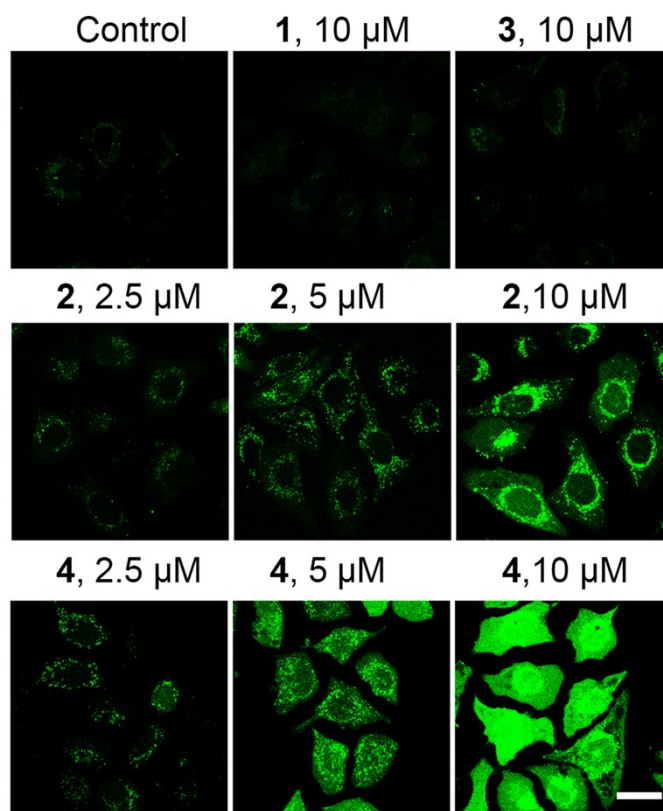


Fig. S22 Intracellular ROS production caused by Ir(III) treatment. A549 cells were treated with **2** and **4** at the indicated concentrations for 6 h. Then the cells were stained with H₂DCFDA and analyzed by confocal microscopy. λ_{ex} : 488 nm; λ_{em} : 530 \pm 20 nm. Scale bar: 10 μm .

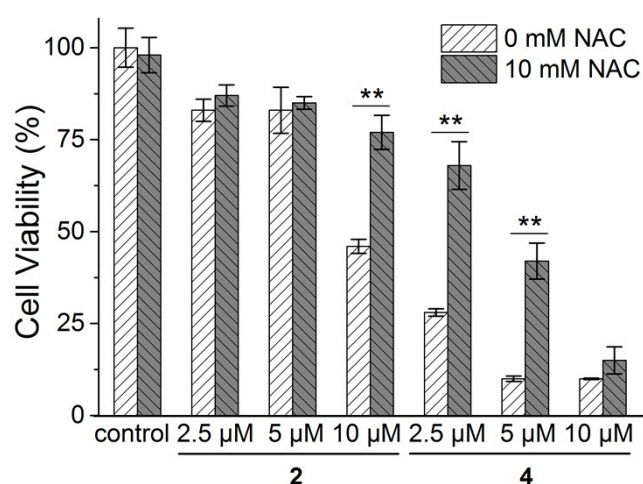


Fig. S23 Impact of NAC on Ir(III)-induced cell death. A549 cells were treated with complexes at the indicated concentrations for 24 h with or without the pretreatment of 10 mM NAC for 1 h. Cell viability was measured by MTT assay. * $p < 0.05$, ** $p < 0.01$.

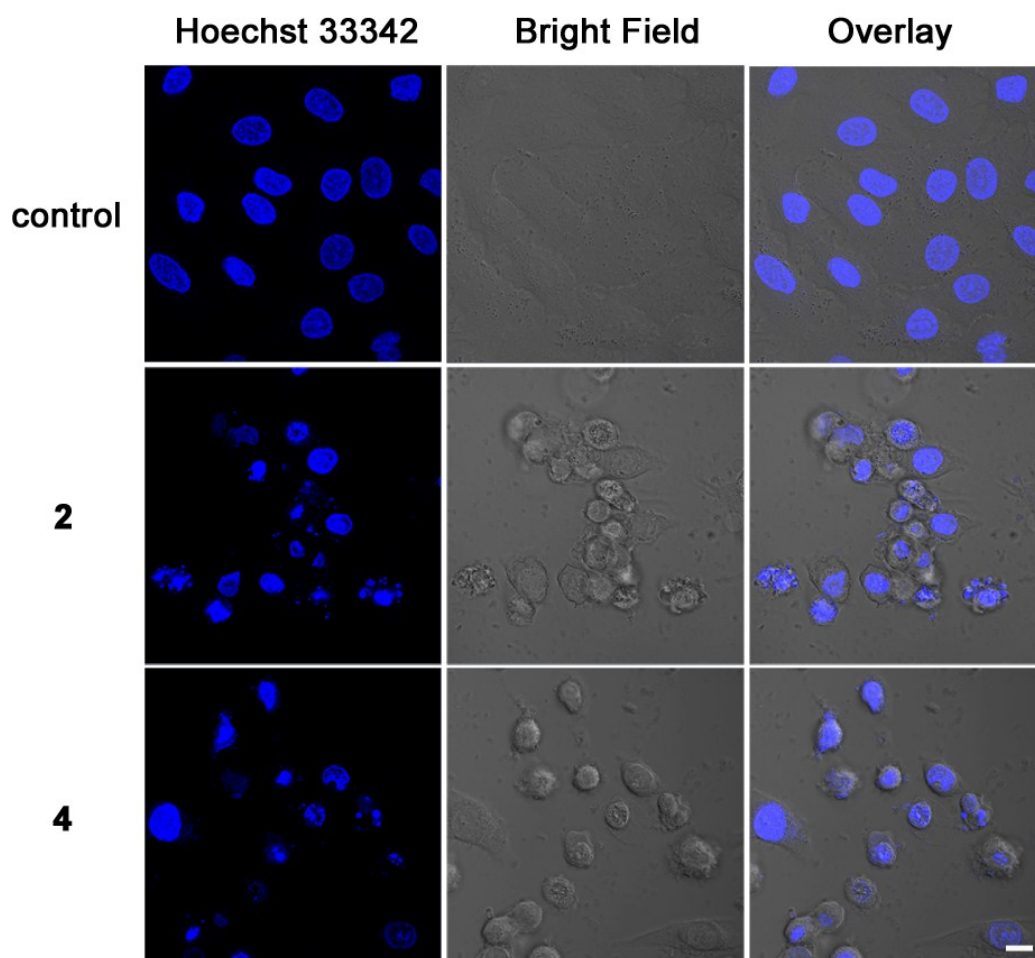


Fig. S24 Characterization of Ir(III)-induced apoptosis by Hoechst 33342 staining. A549 cells were incubated with **2** (10 μ M) and **4** (10 μ M) for 24 h. λ_{ex} : 405 nm; λ_{em} : 460 ± 20 nm. Scale bar: 10 μ m.

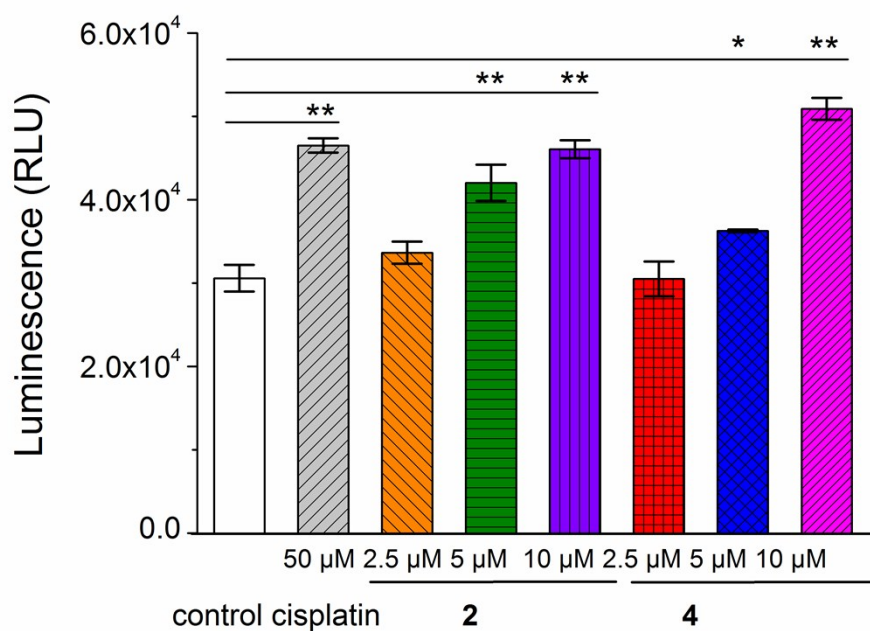


Fig. S25 Activation of caspases-3/7 by Ir(III) treatment. A549 cells were treated with cisplatin, **2** and **4** at the indicated concentrations for 12 h. * $p < 0.05$, ** $p < 0.01$.

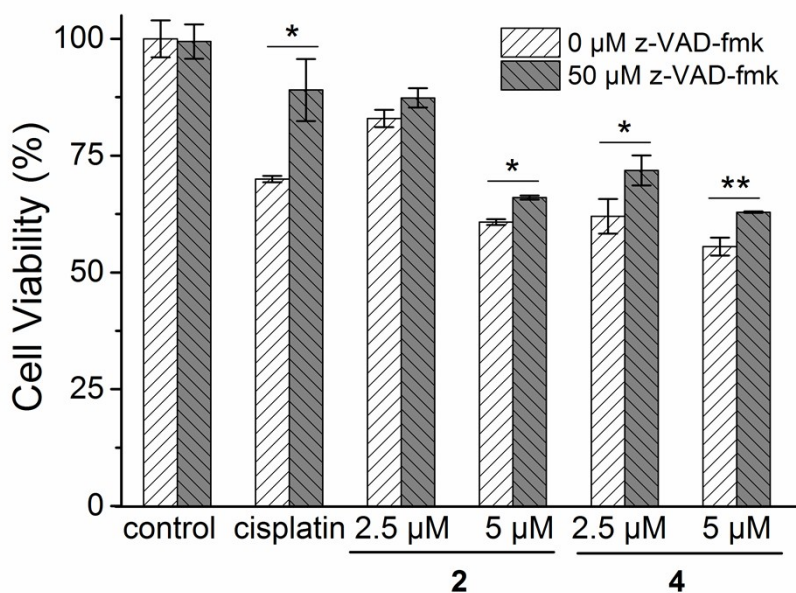


Fig. S26 Impact of z-VAD-fmk on Ir(III)-induced cell death. A549 cells were treated with cisplatin, **2** and **4** for 24 h with or without pretreatment of z-VAD-fmk (50 μM) for 2 h. Cell viability was measured by MTT assay. * $p < 0.05$, ** $p < 0.01$.

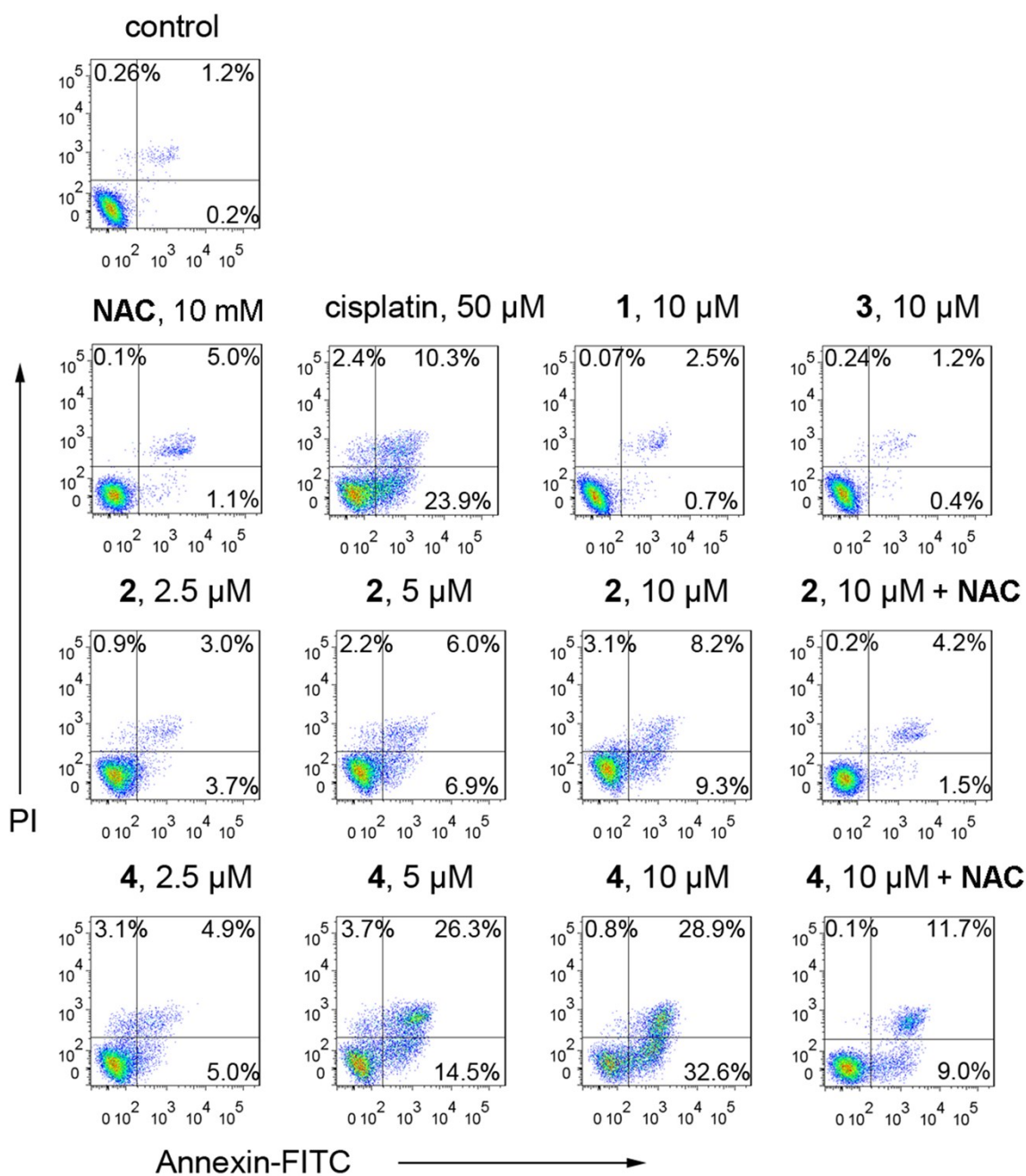


Fig. S27 Annexin V/PI double staining analyzed by flow cytometry. A549 cells were treated with cisplatin, **2** and **4** with or without pretreatment of NAC (10 mM) at the indicated concentrations for 24 h. The fluorescence of FITC ($\lambda_{ex} = 488 \text{ nm}$; $\lambda_{em} = 530 \text{ nm}$) and PI ($\lambda_{ex} = 488 \text{ nm}$; $\lambda_{em} = 630 \text{ nm}$) was analyzed by flow cytometry.

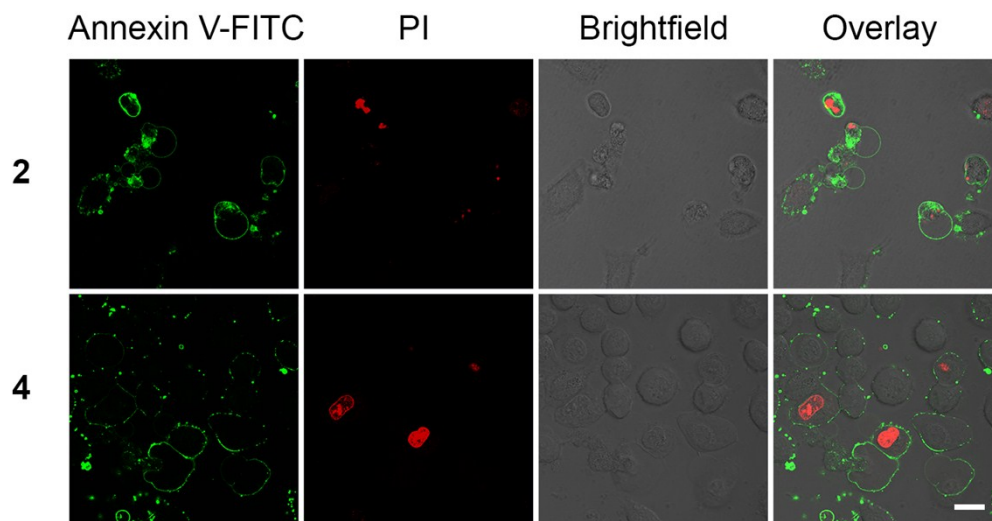


Fig. S28 Annexin V/PI double staining analyzed by confocal microscopy. A549 cells were treated with **2** (10 μ M) and **4** (10 μ M) for 24 h. FITC: $\lambda_{\text{ex}} = 488$ nm; $\lambda_{\text{em}} = 530 \pm 20$ nm. PI: $\lambda_{\text{ex}} = 488$ nm; $\lambda_{\text{em}} = 630 \pm 20$ nm. Scale bar: 10 μ m.

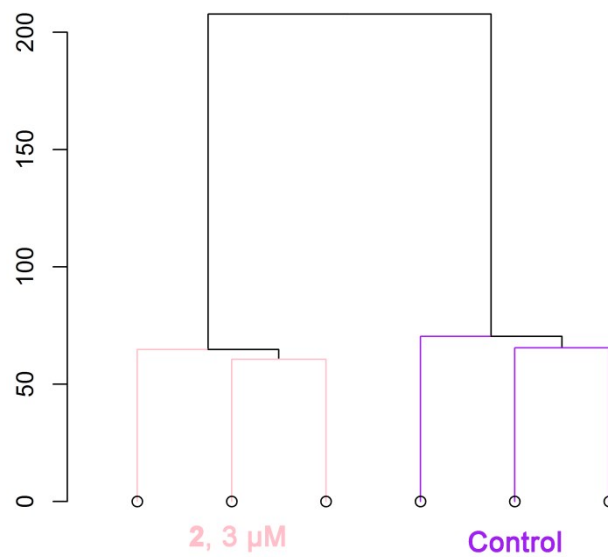


Fig. S29 Cluster analysis of the microarray data using average linkage and Euclidean distance. Each sample was analyzed in triplicate.

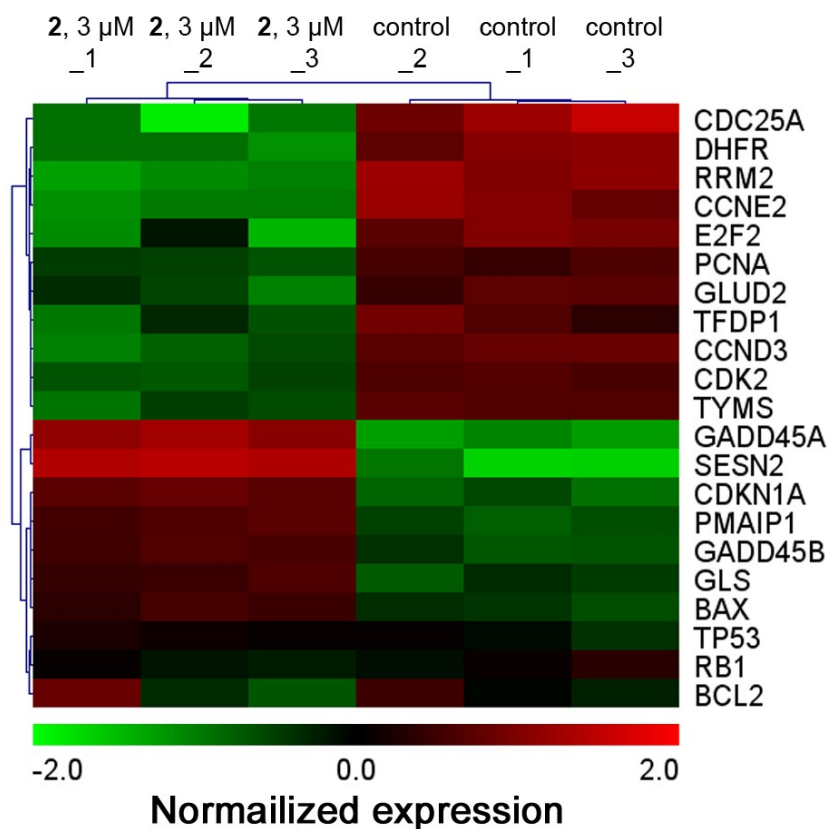


Fig. S30 Heat Map of the 2-induced expression profile of A549 cells to the untreated control. The above 21 genes were selected based on the Kyoto encyclopedia of Genes and Genomes (KEGG) pathways in which they participate phenotype.

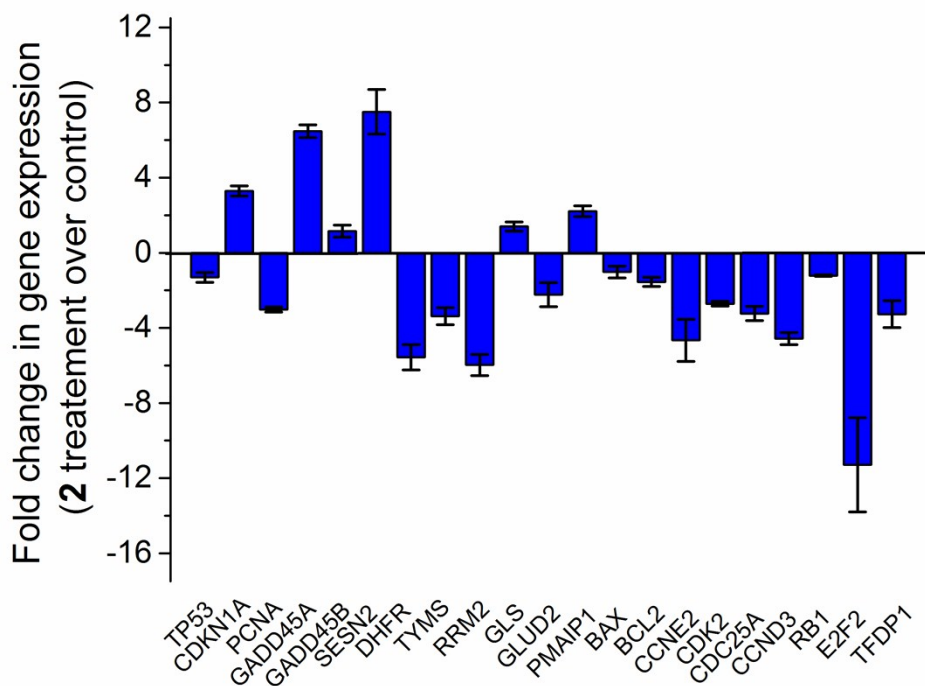


Fig. S31 The fold changes of gene expression caused by Ir(III) treatment determined by RT-PCR. 21 genes were selected to validate the microarray gene expression data.

