Coordinated transcription of *ANRIL* and *P16* genes is silenced by *P16* DNA methylation

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Abstract

Objective: To investigate the relationship between the transcription of *ANRIL*, *P15*, *P14* and *P16* at the same locus and the regulation mechanism of *ANRIL*.

Methods: Publicly available database of Cancer Cell Line Encyclopedia (CCLE) was used in bioinformatic analyses. Methylation of CpG islands was detected by denaturing high performance liquid chromatography (DHPLC). Gene transcript levels were determined using quantitative real-time polymerase chain reaction (qRT-PCR) assays. An engineered *P16*-specific transcription factor and DNA methyltransferase were used to induce *P16*-specific DNA demethylation and methylation.

Results: The expression level of *ANRIL* was positively and significantly correlated with that of *P16* but not with that of *P15* in the CCLE database. This was confirmed in human cell lines and patient colon tissue samples. In addition, *ANRIL* was significantly upregulated in colon cancer tissues. Transcription of *ANRIL* and *P16* was observed only in cell lines in which the *P16* alleles were unmethylated and not in cell lines with fully methylated *P16* alleles. Notably, *P16*-specific methylation significantly decreased transcription of *P16* and *ANRIL* in BGC823 and GES1 cells. In contrast, *P16*-specific demethylation re-activated transcription of *ANRIL* and *P16* in H1299 cells ($P<0.001$). Alteration of *ANRIL* expression was not induced by *P16* expression changes.

Conclusions: *ANRIL* and *P16* are coordinately transcribed in human cells and regulated by the methylation status of the *P16* CpG islands around the transcription start site.

Keywords: *ANRIL*; *P16*; CpG island; DNA methylation; transcriptional regulation

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Introduction

The *P15-P14-P16* (*INK4*) gene locus is a significant genetic susceptibility locus in cancers and cardiovascular disease (1-3). It has also been linked to a number of other pathologies, including intracranial aneurysm, type-2 diabetes, periodontitis, Alzheimer's disease, endometriosis, frailty in the elderly, and glaucoma (4-6). The results of the Cancer Genome Project showed that this locus is the most frequently deleted region in thousands of human cancer genomes (7). While *P16* genetic deletions do occur in cancers, the frequency of *P16* DNA methylation is three times that of deletions (8,9). *P15*, *P14* and *P16* genes coordinately control the G1→S transition in the cell cycle through the cyclin-dependent kinase (CDK) 2/4/6-cyclin D1/E-Rb pathway (10). Higher-order chromatin structure analysis showed that the *P15-P14-P16* chromatin presents in a dynamic compact loop for coordinate repression of these genes through CTCF-binding and that the chromatin decompaction leads to activation of these genes (11,12).

LncRNA *ANRIL* (*CDKN2B-AS1*) is transcribed from the antisense-strand of the *P14* promoter and *P15* gene regions in the *INK4* locus (chr9: 21,994,791–22,120,544 in the hg19 human assembly) (13,14). The preliminary *ANRIL* transcripts are spliced into various mature forms (*Supplementary Figure S1*) (6,15). It was reported that *ANRIL* and *miR31HG* might downregulate *P15* and *P16* transcription through interacting with components of polycomb repressive complex-1 or -2 (PRC-1/-2) (16-19). However, the transcriptional relationship between these genes within the *INK4* locus has not been well studied. The regulatory mechanism of *ANRIL* transcription has rarely been reported (20). In the present study, we report that *P16* DNA methylation may repress *ANRIL* transcription. Bioinformatics and experimental analysis support that *ANRIL* and *P16* are coordinately transcribed in human cells.

Materials and methods

Patients tissue collection

Colon carcinoma along with paired non-cancerous surgical margin samples were collected from 76 patients at the Peking University Cancer Hospital from 2009 to 2011. The Ethics Committee of Peking University Cancer Hospital approved this study. All patients provided written informed consent to participate in the study. The authors had no access to information that could identify individual participants during or after data collection.

Database sources

Gene expression and copy number of 995 cancer cell lines was downloaded from the publicly available database [https://portals.broadinstitute.org/ccle/home] of the Broad-Novartis Cancer Cell Line Encyclopedia (CCLE) (21).

Cell lines and culture

Human cell lines BGC823, MGC803, RKO, H1299, GES1 and SGC7901 were cultured in RPMI1640 medium supplemented with 10% fetal bovine serum (FBS). The human cell lines Caski, Colo205, HeLa, MHCC97H, Siha and SW480 were cultured in Dulbecco's modified eagle medium (DMEM) with 10% FBS. AGS and PC3 were cultured in F12 medium with 10% FBS. All of these cell lines were cultured at 37 °C in 5% CO_2. PC3 cell line was purchased from Cell Line Bank, Chinese Academy of Medical Science. RKO cell line was kindly provided by Dr. Guoren Deng at University of California San Francisco, and SW480 cell line, by Dr. Yuanjia Chen at Peking Union Medical College Hospital. AGS (from Dr. Chengchao Shou), GES1, BGC823, SGC7901, HeLa, Caski, Siha, H1299, Colo205 and MHCC97H cell lines (from Dr. Yang Ke) were obtained from laboratories at Peking University Cancer Hospital/Institute.

RNA extraction and reverse transcription-polymerase chain reaction (RT-PCR)

These cells were harvested when the density reached about 70%. Total RNA was extracted by TRIzol (Invitrogen) and reverse-transcribed using a first-cDNA synthesis kit (Transgen). The expression levels of the *ANRIL*, *P16*, *P15* and *P14* genes were analyzed by quantitative real-time polymerase chain reaction (qRT-PCR) using the corresponding primer sets (*Table 1*). To detect the linear *ANRIL* (NR_003529) expression status in cell lines and tissues, primer sets E3–E4 and E1–E2 were used for qRT-PCR and RT-PCR, respectively. Glyceraldehyde-3-phosphate dehydrogenase (*GAPDH*) was used as a reference gene. Power SYBR Green PCR Master Mix (Fermentas) was used in qRT-PCR (ABI-7500). Relative mRNA level was calculated based on the average Ct value of the target gene and the *GAPDH* reference [$2^{-(\mathrm{Ct}_{\mathrm{target\_gene}}-\mathrm{Ct}_{\mathrm{GAPDH}})}$].

Transfection and construction of vectors

P16-specific siRNAs (5'-ccguaaauguccauuuauatt-3' and 5'-uauaaauggacauuuacggtt-3') were synthesized in GenePharma (Shanghai) and used to transiently transfect cells at a final concentration of 1.0 μg/mL. The negative control was scramble siRNAs (5'-uucuccgaacgugucacgutt-3' and 5'-acgugacacguucggagaatt-3') (GenePharma, Shanghai). The *P16* expression vector was constructed by integrating the wild-type *P16* cDNA into the pIRES2-EGFP vector. A total of 4.5×10^4 cells were transiently transfected with the pIRES2-P16 expression vector, seeded into each well (diameter, 3.48 cm; 6-well microplate; 3 wells/group), and incubated for 48 h. The P16-Dnmt_pTRIPZ and P16-ATF_pcDNA3.1 vectors were constructed as described previously (22,23). These experiments were repeated 2–3 times.

Detection of P16 and P14 methylation by denaturing high performance liquid chromatography (DHPLC)

The methylation status of the *P16* and *P14* CpG islands

Table 1 Sequences of oligonucleotides used as primers in various polymerase chain reaction (PCR)

Gene name	Entrez gene ID	Assay	Oligo name	Primer sequence (5'→3')	Product size (bp)	PCR Tm (°C)
P16	1029	qRT-PCR	P16-F	gctgcccaacgcaccgaata	180	58
			P16-R	accaccagcgtgtccaggaa		
		DHPLC	P16-E1F	tttttagaggatttgagggatagg	392	57
			P16-E1R	ctacctaattccaattcccctacaaactt		
ANRIL	NR_003529	qRT-PCR	E3-E4R	cagcagaaggtgggcagcagat	145	64
			E3-E4F	ttcctcgacagggcaggcaggt		
		RT-PCR	E1-E2R	gggcctcagtggcacatacc	332	65→50
			E1-E2F	tgctctatccgccaatcagg		(–1/cycl)
P15	1030	qRT-PCR	P15-qF	agtcaaccgtttcgggaggcg	168	58
			P15-qR	accaccagcgtgtccaggaag		
P14	1029	qRT-PCR	P14-qF	gccaggggcgcccgccgctg	236	62
			P14-qR	ggcccggtgcagcaccacca		
		DHPLC	P14-F	gttgtttatttttggtgtta	272	51
			P14-R	acctttcctacctaatcttc		
GAPDH	2597	(q)RT-PCR	GAPDH-F	gaaggtgaaggtcggagt	226	62
			GAPDH-R	gaagatggtgatgggatttc		

GAPDH, glyceraldehyde-3-phosphate dehydrogenase; qRT-PCR, quantitative real-time polymerase chain reaction; RT-PCR, reverse transcription-polymerase chain reaction; DHPLC, denaturing high performance liquid chromatography.

was determined using DHPLC as previously described (22,24,25).

Western blotting

Protein extracts were equally loaded into 12% acrylamide gels, electrophoresed, and transferred to PVDF membranes (Millipore). After blocking with 5% fat-free milk in PBS, the membranes were probed with rabbit anti-P16 (Ab50282; Abcam) and mouse anti-GAPDH (60004-1-Ig; Proteintech) which were diluted at 1:3,000 and 1:10,000, respectively. After incubation at room temperature for 1 h, membranes were washed with PBST three times, and incubated with horse radish peroxidase (HRP)-labeled secondary antibody goat anti-rabbit IgG (1:5,000) and anti-mouse IgG (1:10,000), respectively. Signals were visualized using the Enhanced Chemiluminescence kit (Pierce).

Statistical analysis

All statistical analyses were performed using SPSS 18.0 software (SPSS Inc., Chicago, IL, USA). Student's *t*-test was conducted for normally distributed data. The significance of gene expression associations (r) was statistically tested with adjusting gene copy number, and $P<0.05$ was considered statistically significant.

Results

Transcription of ANRIL is significantly correlated with P16 expression

In order to investigate the relationship between transcription levels of the genes within the *INK4* locus, we analyzed the publicly available databases in the CCLE project (21). The *INK4* locus is absent from 298 cell lines [copy number value (CN) <–2.0] and is present in 713 cell lines (*Supplementary File S1*). Because the 298 *INK4* locus-absent cell lines cannot express the locus genes (*Figure 1A*), only the *INK4* allele-containing cell lines were used in the correlation analysis. Unexpectedly, we found that the transcription level of *ANRIL* was positively and significantly correlated with the transcription level of *P16* in the 713 cell lines (r_s=0.254, P<0.001), but was not correlated with transcription levels of *P15* (r_s=–0.015, P=0.701), although the *P16* and *P15* expression levels were correlated with each other (*Figure 1B*). *P16* mRNA levels were still positively correlated with the *ANRIL* expression levels after the gene copy number was adjusted (P<0.001). Among 224 cell lines without the *INK4* locus deletion (CN>0.0), the same phenomenon was consistently observed (*Figure 1C*). These results indicated that *ANRIL* is coordinately transcribed with *P16* but not with *P15*.

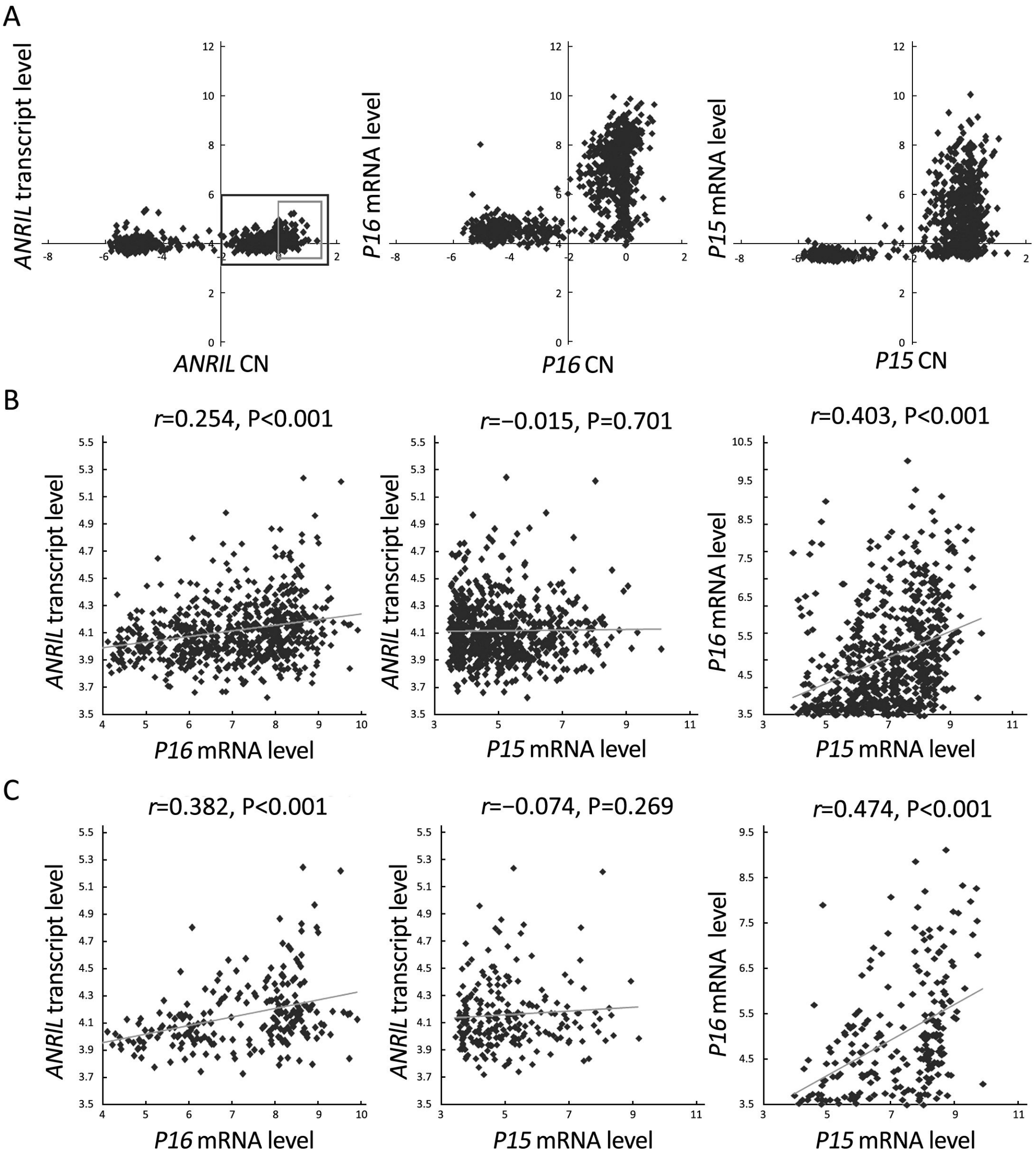

Figure 1 Relationship among *ANRIL*, *P15* and *P16* gene expression in the Cancer Cell Line Encyclopedia (CCLE) project. (A) Gene copy number (CN) is correlated with the corresponding gene expression; Left chart: when no allele is deleted, the CN value ranged from 0 to +2 (gray-line framed); when the target alleles were homogeneously or heterogeneously deleted, the CN value was less than –2 or ranged from –2 to 0 (black-line framed, but not gray-line framed); (B, C) Correlation of the expression levels of the *ANRIL*, *P16* and *P15* genes among human cell lines containing 1 or 2 *INK4* allele(s) (CN values: –2 to +2), and among human cell lines without the *INK4* allele deletion (CN values: 0 to +2), as framed in the top left chart (A). The detailed gene copy number and expression level for each cell line are listed in *Supplementary File S1*.

To confirm these correlations, we analyzed the transcription levels of *ANRIL*, *P16*, *P15* and *P14* genes in a panel of cell lines without the *INK4* deletion using qRT-PCR, and observed the same phenomena. As expected, high level of *ANRIL* transcription was only observed in the *P16*-unmethylated cell lines (Caski, SGC7901, BGC823, GES1, Siha and HeLa), but not in *P16*-methylated cell lines (Colo205, PC3, MHCC97H, RKO, SW480 and AGS) (*Figure 2A*, *3A*, *3B*). *P16* mRNA expression level was closely correlated with *ANRIL* expression level (*r*=0.774, P=0.003), suggesting that *P16* DNA methylation might repress transcription of *ANRIL*. Such an association was not

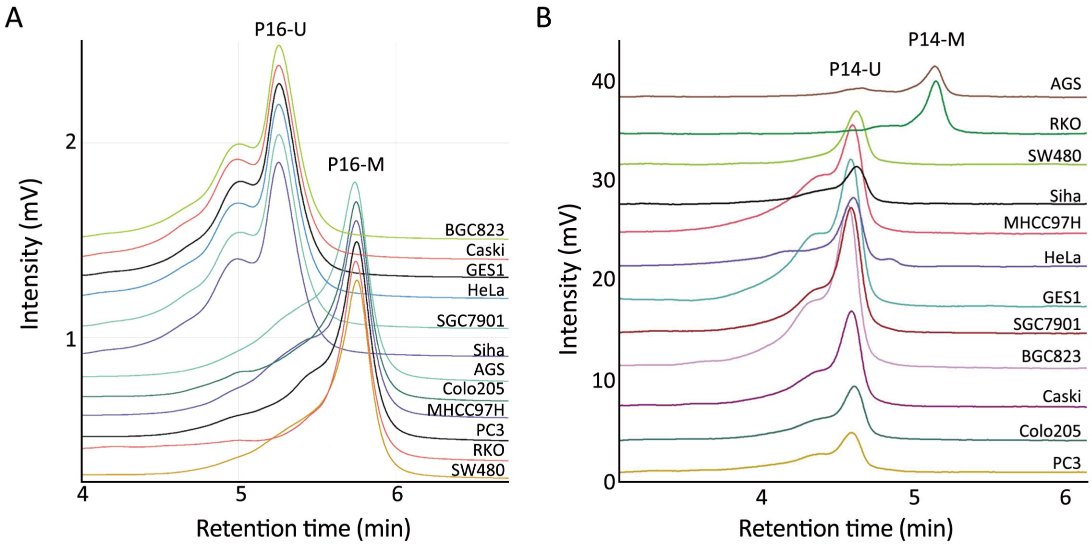

Figure 2 Denaturing high performance liquid chromatography (DHPLC) chromatograms of methylated and unmethylated CpG islands in various cell lines. (A) *P16* CpG islands; (B) *P14* CpG islands.

