

**Table S1.** The list of 15 genes with aberrant low expression in TNBC and lung adenocarcinoma, but not in other cancer, tumor tissues compared with adjacent normal tissues.

| ID      | Entrez Gene Name   | Location            | Type(s)                    |
|---------|--|---------------------|----------------------------|
| ABCC6   | ATP binding cassette subfamily C member 6                | Plasma Membrane     | transporter                |
| ANGPT4  | angiopoietin 4   | Extracellular Space | growth factor              |
| CA3     | carbonic anhydrase 3                                     | Cytoplasm           | enzyme                     |
| CACHD1  | cache domain containing 1                                | Other               | other                      |
| CCND2   | cyclin D2  | Nucleus             | other                      |
| DOCK11  | dedicator of cytokinesis 11                              | Cytoplasm           | other                      |
| FAM47E  | family with sequence similarity 47 member E              | Cytoplasm           | other                      |
| GPR109A | hydroxycarboxylic acid receptor 2                        | Plasma Membrane     | G-protein coupled receptor |
| LIN7    | Alin-7 homolog A, crumbs cell polarity complex component | Plasma Membrane     | other                      |
| LPL     | lipoprotein lipase                                       | Cytoplasm           | enzyme                     |
| PCDHGB7 | protocadherin gamma subfamily B, 7                       | Other               | other                      |
| PTGFR   | prostaglandin F receptor                                 | Plasma Membrane     | G-protein coupled receptor |
| RAPGEF3 | Rap guanine nucleotide exchange factor 3                 | Nucleus             | other                      |
| TACC1   | transforming acidic coiled-coil containing protein 1     | Nucleus             | other                      |
| TGFBR2  | transforming growth factor beta receptor 2               | Plasma Membrane     | kinase                     |

© 2000-2017 QIAGEN. All rights reserved. (Analyzed by Ingenuity Pathway Analysis)

**Table S2.** Demethylation in CCND2 mediated by antroquinonol D in MDA-MB-231 breast cancer cells.

| Demethylation<br>( $\Delta$ Avg_Beta) <sup>a</sup> | Fold change of<br>methylation <sup>b</sup> (%) | GENE<br>NAME | Function              | Reference   |
|--|--|--------------|-----------------------|---|
| -0.200   | 33.343   | CCND2        | Cell cycle regulation | Highly methylation of CCND2 in breast tumor than in normal tissue specimens (11). |

a Demethylation ( $\Delta$  Avg\_Beta) indicates that the change level of DNA methylation in specific gene between DMSO control and D-Antroquinonol treatment. The data was calculated by: D-Antroquinonol.Avg\_Beta – DMSO.Avg\_Beta. “Beta” scores are based on the ratio of methylated signal intensity to the sum of both methylated and unmethylated signals output.

b Fold change of DNA methylation was calculated by: [1-(D-Antroquinonol.Avg\_Beta/DMSO.Avg\_Beta)]\*100.