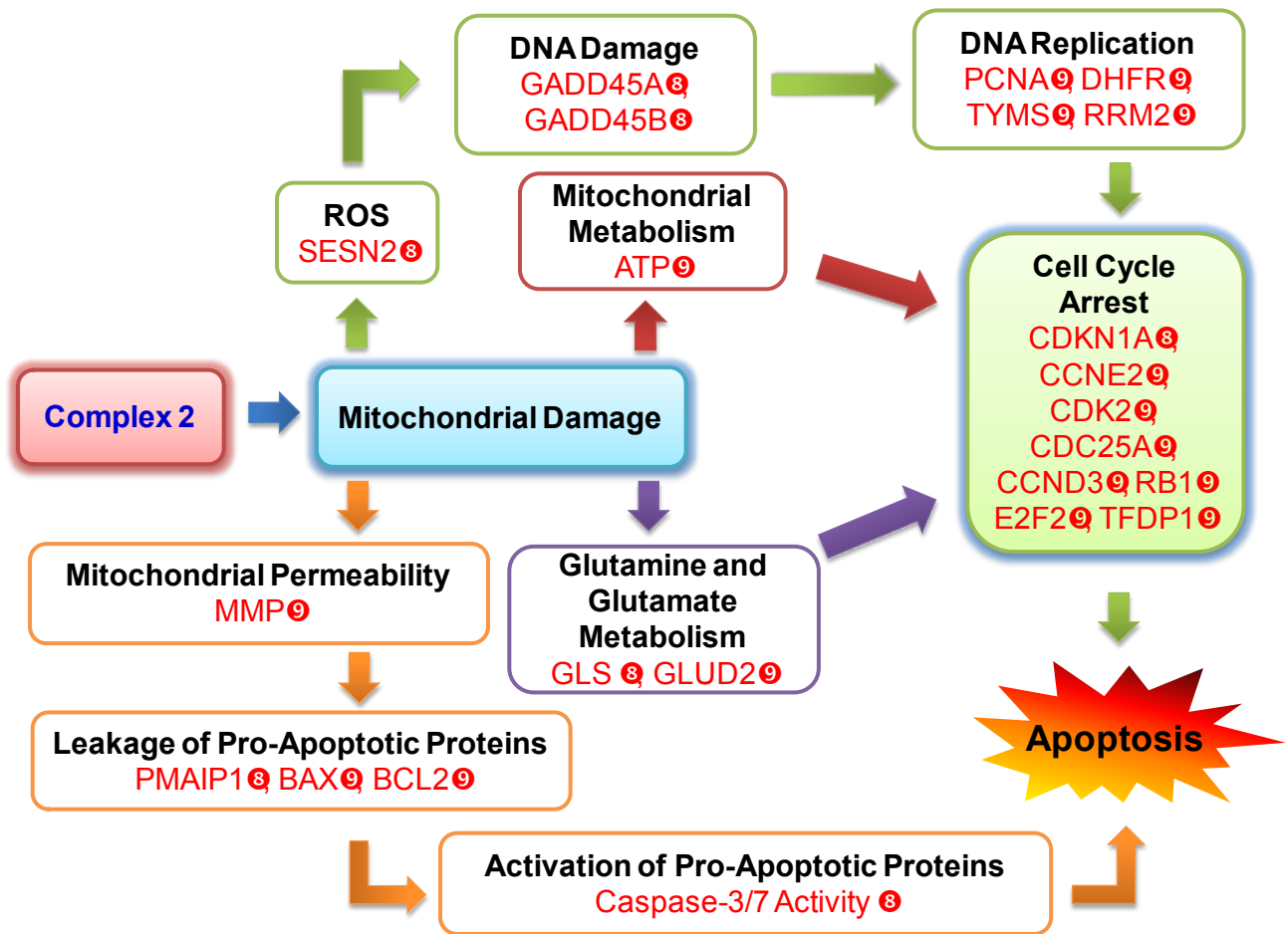


Fig. S32 Proposed mechanisms of action of complex 2.

Table S1 Crystallographic data of **1**, **3** and **4**

Complex	1	3	4
CCDC no.	1452038	1452037	1452036
Empirical formula	2(C ₃₄ H _{27.50} IrN ₄ O ₂)PF ₆	C ₃₄ H ₂₄ F ₄ IrN ₄ O ₂ F ₆ P•C H ₂ Cl ₂	C ₃₄ H ₂₂ Cl ₂ F ₄ IrN ₄ F ₆ P•C 3H ₂ O
Molecular weight	788.78	1018.67	1028.70
Description	Block, red	Block, yellow	Block, yellow
Temperature (K)	250 K	293 K	150 K
λ (Å)	1.54178	0.71073	1.54178
Crystal system	monoclinic	monoclinic	triclinic
Space group	C 2/c	P 21/c	P -1
a (Å)	39.1832(11)	9.3965(1)	10.5808(4)
b (Å)	9.6185(2)	39.4086(6)	13.0767(5)
c (Å)	19.2745(5)	9.8195(2)	14.3976(6)
α (°)	90	90	93.447(3)
β (°)	109.894(2)	104.761(2)	106.228(4)
γ (°)	90	90	97.527(3)
Volume, Å ³	6830.7(3)	3516.18(10)	1886.41(13)
Z	8	4	2
Absorption coefficient (mm ⁻¹)	8.223	4.089	9.338
F(000)	3096.0	1984.0	1004.0
θ _{max} (deg)	73.857	29.464	67.081
Completeness to θ _{max}	0.986	0.898	0.976
Density (calcd) (mg/m ⁻³)	1.534	1.924	1.811
[R _{int}]	0.0204	0.0360	0.0411
Reflections collected/unique	22259/6811	38075/8750	13777/6587
R1 ^a [I > 2σ(I)]	0.0369	0.0264	0.0318
wR2 ^a	0.1039	0.0476	0.0774
GOF ^b	1.020	1.136	1.064

$${}^a R1 = \sum \|F_0| - |F_c| \| / \sum |F_0|, wR2 = \left\{ \frac{\sum [w(F_0^2 - F_c^2)^2]}{\sum [w(F_0^2)^2]} \right\}^{1/2}$$

$${}^b GOF = \left\{ \frac{\sum [w(F_0^2 - F_c^2)^2 / (n - p)]}{\sum [w(F_0^2)^2]} \right\}^{1/2} \text{ where } n \text{ is the number of data and } p \text{ is the number of parameters refined.}$$

Table S2 Selected bond lengths (Å) and bond angles (deg) of **1**, **3** and **4**

Compound	1		3		4	
bond lengths (Å)	Ir1–C1	2.019(5)	Ir1–C12	2.015(3)	Ir1–C12	1.997(4)
	Ir1–C12	2.020(4)	Ir1–C1	2.015(3)	Ir1–C1	2.011(4)
	Ir1–N2	2.044(4)	Ir1–N1	2.043(2)	Ir1–N1	2.045(3)
	Ir1–N1	2.047(4)	Ir1–N2	2.056(2)	Ir1–N2	2.049(3)
	Ir1–N4	2.138(4)	Ir1–N4	2.119(2)	Ir1–N3	2.129(3)
	Ir1–N3	2.143(4)	Ir1–N3	2.127(2)	Ir1–N4	2.142(4)
bond angles (deg)	C1–Ir1–C12	90.23(17)	C12–Ir1–C1	87.40(10)	C12–Ir1–C1	87.80(16)
	C1–Ir1–N2	95.16(17)	C12–Ir1–N1	96.42(10)	C12–Ir1–N1	91.83(15)
	C12–Ir1–N2	80.68(18)	C1–Ir1–N1	80.30(10)	C1–Ir1–N1	80.48(16)
	C1–Ir1–N1	80.15(18)	C12–Ir1–N2	80.53(10)	C12–Ir1–N2	80.56(16)
	C12–Ir1–N1	94.53(18)	C1–Ir1–N2	97.80(10)	C1–Ir1–N2	94.60(16)
	C12–Ir1–N4	95.61(16)	C1–Ir1–N4	99.69(9)	C1–Ir1–N3	97.22(15)
	N2–Ir1–N4	88.16(15)	N1–Ir1–N4	89.74(8)	N1–Ir1–N3	90.71(13)
	N1–Ir1–N4	96.97(16)	N2–Ir1–N4	93.47(9)	N2–Ir1–N3	97.26(14)
	C1–Ir1–N3	97.69(16)	C12–Ir1–N3	96.36(9)	C12–Ir1–N4	98.70(15)
	N2–Ir1–N3	97.85(15)	N1–Ir1–N3	95.66(9)	N1–Ir1–N4	94.76(14)
	N1–Ir1–N3	87.53(15)	N2–Ir1–N3	86.41(9)	N2–Ir1–N4	90.91(14)
	N4–Ir1–N3	76.51(15)	N4–Ir1–N3	76.90(8)	N3–Ir1–N4	76.42(13)

Table S3 Photophysical data of complexes **1–4**

Compounds	Medium	λ_{em}^a/nm	Φ_{em}^b	τ /ns
1	PBS	630	0.017	34.85
	MeCN	615	0.096	74.90
	CH ₂ Cl ₂	603	0.168	201.82
2	PBS	630	0.010	31.84
	MeCN	615	0.033	70.48
	CH ₂ Cl ₂	607	0.041	164.66
3	PBS	560	0.123	289.74
	MeCN	537	0.054	119.45
	CH ₂ Cl ₂	550	0.331	326.94
4	PBS	553	0.082	309.72
	MeCN	555	0.010	162.28
	CH ₂ Cl ₂	573	0.258	242.10

^a Maximum wavelengths of emission spectra (λ_{em}) in nm.

^b The emission quantum yields at room temperature were determined using [Ru(bpy)₃]Cl₂ in aerated H₂O ($\Phi=0.028$) as the reference.¹

^c Decay curves of compounds were recorded by an Edinburgh FLS 920 Spectrometer. All curves were fitted into a two exponential formula $F(t) = A + B_1 \exp(-t/\tau_1) + B_2 \exp(-t/\tau_2) + B_3 \exp(-t/\tau_3)$; $\tau_{avr} = \frac{B_1\tau_1^2 + B_2\tau_2^2 + B_3\tau_3^2}{B_1\tau_1 + B_2\tau_2 + B_3\tau_3}$.

Table S4 Lipophilicity and cellular uptake efficiency of complexes **1–4**

Compound	Lipophilicity ($\log P_{o/w}$) ^a	Amount of iridium(ng per 10 ⁶ cells) ^b
1	0.23	186.24
2	1.28	670.92
3	1.09	212.07
4	2.12	721.45

^a $\log P_{o/w}$ is defined as the logarithmic ratio of Ir(III) concentration in n-octanol to that in the aqueous phase. ^b Amount of iridium in A549 cells was determined by ICP-MS after the cells were incubated with Ir(III) complexes (10 μ M) at 37 °C for 2 h.

Table S5 Treatment information and the number of differentially expressed genes

Compound	Concentration	No. of genes sets (p< 0.05, FC> 2)	No. of up-regulated genes sets (p< 0.05, FC> 2)	No. of down-regulated genes sets (p< 0.05, FC> 2)	No. of probe sets (p< 0.05, FC> 2)
2	3 μ M	1222	507	715	1637

Table S6 List of differentially regulated genes induced by **2** (p < 0.05, Fold Change > 2)

Up-regulated			
Probe Set ID	Gene Symbol	Gene Description	Fold change
213418_at	HSPA6	heat shock 70kDa protein 6 (HSP70B')	79.33965
231947_at	MYCT1	myc target 1	24.04952
217967_s_at	FAM129A	family with sequence similarity 129, member A	23.75726
117_at	HSPA6	heat shock 70kDa protein 6 (HSP70B')	23.26145
213146_at	KDM6B	lysine (K)-specific demethylase 6B	22.9909
224367_at	BEX2	brain expressed X-linked 2	19.51081
206463_s_at	DHRS2	dehydrogenase/reductase (SDR family) member 2	19.45506
233126_s_at	OLAH	oleoyl-ACP hydrolase	17.96261
222945_x_at	OLAH	oleoyl-ACP hydrolase	16.91436
217966_s_at	FAM129A	family with sequence similarity 129, member A	15.99
202672_s_at	ATF3	activating transcription factor 3	13.61979
226725_at	SLFN5	schlafen family member 5	13.22619
219975_x_at	OLAH	oleoyl-ACP hydrolase	12.82565
227099_s_at	C11orf96	chromosome 11 open reading frame 96	12.20198
217074_at	SMOX	spermine oxidase	12.0555
213036_x_at	ATP2A3	ATPase, Ca ²⁺ transporting, ubiquitous	11.31679
238430_x_at	SLFN5	schlafen family member 5	10.36974
1553055_a_at	SLFN5	schlafen family member 5	10.26052
235700_at	CT45A1///CT45A2// /CT45A3///CT45A4/ //CT45A5///CT45A6 ///LOC101060208/// LOC101060210///L OC101060211	cancer/testis antigen family 45, member A1///cancer/testis antigen family 45, member A2///cancer/testis antigen family 45, member A3///cancer/testis antigen family 45, member A4///cancer/testis antigen family 45, member A5///cancer/testis antigen family 45, member A6///cancer/testis antigen family 45 member A3-like///cancer/testis antigen family 45 member A2-like///cancer/testis antigen family 45 member A3-like	10.06079
208868_s_at	GABARAPL1	GABA(A) receptor-associated protein like 1	9.774415

243999_at	SLFN5	schlafen family member 5	9.384396
214636_at	CALCB	calcitonin-related polypeptide beta	9.276074
228846_at	MXD1	MAX dimerization protein 1	9.104825
209383_at	DDIT3	DNA-damage-inducible transcript 3	8.805129
1555788_a_at	TRIB3	tribbles homolog 3 (Drosophila)	7.568183
211506_s_at	IL8	interleukin 8	7.481956
209774_x_at	CXCL2	chemokine (C-X-C motif) ligand 2	7.463029
230383_x_at	SLFN5	schlafen family member 5	7.269395
1555680_a_at	SMOX	spermine oxidase	7.075629
223196_s_at	SESN2	sestrin 2	6.85595
211458_s_at	GABARAPL1///GA BARAPL3	GABA(A) receptor-associated protein like 1///GABA(A) receptors associated protein like 3, pseudogene	6.722471
221778_at	JHDM1D	jumonji C domain containing histone demethylase 1 homolog D (S. cerevisiae)	6.351091
202859_x_at	IL8	interleukin 8	6.326859
230164_at	ZNF621	zinc finger protein 621	6.325591
214079_at	DHRS2	dehydrogenase/reductase (SDR family) member 2	6.31493
214657_s_at	MIR612///NEAT1	microRNA 612///nuclear paraspeckle assembly transcript 1 (non-protein coding)	6.257961
202014_at	PPP1R15A	protein phosphatase 1, regulatory subunit 15A	6.144132
203438_at	STC2	stanniocalcin 2	6.075503
1554980_a_at	ATF3	activating transcription factor 3	5.992451
1567912_s_at	CT45A1///CT45A2// /CT45A3///CT45A4/ //CT45A5///CT45A6 ///LOC101060208/// LOC101060210///L OC101060211	cancer/testis antigen family 45, member A1///cancer/testis antigen family 45, member A2///cancer/testis antigen family 45, member A3///cancer/testis antigen family 45, member A4///cancer/testis antigen family 45, member A5///cancer/testis antigen family 45, member A6///cancer/testis antigen family 45 member A3- like///cancer/testis antigen family 45 member A2- like///cancer/testis antigen family 45 member A3-like	5.976547
207850_at	CXCL3	chemokine (C-X-C motif) ligand 3	5.901013
218145_at	TRIB3	tribbles homolog 3 (Drosophila)	5.898873
225698_at	EPB41L4A-AS1	EPB41L4A antisense RNA 1	5.77958
225381_at	MIR100HG	mir-100-let-7a-2 cluster host gene (non-protein coding)	5.768217
220755_s_at	C6orf48	chromosome 6 open reading frame 48	5.75416
206376_at	SLC6A15	solute carrier family 6 (neutral amino acid transporter), member 15	5.645343
206157_at	PTX3	pentraxin 3, long	5.515035

208893_s_at	DUSP6	dual specificity phosphatase 6	5.491337
204595_s_at	STC1	stanniocalcin 1	5.475359
208869_s_at	GABARAPL1	GABA(A) receptor-associated protein like 1	5.385289
36711_at	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	5.314828
209283_at	CRYAB	crystallin, alpha B	5.245867
229778_at	C12orf39	chromosome 12 open reading frame 39	5.202994
38037_at	HBEGF	heparin-binding EGF-like growth factor	5.099252
203725_at	GADD45A	growth arrest and DNA-damage-inducible, alpha	5.090419
226275_at	MXD1	MAX dimerization protein 1	5.079095
205830_at	CLGN	calmegin	5.043981
232035_at	HIST1H4A///HIST1 H4B///HIST1H4C/// HIST1H4D///HIST1 H4E///HIST1H4F/// HIST1H4H///HIST1 H4I///HIST1H4J///H IST1H4K///HIST1H 4L///HIST2H4A///H IST2H4B///HIST4H 4	histone cluster 1, H4a///histone cluster 1, H4b///histone cluster 1, H4c///histone cluster 1, H4d///histone cluster 1, H4e///histone cluster 1, H4f///histone cluster 1, H4h///histone cluster 1, H4i///histone cluster 1, H4j///histone cluster 1, H4k///histone cluster 1, H4l///histone cluster 2, H4a///histone cluster 2, H4b///histone cluster 4, H4	4.888301
224566_at	MIR612///NEAT1	microRNA 612///nuclear paraspeckle assembly transcript 1 (non-protein coding)	4.861927
1557078_at	SLFN5	schlafen family member 5	4.849515
202843_at	DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9	4.827705
229372_at	GOLT1A	golgi transport 1A	4.758275
37028_at	PPP1R15A	protein phosphatase 1, regulatory subunit 15A	4.746886
225142_at	JHDM1D	jumonji C domain containing histone demethylase 1 homolog D (S. cerevisiae)	4.689666
221009_s_at	ANGPTL4	angiopoietin-like 4	4.585215
219270_at	CHAC1	ChaC, cation transport regulator homolog 1 (E. coli)	4.583573
222900_at	NRIP3	nuclear receptor interacting protein 3	4.580634
227755_at	OTTHUMG000001 78878///RP11- 214C8.5	NULL///NULL	4.543435
221577_x_at	GDF15	growth differentiation factor 15	4.527372
221067_s_at	C12orf39	chromosome 12 open reading frame 39	4.527073
202934_at	HK2	hexokinase 2	4.466961

224841_x_at	GAS5///SNORD44// /SNORD47///SNOR D76///SNORD77///S NORD79///SNORD 80///SNORD81	growth arrest-specific 5 (non-protein coding)///small nucleolar RNA, C/D box 44///small nucleolar RNA, C/D box 47///small nucleolar RNA, C/D box 76///small nucleolar RNA, C/D box 77///small nucleolar RNA, C/D box 79///small nucleolar RNA, C/D box 80///small nucleolar RNA, C/D box 81	4.42811
230493_at	SHISA2	shisa homolog 2 (<i>Xenopus laevis</i>)	4.401241
235191_at	LINC00662	long intergenic non-protein coding RNA 662	4.390994
223195_s_at	SESN2	sestrin 2	4.352908
208892_s_at	DUSP6	dual specificity phosphatase 6	4.339348
219257_s_at	SPHK1	sphingosine kinase 1	4.337762
225957_at	CREBRF	CREB3 regulatory factor	4.336549
215440_s_at	BEX4	brain expressed, X-linked 4	4.335742
203439_s_at	STC2	stanniocalcin 2	4.279082
224741_x_at	GAS5///SNORD44// /SNORD47///SNOR D76///SNORD77///S NORD79///SNORD 80///SNORD81	growth arrest-specific 5 (non-protein coding)///small nucleolar RNA, C/D box 44///small nucleolar RNA, C/D box 47///small nucleolar RNA, C/D box 76///small nucleolar RNA, C/D box 77///small nucleolar RNA, C/D box 79///small nucleolar RNA, C/D box 80///small nucleolar RNA, C/D box 81	4.277033
205193_at	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	4.229065
204596_s_at	STC1	stanniocalcin 1	4.195954
227443_at	LURAP1L	leucine rich adaptor protein 1-like	4.16576
226122_at	PLEKHG1	pleckstrin homology domain containing, family G (with RhoGef domain) member 1	4.14783
202267_at	LAMC2	laminin, gamma 2	4.144789
203234_at	UPP1	uridine phosphorylase 1	4.114868
209457_at	DUSP5	dual specificity phosphatase 5	4.078765
207713_s_at	RBCK1	RanBP-type and C3HC4-type zinc finger containing 1	3.98943
221050_s_at	GTPBP2	GTP binding protein 2	3.985195
239754_at	C17orf76- AS1///SNORD49A// /SNORD49B///SNO RD65	C17orf76 antisense RNA 1///small nucleolar RNA, C/D box 49A///small nucleolar RNA, C/D box 49B///small nucleolar RNA, C/D box 65	3.941277
210357_s_at	SMOX	spermine oxidase	3.935492
235547_at	N4BP2L2	NEDD4 binding protein 2-like 2	3.880942
238825_at	ACRC	acidic repeat containing	3.863544

225220_at	SNHG8///SNORA2 4	small nucleolar RNA host gene 8 (non-protein coding)///small nucleolar RNA, H/ACA box 24	3.838174
204597_x_at	STC1	stanniocalcin 1	3.824257
223484_at	C15orf48	chromosome 15 open reading frame 48	3.816546
242649_x_at	HMG2P46	high mobility group nucleosomal binding domain 2 pseudogene 46	3.763
205100_at	GFPT2	glutamine-fructose-6-phosphate transaminase 2	3.668235
205032_at	ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	3.63873
204411_at	KIF21B	kinesin family member 21B	3.62528
208891_at	DUSP6	dual specificity phosphatase 6	3.605994
207629_s_at	ARHGEF2	Rho/Rac guanine nucleotide exchange factor (GEF) 2	3.600811
224833_at	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	3.595734
237465_at	USP53	ubiquitin specific peptidase 53	3.589891
226650_at	ZFAND2A	zinc finger, AN1-type domain 2A	3.589364
218651_s_at	LARP6	La ribonucleoprotein domain family, member 6	3.572972
207001_x_at	TSC22D3	TSC22 domain family, member 3	3.562951
223940_x_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	3.55823
231202_at	ALDH1L2	aldehyde dehydrogenase 1 family, member L2	3.553949
208763_s_at	TSC22D3	TSC22 domain family, member 3	3.553452
209789_at	CORO2B	coronin, actin binding protein, 2B	3.541628
213272_s_at	TMEM159	transmembrane protein 159	3.522156
204971_at	CSTA	cystatin A (stefin A)	3.509306
230492_s_at	GPCPD1	glycerophosphocholine phosphodiesterase GDE1 homolog (S. cerevisiae)	3.502927
226670_s_at	PABPC1L	poly(A) binding protein, cytoplasmic 1-like	3.482333
218000_s_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	3.452105
238017_at	SDR16C5	short chain dehydrogenase/reductase family 16C, member 5	3.443973
238476_at	CREBRF	CREB3 regulatory factor	3.439102
225033_at	ST3GAL1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	3.437733
201348_at	GPX3	glutathione peroxidase 3 (plasma)	3.400718
222495_at	TMEM167B	transmembrane protein 167B	3.389314
1555355_a_at	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	3.374493
211924_s_at	PLAUR	plasminogen activator, urokinase receptor	3.359371

218451_at	CDCP1	CUB domain containing protein 1	3.347161
213139_at	SNAI2	snail family zinc finger 2	3.332621
1568857_a_at	NBR1	neighbor of BRCA1 gene 1	3.32775
1553142_at	LACC1	laccase (multicopper oxidoreductase) domain containing 1	3.325645
242856_at	AL132709.8///OTT HUMG0000006743 5	NULL///NULL	3.320271
212225_at	EIF1	eukaryotic translation initiation factor 1	3.304097
214696_at	MIR22///MIR22HG	microRNA 22///MIR22 host gene (non-protein coding)	3.300128
218273_s_at	PDP1	pyruvate dehydrogenase phosphatase catalytic subunit 1	3.299827
235146_at	TMCC3	transmembrane and coiled-coil domain family 3	3.285936
1558965_at	PHF21A	PHD finger protein 21A	3.272652
201044_x_at	DUSP1	dual specificity phosphatase 1	3.267757
1569583_at	EREG	epiregulin	3.264414
228082_at	CLMP	CXADR-like membrane protein	3.263171
234932_s_at	CDCP1	CUB domain containing protein 1	3.251179
220266_s_at	KLF4	Kruppel-like factor 4 (gut)	3.250814
223544_at	TMEM79	transmembrane protein 79	3.237858
1553574_at	IFNE	interferon, epsilon	3.234213
203999_at	SYT1	synaptotagmin I	3.229923
213338_at	TMEM158	transmembrane protein 158 (gene/pseudogene)	3.224061
227314_at	ITGA2	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	3.221707
205931_s_at	CREB5///LOC4013 17	cAMP responsive element binding protein 5///uncharacterized LOC401317	3.21155
231779_at	IRAK2	interleukin-1 receptor-associated kinase 2	3.201538
217312_s_at	COL7A1	collagen, type VII, alpha 1	3.191625
219895_at	TMEM255A	transmembrane protein 255A	3.17518
219736_at	TRIM36	tripartite motif containing 36	3.169638
207783_x_at	HUWE1	HECT, UBA and WWE domain containing 1, E3 ubiquitin protein ligase	3.168091
241412_at	BTC	betacellulin	3.164789
209990_s_at	GABBR2	gamma-aminobutyric acid (GABA) B receptor, 2	3.153774
233675_s_at	TPTE2P6	transmembrane phosphoinositide 3-phosphatase and tensin homolog 2 pseudogene 6	3.150281
215072_x_at	C10orf137	chromosome 10 open reading frame 137	3.145296
211343_s_at	COL13A1	collagen, type XIII, alpha 1	3.13756
229228_at	CREB5///LOC4013	cAMP responsive element binding protein	3.135028