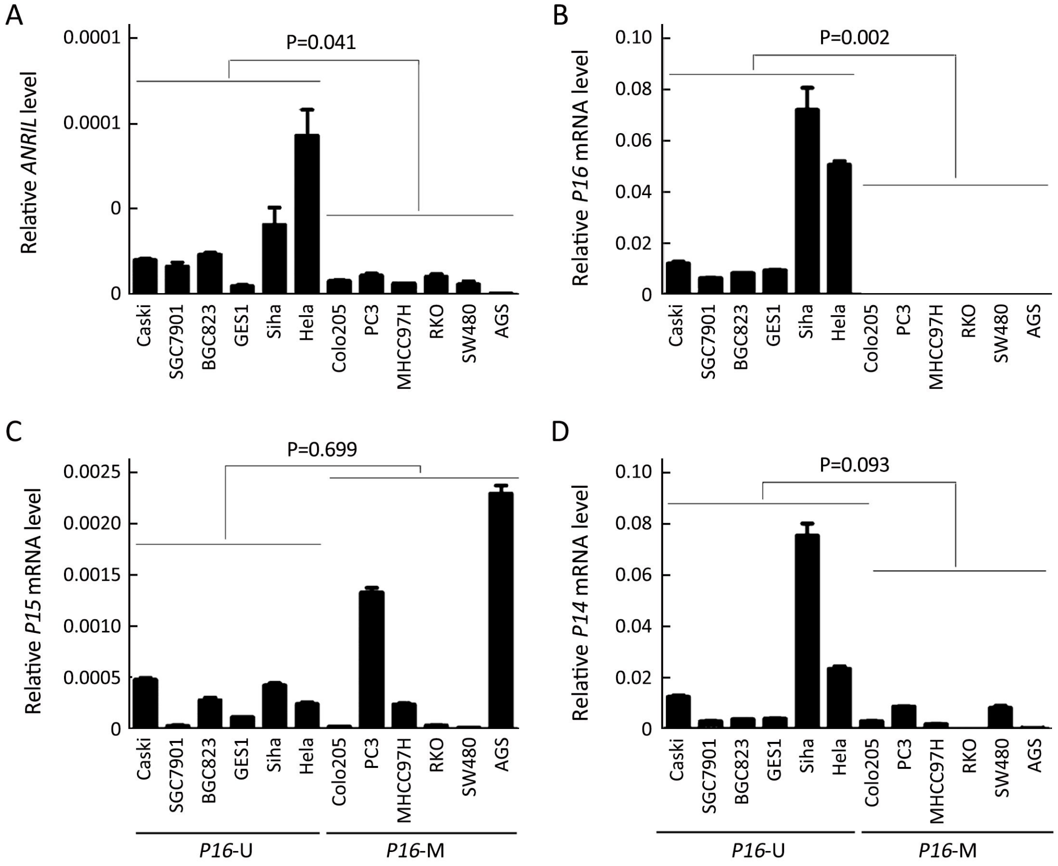

Figure 3 Comparison of the transcription level of the *ANRIL*, *P16*, *P15* and *P14* genes in the *P16*-methylated and -unmethylated cell lines. (A) *ANRIL*; (B) *P16*; (C) *P15*; (D) *P14*.

observed between the *ANRIL* level and the *P15* or *P14* mRNA levels (r=0.090 or 0.297, P=0.780 or 0.349) (*Figure 3C*, *D*).

The positive relationship between the *ANRIL* and *P16* expression levels was further validated in human colon tissue samples. As expected, the *ANRIL* expression level was significantly increased in colon cancer tissues compared to corresponding non-cancerous surgical margins [χ^2 test, 19/76 (25.0%) *vs*. 2/76 (2.6%), P<0.001]. No significant association was observed between the *ANRIL* lncRNA expression level and pTNM stage or other clinicopathological characteristics or overall survival of colon cancer patients (data not shown). Notably, the *P16* mRNA level was significantly higher in the *ANRIL*-positive samples than in the *ANRIL*-negative samples (P<0.001; *Figure 4A*). Once again, the *P15* mRNA expression level was similar to the *ANRIL*-positive samples compared to the *ANRIL*-negative samples (P=0.879; *Figure 4B*). These results indicated that *ANRIL* and *P16* genes are coordinately transcribed in human cells.

Interestingly, the CpG islands around the *P14* transcription start site were methylated only in the AGS and RKO cells but not in the remaining cells (*Figure 2B*). Because the number of the *P14*-methylated cell lines is limited, an association between *ANRIL* transcription and *P14* methylation was not observed.

Transcription repression of ANRIL by P16 DNA methylation

Recently, we constructed a *P16* promoter DNA methyltransferase (*P16*-Dnmt) that can specifically methylate *P16* CpG islands around transcription start sites, and this subsequently leads to silencing of *P16* transcription in human cells but cannot induce *P14* methylation or *P14* repression (20). To elucidate whether methylation of *P16* CpG islands directly leads to the silencing of *ANRIL* transcription, we analyzed the transcription level of *ANRIL* in GES1 and BGC823 cells, in which *P16* CpG islands were methylated by the stably transfected P16-Dnmt_pTRIPZ vector with induction of 0.25 µg/mL doxycycline for 14 days (*Figure 5A*, *C*). qRT-PCR analysis showed that the transcriptional activities of both *P16* and *ANRIL* were significantly decreased, whereas the *P15* mRNA expression level was not changed, and the *P14* mRNA expression level was slightly increased (*Figure 5B*, *D*) in these cell lines.

By contrast, using a *P16*-specific artificial transcription factor (P16-ATF) that can induce demethylation of *P16* CpG islands and reactivate gene expression (*Figure 5E*) (23), we found that transcriptional activities of both *P16* and *ANRIL* were significantly increased (P<0.001), whereas *P15* and *P14* mRNA expression levels were not changed in H1299 cells that were stably transfected with the *P16*-ATF_pcDNA3.1 vector (*Figure 5F*). These results demonstrated that *P16* DNA methylation indeed represses *ANRIL* transcription.

Transcription of ANRIL is not affected by changes in P16 expression

To clarify whether downregulation of *ANRIL* expression is directly caused by *P16* DNA methylation itself or indirectly caused by subsequent *P16* repression, we induced *P16*

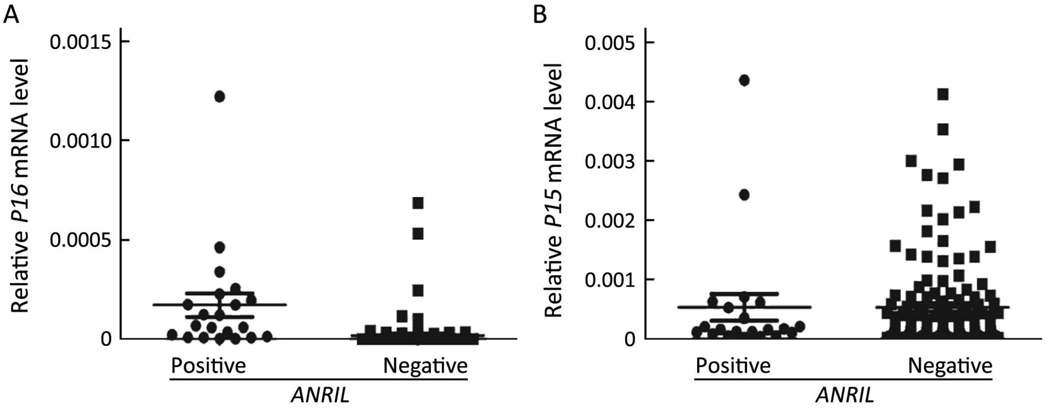

Figure 4 Association between the *ANRIL*, *P16* and *P15* transcription levels in colon tissues. (A) The level of *P16* mRNA in the *ANRIL* expression-positive and -negative samples (P<0.001); (B) The level of *P15* mRNA in the *ANRIL* expression-positive and -negative samples (P=0.879).

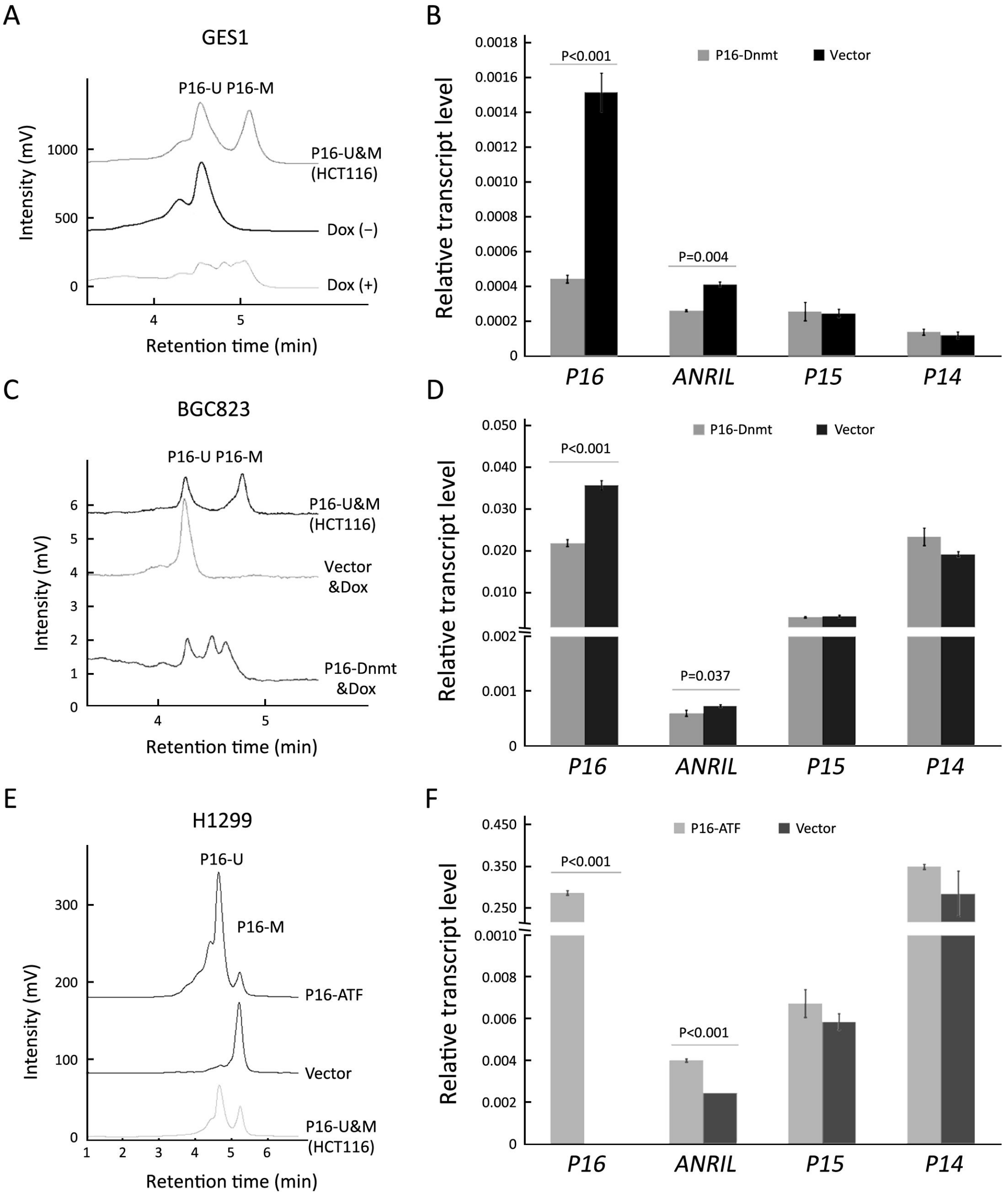

Figure 5 Regulation of *ANRIL* and *P16* transcription by the *P16* promoter methylation changes. (A, C) Denaturing high performance liquid chromatography (DHPLC) chromatograms of methylated- and unmethylated-*P16* CpG islands in the P16-Dnmt stably transfected GES1 and BGC823 cells with or without doxycycline induction for 14 days, respectively. The *P16*-hemimethylated HCT116 cells were used as P16-methylated and -unmethylated (P16-M and -U) control in the DHPLC analysis; (B, D) Repression of *ANRIL* and *P16* transcription in GES1 and BGC823 cells by *P16* DNA methylation, respectively; (E) DHPLC chromatograms of methylated- and unmethylated-*P16* CpG islands in the P16-ATF stably transfected H1299 cells; (F) Reactivation of *ANRIL* and *P16* transcription in H1299 cells by *P16* DNA demethylation.

expression changes in H1299 and BGC823 cells through transient transfection, and found that the *ANRIL* level remained stable following *P16* overexpression and siRNA knockdown (*Figures 6A*, *B*), respectively. Similar result was also obtained in MGC803 cells (*Figure 6C*). These data suggest that it is *P16* methylation itself, but not *P16* downregulation, that leads to the repression of *ANRIL* transcription.

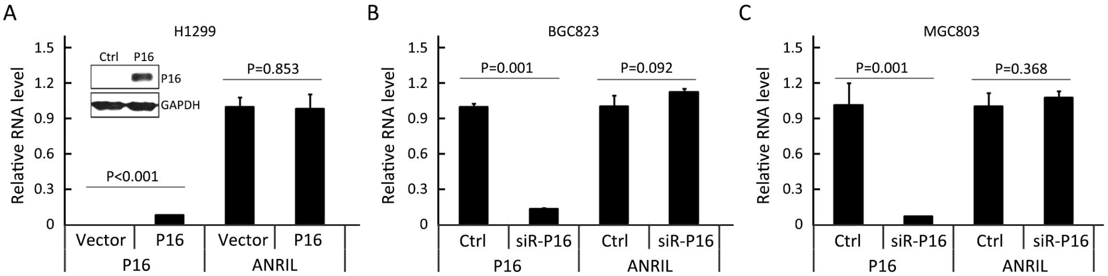

Figure 6 Effects of *P16* expression changes on *ANRIL* transcription. (A) The *ANRIL* and *P16* expression levels in H1299 cells transiently transfected with *P16* expression vector and empty control vector. The inserted image shows the results of Western blotting to monitor the P16 protein amount; (B, C) The *ANRIL* and *P16* expression levels in BGC823 and MGC803 cells transiently transfected with the *P16*-specific siRNA (siR-P16) and scramble RNA control (Ctrl), respectively. These experiments were performed in triplicate. The P-values were obtained in χ^2 test (A) and *t*-student test (B, C), respectively.

Discussion

ANRIL is transcribed from the *INK4* locus and can be spliced into diverse mature forms to regulate gene transcription in the nucleus and to interact with proteins in the cytoplasm (6,15). Consistent with others' reports that *ANRIL* is upregulated in many cancers (26-32), we find that *ANRIL* is also significantly upregulated in colon cancer. The mechanisms of regulation of *ANRIL* transcription have rarely been reported (20). In the present study, we report that the endogenous *ANRIL* and *P16* genes are coordinately transcribed in cancer cells *in vitro* and *in vivo*, and that *P16* methylation may repress *ANRIL* transcription.

ANRIL is considered to be an oncogene, according to its frequent upregulation in many cancers and association with a poor prognosis (26-32). In the present study, we observed significant *ANRIL* upregulation in colon cancer tissues. There was no association between the *ANRIL* lncRNA expression level and prognosis of colon cancer.

There are a number of regulators that co-regulate transcription of *P15*, *P14* and *P16* (10,17,33). It is reasonable to expect that *ANRIL* lncRNA expression correlates with that of the genes in the *INK4* locus. In contrast to another report that *ANRIL* (*CDKN2B-AS*) may repress *P15* expression (34), we did not observe any correlation between the expression levels of *ANRIL* and *P15*, both in a large number of cancer cell lines and in colon tissues. Interestingly, we found a strong positive relationship between the expression levels of *ANRIL* and *P16*. Our experimental evidence strongly supports that the methylation status of the *P16* CpG islands directly affects the transcriptional activity of both *ANRIL* and *P16*, indicating the bi-directional functions of the *P16* promoter. It was previously reported that *P16* methylation was associated with loss of CTCF binding and a chromatin boundary in the *P16* gene (11). The *INK4* chromatin is enriched with the CTCF binding sites and CTCF depletion disrupts the *INK4* chromatin loop formation (12). *P16* methylation may repress *ANRIL* transcription via the *INK4* chromatin conformation changes.

It was reported that *ANRIL* downregulation by siRNA increased the *P16* expression level in cancer cells (18). However, an inverse relationship between the *ANRIL* and *P16* transcription levels was not observed in 224 cancer cell lines without *P16* allele deletion and colon cancer tissues from 76 patients. Instead, higher *P16* mRNA expression was detected in cell lines and tissues with *ANRIL* expression than those without *ANRIL* expression. Endogenous *ANRIL* and *P16* expression levels are positively correlated with each other *in vitro* and *in vivo*.

