## Table S5.

Comparisons of TRIM29 promoter methylation and gene expression for various normal tissues and respective carcinomas in TCGA
(A)

|  | BLCA | BRCA | COAD | LUSC | PAAD | PRAD | READ |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| BRCA | 1 | - | - | - | - | - | - |
| COAD | 0.04378801 | $2.09 \mathrm{E}-05$ | - | - | - | - | - |
| LUSC | 0.09690264 | $2.20 \mathrm{E}-07$ | 1 | - | - | - | - |
| PAAD | 1 | 0.07006369 | 1 | 1 | - | - | - |
| PRAD | $2.68 \mathrm{E}-13$ | $2.91 \mathrm{E}-23$ | $2.74 \mathrm{E}-24$ | $6.56 \mathrm{E}-35$ | $2.20 \mathrm{E}-12$ | - | - |
| READ | 0.06775645 | 0.00112829 | 1 | 1 | 1 | $1.41 \mathrm{E}-15$ | - |
| UCEC | $1.07 \mathrm{E}-06$ | $4.30 \mathrm{E}-19$ | 1 | $1.52 \mathrm{E}-02$ | $1.00 \mathrm{E}+00$ | $6.82 \mathrm{E}-48$ | 1 |

Multiple comparisons of TRIM29 promoter methylation in various normal tissues. TCGA data used as described in methods. Analysis for 5 Illumina probes at the TRIM29 TSS region (probes detailed in supplementary table 3). P-values (average for 5 probes) between groups were calculated by t-test and Bonferroni correction. $\qquad$ $\mathrm{p}<0.05$.
(B)

|  | BLCA | BRCA | COAD | LUSC | PAAD | PRAD | READ |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| BRCA | $1.12 \mathrm{E}-66$ | - | - | - | - | - | - |
| COAD | $1.12 \mathrm{E}-27$ | 0.00161169 | - | - | - | - | - |
| LUSC | 0.06378519 | $8.07 \mathrm{E}-59$ | $4.23 \mathrm{E}-19$ | - | - | - | - |
| PAAD | $1.36 \mathrm{E}-24$ | 1 | 0.17668472 | $4.57 \mathrm{E}-18$ | - | - | - |
| PRAD | $3.29 \mathrm{E}-06$ | $4.57 \mathrm{E}-33$ | $2.81 \mathrm{E}-09$ | 0.21634977 | $1.61 \mathrm{E}-11$ | - | - |
| READ | $3.49 \mathrm{E}-09$ | $2.59 \mathrm{E}-12$ | 0.01105954 | 0.00050761 | $6.08 \mathrm{E}-06$ | 1 | - |
| UCEC | $8.78 \mathrm{E}-45$ | 0.00112701 | 1 | $2.89 \mathrm{E}-35$ | 0.55122249 | $1.75 \mathrm{E}-17$ | $2.98 \mathrm{E}-05$ |

Multiple Comparisons of TRIM29 promoter methylation in various cancers. TCGA data used as described in methods. Analysis for 5 Illumina probes at the TRIM29 TSS region (probes detailed in supplementary table 3). P-values (average for 5 probes) between groups were calculated by t-test and Bonferroni correction. $\square \mathrm{p}<0.05$.
(C)

|  | BLCA | BRCA | LUSC |
| :---: | :---: | :---: | :---: |
| BRCA | 1 | - | - |
| LUSC | 0.00069134 | $9.74 \mathrm{E}-11$ | - |
| PRAD | 0.60609728 | 0.79538649 | $7.69 \mathrm{E}-11$ |

Comparisons of TRIM29 gene expression in various normal tissues. TCGA data used as described in methods. P-values were calculated by t-test and Bonferroni correction. $\qquad$ $\mathrm{P}<0.05$
(D)

|  | BLCA | BRCA | LUSC |
| :---: | :---: | :---: | :---: |
| BRCA | 1 | - | - |
| LUSC | 0.00069134 | $9.74 \mathrm{E}-11$ | - |
| PRAD | 0.60609728 | 0.79538649 | $7.69 \mathrm{E}-11$ |

Comparisons of TRIM29 gene expression in various cancers. TCGA data used as described in methods. P-values were calculated by t-test and Bonferroni correction.$\mathrm{P}<0.05$
(E) Number of samples in TCGA analysis


For all tables: BRCA=breast carcinoma, PRAD=prostate adenocarcinoma, LUSC=lung squamous cell carcinoma, BLCA=bladder carcinoma, $\mathrm{PAAD}=$ pancreatic adenocarcinoma, COAD=colon adenocarcinoma, READ=rectal adenocarcinoma UCEC=uterine-cervix carcinoma. Number of samples in each group is shown in (E).