	17	5///uncharacterized LOC401317	
221841_s_at	KLF4	Kruppel-like factor 4 (gut)	3.118243
226150_at	PPAPDC1B	phosphatidic acid phosphatase type 2 domain containing 1B	3.102143
225524_at	ANTXR2	anthrax toxin receptor 2	3.100708
221827_at	RBCK1	RanBP-type and C3HC4-type zinc finger containing 1	3.075107
228115_at	GAREM	GRB2 associated, regulator of MAPK1	3.071551
214179_s_at	NFE2L1	nuclear factor (erythroid-derived 2)-like 1	3.071297
214753_at	N4BP2L2	NEDD4 binding protein 2-like 2	3.06119
224565_at	MIR612///NEAT1	microRNA 612///nuclear paraspeckle assembly transcript 1 (non-protein coding)	3.047197
202842_s_at	DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9	3.047162
203921_at	CHST2	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2	3.032895
230748_at	SLC16A6	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	3.031163
231894_at	SARS	seryl-tRNA synthetase	3.016467
201466_s_at	JUN	jun proto-oncogene	3.016202
217999_s_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	3.005238
222783_s_at	SMOC1	SPARC related modular calcium binding 1	2.989173
214374_s_at	PPFIBP1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	2.981912
221667_s_at	HSPB8	heat shock 22kDa protein 8	2.981724
220606_s_at	ADPRM	ADP-ribose/CDP-alcohol diphosphatase, manganese-dependent	2.976644
203231_s_at	ATXN1	ataxin 1	2.968378
232184_at	ALS2	amyotrophic lateral sclerosis 2 (juvenile)	2.967341
208960_s_at	KLF6	Kruppel-like factor 6	2.958325
228582_x_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	2.946758
204420_at	FOSL1	FOS-like antigen 1	2.93894
219334_s_at	NABP1	nucleic acid binding protein 1	2.937166
203574_at	NFIL3	nuclear factor, interleukin 3 regulated	2.926328
218468_s_at	GREM1	gremlin 1, DAN family BMP antagonist	2.922122
224568_x_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	2.915679
244070_at	SYNE1	spectrin repeat containing, nuclear envelope 1	2.914922
205227_at	IL1RAP	interleukin 1 receptor accessory protein	2.912328
1558094_s_at	CCDC174	coiled-coil domain containing 174	2.911507
207992_s_at	AMPD3	adenosine monophosphate deaminase 3	2.907378

224826_at	GPCPD1	glycerophosphocholine phosphodiesterase GDE1 homolog (S. cerevisiae)	2.888262
208180_s_at	HIST1H4A///HIST1H4B///HIST1H4C///HIST1H4D///HIST1H4E///HIST1H4F///HIST1H4H///HIST1H4I///HIST1H4J///HIST1H4K///HIST1H4L///HIST2H4A///HIST2H4B///HIST4H4	histone cluster 1, H4a///histone cluster 1, H4b///histone cluster 1, H4c///histone cluster 1, H4d///histone cluster 1, H4e///histone cluster 1, H4f///histone cluster 1, H4h///histone cluster 1, H4i///histone cluster 1, H4j///histone cluster 1, H4k///histone cluster 1, H4l///histone cluster 2, H4a///histone cluster 2, H4b///histone cluster 4, H4	2.879631
201465_s_at	JUN	jun proto-oncogene	2.875144
228037_at	CTD-2267D19.2///OTTHUMG00000179631	NULL///NULL	2.872319
244864_at	OTTHUMG00000017934///RP11-462L8.1	NULL///NULL	2.869684
213112_s_at	SQSTM1	sequestosome 1	2.867512
213976_at	CIZ1	CDKN1A interacting zinc finger protein 1	2.856582
214748_at	N4BP2L2	NEDD4 binding protein 2-like 2	2.853495
231146_at	FAM24B	family with sequence similarity 24, member B	2.844851
231735_s_at	LOC100996467///MALAT1	metastasis-associated lung adenocarcinoma transcript 1-like///metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	2.84092
217998_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	2.823331
223568_s_at	PPAPDC1B	phosphatidic acid phosphatase type 2 domain containing 1B	2.822282
217997_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	2.818357
206243_at	TIMP4	TIMP metalloproteinase inhibitor 4	2.816575
202284_s_at	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	2.81075
209216_at	WDR45	WD repeat domain 45	2.808212
1552546_a_at	LETM2	leucine zipper-EF-hand containing transmembrane protein 2	2.80219
1554168_a_at	SH3KBP1	SH3-domain kinase binding protein 1	2.796641
219496_at	SOWAHC	soyondowah ankyrin repeat domain family member C	2.790832
221920_s_at	SLC25A37	solute carrier family 25 (mitochondrial iron transporter),	2.790642

		member 37	
220585_at	HKDC1	hexokinase domain containing 1	2.786262
226835_s_at	ZFAS1	ZNFX1 antisense RNA 1	2.785478
224915_x_at	ZFAS1	ZNFX1 antisense RNA 1	2.78266
242329_at	CREB5///LOC401317	cAMP responsive element binding protein 5///uncharacterized LOC401317	2.779548
202558_s_at	HSPA13	heat shock protein 70kDa family, member 13	2.778157
228461_at	SH3RF3	SH3 domain containing ring finger 3	2.773869
207536_s_at	TNFRSF9	tumor necrosis factor receptor superfamily, member 9	2.773826
213076_at	ITPKC	inositol-trisphosphate 3-kinase C	2.76973
227458_at	CD274	CD274 molecule	2.768814
221248_s_at	WHSC1L1	Wolf-Hirschhorn syndrome candidate 1-like 1	2.768253
238759_at	CCDC88A	coiled-coil domain containing 88A	2.767407
211692_s_at	BBC3///MIR3190///MIR3191	BCL2 binding component 3///microRNA 3190///microRNA 3191	2.767019
212724_at	RND3	Rho family GTPase 3	2.763135
203998_s_at	SYT1	synaptotagmin I	2.759893
1555832_s_at	KLF6	Kruppel-like factor 6	2.750429
218486_at	KLF11	Kruppel-like factor 11	2.747225
215672_s_at	AHCYL2	adenosylhomocysteinase-like 2	2.746318
208381_s_at	SGPL1	sphingosine-1-phosphate lyase 1	2.741153
206924_at	IL11	interleukin 11	2.739102
207522_s_at	ATP2A3	ATPase, Ca ⁺⁺ transporting, ubiquitous	2.738609
202131_s_at	RIOK3	RIO kinase 3	2.732721
208961_s_at	KLF6	Kruppel-like factor 6	2.731212
226612_at	UBE2QL1	ubiquitin-conjugating enzyme E2Q family-like 1	2.729758
1554741_s_at	FGF7///KGFLP1///KGFLP2	fibroblast growth factor 7///fibroblast growth factor 7 pseudogene///keratinocyte growth factor-like protein 2	2.725005
225540_at	MAP2	microtubule-associated protein 2	2.71542
226675_s_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	2.713382
222572_at	PDP1	pyruvate dehydrogenase phosphatase catalytic subunit 1	2.713084
202147_s_at	IFRD1	interferon-related developmental regulator 1	2.711826
222528_s_at	SLC25A37	solute carrier family 25 (mitochondrial iron transporter), member 37	2.711479
239077_at	CSGALNACT2	chondroitin sulfate N-acetylgalactosaminyltransferase 2	2.709923
225768_at	NR1D2	nuclear receptor subfamily 1, group D, member 2	2.708167
242335_at	SLC25A37	solute carrier family 25 (mitochondrial iron transporter), member 37	2.705237

		member 37	
227530_at	AKAP12	A kinase (PRKA) anchor protein 12	2.705003
1553292_s_at	SGK494	uncharacterized serine/threonine-protein kinase SgK494	2.702525
200632_s_at	NDRG1	N-myc downstream regulated 1	2.701219
202627_s_at	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	2.696476
202920_at	ANK2	ankyrin 2, neuronal	2.696267
227697_at	SOCS3	suppressor of cytokine signaling 3	2.690311
211862_x_at	CFLAR	CASP8 and FADD-like apoptosis regulator	2.688252
224606_at	KLF6	Kruppel-like factor 6	2.686778
242843_at	BCAN	brevican	2.682612
1558678_s_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	2.678856
1554447_at	JPX	JPX transcript, XIST activator (non-protein coding)	2.668041
223774_at	SNHG12///SNORA16A///SNORA44///SNORA61	small nucleolar RNA host gene 12 (non-protein coding)///small nucleolar RNA, H/ACA box 16A///small nucleolar RNA, H/ACA box 44///small nucleolar RNA, H/ACA box 61	2.661464
209878_s_at	RELA	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	2.661096
226886_at	GFPT1	glutamine--fructose-6-phosphate transaminase 1	2.657229
1556097_at	HOMER2	homer homolog 2 (Drosophila)	2.657201
207781_s_at	ZNF711	zinc finger protein 711	2.65673
210845_s_at	PLAUR	plasminogen activator, urokinase receptor	2.653048
204472_at	GEM	GTP binding protein overexpressed in skeletal muscle	2.648446
218136_s_at	SLC25A37	solute carrier family 25 (mitochondrial iron transporter), member 37	2.64827
204977_at	DDX10	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	2.64711
226179_at	SLC25A37	solute carrier family 25 (mitochondrial iron transporter), member 37	2.642503
221156_x_at	CCPG1	cell cycle progression 1	2.640836
228497_at	SLC22A15	solute carrier family 22, member 15	2.635145
226227_x_at	ZFAS1	ZNFX1 antisense RNA 1	2.633314
228519_x_at	CIRBP	cold inducible RNA binding protein	2.632777
209435_s_at	ARHGEF2	Rho/Rac guanine nucleotide exchange factor (GEF) 2	2.631956
203821_at	HBEGF	heparin-binding EGF-like growth factor	2.627046
208966_x_at	IFI16	interferon, gamma-inducible protein 16	2.624607
206618_at	IL18R1	interleukin 18 receptor 1	2.622

218456_at	CAPRN2	caprin family member 2	2.619609
232355_at	SNORD114-3	small nucleolar RNA, C/D box 114-3	2.618499
210794_s_at	MEG3	maternally expressed 3 (non-protein coding)	2.613246
225146_at	FAM219A	family with sequence similarity 219, member A	2.609178
231067_s_at	AKAP12	A kinase (PRKA) anchor protein 12	2.604141
209750_at	NR1D2	nuclear receptor subfamily 1, group D, member 2	2.603701
208322_s_at	ST3GAL1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	2.601995
203330_s_at	STX5	syntaxin 5	2.588852
214452_at	BCAT1	branched chain amino-acid transaminase 1, cytosolic	2.587552
1570425_s_at	LATS1	large tumor suppressor kinase 1	2.582856
200670_at	XBP1	X-box binding protein 1	2.577027
226099_at	ELL2	elongation factor, RNA polymerase II, 2	2.568316
217988_at	CCNB1IP1	cyclin B1 interacting protein 1, E3 ubiquitin protein ligase	2.563631
226206_at	MAFK	v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian)	2.563341
202847_at	PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	2.56176
225956_at	CREBRF	CREB3 regulatory factor	2.560003
224763_at	LOC100506548//R PL37	uncharacterized LOC100506548//ribosomal protein L37	2.557715
1559393_at	ALDH1L2	aldehyde dehydrogenase 1 family, member L2	2.556477
206777_s_at	CRYBB2//CRYBB 2P1	crystallin, beta B2//crystallin, beta B2 pseudogene 1	2.555645
1559315_s_at	SOCS2-AS1	SOCS2 antisense RNA 1	2.555293
1558305_at	GIGYF2	GRB10 interacting GYF protein 2	2.546257
228937_at	LACC1	laccase (multicopper oxidoreductase) domain containing 1	2.545712
1559640_at	ANKFN1	ankyrin-repeat and fibronectin type III domain containing 1	2.543106
203594_at	RTCA	RNA 3'-terminal phosphate cyclase	2.538703
224559_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	2.536869
209925_at	OCLN	occludin	2.535927
206332_s_at	IFI16	interferon, gamma-inducible protein 16	2.534263
213419_at	APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2	2.528748
213462_at	NPAS2	neuronal PAS domain protein 2	2.528271
242162_at	DAW1	dynein assembly factor with WDR repeat domains 1	2.52772
1554767_s_at	CRYZL1	crystallin, zeta (quinone reductase)-like 1	2.523594
225699_at	SNHG15//SNORA 9	small nucleolar RNA host gene 15 (non-protein coding)//small nucleolar RNA, H/ACA box 9	2.523236

242239_at	ARL5B-AS1	ARL5B antisense RNA 1	2.51786
1555875_at	SRGAP1	SLIT-ROBO Rho GTPase activating protein 1	2.514128
213656_s_at	KLC1	kinesin light chain 1	2.513991
227091_at	CCDC146	coiled-coil domain containing 146	2.510509
203505_at	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	2.506639
227905_s_at	AZI2	5-azacytidine induced 2	2.505061
227301_at	CCT6P1///CCT6P3	chaperonin containing TCP1, subunit 6 (zeta) pseudogene 1///chaperonin containing TCP1, subunit 6 (zeta) pseudogene 3	2.502565
241844_x_at	TMEM156	transmembrane protein 156	2.493211
205047_s_at	ASNS	asparagine synthetase (glutamine-hydrolyzing)	2.490488
228184_at	DISP1	dispatched homolog 1 (Drosophila)	2.489486
204286_s_at	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	2.489024
223333_s_at	ANGPTL4	angiopoietin-like 4	2.487071
227865_at	IDNK	idnK, gluconokinase homolog (E. coli)	2.483796
212985_at	APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2	2.476238
227529_s_at	AKAP12	A kinase (PRKA) anchor protein 12	2.472081
219557_s_at	NRIP3	nuclear receptor interacting protein 3	2.471858
202643_s_at	TNFAIP3	tumor necrosis factor, alpha-induced protein 3	2.470986
223082_at	SH3KBP1	SH3-domain kinase binding protein 1	2.470821
217996_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	2.466336
1552658_a_at	NAV3	neuron navigator 3	2.465748
209295_at	TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	2.458366
212099_at	RHOB	ras homolog family member B	2.456874
214091_s_at	GPX3	glutathione peroxidase 3 (plasma)	2.453612
40148_at	APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2	2.452102
226181_at	TUBE1	tubulin, epsilon 1	2.449279
1554465_s_at	KRBOX4///ZNF674	KRAB box domain containing 4///zinc finger protein 674	2.448469
1554462_a_at	DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9	2.447333
227034_at	SOWAHC	sosondowah ankyrin repeat domain family member C	2.447017
242663_at	LINC00662	long intergenic non-protein coding RNA 662	2.446314
219578_s_at	CPEB1	cytoplasmic polyadenylation element binding protein 1	2.444868
231791_at	ASAH2B	N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2B	2.442464
221551_x_at	ST6GALNAC4	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4	2.440624

227027_at	GFPT1	glutamine--fructose-6-phosphate transaminase 1	2.440355
1553672_at	ENAH	enabled homolog (Drosophila)	2.43872
215318_at	MINOS1P1	mitochondrial inner membrane organizing system 1 pseudogene 1	2.437612
200758_s_at	NFE2L1	nuclear factor (erythroid-derived 2)-like 1	2.434443
205386_s_at	MDM2	MDM2 oncogene, E3 ubiquitin protein ligase	2.433793
223805_at	OSBPL6	oxysterol binding protein-like 6	2.433437
205302_at	IGFBP1	insulin-like growth factor binding protein 1	2.429466
227649_s_at	SRGAP2///SRGAP2 D	SLIT-ROBO Rho GTPase activating protein 2///SLIT- ROBO Rho GTPase activating protein 2D	2.428722
206101_at	ECM2	extracellular matrix protein 2, female organ and adipocyte specific	2.427659
223773_s_at	SNHG12///SNORA 16A///SNORA44///S NORA61	small nucleolar RNA host gene 12 (non-protein coding)///small nucleolar RNA, H/ACA box 16A///small nucleolar RNA, H/ACA box 44///small nucleolar RNA, H/ACA box 61	2.426703
1569106_s_at	SETD5	SET domain containing 5	2.422549
228438_at	LOC100132891	uncharacterized LOC100132891	2.417212
228482_at	CDRT4///TVP23C- CDRT4	CMT1A duplicated region transcript 4///TVP23C-CDRT4 readthrough	2.415728
209034_at	PNRC1	proline-rich nuclear receptor coactivator 1	2.415453
201294_s_at	WSB1	WD repeat and SOCS box containing 1	2.410441
226425_at	CLIP4	CAP-GLY domain containing linker protein family, member 4	2.406532
204136_at	COL7A1	collagen, type VII, alpha 1	2.405578
220169_at	TMEM156	transmembrane protein 156	2.401513
230244_at	C2orf82	chromosome 2 open reading frame 82	2.400543
218851_s_at	SFT2D3///WDR33	SFT2 domain containing 3///WD repeat domain 33	2.396937
222502_s_at	UFM1	ubiquitin-fold modifier 1	2.395208
203827_at	WIPI1	WD repeat domain, phosphoinositide interacting 1	2.394806
222872_x_at	NABP1	nucleic acid binding protein 1	2.391438
209333_at	ULK1	unc-51-like kinase 1 (C. elegans)	2.39078
222903_s_at	CPEB1	cytoplasmic polyadenylation element binding protein 1	2.389823
222408_s_at	YPEL5	yippee-like 5 (Drosophila)	2.389249
232281_at	LINC00662	long intergenic non-protein coding RNA 662	2.387817
203504_s_at	ABCA1	ATP-binding cassette, sub-family A (ABC1), member 1	2.386329
1568609_s_at	FLJ39739///LINC00 623///LINC00869///	uncharacterized FLJ39739///long intergenic non-protein coding RNA 623///long intergenic non-protein coding RNA	2.384505

	LINC00875///LOC728875	869///long intergenic non-protein coding RNA 875///uncharacterized LOC728875	
222728_s_at	MIR1304///SNORA18///SNORA32///SNORA40///SNORA8///SNORD5///TAF1D	microRNA 1304///small nucleolar RNA, H/ACA box 1///small nucleolar RNA, H/ACA box 18///small nucleolar RNA, H/ACA box 32///small nucleolar RNA, H/ACA box 40///small nucleolar RNA, H/ACA box 8///small nucleolar RNA, C/D box 5///TATA box binding protein (TBP)-associated factor, RNA polymerase I, D, 41kDa	2.38441
204285_s_at	PMAIP1	phorbol-12-myristate-13-acetate-induced protein 1	2.382668
1554256_a_at	PCNXL2	pecanex-like 2 (Drosophila)	2.381159
217142_at	OTTHUMG00000014809///RP1-14209.1	NULL///NULL	2.378327
1553992_s_at	NBR2	neighbor of BRCA1 gene 2 (non-protein coding)	2.375671
229422_at	NRD1	nardilysin (N-arginine dibasic convertase)	2.37531
214787_at	DENND4A	DENN/MADD domain containing 4A	2.373455
229050_s_at	SNHG7///SNORA17///SNORA43	small nucleolar RNA host gene 7 (non-protein coding)///small nucleolar RNA, H/ACA box 17///small nucleolar RNA, H/ACA box 43	2.372049
215071_s_at	HIST1H2AC	histone cluster 1, H2ac	2.371237
1557302_at	ZNF585B	zinc finger protein 585B	2.369799
204693_at	CDC42EP1	CDC42 effector protein (Rho GTPase binding) 1	2.366787
212307_s_at	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase	2.363809
226384_at	PPAPDC1B	phosphatidic acid phosphatase type 2 domain containing 1B	2.363273
225701_at	AKNA	AT-hook transcription factor	2.36327
223577_x_at	LOC100996467	metastasis-associated lung adenocarcinoma transcript 1-like	2.361653
222498_at	AZI2	5-azacytidine induced 2	2.358719
213988_s_at	SAT1	spermidine/spermine N1-acetyltransferase 1	2.354539
211795_s_at	FYB	FYN binding protein	2.352921
235414_at	ZNF383	zinc finger protein 383	2.35161
221988_at	SMIM7	small integral membrane protein 7	2.351187
218912_at	GCC1	GRIP and coiled-coil domain containing 1	2.349992
204203_at	CEBPG	CCAAT/enhancer binding protein (C/EBP), gamma	2.3494
231412_at	LOC100506342	uncharacterized LOC100506342	2.348272
208786_s_at	MAP1LC3B	microtubule-associated protein 1 light chain 3 beta	2.347351
221843_s_at	TLDC1	TBC/LysM-associated domain containing 1	2.345882

235584_at	LOC285033	uncharacterized LOC285033	2.344002
229940_at	SETD3	SET domain containing 3	2.342829
206273_at	SLMO1	slowmo homolog 1 (Drosophila)	2.3384
212171_x_at	VEGFA	vascular endothelial growth factor A	2.336545
1558249_s_at	STX16	syntaxin 16	2.335867
221876_at	ZNF783	zinc finger family member 783	2.335238
233229_at	SCFD1	sec1 family domain containing 1	2.334828
224657_at	ERRFI1	ERBB receptor feedback inhibitor 1	2.334793
236261_at	OSBPL6	oxysterol binding protein-like 6	2.3346
228575_at	IL20RB	interleukin 20 receptor beta	2.332198
1560402_at	GAS5	growth arrest-specific 5 (non-protein coding)	2.32794
228005_at	ZXDB	zinc finger, X-linked, duplicated B	2.327882
213919_at	DNAJC4	DnaJ (Hsp40) homolog, subfamily C, member 4	2.325577
211354_s_at	LEPR	leptin receptor	2.32506
230031_at	HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	2.322999
229069_at	SARNP	SAP domain containing ribonucleoprotein	2.322386
208523_x_at	HIST1H2BC///HIST1H2BE///HIST1H2BF///HIST1H2BG///HIST1H2BI	histone cluster 1, H2bc///histone cluster 1, H2be///histone cluster 1, H2bf///histone cluster 1, H2bg///histone cluster 1, H2bi	2.320375
219371_s_at	KLF2	Kruppel-like factor 2 (lung)	2.320352
225842_at	PHLDA1	pleckstrin homology-like domain, family A, member 1	2.319554
239233_at	CCDC88A	coiled-coil domain containing 88A	2.318928
1554053_at	SPTLC1	serine palmitoyltransferase, long chain base subunit 1	2.316571
200920_s_at	BTG1	B-cell translocation gene 1, anti-proliferative	2.315529
224567_x_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	2.310717
204823_at	NAV3	neuron navigator 3	2.307372
220393_at	LGSN	lengsin, lens protein with glutamine synthetase domain	2.305646
205729_at	OSMR	oncostatin M receptor	2.305142
65438_at	TLDC1	TBC/LysM-associated domain containing 1	2.304234
231813_s_at	COG1	component of oligomeric golgi complex 1	2.302033
209706_at	NKX3-1	NK3 homeobox 1	2.301247
202146_at	IFRD1	interferon-related developmental regulator 1	2.300902
224441_s_at	USP45	ubiquitin specific peptidase 45	2.300807
215012_at	ZNF451	zinc finger protein 451	2.299076
231856_at	KIAA1244	KIAA1244	2.296096

