<table>
<thead>
<tr>
<th></th>
<th>Right colon cancer</th>
<th>Left colon cancer</th>
<th>Rectal cancer</th>
<th>p value</th>
<th>Statistical method</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of cases</td>
<td>35</td>
<td>36</td>
<td>35</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Age at diagnosis (median ± SD)</td>
<td>68 ± 9.9</td>
<td>69.5 ± 10.1</td>
<td>69 ± 9.2</td>
<td>0.902</td>
<td>Kruskal-Wallis test</td>
</tr>
<tr>
<td>Sex (Male : Female)</td>
<td>17:18</td>
<td>21:15</td>
<td>24 :11</td>
<td>0.237</td>
<td></td>
</tr>
<tr>
<td>AJCC cancer stage</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>I</td>
<td>9</td>
<td>6</td>
<td>8</td>
<td></td>
<td></td>
</tr>
<tr>
<td>II</td>
<td>13</td>
<td>14</td>
<td>10</td>
<td>0.762</td>
<td>χ² test</td>
</tr>
<tr>
<td>III</td>
<td>13</td>
<td>16</td>
<td>17</td>
<td></td>
<td></td>
</tr>
<tr>
<td>IV</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lymph node metastasis (+)</td>
<td>13</td>
<td>16</td>
<td>17</td>
<td>0.620</td>
<td></td>
</tr>
<tr>
<td>(-)</td>
<td>22</td>
<td>20</td>
<td>18</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Pathological type</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Differentiated</td>
<td>34</td>
<td>36</td>
<td>34</td>
<td>0.547</td>
<td>Fisher’s exact test</td>
</tr>
<tr>
<td>Poorly</td>
<td>1</td>
<td>0</td>
<td>1</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

AJCC, American Joint Committee on Cancer
Table S2. *KRAS* mutations identified in 106 CRC tissues.

<table>
<thead>
<tr>
<th>Mutations</th>
<th>Number of tumors</th>
<th>Frequency (%)</th>
<th>Patient ID</th>
</tr>
</thead>
<tbody>
<tr>
<td>G12V</td>
<td>16</td>
<td>15.1%</td>
<td>322, 326, 336, 342, 343, 373, 380, 388, 413, 422, 426, 481, 505, 519, 521, 556</td>
</tr>
<tr>
<td>G12D</td>
<td>7</td>
<td>6.6%</td>
<td>275, 316, 361, 410, 444, 464, 558</td>
</tr>
<tr>
<td>G12S</td>
<td>3</td>
<td>2.8%</td>
<td>321, 330, 534</td>
</tr>
<tr>
<td>G12C</td>
<td>3</td>
<td>2.8%</td>
<td>285, 360, 428</td>
</tr>
<tr>
<td>G12A</td>
<td>1</td>
<td>0.9%</td>
<td>472</td>
</tr>
<tr>
<td>G13D</td>
<td>9</td>
<td>8.5%</td>
<td>313, 341, 374, 419, 456, 473, 478, 484, 557</td>
</tr>
<tr>
<td>G13C</td>
<td>1</td>
<td>0.9%</td>
<td>311</td>
</tr>
<tr>
<td>G13R</td>
<td>1</td>
<td>0.9%</td>
<td>425</td>
</tr>
<tr>
<td>A59E</td>
<td>1</td>
<td>0.9%</td>
<td>347</td>
</tr>
</tbody>
</table>
Table S3. Relationship between CIMP and *BRAF* or *KRAS* mutations.

<table>
<thead>
<tr>
<th></th>
<th>CIMP-positive</th>
<th>CIMP-negative</th>
<th>p value</th>
<th>Statistical method</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>BRAF</em> mut (+)</td>
<td>5</td>
<td>0</td>
<td>0.001</td>
<td></td>
</tr>
<tr>
<td><em>BRAF</em> mut (-)</td>
<td>20</td>
<td>81</td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>KRAS</em> mut (+)</td>
<td>11</td>
<td>31</td>
<td>0.387</td>
<td>Fisher's exact test</td>
</tr>
<tr>
<td><em>KRAS</em> mut (-)</td>
<td>14</td>
<td>50</td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>KRAS</em> G13D (+)</td>
<td>2</td>
<td>7</td>
<td>0.642</td>
<td></td>
</tr>
<tr>
<td><em>KRAS</em> G13D (-)</td>
<td>23</td>
<td>74</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*BRAF* mut: *BRAF* mutation (V600E), *KRAS* mut: all *KRAS* mutations
Table S4. MAFG consensus binding sites in the iDMRs.

