**Supplementary Table 1** The main clinical data, including histological grades and TNM stages of 14 human subjects and TES levels of the CRC tissue samples

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **No.** | **Gender** | **Age (Years)** | **T** | **N** | **M** | **histological grade** | **Tumor TES level****(TES/GAPDH)** |
| 1234567891011121314 | MaleFemaleMaleMaleFemaleFemaleMaleMaleMaleMaleMaleFemaleMaleFemale | 4253615444595071585924565954 | 44444444444444 | 02112111012211 | 00101010000000 | High-gradeHigh-gradeHigh-gradeHigh-gradeHigh-gradeLow-gradeHigh-gradeHigh-gradeHigh-gradeHigh-gradeHigh-gradeHigh-gradeHigh-gradeHigh-grade | 0.2812748710.1101493180.4266089350.1094278750.5466877580.6250257780.5373006840.0072693910.126548240.0883452950.0088359720.3014603120.0683394510.513558938 |

**Supplementary Table 2** The Broder's grade and Duke's classification of the original tumors and TES levels of the CRC cell lines

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Cell line** | **Duke's stage** | **Broders' grade** | **Differentiation of the original tumor** | **Histological grades** |  |
| Caco-2DLD-1HCT116HT-29SW480RKOSW620LoVo | NDCNDNDBND CC | ⅡⅢ/ⅣⅢ/ⅣⅠⅣⅢ/ⅣⅣⅣ | ModeratePoorModerate/ PoorModerately wellPoorPoorPoorModerately well | Low-gradeHigh-gradeHigh-gradeLow-gradeHigh-gradeHigh-gradeHigh-gradeLow-grade |  |

**ND：Not determined**

**Supplementary Table 3** The primers used for RT-qPCR

|  |  |
| --- | --- |
| **Gene** | **Primer Sequence (Forward and Reverse)** |
| GAPDHp21p53Nkx2.5 | 5'- CCACTCCTCCACCTTTGAC -3'5'- ACCCTGTTGCTGTAGCCA -3'5’- TGTGGACCTGTCACTGTCTT -3’5’- TAGGGCTTCCTCTTGGAGA -3’5’- TTTCCGTCTGGGCTTCT -3’5’- GCTGTGACTGCTTGTAGATGG -3’5’- GGGATGGTAAACCGTGTCTGG -3’5’- TAGTTGCTGTTGGACTGTGAAGG -3’ |

**Supplementary Table 4** The primers used for amplifying the exonic regions of TP53

|  |  |
| --- | --- |
| **Exon** | **Primer Sequence (Forward and Reverse)** |
| E1E2/3E4/5E6E7/8E9E10E11 | 5'- GTTAGTATCTACGGCACCAGGTC -3'5'- CTCTAGCCAAGCTTCCATCCCAC -3'5’- CCACAGGAAGCCGAGCTGTCTC -3’5’- CACTGACAGGAAGCCAAAGGGTG -3’5’- CAATCCCAGCACTCTCAAAGAG -3’5’- GGGTTATAGGGAGGTCAAATAAGC -3’5’- CTCCCCTGCTTGCCACAGGTC -3’5’- GTAGGTGGAGGAGAAGCCACAGG -3’5'- GACAGGTAGGACCTGATTTCC -3'5'- GGTATAAGTTGGTGTTCTGAAG -3'5’- CTTCAGGTACTAAGTCTTGGGAC -3’5’- GCTAGGCTAAGCTATGATGTTCC -3’5’- GCTGTATAGGTACTTGAAGTGCAG -3’5’- CAGGGCTGGGACCCAATGAGATGG -3’5’- GATTTGAATTCCCGTTGTCCCAG -3’5’- GACCCAGTCTCCAGCCTTTGTTC -3’ |