223569_at	PPAPDC1B	phosphatidic acid phosphatase type 2 domain containing 1B	2.293404
235338_s_at	SETDB2	SET domain, bifurcated 2	2.292326
238553_at	AGAP9///BMS1P1// /BMS1P5///LOC100 996797	ArfGAP with GTPase domain, ankyrin repeat and PH domain 9///BMS1 pseudogene 1///BMS1 pseudogene 5///uncharacterized LOC100996797	2.292105
210587_at	INHBE	inhibin, beta E	2.290544
1569086_at	LOC100287177	uncharacterized LOC100287177	2.2846
219603_s_at	ZNF226	zinc finger protein 226	2.283952
235533_at	COX19	cytochrome c oxidase assembly homolog 19 (S. cerevisiae)	2.279964
221218_s_at	TPK1	thiamin pyrophosphokinase 1	2.278434
201464_x_at	JUN	jun proto-oncogene	2.278311
224610_at	SNHG1///SNORD2 2///SNORD25///SN ORD26///SNORD27 ///SNORD28///SNO RD29///SNORD31	small nucleolar RNA host gene 1 (non-protein coding)///small nucleolar RNA, C/D box 22///small nucleolar RNA, C/D box 25///small nucleolar RNA, C/D box 26///small nucleolar RNA, C/D box 27///small nucleolar RNA, C/D box 28///small nucleolar RNA, C/D box 29///small nucleolar RNA, C/D box 31	2.278257
201858_s_at	SRGN	serglycin	2.277747
235065_at	GAREM	GRB2 associated, regulator of MAPK1	2.277205
240983_s_at	CARS	cysteinyl-tRNA synthetase	2.27703
202129_s_at	RIOK3	RIO kinase 3	2.276902
200629_at	WARS	tryptophanyl-tRNA synthetase	2.275692
200759_x_at	NFE2L1	nuclear factor (erythroid-derived 2)-like 1	2.275667
225527_at	CEBPB	CCAAT/enhancer binding protein (C/EBP), gamma	2.273365
205599_at	TRAF1	TNF receptor-associated factor 1	2.273049
241985_at	JMY	junction mediating and regulatory protein, p53 cofactor	2.272324
1554274_a_at	SSH1	slingshot protein phosphatase 1	2.270624
221107_at	CHRNA9	cholinergic receptor, nicotinic, alpha 9 (neuronal)	2.270118
1554014_at	CHD2///LOC10050 7217	chromodomain helicase DNA binding protein 2///uncharacterized LOC100507217	2.257418
223494_at	MGEA5	meningioma expressed antigen 5 (hyaluronidase)	2.256515
225756_at	CSNK1E	casein kinase 1, epsilon	2.255719
223401_at	ADPRM	ADP-ribose/CDP-alcohol diphosphatase, manganese-dependent	2.25516
212811_x_at	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	2.254712
234106_s_at	FLYWCH1	FLYWCH-type zinc finger 1	2.254477

1557828_a_at	C5orf28	chromosome 5 open reading frame 28	2.253291
206175_x_at	ZNF222	zinc finger protein 222	2.251657
221638_s_at	STX16	syntaxin 16	2.250599
39548_at	NPAS2	neuronal PAS domain protein 2	2.249541
243868_at	RFX3	regulatory factor X, 3 (influences HLA class II expression)	2.249192
205596_s_at	SMURF2	SMAD specific E3 ubiquitin protein ligase 2	2.248812
1568954_s_at	C16orf72	chromosome 16 open reading frame 72	2.248739
204090_at	STK19	serine/threonine kinase 19	2.248657
226700_at	U2AF1L4	U2 small nuclear RNA auxiliary factor 1-like 4	2.245012
205655_at	MDM4	Mdm4 p53 binding protein homolog (mouse)	2.243159
224835_at	GPCPD1	glycerophosphocholine phosphodiesterase GDE1 homolog (S. cerevisiae)	2.242471
232080_at	HECW2	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	2.238717
234976_x_at	MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	2.236287
221211_s_at	MAP3K7CL	MAP3K7 C-terminal like	2.235214
202375_at	SEC24D	SEC24 family, member D (S. cerevisiae)	2.234397
217649_at	ZFAND5	zinc finger, AN1-type domain 5	2.23399
212816_s_at	CBS	cystathionine-beta-synthase	2.233412
216250_s_at	LPXN	leupaxin	2.232681
217373_x_at	MDM2	MDM2 oncogene, E3 ubiquitin protein ligase	2.230853
207564_x_at	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase	2.228693
202500_at	DNAJB2	DnaJ (Hsp40) homolog, subfamily B, member 2	2.22866
204182_s_at	ZBTB43	zinc finger and BTB domain containing 43	2.225937
1554661_s_at	CNST	consortin, connexin sorting protein	2.224957
225018_at	SPIRE1	spire homolog 1 (Drosophila)	2.223818
207949_s_at	ICA1	islet cell autoantigen 1, 69kDa	2.223267
242477_at	TTC39B	tetratricopeptide repeat domain 39B	2.222664
225034_at	ST3GAL1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	2.221453
230815_at	LOC389765	kinesin family member 27 pseudogene	2.220373
228661_s_at	LOC100506029//L	uncharacterized LOC100506029//uncharacterized	2.219402
	OC100506051	LOC100506051	
202887_s_at	DDIT4	DNA-damage-inducible transcript 4	2.217444
222621_at	DNAJC1	DnaJ (Hsp40) homolog, subfamily C, member 1	2.214092
204584_at	L1CAM	L1 cell adhesion molecule	2.213295
215037_s_at	BCL2L1	BCL2-like 1	2.21263
213124_at	ZNF473	zinc finger protein 473	2.211437

225573_at	ACAD11///NPHP3// /NPHP3-ACAD11	acyl-CoA dehydrogenase family, member 11///nephronophthisis 3 (adolescent)//NPHP3-ACAD11 readthrough	2.210854
209305_s_at	GADD45B	growth arrest and DNA-damage-inducible, beta	2.209988
230131_x_at	ARSD	arylsulfatase D	2.209581
213836_s_at	WIPI1	WD repeat domain, phosphoinositide interacting 1	2.20932
1555781_at	PQLC2	PQ loop repeat containing 2	2.209162
206153_at	CYP4F11	cytochrome P450, family 4, subfamily F, polypeptide 11	2.208324
204906_at	RPS6KA2	ribosomal protein S6 kinase, 90kDa, polypeptide 2	2.206362
232392_at	SRSF3	serine/arginine-rich splicing factor 3	2.205913
1553995_a_at	NT5E	5'-nucleotidase, ecto (CD73)	2.205871
224558_s_at	MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	2.205597
210405_x_at	TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	2.204491
209912_s_at	AP5Z1///MIR4656	adaptor-related protein complex 5, zeta 1 subunit///microRNA 4656	2.202911
215948_x_at	ZMYM5	zinc finger, MYM-type 5	2.201186
224952_at	TANC2	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	2.200957
239843_at	RIT1	Ras-like without CAAX 1	2.197459
238575_at	OSBPL6	oxysterol binding protein-like 6	2.192036
226621_at	OSMR	oncostatin M receptor	2.189159
213286_at	ZFR	zinc finger RNA binding protein	2.188917
227223_at	RBM39	RNA binding motif protein 39	2.188839
203585_at	ZNF185	zinc finger protein 185 (LIM domain)	2.187156
203728_at	BAK1	BCL2-antagonist/killer 1	2.185864
223231_at	TATDN1	TatD DNase domain containing 1	2.181537
213554_s_at	CDV3	CDV3 homolog (mouse)	2.180924
230083_at	USP53	ubiquitin specific peptidase 53	2.18038
242956_at	IDH1	isocitrate dehydrogenase 1 (NADP+), soluble	2.179576
222529_at	SLC25A37	solute carrier family 25 (mitochondrial iron transporter), member 37	2.178238
228284_at	TLE1	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	2.177768
225327_at	FAM214A	family with sequence similarity 214, member A	2.177497
204523_at	ZNF140	zinc finger protein 140	2.17491
217831_s_at	NSFL1C	NSFL1 (p97) cofactor (p47)	2.174256
204402_at	RHBDD3	rhomboid domain containing 3	2.173858

203542_s_at	KLF9	Kruppel-like factor 9	2.173224
231836_at	HKR1///LOC100507342	HKR1, GLI-Kruppel zinc finger family member///uncharacterized LOC100507342	2.170658
221782_at	DNAJC10	DnaJ (Hsp40) homolog, subfamily C, member 10	2.170447
225632_s_at	ISY1-RAB43///RAB43	ISY1-RAB43 readthrough///RAB43, member RAS oncogene family	2.169995
223674_s_at	CDC42SE1	CDC42 small effector 1	2.169404
202644_s_at	TNFAIP3	tumor necrosis factor, alpha-induced protein 3	2.168567
200664_s_at	DNAJB1	DnaJ (Hsp40) homolog, subfamily B, member 1	2.167792
205969_at	AADAC	arylamide deacetylase	2.167143
209166_s_at	MAN2B1	mannosidase, alpha, class 2B, member 1	2.165101
200797_s_at	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	2.164572
241359_at	TLCD2	TLC domain containing 2	2.163458
242691_at	CTC-444N24.11///OTTH UMG00000183241	NULL///NULL	2.162664
213650_at	GOLGA8A///GOLGA8B	golgin A8 family, member A///golgin A8 family, member B	2.160147
205567_at	CHST1	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	2.15819
218368_s_at	TNFRSF12A	tumor necrosis factor receptor superfamily, member 12A	2.156055
209217_s_at	WDR45	WD repeat domain 45	2.155851
47773_at	FBXO42	F-box protein 42	2.153826
210517_s_at	AKAP12	A kinase (PRKA) anchor protein 12	2.148598
218376_s_at	MICAL1	microtubule associated monooxygenase, calponin and LIM domain containing 1	2.147521
1554015_a_at	CHD2///LOC100507217	chromodomain helicase DNA binding protein 2///uncharacterized LOC100507217	2.144557
212810_s_at	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	2.144454
203543_s_at	KLF9	Kruppel-like factor 9	2.143329
236696_at	U2SURP	U2 snRNP-associated SURP domain containing	2.142561
206583_at	KRBOX4	KRAB box domain containing 4	2.141938
33304_at	ISG20	interferon stimulated exonuclease gene 20kDa	2.141504
221765_at	UGCG	UDP-glucose ceramide glucosyltransferase	2.141113
225314_at	OCIAD2	OCIA domain containing 2	2.14068
233085_s_at	NABP1	nucleic acid binding protein 1	2.137576
228749_at	ZDBF2	zinc finger, DBF-type containing 2	2.134101
206833_s_at	ACYP2	acylphosphatase 2, muscle type	2.13405

200628_s_at	WARS	tryptophanyl-tRNA synthetase	2.133948
219340_s_at	CLN8	ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation)	2.133868
219926_at	POPDC3	popeye domain containing 3	2.132836
218954_s_at	BRF2	BRF2, RNA polymerase III transcription initiation factor 50 kDa subunit	2.132644
213672_at	MARS	methionyl-tRNA synthetase	2.131914
227213_at	ADAT2	adenosine deaminase, tRNA-specific 2	2.130954
225912_at	TP53INP1	tumor protein p53 inducible nuclear protein 1	2.130941
233070_at	ZNF197	zinc finger protein 197	2.130181
220937_s_at	ST6GALNAC4	ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4	2.12604
221812_at	FBXO42	F-box protein 42	2.124699
202628_s_at	SERPINE1	serpin peptidase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	2.121895
213359_at	HNRNPD	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	2.121284
204106_at	TESK1	testis-specific kinase 1	2.12097
219959_at	MOCOS	molybdenum cofactor sulfurase	2.11891
216375_s_at	ETV5	ets variant 5	2.118788
201471_s_at	SQSTM1	sequestosome 1	2.118443
225285_at	BCAT1	branched chain amino-acid transaminase 1, cytosolic	2.115256
236321_at	FAM200B	family with sequence similarity 200, member B	2.114751
235610_at	ALKBH8	alkB, alkylation repair homolog 8 (E. coli)	2.113852
1554161_at	SLC25A27	solute carrier family 25, member 27	2.110021
235727_at	KLHL28	kelch-like family member 28	2.108067
232436_at	ZNF274	zinc finger protein 274	2.107748
224798_s_at	FAM219B	family with sequence similarity 219, member B	2.105731
210547_x_at	ICA1	islet cell autoantigen 1, 69kDa	2.104756
201631_s_at	IER3	immediate early response 3	2.104178
222385_x_at	SEC61A1	Sec61 alpha 1 subunit (S. cerevisiae)	2.103707
216902_s_at	RRN3///RRN3P1///RRN3P2	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae)///RNA polymerase I transcription factor homolog (S. cerevisiae) pseudogene 1///RNA polymerase I transcription factor homolog (S. cerevisiae) pseudogene 2	2.101407
206967_at	CCNT1	cyclin T1	2.100634
209610_s_at	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	2.099833

242807_at	FSD1L	fibronectin type III and SPRY domain containing 1-like	2.095492
203232_s_at	ATXN1	ataxin 1	2.095098
238912_x_at	C9orf85	chromosome 9 open reading frame 85	2.093493
208934_s_at	LGALS8	lectin, galactoside-binding, soluble, 8	2.089767
214446_at	ELL2	elongation factor, RNA polymerase II, 2	2.088218
217185_s_at	ZNF259///ZNF259P 1	zinc finger protein 259///zinc finger protein 259 pseudogene 1	2.08758
226562_at	ZSCAN29	zinc finger and SCAN domain containing 29	2.086776
203814_s_at	NQO2	NAD(P)H dehydrogenase, quinone 2	2.085545
221781_s_at	DNAJC10	DnaJ (Hsp40) homolog, subfamily C, member 10	2.084709
219550_at	ROBO3	roundabout, axon guidance receptor, homolog 3 (Drosophila)	2.082416
39549_at	NPAS2	neuronal PAS domain protein 2	2.082335
225065_x_at	C17orf76- AS1//SNORD49A// /SNORD49B//SNO RD65	C17orf76 antisense RNA 1///small nucleolar RNA, C/D box 49A///small nucleolar RNA, C/D box 49B///small nucleolar RNA, C/D box 65	2.082303
230435_at	FAM228B	family with sequence similarity 228, member B	2.082228
204958_at	PLK3	polo-like kinase 3	2.079594
1554589_at	LENG9	leukocyte receptor cluster (LRC) member 9	2.079241
224806_at	TRIM25	tripartite motif containing 25	2.079015
218004_at	BSDC1	BSD domain containing 1	2.078615
1554008_at	OSMR	oncostatin M receptor	2.077414
224204_x_at	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2	2.076938
235427_at	CFLAR	CASP8 and FADD-like apoptosis regulator	2.076203
202083_s_at	SEC14L1	SEC14-like 1 (S. cerevisiae)	2.075801
230277_at	LOC100289187	transmembrane protein 225-like	2.075517
209967_s_at	CREM	cAMP responsive element modulator	2.074638
208540_x_at	S100A11P1///S100 A11P1	S100 calcium binding protein A11 pseudogene 1///NULL	2.074217
242324_x_at	CCBE1	collagen and calcium binding EGF domains 1	2.074116
203556_at	ZHX2	zinc fingers and homeoboxes 2	2.073705
228923_at	S100A6	S100 calcium binding protein A6	2.071085
218955_at	BRF2	BRF2, RNA polymerase III transcription initiation factor 50 kDa subunit	2.069404
200766_at	CTSD	cathepsin D	2.06924
232087_at	CXorf23	chromosome X open reading frame 23	2.068774
214841_at	CNIH3	cornichon homolog 3 (Drosophila)	2.067396

209360_s_at	LOC100506403//R UNX1	uncharacterized LOC100506403//runt-related transcription factor 1	2.063978
1554095_at	RBM33	RNA binding motif protein 33	2.061843
212501_at	CEBPB	CCAAT/enhancer binding protein (C/EBP), beta	2.061806
241418_at	LOC344887	NmrA-like family domain containing 1 pseudogene	2.060765
201474_s_at	ITGA3	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	2.059272
244698_at	CDRT4//TVP23C- CDRT4	CMT1A duplicated region transcript 4//TVP23C-CDRT4 readthrough	2.058758
205780_at	BIK	BCL2-interacting killer (apoptosis-inducing)	2.058593
1553031_at	GPR115	G protein-coupled receptor 115	2.057112
1564856_s_at	LOC727924	uncharacterized LOC727924	2.054899
1555938_x_at	VIM	vimentin	2.053823
213142_x_at	GSAP	gamma-secretase activating protein	2.052251
200898_s_at	MGEA5	meningioma expressed antigen 5 (hyaluronidase)	2.052147
217783_s_at	YPEL5	yippee-like 5 (Drosophila)	2.049307
209611_s_at	SLC1A4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	2.04909
221260_s_at	CSRNP2	cysteine-serine-rich nuclear protein 2	2.049054
206182_at	ZNF134	zinc finger protein 134	2.048814
221813_at	FBXO42	F-box protein 42	2.048046
238295_at	TEFM	transcription elongation factor, mitochondrial	2.046329
214090_at	PAWR	PRKC, apoptosis, WT1, regulator	2.045732
202344_at	HSF1	heat shock transcription factor 1	2.045701
204937_s_at	ZNF274	zinc finger protein 274	2.04422
218972_at	TTC17	tetratricopeptide repeat domain 17	2.043144
226038_at	LONRF1	LON peptidase N-terminal domain and ring finger 1	2.042299
216080_s_at	FADS3	fatty acid desaturase 3	2.04225
218050_at	UFM1	ubiquitin-fold modifier 1	2.04192
207630_s_at	CREM	cAMP responsive element modulator	2.0411
222716_s_at	SNX24	sorting nexin 24	2.040883
218064_s_at	AKAP8L	A kinase (PRKA) anchor protein 8-like	2.040855
1552472_a_at	ACAP2	ArfGAP with coiled-coil, ankyrin repeat and PH domains 2	2.040733
1562309_s_at	LOC100506695//P HF21B	uncharacterized LOC100506695//PHD finger protein 21B	2.04053
218769_s_at	ANKRA2	ankyrin repeat, family A (RFXANK-like), 2	2.039426
213281_at	JUN	jun proto-oncogene	2.038826
229297_at	GPATCH2L	G patch domain containing 2-like	2.038079

212614_at	ARID5B	AT rich interactive domain 5B (MRF1-like)	2.036191
222784_at	SMOC1	SPARC related modular calcium binding 1	2.03564
214023_x_at	TUBB2B	tubulin, beta 2B class IIb	2.034431
226517_at	BCAT1	branched chain amino-acid transaminase 1, cytosolic	2.033532
204421_s_at	FGF2	fibroblast growth factor 2 (basic)	2.033458
205266_at	LIF	leukemia inhibitory factor	2.029719
234611_at	LGALS8-AS1	LGALS8 antisense RNA 1	2.029152
223888_s_at	LARS	leucyl-tRNA synthetase	2.029125
205146_x_at	APBA3	amyloid beta (A4) precursor protein-binding, family A, member 3	2.028785
211071_s_at	MLLT11	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11	2.028623
227492_at	OCLN	occludin	2.028286
225753_at	ZNF513	zinc finger protein 513	2.028019
238327_at	ODF3B	outer dense fiber of sperm tails 3B	2.027395
201751_at	JOSD1	Josephin domain containing 1	2.02736
200054_at	ZNF259	zinc finger protein 259	2.026797
205943_at	TDO2	tryptophan 2,3-dioxygenase	2.02608
242140_at	ERVK3-1	endogenous retrovirus group K3, member 1	2.025781
213038_at	RNF19B	ring finger protein 19B	2.025222
221683_s_at	CEP290	centrosomal protein 290kDa	2.025084
220991_s_at	RNF32	ring finger protein 32	2.023413
1554807_a_at	SPIRE1	spire homolog 1 (Drosophila)	2.021862
1553575_at	ND6	NADH dehydrogenase, subunit 6 (complex I)	2.020848
208785_s_at	MAP1LC3B	microtubule-associated protein 1 light chain 3 beta	2.018754
202266_at	TDP2	tyrosyl-DNA phosphodiesterase 2	2.018523
203736_s_at	PPFIBP1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	2.018496
207064_s_at	AOC2	amine oxidase, copper containing 2 (retina-specific)	2.01756
244804_at	SQSTM1	sequestosome 1	2.015149
1552360_a_at	TIRAP	toll-interleukin 1 receptor (TIR) domain containing adaptor protein	2.014893
1554036_at	ZBTB24	zinc finger and BTB domain containing 24	2.013084
210999_s_at	GRB10	growth factor receptor-bound protein 10	2.012749
221899_at	N4BP2L2	NEDD4 binding protein 2-like 2	2.012719
219520_s_at	WWC3	WWC family member 3	2.011966
227614_at	HKDC1	hexokinase domain containing 1	2.009651
1561760_s_at	LOC645513	uncharacterized LOC645513	2.009327
204567_s_at	ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	2.008924

203157_s_at	GLS	glutaminase	2.008544
222662_at	PPP1R3B	protein phosphatase 1, regulatory subunit 3B	2.007346
1553972_a_at	CBS	cystathionine-beta-synthase	2.007259
212819_at	ASB1	ankyrin repeat and SOCS box containing 1	2.006277
222031_at	LOC100506453//L OC389906//LOC44 1528	uncharacterized LOC100506453//zinc finger protein 839 pseudogene//uncharacterized LOC441528	2.004015
227266_s_at	FYB	FYN binding protein	2.00374
218647_s_at	YRDC	yrdC domain containing (E. coli)	2.003226
222235_s_at	CSGALNACT2	chondroitin sulfate N-acetylgalactosaminyltransferase 2	2.002278
204698_at	ISG20	interferon stimulated exonuclease gene 20kDa	2.00114
1554097_a_at	MIR31HG	MIR31 host gene (non-protein coding)	2.001036

Down-regulated

Probe Set ID	Gene Symbol	Gene Description	Fold change
229569_at	OTTHUMG000001 80314//RP1- 193H18.2	NULL//NULL	0.021515
244111_at	KRT222	keratin 222	0.034321
209937_at	TM4SF4	transmembrane 4 L six family member 4	0.042976
225815_at	CPLX2	complexin 2	0.063556
238199_x_at	COX3	cytochrome c oxidase III	0.064215
225645_at	EHF	ets homologous factor	0.06901
208323_s_at	ANXA13	annexin A13	0.082018
208096_s_at	COL21A1	collagen, type XXI, alpha 1	0.093902
243864_at	CCDC80	coiled-coil domain containing 80	0.096765
1557795_s_at	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	0.096768
219990_at	E2F8	E2F transcription factor 8	0.102116
220639_at	TM4SF20	transmembrane 4 L six family member 20	0.114088
204988_at	FGB	fibrinogen beta chain	0.114767
203757_s_at	CEACAM6	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)	0.11837
226189_at	ITGB8	integrin, beta 8	0.119617
203913_s_at	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	0.123116
202831_at	GPX2	glutathione peroxidase 2 (gastrointestinal)	0.125255
213960_at	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	0.128718
225207_at	PDK4	pyruvate dehydrogenase kinase, isozyme 4	0.137155
203914_x_at	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	0.137594