P16 is a weakly expressed nucleic protein that inhibits CDK4 activity in normal human cells (1). Although *P16* expression is epigenetically repressed in approximately 30%–40% of cancers (8,9,35-38), strong cytoplasmic P16 staining could be detected in some cancers, especially in the human papillomavirus (HPV) infection-related cancers (i.e., cervical, oral, skin and thyroid cancers) (39-42). Interestingly, according to the publicly available database in the Human Protein Atlas project, the majority of P16 proteins are incorrectly located in the cytoplasm of P16 staining-positive cancer cells from multiple cancer types (i.e., breast, colon, gliocyte, liver, lung, melanocyte, ovarian, prostate, stomach, and urothelial tract), where HPV infection has not been reported (*Supplementary Figure S2*) (43). Cytoplasmic P16 cannot function as a tumor suppressor in cells. It is worth studying whether the cytoplasmic compartmentalization of P16 in cancer cells leads to adaptive upregulation of *ANRIL* transcription in cancer cells.

Conclusions

ANRIL is coordinately transcribed with *P16* in human cells. The methylation status of the *P16* CpG islands around the transcription start site controls the transcription of the *ANRIL* and *P16* genes.

Acknowledgements

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Footnote

Conflicts of Interest: The authors have no conflicts of interest to declare.

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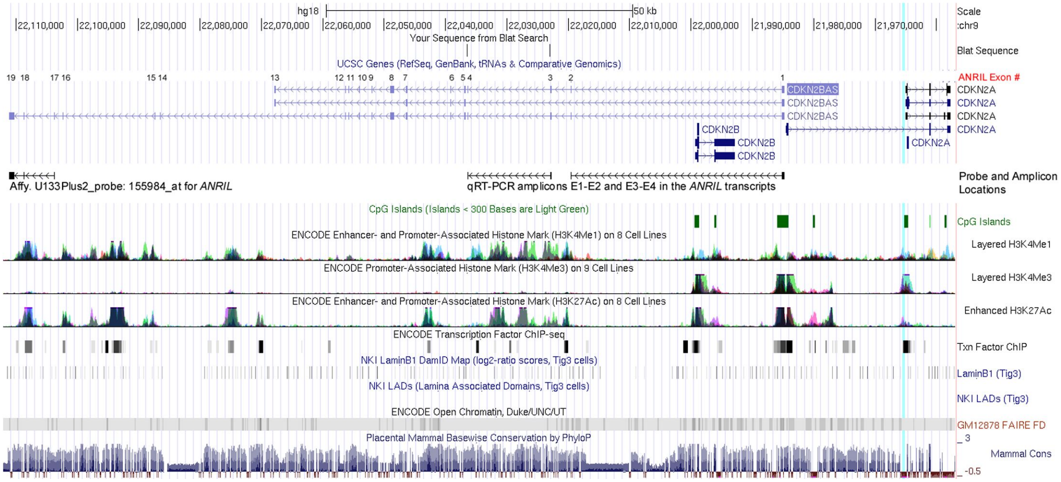

Figure S1 Graphic view of *ANRIL* (*CDKN2BAS*), *P15* (*CDKN2B*), *P16* and *P14* (*CDKN2A*) genes in *INK4* locus. The location information of the *ANRIL*-specific probe used in the Affy. U133 Plus 2.0 platform and the qRT-PCR amplicon in the *ANRIL* transcripts analyzed in the present study are also marked. This image was adapted from the University of California Santa Cruz (UCSC) Gene Brower.

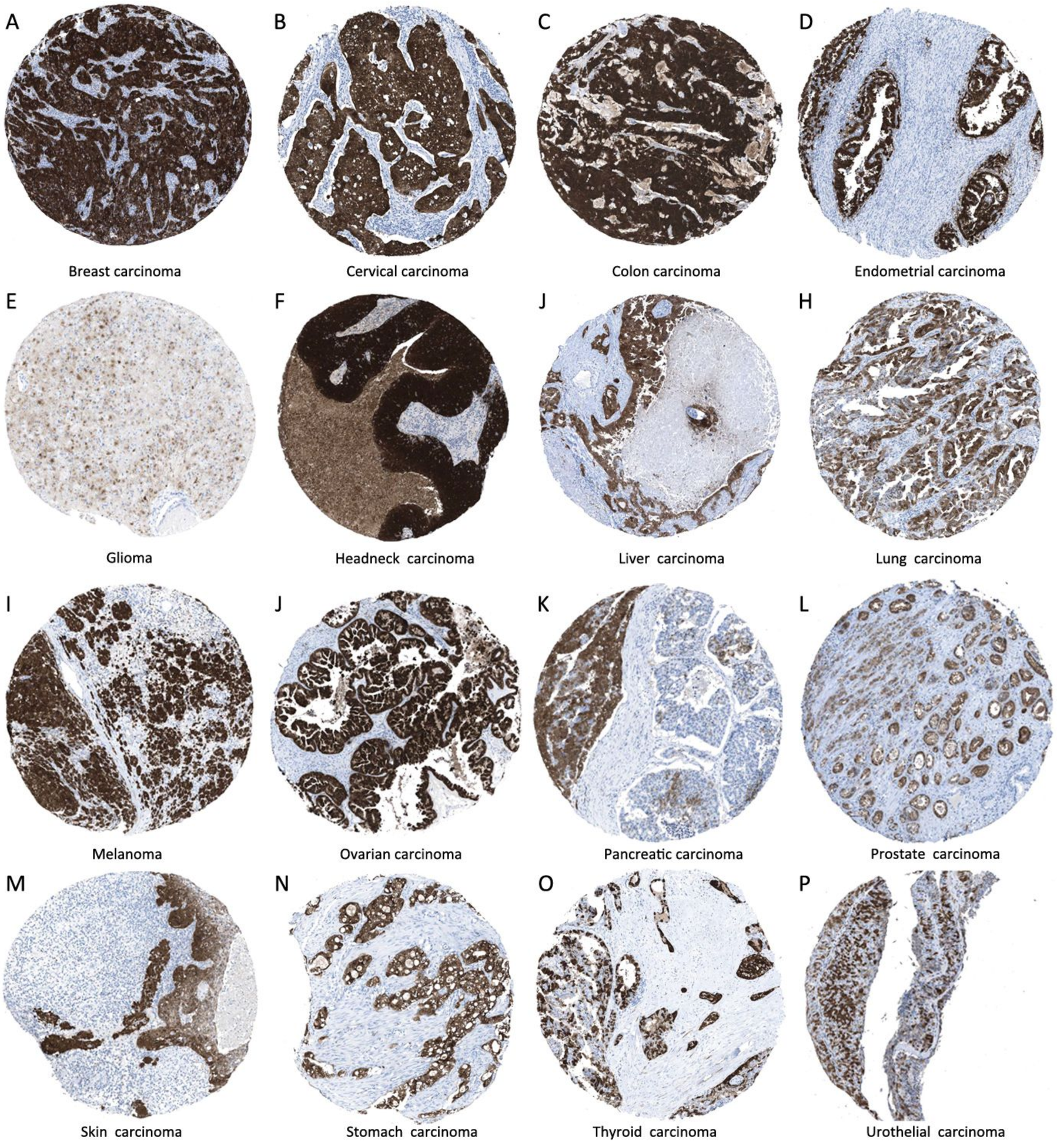

Figure S2 Images of the immunohistochemitry staining of P16 protein in carcinomas from various organs using the P16-specific antibody CAB018232. These images are adapted from the publicly available website [http://www.proteinatlas.org/ENSG00000147889-CDKN2A/cancer] the Human Protein Atlas Project (44). A-P: Breast, cervical, colon, endometrial, gliocyte, head and neck, liver, lung, melanocyte, ovarian, pancreatic, prostate, skin, stomach, thyroid, and urothelial carcinomas.

File S1

Cell name_Organ	Copy number value			Relative RNA level		
	CDKN2BAS	CDKN2B	CDKN2A	CDKN2A	CDKN2B	CDKN2BAS1
NCIH1648_LUNG	–5.82	–5.82	–5.70	4.45	3.50	3.95
WM88_SKIN	–5.65	–5.38	–5.65	4.62	3.35	4.76
ISTMES2_PLEURA	–5.56	–5.49	–5.56	4.83	3.81	4.11
HCC1500_BREAST	–5.40	–5.34	–5.40	4.61	3.63	4.00
SW1573_LUNG	–5.40	–5.10	–5.40	4.19	3.57	3.89
THP1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–5.50	–5.50	–5.40	4.28	3.72	4.12
LU99_LUNG	–5.39	–5.38	–5.39	4.97	3.68	3.97
IGR1_SKIN	–5.39	–5.32	–5.39	4.09	3.65	3.79
HEL9217_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–5.51	–5.51	–5.39	4.49	3.64	4.01
BICR6_UPPER_AERODIGESTIVE_TRACT	–5.38	–1.73	–5.38	6.00	4.64	3.68
BICR16_UPPER_AERODIGESTIVE_TRACT	–5.38	–4.80	–5.38	4.81	3.56	3.97
COLO741_SKIN	–5.41	–5.41	–5.37	4.10	3.52	4.01
NCIH1437_LUNG	–5.56	–5.56	–5.33	4.48	3.65	4.01
NCIH647_LUNG	–5.36	–5.36	–5.29	4.51	3.67	3.84
U138MG_CENTRAL_NERVOUS_SYSTEM	–5.29	–5.05	–5.29	4.49	3.69	3.79
NUDHL1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–5.47	–5.47	–5.26	4.95	3.99	4.14
LUDLU1_LUNG	–5.24	–5.03	–5.24	4.69	3.77	3.79
DAOY_CENTRAL_NERVOUS_SYSTEM	–5.24	–4.90	–5.24	4.57	3.36	4.02
TM31_CENTRAL_NERVOUS_SYSTEM	–5.39	–5.39	–5.24	4.21	3.63	3.80
HUPT4_PANCREAS	–5.62	–5.62	–5.23	4.41	3.55	3.81
TC71_BONE	–1.12	–1.12	–5.20	4.73	3.91	3.93
CGTHW1_THYROID	–5.19	–5.15	–5.19	4.12	3.44	3.89
RERFLCSQ1_LUNG	–5.19	–4.92	–5.19	4.23	3.41	3.80
1321N1_CENTRAL_NERVOUS_SYSTEM	–5.18	–4.90	–5.18	4.50	3.61	3.97
SNU16_STOMACH	–5.18	–5.08	–5.18	4.23	3.55	3.88
HT1080_SOFT_TISSUE	–5.14	–4.51	–5.14	4.55	3.63	4.28
TUHR14TKB_KIDNEY	–5.13	–4.93	–5.13	4.80	3.72	3.70
HDMYZ_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–5.12	–4.70	–5.12	4.18	3.38	3.84
OCILY3_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–5.13	–5.13	–5.12	4.41	3.74	3.90
SW1271_LUNG	–5.25	–5.25	–5.10	4.15	3.46	3.95
JM1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–5.14	–5.14	–5.09	4.82	3.84	3.96
A2058_SKIN	–5.09	–0.14	–5.09	8.04	6.67	3.89
HCC4006_LUNG	–5.56	–5.56	–5.07	4.59	3.34	4.11
DKMG_CENTRAL_NERVOUS_SYSTEM	–5.32	–5.32	–5.07	4.55	3.40	3.99
JURLMK1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–5.05	–4.87	–5.05	4.38	3.54	4.16
SKOV3_OVARY	–5.24	–5.24	–5.05	4.43	3.61	3.82
CMK115_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–5.10	–5.10	–5.05	4.46	3.62	4.05
MOLT13_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–5.05	–5.01	–5.05	4.89	3.42	4.29
143B_BONE	–5.06	–5.06	–5.03	4.68	3.53	3.78
SF126_CENTRAL_NERVOUS_SYSTEM	–5.16	–5.16	–5.02	5.05	3.36	3.97
KYO1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–5.00	–4.85	–5.00	4.63	3.48	4.19

File S1 (*continued*)

File S1 (*continued*)

Cell name_Organ	Copy number value			Relative RNA level		
	CDKN2BAS	CDKN2B	CDKN2A	CDKN2A	CDKN2B	CDKN2BAS1
RCC4_KIDNEY	–5.00	–4.64	–5.00	5.09	3.47	3.76
TE6_OESOPHAGUS	–5.00	–4.94	–5.00	4.58	3.66	3.77
CADOES1_BONE	–4.99	–4.79	–4.99	4.48	3.46	3.97
COV504_OVARY	–5.60	–5.60	–4.98	4.54	3.52	4.03
SF295_CENTRAL_NERVOUS_SYSTEM	–5.07	–5.07	–4.98	4.76	3.61	3.97
KU1919_URINARY_TRACT	–4.97	–4.90	–4.97	4.13	3.42	3.81
HCC38_BREAST	–5.42	–5.42	–4.97	4.24	3.65	3.84
TE9_OESOPHAGUS	–5.81	–5.81	–4.96	4.53	3.53	3.87
DOHH2_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–4.98	–4.98	–4.95	4.20	3.59	4.27
CAS1_CENTRAL_NERVOUS_SYSTEM	–5.59	–5.59	–4.90	5.16	3.67	3.72
NCIH2023_LUNG	–1.28	–1.28	–4.89	4.42	5.01	3.85
SW1710_URINARY_TRACT	–0.79	–0.79	–4.89	4.13	4.98	4.10
TE8_OESOPHAGUS	–4.88	–4.81	–4.88	4.01	3.29	4.26
LN229_CENTRAL_NERVOUS_SYSTEM	–5.54	–5.54	–4.88	4.68	3.75	3.95
HMC18_BREAST	–5.55	–5.55	–4.86	5.07	3.67	4.18
YAPC_PANCREAS	–5.25	–5.25	–4.86	5.47	3.85	3.87
TE15_OESOPHAGUS	–4.86	–4.76	–4.86	4.48	3.51	3.79
VMRCRCZ_KIDNEY	–5.23	–5.23	–4.84	4.53	3.92	3.79
PANC0327_PANCREAS	–5.31	–5.31	–4.79	4.14	3.53	4.87
SW1088_CENTRAL_NERVOUS_SYSTEM	–5.51	–5.51	–4.79	4.64	3.64	3.88
NCIH1651_LUNG	–4.79	–4.78	–4.79	4.32	3.59	3.81
SNB19_CENTRAL_NERVOUS_SYSTEM	–4.96	–4.96	–4.78	4.19	3.57	4.13
NCIH322_LUNG	–5.45	–5.45	–4.78	4.83	3.99	3.78
TE11_OESOPHAGUS	–5.25	–5.25	–4.78	4.55	3.49	3.89
BICR31_UPPER_AERODIGESTIVE_TRACT	–4.77	–0.55	–4.77	4.91	6.03	3.91
SNU449_LIVER	–4.99	–4.99	–4.76	4.32	3.66	4.23
TUHR10TKB_KIDNEY	–5.50	–5.50	–4.75	3.90	3.39	3.91
KYSE450_OESOPHAGUS	–4.74	0.42	–4.74	4.38	5.84	3.78
WM115_SKIN	–5.27	–5.27	–4.74	4.23	3.52	4.04
MCF7_BREAST	–2.43	–2.43	–4.74	4.59	4.63	4.55
DBTRG05MG_CENTRAL_NERVOUS_SYSTEM	–4.99	–4.99	–4.73	4.59	3.49	3.68
KMRC1_KIDNEY	–5.49	–5.49	–4.73	5.21	3.55	3.84
UMUC3_URINARY_TRACT	–4.71	–4.60	–4.71	4.68	3.64	4.11
BC3C_URINARY_TRACT	–5.19	–5.19	–4.71	4.32	3.56	4.02
SH4_SKIN	–4.71	–4.48	–4.71	3.93	3.63	3.96
A375_SKIN	–4.76	–4.76	–4.69	4.77	3.50	3.93
NCIH1650_LUNG	–5.43	–5.43	–4.67	4.28	3.42	3.90
CAL62_THYROID	–4.74	–4.74	–4.67	4.45	3.56	4.17
MDAMB231_BREAST	–4.75	–4.75	–4.66	4.97	3.76	4.02
KP2_PANCREAS	–4.75	–4.75	–4.65	4.43	3.61	3.82
A498_KIDNEY	–4.98	–4.98	–4.65	4.53	3.42	3.87

File S1 (*continued*)

File S1 (*continued*)