**Table S3.** CCND2 mRNA expression in relation to the clinical parameters of lung cancer.<sup>1</sup>

| Characteristics             | CCND2 mRNA |          |            |                 | CCND2 methylation           |             |              |                                |
|-----------------------------|------------|----------|------------|-----------------|-----------------------------|-------------|--------------|--------------------------------|
|                             | Total<br>n | Low<br>n | Low<br>(%) | Normal<br>n (%) | Total<br>n                  | Low<br>n(%) | High<br>n(%) |                                |
| <b>Overall</b>              | 1019       | 630      | (61.8)     | 389             | (38.2)                      | 828         | 626(75.6)    | 202(24.4)                      |
| <b>Age</b>                  | 1010       | 628      | (62.2)     | 382             | (37.8)                      | 819         | 618(75.5)    | 201(24.5)                      |
| < 65                        | 437        | 271      | (62.0)     | 166             | (38.0)                      | 362         | 254(70.2)    | 108(29.8) <sup>0.002</sup>     |
| ≥ 65                        | 573        | 357      | (62.3)     | 4               | (37.7)                      | 457         | 364(79.6)    | 93(20.4)                       |
| <b>Gender</b>               | 1019       | 630      | (61.8)     | 389             | (38.2)                      | 828         | 626(75.6)    | 202(24.4)                      |
| Female                      | 407        | 264      | (64.9)     | 143             | (35.1)                      | 340         | 233(68.5)    | 107(31.5) <sup>&lt;0.001</sup> |
| Male                        | 612        | 366      | (59.8)     | 246             | (40.2)                      | 488         | 293(80.5)    | 95(19.5)                       |
| <b>Tumor type</b>           | 1019       | 630      | (61.8)     | 389             | (38.2)                      | 828         | 626(75.6)    | 202(24.4)                      |
| Squamous carcinoma          | 504        | 250      | (49.6)     | 254             | (50.4)                      | 370         | 358(96.8)    | 12(3.2)                        |
| Adenocarcinoma              | 515        | 380      | (73.8)     | 135             | (26.2) <sup>&lt;0.001</sup> | 458         | 268(58.5)    | 190(41.5) <sup>&lt;0.001</sup> |
| <b>Tumor stage</b>          | 1007       | 621      | (61.7)     | 386             | (38.3)                      | 820         | 622(75.9)    | 198(24.1)                      |
| I                           | 520        | 308      | (59.2)     | 212             | (40.8)                      | 420         | 320(76.2)    | 100(23.8)                      |
| II                          | 285        | 178      | (62.5)     | 107             | (37.5)                      | 247         | 188(76.1)    | 59(23.9)                       |
| III                         | 169        | 108      | (63.9)     | 61              | (36.1)                      | 129         | 96(74.4)     | 33(25.6)                       |
| IV                          | 33         | 27       | (81.8)     | 6               | (18.2)                      | 24          | 18(75.0)     | 6(25.0)                        |
| <b>Primary tumor</b>        | 1016       | 628      | (61.8)     | 388             | (38.2)                      | 825         | 624(75.6)    | 201(24.4)                      |
| T1                          | 284        | 167      | (58.8)     | 117             | (41.2)                      | 245         | 192(78.4)    | 53(21.6)                       |
| T2                          | 571        | 363      | (63.6)     | 208             | (36.4)                      | 450         | 333(74.0)    | 117(26.0)                      |
| T3                          | 118        | 76       | (64.4)     | 42              | (35.6)                      | 101         | 76(75.2)     | 25(24.8)                       |
| T4                          | 43         | 22       | (51.2)     | 21              | (48.8)                      | 29          | 23(79.3)     | 6(20.7)                        |
| <b>Regional lymph nodes</b> | 1013       | 626      | (61.8)     | 387             | (38.2)                      | 823         | 623(75.7)    | 200(24.3)                      |
| N0                          | 663        | 399      | (60.2)     | 264             | (39.8)                      | 546         | 419(76.7)    | 127(23.3)                      |
| N1                          | 229        | 136      | (59.4)     | 93              | (40.6)                      | 182         | 135(74.2)    | 47(25.8)                       |
| N2                          | 114        | 86       | (75.4)     | 28              | (24.6)                      | 94          | 68(72.3)     | 26(27.7)                       |
| N3                          | 7          | 5        | (71.4)     | 2               | (28.6) <sup>0.014</sup>     | 1           | 1(100.0)     | 0(0.0)                         |
| <b>Distant metastasis</b>   | 1016       | 629      | (61.9)     | 387             | (38.1)                      | 825         | 625(75.8)    | 200(24.2)                      |
| No distant metastasis       | 983        | 602      | (61.2)     | 381             | (38.8)                      | 801         | 607(75.8)    | 18(24.2)                       |
| Distant metastasis          | 33         | 27       | (81.8)     | 6               | (18.2) <sup>0.017</sup>     | 24          | 18(75.0)     | 6(25.0)                        |

- These results were analyzed by the Pearson  $\chi^2$  test. P values with significance are shown as superscripts.
- When the CCND2 expression level in lung tumors was less than half of the mean of CCND2 expression levels in adjacent normal lung tissues was defined as low expression from TCGA data set using RNA sequencing analysis.

3. \*, P < 0.05; \*\*, P < 0.001.

**Table S4.** CCND2 mRNA expression and promoter hypermethylation in relation to the clinical parameters of breast cancer.<sup>1</sup>