213894_at	THSD7A	thrombospondin, type I, domain containing 7A	0.140671
206291_at	NTS	neurotensin	0.143579
211657_at	CEACAM6	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)	0.144887
205216_s_at	APOH	apolipoprotein H (beta-2-glycoprotein I)	0.147119
204259_at	MMP7	matrix metalloproteinase 7 (matrilysin, uterine)	0.148167
221521_s_at	GINS2	GINS complex subunit 2 (Psf2 homolog)	0.150469
203932_at	HLA-DMB	major histocompatibility complex, class II, DM beta	0.150584
224209_s_at	GDA	guanine deaminase	0.150902
227966_s_at	CCDC74A///CCDC 74B	coiled-coil domain containing 74A///coiled-coil domain containing 74B	0.152902
215311_at	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	0.153963
223274_at	TCF19	transcription factor 19	0.155603
204317_at	TRMU	tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase	0.156918
223570_at	MCM10	minichromosome maintenance complex component 10	0.156962
218755_at	KIF20A	kinesin family member 20A	0.159961
222962_s_at	MCM10	minichromosome maintenance complex component 10	0.161416
204159_at	CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	0.162654
211548_s_at	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	0.163773
205698_s_at	MAP2K6	mitogen-activated protein kinase kinase 6	0.163951
206026_s_at	TNFAIP6	tumor necrosis factor, alpha-induced protein 6	0.164928
228038_at	SOX2	SRY (sex determining region Y)-box 2	0.16698
211549_s_at	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	0.167116
202107_s_at	MCM2	minichromosome maintenance complex component 2	0.1713
201884_at	CEACAM5	carcinoembryonic antigen-related cell adhesion molecule 5	0.173973
214920_at	THSD7A	thrombospondin, type I, domain containing 7A	0.174741
212023_s_at	MKI67	antigen identified by monoclonal antibody Ki-67	0.17562
48808_at	DHFR	dihydrofolate reductase	0.175821
39248_at	AQP3	aquaporin 3 (Gill blood group)	0.17628
222696_at	AXIN2	axin 2	0.178204
226535_at	ITGB6	integrin, beta 6	0.178636
216238_s_at	FGB	fibrinogen beta chain	0.179157
218807_at	VAV3	vav 3 guanine nucleotide exchange factor	0.179418
228969_at	AGR2	anterior gradient 2 homolog (<i>Xenopus laevis</i>)	0.182232
1557128_at	FAM111B	family with sequence similarity 111, member B	0.182317
204695_at	CDC25A	cell division cycle 25A	0.185194
223312_at	PRADC1	protease-associated domain containing 1	0.18538

204684_at	NPTX1	neuronal pentraxin I	0.189952
229242_at	TNFSF15	tumor necrosis factor (ligand) superfamily, member 15	0.190608
220651_s_at	MCM10	minichromosome maintenance complex component 10	0.191247
228849_at	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	0.191374
209891_at	SPC25	SPC25, NDC80 kinetochore complex component	0.192016
206025_s_at	TNFAIP6	tumor necrosis factor, alpha-induced protein 6	0.192414
212141_at	MCM4	minichromosome maintenance complex component 4	0.194
212094_at	PEG10	paternally expressed 10	0.195268
211538_s_at	HSPA2	heat shock 70kDa protein 2	0.195517
218704_at	RNF43	ring finger protein 43	0.196572
201791_s_at	DHCR7	7-dehydrocholesterol reductase	0.19674
206368_at	CPLX2	complexin 2	0.201206
212949_at	NCAPH	non-SMC condensin I complex, subunit H	0.201379
228401_at	ATAD2	ATPase family, AAA domain containing 2	0.201489
1556325_at	FILIP1	filamin A interacting protein 1	0.201922
201131_s_at	CDH1	cadherin 1, type 1, E-cadherin (epithelial)	0.202758
235588_at	ESCO2	establishment of sister chromatid cohesion N-acetyltransferase 2	0.203529
215942_s_at	GTSE1	G-2 and S-phase expressed 1	0.204144
223307_at	CDCA3	cell division cycle associated 3	0.204411
226456_at	RMI2	RecQ mediated genome instability 2	0.205036
209863_s_at	TP63	tumor protein p63	0.205567
203213_at	CDK1	cyclin-dependent kinase 1	0.205943
239680_at	WDR76	WD repeat domain 76	0.206283
206462_s_at	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	0.207462
209464_at	AURKB	aurora kinase B	0.207891
204318_s_at	GTSE1	G-2 and S-phase expressed 1	0.210062
201890_at	RRM2	ribonucleotide reductase M2	0.210171
230836_at	ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	0.210783
211685_s_at	NCALD	neurocalcin delta	0.211201
215025_at	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	0.211161
205960_at	PDK4	pyruvate dehydrogenase kinase, isozyme 4	0.211841
212203_x_at	IFITM3	interferon induced transmembrane protein 3	0.213792
204444_at	KIF11	kinesin family member 11	0.215041
1553402_a_at	HFE	hemochromatosis	0.216854
204975_at	EMP2	epithelial membrane protein 2	0.21706
1553588_at	ND3//SH3KBP1	NADH dehydrogenase, subunit 3 (complex I)//SH3-	0.218985

		domain kinase binding protein 1	
241607_at	LOC730102	quinone oxidoreductase-like protein 2 pseudogene	0.219679
230087_at	PRIMA1	proline rich membrane anchor 1	0.219987
221436_s_at	CDCA3	cell division cycle associated 3	0.220117
217033_x_at	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	0.22012
209173_at	AGR2	anterior gradient 2 homolog (Xenopus laevis)	0.222991
1555677_s_at	SMC1A	structural maintenance of chromosomes 1A	0.223441
211713_x_at	KIAA0101	KIAA0101	0.224622
207843_x_at	CYB5A	cytochrome b5 type A (microsomal)	0.224751
212021_s_at	MKI67	antigen identified by monoclonal antibody Ki-67	0.224782
225078_at	EMP2	epithelial membrane protein 2	0.226145
209773_s_at	RRM2	ribonucleotide reductase M2	0.226712
218115_at	ASF1B	anti-silencing function 1B histone chaperone	0.227253
202508_s_at	SNAP25	synaptosomal-associated protein, 25kDa	0.227942
202338_at	TK1	thymidine kinase 1, soluble	0.228399
220084_at	C14orf105	chromosome 14 open reading frame 105	0.228701
216598_s_at	CCL2	chemokine (C-C motif) ligand 2	0.228708
210377_at	ACSM3	acyl-CoA synthetase medium-chain family member 3	0.229013
203418_at	CCNA2	cyclin A2	0.229637
212095_s_at	MTUS1	microtubule associated tumor suppressor 1	0.229845
212020_s_at	MKI67	antigen identified by monoclonal antibody Ki-67	0.230159
212022_s_at	MKI67	antigen identified by monoclonal antibody Ki-67	0.231332
214433_s_at	SELENBP1	selenium binding protein 1	0.231871
204051_s_at	SFRP4	secreted frizzled-related protein 4	0.232082
1554408_a_at	TK1	thymidine kinase 1, soluble	0.234726
202532_s_at	DHFR	dihydrofolate reductase	0.235281
202067_s_at	LDLR	low density lipoprotein receptor	0.2356
213075_at	OLFML2A	olfactomedin-like 2A	0.235686
204126_s_at	CDC45	cell division cycle 45	0.236177
218857_s_at	ASRGL1	asparaginase like 1	0.236374
240365_at	LINC00669	long intergenic non-protein coding RNA 669	0.236489
227578_at	TMPO-AS1	TMPO antisense RNA 1	0.237588
1557217_a_at	FANCB	Fanconi anemia, complementation group B	0.238529
201710_at	MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	0.238932
224221_s_at	VAV3	vav 3 guanine nucleotide exchange factor	0.239093
209847_at	CDH17	cadherin 17, LI cadherin (liver-intestine)	0.24074
211814_s_at	CCNE2	cyclin E2	0.242154

200862_at	DHCR24	24-dehydrocholesterol reductase	0.242448
227209_at	CNTN1	contactin 1	0.243455
205226_at	PDGFRL	platelet-derived growth factor receptor-like	0.243859
219734_at	SIDT1	SID1 transmembrane family, member 1	0.244256
225079_at	EMP2	epithelial membrane protein 2	0.244455
222037_at	MCM4	minichromosome maintenance complex component 4	0.246297
221591_s_at	FAM64A	family with sequence similarity 64, member A	0.246507
227202_at	CNTN1	contactin 1	0.247898
231534_at	CDK1	cyclin-dependent kinase 1	0.248025
206385_s_at	ANK3	ankyrin 3, node of Ranvier (ankyrin G)	0.250777
204603_at	EXO1	exonuclease 1	0.25116
222557_at	STMN3	stathmin-like 3	0.251447
215115_x_at	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	0.252149
219737_s_at	PCDH9	protocadherin 9	0.252763
208955_at	DUT	deoxyuridine triphosphatase	0.254113
212093_s_at	MTUS1	microtubule associated tumor suppressor 1	0.25736
202534_x_at	DHFR	dihydrofolate reductase	0.257522
205034_at	CCNE2	cyclin E2	0.257889
218019_s_at	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	0.258188
203699_s_at	DIO2	deiodinase, iodothyronine, type II	0.258624
218726_at	HJURP	Holliday junction recognition protein	0.258743
221703_at	BRIP1	BRCA1 interacting protein C-terminal helicase 1	0.260332
229551_x_at	ZNF367	zinc finger protein 367	0.261871
1558217_at	SLFN13	schlafen family member 13	0.262674
212636_at	QKI	QKI, KH domain containing, RNA binding	0.26327
214804_at	CENPI	centromere protein I	0.263387
213543_at	SGCD	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	0.264594
218711_s_at	SDPR	serum deprivation response	0.265928
215388_s_at	CFH//CFHR1	complement factor H//complement factor H-related 1	0.266878
219650_at	ERCC6L	excision repair cross-complementing rodent repair deficiency, complementation group 6-like	0.267048
226747_at	TXNDC16	thioredoxin domain containing 16	0.267407
201309_x_at	NREP	neuronal regeneration related protein	0.267723
201315_x_at	IFITM2	interferon induced transmembrane protein 2	0.267756
202503_s_at	KIAA0101	KIAA0101	0.268052
234465_at	EME1	essential meiotic endonuclease 1 homolog 1 (S. pombe)	0.268442
227703_s_at	SYTL4	synaptotagmin-like 4	0.268684

229159_at	THSD7A	thrombospondin, type I, domain containing 7A	0.269014
219690_at	IGFLR1	IGF-like family receptor 1	0.269437
204897_at	PTGER4	prostaglandin E receptor 4 (subtype EP4)	0.269551
218741_at	CENPM	centromere protein M	0.269613
204768_s_at	FEN1	flap structure-specific endonuclease 1	0.269721
209366_x_at	CYB5A	cytochrome b5 type A (microsomal)	0.269929
222608_s_at	ANLN	anillin, actin binding protein	0.269929
219148_at	PBK	PDZ binding kinase	0.270378
204727_at	WDHD1	WD repeat and HMG-box DNA binding protein 1	0.271595
59437_at	C9orf116	chromosome 9 open reading frame 116	0.272814
212092_at	PEG10	paternally expressed 10	0.273139
219502_at	NEIL3	nei endonuclease VIII-like 3 (E. coli)	0.273691
202094_at	BIRC5	baculoviral IAP repeat containing 5	0.273854
206632_s_at	APOBEC3B	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	0.27393
201627_s_at	INSIG1	insulin induced gene 1	0.274309
239093_at	HOGA1	4-hydroxy-2-oxoglutarate aldolase 1	0.274494
203976_s_at	CHAF1A	chromatin assembly factor 1, subunit A (p150)	0.27451
205623_at	ALDH3A1	aldehyde dehydrogenase 3 family, member A1	0.274722
203242_s_at	PDLIM5	PDZ and LIM domain 5	0.275647
205305_at	FGL1	fibrinogen-like 1	0.275783
235178_x_at	ESCO2	establishment of sister chromatid cohesion N-acetyltransferase 2	0.27636
214033_at	ABCC6	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	0.276559
222797_at	DPYSL5	dihydropyrimidinase-like 5	0.276835
216804_s_at	PDLIM5	PDZ and LIM domain 5	0.277076
200831_s_at	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	0.277092
204767_s_at	FEN1	flap structure-specific endonuclease 1	0.277212
212096_s_at	MTUS1	microtubule associated tumor suppressor 1	0.277792
203276_at	LMNB1	lamin B1	0.278727
207183_at	GPR19	G protein-coupled receptor 19	0.278922
211194_s_at	TP63	tumor protein p63	0.279171
204359_at	FLRT2//LOC100506718	fibronectin leucine rich transmembrane protein 2//uncharacterized LOC100506718	0.279395
202712_s_at	CKMT1A//CKMT1B	creatine kinase, mitochondrial 1A//creatine kinase, mitochondrial 1B	0.27942
1555004_a_at	RBL1	retinoblastoma-like 1 (p107)	0.279741

204179_at	MB	myoglobin	0.281187
225242_s_at	CCDC80	coiled-coil domain containing 80	0.281311
238222_at	GKN2	gastrokine 2	0.281374
205909_at	POLE2	polymerase (DNA directed), epsilon 2, accessory subunit	0.281521
215726_s_at	CYB5A	cytochrome b5 type A (microsomal)	0.282573
230730_at	SGCD	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	0.282917
201431_s_at	DPYSL3	dihydropyrimidinase-like 3	0.283532
210983_s_at	MCM7	minichromosome maintenance complex component 7	0.283667
212148_at	PBX1	pre-B-cell leukemia homeobox 1	0.284497
210334_x_at	BIRC5	baculoviral IAP repeat containing 5	0.284648
202555_s_at	MYLK	myosin light chain kinase	0.284852
212142_at	MCM4	minichromosome maintenance complex component 4	0.284893
230261_at	ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	0.285786
235343_at	VASH2	vasohibin 2	0.286068
1552619_a_at	ANLN	anillin, actin binding protein	0.286565
207828_s_at	CENPF	centromere protein F, 350/400kDa	0.286626
208373_s_at	P2RY6	pyrimidinergic receptor P2Y, G-protein coupled, 6	0.287485
203764_at	DLGAP5	discs, large (Drosophila) homolog-associated protein 5	0.288104
225826_at	MMAB	methylmalonic aciduria (cobalamin deficiency) cblB type	0.288129
216237_s_at	MCM5	minichromosome maintenance complex component 5	0.289008
242943_at	ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	0.289711
204026_s_at	ZWINT	ZW10 interacting kinetochore protein	0.289932
212560_at	SORL1	sortilin-related receptor, L(DLR class) A repeats containing	0.289949
65517_at	AP1M2	adaptor-related protein complex 1, mu 2 subunit	0.290058
218261_at	AP1M2	adaptor-related protein complex 1, mu 2 subunit	0.290907
206549_at	INSL4	insulin-like 4 (placenta)	0.291103
225911_at	NPNT	nephronectin	0.291699
201930_at	MCM6	minichromosome maintenance complex component 6	0.291781
210145_at	PLA2G4A	phospholipase A2, group IVA (cytosolic, calcium-dependent)	0.292121
208343_s_at	NR5A2	nuclear receptor subfamily 5, group A, member 2	0.292919
205882_x_at	ADD3	adducin 3 (gamma)	0.294128
230081_at	PLCXD3	phosphatidylinositol-specific phospholipase C, X domain containing 3	0.294402
210074_at	CTSL2	cathepsin L2	0.294992

222925_at	DCDC2	doublecortin domain containing 2	0.295847
210559_s_at	CDK1	cyclin-dependent kinase 1	0.29587
224210_s_at	PXMP4	peroxisomal membrane protein 4, 24kDa	0.297072
211203_s_at	CNTN1	contactin 1	0.297225
223700_at	MND1	meiotic nuclear divisions 1 homolog (S. cerevisiae)	0.297393
227480_at	SUSD2	sushi domain containing 2	0.297814
212412_at	PDLIM5	PDZ and LIM domain 5	0.298121
220085_at	HELLS	helicase, lymphoid-specific	0.299009
1553973_a_at	SPINK6	serine peptidase inhibitor, Kazal type 6	0.299884
226030_at	ACADSB	acyl-CoA dehydrogenase, short/branched chain	0.299901
236190_at	CTD- 2576D5.4///OTTHU MG00000177273	NULL///NULL	0.299964
203228_at	PAFAH1B3	platelet-activating factor acetylhydrolase 1b, catalytic subunit 3 (29kDa)	0.300228
224496_s_at	TMEM107	transmembrane protein 107	0.302419
204602_at	DKK1	dickkopf WNT signaling pathway inhibitor 1	0.302522
202869_at	OAS1	2'-5'-oligoadenylate synthetase 1, 40/46kDa	0.303927
223204_at	FAM198B	family with sequence similarity 198, member B	0.304427
205552_s_at	OAS1	2'-5'-oligoadenylate synthetase 1, 40/46kDa	0.304459
207590_s_at	CENPI	centromere protein I	0.305377
204817_at	ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)	0.305418
229097_at	DIAPH3	diaphanous homolog 3 (Drosophila)	0.305595
224823_at	MYLK	myosin light chain kinase	0.306662
228361_at	E2F2	E2F transcription factor 2	0.307157
201328_at	ETS2	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	0.307374
222036_s_at	MCM4	minichromosome maintenance complex component 4	0.307432
210964_s_at	GYG2	glycogenin 2	0.307559
211792_s_at	CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	0.30776
221957_at	PDK3	pyruvate dehydrogenase kinase, isozyme 3	0.307964
233938_at	C11orf86	chromosome 11 open reading frame 86	0.30816
200832_s_at	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	0.308223
222843_at	FIGNL1	fidgetin-like 1	0.308335
203608_at	ALDH5A1	aldehyde dehydrogenase 5 family, member A1	0.309341
216384_x_at	LOC100506248///L OC728026///MIR12 44-1///MIR1244-	prothymosin alpha-like///prothymosin alpha-like///microRNA 1244-1///microRNA 1244-2///microRNA 1244-3///prothymosin, alpha	0.309484

	2///MIR1244-		
	3///PTMA		
217555_at	SMC1A	structural maintenance of chromosomes 1A	0.309517
205296_at	RBL1	retinoblastoma-like 1 (p107)	0.30985
218782_s_at	ATAD2	ATPase family, AAA domain containing 2	0.312409
201790_s_at	DHCR7	7-dehydrocholesterol reductase	0.312441
205235_s_at	KIF20B	kinesin family member 20B	0.312452
219232_s_at	EGLN3	egl nine homolog 3 (C. elegans)	0.312806
228375_at	IGSF11	immunoglobulin superfamily, member 11	0.313265
219918_s_at	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	0.313277
218662_s_at	NCAPG	non-SMC condensin I complex, subunit G	0.313782
221520_s_at	CDCA8	cell division cycle associated 8	0.314098
228773_at	LOC100506100	uncharacterized LOC100506100	0.314142
219493_at	SHCBP1	SHC SH2-domain binding protein 1	0.315027
217377_x_at	NTRK3	neurotrophic tyrosine kinase, receptor, type 3	0.315728
203214_x_at	CDK1	cyclin-dependent kinase 1	0.315872
1552921_a_at	FIGNL1	fidgetin-like 1	0.315906
227896_at	BCCIP	BRCA2 and CDKN1A interacting protein	0.317222
203145_at	SPAG5	sperm associated antigen 5	0.317375
202095_s_at	BIRC5	baculoviral IAP repeat containing 5	0.318235
50965_at	RAB26	RAB26, member RAS oncogene family	0.318619
225655_at	UHRF1	ubiquitin-like with PHD and ring finger domains 1	0.318841
202068_s_at	LDLR	low density lipoprotein receptor	0.318853
204867_at	GCHFR	GTP cyclohydrolase I feedback regulator	0.318858
209680_s_at	KIFC1	kinesin family member C1	0.319313
223170_at	TMEM98	transmembrane protein 98	0.319432
243840_at	CLSPN	claspin	0.319622
219528_s_at	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)	0.319916
203243_s_at	PDLIM5	PDZ and LIM domain 5	0.321041
223556_at	HELLS	helicase, lymphoid-specific	0.322936
202533_s_at	DHFR	dihydrofolate reductase	0.323846
1553589_a_at	PDZK1IP1	PDZK1 interacting protein 1	0.324471
206348_s_at	PDK3	pyruvate dehydrogenase kinase, isozyme 3	0.324546
223229_at	UBE2T	ubiquitin-conjugating enzyme E2T (putative)	0.32536
1554485_s_at	TMEM37	transmembrane protein 37	0.325536
205014_at	FGFBP1	fibroblast growth factor binding protein 1	0.326026
202761_s_at	SYNE2	spectrin repeat containing, nuclear envelope 2	0.326303

205436_s_at	H2AFX	H2A histone family, member X	0.326478
204162_at	NDC80	NDC80 kinetochore complex component	0.326793
225792_at	HOOK1	hook homolog 1 (Drosophila)	0.327012
1556037_s_at	HHIP	hedgehog interacting protein	0.327073
238977_at	MCM6	minichromosome maintenance complex component 6	0.327255
236129_at	GALNT5	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 5 (GalNAc-T5)	0.327835
231130_at	FKBP7	FK506 binding protein 7	0.32792
234980_at	TMEM56	transmembrane protein 56	0.328353
218875_s_at	FBXO5	F-box protein 5	0.328476
213226_at	CCNA2	cyclin A2	0.32869
204728_s_at	WDHD1	WD repeat and HMG-box DNA binding protein 1	0.329671
219195_at	PPARGC1A	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha	0.330029
205403_at	IL1R2	interleukin 1 receptor, type II	0.330277
206102_at	GINS1	GINS complex subunit 1 (Psf1 homolog)	0.330401
235609_at	BRIP1	BRCA1 interacting protein C-terminal helicase 1	0.33046
201585_s_at	LOC100996496//S FPQ	uncharacterized LOC100996496//splicing factor proline/glutamine-rich	0.332168
202580_x_at	FOXO1	forkhead box M1	0.332584
202590_s_at	PDK2	pyruvate dehydrogenase kinase, isozyme 2	0.332792
218400_at	OAS3	2'-5'-oligoadenylate synthetase 3, 100kDa	0.33298
218663_at	NCAPG	non-SMC condensin I complex, subunit G	0.333067
227350_at	HELLS	helicase, lymphoid-specific	0.333118
226433_at	RNF157	ring finger protein 157	0.334192
238529_at	OTTHUMG000001 78927//RP11- 196G18.23	NULL//NULL	0.33568
38158_at	ESPL1	extra spindle pole bodies homolog 1 (S. cerevisiae)	0.336287
208530_s_at	RARB	retinoic acid receptor, beta	0.336918
201626_at	INSIG1	insulin induced gene 1	0.337555
213906_at	MYBL1	v-myb myeloblastosis viral oncogene homolog (avian)-like 1	0.339205
201700_at	CCND3	cyclin D3	0.339586
205158_at	RNASE4	ribonuclease, RNase A family, 4	0.339816
204886_at	PLK4	polo-like kinase 4	0.341694
228293_at	DEPDC7	DEP domain containing 7	0.342206
235890_at	TBL1XR1	transducin (beta)-like 1 X-linked receptor 1	0.342224

205792_at	WISP2	WNT1 inducible signaling pathway protein 2	0.343816
220520_s_at	NUP62CL	nucleoporin 62kDa C-terminal like	0.343997
204826_at	CCNF	cyclin F	0.344045
208368_s_at	BRCA2	breast cancer 2, early onset	0.344207
218865_at		1-Mar mitochondrial amidoxime reducing component 1	0.34443
216945_x_at	PASK	PAS domain containing serine/threonine kinase	0.344519
222764_at	ASRGL1	asparaginase like 1	0.345288
207746_at	POLQ	polymerase (DNA directed), theta	0.345402
222039_at	KIF18B	kinesin family member 18B	0.34584
208795_s_at	MCM7	minichromosome maintenance complex component 7	0.345925
204146_at	RAD51AP1	RAD51 associated protein 1	0.346065
219383_at	PRR5L	proline rich 5 like	0.346146
223759_s_at	GSG2	germ cell associated 2 (haspin)	0.346266
220087_at	BCMO1	beta-carotene 15,15'-monooxygenase 1	0.346269
210064_s_at	UPK1B	uroplakin 1B	0.346383
218944_at	PYCRL	pyrroline-5-carboxylate reductase-like	0.346392
239576_at	MTUS1	microtubule associated tumor suppressor 1	0.34645
201430_s_at	DPYSL3	dihydropyrimidinase-like 3	0.346694
218883_s_at	MLF1IP	MLF1 interacting protein	0.347543
202994_s_at	FBLN1	fibulin 1	0.348013
203022_at	RNASEH2A	ribonuclease H2, subunit A	0.3482
205046_at	CENPE	centromere protein E, 312kDa	0.348338
217564_s_at	CPS1	carbamoyl-phosphate synthase 1, mitochondrial	0.348432
242655_at	BARD1	BRCA1 associated RING domain 1	0.348502
210174_at	NR5A2	nuclear receptor subfamily 5, group A, member 2	0.348664
203636_at	MID1	midline 1 (Opitz/BBB syndrome)	0.348679
235572_at	SPC24	SPC24, NDC80 kinetochore complex component	0.349405
202218_s_at	FADS2	fatty acid desaturase 2	0.349592
203184_at	FBN2	fibrillin 2	0.349623
226552_at	IER5L	immediate early response 5-like	0.350246
228865_at	C1orf116	chromosome 1 open reading frame 116	0.351527
236300_at	PDE3A	phosphodiesterase 3A, cGMP-inhibited	0.352041
1557218_s_at	FANCB	Fanconi anemia, complementation group B	0.352207
202944_at	NAGA	N-acetylgalactosaminidase, alpha-	0.352588
229649_at	NRXN3	neurexin 3	0.353133
214745_at	PLCH1	phospholipase C, eta 1	0.353544
203755_at	BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B	0.353613
206140_at	LHX2	LIM homeobox 2	0.353735

