

Table SI. Summary of the sequencing metrics.

Sample name	Raw data		Clean data				
	Reads, n	Bases, bp	Reads, n	Bases, bp	GC content, %	Q20, %	Q30, %
Control-1	60,388,502	9,058,275,300	59,455,183	8,858,546,410	51.17	98.88	95.97
Control-2	44,595,947	6,689,392,050	43,987,766	6,555,412,406	49.32	98.94	96.09
Control-3	73,357,336	11,003,600,400	71,966,962	10,721,514,193	50.92	98.82	95.75
Cisplatin-1	93,867,181	14,080,077,150	92,345,188	13,764,049,654	50.32	98.89	95.93
Cisplatin-2	49,631,973	7,444,795,950	48,764,662	7,261,938,717	50.41	98.74	95.52
Cisplatin-3	55,951,060	8,392,659,000	55,170,132	8,221,835,359	50.48	98.86	95.86
Cisplatin + Tet-1	52,795,963	7,919,394,450	51,949,411	7,745,648,710	50.11	98.93	96.06
Cisplatin + Tet-2	52,985,060	7,947,759,000	52,249,801	7,788,219,058	49.64	98.92	96.03
Cisplatin + Tet-3	60,460,425	9,069,063,750	59,561,540	8,875,242,724	49.98	98.91	96.05
Average	60,448,161	9,067,224,117	59,494,516	8,865,823,026	50.26	98.88	95.91

Table SII. GO biological processes and KEGG pathways associated with the 432 differentially expressed genes specifically induced by combination of cisplatin and tetramethylpyrazine vs. control.

A, Downregulated genes, GO terms

Term	Count	P-value	Gene name
GO:0042254, ribosome biogenesis	18	1.13x10 ⁻¹⁴	EIF6, NAF1, EXOSC4, EXOSC1, FBL, MRTO4, IMP3, CDKN2A, NPM1, PES1, etc.
GO:0022613, ribonucleoprotein complex biogenesis	19	2.43x10 ⁻¹⁴	EIF6, NAF1, EXOSC4, NIP7, FBL,IMP3, CDKN2A, PRMT5, NPM1, PES1, etc.
GO:0034470, ncRNA processing	19	3.02x10 ⁻¹³	NAF1, EXOSC4, RRP9, QTRT1, BOP1, IMP3, CDKN2A, WDR4, TSEN2, NSUN2, etc.
GO:0034660, ncRNA metabolic process	20	2.08x10 ⁻¹²	NAF1, EXOSC4, RRP9, QTRT1, BOP1, IMP3, CDKN2A, WDR4, TSEN2, NSUN2, etc.
GO:0006364, rRNA processing	12	8.24x10 ⁻¹⁰	RCL1, NAF1, IMP3, PA2G4, CDKN2A, NOP2, EXOSC4, EXOSC1, BOP1, RRP9, etc.
GO:0016072, rRNA metabolic process	12	9.56x10 ⁻¹⁰	RCL1, NAF1, IMP3, PA2G4, CDKN2A, NOP2, EXOSC4, EXOSC1, BOP1, RRP9, etc.
GO:0006396, RNA processing	24	1.27x10 ⁻⁹	EIF6, NAF1, EXOSC4, NIP7, FBL,IMP3, CDKN2A, PRMT5, NPM1, PES1, etc.
GO:0034622, cellular macromolecular complex assembly	13	8.64x10 ⁻⁶	EIF6, HIST1H2AB, HIST1H4K, FKBP4, NIP7, FLNA, WNT2, PRMT5, HIST1H2AI, HIST1H3B, CACNA1A, etc.
GO:0008033, tRNA processing	8	1.63x10 ⁻⁵	ELAC2, PUS1, WDR4, QTRT1, TSEN2, NSUN2, RPP40, FBL
GO:0034621, cellular macromolecular complex subunit organization	13	2.91x10 ⁻⁵	EIF6, HIST1H2AB, FKBP4, NIP7, FLNA, WNT2, PRMT5, H2AFZ, HIST1H2AI, CACNA1A, TUBA1C, etc.
GO:0065003, macromolecular complex assembly	15	4.02x10 ⁻⁵	EIF6, HIST1H2AB, HIST1H4K, NIP7, FKBP4, FLNA, WNT2, PRMT5, MYC, TUBA1C, CACNA1A, etc.
GO:0006399, tRNA metabolic process	9	5.10x10 ⁻⁵	ELAC2, PUS1, WDR4, YARS2, QTRT1, TSEN2, NSUN2, RPP40, FBL
GO:0043933, macromolecular complex subunit organization	15	9.73x10 ⁻⁵	EIF6, HIST1H2AB, HIST1H4K, NIP7, FKBP4, FLNA, WNT2, PRMT5, MYC, TUBA1C, CACNA1A, etc.
GO:0006412, translation	13	3.52x10 ⁻⁴	EIF6, RPL26, EIF5A, RPL36, RPL37, RPS5, RPS19, RPL41, RPLP1, GM10020, etc.
GO:0008203, cholesterol metabolic process	6	1.31x10 ⁻³	CYP51, LDLR, FDPS, HMGCS1, PCSK9, SREBF2
GO:0005996, monosaccharide metabolic process	9	1.77x10 ⁻³	CSGALNACT1, GALK1, ATF4, LDHA, GMDS, MYC, FABP5, CACNA1A, ENO1
GO:0016125, sterol metabolic process	6	2.01x10 ⁻³	CYP51, LDLR, FDPS, HMGCS1, PCSK9, SREBF2
GO:0019318, hexose metabolic process	8	3.61x10 ⁻³	GALK1, ATF4, LDHA, GMDS, MYC, FABP5, CACNA1A, ENO1
GO:0006334, nucleosome assembly	5	1.03x10 ⁻²	HIST1H2AB, HIST1H4K, HIST1H2AI, H2AFZ, HIST1H3B, HIST1H3H
GO:0031497, chromatin assembly	5	1.13x10 ⁻²	HIST1H2AB, HIST1H4K, HIST1H2AI, H2AFZ, HIST1H3B, HIST1H3H