| Characteristics          | Total |            | CCND2 mRNA                      |                | CCND2 Methylation         |  |
|--------------------------|-------|------------|---------------------------------|----------------|---------------------------|--|
|                          | n     | n          | Low (%)                         | High n (%)     | n (%)                     | n (%)                                  |
| <b>Overall</b>           | 761   | 183        | (24.0)                          | 578 (76.0)     | 623                       | 86 (13.8)                              |
| <b>Age</b>               | 761   | 183        | (24.0)                          | 578 (76.0)     | 623                       | 86 (13.8)                              |
| < 65                     | 551   | 121 (22.0) | 430 (78.0) <sup>0.029</sup>     | 453 399 (88.1) | 54 (86.2)                 | 54 (11.9) <sup>0.026</sup> (13.8)      |
| ≥ 65                     | 210   | 62 (29.5)  | 148 (70.5)                      | 170 138 (81.2) | 32 (86.2)                 | 32 (18.8) (11.9)                       |
| <b>Race</b>              | 525   | 117 (22.3) | 407 (77.7)                      | 433 371 (85.7) | 62 (86.4)                 | 62 (14.3) (46) (13.6) <sup>0.722</sup> |
| White                    | 421   | 82 (19.5)  | 33.9 (80.5) <sup>0.003</sup>    | 338 292 (86.4) | 46 (82.8)                 | 46 (17.2) (11)                         |
| Black/African American   | 72    | 27 (37.5)  | 45 (62.5)                       | 64 53 (83.9)   | 5 (82.8)                  | 5 (0.0) (0)                            |
| Asian                    | 32    | 8 (25.0)   | 24 (75.0)                       | 31 26 (83.9)   | 5 (16.1) (5)              | 5 (16.1) (11)                          |
| <b>Menopause State</b>   | 480   | 117 (22.3) | 407 (77.7)                      | 404 347 (85.9) | 57 (87.4)                 | 57 (14.1) (46) (13.6) <sup>0.242</sup> |
| Premenopause             | 123   | 23 (18.7)  | 100 (81.3) <sup>0.536</sup>     | 103 90 (87.4)  | 0 (100.0)                 | 0 (0.0) (0)                            |
| Perimenopause            | 16    | 3 (18.8)   | 13 (81.3)                       | 14 14 (100.0)  | 11 (84.7)                 | 11 (15.3) (11)                         |
| Postmenopause            | 341   | 79 (23.2)  | 262 (76.8)                      | 287 243 (84.7) | 1 (14.1)                  | 1 (14.1) (11)                          |
| <b>Histological Type</b> | 714   | 166 (23.2) | 548 (76.8)                      | 582 347 (85.9) | 57 (82.2)                 | 57 (14.1) (27) (17.8) <sup>0.356</sup> |
| ILC                      | 170   | 25 (14.7)  | 145 (85.3) <sup>&lt;0.001</sup> | 152 125 (82.2) | 53 (13.3)                 | 53 (13.3) (53)                         |
| IDC                      | 504   | 128 (25.4) | 376 (74.6)                      | 400 347 (86.8) | 15 (21.4)                 | 15 (21.4) (3)                          |
| Mucinous Carcinoma       | 15    | 11 (73.3)  | 4 (26.7)                        | 14 11 (78.6)   | 1 (6.3)                   | 1 (6.3) (1)                            |
| Mixed type               | 25    | 2 (8.0)    | 23 (92.0)                       | 16 15 (93.8)   | 1 (16.7)                  | 1 (16.7) (1)                           |
| <b>Tumor Stage</b>       | 535   | 117 (21.9) | 418 (78.1)                      | 440 379 (86.1) | 61 (88.6)                 | 61 (13.9) (8) (11.4) <sup>0.181</sup>  |
| I                        | 86    | 14 (16.3)  | 72 (83.7) <sup>0.371</sup>      | 70 62 (88.6)   | 41 (91.1)                 | 41 (17.0) (41)                         |
| II                       | 299   | 73 (24.4)  | 226 (75.6)                      | 241 200 (83.0) | 11 (91.1)                 | 11 (8.9) (11)                          |
| III                      | 142   | 28 (19.7)  | 114 (80.3)                      | 123 112 (91.1) | 1 (24.4)                  | 1 (8.9) (1)                            |
| IV                       | 8     | 2 (25.0)   | 6 (75.0)                        | 6 5 (83.3)     | 1 (16.7)                  | 1 (16.7) (1)                           |
| <b>ER</b>                | 535   | 121 (22.6) | 414 (77.4)                      | 443 381 (86.0) | 62 (89.3)                 | 62 (14.0) (11) (10.7) <sup>0.268</sup> |
| Negative                 | 117   | 33 (28.2)  | 84 (71.8) <sup>0.102</sup>      | 103 92 (89.3)  | 51 (15.0)                 | 51 (15.0) (51)                         |
| Positive                 | 418   | 88 (21.1)  | 330 (78.9)                      | 340 289 (85.0) | 1 (14.0)                  | 1 (14.0) (1)                           |
| <b>PR</b>                | 533   | 121 (22.7) | 412 (77.3)                      | 442 380 (86.0) | 62 (86.0)                 | 62 (14.0) (11) (14.0) <sup>0.986</sup> |
| Negative                 | 169   | 50 (29.6)  | 119 (70.4) <sup>0.010</sup>     | 143 123 (86.0) | 51 (14.0)                 | 51 (14.0) (51)                         |
| Positive                 | 364   | 71 (19.5)  | 293 (80.5)                      | 299 257 (86.0) | 1 (24.4)                  | 1 (24.4) (1)                           |
| <b>HER2</b>              | 463   | 99 (21.4)  | 364 (78.6)                      | 385 331 (86.0) | 54 (87.4)                 | 54 (14.0) (43) (12.6) <sup>0.032</sup> |
| Negative                 | 404   | 91 (22.5)  | 313 (77.5) <sup>0.117</sup>     | 340 297 (87.4) | 11 (75.6)                 | 11 (24.4) (11)                         |
| Positive                 | 59    | 8 (13.6)   | 51 (86.4)                       | 45 34 (75.6)   | 9 (13.2) <sup>0.781</sup> | 9 (14.5) (9)                           |
| <b>TRBC</b>              | 515   | 115 (22.3) | 400 (77.7)                      | 426 365 (85.7) | 61 (86.8)                 | 61 (14.3) (9) (13.2) <sup>0.781</sup>  |
| Negative                 | 76    | 25 (32.9)  | 51 (67.1) <sup>0.017</sup>      | 68 59 (86.8)   | 52 (14.5)                 | 52 (14.5) (52)                         |
| Positive                 | 439   | 90 (20.5)  | 349 (79.5)                      | 358 306 (85.5) | 1 (14.3)                  | 1 (14.3) (1)                           |

- These results were analyzed by the Pearson  $\chi^2$  test. P values with significance are shown as superscripts.
- When the CCND2 expression level in breast tumors was less than half of the mean of CCND2 expression levels in adjacent normalbreast tissues was defined as low expression from TCGA data set using RNA sequencing analysis.