201034_at	ADD3	adducin 3 (gamma)	0.354267
218477_at	TMEM14A	transmembrane protein 14A	0.354785
204615_x_at	IDI1	isopentenyl-diphosphate delta isomerase 1	0.354801
212151_at	PBX1	pre-B-cell leukemia homeobox 1	0.355185
205692_s_at	CD38	CD38 molecule	0.355345
209772_s_at	CD24	CD24 molecule	0.355838
216228_s_at	WDHD1	WD repeat and HMG-box DNA binding protein 1	0.356185
202388_at	RGS2	regulator of G-protein signaling 2, 24kDa	0.356294
204128_s_at	RFC3	replication factor C (activator 1) 3, 38kDa	0.356781
211519_s_at	KIF2C	kinesin family member 2C	0.357186
220295_x_at	DEPDC1	DEP domain containing 1	0.357191
220441_at	DNAJC22	DnaJ (Hsp40) homolog, subfamily C, member 22	0.358024
213891_s_at	TCF4	transcription factor 4	0.358056
201755_at	MCM5	minichromosome maintenance complex component 5	0.358406
218039_at	NUSAP1	nucleolar and spindle associated protein 1	0.358672
226936_at	CENPW	centromere protein W	0.358722
213425_at	WNT5A	wingless-type MMTV integration site family, member 5A	0.358793
213171_s_at	MMP24	matrix metalloproteinase 24 (membrane-inserted)	0.359136
206364_at	KIF14	kinesin family member 14	0.359406
203178_at	GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	0.359421
223381_at	NUF2	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)	0.359991
232362_at	CCDC18	coiled-coil domain containing 18	0.360706
218308_at	TACC3	transforming, acidic coiled-coil containing protein 3	0.361128
210220_at	FZD2	frizzled family receptor 2	0.361895
203700_s_at	DIO2	deiodinase, iodothyronine, type II	0.36194
203625_x_at	SKP2	S-phase kinase-associated protein 2, E3 ubiquitin protein ligase	0.362956
234863_x_at	FBXO5	F-box protein 5	0.363264
201753_s_at	ADD3	adducin 3 (gamma)	0.363754
228507_at	PDE3A	phosphodiesterase 3A, cGMP-inhibited	0.364124
218248_at	FAM111A	family with sequence similarity 111, member A	0.364207
218285_s_at	BDH2	3-hydroxybutyrate dehydrogenase, type 2	0.364393
215695_s_at	GYG2	glycogenin 2	0.364579
217853_at	TNS3	tensin 3	0.365002
228323_at	CASC5	cancer susceptibility candidate 5	0.365324
219512_at	DSN1	DSN1, MIND kinetochore complex component, homolog	0.365567

(<i>S. cerevisiae</i>)			
222717_at	SDPR	serum deprivation response	0.365724
208978_at	CRIP2	cysteine-rich protein 2	0.367123
210821_x_at	CENPA	centromere protein A	0.367562
218901_at	PLSCR4	phospholipid scramblase 4	0.367854
218009_s_at	PRC1	protein regulator of cytokinesis 1	0.367962
231855_at	KIAA1524	KIAA1524	0.36801
202726_at	LIG1	ligase I, DNA, ATP-dependent	0.368286
213787_s_at	EBP	emopamil binding protein (sterol isomerase)	0.368507
204887_s_at	PLK4	polo-like kinase 4	0.36857
227165_at	SKA3	spindle and kinetochore associated complex subunit 3	0.369697
236641_at	KIF14	kinesin family member 14	0.370899
204835_at	POLA1	polymerase (DNA directed), alpha 1, catalytic subunit	0.371123
1554997_a_at	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	0.371209
213253_at	SMC2	structural maintenance of chromosomes 2	0.371325
205670_at	GAL3ST1	galactose-3-O-sulfotransferase 1	0.372113
219667_s_at	BANK1	B-cell scaffold protein with ankyrin repeats 1	0.372697
225355_at	NEURL1B	neuralized homolog 1B (<i>Drosophila</i>)	0.372834
204822_at	TTK	TTK protein kinase	0.373001
201774_s_at	NCAPD2	non-SMC condensin I complex, subunit D2	0.373345
219978_s_at	NUSAP1	nucleolar and spindle associated protein 1	0.37337
212206_s_at	H2AFV	H2A histone family, member V	0.373677
213227_at	PGRMC2	progesterone receptor membrane component 2	0.37408
225687_at	FAM83D	family with sequence similarity 83, member D	0.374534
212801_at	CIT///MIR1178	citron (rho-interacting, serine/threonine kinase 21)///microRNA 1178	0.375653
228868_x_at	CDT1	chromatin licensing and DNA replication factor 1	0.37676
210567_s_at	SKP2	S-phase kinase-associated protein 2, E3 ubiquitin protein ligase	0.377063
204766_s_at	NUDT1	nudix (nucleoside diphosphate linked moiety X)-type motif 1	0.377679
237563_s_at	OTTHUMG00000039487///RP11-295G20.2	NULL///NULL	0.377819
203209_at	RFC5	replication factor C (activator 1) 5, 36.5kDa	0.377856
213008_at	FANCI	Fanconi anemia, complementation group I	0.377937
203967_at	CDC6	cell division cycle 6	0.37804

222680_s_at	DTL	denticleless E3 ubiquitin protein ligase homolog (Drosophila)	0.3789
205795_at	NRXN3	neurexin 3	0.378939
209980_s_at	SHMT1	serine hydroxymethyltransferase 1 (soluble)	0.379693
210052_s_at	TPX2	TPX2, microtubule-associated, homolog (Xenopus laevis)	0.379776
224753_at	CDCA5	cell division cycle associated 5	0.380136
237515_at	TMEM56	transmembrane protein 56	0.380214
219000_s_at	DSCC1	DNA replication and sister chromatid cohesion 1	0.380347
209932_s_at	DUT	deoxyuridine triphosphatase	0.380642
223395_at	ABI3BP	ABI family, member 3 (NESH) binding protein	0.380718
1563933_a_at	PLD5	phospholipase D family, member 5	0.381053
201555_at	MCM3	minichromosome maintenance complex component 3	0.381153
229610_at	CKAP2L	cytoskeleton associated protein 2-like	0.381415
202735_at	EBP	emopamil binding protein (sterol isomerase)	0.381625
230021_at	TICRR	TOPBP1-interacting checkpoint and replication regulator	0.381633
205673_s_at	ASB9	ankyrin repeat and SOCS box containing 9	0.382029
1553120_at	CLSPN	claspin	0.382108
218350_s_at	GMNN	geminin, DNA replication inhibitor	0.382426
208337_s_at	NR5A2	nuclear receptor subfamily 5, group A, member 2	0.382665
219304_s_at	PDGFD	platelet derived growth factor D	0.382809
209754_s_at	TMPO	thymopoietin	0.383343
203432_at	TMPO	thymopoietin	0.38341
227756_at	FAM81A	family with sequence similarity 81, member A	0.3837
226625_at	TGFBR3	transforming growth factor, beta receptor III	0.384147
224910_at	CARHSP1	calcium regulated heat stable protein 1, 24kDa	0.384521
214727_at	BRCA2	breast cancer 2, early onset	0.384767
221042_s_at	CLMN	calmin (calponin-like, transmembrane)	0.385298
209735_at	ABCG2	ATP-binding cassette, sub-family G (WHITE), member 2	0.385362
226574_at	PSPC1	paraspeckle component 1	0.385584
201141_at	GPNMB	glycoprotein (transmembrane) nmb	0.385959
228489_at	TM4SF18	transmembrane 4 L six family member 18	0.386064
213007_at	FANCI	Fanconi anemia, complementation group I	0.386505
225295_at	SLC39A10	solute carrier family 39 (zinc transporter), member 10	0.386566
210963_s_at	GYG2	glycogenin 2	0.38657
205559_s_at	PCSK5	proprotein convertase subtilisin/kexin type 5	0.386942
203362_s_at	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	0.387705
201310_s_at	NREP	neuronal regeneration related protein	0.387737
227928_at	PARPBP	PARP1 binding protein	0.387746

1555826_at	BIRC5	baculoviral IAP repeat containing 5	0.387909
228796_at	CPNE4	copine IV	0.388223
219408_at	PRMT7	protein arginine methyltransferase 7	0.388323
221731_x_at	VCAN	versican	0.388462
204633_s_at	RPS6KA5	ribosomal protein S6 kinase, 90kDa, polypeptide 5	0.388718
228057_at	DDIT4L	DNA-damage-inducible transcript 4-like	0.389314
200783_s_at	STMN1	stathmin 1	0.389421
228302_x_at	CAMK2N1	calcium/calmodulin-dependent protein kinase II inhibitor 1	0.389699
204748_at	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	0.389756
226923_at	SCFD2	sec1 family domain containing 2	0.390072
219531_at	CEP72	centrosomal protein 72kDa	0.390169
222777_s_at	WHSC1	Wolf-Hirschhorn syndrome candidate 1	0.390237
202507_s_at	SNAP25	synaptosomal-associated protein, 25kDa	0.390536
226279_at	PRSS23	protease, serine, 23	0.390928
215143_at	DPY19L2P2	dpy-19-like 2 pseudogene 2 (C. elegans)	0.391265
232563_at	ZNF684	zinc finger protein 684	0.391542
204404_at	SLC12A2	solute carrier family 12 (sodium/potassium/chloride transporters), member 2	0.39208
205345_at	BARD1	BRCA1 associated RING domain 1	0.392214
222740_at	ATAD2	ATPase family, AAA domain containing 2	0.392657
214051_at	LOC101060235//TMSB15B	thymosin beta-15B-like//thymosin beta 15a//thymosin beta 15B	0.393055
217590_s_at	TRPA1	transient receptor potential cation channel, subfamily A, member 1	0.393562
204127_at	RFC3	replication factor C (activator 1) 3, 38kDa	0.393633
203799_at	CD302//LY75-CD302	CD302 molecule//LY75-CD302 readthrough	0.393877
225171_at	ARHGAP18	Rho GTPase activating protein 18	0.394199
213228_at	PDE8B	phosphodiesterase 8B	0.3942
211804_s_at	CDK2	cyclin-dependent kinase 2	0.394203
201292_at	TOP2A	topoisomerase (DNA) II alpha 170kDa	0.394481
205768_s_at	SLC27A2	solute carrier family 27 (fatty acid transporter), member 2	0.394679
1555573_at	TTC40	tetratricopeptide repeat domain 40	0.394681
1557756_a_at	CEP128	centrosomal protein 128kDa	0.394895
204962_s_at	CENPA//SLC35F6	centromere protein A//solute carrier family 35, member F6	0.39548
238590_x_at	TMEM107	transmembrane protein 107	0.395585

235088_at	C4orf46	chromosome 4 open reading frame 46	0.39616
204279_at	PSMB9	proteasome (prosome, macropain) subunit, beta type, 9	0.396391
229538_s_at	IQGAP3	IQ motif containing GTPase activating protein 3	0.396413
228069_at	MTFR2	mitochondrial fission regulator 2	0.396478
213131_at	OLFM1	olfactomedin 1	0.396506
206118_at	STAT4	signal transducer and activator of transcription 4	0.396691
209172_s_at	CENPF	centromere protein F, 350/400kDa	0.398124
204709_s_at	KIF23	kinesin family member 23	0.398442
204731_at	TGFBR3	transforming growth factor, beta receptor III	0.398446
210761_s_at	GRB7	growth factor receptor-bound protein 7	0.39881
202995_s_at	FBLN1	fibulin 1	0.398955
230418_s_at	GALNT16	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 16	0.399356
1554696_s_at	TYMS	thymidylate synthetase	0.400055
219014_at	PLAC8	placenta-specific 8	0.400096
219076_s_at	PXMP2	peroxisomal membrane protein 2, 22kDa	0.400624
219510_at	POLQ	polymerase (DNA directed), theta	0.401048
203509_at	SORL1	sortilin-related receptor, L(DLR class) A repeats containing	0.401545
205733_at	BLM	Bloom syndrome, RecQ helicase-like	0.401592
228646_at	PPP1R1C	protein phosphatase 1, regulatory (inhibitor) subunit 1C	0.402065
215629_s_at	DLEU2///DLEU2L	deleted in lymphocytic leukemia 2 (non-protein coding)///deleted in lymphocytic leukemia 2-like	0.402473
238015_at	C4orf46	chromosome 4 open reading frame 46	0.402905
201650_at	KRT19	keratin 19	0.403387
1556499_s_at	COL1A1	collagen, type I, alpha 1	0.403449
201291_s_at	TOP2A	topoisomerase (DNA) II alpha 170kDa	0.403574
221011_s_at	LBH	limb bud and heart development	0.403808
207165_at	HMMR	hyaluronan-mediated motility receptor (RHAMM)	0.403914
227743_at	MYO15B	myosin XVB pseudogene	0.404073
40837_at	TLE2	transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)	0.404338
221748_s_at	TNS1	tensin 1	0.404758
225835_at	SLC12A2	solute carrier family 12 (sodium/potassium/chloride transporters), member 2	0.405116
204441_s_at	POLA2	polymerase (DNA directed), alpha 2, accessory subunit	0.405125
201752_s_at	ADD3	adducin 3 (gamma)	0.405258
213695_at	PON3	paraoxonase 3	0.405277
226350_at	CHML	choroideremia-like (Rab escort protein 2)	0.405423

1559005_s_at	CNTLN	centlein, centrosomal protein	0.405522
212494_at	TENC1	tensin like C1 domain containing phosphatase (tensin 2)	0.40577
218619_s_at	SUV39H1	suppressor of variegation 3-9 homolog 1 (Drosophila)	0.406139
231810_at	BRI3BP	BRI3 binding protein	0.406815
208596_s_at	UGT1A1///UGT1A1 0///UGT1A3///UGT 1A4///UGT1A5///U GT1A6///UGT1A7// /UGT1A8///UGT1A 9	UDP glucuronosyltransferase 1 family, polypeptide A1///UDP glucuronosyltransferase 1 family, polypeptide A10///UDP glucuronosyltransferase 1 family, polypeptide A3///UDP glucuronosyltransferase 1 family, polypeptide A4///UDP glucuronosyltransferase 1 family, polypeptide A5///UDP glucuronosyltransferase 1 family, polypeptide A6///UDP glucuronosyltransferase 1 family, polypeptide A7///UDP glucuronosyltransferase 1 family, polypeptide A8///UDP glucuronosyltransferase 1 family, polypeptide A9	0.406951
242560_at	FANCD2	Fanconi anemia, complementation group D2	0.406972
204378_at	BCAS1	breast carcinoma amplified sequence 1	0.407035
205253_at	PBX1	pre-B-cell leukemia homeobox 1	0.407599
238444_at	ZNF618	zinc finger protein 618	0.407715
204513_s_at	ELMO1	engulfment and cell motility 1	0.408173
230061_at	TM4SF18	transmembrane 4 L six family member 18	0.408308
225516_at	SLC7A2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	0.408572
235256_s_at	GALM	galactose mutarotase (aldose 1-epimerase)	0.408682
204920_at	CPS1	carbamoyl-phosphate synthase 1, mitochondrial	0.408936
238868_at	UACA	uveal autoantigen with coiled-coil domains and ankyrin repeats	0.409225
201906_s_at	CTDSPL	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	0.409383
225108_at	AGPS	alkylglycerone phosphate synthase	0.409426
232244_at	KIAA1161	KIAA1161	0.4095
205833_s_at	PART1	prostate androgen-regulated transcript 1 (non-protein coding)	0.409779
226402_at	CYP2U1	cytochrome P450, family 2, subfamily U, polypeptide 1	0.409998
204836_at	GLDC	glycine dehydrogenase (decarboxylating)	0.410388
218227_at	NUBP2	nucleotide binding protein 2	0.410462
1555486_a_at	PRR5L	proline rich 5 like	0.411081
205560_at	PCSK5	proprotein convertase subtilisin/kexin type 5	0.411208
222802_at	EDN1	endothelin 1	0.411242

204532_x_at	UGT1A1///UGT1A1 0///UGT1A4///UGT 1A6///UGT1A8///U GT1A9	UDP glucuronosyltransferase 1 family, polypeptide A1///UDP glucuronosyltransferase 1 family, polypeptide A10///UDP glucuronosyltransferase 1 family, polypeptide A4///UDP glucuronosyltransferase 1 family, polypeptide A6///UDP glucuronosyltransferase 1 family, polypeptide A8///UDP glucuronosyltransferase 1 family, polypeptide A9	0.41136
201904_s_at	CTDSPL	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	0.41158
202671_s_at	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	0.41163
222391_at	TMEM30A	transmembrane protein 30A	0.411654
208881_x_at	IDI1	isopentenyl-diphosphate delta isomerase 1	0.412396
209267_s_at	SLC39A8	solute carrier family 39 (zinc transporter), member 8	0.412464
1554768_a_at	MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	0.41259
212281_s_at	TMEM97	transmembrane protein 97	0.412944
211708_s_at	SCD	stearoyl-CoA desaturase (delta-9-desaturase)	0.413046
203968_s_at	CDC6	cell division cycle 6	0.413467
210540_s_at	B4GALT4	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 4	0.413524
226288_s_at	NLGN2	neuroligin 2	0.41364
205519_at	WDR76	WD repeat domain 76	0.413726
218493_at	SNRNP25	small nuclear ribonucleoprotein 25kDa (U11/U12)	0.41393
202183_s_at	KIF22	kinesin family member 22	0.413977
205311_at	DDC	dopa decarboxylase (aromatic L-amino acid decarboxylase)	0.413995
203856_at	VRK1	vaccinia related kinase 1	0.413995
228124_at	ABHD12	abhydrolase domain containing 12	0.414183
218585_s_at	DTL	denticleless E3 ubiquitin protein ligase homolog (Drosophila)	0.414989
204147_s_at	TFDP1	transcription factor Dp-1	0.415485
208998_at	UCP2	uncoupling protein 2 (mitochondrial, proton carrier)	0.415769
226961_at	PRR15	proline rich 15	0.415798
204510_at	CDC7	cell division cycle 7	0.416757
209408_at	KIF2C	kinesin family member 2C	0.417097
219428_s_at	PXMP4	peroxisomal membrane protein 4, 24kDa	0.417396
236029_at	FAT3	FAT atypical cadherin 3	0.417463
224944_at	TMPO	thymopoietin	0.417648
224659_at	SEPN1	selenoprotein N, 1	0.418099
211571_s_at	VCAN	versican	0.418191

219703_at	MNS1	meiosis-specific nuclear structural 1	0.418801
229506_at	PPM1L	protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent, 1L	0.419801
232278_s_at	DEPDC1	DEP domain containing 1	0.419873
1555867_at	GNG4	guanine nucleotide binding protein (G protein), gamma 4	0.419955
230165_at	SGOL2	shugoshin-like 2 (S. pombe)	0.420053
219523_s_at	TENM3	teneurin transmembrane protein 3	0.420244
204252_at	CDK2	cyclin-dependent kinase 2	0.420634
213344_s_at	H2AFX	H2A histone family, member X	0.421065
213712_at	ELOVL2	ELOVL fatty acid elongase 2	0.421117
218051_s_at	NT5DC2	5'-nucleotidase domain containing 2	0.421391
238945_at	ACER3	alkaline ceramidase 3	0.421451
220840_s_at	C1orf112	chromosome 1 open reading frame 112	0.421922
1557779_at	OTTHUMG000000 18252///RP11- 346D6.6	NULL///NULL	0.422256
219219_at	TMEM160	transmembrane protein 160	0.423028
222118_at	CENPN	centromere protein N	0.423258
232270_at	C9orf3///LOC10050 7319	chromosome 9 open reading frame 3///uncharacterized LOC100507319	0.423395
222895_s_at	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)	0.423617
235029_at	GINS4	GINS complex subunit 4 (Sld5 homolog)	0.42409
209709_s_at	HMMR	hyaluronan-mediated motility receptor (RHAMM)	0.424413
206837_at	ALX1	ALX homeobox 1	0.424422
225166_at	ARHGAP18	Rho GTPase activating protein 18	0.424602
228729_at	CCNB1	cyclin B1	0.424692
232238_at	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	0.424778
210447_at	GLUD2	glutamate dehydrogenase 2	0.425072
206316_s_at	KNTC1	kinetochore associated 1	0.425201
222492_at	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	0.425548
204092_s_at	AURKA	aurora kinase A	0.425667
223551_at	PKIB	protein kinase (cAMP-dependent, catalytic) inhibitor beta	0.425955
215646_s_at	VCAN	versican	0.426177
218108_at	UBR7	ubiquitin protein ligase E3 component n-recogin 7 (putative)	0.426262
212413_at		6-Sep septin 6	0.426735
1558487_a_at	TMED4	transmembrane emp24 protein transport domain containing 4	0.426936

204619_s_at	VCAN	versican	0.427632
1556629_a_at	SNAP25	synaptosomal-associated protein, 25kDa	0.427812
266_s_at	CD24	CD24 molecule	0.427915
227545_at	BARD1	BRCA1 associated RING domain 1	0.427993
205176_s_at	ITGB3BP	integrin beta 3 binding protein (beta3-endonexin)	0.428005
209389_x_at	DBI	diazepam binding inhibitor (GABA receptor modulator, acyl-CoA binding protein)	0.428405
201377_at	UBAP2L	ubiquitin associated protein 2-like	0.42897
205822_s_at	HMGCS1	3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble)	0.42929
218701_at	LACTB2	lactamase, beta 2	0.429399
224372_at	C10orf99///CCDC104 4///ND4	chromosome 10 open reading frame 99///coiled-coil domain containing 104///NADH dehydrogenase, subunit 4 (complex I)	0.429479
204240_s_at	SMC2	structural maintenance of chromosomes 2	0.429535
219588_s_at	NCAPG2	non-SMC condensin II complex, subunit G2	0.429573
218018_at	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase	0.429716
224856_at	FKBP5	FK506 binding protein 5	0.429966
208808_s_at	HMGB2	high mobility group box 2	0.430016
222958_s_at	DEPDC1	DEP domain containing 1	0.430021
238055_at	LOC100505549	uncharacterized LOC100505549	0.430505
202870_s_at	CDC20	cell division cycle 20	0.430702
223220_s_at	PARP9	poly (ADP-ribose) polymerase family, member 9	0.430703
243445_at	BNC2	basonuclin 2	0.43089
211088_s_at	PLK4	polo-like kinase 4	0.431287
211080_s_at	NEK2	NIMA-related kinase 2	0.431411
201896_s_at	PSRC1	proline/serine-rich coiled-coil 1	0.432032
205080_at	RARB	retinoic acid receptor, beta	0.432153
1556579_s_at	IGSF10	immunoglobulin superfamily, member 10	0.43242
211070_x_at	DBI	diazepam binding inhibitor (GABA receptor modulator, acyl-CoA binding protein)	0.432445
206884_s_at	SCEL	sciellin	0.432627
210956_at	LOC100996758///L OC101060446///NP Y4R	neuropeptide Y receptor type 4-like///neuropeptide Y receptor type 4-like///neuropeptide Y receptor Y4	0.43279
219306_at	KIF15	kinesin family member 15	0.432826
212282_at	TMEM97	transmembrane protein 97	0.432935
1552278_a_at	SLC46A1	solute carrier family 46 (folate transporter), member 1	0.432971
230720_at	RNF182	ring finger protein 182	0.433129