Cell name_Organ	Copy number value			Relative RNA level		
	CDKN2BAS	CDKN2B	CDKN2A	CDKN2A	CDKN2B	CDKN2BAS1
C32_SKIN	–0.97	–0.97	–4.65	4.83	5.54	4.15
F36P_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–5.40	–5.40	–4.64	4.48	3.55	4.09
GB1_CENTRAL_NERVOUS_SYSTEM	–5.29	–5.29	–4.64	4.27	3.34	3.87
PK45H_PANCREAS	–4.93	–4.93	–4.63	4.64	3.41	4.04
CMK86_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–5.40	–5.40	–4.63	4.98	3.49	3.92
EBC1_LUNG	–5.29	–5.29	–4.62	4.55	3.68	4.02
HUT78_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–4.98	–4.98	–4.61	4.92	3.87	4.27
SNU1105_CENTRAL_NERVOUS_SYSTEM	–4.61	–4.57	–4.61	4.27	3.55	3.90
NCIH2126_LUNG	–4.71	–4.71	–4.60	4.41	3.56	3.90
YH13_CENTRAL_NERVOUS_SYSTEM	–5.50	–5.50	–4.60	4.33	3.57	3.84
RKN_SOFT_TISSUE	–5.63	–5.63	–4.60	4.73	3.71	4.51
SNU466_CENTRAL_NERVOUS_SYSTEM	–4.89	–4.89	–4.60	5.24	3.56	4.17
JHUEM3_ENDOMETRIUM	–4.59	–0.79	–4.59	4.23	6.01	3.93
NCIH2452_PLEURA	–5.13	–5.13	–4.59	3.98	3.56	4.13
SET2_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–4.59	–4.59	–4.59	4.58	3.56	4.02
NUGC2_STOMACH	–5.18	–5.18	–4.58	4.09	3.68	3.87
RCC10RGB_KIDNEY	–5.14	–5.14	–4.56	4.41	3.34	3.99
SKHEP1_LIVER	–5.10	–5.10	–4.56	4.95	3.38	3.81
SU8686_PANCREAS	–5.38	–5.38	–4.54	4.57	3.49	4.24
MKN45_STOMACH	–4.97	–4.97	–4.54	4.56	3.67	3.99
NCIH460_LUNG	–5.36	–5.36	–4.54	4.13	3.53	3.90
SNU738_CENTRAL_NERVOUS_SYSTEM	–5.03	–5.03	–4.54	4.30	3.45	3.97
AM38_CENTRAL_NERVOUS_SYSTEM	–4.65	–4.65	–4.54	4.47	3.65	3.91
SKLU1_LUNG	–5.30	–5.30	–4.54	4.27	3.78	3.86
COLO680N_OESOPHAGUS	–5.18	–5.18	–4.53	4.77	3.49	3.87
NCIH28_PLEURA	–5.24	–5.24	–4.53	4.33	3.70	3.96
CMLT1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–4.53	–4.53	–4.53	4.61	3.60	4.30
A549_LUNG	–4.84	–4.84	–4.49	4.86	3.53	4.06
MUTZ5_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–5.12	–5.12	–4.49	4.53	3.68	3.94
UMRC6_KIDNEY	–4.73	–4.73	–4.48	5.38	3.57	3.81
HEC50B_ENDOMETRIUM	–5.54	–5.54	–4.48	4.59	3.59	4.25
NCIH1755_LUNG	–5.21	–5.21	–4.48	4.40	3.60	3.68
LOXIMVI_SKIN	–4.46	0.30	–4.46	4.76	6.47	4.10
HTK_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–4.63	–4.63	–4.46	4.16	3.89	3.74
HOS_BONE	–5.16	–5.16	–4.46	4.12	3.47	4.17
HT144_SKIN	–5.20	–5.20	–4.45	4.95	3.60	4.14
EM2_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–5.28	–5.28	–4.44	4.94	3.48	3.91
SNU1196_BILIARY_TRACT	–5.15	–5.15	–4.44	4.56	3.71	4.08
HUPT3_PANCREAS	–5.20	–5.20	–4.43	4.19	3.65	4.13
VMRCLCD_LUNG	–4.67	–4.67	–4.43	4.98	3.59	3.96
WM2664_SKIN	–4.99	–4.99	–4.43	4.49	3.44	3.86

File S1 (*continued*)

File S1 (*continued*)

Cell name_Organ	Copy number value			Relative RNA level		
	CDKN2BAS	CDKN2B	CDKN2A	CDKN2A	CDKN2B	CDKN2BAS1
LAMA84_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–4.76	–4.76	–4.42	4.64	3.56	4.19
ONS76_CENTRAL_NERVOUS_SYSTEM	–0.22	–0.22	–4.42	4.73	3.75	3.95
H4_CENTRAL_NERVOUS_SYSTEM	–5.10	–5.10	–4.42	4.23	3.53	3.80
ACHN_KIDNEY	–0.16	–0.16	–4.41	4.28	5.14	3.86
DANG_PANCREAS	–4.94	–4.94	–4.41	4.19	3.64	3.96
MALME3M_SKIN	–4.85	–4.85	–4.41	5.00	3.46	3.79
JURKAT_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–5.14	–5.14	–4.39	4.24	3.55	3.96
HCC1806_BREAST	–5.25	–5.25	–4.39	4.57	3.72	3.81
REH_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–5.09	–5.09	–4.39	4.51	3.49	3.94
SUPB15_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–4.38	–2.54	–4.38	4.70	3.73	4.13
HS683_CENTRAL_NERVOUS_SYSTEM	–5.12	–5.12	–4.38	4.33	3.46	3.93
JL1_PLEURA	–5.03	–5.03	–4.36	4.27	3.57	4.05
TE14_OESOPHAGUS	–4.60	–4.60	–4.36	4.31	3.62	3.93
RT112_URINARY_TRACT	–5.01	–5.01	–4.36	4.16	3.53	3.93
MOLT4_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.09	–0.09	–4.34	4.47	3.78	4.66
SCC25_UPPER_AERODIGESTIVE_TRACT	–0.64	–0.64	–4.34	4.74	4.99	3.79
SNU387_LIVER	–4.98	–4.98	–4.34	4.98	3.67	3.84
BXPC3_PANCREAS	–4.45	–4.45	–4.33	4.99	3.48	3.88
PECAPJ34CLONEC12_UPPER_AERODIGESTIVE_TRACT	–4.87	–4.87	–4.33	4.18	3.87	3.73
NCIH1793_LUNG	–4.32	–0.06	–4.32	4.44	7.14	3.91
KYSE180_OESOPHAGUS	–5.62	–5.62	–4.32	4.99	3.64	3.95
COLO679_SKIN	–4.32	–1.01	–4.32	4.33	7.62	3.97
SNU489_CENTRAL_NERVOUS_SYSTEM	–4.88	–4.88	–4.32	4.43	3.61	3.78
MELJUSO_SKIN	–5.07	–5.07	–4.32	4.07	3.69	4.07
NCIH2122_LUNG	–5.08	–5.08	–4.32	4.05	3.63	3.94
PANC0213_PANCREAS	–5.31	–5.31	–4.32	4.13	3.48	3.81
ALLSIL_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–4.92	–4.92	–4.31	4.24	3.70	4.03
BFTC909_KIDNEY	–5.10	–5.10	–4.31	4.24	3.50	3.94
NALM19_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–4.30	–4.30	–4.30	4.15	3.54	4.08
HCC1171_LUNG	–5.00	–5.00	–4.29	4.12	3.56	3.65
JHOM1_OVARY	–4.55	–4.55	–4.29	4.53	3.51	3.93
UACC62_SKIN	–5.08	–5.08	–4.29	4.22	3.65	4.02
HUG1N_STOMACH	–5.40	–5.40	–4.29	4.47	3.63	3.83
NCCSTCK140_STOMACH	–4.41	–4.41	–4.29	4.74	3.48	3.91
SNU840_OVARY	–4.28	–4.28	–4.28	4.57	3.68	3.96
HLC1_LUNG	–4.28	–4.28	–4.28	4.25	3.51	4.05
ISTMES1_PLEURA	–4.72	–4.72	–4.28	4.31	3.57	3.95
WM1799_SKIN	–0.22	–0.22	–4.28	4.24	5.14	4.28
GRANTA519_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–4.63	–4.63	–4.27	4.44	3.54	4.08
PF382_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–5.30	–5.30	–4.27	5.20	3.54	4.28
NCIH2052_PLEURA	–5.15	–5.15	–4.27	4.37	3.61	3.94

File S1 (*continued*)

File S1 (*continued*)

Cell name_Organ	Copy number value			Relative RNA level		
	CDKN2BAS	CDKN2B	CDKN2A	CDKN2A	CDKN2B	CDKN2BAS1
LCLC103H_LUNG	–4.59	–4.59	–4.26	4.32	3.44	3.96
TE10_OESOPHAGUS	–4.95	–4.95	–4.25	4.86	3.64	4.12
RMGI_OVARY	–0.02	–0.02	–4.25	5.18	4.55	3.80
OCILY19_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–4.91	–4.91	–4.25	4.69	3.70	4.17
SKMEL5_SKIN	–4.24	–4.24	–4.24	4.33	3.49	3.95
BECKER_CENTRAL_NERVOUS_SYSTEM	–0.35	–0.35	–4.24	4.24	5.47	3.98
NALM6_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–5.05	–5.05	–4.23	4.64	3.55	4.17
SF172_CENTRAL_NERVOUS_SYSTEM	–4.93	–4.93	–4.22	4.73	3.47	3.85
KYSE70_OESOPHAGUS	–5.30	–5.30	–4.22	4.90	3.56	3.98
P12ICHIKAWA_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–4.20	–0.29	–4.20	4.55	3.68	5.28
NOMO1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–5.09	–5.09	–4.19	4.49	3.41	4.00
NCIH1838_LUNG	–5.01	–5.01	–4.18	4.63	3.69	4.10
RS411_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–4.77	–4.77	–4.17	4.45	3.51	3.89
SLR21_KIDNEY	–4.17	–4.17	–4.17	4.33	3.58	4.05
CAKI1_KIDNEY	–5.11	–5.11	–4.14	4.79	3.83	4.10
NCIH3255_LUNG	–4.13	–4.13	–4.13	4.33	3.32	3.72
LOUNH91_LUNG	–4.72	–4.72	–4.13	4.48	3.78	4.29
MHHCALL2_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–4.69	–4.69	–4.12	4.35	3.30	5.32
SNU410_PANCREAS	–4.82	–4.82	–4.11	4.55	3.57	3.94
LC1SQSF_LUNG	–4.70	–4.70	–4.11	4.83	3.50	3.85
NB4_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–4.70	–4.70	–4.11	4.61	3.70	4.27
NCIH1944_LUNG	–4.72	–4.72	–4.09	4.31	3.55	4.14
786O_KIDNEY	–4.96	–4.96	–4.09	4.64	3.77	4.42
KYSE510_OESOPHAGUS	–4.48	–4.48	–4.08	4.70	3.67	3.99
SNU201_CENTRAL_NERVOUS_SYSTEM	–4.82	–4.82	–4.08	4.28	3.56	3.94
MHHCALL3_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–4.08	–0.94	–4.08	5.09	3.57	4.50
GOS3_CENTRAL_NERVOUS_SYSTEM	–4.97	–4.97	–4.08	4.58	3.68	4.12
SNU668_STOMACH	–4.06	–4.06	–4.06	4.78	3.45	3.94
TCCPAN2_PANCREAS	–4.05	–4.05	–4.05	4.78	3.64	3.80
LN18_CENTRAL_NERVOUS_SYSTEM	–4.05	–4.05	–4.05	4.69	3.55	3.82
KE37_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–4.03	–0.02	–4.03	4.53	3.82	4.25
RT11284_URINARY_TRACT	–4.65	–4.65	–4.02	4.12	3.85	3.84
CAL54_KIDNEY	–4.68	–4.68	–4.02	4.25	3.61	4.06
CAKI2_KIDNEY	–4.00	–4.00	–4.00	4.16	3.54	3.77
MHHCALL4_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–3.99	–3.99	–3.99	5.05	3.53	4.26
SNU478_BILIARY_TRACT	–4.47	–4.47	–3.97	5.10	3.72	4.17
NALM1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–4.60	–4.60	–3.95	4.64	3.54	4.39
UOK101_KIDNEY	–4.26	–4.26	–3.95	4.47	3.52	3.88
MG63_BONE	–4.71	–4.71	–3.94	4.91	3.56	3.97
U178_CENTRAL_NERVOUS_SYSTEM	–4.75	–4.75	–3.91	4.64	3.70	3.85
KPL1_BREAST	–1.50	–1.50	–3.90	4.89	5.36	4.51

File S1 (*continued*)

File S1 (*continued*)

Cell name_Organ	Copy number value			Relative RNA level		
	CDKN2BAS	CDKN2B	CDKN2A	CDKN2A	CDKN2B	CDKN2BAS1
PEER_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.02	0.02	–3.90	4.94	3.82	4.63
KLM1_PANCREAS	–3.89	–3.89	–3.89	4.71	3.43	3.80
U118MG_CENTRAL_NERVOUS_SYSTEM	–4.64	–4.64	–3.88	4.68	3.44	3.66
MIAPACA2_PANCREAS	–4.70	–4.70	–3.86	4.40	3.54	3.79
HCC15_LUNG	–4.55	–4.55	–3.84	4.78	3.46	4.45
NCIH1869_LUNG	–4.70	–4.70	–3.83	4.96	3.55	3.96
SCC9_UPPER_AERODIGESTIVE_TRACT	–3.78	–3.78	–3.78	4.45	3.74	3.87
LC1F_LUNG	–3.77	–3.77	–3.77	4.81	3.51	4.05
SKMES1_LUNG	–4.71	–4.71	–3.75	4.67	3.78	4.15
SNU1079_BILIARY_TRACT	–3.73	–3.73	–3.73	4.84	3.57	4.11
UMRC2_KIDNEY	–4.43	–4.43	–3.72	4.58	3.52	4.02
A101D_SKIN	–5.67	–5.67	–3.72	3.98	3.47	4.10
KMRC20_KIDNEY	–4.89	–4.89	–3.72	4.40	3.56	4.08
KNS81_CENTRAL_NERVOUS_SYSTEM	–3.72	–3.72	–3.72	4.26	3.76	4.08
LMSU_STOMACH	–4.90	–4.90	–3.66	4.51	3.46	3.99
K562_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–3.58	–3.58	–3.58	4.51	3.41	4.19
MESSA_SOFT_TISSUE	–4.86	–4.86	–3.57	4.06	3.75	3.88
MOLP8_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–5.18	–5.18	–3.51	5.02	3.61	4.17
KG1C_CENTRAL_NERVOUS_SYSTEM	–3.51	–3.51	–3.51	4.66	3.74	4.06
A172_CENTRAL_NERVOUS_SYSTEM	–5.12	–5.12	–3.47	4.45	3.52	4.09
BT20_BREAST	–3.46	–3.46	–3.46	4.61	3.45	3.79
PK1_PANCREAS	–5.83	–5.83	–3.46	4.33	3.68	3.73
NMCG1_CENTRAL_NERVOUS_SYSTEM	–4.81	–3.44	–3.44	3.85	3.59	3.98
HCC1395_BREAST	–3.44	–3.44	–3.44	4.23	3.60	3.89
MOLM13_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–5.86	–5.86	–3.42	4.95	3.60	4.03
NCIH1666_LUNG	–4.68	–4.68	–3.42	3.97	3.56	3.76
JHOS2_OVARY	–5.27	–5.27	–3.41	5.24	3.56	4.14
NCIH2228_LUNG	–5.18	–5.18	–3.39	4.02	3.58	3.85
NCIH292_LUNG	–5.18	–5.18	–3.37	4.74	3.59	3.67
A673_BONE	–5.13	–5.13	–3.37	4.37	3.65	3.78
MOLT16_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–5.34	–5.34	–3.36	4.69	3.53	4.71
TYKNU_OVARY	–3.35	–3.35	–3.35	4.49	3.64	4.65
NCIH1563_LUNG	–5.25	–5.25	–3.32	4.60	3.50	3.94
KNS60_CENTRAL_NERVOUS_SYSTEM	–5.28	–5.28	–3.30	4.08	3.49	3.89
CAL29_URINARY_TRACT	–4.99	–4.99	–3.29	4.53	3.57	4.04
JHOS4_OVARY	–5.27	–5.27	–3.28	4.60	3.58	3.58
ECGI10_OESOPHAGUS	0.76	0.76	–3.24	4.93	7.61	4.06
A3KAW_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–5.21	–5.21	–3.23	4.72	3.89	4.16
SLR26_KIDNEY	–5.12	–5.12	–3.21	4.42	3.34	3.78
LI7_LIVER	–4.96	–4.96	–3.20	4.34	3.36	4.61
SUPT1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–5.71	–5.71	–3.18	4.88	4.12	4.36

File S1 (*continued*)

File S1 (*continued*)

Cell name_Organ	Copy number value			Relative RNA level		
	CDKN2BAS	CDKN2B	CDKN2A	CDKN2A	CDKN2B	CDKN2BAS1
JHOC5_OVARY	–5.87	–5.87	–3.17	4.25	3.44	4.09
PANC0813_PANCREAS	–4.69	–4.69	–3.17	5.00	3.63	3.86
CAPAN1_PANCREAS	–4.84	–4.84	–3.15	4.28	3.61	3.71
SW780_URINARY_TRACT	–5.09	–5.09	–3.15	4.74	3.58	3.91
OVTOKO_OVARY	–3.15	–3.15	–3.15	4.90	4.01	3.97
EFM19_BREAST	–5.29	–5.29	–3.13	4.23	3.51	4.05
NCIH838_LUNG	–4.94	–4.94	–3.12	4.71	3.62	4.01
REC1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–5.03	–5.03	–3.09	4.13	3.62	4.06
NCIH2170_LUNG	–5.40	–5.40	–3.07	4.12	3.55	4.05
T98G_CENTRAL_NERVOUS_SYSTEM	–0.22	–0.22	–3.06	4.49	7.33	4.47
SKMEL24_SKIN	–5.00	–5.00	–3.06	3.97	3.52	4.38
RT4_URINARY_TRACT	–4.93	–4.93	–3.00	4.54	3.44	4.14
TUHR4TKB_KIDNEY	–3.00	–3.00	–3.00	5.41	4.73	4.00
RPMI8402_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–5.07	–5.07	–2.99	4.52	3.50	4.20
GAMG_CENTRAL_NERVOUS_SYSTEM	–5.09	–5.09	–2.97	4.12	3.31	3.91
NUGC4_STOMACH	–5.28	–5.28	–2.97	5.17	3.65	4.04
SW900_LUNG	–4.69	–4.69	–2.94	4.84	3.80	3.87
OUMS27_BONE	–4.78	–4.78	–2.94	4.44	3.63	4.10
G361_SKIN	–0.47	–0.47	–2.94	4.38	5.62	3.97
SW1990_PANCREAS	–5.41	–5.41	–2.93	4.70	3.66	4.19
U251MG_CENTRAL_NERVOUS_SYSTEM	–4.94	–4.94	–2.91	4.06	3.47	3.98
KS1_CENTRAL_NERVOUS_SYSTEM	–4.93	–4.93	–2.89	4.68	3.50	4.03
BV173_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–2.89	–2.89	–2.89	4.57	3.51	4.29
PANC0504_PANCREAS	–4.99	–4.99	–2.84	4.17	3.49	4.17
SW579_THYROID	–4.94	–4.94	–2.84	4.38	3.60	3.93
NCIH2405_LUNG	–2.84	–2.84	–2.84	4.24	3.46	4.05
CMK_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–4.44	–4.44	–2.83	4.86	3.49	4.35
COLO678_LARGE_INTESTINE	–4.59	–4.59	–2.80	4.98	3.47	4.08
YKG1_CENTRAL_NERVOUS_SYSTEM	–4.63	–4.63	–2.79	4.51	3.33	5.41
U87MG_CENTRAL_NERVOUS_SYSTEM	–4.53	–4.53	–2.78	3.79	3.43	3.90
RERFLCAD1_LUNG	–4.88	–4.88	–2.78	4.17	3.58	3.78
BFTC905_URINARY_TRACT	–4.73	–4.73	–2.77	4.50	3.60	4.15
HCC2935_LUNG	–4.43	–4.43	–2.76	4.07	3.52	3.92
42MGBA_CENTRAL_NERVOUS_SYSTEM	–4.43	–4.43	–2.71	4.29	3.34	3.86
MM1S_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–2.69	–2.69	–2.69	4.52	3.76	3.88
HCC95_LUNG	–4.48	–4.48	–2.69	4.69	3.56	4.06
PECAPJ15_UPPER_AERODIGESTIVE_TRACT	–2.68	–2.68	–2.68	4.56	4.05	3.94
KP4_PANCREAS	–4.83	–4.83	–2.65	4.65	3.57	4.19
OSRC2_KIDNEY	–4.27	–4.27	–2.60	4.40	3.40	4.14
BICR18_UPPER_AERODIGESTIVE_TRACT	–4.33	–4.33	–2.48	4.45	3.57	4.05
ACCMESO1_PLEURA	–4.11	–4.11	–2.48	4.50	3.33	3.96
HEYA8_OVARY	–4.39	–4.39	–2.47	5.02	3.55	3.97