<table>
<thead>
<tr>
<th>DMR</th>
<th>Analyzed region</th>
<th>Strand</th>
<th>MAFG consensus binding site</th>
<th>Number of consensus binding sites</th>
<th>Frequency of MAFG consensus binding site per 1 Kb</th>
</tr>
</thead>
<tbody>
<tr>
<td>PPIEL</td>
<td>chr1: 40024626-40025540 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>ARHI-CG1</td>
<td>chr1: 68515433-68517545 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>ARHI-CG2</td>
<td>chr1: 68512505-68513486 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>ZDBF2</td>
<td>chr2: 207114563-207136544 -1</td>
<td>AGATAGCGCAGAATCTGCTGAAA</td>
<td>5</td>
<td>0.23</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>AATTGGCTTAGAGAGGACGATCAG</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>CTGATGCTCTCTAGCAAAATT</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>AGAGGCGCTGAGTTATGGTTAT</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>ATAAACATCACTCAGCATT</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NAP1L5</td>
<td>chr4: 89618184-89619237 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>FAM50B</td>
<td>chr6: 3849082-3850359 -1</td>
<td>GATGCGCTGCTTCAGACACCT</td>
<td>2</td>
<td>1.56</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>GAGGCTGTGAAAGCCGGCGCATC</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ZAC</td>
<td>chr6: 144328076-144329888 -1</td>
<td>AGATTGCTTACTTGGCCATAG</td>
<td>2</td>
<td>1.10</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>CATGTGCTAAGTAGACATCT</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GRB10-DMR</td>
<td>chr7: 50848726-50853132 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>PEG10</td>
<td>chr7: 94285537-94287960 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>PEG1</td>
<td>chr7: 130130122-130134388 -1</td>
<td>CAAATGCTGATTTAGCACCTA</td>
<td>2</td>
<td>0.47</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>TAGGTGCTAAATGACATCTT</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>LOC728024</td>
<td>chr8: 37604992-37606088 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>TRAPPC9</td>
<td>chr8: 141108147-141111081 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>H19promoter</td>
<td>chr11: 2018812-2024740 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>H19DMR</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>IGF2-DMR</td>
<td>chr11: 2153991-2155112 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>IGF2-DMR0</td>
<td>chr11: 2168333-2169768 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>KvDMR1</td>
<td>chr11: 2719948-2722259 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>RB1</td>
<td>chr13: 48892341-48895763 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>MEG3</td>
<td>chr14: 101290524-101293978 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>MEG8</td>
<td>chr14: 101370741-101371419 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>MAGEL2</td>
<td>chr15: 23892425-23894029 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>NDN</td>
<td>chr15: 23931451-23932759 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>SNRPN</td>
<td>chr15: 25200004-25201976 -1</td>
<td>CCTCTGCTGCGTCTGCCCGAACC</td>
<td>2</td>
<td>1.01</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>GTTGCGCAGACCGCAGCAGAGG</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>IGF1R</td>
<td>chr15: 99408496-99409650 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>ZNF597(3')</td>
<td>chr16: 3481801-3482388 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>ZNF597(TSS)</td>
<td>chr16: 3492828-3494463 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>ZNF331(1)</td>
<td>chr19: 54040510-54042212 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>ZNF331(2)</td>
<td>chr19: 54057086-54058425 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>PEG3</td>
<td>chr19: 57348493-57353271 -1</td>
<td>GGTGTGCGAGTAGGCGCCTGT</td>
<td>1</td>
<td>0.21</td>
<td></td>
</tr>
<tr>
<td>USP29</td>
<td>chr19: 57629548-57631498 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>L3MBTL</td>
<td>chr20: 42142365-42144040 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>NESPP55</td>
<td>chr20: 57414039-57418612 -1</td>
<td>TTGGTGCTGCTGTACGACGAGC</td>
<td>2</td>
<td>0.44</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>GCTCTGAGTCAGCCCAGCAGAAC</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NESPAS-GNASXL</td>
<td>chr20: 57425649-57428033 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>GNAS1A</td>
<td>chr20: 57463265-57465201 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>GNASXL</td>
<td>chr20: 57428905-57431463 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>WRB</td>
<td>chr21: 40757510-40758276 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>NHP2L1</td>
<td>chr22: 42077774-42078873 -</td>
<td>non</td>
<td>non</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

1The analyzed regions were shown using the UCSC hg19 reference genome.
2Forward strand and reverse strand were indicated in 1 and -1, respectively.
3MAFG consensus binding site was identified by the JASPAR database. The relative profile score threshold was set at 80%.
Table S5. *IGF2* imprinting status in paired tumors and normal mucosae.