220327_at	VGLL3	vestigial like 3 (Drosophila)	0.433487
209008_x_at	KRT8	keratin 8	0.433525
35820_at	GM2A	GM2 ganglioside activator	0.433636
205406_s_at	SPA17	sperm autoantigenic protein 17	0.433701
232155_at	RNF213	ring finger protein 213	0.433755
226346_at	MEX3A	mex-3 homolog A (C. elegans)	0.434129
208650_s_at	CD24	CD24 molecule	0.434357
217099_s_at	GEMIN4	gem (nuclear organelle) associated protein 4	0.434628
203753_at	TCF4	transcription factor 4	0.434768
244153_at	ZNF207	zinc finger protein 207	0.434824
224954_at	SHMT1	serine hydroxymethyltransferase 1 (soluble)	0.434927
213599_at	OIP5	Opa interacting protein 5	0.43502
205759_s_at	SULT2B1	sulfotransferase family, cytosolic, 2B, member 1	0.43519
206347_at	PDK3	pyruvate dehydrogenase kinase, isozyme 3	0.435321
208079_s_at	AURKA	aurora kinase A	0.435448
235545_at	DEPDC1	DEP domain containing 1	0.435825
202240_at	PLK1	polo-like kinase 1	0.43592
227449_at	EPHA4	EPH receptor A4	0.435976
205441_at	OCEL1	occludin/ELL domain containing 1	0.435986
223599_at	TRIM6	tripartite motif containing 6	0.436346
215125_s_at	UGT1A1///UGT1A1 0///UGT1A3///UGT 1A4///UGT1A5///U GT1A6///UGT1A7// /UGT1A8///UGT1A 9	UDP glucuronosyltransferase 1 family, polypeptide A1///UDP glucuronosyltransferase 1 family, polypeptide A10///UDP glucuronosyltransferase 1 family, polypeptide A3///UDP glucuronosyltransferase 1 family, polypeptide A4///UDP glucuronosyltransferase 1 family, polypeptide A5///UDP glucuronosyltransferase 1 family, polypeptide A6///UDP glucuronosyltransferase 1 family, polypeptide A7///UDP glucuronosyltransferase 1 family, polypeptide A8///UDP glucuronosyltransferase 1 family, polypeptide A9	0.436452
202023_at	EFNA1	ephrin-A1	0.436702
211569_s_at	HADH	hydroxyacyl-CoA dehydrogenase	0.436818
226980_at	DEPDC1B	DEP domain containing 1B	0.436909
217520_x_at	LOC283683///LOC6 46278	uncharacterized LOC283683///programmed cell death 6 interacting protein pseudogene	0.436919
239824_s_at	TMEM107	transmembrane protein 107	0.436984
236115_at	HTR7P1	5-hydroxytryptamine (serotonin) receptor 7 pseudogene 1	0.437057
226661_at	CDCA2	cell division cycle associated 2	0.437373

230398_at	TNS4	tensin 4	0.437379
209642_at	BUB1	BUB1 mitotic checkpoint serine/threonine kinase	0.437962
202245_at	LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	0.438473
205609_at	ANGPT1	angiopoietin 1	0.438482
203637_s_at	MID1	midline 1 (Opitz/BBB syndrome)	0.438774
228273_at	PRR11	proline rich 11	0.438996
207030_s_at	CSRP2	cysteine and glycine-rich protein 2	0.439315
201625_s_at	INSIG1	insulin induced gene 1	0.439604
1552485_at	LACTB	lactamase, beta	0.439706
216952_s_at	LMNB2	lamin B2	0.439758
205053_at	PRIM1	primase, DNA, polypeptide 1 (49kDa)	0.439931
212386_at	TCF4	transcription factor 4	0.440156
1558501_at	DNM3	dynamamin 3	0.440444
227476_at	LPGAT1	lysophosphatidylglycerol acyltransferase 1	0.440648
204588_s_at	SLC7A7	solute carrier family 7 (amino acid transporter light chain, y+L system), member 7	0.440826
221305_s_at	UGT1A8///UGT1A9	UDP glucuronosyltransferase 1 family, polypeptide A8///UDP glucuronosyltransferase 1 family, polypeptide A9	0.441349
216733_s_at	GATM	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	0.441562
203210_s_at	RFC5	replication factor C (activator 1) 5, 36.5kDa	0.441921
223785_at	FANCI	Fanconi anemia, complementation group I	0.442378
212830_at	MEGF9	multiple EGF-like-domains 9	0.442722
212205_at	H2AFV	H2A histone family, member V	0.44356
209753_s_at	TMPO	thymopoietin	0.443701
218355_at	KIF4A	kinesin family member 4A	0.444412
216026_s_at	POLE	polymerase (DNA directed), epsilon, catalytic subunit	0.444483
240259_at	FLRT2///LOC100506718	fibronectin leucine rich transmembrane protein 2///uncharacterized LOC100506718	0.444759
235266_at	ATAD2	ATPase family, AAA domain containing 2	0.445086
212126_at	CBX5	chromobox homolog 5	0.445131
1569114_at	AC099850.1///OTT HUMG0000013207 9	NULL///NULL	0.44516
1557336_at	OTTHUMG000001 58739///RP11- 81N13.1	NULL///NULL	0.445177

204529_s_at	TOX	thymocyte selection-associated high mobility group box	0.445839
204558_at	RAD54L	RAD54-like (<i>S. cerevisiae</i>)	0.445875
202586_at	POLR2L	polymerase (RNA) II (DNA directed) polypeptide L, 7.6kDa	0.445938
225716_at	BRI3BP	BRI3 binding protein	0.446144
205990_s_at	WNT5A	wingless-type MMTV integration site family, member 5A	0.446285
222146_s_at	TCF4	transcription factor 4	0.446305
219262_at	SUV39H2	suppressor of variegation 3-9 homolog 2 (<i>Drosophila</i>)	0.44645
226390_at	STARD4	StAR-related lipid transfer (START) domain containing 4	0.446472
228530_at	MZT1	mitotic spindle organizing protein 1	0.446595
235678_at	GM2A	GM2 ganglioside activator	0.446973
219630_at	PDZK1IP1	PDZK1 interacting protein 1	0.447336
227420_at	TNFAIP8L1	tumor necrosis factor, alpha-induced protein 8-like 1	0.447442
218542_at	CEP55	centrosomal protein 55kDa	0.447517
225968_at	PRICKLE2	prickle homolog 2 (<i>Drosophila</i>)	0.44761
229305_at	MLF1IP	MLF1 interacting protein	0.447635
230696_at	LOC100289092	uncharacterized LOC100289092	0.447893
219038_at	MORC4	MORC family CW-type zinc finger 4	0.447917
227197_at	ARHGEF26	Rho guanine nucleotide exchange factor (GEF) 26	0.448882
225592_at	NRM	nurim (nuclear envelope membrane protein)	0.44899
227211_at	PHF19	PHD finger protein 19	0.449117
226010_at	SLC25A23	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23	0.449153
218693_at	TSPAN15	tetraspanin 15	0.449196
225650_at	SAMD1	sterile alpha motif domain containing 1	0.449343
212279_at	TMEM97	transmembrane protein 97	0.449612
204717_s_at	SLC29A2	solute carrier family 29 (nucleoside transporters), member 2	0.449869
1553569_at	COX2///OAF///TLE 1	cytochrome c oxidase subunit II///OAF homolog (<i>Drosophila</i>)///transducin-like enhancer of split 1 (E(sp1) homolog, <i>Drosophila</i>)	0.449877
213647_at	DNA2	DNA replication helicase/nuclease 2	0.449979
240806_at	RPL15	ribosomal protein L15	0.450067
238756_at	GAS2L3	growth arrest-specific 2 like 3	0.450252
212387_at	TCF4	transcription factor 4	0.450975
218309_at	CAMK2N1	calcium/calmodulin-dependent protein kinase II inhibitor 1	0.451267
230738_at	OTTHUMG000001 78927///RP11-	NULL///NULL	0.451313

	196G18.23		
203186_s_at	S100A4	S100 calcium binding protein A4	0.451315
1553690_at	SGOL1	shugoshin-like 1 (<i>S. pombe</i>)	0.451369
201036_s_at	HADH	hydroxyacyl-CoA dehydrogenase	0.451481
222077_s_at	RACGAP1	Rac GTPase activating protein 1	0.451615
208651_x_at	CD24	CD24 molecule	0.451936
1553810_a_at	KIAA1524	KIAA1524	0.452008
228959_at	PDK3	pyruvate dehydrogenase kinase, isozyme 3	0.452428
228654_at	SPIN4	spindlin family, member 4	0.452574
1555758_a_at	CDKN3	cyclin-dependent kinase inhibitor 3	0.452578
210380_s_at	CACNA1G	calcium channel, voltage-dependent, T type, alpha 1G subunit	0.452644
228039_at	DDX46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	0.452743
212385_at	TCF4	transcription factor 4	0.452896
1553551_s_at	ND2	MTND2	0.453234
226590_at	ZNF618	zinc finger protein 618	0.453759
224909_s_at	PREX1	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1	0.453819
227678_at	XRCC6BP1	XRCC6 binding protein 1	0.453842
230592_at	NSL1	NSL1, MIND kinetochore complex component, homolog (<i>S. cerevisiae</i>)	0.454018
234987_at	SAMHD1	SAM domain and HD domain 1	0.454129
238443_at	TFAM	transcription factor A, mitochondrial	0.454181
213587_s_at	ATP6V0E2	ATPase, H ⁺ transporting V0 subunit e2	0.454356
205339_at	STIL	SCL/TAL1 interrupting locus	0.454553
211767_at	GINS4	GINS complex subunit 4 (<i>Sld5</i> homolog)	0.454618
223545_at	FANCD2	Fanconi anemia, complementation group D2	0.454887
51192_at	SSH3	slingshot protein phosphatase 3	0.455404
226355_at	POC1A	POC1 centriolar protein homolog A (<i>Chlamydomonas</i>)	0.45549
206805_at	SEMA3A	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	0.45557
207717_s_at	PKP2	plakophilin 2	0.455601
202705_at	CCNB2	cyclin B2	0.455722
202126_at	PRPF4B	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	0.456693
229459_at	FAM19A5	family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	0.457216
226234_at	GDF11	growth differentiation factor 11	0.457458
219612_s_at	FGG	fibrinogen gamma chain	0.457687

234936_s_at	CC2D2A	coiled-coil and C2 domain containing 2A	0.457904
203975_s_at	CHAF1A	chromatin assembly factor 1, subunit A (p150)	0.457916
204775_at	CHAF1B	chromatin assembly factor 1, subunit B (p60)	0.458109
241710_at	LOC728819	hCG1645220	0.458156
226029_at	VANGL2	VANGL planar cell polarity protein 2	0.458615
235919_at	CEP78	centrosomal protein 78kDa	0.458665
202464_s_at	PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	0.45875
228821_at	ST6GAL2	ST6 beta-galactosamide alpha-2,6-sialyltransferase 2	0.458802
209771_x_at	CD24	CD24 molecule	0.458872
219738_s_at	PCDH9	protocadherin 9	0.458995
232067_at	FAXC	failed axon connections homolog (Drosophila)	0.460569
229189_s_at	LOC100507376	uncharacterized LOC100507376	0.461419
243688_at	MGC45800	uncharacterized LOC90768	0.461595
209608_s_at	ACAT2	acetyl-CoA acetyltransferase 2	0.462467
209031_at	CADM1	cell adhesion molecule 1	0.462488
214710_s_at	CCNB1	cyclin B1	0.462761
202546_at	VAMP8	vesicle-associated membrane protein 8	0.463274
225777_at	SAPCD2	suppressor APC domain containing 2	0.463379
226287_at	CCDC34	coiled-coil domain containing 34	0.463381
208511_at	PTTG3P	pituitary tumor-transforming 3, pseudogene	0.463417
240382_at	OTTHUMG000001	NULL//NULL	0.463484
	75897//RP3-		
	512B11.3		
231472_at	FBXO15	F-box protein 15	0.463881
214295_at	KIAA0485	uncharacterized LOC57235	0.464042
212737_at	GM2A	GM2 ganglioside activator	0.464091
207126_x_at	UGT1A1//UGT1A1	UDP glucuronosyltransferase 1 family, polypeptide	0.464119
	0//UGT1A4//UGT	A1//UDP glucuronosyltransferase 1 family, polypeptide	
	1A6//UGT1A8//U	A10//UDP glucuronosyltransferase 1 family, polypeptide	
	GT1A9	A4//UDP glucuronosyltransferase 1 family, polypeptide	
		A6//UDP glucuronosyltransferase 1 family, polypeptide	
		A8//UDP glucuronosyltransferase 1 family, polypeptide	
		A9	
220223_at	ATAD5	ATPase family, AAA domain containing 5	0.464203
201015_s_at	JUP	junction plakoglobin	0.464496
221909_at	RNFT2	ring finger protein, transmembrane 2	0.464542
1556821_x_at	DLEU2	deleted in lymphocytic leukemia 2 (non-protein coding)	0.464704
222482_at	SSBP3	single stranded DNA binding protein 3	0.465048

209714_s_at	CDKN3	cyclin-dependent kinase inhibitor 3	0.465194
213429_at	BICC1	bicaudal C homolog 1 (Drosophila)	0.465228
205085_at	ORC1	origin recognition complex, subunit 1	0.465253
201697_s_at	DNMT1	DNA (cytosine-5-)-methyltransferase 1	0.46551
224734_at	HMGB1	high mobility group box 1	0.465513
216870_x_at	DLEU2	deleted in lymphocytic leukemia 2 (non-protein coding)	0.465749
204646_at	DPYD	dihydropyrimidine dehydrogenase	0.465766
218966_at	MYO5C	myosin VC	0.465857
208549_x_at	PTMA	prothymosin, alpha	0.466212
203911_at	RAP1GAP	RAP1 GTPase activating protein	0.466656
203302_at	DCK	deoxycytidine kinase	0.467212
220885_s_at	CENPJ	centromere protein J	0.467318
1552370_at	C4orf33	chromosome 4 open reading frame 33	0.467331
220060_s_at	PARPBP	PARP1 binding protein	0.467347
235970_at	LCORL	ligand dependent nuclear receptor corepressor-like	0.467407
207747_s_at	DOK4	docking protein 4	0.467931
227236_at	TSPAN2	tetraspanin 2	0.468254
204547_at	RAB40B	RAB40B, member RAS oncogene family	0.468732
218717_s_at	LEPREL1	leprecan-like 1	0.468894
207052_at	HAVCR1	hepatitis A virus cellular receptor 1	0.468919
204492_at	ARHGAP11A	Rho GTPase activating protein 11A	0.46898
222848_at	CENPK	centromere protein K	0.469243
201202_at	PCNA	proliferating cell nuclear antigen	0.469321
224964_s_at	GNG2	guanine nucleotide binding protein (G protein), gamma 2	0.469491
225182_at	TMEM50B	transmembrane protein 50B	0.469604
207559_s_at	ZMYM3	zinc finger, MYM-type 3	0.469653
205229_s_at	COCH	cochlin	0.469849
234974_at	GALM	galactose mutarotase (aldose 1-epimerase)	0.470236
206027_at	S100A3	S100 calcium binding protein A3	0.470646
218500_at	THEM6	thioesterase superfamily member 6	0.470681
1552256_a_at	SCARB1	scavenger receptor class B, member 1	0.470759
242979_at	IRS1	insulin receptor substrate 1	0.470903
235846_at	FSBP///RAD54B	fibrinogen silencer binding protein///RAD54 homolog B (<i>S. cerevisiae</i>)	0.471206
213839_at	CLMN	calmin (calponin-like, transmembrane)	0.471326
224693_at	FAM210B	family with sequence similarity 210, member B	0.471797
204620_s_at	VCAN	versican	0.472196
204033_at	TRIP13	thyroid hormone receptor interactor 13	0.472524

206094_x_at	UGT1A1///UGT1A10///UGT1A3///UGT1A4///UGT1A5///UGT1A6///UGT1A7///UGT1A8///UGT1A9	UDP glucuronosyltransferase 1 family, polypeptide A1///UDP glucuronosyltransferase 1 family, polypeptide A10///UDP glucuronosyltransferase 1 family, polypeptide A3///UDP glucuronosyltransferase 1 family, polypeptide A4///UDP glucuronosyltransferase 1 family, polypeptide A5///UDP glucuronosyltransferase 1 family, polypeptide A6///UDP glucuronosyltransferase 1 family, polypeptide A7///UDP glucuronosyltransferase 1 family, polypeptide A8///UDP glucuronosyltransferase 1 family, polypeptide A9	0.472652
220945_x_at	MANSC1	MANSC domain containing 1	0.472656
225759_x_at	CLMN	calmin (calponin-like, transmembrane)	0.472723
230312_at	LOC100507312	uncharacterized LOC100507312	0.472796
237159_x_at	AP1S3	adaptor-related protein complex 1, sigma 3 subunit	0.472807
1553570_x_at	COX2///OAF///TLE1	cytochrome c oxidase subunit II///OAF homolog (Drosophila)///transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	0.473044
210006_at	ABHD14A	abhydrolase domain containing 14A	0.473113
204315_s_at	GTSE1	G-2 and S-phase expressed 1	0.473198
211040_x_at	GTSE1	G-2 and S-phase expressed 1	0.47349
226630_at	MIS18BP1	MIS18 binding protein 1	0.473565
201759_at	TBCD	tubulin folding cofactor D	0.473654
243582_at	SH3RF2	SH3 domain containing ring finger 2	0.474208
212361_s_at	ATP2A2	ATPase, Ca ²⁺ transporting, cardiac muscle, slow twitch 2	0.474225
212372_at	MYH10	myosin, heavy chain 10, non-muscle	0.474301
219663_s_at	TMEM121	transmembrane protein 121	0.474361
204579_at	FGFR4	fibroblast growth factor receptor 4	0.474362
204641_at	NEK2	NIMA-related kinase 2	0.474435
218904_s_at	C9orf40	chromosome 9 open reading frame 40	0.474455
224950_at	PTGFRN	prostaglandin F2 receptor inhibitor	0.47447
213666_at	6-Sep	septin 6	0.474844
231846_at	FOXRED2	FAD-dependent oxidoreductase domain containing 2	0.474995
217905_at	MCMBP	minichromosome maintenance complex binding protein	0.475188
205141_at	ANG	angiogenin, ribonuclease, RNase A family, 5	0.475499
205769_at	SLC27A2	solute carrier family 27 (fatty acid transporter), member 2	0.475534
229002_at	FAM69B	family with sequence similarity 69, member B	0.475636
227055_at	METTL7B	methyltransferase like 7B	0.47603
228949_at	WLS	wntless homolog (Drosophila)	0.476506

235964_x_at	SAMHD1	SAM domain and HD domain 1	0.477091
229513_at	STRBP	spermatid perinuclear RNA binding protein	0.477212
218300_at	PAGR1	PAXIP1 associated glutamate-rich protein 1	0.477351
201510_at	ELF3	E74-like factor 3 (ets domain transcription factor, epithelial-specific)	0.477625
228255_at	TMEM237	transmembrane protein 237	0.477773
202950_at	CRYZ	crystallin, zeta (quinone reductase)	0.478561
213397_x_at	RNASE4	ribonuclease, RNase A family, 4	0.478849
202308_at	SREBF1	sterol regulatory element binding transcription factor 1	0.479131
206204_at	GRB14	growth factor receptor-bound protein 14	0.47928
226990_at	CAPRN1	cell cycle associated protein 1	0.479994
230109_at	PDE7B	phosphodiesterase 7B	0.480108
209691_s_at	DOK4	docking protein 4	0.480218
224947_at	RNF26	ring finger protein 26	0.480302
216379_x_at	CD24	CD24 molecule	0.480649
221258_s_at	KIF18A	kinesin family member 18A	0.481609
1565951_s_at	CHML	choroideremia-like (Rab escort protein 2)	0.481737
234733_s_at	FANCM	Fanconi anemia, complementation group M	0.481969
213582_at	ATP11A	ATPase, class VI, type 11A	0.482397
223707_at	RPL27A//SNORA3	ribosomal protein L27a//small nucleolar RNA, H/ACA box 3	0.482792
230772_at	HNF4A	hepatocyte nuclear factor 4, alpha	0.48283
211719_x_at	FN1	fibronectin 1	0.483032
228168_at	ATP5G3	ATP synthase, H ⁺ transporting, mitochondrial Fo complex, subunit C3 (subunit 9)	0.483094
205189_s_at	FANCC	Fanconi anemia, complementation group C	0.483388
210495_x_at	FN1	fibronectin 1	0.483577
225298_at	PNKD	paroxysmal nonkinesigenic dyskinesia	0.483612
227212_s_at	PHF19	PHD finger protein 19	0.483631
213358_at	SOGA2	SOGA family member 2	0.483808
203217_s_at	ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	0.483908
208956_x_at	DUT	deoxyuridine triphosphatase	0.484111
209108_at	TSPAN6	tetraspanin 6	0.484634
209048_s_at	ZMYND8	zinc finger, MYND-type containing 8	0.48529
212067_s_at	C1R	complement component 1, r subcomponent	0.485293
204825_at	MELK	maternal embryonic leucine zipper kinase	0.485319
236208_at	MOCS2	molybdenum cofactor synthesis 2	0.485401
208107_s_at	LOC81691	exonuclease NEF-sp	0.485638

213534_s_at	PASK	PAS domain containing serine/threonine kinase	0.485949
243176_at	ARL5A	ADP-ribosylation factor-like 5A	0.485995
221750_at	HMGCS1	3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble)	0.486689
218529_at	CD320	CD320 molecule	0.486833
223385_at	CYP2S1	cytochrome P450, family 2, subfamily S, polypeptide 1	0.487463
203560_at	GGH	gamma-glutamyl hydrolase (conjugase, foylpolymagglutamyl hydrolase)	0.487526
215215_s_at	LOC81691	exonuclease NEF-sp	0.487598
210871_x_at	SSX2IP	synovial sarcoma, X breakpoint 2 interacting protein	0.487667
228559_at	CENPN	centromere protein N	0.487739
219416_at	SCARA3	scavenger receptor class A, member 3	0.487832
226278_at	SVIP	small VCP/p97-interacting protein	0.48806
230793_at	LRRRC16A	leucine rich repeat containing 16A	0.488132
227262_at	HAPLN3	hyaluronan and proteoglycan link protein 3	0.488597
202954_at	UBE2C	ubiquitin-conjugating enzyme E2C	0.489045
229269_x_at	SSBP4	single stranded DNA binding protein 4	0.489329
1554242_a_at	COCH	cochlin	0.489837
239272_at	MMP28	matrix metalloproteinase 28	0.490138
212876_at	B4GALT4	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 4	0.490333
228205_at	TKT	transketolase	0.490523
31874_at	GAS2L1	growth arrest-specific 2 like 1	0.491256
228381_at	ATF7IP2///LOC100287628	activating transcription factor 7 interacting protein 2///uncharacterized LOC100287628	0.491528
216508_x_at	HMGB1P4///HMGB1P4	high mobility group box 1 pseudogene 4///NULL	0.491701
202428_x_at	DBI	diazepam binding inhibitor (GABA receptor modulator, acyl-CoA binding protein)	0.491762
213899_at	METAP2	methionyl aminopeptidase 2	0.492001
210046_s_at	IDH2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	0.492389
1553538_s_at	COX1	cytochrome c oxidase subunit I	0.492512
222809_x_at	CCDC85C	coiled-coil domain containing 85C	0.492553
219070_s_at	MOSPD3	motile sperm domain containing 3	0.492967
228298_at	PCED1B	PC-esterase domain containing 1B	0.493215
206006_s_at	KIAA1009	KIAA1009	0.493481
210007_s_at	GPD2	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	0.49353
229006_at	LOC100507487	uncharacterized LOC100507487	0.494229
213067_at	MYH10	myosin, heavy chain 10, non-muscle	0.494245