File S1 (*continued*)

File S1 (*continued*)

Cell name_Organ	Copy number value			Relative RNA level		
	CDKN2BAS	CDKN2B	CDKN2A	CDKN2A	CDKN2B	CDKN2BAS1
S117_SOFT_TISSUE	-4.53	-4.53	-2.46	4.70	3.62	4.05
NCIH1623_LUNG	-3.55	-3.55	-2.40	6.24	5.07	3.95
UT7_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	-4.52	-4.52	-2.39	4.65	3.60	4.01
PANC1_PANCREAS	-4.31	-4.31	-2.37	4.32	3.72	4.13
EOL1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	-4.69	-4.69	-2.36	4.53	3.69	4.28
MSTO211H_PLEURA	-5.14	-5.14	-2.26	4.93	3.40	4.18
GSU_STOMACH	-2.26	-2.26	-2.26	4.83	3.48	3.76
HEL_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	-4.42	-4.42	-2.22	4.31	3.49	4.20
LCLC97TM1_LUNG	-4.80	-4.80	-2.18	4.23	3.39	4.33
SR786_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	-2.04	-2.04	-2.04	6.03	3.72	4.37
KYSE140_OESOPHAGUS	-3.77	-3.77	-1.99	4.51	3.69	4.21
SKNDZ_AUTONOMIC_GANGLIA	-1.94	-1.94	-1.94	6.64	3.80	4.31
BT474_BREAST	-1.82	-1.82	-1.82	5.03	3.80	4.00
BICR22_UPPER_AERODIGESTIVE_TRACT	0.13	0.13	-1.79	4.55	7.96	3.98
RDES_BONE	-1.64	-1.64	-1.64	6.96	3.82	4.43
SQ1_LUNG	-1.62	-1.62	-1.62	6.65	4.08	4.14
CAL78_BONE	-1.62	-1.62	-1.62	7.20	4.13	3.98
HCC1143_BREAST	-1.62	-1.62	-1.62	6.34	6.09	4.08
PATU8988S_PANCREAS	-1.60	-1.60	-1.60	6.90	4.27	4.07
SKLMS1_SOFT_TISSUE	-1.56	-1.56	-1.56	6.83	5.13	3.67
RVH421_SKIN	-1.56	-1.56	-1.56	4.41	4.60	4.13
OCIAML5_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	-1.50	-1.50	-1.50	6.34	3.64	4.25
SNU213_PANCREAS	-1.44	-1.44	-1.44	8.11	6.91	3.77
HS294T_SKIN	-1.43	-1.43	-1.43	4.61	3.51	3.90
KYSE520_OESOPHAGUS	-1.43	-1.43	-1.43	7.57	5.31	3.85
NCIH716_LARGE_INTESTINE	-1.41	-1.41	-1.41	6.83	4.81	4.11
CORL105_LUNG	-1.40	-1.40	-1.40	6.02	5.70	3.91
SKES1_BONE	-1.31	-1.31	-1.31	7.16	3.55	4.07
KYSE270_OESOPHAGUS	-1.29	-1.29	-1.29	7.71	3.89	3.75
LS123_LARGE_INTESTINE	-1.28	-1.28	-1.28	6.52	6.09	4.16
HUH1_LIVER	-1.28	-1.28	-1.28	6.91	6.43	4.05
WM983B_SKIN	-1.28	-1.28	-1.28	7.54	4.92	3.95
NCIH854_LUNG	-1.25	-1.25	-1.25	6.46	7.39	4.12
NCIH2087_LUNG	-1.25	-1.25	-1.25	7.74	3.90	4.37
COLO320_LARGE_INTESTINE	-1.23	-1.23	-1.23	6.08	3.57	4.07
NCIH1792_LUNG	-1.23	-1.23	-1.23	7.95	5.56	3.96
ABC1_LUNG	-1.23	-1.23	-1.23	7.08	6.06	4.11
MORCPR_LUNG	-1.23	-1.23	-1.23	6.39	5.18	3.93
RERFGC1B_STOMACH	-1.22	-1.22	-1.22	6.39	4.94	3.97
UMUC1_URINARY_TRACT	-1.22	-1.22	-1.22	5.52	6.90	3.90
NCIH441_LUNG	-1.22	-1.22	-1.22	6.17	4.18	4.09

File S1 (*continued*)

File S1 (*continued*)

Cell name_Organ	Copy number value			Relative RNA level		
	CDKN2BAS	CDKN2B	CDKN2A	CDKN2A	CDKN2B	CDKN2BAS1
PLCPRF5_LIVER	−1.21	−1.21	−1.21	6.83	3.84	3.85
SLR25_KIDNEY	−1.20	−1.20	−1.20	6.18	3.70	3.96
HCC2279_LUNG	−1.20	−1.20	−1.20	4.36	3.49	3.84
T84_LARGE_INTESTINE	−1.19	−1.19	−1.19	5.87	3.96	4.02
NCIH727_LUNG	−1.19	−1.19	−1.19	6.84	5.79	4.62
PSN1_PANCREAS	−1.18	−1.18	−1.18	4.12	6.49	3.87
ALEXANDERCELLS_LIVER	−1.18	−1.18	−1.18	6.93	3.57	4.06
NCIH1703_LUNG	−1.17	−1.17	−1.17	8.25	4.86	4.46
CORL23_LUNG	0.01	0.01	−1.16	7.99	6.72	4.06
SNU216_STOMACH	−1.15	−1.15	−1.15	7.57	6.71	4.41
NCIH23_LUNG	−1.14	−1.14	−1.14	6.46	3.75	4.00
ASPC1_PANCREAS	−1.14	−1.14	−1.14	8.50	8.51	4.56
MKN74_STOMACH	−1.13	−1.13	−1.13	5.89	4.86	4.08
MDAMB361_BREAST	−1.70	−1.70	−1.12	5.40	3.81	4.00
TE4_OESOPHAGUS	−1.08	−1.08	−1.08	6.87	6.79	3.76
MDAMB453_BREAST	−1.07	−1.07	−1.07	5.91	3.84	4.24
SH10TC_STOMACH	−1.07	−1.07	−1.07	7.28	6.01	4.13
SNU886_LIVER	−1.07	−1.07	−1.07	7.80	5.86	3.63
SNU1076_UPPER_AERODIGESTIVE_TRACT	−1.05	−1.05	−1.05	7.79	7.36	4.33
HS852T_SKIN	−1.03	−1.03	−1.03	5.67	4.18	3.99
SKNAS_AUTONOMIC_GANGLIA	−1.02	−1.02	−1.02	5.48	3.65	3.72
RD_SOFT_TISSUE	−1.01	−1.01	−1.01	7.67	5.21	4.31
SNUC4_LARGE_INTESTINE	−1.01	−1.01	−1.01	4.27	3.69	3.92
NCIH2342_LUNG	−1.00	−1.00	−1.00	6.66	5.33	4.00
MHHES1_BONE	−1.00	−1.00	−1.00	5.73	3.48	4.15
TOLEDO_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	−0.99	−0.95	−0.99	6.47	3.55	4.14
RERFLCAI_LUNG	−0.98	−0.98	−0.98	7.15	4.51	3.97
SUPM2_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	−0.98	−0.98	−0.98	6.64	3.44	4.13
SNU5_STOMACH	−0.97	−0.97	−0.97	6.15	6.15	4.36
LOUCY_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	−0.97	−0.97	−0.97	6.96	3.72	4.07
HUTU80_SMALL_INTESTINE	−0.97	0.01	−0.97	6.61	5.55	4.00
CCFSTTG1_CENTRAL_NERVOUS_SYSTEM	−0.97	−0.97	−0.97	7.95	5.70	3.94
SCABER_URINARY_TRACT	−0.97	−0.97	−0.97	7.80	4.83	3.95
59M_OVARY	−0.97	−0.97	−0.97	5.87	4.49	3.92
MEWO_SKIN	−0.96	−0.96	−0.96	5.76	4.91	4.25
TT_THYROID	−0.96	−0.96	−0.96	4.36	3.42	4.13
CAL33_UPPER_AERODIGESTIVE_TRACT	−0.95	−0.95	−0.95	6.12	5.93	3.77
RH30_SOFT_TISSUE	−0.93	−0.93	−0.93	8.13	4.64	4.02
SKMM2_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	−0.93	−0.93	−0.93	7.01	3.69	3.98
NCIH226_LUNG	−0.92	−0.92	−0.92	4.79	4.77	4.00
SLR23_KIDNEY	−0.92	−0.92	−0.92	5.49	4.55	3.80

File S1 (*continued*)

File S1 (*continued*)

Cell name_Organ	Copy number value			Relative RNA level		
	CDKN2BAS	CDKN2B	CDKN2A	CDKN2A	CDKN2B	CDKN2BAS1
SKMEL2_SKIN	–0.92	–0.92	–0.92	6.27	4.06	3.82
SNU1214_UPPER_AERODIGESTIVE_TRACT	–0.91	–0.91	–0.91	6.01	6.45	3.96
SJSA1_BONE	–0.90	–0.90	–0.90	7.90	6.51	4.01
CHAGOK1_LUNG	–0.90	–0.90	–0.90	6.89	4.15	4.14
HL60_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.90	–0.90	–0.90	6.00	4.09	4.14
NCIH1915_LUNG	–0.90	–0.90	–0.90	8.18	4.04	4.21
OVKATE_OVARY	–0.89	–0.89	–0.89	6.90	4.45	3.87
G292CLONEA141B1_BONE	–0.89	–0.89	–0.89	7.97	4.38	3.86
RI1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.88	–0.88	–0.88	8.36	3.77	4.21
A704_KIDNEY	–0.87	–0.87	–0.87	5.25	3.92	4.66
EFM192A_BREAST	–0.87	–0.87	–0.87	6.11	4.81	4.16
KASUMI1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.86	–0.86	–0.86	5.22	3.66	4.13
NCIH2347_LUNG	–0.86	–0.86	–0.86	7.14	4.83	4.02
AZ521_STOMACH	–0.86	0.00	–0.86	6.44	6.07	4.13
SNUC2A_LARGE_INTESTINE	–0.85	–0.85	–0.85	6.86	4.24	4.07
EFO27_OVARY	–0.85	–0.85	–0.85	7.98	4.90	3.93
769P_KIDNEY	–0.85	–0.85	–0.85	4.55	4.94	4.07
SKMEL3_SKIN	–0.84	–0.84	–0.84	6.43	3.85	3.96
L363_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.84	–0.84	–0.84	7.20	3.77	4.76
K029AX_SKIN	–0.83	–0.83	–0.83	7.57	4.96	4.05
MEC1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.83	–0.83	–0.83	6.05	3.54	4.05
SUPT11_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.83	–0.83	–0.83	7.61	3.73	4.22
HEC1A_ENDOMETRIUM	–0.83	–0.83	–0.83	6.63	3.82	4.08
TC32_BONE	–0.83	–0.83	–0.83	4.72	3.69	4.17
PK59_PANCREAS	–0.82	–0.82	–0.82	7.09	7.53	4.17
JEKO1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.81	–0.81	–0.81	7.70	3.66	4.12
KMRC2_KIDNEY	–0.80	–0.80	–0.80	6.12	4.47	3.67
C2BBE1_LARGE_INTESTINE	–0.80	–0.80	–0.80	5.91	4.39	4.05
NCIH1975_LUNG	–0.79	–0.79	–0.79	6.06	5.71	4.34
SNU1272_KIDNEY	–0.79	–0.79	–0.79	6.62	4.41	4.04
PECAPJ41CLONED2_UPPER_AERODIGESTIVE_TRACT	–0.79	–0.79	–0.79	6.06	5.53	3.98
JHH5_LIVER	–0.78	–0.78	–0.78	7.81	7.16	4.34
SUDHL1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.78	–0.78	–0.78	7.01	3.51	4.68
SHP77_LUNG	–0.76	–0.76	–0.76	6.98	3.60	4.06
HCC1419_BREAST	–0.76	–0.76	–0.76	5.31	3.96	4.28
BEN_LUNG	–0.75	–0.75	–0.75	6.15	4.32	4.30
OV90_OVARY	–0.75	–0.75	–0.75	7.59	5.23	4.13
JHH2_LIVER	–0.75	–0.75	–0.75	7.89	9.32	4.11
HS742T_BREAST	–0.74	–0.74	–0.74	6.68	7.86	3.83
NCIH2030_LUNG	–0.74	–0.74	–0.74	6.60	5.14	4.04
IPC298_SKIN	–0.72	–0.72	–0.72	8.22	5.17	4.06

File S1 (*continued*)

File S1 (*continued*)

Cell name_Organ	Copy number value			Relative RNA level		
	CDKN2BAS	CDKN2B	CDKN2A	CDKN2A	CDKN2B	CDKN2BAS1
TT2609C02_THYROID	–0.72	–0.72	–0.72	7.48	4.34	4.03
HEC1B_ENDOMETRIUM	–0.72	–0.72	–0.72	6.42	3.72	3.96
NCIH1435_LUNG	–0.71	–0.71	–0.71	6.22	5.19	4.04
SKMEL1_SKIN	–0.71	–0.71	–0.71	7.17	4.94	3.88
RMUGS_OVARY	–0.71	–0.71	–0.71	5.40	3.97	4.16
HCC1897_LUNG	–0.70	–0.70	–0.70	7.48	4.37	3.98
T24_URINARY_TRACT	–0.70	–0.70	–0.70	7.26	4.36	3.95
SKMEL31_SKIN	–0.69	0.30	–0.69	4.17	6.27	3.81
KNS42_CENTRAL_NERVOUS_SYSTEM	–0.04	–0.04	–0.69	7.16	4.41	4.01
CORL24_LUNG	–0.69	–0.69	–0.69	7.71	5.72	4.31
SKMEL30_SKIN	–0.68	–0.68	–0.68	7.82	5.19	3.97
SNU349_KIDNEY	–0.68	–0.68	–0.68	7.28	4.91	3.75
SCC15_UPPER_AERODIGESTIVE_TRACT	–0.68	–0.68	–0.68	7.52	7.44	4.18
NCIH1105_LUNG	–0.67	–0.67	–0.67	7.14	4.35	4.45
NCIH1581_LUNG	–0.67	–0.67	–0.67	6.91	4.33	4.16
YD8_UPPER_AERODIGESTIVE_TRACT	–0.67	–0.67	–0.67	7.95	7.73	4.19
NCIH2286_LUNG	–0.67	–0.67	–0.67	7.09	5.04	4.11
NCIH358_LUNG	–0.67	–0.67	–0.67	7.75	5.36	3.91
TEN_ENDOMETRIUM	–0.67	–0.67	–0.67	8.41	4.41	3.87
MOGGUVW_CENTRAL_NERVOUS_SYSTEM	–0.66	–0.66	–0.66	7.99	5.82	3.85
NCIH211_LUNG	–0.66	–0.66	–0.66	6.01	3.65	3.86
CFPAC1_PANCREAS	–0.66	–0.66	–0.66	8.11	5.89	3.87
VMRCLCP_LUNG	–0.65	–0.65	–0.65	4.41	3.61	3.89
PANC0203_PANCREAS	–0.65	–0.65	–0.65	7.47	5.28	4.17
HCC78_LUNG	–0.64	–0.64	–0.64	6.00	4.04	4.47
PC14_LUNG	–0.64	–0.64	–0.64	8.71	6.10	4.11
NCIH1573_LUNG	–0.64	–0.64	–0.64	7.40	5.62	4.23
PECAPJ49_UPPER_AERODIGESTIVE_TRACT	–0.64	–0.64	–0.64	7.71	4.79	4.11
CORL311_LUNG	–0.64	–0.64	–0.64	7.29	4.07	4.22
CAPAN2_PANCREAS	–0.64	–0.64	–0.64	8.82	5.97	4.12
BHY_UPPER_AERODIGESTIVE_TRACT	–0.63	–0.63	–0.63	6.16	6.60	4.46
NCIH2171_LUNG	–0.63	–0.63	–0.63	7.49	3.83	3.90
RH41_SOFT_TISSUE	–0.63	–0.63	–0.63	7.67	3.64	4.12
SNU245_BILIARY_TRACT	–0.63	–0.63	–0.63	5.14	3.80	4.25
MKN1_STOMACH	–0.63	–0.63	–0.63	8.06	5.70	4.08
ML1_THYROID	–0.63	–0.63	–0.63	7.48	6.27	4.17
COV362_OVARY	–0.62	–0.62	–0.62	8.49	3.93	4.04
HT1197_URINARY_TRACT	–0.62	–0.62	–0.62	6.07	5.03	4.14
MELHO_SKIN	–0.61	–0.61	–0.62	5.31	4.79	4.28
IGR37_SKIN	–0.61	–0.61	–0.61	4.35	4.04	3.97
UACC257_SKIN	–0.61	–0.61	–0.61	7.61	4.50	4.04

