Table S4
TRIM29 CpG island genomic sequence, Illumina probes details and primers for Q-MSP and RT-PCR.

(A)

TRIM29 CpG island genomic sequence, 648 bases, chr11:119513116-119513764 (located 300 b away from TSS at chr11:119514073). From NCBI Reference Sequence: NC_000011.9, Homo sapiens chromosome 11, GRCh37.p2 primary reference assembly. The Illumina infinium methylation array 450K probes are marked in 5 colors as listed in B.

(B)

<table>
<thead>
<tr>
<th>IlmnID</th>
<th>SourceSeq</th>
<th>Chr</th>
<th>Coordinate_36</th>
</tr>
</thead>
<tbody>
<tr>
<td>cg20655548</td>
<td>GATTCTTGCTCCTGGAACATGCAAGGTAGCAGATGCAGGTCTGGTCG</td>
<td>11</td>
<td>119513235</td>
</tr>
<tr>
<td>cg12261660</td>
<td>ACACCAAGCAGACTTGACCGCTCTGCTGCTGCGATGCGGTCG</td>
<td>11</td>
<td>11953404</td>
</tr>
<tr>
<td>cg17971587</td>
<td>AAAAGGCGAGCTGCAAGTCATTTCTCGGAGTCCGGAAGCCACAGC</td>
<td>11</td>
<td>11953533</td>
</tr>
<tr>
<td>cg13285004</td>
<td>CGGGAGCGACAAAGACTCCACTTCCACTTGATGCTGATGCCG</td>
<td>11</td>
<td>11953694</td>
</tr>
<tr>
<td>cg13625403</td>
<td>TAGTTGAGTTTGCTGCTCCCCAGGCAGACTGATGCTGAGTCG</td>
<td>11</td>
<td>11953720</td>
</tr>
</tbody>
</table>

TRIM29 Illumina probes: detailed list of the 5 probes that were analyzed in ENCODE and in TCGA.
Illumina Infinium methylation array 27K results for TRIM29 probe # cg13625403 – methylation was measured as average beta 0-1.

(D) Primers for TRIM29 Q-MSP

Design was based on the NCBI Reference Sequence: NC_000011.9, Homo sapiens chromosome 11, GRCh37.p2 primary reference assembly. Note that the sequence was adjusted for methylation dependent CT conversion by sodium bisulfite.

Unmethylated: TRIM29 FUM (forward) TTTAGTTTGTTGAGTTTGGGGAT TRIM29 RUM (reverse) CACTAAAAACCTACAATAACAACA

Methylated: TRIM 29 FM (forward) AGTTTGTCAGTTCCGGGAC TRIM 29 RM (reverse) ACTAAAAACCTACGTACGACG

(E) Primers for gene expression

Design was based on the NCBI Reference Sequence: NM_012101.3 and used NCBI primer blast program.

TRIM29_GEXF (forward) CTGACAATGACCTGCC CGT TRIM29_GEXR (reverse) CCTTGGGGCTTTGGCTC CG CAT

\[
\begin{array}{|c|c|c|}
\hline
\text{Tissue type} & \text{Ave. beta} & \text{Tissue type} & \text{Ave. beta} \\
\hline
\text{negative control} \_1 & 0.020 & \text{colon} \_1 & 0.935 \\
\text{negative control} \_2 & 0.062 & \text{colon} \_2 & 0.911 \\
\text{positive control} \_1 & 0.911 & \text{lung} \_1 & 0.957 \\
\text{positive control} \_2 & 0.861 & \text{lung} \_2 & 0.944 \\
\text{breast} \_1 & 0.488 & \text{endometrium} \_1 & 0.968 \\
\text{breast} \_2 & 0.501 & \text{endometrium} \_2 & 0.955 \\
\text{breast} \_3 & 0.518 & \text{WBC} \_1 & 0.956 \\
\text{breast} \_4 & 0.651 & \text{WBC} \_2 & 0.955 \\
\text{breast} \_5 & 0.545 & \text{WBC} \_3 & 0.959 \\
\text{breast} \_6 & 0.454 & & \\
\hline
\end{array}
\]