B, Downregulated genes, KEGG pathways

Term	Count	P-value	Gene name
mmu03010, Ribosome	10	1.67x10 ⁻⁶	RPS19, RPL41, RPLP1, GM10020, RPL26, RPL3, RPL10, RPL36, RPL37, RPS5
mmu00670, One carbon pool by folate	3	1.75x10 ⁻²	SHMT2, ATIC, GART
mmu04510, Focal adhesion	7	4.16x10 ⁻²	ACTG1, CCND1, COL2A1, ZYX, VASP, FLNA, MYL9
mmu05322, Systemic lupus erythematosus	5	4.33x10 ⁻²	HIST1H2AB, HIST1H4K, HIST1H2AI, H2AFZ, HIST1H3B, HIST1H3H

C, Upregulated genes, GO terms

Term	Count	P-value	Gene name
GO:0000280, nuclear division	7	6.71x10 ⁻⁴	HAUS3, KNTC1, POLN, NUSAP1, NDC80, CEP55, NCAPD3

Table SII. Continued.

C, Upregulated genes, GO terms			
Term	Count	P-value	Gene name
GO:0007067, mitosis	7	6.71x10 ⁻⁴	HAUS3, KNTC1, POLN, NUSAP1, NDC80, CEP55, NCAPD3
GO:0000087, M phase of mitotic cycle cell	7	7.48x10 ⁻⁴	HAUS3, KNTC1, POLN, NUSAP1, NDC80, CEP55, NCAPD3
GO:0048285, organelle fission	7	8.10x10 ⁻⁴	HAUS3, KNTC1, POLN, NUSAP1, NDC80, CEP55, NCAPD3
GO:0051301, cell division	8	9.71x10 ⁻⁴	CDK19, HAUS3, KNTC1, POLN, NUSAP1, NDC80, CEP55, NCAPD3
GO:0022402, cell cycle process	9	1.54x10 ⁻³	GAS2L3, HAUS3, KNTC1, POLN, NUSAP1, NDC80, CEP55, BRCA1, NCAPD3
GO:0000278, mitotic cell cycle	7	2.42x10 ⁻³	HAUS3, KNTC1, POLN, NUSAP1, NDC80, CEP55, NCAPD3
GO:0006986, response to unfolded protein	4	3.40x10 ⁻³	UPF2, EDEM3, DNAJC3, VARS
GO:0000226, microtubule cytoskeleton organization	5	3.44x10 ⁻³	HAUS3, POLN, NUSAP1, NDC80, BRCA1
GO:0051297, centrosome organization	3	4.46x10 ⁻³	HAUS3, POLN, BRCA1
GO:0000279, M phase	7	5.00x10 ⁻³	HAUS3, KNTC1, POLN, NUSAP1, NDC80, CEP55, NCAPD3
GO:0031023, microtubule organizing center organization	3	6.05x10 ⁻³	HAUS3, POLN, BRCA1
GO:0007049, cell cycle	10	6.87x10 ⁻³	GAS2L3, HAUS3, KNTC1, POLN, NUSAP1, NDC80, CEP55, CCNDBP1, BRCA1, NCAPD3
GO:0007010, cytoskeleton organization	7	9.75x10 ⁻³	PRPH, HAUS3, SORBS1, POLN, NUSAP1, NDC80, BRCA1
GO:0022403, cell cycle phase	7	1.00x10 ⁻²	HAUS3, KNTC1, POLN, NUSAP1, NDC80, CEP55, NCAPD3
GO:0007051, spindle organization	3	1.06x10 ⁻²	HAUS3, POLN, NDC80
GO:0043065, positive regulation of apoptosis	6	1.26x10 ⁻²	SERINC3, CASP3, CASP4, IL18, BRCA1, BCL2L11
GO:0051789, response to protein stimulus	4	1.27x10 ⁻²	UPF2, EDEM3, DNAJC3, VARS
GO:0043068, positive regulation of programmed cell death	6	1.30x10 ⁻²	SERINC3, CASP3, CASP4, IL18, BRCA1, BCL2L11
GO:0010942, positive regulation of cell death	6	1.34x10 ⁻²	SERINC3, CASP3, CASP4, IL18, BRCA1, BCL2L11
D, Upregulated genes, KEGG pathways			
Term	Count	P-value	Gene name
mmu05200, Pathways in cancer	8	1.11x10 ⁻³	CASP3, PTGS2, WNT9A, TCF7L1, CHUK, CSF2RA, FZD6, CTNNA2
mmu04520, Adherens junction	4	7.01x10 ⁻³	PTPRJ, SORBS1, TCF7L1, CTNNA2
mmu05217, Basal cell carcinoma	3	3.31x10 ⁻²	WNT9A, TCF7L1, FZD6
mmu04621, NOD-like receptor signaling pathway	3	4.12x10 ⁻²	IL18, TAB2, CHUK
GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.			