File S1 (*continued*)

File S1 (*continued*)

Cell name_Organ	Copy number value			Relative RNA level		
	CDKN2BAS	CDKN2B	CDKN2A	CDKN2A	CDKN2B	CDKN2BAS1
OCIM1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.61	–0.61	–0.61	8.53	6.95	4.03
UACC893_BREAST	–0.60	–0.60	–0.60	5.72	5.00	3.98
MINO_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.60	–0.60	–0.60	8.06	3.82	4.26
TT_OESOPHAGUS	–0.59	–0.59	–0.59	7.07	7.00	4.13
BCPAP_THYROID	–0.58	–0.58	–0.58	7.14	4.25	3.95
SNU503_LARGE_INTESTINE	–0.58	–0.58	–0.58	7.41	7.40	4.02
WM793_SKIN	–0.58	–0.58	–0.58	7.59	4.33	4.08
MDAMB436_BREAST	–0.57	–0.57	–0.57	7.65	4.17	3.77
YD15_SALIVARY_GLAND	–0.56	–0.56	–0.56	7.30	4.17	4.02
BHT101_THYROID	–0.55	–0.55	–0.55	7.89	7.96	4.05
COLO829_SKIN	–0.55	–0.55	–0.55	9.15	7.69	4.29
TE1_OESOPHAGUS	–0.54	–0.54	–0.54	8.05	5.74	3.98
HDQP1_BREAST	–0.54	–0.54	–0.54	8.83	6.60	4.04
NCIH650_LUNG	–0.54	–0.54	–0.54	7.65	5.84	3.92
PATU8988T_PANCREAS	–0.53	–0.53	–0.53	7.39	3.97	4.23
SCC4_UPPER_AERODIGESTIVE_TRACT	–0.53	–0.53	–0.53	6.12	5.78	3.95
SNU308_BILIARY_TRACT	–0.52	–0.52	–0.52	7.81	6.57	4.08
KYSE150_OESOPHAGUS	–0.52	–0.52	–0.52	7.98	6.70	4.22
JHH7_LIVER	–0.52	–0.52	–0.52	7.20	4.64	4.04
CAOV3_OVARY	–0.52	–0.52	–0.52	8.06	4.93	4.11
HS729_SOFT_TISSUE	–0.51	–0.51	–0.51	8.13	5.74	3.94
SW948_LARGE_INTESTINE	–0.51	–0.51	–0.51	6.51	3.84	3.99
U2OS_BONE	–0.50	–0.50	–0.50	4.34	3.61	4.08
MKN7_STOMACH	–0.50	–0.50	–0.50	7.44	7.69	4.02
FADU_UPPER_AERODIGESTIVE_TRACT	–0.50	–0.50	–0.50	6.87	4.69	3.96
KYSE30_OESOPHAGUS	–0.50	–0.50	–0.50	6.45	7.99	4.01
SNU475_LIVER	–0.49	–0.49	–0.49	7.52	6.00	3.91
DMS114_LUNG	–0.49	–0.49	–0.49	6.42	3.96	4.24
COLO818_SKIN	–0.30	–0.30	–0.49	4.47	6.15	4.03
HPAC_PANCREAS	–0.49	–0.49	–0.49	7.04	7.07	4.25
EW8_BONE	–0.48	–0.48	–0.48	6.75	3.68	3.68
	–0.48	–0.48	–0.48	8.42	7.04	3.94
PC3_PROSTATE	–0.48	–0.48	–0.48	7.09	5.38	3.88
EVSAT_BREAST	–0.48	–0.48	–0.48	5.92	3.96	4.12
RERFLCAD2_LUNG	–0.47	–0.47	–0.47	7.90	5.27	4.02
EWS502_BONE	–0.47	–0.47	–0.47	7.28	3.53	4.28
HARA_LUNG	–0.45	–0.45	–0.45	9.35	5.42	4.11
L428_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.45	–0.45	–0.45	7.34	3.54	3.97
DETROIT562_UPPER_AERODIGESTIVE_TRACT	–0.41	–0.41	–0.44	5.96	5.29	3.86
NCIH747_LARGE_INTESTINE	–0.44	–0.44	–0.44	7.97	7.18	4.11
T47D_BREAST	–0.44	–0.44	–0.44	6.43	4.29	4.34

File S1 (*continued*)

File S1 (*continued*)

Cell name_Organ	Copy number value			Relative RNA level		
	CDKN2BAS	CDKN2B	CDKN2A	CDKN2A	CDKN2B	CDKN2BAS1
IALM_LUNG	–0.37	0.11	–0.44	8.44	5.07	3.87
KARPAS620_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.43	–0.43	–0.43	6.44	3.59	4.16
MEG01_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.43	–0.43	–0.43	8.82	5.05	4.22
A253_SALIVARY_GLAND	–0.43	–0.43	–0.43	6.81	4.97	4.03
COLO849_SKIN	–0.42	–0.42	–0.42	10.00	5.62	4.13
GCT_SOFT_TISSUE	–0.42	–0.42	–0.42	7.78	4.45	4.08
KE39_STOMACH	–0.42	–0.42	–0.42	7.58	8.10	3.95
OVCAR4_OVARY	0.60	–0.42	–0.42	8.45	7.01	3.84
SLR20_KIDNEY	–0.42	–0.42	–0.42	7.49	4.99	3.82
CALU1_LUNG	–0.41	–0.41	–0.41	7.81	5.75	4.20
OUMS23_LARGE_INTESTINE	–0.41	–0.41	–0.41	7.24	4.62	3.73
KP3_PANCREAS	–0.40	–0.40	–0.40	8.58	6.19	4.42
HCC1954_BREAST	–0.40	–0.40	–0.40	7.28	5.27	4.08
QGP1_PANCREAS	–0.40	–0.40	–0.40	6.92	4.95	4.20
HT55_LARGE_INTESTINE	–0.40	–0.40	–0.40	4.67	3.66	4.11
CALU6_LUNG	–0.95	–0.39	–0.39	8.43	8.14	4.20
KMS21BM_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.39	–0.39	–0.39	6.66	3.73	4.14
GCIY_STOMACH	–0.38	–0.38	–0.38	8.11	4.74	3.99
SNU878_LIVER	–0.38	–0.38	–0.38	7.80	6.01	3.92
HLF_LIVER	–0.38	–0.38	–0.38	7.24	5.02	3.97
F5_CENTRAL_NERVOUS_SYSTEM	–0.38	–0.38	–0.38	5.79	4.06	3.85
DND41_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.38	–0.38	–0.38	8.35	3.81	4.42
SW1116_LARGE_INTESTINE	–0.38	–0.38	–0.38	7.08	5.26	4.12
MDST8_LARGE_INTESTINE	–0.38	–0.38	–0.38	6.08	4.87	4.19
COLO783_SKIN	–0.37	–0.37	–0.37	7.89	4.84	4.20
NCIH1693_LUNG	–0.37	–0.37	–0.37	8.19	7.12	3.84
NCIH510_LUNG	–0.37	–0.37	–0.37	7.47	3.68	4.15
COLO800_SKIN	–0.37	–0.37	–0.37	4.68	6.65	4.10
PANC0403_PANCREAS	–0.37	–0.37	–0.37	7.29	5.46	4.16
KCIMOH1_PANCREAS	–0.37	–0.37	–0.37	7.12	8.23	4.17
HS944T_SKIN	–0.36	–0.36	–0.36	8.33	4.68	4.17
KYSE410_OESOPHAGUS	–0.36	–0.36	–0.36	7.94	6.49	4.03
HK2_KIDNEY	–0.36	–0.36	–0.36	7.59	4.13	4.00
NCIH2291_LUNG	–0.36	–0.36	–0.36	7.73	6.77	3.94
SKBR3_BREAST	–0.35	–0.35	–0.35	6.44	5.34	3.98
KLE_ENDOMETRIUM	–0.35	–0.35	–0.35	8.84	4.57	4.00
HLE_LIVER	–0.35	–0.35	–0.35	7.30	3.92	4.05
NCIH82_LUNG	–0.35	–0.35	–0.35	7.91	3.73	4.14
T3M4_PANCREAS	–0.35	–0.35	–0.35	6.13	5.39	4.03
CALU3_LUNG	–0.34	–0.34	–0.34	8.42	5.38	4.23
EFO21_OVARY	–0.34	–0.34	–0.34	7.83	5.88	3.94

File S1 (*continued*)

File S1 (*continued*)

Cell name_Organ	Copy number value			Relative RNA level		
	CDKN2BAS	CDKN2B	CDKN2A	CDKN2A	CDKN2B	CDKN2BAS1
PL21_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.34	–0.34	–0.34	7.86	3.49	4.45
MDAMB468_BREAST	–0.34	–0.34	–0.34	7.97	5.61	3.91
UACC812_BREAST	–0.34	–0.34	–0.34	4.64	3.92	4.22
OVSAHO_OVARY	–0.34	–0.34	–0.34	7.30	4.41	4.31
DMS53_LUNG	–0.34	–0.34	–0.34	6.35	3.79	4.00
HS578T_BREAST	–0.26	–0.26	–0.33	4.34	6.58	4.00
GSS_STOMACH	–0.33	–0.33	–0.33	7.18	4.13	3.77
RERFLCKJ_LUNG	–0.33	–0.33	–0.33	7.56	6.97	4.27
GMS10_CENTRAL_NERVOUS_SYSTEM	–0.33	–0.33	–0.33	8.36	5.65	4.31
SNU61_LARGE_INTESTINE	–0.33	–0.33	–0.33	6.62	4.59	3.90
NCIH1395_LUNG	–0.33	–0.33	–0.33	5.82	3.75	3.94
HPAFII_PANCREAS	–0.33	–0.33	–0.33	8.94	8.25	3.87
BT483_BREAST	–0.33	–0.33	–0.33	4.60	4.22	4.24
NCIH2085_LUNG	–0.32	–0.32	–0.32	7.86	7.11	4.13
KMBC2_URINARY_TRACT	–0.32	–0.32	–0.32	8.43	8.75	4.12
TALL1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.32	–0.32	–0.32	6.84	3.66	4.36
GRM_SKIN	–0.32	–0.32	–0.32	4.22	6.08	3.91
HUH6_LIVER	–0.31	–0.31	–0.31	6.20	3.87	3.95
DU145_PROSTATE	–0.31	–0.31	–0.31	8.83	5.21	3.74
KNS62_LUNG	–0.30	–0.30	–0.30	7.75	6.19	3.95
OV56_OVARY	–0.30	–0.30	–0.30	8.80	6.57	4.07
NCIH1568_LUNG	–0.30	–0.30	–0.30	5.57	6.90	4.19
COV644_OVARY	–0.30	–0.30	–0.30	7.76	6.26	4.18
NCIH1734_LUNG	–0.29	–0.29	–0.29	8.62	4.38	4.26
FU97_STOMACH	–0.29	–0.29	–0.29	6.23	3.73	3.89
OE19_OESOPHAGUS	–0.29	–0.29	–0.29	5.71	3.88	4.17
KU812_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.28	–0.28	–0.28	5.32	3.51	4.46
CCK81_LARGE_INTESTINE	–0.28	–0.28	–0.28	4.80	3.66	4.03
KURAMOCHI_OVARY	–0.28	–0.28	–0.28	8.24	4.58	3.93
U937_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.27	–0.27	–0.27	7.61	3.81	3.93
HUH7_LIVER	–0.27	–0.27	–0.27	7.15	6.24	4.04
COV318_OVARY	–0.27	–0.27	–0.27	8.45	5.12	4.13
NCIH810_LUNG	–0.27	–0.27	–0.27	8.13	4.23	4.17
HS936T_SKIN	–0.26	–0.26	–0.26	7.44	4.61	4.04
NCIH1385_LUNG	–0.26	–0.26	–0.26	4.39	3.56	4.06
JIMT1_BREAST	–0.26	–0.26	–0.26	8.33	6.22	3.97
KHM1B_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.26	–0.26	–0.26	6.56	3.94	4.30
CAL12T_LUNG	–0.26	–0.26	–0.26	6.81	6.34	3.99
AU565_BREAST	–0.26	–0.26	–0.26	6.17	3.83	4.25
RPMI7951_SKIN	–0.26	–0.26	–0.26	8.40	4.76	4.41
HS695T_SKIN	–0.25	–0.25	–0.25	4.85	8.50	4.07

File S1 (*continued*)

File S1 (*continued*)

Cell name_Organ	Copy number value			Relative RNA level		
	CDKN2BAS	CDKN2B	CDKN2A	CDKN2A	CDKN2B	CDKN2BAS1
HCC366_LUNG	–0.25	–0.25	–0.25	7.88	5.18	4.15
OVMANA_OVARY	–0.25	–0.25	–0.25	7.75	4.82	4.12
HEC108_ENDOMETRIUM	–0.25	–0.25	–0.25	5.12	4.75	3.91
TE5_OESOPHAGUS	–0.25	–0.25	–0.25	4.41	5.64	4.03
NCIH1781_LUNG	–0.25	–0.25	–0.25	8.50	5.45	4.15
SNU398_LIVER	–0.25	–0.25	–0.25	7.27	4.62	4.00
SW480_LARGE_INTESTINE	–0.25	–0.25	–0.25	6.99	4.56	4.09
MDAMB175VII_BREAST	–0.25	–0.25	–0.25	5.38	4.60	3.91
AMO1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.24	–0.24	–0.24	6.51	3.91	4.05
NCIH2227_LUNG	–0.24	–0.24	–0.24	7.49	4.65	4.48
647V_URINARY_TRACT	–0.24	–0.24	–0.24	9.07	7.86	4.14
NB1_AUTONOMIC_GANGLIA	–0.23	–0.23	–0.23	4.44	3.66	3.89
OAW42_OVARY	–0.23	–0.23	–0.23	6.91	3.76	4.23
NCIH1299_LUNG	–0.23	–0.23	–0.23	7.72	5.96	4.09
SNU685_ENDOMETRIUM	–0.22	–0.22	–0.22	8.67	4.95	3.85
ZR7530_BREAST	–0.21	–0.21	–0.21	4.77	3.92	4.27
NCIH2110_LUNG	–0.21	–0.21	–0.21	8.27	5.47	3.90
CAOV4_OVARY	–0.21	–0.21	–0.21	7.90	5.72	4.10
RPMI8226_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.21	–0.21	–0.21	7.75	3.89	4.12
NUGC3_STOMACH	0.60	–0.21	–0.21	7.06	5.32	4.30
OVCAR8_OVARY	–0.21	–0.21	–0.21	8.43	5.25	3.98
NCIH1341_LUNG	–0.21	–0.21	–0.21	8.44	5.80	4.52
DV90_LUNG	–0.20	–0.20	–0.20	7.23	4.27	4.02
SIGM5_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.20	–0.20	–0.20	7.35	3.58	4.31
OCUM1_STOMACH	–0.20	–0.20	–0.20	6.05	5.98	3.99
MOLM6_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.20	–0.20	–0.20	5.70	3.67	4.38
SKMEL28_SKIN	–0.20	–0.20	–0.20	8.04	6.15	4.13
NCIH661_LUNG	–0.20	–0.20	–0.20	7.30	4.87	4.18
HS746T_STOMACH	–0.19	–0.19	–0.19	7.35	4.70	4.15
HUH28_BILIARY_TRACT	–0.19	–0.19	–0.19	8.38	6.94	4.47
COLO792_SKIN	–0.18	–0.18	–0.18	6.35	4.45	4.04
C3A_LIVER	–0.18	–0.18	–0.18	4.60	3.70	4.13
MFE280_ENDOMETRIUM	–0.18	–0.18	–0.18	8.53	4.06	4.23
SJRH30_SOFT_TISSUE	–0.17	–0.17	–0.17	8.01	3.84	4.24
HCC1195_LUNG	–0.17	–0.17	–0.17	5.28	3.81	4.10
VMCUB1_URINARY_TRACT	–0.17	–0.17	–0.17	8.44	5.73	4.35
SNU601_STOMACH	–0.17	–0.17	–0.17	4.34	4.32	3.89
TF1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.16	–0.16	–0.16	9.09	4.21	4.20
NCIH2444_LUNG	–0.16	–0.16	–0.16	7.04	6.65	4.04
NCIH1694_LUNG	–0.16	–0.16	–0.16	8.33	4.00	4.70
DEL_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.16	–0.16	–0.16	6.64	3.77	4.25

File S1 (*continued*)

File S1 (*continued*)