**Table S5.** Methylation levels of CCND2 promoter through pyrosequencing.

| <b>Cells</b> | <b>Treatment</b> | <b>Position</b> | <b>1</b> | <b>2</b> | <b>3</b> | <b>4</b> | <b>5</b> | <b>6</b> |
|--------------|------------------|-----------------|----------|----------|----------|----------|----------|----------|
| CL1-5        | DMSO             | Methylation (%) | 7        | 10       | 5        | 17       | 11       | 10       |
|              | Antroquinonol    | Methylation (%) | 10       | 11       | 6        | 16       | 14       | 10       |
|              | Antroquinonol D  | Methylation (%) | 11       | 12       | 5        | 17       | 13       | 10       |
| H1299        | DMSO             | Methylation (%) | 16       | 13       | 7        | 23       | 25       | 27       |
|              | Antroquinonol    | Methylation (%) | 14       | 12       | 7        | 20       | 24       | 24       |
|              | Antroquinonol D  | Methylation (%) | 14       | 26       | 8        | 22       | 26       | 25       |

**Table S6.** List of primer sequences and reaction conditions used in the study.

| Real-time RT-PCR <sup>a</sup> |              | Sequence (5' to 3')                        | Probe | Tm<br>(°C) |
|-------------------------------|--------------|--|-------|------------|
| <i>CCND2</i>                  | Forward      | GGACATCCAACCCTACATGC                       | #49   | 60         |
|                               | Reverse      | CGCACTTCTGTCCTCACAG                        |       |            |
| <i>COL4A2</i>                 | Forward      | CCAGGACAGAAAGGAGACCA                       | #1    | 60         |
|                               | Reverse      | GGTGTGATGCCTGGAAC                          |       |            |
| <i>FOXN3</i>                  | Forward      | ATCAGGCACCTTCTCCTCAA                       | #15   | 60         |
|                               | Reverse      | TCTCAGCAGTGTGAGGCCATC                      |       |            |
| <i>GAPDH</i>                  | Forward      | AGCCACATCGCTCAGACAC                        | #60   | 60         |
|                               | Reverse      | GCCCAATACGACCAAATCC                        |       |            |
| <i>RPS6KA2</i>                | Forward      | CAGTTGCTGGAACTATGGAAAA                     | #39   | 60         |
|                               | Reverse      | TCCAGGTTGAGATCCTCCTCT                      |       |            |
| <i>RXRA</i>                   | Forward      | ACATGCAGATGGACAAGACG                       | #26   | 60         |
|                               | Reverse      | TCGAGAGCCCCCTGGAGT                         |       |            |
| <i>TAOK1</i>                  | Forward      | TCGTAATCGAGAACACTTGCT                      | #56   | 60         |
|                               | Reverse      | CTTGCATTGCCTCGTAACC                        |       |            |
| <i>FANCC</i>                  | Forward      | ATCAGGCACCTTCTCCTCAA                       | #15   | 60         |
|                               | Reverse      | TCTCAGCAGTGTGAGGCCATC                      |       |            |
| <i>CACNA1A</i>                | Forward      | TCGCCGAGGATGAAACTG                         | #32   | 60         |
|                               | Reverse      | GCTTTCTTATGGTGGTCTCC                       |       |            |
| <i>CDH15</i>                  | Forward      | GGACATCGCCGACTTCAT                         | #75   | 60         |
|                               | Reverse      | GGCACACTGGGTCACTATC                        |       |            |
| <i>ASB9</i>                   | Forward      | AAACAAGGGGGCATGGAT                         | #72   | 60         |
|                               | Reverse      | ACCAATCAGACACAGCATCG                       |       |            |
| <i>DAPK1</i>                  | Forward      | CCCAGTTGAAGAACCCATAGC                      | #49   | 60         |
|                               | Reverse      | CGAGGAACATTATCATGATGTCAG                   |       |            |
| <i>FOXN3</i>                  | Forward      | GCTTTGAATACTCCCCCTGA                       | #65   | 60         |
|                               | Reverse      | GCGCTCCATTGGATCA                           |       |            |
| <i>FOXP3</i>                  | Forward      | GAGAAGCTGAGTGCCATGC                        | #20   | 60         |
|                               | Reverse      | AGCCCTTGTGCGGATGATG                        |       |            |
| <i>HOXD10</i>                 | Forward      | CTGAGGCTCTCCGTGTCCAGT                      | #2    | 60         |
|                               | Reverse      | GCTGGTTGGTGTATCAGACTTG                     |       |            |
| <i>LRP1B</i>                  | Forward      | CGTGAATTGTGTCTCCCAGA                       | #76   | 60         |
|                               | Reverse      | GGGGCACTTGATTCTACCTC                       |       |            |
| <i>RARB</i>                   | Forward      | TTGTGTTCACCTTGCCAAC                        | #51   | 60         |
|                               | Reverse      | TTTGTGTTCCCTCAAGGTC                        |       |            |
| <i>RHOBTB3</i>                | Forward      | CCACCTCAACTGAACAAACCA                      | #41   | 60         |
|                               | Reverse      | GGCAGCAGAACAGCAAGTTA                       |       |            |
| <i>SOX4</i>                   | Forward      | AGCCGGAGGAGGAGATGT                         | #20   | 60         |
|                               | Reverse      | TTCTCGGGTCATTCCTAGC                        |       |            |
| <i>TBC1D8</i>                 | Forward      | CCGAGCCAGATACCAAG                          | #85   | 60         |
|                               | Reverse      | GAAAGCCCGGAAGAACTCA                        |       |            |
| <i>TCERG1L</i>                | Forward      | ACATGCTGCTGGAGAGAGG                        | #14   | 60         |
|                               | Reverse      | GGTCAAACACGATTGTGTAATT                     |       |            |
| <i>THBS4</i>                  | Forward      | CCTGAGACCATTGAATTGAGG                      | #6    | 60         |
|                               | Reverse      | ACCAGCTCAGCTCTCCAA                         |       |            |
| Pyrosequencing                |              |  |       |            |
| <i>CCND2</i>                  | Bis-Forward  | GAGGGAGGGAGAGATTGAAAG                      | 60.2  |            |
|                               | Bio- Reverse | ATCCTCCCCCTAAACTAATCT                      |       |            |
|                               | Seq- Forward | GGGAGGAGGAATTAGA                           |       |            |
| qMSP                          |              |  |       |            |
| <i>CCND2</i>                  | Forward      | CGTTAGAGTACGTGTTAGGGTCGATC                 | 60    |            |
|                               | Reverse      | CGAAAACATAAAACCTCCACGCT                    |       |            |
|                               | LNA-probe    | 56-FAM/AA TCG CCG C/ZEN/C AAC ACG /3IABKFQ |       |            |