225684_at	SKA2	spindle and kinetochore associated complex subunit 2	0.494518
203046_s_at	TIMELESS	timeless circadian clock	0.494824
213379_at	COQ2	coenzyme Q2 4-hydroxybenzoate polyprenyltransferase	0.494862
227502_at	OTTHUMG000001 57537///RP5- 894A10.2	NULL//NULL	0.494989
225173_at	ARHGAP18	Rho GTPase activating protein 18	0.495176
221245_s_at	FZD5	frizzled family receptor 5	0.495498
203474_at	IQGAP2	IQ motif containing GTPase activating protein 2	0.495744
223513_at	CENPJ	centromere protein J	0.495836
203554_x_at	PTTG1	pituitary tumor-transforming 1	0.496641
228542_at	MRS2	MRS2 magnesium transporter	0.497372
202145_at	LY6E	lymphocyte antigen 6 complex, locus E	0.497635
1555123_at	ST6GAL2	ST6 beta-galactosamide alpha-2,6-sialyltransferase 2	0.497699
219448_at	TMEM70	transmembrane protein 70	0.4978
229338_at	LOC100289361	uncharacterized LOC100289361	0.497817
209780_at	PHTF2	putative homeodomain transcription factor 2	0.498279
212218_s_at	FASN	fatty acid synthase	0.498531
222805_at	MANEA	mannosidase, endo-alpha	0.498603
214439_x_at	BIN1	bridging integrator 1	0.498947
201663_s_at	SMC4	structural maintenance of chromosomes 4	0.499294
227983_at	RILPL2	Rab interacting lysosomal protein-like 2	0.499755
203722_at	ALDH4A1	aldehyde dehydrogenase 4 family, member A1	0.499927
214814_at	YTHDC1	YTH domain containing 1	0.499964

Table S7 Top 10 pharmaceutical perturbagens displaying positive correlation with **2** identified by the Connectivity Map (cmap) analysis

Rank	Cmap name	Score	Description
1	Spiperone	1	D2 dopamine receptor agonist
2	Thioridazine	0.984	D2 dopamine receptor agonist
3	Celastrol	0.981	Proteasome inhibitor
4	MG-262	0.978	Proteasome inhibitor
5	15-delta prostaglandin J2	0.978	Specific activator of the peroxisome proliferator-activated receptor gamma (PPAR- γ)
6	5224221	0.938	N/A
7	Pyruvium	0.926	Inhibitor of mitochondrial respiration
8	Ivermectin	0.919	Selectively and high-affinity binder of glutamate-gated chloride channels (GluCl _s)
9	Prenylamine	0.913	Calcium channel blocker
10	Phenoxybenzamine	0.91	Adrenergic alpha-antagonist

Table S8 Top 25 GO terms enriched with differentially expressed genes with corresponding Fisher's exact test with a multiple testing correction

GO term	category	p-value	False discovery rate (FDR)	The number of differentially expressed genes in this term
Mitotic cell cycle	Biological process	1.92E-27	8.68E-24	100
Mitotic nuclear division	Biological process	2.17E-16	4.92E-13	57
Nucleoplasm	Cellular component	3.04E-12	4.58E-09	128
DNA replication	Biological process	6.63E-12	7.50E-09	35
Chromosome, centromeric region	Cellular component	2.03E-11	1.84E-08	22
Kinetochores	Cellular component	6.52E-11	4.92E-08	27
G-protein coupled receptor activity	Molecular function	7.14E-11	4.62E-08	5
DNA strand elongation involved in DNA replication	Biological process	1.56E-10	8.84E-08	17
G-protein coupled receptor signaling pathway	Biological process	2.78E-10	1.40E-07	12
Chromosome segregation	Biological process	1.02E-09	4.63E-07	22
G1/S transition of mitotic cell cycle	Biological process	1.12E-09	4.61E-07	34
Mitotic sister chromatid segregation	Biological process	3.38E-09	1.28E-06	13
Cytosol	Cellular component	8.21E-09	2.86E-06	224
DNA replication initiation	Biological process	1.24E-07	4.00E-05	12
DNA repair	Biological process	1.91E-07	5.77E-05	42
Spindle	Cellular component	1.92E-07	5.43E-05	18
Microtubule binding	Molecular function	2.52E-07	6.72E-05	30
Regulation of transcription involved in G1/S transition of mitotic cell cycle	Biological process	5.43E-07	1.37E-04	11
Protein binding	Molecular function	9.40E-07	2.24E-04	477
Cell proliferation	Biological process	1.29E-06	2.91E-04	47
Spindle microtubule	Cellular component	1.99E-06	4.28E-04	12
Spindle pole	Cellular component	2.27E-06	4.66E-04	16
Telomere maintenance via semi-conservative replication	Biological process	2.36E-06	4.65E-04	10
Oocyte maturation	Biological process	2.39E-06	4.50E-04	9
Nucleolus	Cellular component	2.98E-06	5.40E-04	145

Table S9 Kyoto encyclopedia of Genes and Genomes (KEGG) pathways enriched with differentially expressed genes with corresponding Fisher's exact test p values < 0.05.

Pathway name	Pathway classification	p-value	FDR	The number of differentially expressed genes in this pathway	Ratio ^a
Cell cycle	Cellular Processes; Cell growth and death	2.52E-13	6.55E-11	36	0.290
DNA replication	Genetic Information Processing; Replication and repair	1.37E-10	1.78E-08	17	0.472
p53 signaling pathway	Cellular Processes; Cell growth and death	7.34E-06	0.000637	16	0.235
TNF signaling pathway	Environmental Information Processing; Signal transduction	2.09E-03	0.07747	16	0.145
One carbon pool by folate	Metabolism; Metabolism of cofactors and vitamins	4.06E-03	0.105562	5	0.250
Ribosome	Genetic Information Processing; Translation	4.10E-03	0.096836	1	0.007
D-Glutamine and D-glutamate metabolism	Metabolism; Metabolism of other amino acids	4.55E-03	0.098476	2	0.500
Alanine, aspartate and glutamate metabolism	Metabolism; Amino acid metabolism	5.15E-03	0.103075	7	0.194
Glycosaminoglycan biosynthesis - keratan sulfate	Metabolism; Glycan biosynthesis and metabolism	6.05E-03	0.112387	4	0.267
Pyrimidine metabolism	Metabolism; Nucleotide metabolism	8.01E-03	0.138874	14	0.133
Base excision repair	Genetic Information Processing; Replication and repair	1.19E-02	0.192785	6	0.182
FoxO signaling pathway	Environmental Information Processing; Signal transduction	1.35E-02	0.206175	16	0.120
Fatty acid biosynthesis	Metabolism; Lipid metabolism	1.40E-02	0.191025	2	0.333
Butanoate metabolism	Metabolism; Carbohydrate metabolism	1.42E-02	0.184938	5	0.192

Natural killer cell mediated cytotoxicity	Organismal Systems; Immune system	1.94E-02	0.229206	2	0.015
Tight junction	Cellular Processes; Cellular commiunity	1.94E-02	0.240121	2	0.015
Folate biosynthesis	Metabolism; Metabolism of cofactors and vitamins	2.60E-02	0.260466	3	0.214
Fatty acid metabolism	Metabolism; Overview	2.66E-02	0.255976	7	0.146
Pathways in cancer	Human Diseases; Cancers	3.03E-02	0.281658	31	0.095
NF-kappa B signaling pathway	Environmental Information Processing; Signal transduction	3.24E-02	0.280621	11	0.121
Glycosphingolipid biosynthesis - ganglio series	Metabolism; Glycan biosynthesis and metabolism	3.27E-02	0.273989	3	0.200
Arginine and proline metabolism	Metabolism; Amino acid metabolism	3.33E-02	0.270908	8	0.133
Mismatch repair	Genetic Information Processing; Replication and repair	3.39E-02	0.267267	4	0.174
Wnt signaling pathway	Environmental Information Processing; Signal transduction	3.99E-02	0.287977	15	0.108
Synthesis and degradation of ketone bodies	Metabolism; Lipid metabolism	4.10E-02	0.287773	2	0.222
mRNA surveillance pathway	Genetic Information Processing; Translation	4.31E-02	0.280182	1	0.011
2-Oxocarboxylic acid metabolism	Metabolism; Overview	4.88E-02	0.302333	3	0.176
RNA transport	Genetic Information Processing; Translation	4.89E-02	0.295868	4	0.025

^a The ratio is calculated by dividing the number of differentially expressed genes found in the pathway by the total number of genes involved in this pathway.

Table S10 Primers and sequences of the selected genes studied in RT-PCR

Primer Name	Sequence(5'to3')
PCNA_at-F	TGCAGATGTACCCCTTGTTG
PCNA_at-R	CCTTCTTCATCCTCGATCTTG
CCND3_at-F	CTTTGAGCACAACTTTAAGAGGACAT
CCND3_at-R	AAGGGAGGAAAACAGCAACCA
RRM2_at-F	GGCTTTGTCTTGCATTGTGA
RRM2_at-R	GCTGGCAGAAGTTAATCCTCA
CDKN1A_at-F	CAGCGACCTTCCTCATCCA
CDKN1A_at-R	TCCTTGTTCCGCTGCTAATCA
DHFR_at-F	TTTGGAAAAACCCATGAAGG
DHFR_at-R	TGGCTCCAAAAGTCTTACAATG
GLS_at-F	CACTGCCCTCCCATTACCTA
GLS_at-R	AAGCTCAAGCATGGGAACAG
GADD45A_at-F	GGGCTGAGTGAGTTCAACTACATG
GADD45A_at-R	CCTTCTTCATTTTCACCTCTTTCC
TFDP1_at-F	TGCCGAAGACCTTAAAATGG
TFDP1_at-R	TTCCCTGAGCCATTTCTGTC
CDK2_at-F	TCTGACGTCCACCTCCTACC
CDK2_at-R	TTTTACCCATGCCCTCACTC
PMAIP1_at-F	CTGGCCTACTGTGAAGGGAGAT
PMAIP1_at-R	AAACACCAAAAACAGCAACAACA
CDC25A_at-F	TCTCTCCCCTCTTACCTCAACTTC
CDC25A_at-R	TCAAACCCGTAACACAGCAACT
GADD45B_at-F	CGCCCTGCAAATCCACTT
GADD45B_at-R	ACCCGCACGATGTTGATGT
GLUD2_at-F	GGAAGGGACAGTCAAGAGCA
GLUD2_at-R	CTGAAAAGGCCACACACCTT
CCNE2_at-F	TCAGAAAAGGGGGACAGTTG
CCNE2_at-R	TGCTCTTCGGTGGTGTGATA
SESN2_at-F	AAGATCAGGGACCCCATTTTC
SESN2_at-R	CAGGAGAGGGGACAGATGAG
E2F2_at-F	GGTGTCCCTTTTCCACAGTAATG

E2F2_at-R	AAGCTTGACCACCTCCCTCTTC
TYMS_at-F	ATCAAGGGATCCACAAATGC
TYMS_at-R	AGGCTGTCCAAAAAGTCTCG
TP53_at-F	GACTGGGTCTCGCTTTGTTG
TP53_at-R	TGCAGTAAGCCAAGATCACG
RB1_at-F	CTCCATTTTCATCATTGTTTCTGC
RB1_at-R	CACGATCTCTGAAGTTCCTAAAA
BAX_at-F	CCAAGAAGCTGAGCGAGTGT
BAX_at-R	ATCCTCTGCAGCTCCATGTT
BCL2_at-F	GGCCCTCCAGATAGCTCATT
BCL2_at-R	TCCCCAAAAGAAATGCAATC
gapdh(Hs)Forward Primer	TGACTTCAACAGCGACACCCA
gapdh(Hs)Reverse Primer	CACCCTGTTGCTGTAGCCAAA

Table S11 Functions of the selected genes studied in RT-PCR^a

Gene Name	Functions
TP53	This gene encodes a tumor suppressor protein containing transcriptional activation, DNA binding, and oligomerization domains. The encoded protein responds to diverse cellular stresses to regulate expression of target genes, thereby inducing cell cycle arrest, apoptosis, senescence, DNA repair, or changes in metabolism. Mutations in this gene are associated with a variety of human cancers, including hereditary cancers such as Li-Fraumeni syndrome. Alternative splicing of this gene and the use of alternate promoters result in multiple transcript variants and isoforms. Additional isoforms have also been shown to result from the use of alternate translation initiation codons.
CDKN1A	This gene encodes a potent cyclin-dependent kinase inhibitor. The encoded protein binds to and inhibits the activity of cyclin-cyclin-dependent kinase2 or -cyclin-dependent kinase4 complexes, and thus functions as a regulator of cell cycle progression at G1. The expression of this gene is tightly controlled by the tumor suppressor protein p53, through which this protein mediates the p53-dependent cell cycle G1 phase arrest in response to a variety of stress stimuli. This protein can interact with proliferating cell nuclear antigen, a DNA polymerase accessory factor, and plays a regulatory role in S phase DNA replication and DNA damage repair. This protein was reported to be specifically cleaved by CASP3-like caspases, which thus leads to a dramatic activation of cyclin-dependent kinase2, and may be instrumental in the execution of apoptosis following caspase activation. Mice that lack this gene have the ability to regenerate damaged or missing tissue. Multiple alternatively spliced variants have been found for this gene.
PCNA	The protein encoded by this gene is found in the nucleus and is a cofactor of DNA polymerase delta. The encoded protein acts as a homotrimer and helps increase the processivity of leading strand synthesis during DNA replication. In response to DNA damage, this protein is ubiquitinated and is involved in the RAD6-dependent DNA repair pathway. Two transcript variants encoding the same protein have been found for this gene. Pseudogenes of this gene have been described on chromosome 4 and on the X chromosome.
GADD45A	This gene is a member of a group of genes whose transcript levels are increased following stressful growth arrest conditions and treatment with DNA-damaging

agents. The protein encoded by this gene responds to environmental stresses by mediating activation of the p38/JNK pathway via MTK1/MEKK4 kinase. The DNA damage-induced transcription of this gene is mediated by both p53-dependent and -independent mechanisms. Alternatively spliced transcript variants encoding distinct isoforms have been found for this gene.

- GADD45B** This gene is a member of a group of genes whose transcript levels are increased following stressful growth arrest conditions and treatment with DNA-damaging agents. The genes in this group respond to environmental stresses by mediating activation of the p38/JNK pathway. This activation is mediated via their proteins binding and activating MTK1/MEKK4 kinase, which is an upstream activator of both p38 and JNK MAPKs. The function of these genes or their protein products is involved in the regulation of growth and apoptosis. These genes are regulated by different mechanisms, but they are often coordinately expressed and can function cooperatively in inhibiting cell growth.
- SESN2** This gene encodes a member of the sestrin family of PA26-related proteins. The encoded protein may function in the regulation of cell growth and survival. This protein may be involved in cellular response to different stress conditions.
- DHFR** Dihydrofolate reductase converts dihydrofolate into tetrahydrofolate, a methyl group shuttle required for the de novo synthesis of purines, thymidylic acid, and certain amino acids. While the functional dihydrofolate reductase gene has been mapped to chromosome 5, multiple intronless processed pseudogenes or dihydrofolate reductase-like genes have been identified on separate chromosomes. Dihydrofolate reductase deficiency has been linked to megaloblastic anemia. Several transcript variants encoding different isoforms have been found for this gene.
- TYMS** Thymidylate synthase catalyzes the methylation of deoxyuridylate to deoxythymidylate using 5,10-methylenetetrahydrofolate (methylene-THF) as a cofactor. This function maintains the dTMP (thymidine-5-prime monophosphate) pool critical for DNA replication and repair. The enzyme has been of interest as a target for cancer chemotherapeutic agents. It is considered to be the primary site of action for 5-fluorouracil, 5-fluoro-2-prime-deoxyuridine, and some folate analogs. Expression of this gene and that of a naturally occurring antisense transcript rTSalpha (GeneID:55556) vary inversely when cell-growth progresses from late-log to plateau phase.

- RRM2** This gene encodes one of two non-identical subunits for ribonucleotide reductase. This reductase catalyzes the formation of deoxyribonucleotides from ribonucleotides. Synthesis of the encoded protein (M2) is regulated in a cell-cycle dependent fashion. Transcription from this gene can initiate from alternative promoters, which results in two isoforms that differ in the lengths of their N-termini. Related pseudogenes have been identified on chromosomes 1 and X.
- GLS** This gene encodes the K-type mitochondrial glutaminase. The encoded protein is an phosphate-activated amidohydrolase that catalyzes the hydrolysis of glutamine to glutamate and ammonia. This protein is primarily expressed in the brain and kidney plays an essential role in generating energy for metabolism, synthesizing the brain neurotransmitter glutamate and maintaining acid-base balance in the kidney. Alternate splicing results in multiple transcript variants.
- GLUD2** The protein encoded by this gene is localized to the mitochondrion and acts as a homohexamer to recycle glutamate during neurotransmission. The encoded enzyme catalyzes the reversible oxidative deamination of glutamate to alpha-ketoglutarate. This gene is intronless.
- PMAIP1** The protein encoded by this gene is termed Noxa. Noxa transcription and protein expression can be activated by multiple apoptotic signals in a p53-dependent as well as -independent manner. Overexpressed Noxa protein localizes preferentially to mitochondria and promotes mitochondrial dysfunction, which exerts its proapoptotic function mainly by neutralizing the prosurvival Bcl2 proteins Mcl1/A1, facilitating activation of Bax and/or Bak proteins.
- BAX** The protein encoded by this gene belongs to the BCL2 protein family. BCL2 family members form hetero- or homodimers and act as anti- or pro-apoptotic regulators that are involved in a wide variety of cellular activities. This protein forms a heterodimer with BCL2, and functions as an apoptotic activator. This protein is reported to interact with, and increase the opening of, the mitochondrial voltage-dependent anion channel (VDAC), which leads to the loss in membrane potential and the release of cytochrome c. The expression of this gene is regulated by the tumor suppressor P53 and has been shown to be involved in P53-mediated apoptosis. Multiple alternatively spliced transcript variants, which encode different isoforms, have been reported for this gene.
- BCL2** This gene encodes an integral outer mitochondrial membrane protein that blocks the

apoptotic death of some cells such as lymphocytes. Constitutive expression of BCL2, such as in the case of translocation of BCL2 to Ig heavy chain locus, is thought to be the cause of follicular lymphoma. Alternative splicing results in multiple transcript variants.

CCNE2 The protein encoded by this gene belongs to the highly conserved cyclin family, whose members are characterized by a dramatic periodicity in protein abundance through the cell cycle. Cyclins function as regulators of CDK kinases. Different cyclins exhibit distinct expression and degradation patterns which contribute to the temporal coordination of each mitotic event. This cyclin forms a complex with and functions as a regulatory subunit of CDK2. This cyclin has been shown to specifically interact with CIP/KIP family of CDK inhibitors, and plays a role in cell cycle G1/S transition. The expression of this gene peaks at the G1-S phase and exhibits a pattern of tissue specificity distinct from that of cyclin E1. A significantly increased expression level of this gene was observed in tumor-derived cells.

CDK2 This gene encodes a member of a family of serine/threonine protein kinases that participate in cell cycle regulation. The encoded protein is the catalytic subunit of the cyclin-dependent protein kinase complex, which regulates progression through the cell cycle. Activity of this protein is especially critical during the G1 to S phase transition. This protein associates with and regulated by other subunits of the complex including cyclin A or E, CDK inhibitor p21Cip1 (CDKN1A), and p27Kip1 (CDKN1B). Alternative splicing results in multiple transcript variants.

CDC25A CDC25A is a member of the CDC25 family of phosphatases. CDC25A is required for progression from G1 to the S phase of the cell cycle. It activates the cyclin-dependent kinase CDC2 by removing two phosphate groups. CDC25A is specifically degraded in response to DNA damage, which prevents cells with chromosomal abnormalities from progressing through cell division. CDC25A is an oncogene, although its exact role in oncogenesis has not been demonstrated. Two transcript variants encoding different isoforms have been found for this gene.

CCND3 The protein encoded by this gene belongs to the highly conserved cyclin family, whose members are characterized by a dramatic periodicity in protein abundance through the cell cycle. Cyclins function as regulators of CDK kinases. Different cyclins exhibit distinct expression and degradation patterns which contribute to the temporal coordination of each mitotic event. This cyclin forms a complex with and

functions as a regulatory subunit of CDK4 or CDK6, whose activity is required for cell cycle G1/S transition. This protein has been shown to interact with and be involved in the phosphorylation of tumor suppressor protein Rb. The CDK4 activity associated with this cyclin was reported to be necessary for cell cycle progression through G2 phase into mitosis after UV radiation. Several transcript variants encoding different isoforms have been found for this gene.

- RB1 The protein encoded by this gene is a negative regulator of the cell cycle and was the first tumor suppressor gene found. The encoded protein also stabilizes constitutive heterochromatin to maintain the overall chromatin structure. The active, hypophosphorylated form of the protein binds transcription factor E2F1. Defects in this gene are a cause of childhood cancer retinoblastoma (RB), bladder cancer, and osteogenic sarcoma.
- E2F2 The protein encoded by this gene is a member of the E2F family of transcription factors. The E2F family plays a crucial role in the control of cell cycle and action of tumor suppressor proteins and is also a target of the transforming proteins of small DNA tumor viruses. The E2F proteins contain several evolutionally conserved domains found in most members of the family. These domains include a DNA binding domain, a dimerization domain which determines interaction with the differentiation regulated transcription factor proteins (DP), a transactivation domain enriched in acidic amino acids, and a tumor suppressor protein association domain which is embedded within the transactivation domain. This protein and another 2 members, E2F1 and E2F3, have an additional cyclin binding domain. This protein binds specifically to retinoblastoma protein pRB in a cell-cycle dependent manner, and it exhibits overall 46% amino acid identity to E2F1.
- TFDP1 This gene encodes a member of a family of transcription factors that heterodimerize with E2F proteins to enhance their DNA-binding activity and promote transcription from E2F target genes. The encoded protein functions as part of this complex to control the transcriptional activity of numerous genes involved in cell cycle progression from G1 to S phase. Alternative splicing results in multiple transcript variants. Pseudogenes of this gene are found on chromosomes 1, 15, and X.

^aThe functions of the genes are adapted from PubMed.

Supporting references

1. G. A. Crosby and J. N. Demas, *J. Phys. Chem.*, 1971, **75**, 991-1024.
2. S. Sprouse, K. A. King, P. J. Spellane and R. J. Watts, *J. Am. Chem. Soc.*, 1984, **106**, 6647-6653.
3. Y. You and S. Y. Park, *J. Am. Chem. Soc.*, 2005, **127**, 12438-12439.
4. G. M. Sheldrick, *Acta Crystallogr. A*, 2008, **64**, 112-122.
5. M. J. McKeage, S. J. Berners-Price, P. Galettis, R. J. Bowen, W. Brouwer, L. Ding, L. Zhuang and B. C. Baguley, *Cancer Chemother. Pharmacol.*, 2000, **46**, 343-350.
6. S. K. Leung, H. W. Liu and K. K. Lo, *Chem. Commun.*, 2011, **47**, 10548-10550.
7. Y. Li, C. P. Tan, W. Zhang, L. He, L. N. Ji and Z. W. Mao, *Biomaterials*, 2015, **39**, 95-104.
8. M. R. Eftink and C. A. Ghiron, *Biochemistry*, 1976, **15**, 672-680.