Cell name_Organ	Copy number value			Relative RNA level		
	CDKN2BAS	CDKN2B	CDKN2A	CDKN2A	CDKN2B	CDKN2BAS1
SNU520_STOMACH	–0.16	–0.16	–0.16	6.27	4.54	4.13
NCIH2172_LUNG	–0.15	–0.15	–0.15	8.44	6.60	4.14
SUDHL8_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.15	–0.15	–0.15	8.07	3.78	4.42
HCC44_LUNG	–0.15	–0.15	–0.15	8.95	6.25	3.89
MCAS_OVARY	–0.15	–0.15	–0.15	6.33	6.65	4.04
NCIH1355_LUNG	–0.15	–0.15	–0.15	8.00	6.62	4.15
KCL22_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.14	–0.14	–0.14	5.59	3.40	3.88
SW1463_LARGE_INTESTINE	–0.14	–0.14	–0.14	7.22	4.37	3.86
FTC133_THYROID	–0.14	–0.14	–0.14	8.59	5.38	4.12
MHHNB11_AUTONOMIC_GANGLIA	–0.14	–0.14	–0.14	4.88	3.79	4.00
COLO684_ENDOMETRIUM	–0.14	–0.14	–0.14	8.25	4.19	3.84
JHH4_LIVER	–0.13	–0.13	–0.13	7.86	6.57	4.00
SUDHL4_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.13	–0.13	–0.13	7.41	3.76	4.32
SW620_LARGE_INTESTINE	–0.13	–0.13	–0.13	7.35	5.00	4.16
LP1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.13	–0.13	–0.13	7.35	5.26	4.49
NCIH522_LUNG	–0.13	–0.13	–0.13	8.54	6.03	4.07
HEPG2_LIVER	–0.13	–0.13	–0.13	5.04	3.75	3.96
SNU761_LIVER	–0.13	–0.13	–0.13	6.43	7.80	4.14
AML193_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.13	–0.13	–0.13	7.98	3.62	4.67
NCIH196_LUNG	–0.12	–0.12	–0.12	8.14	7.29	4.32
MC116_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.12	–0.12	–0.12	8.05	3.77	4.03
OV7_OVARY	–0.12	–0.12	–0.12	8.95	5.31	3.96
HT29_LARGE_INTESTINE	–0.11	–0.11	–0.11	8.12	4.46	3.95
OCIAML2_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.11	–0.11	–0.11	7.33	3.85	4.13
OPM2_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.11	–0.11	–0.11	8.15	5.09	4.67
IMR32_AUTONOMIC_GANGLIA	–0.11	–0.11	–0.11	4.83	3.66	4.05
HT1376_URINARY_TRACT	–0.11	–0.11	–0.11	7.89	5.94	4.88
OCIAML3_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.11	–0.11	–0.11	4.57	3.76	4.14
TE441T_SOFT_TISSUE	–0.11	–0.11	–0.11	5.80	3.89	4.12
LOVO_LARGE_INTESTINE	–0.11	–0.11	–0.11	5.36	4.35	3.98
SBC5_LUNG	–0.11	–0.11	–0.11	8.52	4.31	3.81
KMS26_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.10	–0.10	–0.10	8.61	6.53	4.29
HCC1428_BREAST	–0.10	–0.10	–0.10	6.27	4.26	4.10
NCIH2009_LUNG	–0.10	–0.10	–0.10	8.91	4.97	4.30
JHUEM2_ENDOMETRIUM	–0.10	–0.10	–0.10	6.30	3.96	4.26
COLO704_OVARY	–0.10	–0.10	–0.10	8.37	4.21	4.24
D341MED_CENTRAL_NERVOUS_SYSTEM	–0.09	–0.09	–0.09	5.85	3.60	4.16
AN3CA_ENDOMETRIUM	–0.09	–0.09	–0.09	7.76	3.70	4.35
OE33_OESOPHAGUS	–0.09	–0.09	–0.09	8.54	6.06	4.17
OVK18_OVARY	–0.09	–0.09	–0.09	5.49	3.77	3.91
NCIH524_LUNG	–0.08	–0.08	–0.08	8.16	4.15	3.98

File S1 (*continued*)

File S1 (*continued*)

Cell name_Organ	Copy number value			Relative RNA level		
	CDKN2BAS	CDKN2B	CDKN2A	CDKN2A	CDKN2B	CDKN2BAS1
RCM1_LARGE_INTESTINE	–0.08	–0.08	–0.08	6.84	5.44	4.01
SNU719_STOMACH	–0.08	–0.08	–0.08	4.47	7.65	3.85
2313287_STOMACH	–0.08	–0.08	–0.08	6.08	5.79	3.91
YMB1_BREAST	–0.08	–0.08	–0.08	5.89	4.02	4.24
8MGBA_CENTRAL_NERVOUS_SYSTEM	–0.08	–0.08	–0.08	8.93	7.98	4.18
KMS18_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.08	–0.08	–0.08	5.72	3.61	3.90
G402_SOFT_TISSUE	–0.07	–0.07	–0.07	5.71	3.73	4.20
PFEIFFER_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.07	–0.07	–0.07	6.37	3.56	4.41
639V_URINARY_TRACT	–0.07	–0.07	–0.07	8.42	5.25	4.41
NCIH2066_LUNG	–0.07	–0.07	–0.07	8.31	6.58	4.25
WSUDLCL2_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.07	–0.07	–0.07	7.57	3.69	4.25
MDAMB415_BREAST	–0.07	–0.07	–0.07	7.24	5.22	4.17
RL_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.07	–0.07	–0.07	7.31	3.86	4.24
LU65_LUNG	0.47	–0.07	–0.07	9.06	6.85	4.29
EFE184_ENDOMETRIUM	–0.07	–0.07	–0.07	8.58	6.75	3.94
ME1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.07	–0.07	–0.07	5.93	3.73	4.15
GI1_CENTRAL_NERVOUS_SYSTEM	–0.07	–0.07	–0.07	9.26	5.66	4.36
HS939T_SKIN	–0.06	–0.06	–0.06	5.69	5.90	4.18
SUDHL10_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.06	–0.06	–0.06	7.98	3.65	4.27
ST486_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.06	–0.06	–0.06	8.27	4.05	4.41
KASUMI6_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.06	–0.06	–0.06	6.15	3.58	4.10
SHSY5Y_AUTONOMIC_GANGLIA	–0.06	–0.06	–0.06	4.91	3.60	4.00
KO52_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.06	–0.06	–0.06	5.49	3.46	3.86
RAJI_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.06	–0.06	–0.06	7.43	3.91	4.13
ECC12_STOMACH	–0.06	–0.06	–0.06	7.96	5.51	4.31
HS611T_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.06	–0.06	–0.06	5.53	3.68	3.71
RCHACV_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.06	–0.06	–0.06	5.77	3.65	4.28
ZR751_BREAST	–0.06	–0.06	–0.06	5.82	4.09	3.97
BL41_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.06	–0.06	–0.06	7.79	3.74	4.19
RKO_LARGE_INTESTINE	–0.06	–0.06	–0.06	4.87	5.06	4.27
GDM1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.06	–0.06	–0.06	4.77	3.45	4.21
NCO2_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.06	–0.06	–0.06	9.19	5.65	4.35
CORL88_LUNG	–0.05	–0.05	–0.05	7.98	4.59	4.73
SCLC21H_LUNG	–0.05	–0.05	–0.05	8.29	4.43	4.34
SW1353_BONE	–0.05	–0.05	–0.05	6.10	6.15	3.98
SNU899_UPPER_AERODIGESTIVE_TRACT	–0.05	–0.05	–0.05	8.61	6.64	4.20
CL40_LARGE_INTESTINE	–0.05	–0.05	–0.05	5.98	5.24	3.89
KYM1_SOFT_TISSUE	–0.04	–0.04	–0.04	4.96	3.46	3.98
ISHIKAWAHERAKLIO02ER_ENDOMETRIUM	–0.04	–0.04	–0.04	8.25	4.45	4.17
KPNRTBM1_AUTONOMIC_GANGLIA	–0.04	–0.04	–0.04	4.91	3.49	4.06
RL952_ENDOMETRIUM	–0.04	–0.04	–0.04	7.78	4.98	4.15

File S1 (*continued*)

File S1 (*continued*)

Cell name_Organ	Copy number value			Relative RNA level		
	CDKN2BAS	CDKN2B	CDKN2A	CDKN2A	CDKN2B	CDKN2BAS1
KPNSI9S_AUTONOMIC_GANGLIA	–0.04	–0.04	–0.04	5.44	5.50	3.76
KE97_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.04	–0.04	–0.04	5.65	3.62	3.94
KARPAS422_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.04	–0.04	–0.04	6.52	3.90	4.64
SNU423_LIVER	–0.04	–0.04	–0.04	7.59	4.98	4.16
22RV1_PROSTATE	–0.04	–0.04	–0.04	6.91	3.90	4.15
A4FUK_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.04	–0.04	–0.04	7.41	3.83	4.22
CA46_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.04	–0.04	–0.04	7.63	3.79	3.92
HCT116_LARGE_INTESTINE	–0.04	–0.04	–0.04	6.73	4.05	3.91
P3HR1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.04	–0.04	–0.04	6.77	3.89	4.76
ESS1_ENDOMETRIUM	–0.04	–0.04	–0.04	8.90	4.18	4.22
MONOMAC1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.04	–0.04	–0.04	8.69	4.44	4.41
A204_SOFT_TISSUE	–0.04	–0.04	–0.04	5.77	3.86	3.88
JK1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.04	–0.04	–0.04	4.99	9.01	4.45
SKNSH_AUTONOMIC_GANGLIA	–0.03	–0.03	–0.03	5.17	4.08	4.19
SW48_LARGE_INTESTINE	–0.03	–0.03	–0.03	4.46	4.32	4.01
BL70_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.03	–0.03	–0.03	7.99	3.95	4.25
VMRCRCW_KIDNEY	–0.03	–0.03	–0.03	8.58	5.51	4.19
G401_SOFT_TISSUE	–0.03	–0.03	–0.03	5.20	3.48	4.14
DAUDI_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.03	–0.03	–0.03	6.87	3.54	4.05
SNU175_LARGE_INTESTINE	–0.03	–0.03	–0.03	5.29	3.52	4.07
HS172T_URINARY_TRACT	–0.03	–0.03	–0.03	5.89	5.73	3.96
CORL95_LUNG	–0.03	–0.03	–0.03	9.20	5.13	4.44
CI1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.03	–0.03	–0.03	7.14	3.93	4.14
HS940T_SKIN	–0.03	–0.03	–0.03	5.88	5.30	4.03
M07E_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.03	–0.03	–0.03	6.67	4.19	3.98
CHP126_AUTONOMIC_GANGLIA	–0.02	–0.02	–0.02	5.19	3.60	4.10
KOPN8_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.02	–0.02	–0.02	7.51	3.71	4.18
NCIH508_LARGE_INTESTINE	–0.02	–0.02	–0.02	6.25	4.40	4.10
HCT15_LARGE_INTESTINE	–0.02	–0.02	–0.02	4.75	3.88	3.88
TOV21G_OVARY	–0.02	–0.02	–0.02	5.30	3.78	3.91
697_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.02	–0.02	–0.02	4.31	3.80	4.39
JHH6_LIVER	–0.02	–0.02	–0.02	6.84	6.45	4.99
NAMALWA_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.02	–0.02	–0.02	8.17	3.50	3.93
SNU81_LARGE_INTESTINE	–0.02	–0.02	–0.02	6.86	5.65	4.00
AGS_STOMACH	–0.02	–0.02	–0.02	3.95	7.69	4.19
MV411_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.02	–0.02	–0.02	7.70	3.87	3.91
SNU407_LARGE_INTESTINE	–0.02	–0.02	–0.02	5.31	4.12	3.96
NCIH660_PROSTATE	–0.02	–0.02	–0.02	8.20	4.63	4.30
BDCM_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.02	–0.02	–0.02	5.57	3.46	4.18
RERFLCMS_LUNG	–0.02	–0.02	–0.02	8.47	7.08	3.98
TGBC11TKB_STOMACH	–0.02	–0.02	–0.02	7.24	5.11	3.91

File S1 (*continued*)

File S1 (*continued*)

Cell name_Organ	Copy number value			Relative RNA level		
	CDKN2BAS	CDKN2B	CDKN2A	CDKN2A	CDKN2B	CDKN2BAS1
IM95_STOMACH	–0.02	–0.02	–0.02	4.42	4.06	3.96
SNGM_ENDOMETRIUM	–0.02	–0.02	–0.02	6.59	4.28	3.78
SNUC5_LARGE_INTESTINE	–0.01	–0.01	–0.01	7.57	6.25	4.14
HS819T_BONE	–0.01	–0.01	–0.01	6.62	6.24	3.94
EB1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.01	–0.01	–0.01	7.78	3.66	3.98
OCILY10_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.01	–0.01	–0.01	6.99	3.92	4.06
JHUEM1_ENDOMETRIUM	–0.01	–0.01	–0.01	6.32	4.08	4.19
HH_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.01	–0.01	–0.01	7.52	3.85	4.35
HS618T_LUNG	–0.01	–0.01	–0.01	6.37	4.97	3.93
JVM2_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.01	–0.01	–0.01	5.65	3.53	4.22
MJ_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	–0.01	–0.01	–0.01	5.83	3.70	3.89
MFE296_ENDOMETRIUM	–0.01	–0.01	–0.01	6.89	3.78	3.96
NCIH2106_LUNG	–0.01	–0.01	–0.01	8.28	4.67	3.98
HS888T_BONE	–0.01	–0.01	–0.01	6.62	5.23	4.03
SNU1077_ENDOMETRIUM	–0.01	–0.01	–0.01	8.49	6.43	3.77
HS863T_BONE	–0.01	–0.01	–0.01	5.71	4.71	4.08
HS737T_BONE	–0.01	–0.01	–0.01	6.86	6.71	3.85
HS343T_BREAST	–0.01	–0.01	–0.01	6.00	5.86	3.95
PRECLH_PROSTATE	–0.01	–0.01	–0.01	8.03	5.52	3.92
HS934T_SKIN	0.00	0.00	0.00	5.80	4.49	4.13
SW1417_LARGE_INTESTINE	0.00	0.00	0.00	4.96	3.78	4.08
HUT102_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.00	0.00	0.00	5.97	4.15	4.29
GP2D_LARGE_INTESTINE	0.00	0.00	0.00	4.80	3.59	4.14
SNU1_STOMACH	0.00	0.00	0.00	6.51	4.31	4.09
HS895T_SKIN	0.00	0.00	0.00	7.12	4.58	3.91
TIG3TD_LUNG	0.00	0.00	0.00	6.61	4.52	4.09
BICR56_UPPER_AERODIGESTIVE_TRACT	0.00	0.00	0.00	7.62	10.07	3.99
BJHTERT_SKIN	0.00	0.00	0.00	5.60	4.50	3.94
HS739T_BREAST	0.00	0.00	0.00	6.99	8.10	3.98
CW2_LARGE_INTESTINE	0.00	0.00	0.00	4.83	3.62	3.98
HS688AT_SKIN	0.00	0.00	0.00	5.81	4.41	4.17
DMS273_LUNG	0.00	0.00	0.00	8.77	3.72	4.20
TE125T_SOFT_TISSUE	0.00	0.00	0.00	6.03	4.68	4.00
HS604T_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.00	0.00	0.00	6.56	4.99	4.02
HEC251_ENDOMETRIUM	0.00	0.00	0.00	8.58	4.76	4.19
NUDUL1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.00	0.00	0.00	8.16	3.73	4.69
TO175T_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.00	0.00	0.00	5.89	5.08	3.84
JHH1_LIVER	0.00	0.00	0.00	7.38	4.54	3.94
HS281T_BREAST	0.00	0.00	0.00	5.98	5.59	4.09
HS606T_BREAST	0.00	0.00	0.00	6.08	6.37	3.88
HCC1937_BREAST	0.00	0.00	0.00	8.55	7.42	3.83

File S1 (*continued*)

File S1 (*continued*)

Cell name_Organ	Copy number value			Relative RNA level		
	CDKN2BAS	CDKN2B	CDKN2A	CDKN2A	CDKN2B	CDKN2BAS1
HS822T_BONE	0.00	0.00	0.00	6.17	5.29	3.99
P31FUJ_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.00	0.00	0.00	8.07	3.76	4.21
DLD1_LARGE_INTESTINE	0.01	0.01	0.01	4.42	3.70	3.91
HS821T_BONE	0.01	0.01	0.01	5.82	5.26	3.95
A2780_OVARY	0.01	0.01	0.01	5.36	3.54	4.08
HS274T_BREAST	0.01	0.01	0.01	5.31	4.91	4.06
MDAPCA2B_PROSTATE	0.01	0.01	0.01	3.97	3.72	4.04
HS616T_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.01	0.01	0.01	6.44	6.97	3.98
HS706T_BONE	0.01	0.01	0.01	4.86	7.92	4.14
T173_BONE	0.01	0.01	0.01	6.65	5.50	3.85
NCIH841_LUNG	0.01	0.01	0.01	8.01	6.19	4.28
NH6_AUTONOMIC_GANGLIA	0.01	0.01	0.01	5.30	4.14	4.18
KMS27_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.01	0.01	0.01	7.82	4.74	4.44
CAL148_BREAST	0.01	0.01	0.01	6.33	3.66	4.11
HS600T_SKIN	0.01	0.01	0.01	6.27	5.39	3.75
COLO668_LUNG	0.01	0.01	0.01	7.94	3.74	4.14
NCIH1048_LUNG	0.01	0.01	0.01	8.45	4.45	4.43
HS839T_SKIN	0.01	0.01	0.01	6.01	4.45	4.15
HCC1569_BREAST	0.01	0.01	0.01	9.07	5.57	4.03
TE159T_SOFT_TISSUE	0.01	0.01	0.01	6.11	4.12	3.95
HS698T_LARGE_INTESTINE	0.01	0.01	0.01	5.56	5.07	3.81
JVM3_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.01	0.01	0.01	5.73	3.64	4.00
COV434_OVARY	0.01	0.01	0.01	7.17	3.90	4.32
KMS34_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.01	0.01	0.01	8.60	5.79	4.60
IGROV1_OVARY	0.01	0.01	0.01	5.76	3.75	4.16
JHOM2B_OVARY	0.01	0.01	0.01	8.23	7.23	4.18
HLFA_LUNG	0.01	0.01	0.01	6.76	4.85	3.99
HS675T_LARGE_INTESTINE	0.01	0.01	0.01	5.41	4.20	4.27
KG1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.01	0.01	0.01	5.32	3.62	4.03
OELE_OVARY	0.01	0.01	0.01	8.42	5.27	4.08
HS751T_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.02	0.02	0.02	5.53	5.12	4.07
SUDHL5_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.02	0.02	0.02	7.30	3.91	4.58
CPCN_LUNG	0.02	0.02	0.02	8.29	5.05	4.67
HCC827_LUNG	0.02	0.02	0.02	8.96	6.58	3.99
DM3_PLEURA	0.02	0.02	0.02	7.01	4.57	3.88
L33_PANCREAS	0.02	0.02	0.02	8.08	4.95	3.79
CAL51_BREAST	0.02	0.02	0.02	5.94	3.69	4.03
HMEL_BREAST	0.02	0.02	0.02	6.33	6.52	4.17
EPLC272H_LUNG	0.02	0.02	0.02	7.32	5.72	4.25
MPP89_PLEURA	0.02	0.02	0.02	8.86	5.80	4.24
SNU1040_LARGE_INTESTINE	0.02	0.02	0.02	5.25	4.44	4.00