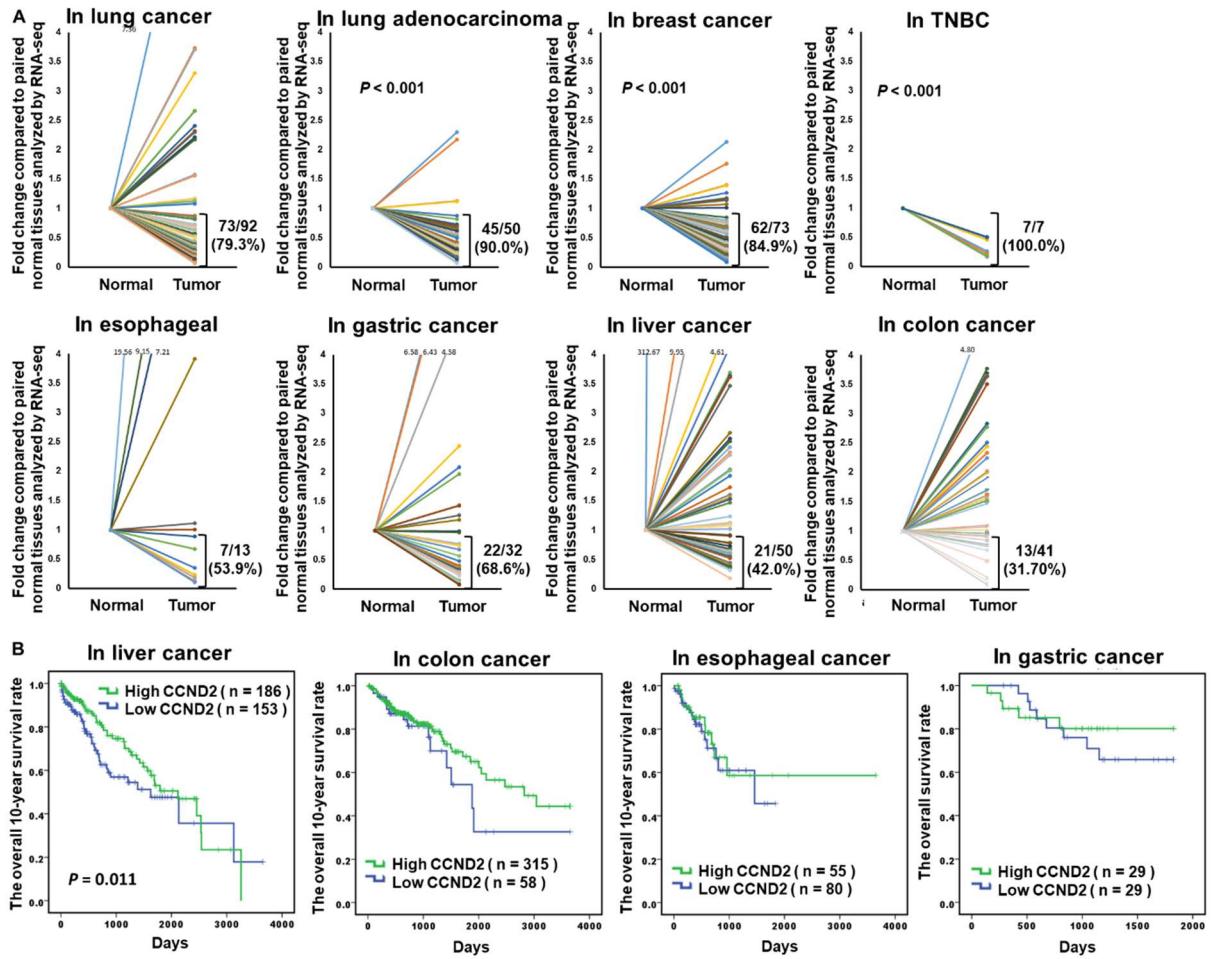
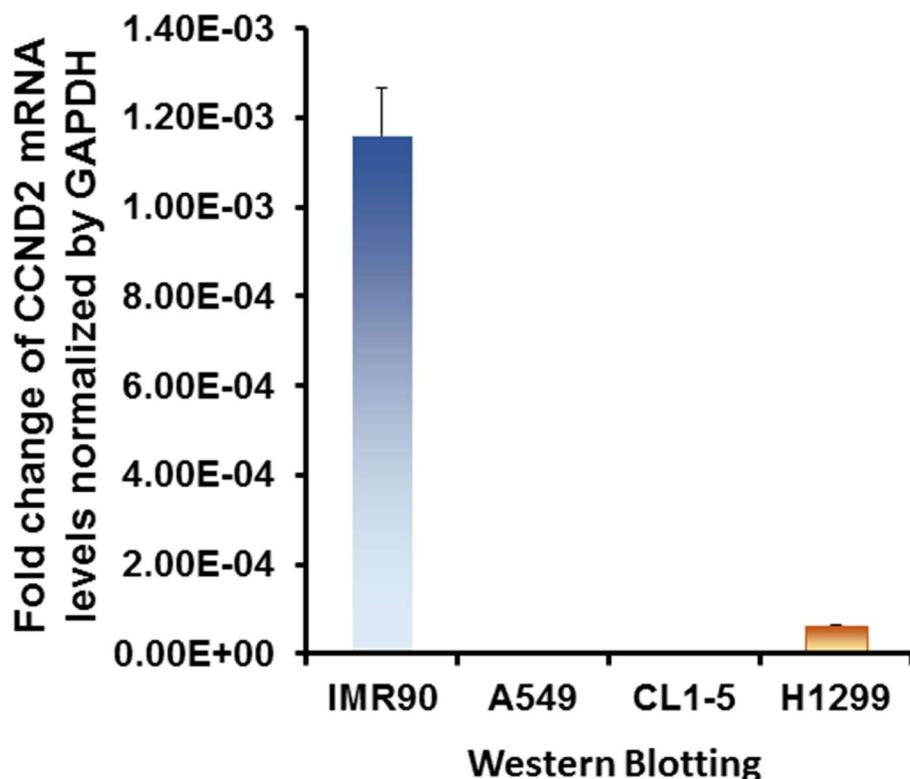