File S1 (*continued*)

File S1 (*continued*)

Cell name_Organ	Copy number value			Relative RNA level		
	CDKN2BAS	CDKN2B	CDKN2A	CDKN2A	CDKN2B	CDKN2BAS1
KASUMI2_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.02	0.02	0.02	5.65	3.48	4.14
HUNS1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.02	0.02	0.02	6.02	3.79	4.05
MOTN1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.02	0.02	0.02	8.15	4.48	4.39
SW403_LARGE_INTESTINE	0.02	0.02	0.02	4.82	3.62	3.91
KELLY_AUTONOMIC_GANGLIA	0.02	0.02	0.02	7.05	3.73	3.84
HS840T_UPPER_AERODIGESTIVE_TRACT	0.02	0.02	0.02	6.51	4.44	3.95
U266B1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.02	0.02	0.02	6.64	5.09	4.42
EHEB_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.02	0.02	0.02	5.54	3.68	4.16
TCCSUP_URINARY_TRACT	0.02	0.02	0.02	9.71	7.57	3.84
HPBALL_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.02	0.02	0.02	7.50	3.52	4.32
HS229T_LUNG	0.03	0.03	0.03	6.25	4.18	3.98
SALE_LUNG	0.03	0.03	0.03	7.68	5.96	3.90
DU4475_BREAST	0.03	0.03	0.03	6.68	5.05	4.25
KMM1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.03	0.03	0.03	8.11	5.37	3.99
KMS11_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.03	0.03	0.03	8.59	4.61	4.52
LS180_LARGE_INTESTINE	0.03	0.03	0.03	4.10	3.55	4.04
MFE319_ENDOMETRIUM	0.03	0.03	0.03	7.88	4.07	3.98
COLO205_LARGE_INTESTINE	0.03	0.03	0.03	7.12	4.06	4.28
NCIH1155_LUNG	0.03	0.03	0.03	8.56	4.93	4.39
SNU46_UPPER_AERODIGESTIVE_TRACT	0.03	0.03	0.03	8.29	5.39	4.06
EN_ENDOMETRIUM	0.04	0.04	0.04	7.90	4.23	3.95
TE617T_SOFT_TISSUE	0.04	0.04	0.04	7.18	4.69	4.09
NCIH929_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.04	0.04	0.04	6.35	4.01	4.35
HEC265_ENDOMETRIUM	0.04	0.04	0.04	5.11	4.68	4.05
BCP1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.04	0.04	0.04	7.50	4.40	3.91
SNU1197_LARGE_INTESTINE	0.10	0.04	0.04	7.84	7.87	4.04
PCM6_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.04	0.04	0.04	7.78	8.89	4.41
LS411N_LARGE_INTESTINE	0.04	0.04	0.04	4.93	4.06	3.96
HS870T_BONE	0.04	0.04	0.04	6.50	4.20	4.10
NCIH596_LUNG	0.04	0.04	0.04	8.66	6.03	4.03
HCC2218_BREAST	0.04	0.04	0.04	5.66	5.27	4.07
HUCCT1_BILIARY_TRACT	0.05	0.05	0.05	7.89	6.47	4.01
KMRC3_KIDNEY	0.05	0.05	0.05	6.96	5.29	4.14
HEKTE_KIDNEY	0.05	0.05	0.05	8.49	6.87	4.14
MONOMAC6_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.06	0.06	0.06	8.52	3.78	4.54
CL34_LARGE_INTESTINE	0.06	0.06	0.06	6.37	4.24	3.87
M059K_CENTRAL_NERVOUS_SYSTEM	0.06	0.06	0.06	8.27	5.51	4.26
LNCAPCLONEFGC_PROSTATE	0.06	0.06	0.06	5.93	3.70	4.24
KM12_LARGE_INTESTINE	0.07	0.07	0.07	8.06	4.56	4.24
HEC151_ENDOMETRIUM	0.07	0.07	0.07	4.89	4.05	3.85
CL11_LARGE_INTESTINE	0.07	0.07	0.07	7.75	6.90	4.08

File S1 (*continued*)

File S1 (*continued*)

Cell name_Organ	Copy number value			Relative RNA level		
	CDKN2BAS	CDKN2B	CDKN2A	CDKN2A	CDKN2B	CDKN2BAS1
SKNMC_BONE	0.07	0.07	0.07	7.91	3.65	4.27
NCIH1436_LUNG	0.07	0.07	0.07	7.98	4.73	4.39
NCIH1963_LUNG	0.07	0.07	0.07	8.59	5.54	4.83
SEM_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.07	0.07	0.07	8.44	3.65	4.11
IGR39_SKIN	0.07	0.07	0.07	4.40	4.50	3.94
NCIH209_LUNG	0.07	0.07	0.07	8.18	5.05	4.45
NCIH1339_LUNG	0.07	0.07	0.07	5.79	4.65	4.48
NCIH2081_LUNG	0.07	0.07	0.07	8.17	4.54	4.52
KARPAS299_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.07	0.07	0.07	7.54	3.85	4.30
HEC59_ENDOMETRIUM	0.07	0.07	0.07	5.90	3.55	4.16
KPNYN_AUTONOMIC_GANGLIA	0.08	0.08	0.08	4.54	3.76	4.13
KMH2_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.08	0.08	0.08	4.37	3.62	4.00
D283MED_CENTRAL_NERVOUS_SYSTEM	0.08	0.08	0.08	4.71	3.75	3.86
ONCODG1_OVARY	0.08	0.08	0.08	8.41	5.01	4.19
SNU324_PANCREAS	0.08	0.08	0.08	8.11	4.12	4.06
OC314_OVARY	0.08	0.08	0.08	8.28	4.69	3.95
NCIH1373_LUNG	0.08	0.08	0.08	7.75	7.43	4.36
SIMA_AUTONOMIC_GANGLIA	0.08	0.08	0.08	4.69	3.64	3.96
NCIH1618_LUNG	0.09	0.09	0.09	8.13	4.74	4.29
HEP3B217_LIVER	0.09	0.09	0.09	8.49	5.36	4.18
DMS454_LUNG	0.09	0.09	0.09	8.07	5.09	4.18
OC316_OVARY	0.09	0.09	0.09	8.24	4.64	4.14
CORL51_LUNG	0.09	0.09	0.09	8.27	5.41	3.95
GA10_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.09	0.09	0.09	8.19	4.01	4.04
MDAMB134VI_BREAST	0.10	0.10	0.10	6.06	4.66	4.80
CORL279_LUNG	0.10	0.10	0.10	8.85	5.80	3.80
HT_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.10	0.10	0.10	6.82	3.76	4.29
SKNBE2_AUTONOMIC_GANGLIA	0.10	0.10	0.10	5.78	3.70	3.92
CORL47_LUNG	0.10	0.10	0.10	8.81	4.19	4.21
SKUT1_SOFT_TISSUE	0.10	0.10	0.10	9.33	6.08	4.19
SNUC1_LARGE_INTESTINE	0.11	0.11	0.11	5.05	4.78	4.01
HSC2_UPPER_AERODIGESTIVE_TRACT	0.11	0.11	0.11	8.16	6.94	3.96
OVISE_OVARY	0.12	0.12	0.12	8.12	4.63	3.84
CAL27_UPPER_AERODIGESTIVE_TRACT	0.13	0.13	0.13	6.35	6.70	4.00
HCC1599_BREAST	0.13	0.13	0.13	8.14	6.40	4.18
DMS153_LUNG	0.13	0.13	0.13	8.51	4.69	4.14
YD38_UPPER_AERODIGESTIVE_TRACT	0.13	0.13	0.13	7.79	6.58	4.26
COLO775_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.14	0.14	0.14	7.40	3.79	3.87
CHL1_SKIN	0.15	0.15	0.15	6.09	4.18	4.08
MOLM16_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.15	0.15	0.15	9.89	3.97	4.13
KMS20_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.15	0.15	0.15	7.35	3.63	4.38

File S1 (*continued*)

File S1 (*continued*)

Cell name_Organ	Copy number value			Relative RNA level		
	CDKN2BAS	CDKN2B	CDKN2A	CDKN2A	CDKN2B	CDKN2BAS1
KATOIII_STOMACH	0.15	0.15	0.15	4.27	4.31	4.03
SW837_LARGE_INTESTINE	0.15	0.15	0.15	7.38	5.23	3.98
HS766T_PANCREAS	0.16	0.16	0.16	8.00	7.30	4.07
CL14_LARGE_INTESTINE	0.16	0.16	0.16	6.08	5.18	3.97
ECC10_STOMACH	0.16	0.16	0.16	8.44	5.08	4.11
SW1783_CENTRAL_NERVOUS_SYSTEM	0.16	0.16	0.16	8.74	6.34	4.02
SKNFI_AUTONOMIC_GANGLIA	0.17	0.17	0.17	4.84	3.94	3.97
KIJK_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.17	0.17	0.17	6.32	3.66	4.11
ES2_OVARY	0.17	0.17	0.17	8.60	4.44	4.12
HT115_LARGE_INTESTINE	0.17	0.17	0.17	7.24	4.29	3.73
KMS12BM_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.18	0.18	0.18	8.37	4.46	4.03
HMCB_SKIN	0.18	0.18	0.18	6.16	4.16	4.03
J82_URINARY_TRACT	0.18	0.18	0.18	8.37	5.79	4.11
LS1034_LARGE_INTESTINE	0.19	0.19	0.19	4.21	3.63	3.94
NCIH2029_LUNG	0.19	0.19	0.19	8.10	4.84	4.87
CAMA1_BREAST	0.20	0.20	0.20	6.75	4.87	4.28
HCC33_LUNG	0.20	0.20	0.20	8.39	5.35	4.42
HCC1187_BREAST	0.20	0.20	0.20	7.93	4.54	4.06
CHP212_AUTONOMIC_GANGLIA	0.21	0.21	0.21	5.76	4.85	4.01
NCIN87_STOMACH	0.21	0.21	0.21	8.45	6.21	4.30
NCIH2196_LUNG	0.21	0.21	0.21	8.56	5.07	4.16
HEC6_ENDOMETRIUM	0.21	0.21	0.21	4.59	5.72	3.98
NCIH520_LUNG	0.22	0.22	0.22	8.15	4.30	4.46
PANC1005_PANCREAS	0.22	0.22	0.22	8.28	5.97	4.07
DB_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.22	0.22	0.22	4.80	3.53	3.91
SKM1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.23	0.23	0.23	8.03	3.51	4.19
PATU8902_PANCREAS	0.23	0.23	0.23	7.98	5.03	4.14
KMS28BM_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.23	0.23	0.23	8.28	4.10	4.39
LK2_LUNG	0.25	0.25	0.25	8.67	4.64	4.07
DMS79_LUNG	0.25	0.25	0.25	8.35	4.43	4.65
SUIT2_PANCREAS	–5.23	–5.23	0.25	5.63	3.42	4.01
PL45_PANCREAS	0.25	0.25	0.25	8.37	6.74	4.10
JMSU1_URINARY_TRACT	0.25	0.25	0.25	8.91	6.67	4.07
SNU182_LIVER	0.26	0.26	0.26	8.73	9.14	3.99
SNU283_LARGE_INTESTINE	0.26	0.26	0.26	6.57	4.11	3.95
MDAMB435S_SKIN	0.28	0.28	0.28	8.14	4.99	4.45
TOV112D_OVARY	0.29	0.29	0.29	7.68	3.83	4.07
OAW28_OVARY	0.29	0.29	0.29	8.51	5.22	4.16
HS571T_OVARY	0.30	0.30	0.30	5.71	5.21	4.01
MDAMB157_BREAST	0.31	0.31	0.31	8.67	7.01	4.41
FTC238_THYROID	0.31	0.31	0.31	8.71	5.96	4.23

File S1 (*continued*)

File S1 (*continued*)

Cell name_Organ	Copy number value			Relative RNA level		
	CDKN2BAS	CDKN2B	CDKN2A	CDKN2A	CDKN2B	CDKN2BAS1
NIHOVCAR3_OVARY	0.31	0.31	0.31	8.64	6.22	4.04
MEC2_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.33	0.33	0.33	6.48	3.73	4.18
L1236_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.34	0.34	0.34	8.52	6.90	4.23
HSC3_UPPER_AERODIGESTIVE_TRACT	0.34	0.34	0.34	6.54	4.74	4.33
LXF289_LUNG	0.35	0.35	0.35	8.04	7.16	4.11
VCAP_PROSTATE	0.35	0.35	0.35	4.94	3.61	3.92
NCIH526_LUNG	0.35	0.35	0.35	8.20	4.39	4.24
MOLP2_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.37	0.37	0.37	6.19	4.82	4.10
NCIH446_LUNG	0.37	0.37	0.37	8.35	5.05	4.16
SNU626_CENTRAL_NERVOUS_SYSTEM	0.37	0.37	0.37	8.66	5.70	4.24
FUOV1_OVARY	0.37	0.37	0.37	8.07	5.49	4.17
5637_URINARY_TRACT	0.38	0.38	0.38	9.05	5.41	4.10
NCIH1930_LUNG	0.38	0.38	0.38	8.03	4.51	4.34
KALS1_CENTRAL_NERVOUS_SYSTEM	0.39	0.39	0.39	9.51	8.00	5.22
NCIH146_LUNG	0.41	0.41	0.41	8.48	4.18	4.25
HSC4_UPPER_AERODIGESTIVE_TRACT	0.42	0.42	0.42	6.70	6.84	4.46
MOGGCCM_CENTRAL_NERVOUS_SYSTEM	0.42	0.42	0.42	9.58	7.26	4.18
LS513_LARGE_INTESTINE	0.43	0.43	0.43	5.08	3.63	4.01
NCIH1836_LUNG	0.43	0.43	0.43	8.95	7.33	4.81
NCIH69_LUNG	0.44	0.44	0.44	8.48	4.43	4.17
8305C_THYROID	0.46	0.46	0.46	8.13	4.67	4.18
HGC27_STOMACH	0.46	0.46	0.46	8.28	4.33	3.85
SNU8_OVARY	0.47	0.47	0.47	8.95	7.78	4.19
YD10B_UPPER_AERODIGESTIVE_TRACT	0.47	0.47	0.47	6.90	7.30	4.57
EB2_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.48	0.48	0.48	8.05	3.89	4.00
EJM_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.49	0.49	0.49	8.20	7.39	3.97
8505C_THYROID	0.49	0.49	0.49	7.08	4.24	4.49
NCIH1092_LUNG	0.50	0.50	0.50	8.64	5.21	5.25
L540_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.51	0.51	0.51	4.82	3.74	4.10
SUDHL6_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.51	0.51	0.51	7.85	3.73	4.27
BT549_BREAST	0.53	0.53	0.53	9.73	6.81	4.17
CAL851_BREAST	0.54	0.54	0.54	9.26	8.36	4.02
HCC202_BREAST	0.55	0.55	0.55	6.90	6.11	4.35
CJM_SKIN	0.55	0.55	0.55	8.07	8.22	4.22
NCIH1184_LUNG	0.55	0.55	0.55	8.60	4.78	4.78
NCIH2141_LUNG	0.57	0.57	0.57	8.48	5.30	4.57
SNU620_STOMACH	0.62	0.62	0.62	5.89	5.51	4.01
HCC56_LARGE_INTESTINE	0.67	0.67	0.67	5.18	4.13	3.78
SKCO1_LARGE_INTESTINE	0.74	0.74	0.74	4.97	4.42	4.05
NCIH889_LUNG	0.78	0.78	0.78	8.90	4.16	4.97
SNU119_OVARY	0.83	0.83	0.83	9.13	7.75	4.09

File S1 (*continued*)

File S1 (*continued*)

Cell name_Organ	Copy number value			Relative RNA level		
	CDKN2BAS	CDKN2B	CDKN2A	CDKN2A	CDKN2B	CDKN2BAS1
HDLM2_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	0.83	0.83	0.83	7.89	3.61	4.51
HCC2157_BREAST	0.91	0.91	0.91	8.50	4.41	4.17
NCIH1876_LUNG	0.96	0.96	0.96	8.98	5.44	4.77
HCC70_BREAST	1.01	1.01	1.01	9.68	8.28	4.17
SUPHD1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE	1.31	1.31	1.31	5.84	3.62	4.14