Figure S1 *CCND2* mRNA expression level and its correlation with survival in lung, breast, liver, colon, and gastric cancers. Data for mRNA expression level assayed through RNA sequencing and survival data were collected from TCGA. (A) The fold changes of normal tissues and tumors for RNA sequencing were normalised using the data of paired adjacent normal tissues. (B) Kaplan–Meier survival curves were used to compare the overall and 10-year survival between cancer patients with low and high *CCND2* mRNA expression level in lung cancer, breast cancer, liver cancer, and colon cancer. Because the follow-up time for gastric cancer patients was less than 10 years, only overall survival was analysed in these patients.

**Figure S2**

**Real-time RT-PCR**



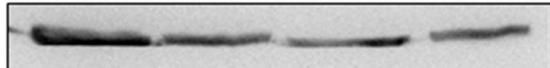
**Western Blotting**

IMR-90 A549 CL1-5 H1299

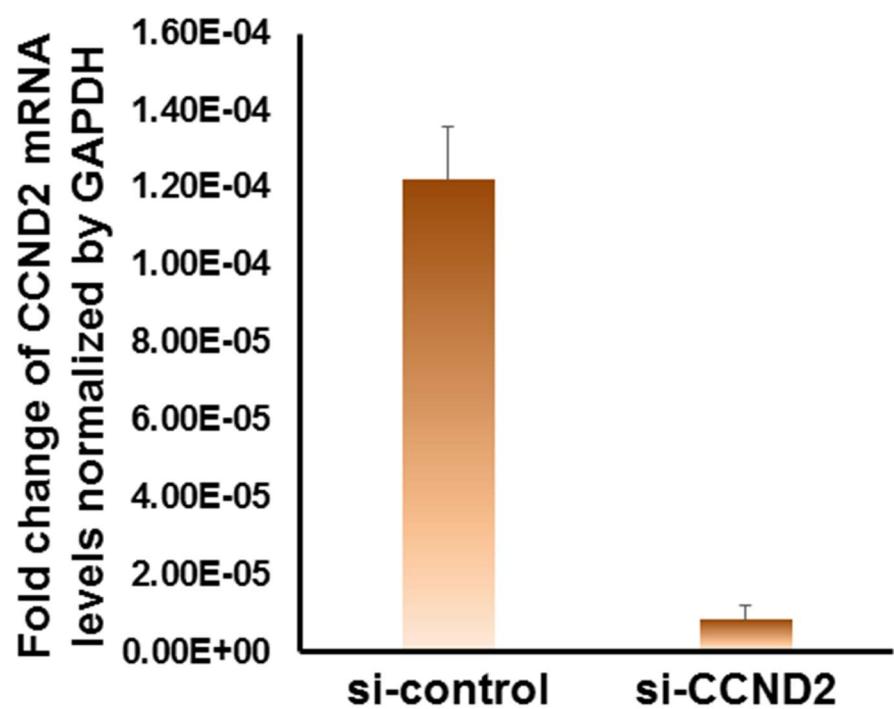
**CCND2**



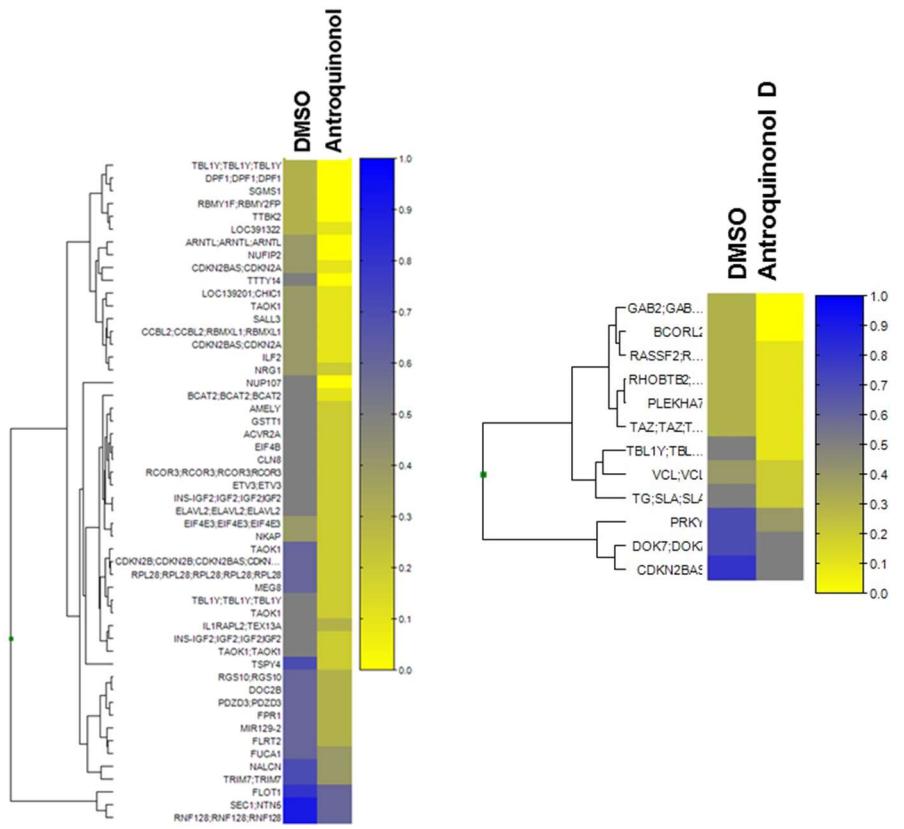
**ACTB**



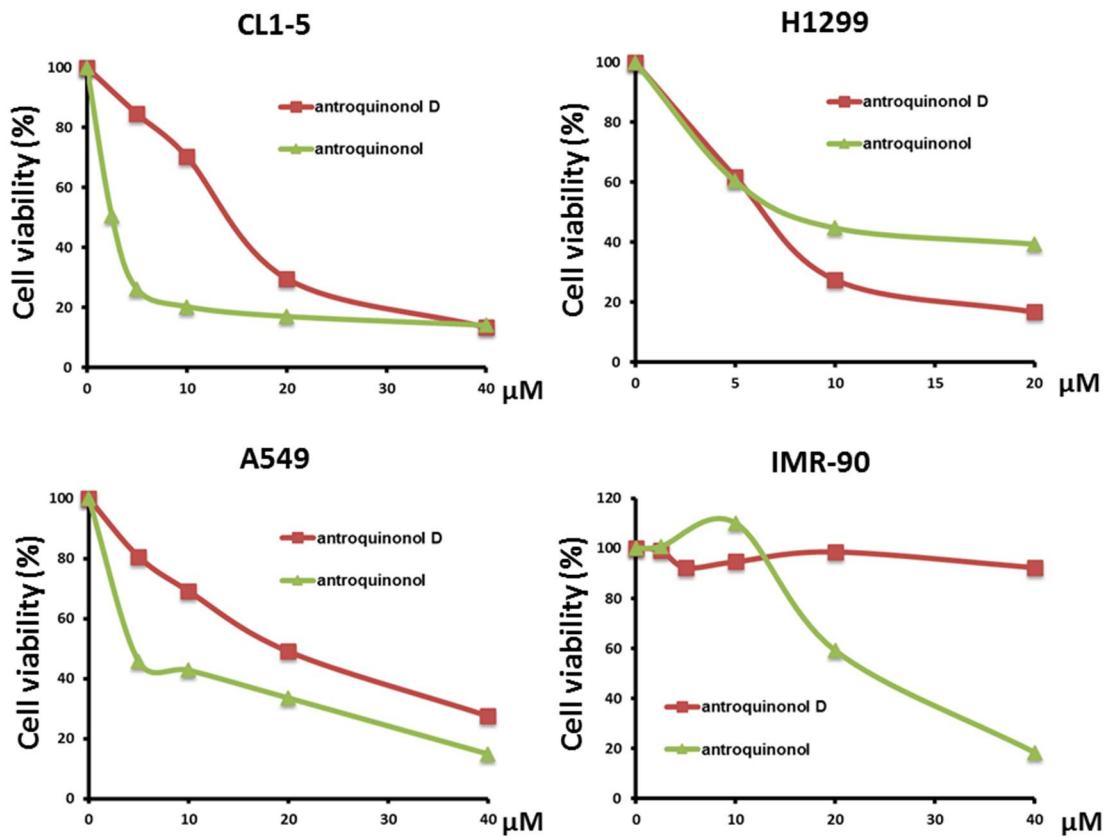
**Figure S2.** *CCND2* mRNA and protein expression in lung cancer and normal cell lines.



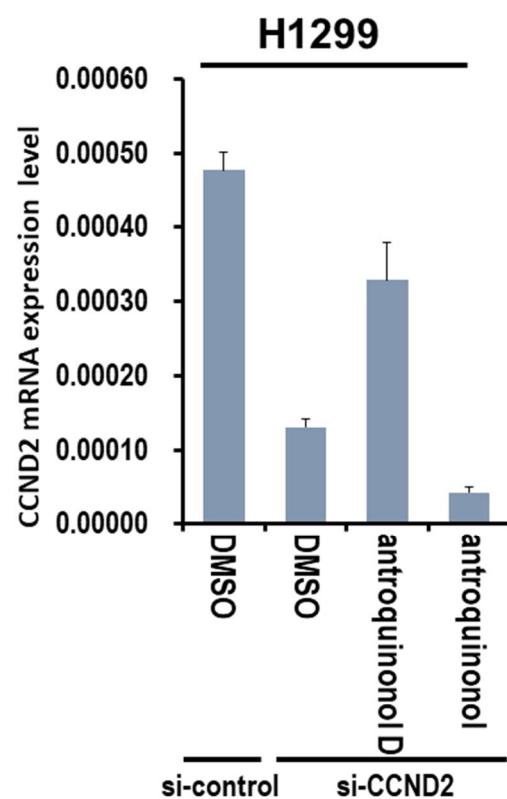
**Figure S3.** CCND2 mRNA expression level when treated with si-control or si-CCND2.



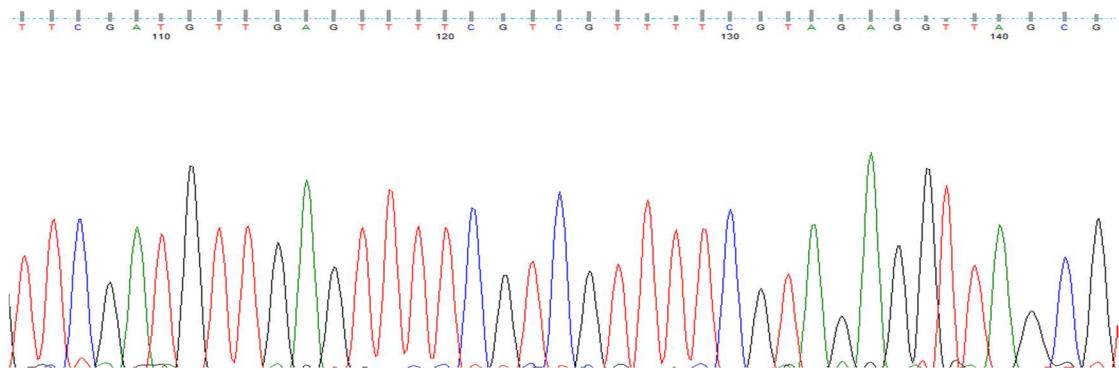
**Figure S4.** Heatmap of demethylation genes followed by antroquinonol D and antroquinonol.



**Figure S5.** Cell viability curve of antroquinonol D and antroquinonol.



**Figure S6.** The CCND2 mRNA expression followed by si-CCND2 and drug treatment.



**Figure S7.** The qPCR end product for *CCND2* methylation was analyzed by bisulfite sequencing.

## References

1. Ganzinelli M, Mariani P, Cattaneo D, et al. Expression of DNA repair genes in ovarian cancer samples: biological and clinical considerations. *Eur J Cancer* 2011; 47: 1086-94.
2. Morey Kinney SR, Smiraglia DJ, James SR, Moser MT, Foster BA, Karpf AR. Stage-specific alterations of DNA methyltransferase expression, DNA hypermethylation, and DNA hypomethylation during prostate cancer progression in the transgenic adenocarcinoma of mouse prostate model. *Mol Cancer Res* 2008; 6: 1365-74.
3. Castro M, Grau L, Puerta P, et al. Multiplexed methylation profiles of tumor suppressor genes and clinical outcome in lung cancer. *J Transl Med* 2010; 8: 86.
4. Yamada S, Nomoto S, Fujii T, et al. Frequent promoter methylation of M-cadherin in hepatocellular carcinoma is associated with poor prognosis. *Anticancer Res* 2007; 27: 2269-74.
5. Tokuoka M, Miyoshi N, Hitora T, et al. Clinical significance of ASB9 in human colorectal cancer. *Int J Oncol* 2010; 37: 1105-11.
6. Bignone PA, Lee KY, Liu Y, et al. RPS6KA2, a putative tumour suppressor gene at 6q27 in sporadic epithelial ovarian cancer. *Oncogene* 2007; 26: 683-700.
7. He XP, Li ZS, Zhu RM, et al. Effects of recombinant human canstatin protein in the treatment of pancreatic cancer. *World J Gastroenterol* 2006; 12: 6652-7.
8. L'Esperance S, Popa I, Bachvarova M, et al. Gene expression profiling of paired ovarian tumors obtained prior to and following adjuvant chemotherapy: molecular signatures of chemoresistant tumors. *Int J Oncol* 2006; 29: 5-24.
9. Chen YJ, Liao CT, Chen PJ, et al. Downregulation of Ches1 and other novel genes in oral cancer cells chronically exposed to areca nut extract. *Head Neck* 2011; 33: 257-66.
10. Chang H, Mohabir N, Done S, Hamel PA. Loss of ALX4 expression in epithelial cells and adjacent stromal cells in breast cancer. *J Clin Pathol* 2009; 62: 908-14.
11. Zhu W, Qin W, Hewett JE, Sauter ER. Quantitative evaluation of DNA hypermethylation in malignant and benign breast tissue and fluids. *Int J Cancer* 2010; 126: 474-82.