<table>
<thead>
<tr>
<th>Tumor</th>
<th>MOI</th>
<th>LOI</th>
<th>p value</th>
<th>Statistical method</th>
</tr>
</thead>
<tbody>
<tr>
<td>Normal mucosa</td>
<td>4</td>
<td>3</td>
<td>0.225</td>
<td>Fisher's exact test</td>
</tr>
<tr>
<td></td>
<td>10</td>
<td>22</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

MOI, maintenance of imprinting; LOI, loss of imprinting
Table S6. Relationship between *IGF2*-DMR2 hypomethylation and *IGF2* LOI in tumors.

<table>
<thead>
<tr>
<th>IGF2-DMR2 hypomethylation</th>
<th>Number of MOI cases</th>
<th>Number of LOI cases</th>
<th>p value</th>
<th>Statistical method</th>
</tr>
</thead>
<tbody>
<tr>
<td>(+)</td>
<td>5</td>
<td>14</td>
<td>0.326</td>
<td>χ² test</td>
</tr>
<tr>
<td>(-)</td>
<td>9</td>
<td>13</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

MOI, maintenance of imprinting; LOI, loss of imprinting
Table S7. Relationship between clinicopathological factors and HyMiD status.

<table>
<thead>
<tr>
<th></th>
<th>HyMiD-positive</th>
<th>HyMiD-negative</th>
<th>p value</th>
<th>Statistical method</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of cases</td>
<td>55</td>
<td>51</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Age at diagnosis (Median ± SD)</td>
<td>70.0 ± 10.0</td>
<td>68.0 ± 9.8</td>
<td>0.850</td>
<td>Kruskal-Wallis test</td>
</tr>
<tr>
<td>Sex</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>27/55 (49.1%)</td>
<td>35/51 (68.6%)</td>
<td>0.032</td>
<td></td>
</tr>
<tr>
<td>Female</td>
<td>28/55 (50.9%)</td>
<td>16/51 (31.4%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Tumor location</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Right</td>
<td>18/55 (32.7%)</td>
<td>17/51 (33.3%)</td>
<td>0.567</td>
<td></td>
</tr>
<tr>
<td>Left</td>
<td>21/55 (38.2%)</td>
<td>15/51 (29.4%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Rectum</td>
<td>16/55 (29.1%)</td>
<td>19/51 (37.3%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Pathological type</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Differentiated</td>
<td>54/55 (98.2%)</td>
<td>50/51 (98.0%)</td>
<td>0.733</td>
<td>Fisher's exact test</td>
</tr>
<tr>
<td>Poorly</td>
<td>1/55 (1.8%)</td>
<td>1/51 (2.0%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lymph node metastasis</td>
<td>22/55 (40.0%)</td>
<td>24/51 (47.1%)</td>
<td>0.296</td>
<td></td>
</tr>
<tr>
<td>Lymphatic invasion</td>
<td>28/55 (50.9%)</td>
<td>27/51 (52.9%)</td>
<td>0.494</td>
<td></td>
</tr>
<tr>
<td>Vascular invasion</td>
<td>16/55 (29.1%)</td>
<td>16/51 (31.4%)</td>
<td>0.482</td>
<td></td>
</tr>
<tr>
<td>AJCC cancer stage</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>I</td>
<td>17/55 (30.9%)</td>
<td>6/51 (11.8%)</td>
<td>0.053</td>
<td></td>
</tr>
<tr>
<td>II</td>
<td>16/55 (29.1%)</td>
<td>21/51 (41.2%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>III</td>
<td>22/55 (40.0%)</td>
<td>24/51 (47.0%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Tumor size (Median ± SD) (mm)</td>
<td>45.0 ± 18.6</td>
<td>42.0 ± 16.0</td>
<td>0.556</td>
<td>Mann-Whitney U test</td>
</tr>
<tr>
<td>Survival rate</td>
<td>0.992</td>
<td>0.876</td>
<td>0.453</td>
<td>Log-rank test</td>
</tr>
</tbody>
</table>

AJCC, American Joint Committee on Cancer
Table S8. Relationship between clinicopathological factors and IG2-DMR0 hypomethylation.

<table>
<thead>
<tr>
<th></th>
<th>IG2-DMR0 hypomethylation (+)</th>
<th>IG2-DMR0 hypomethylation (-)</th>
<th>p value</th>
<th>Statistical method</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of cases</td>
<td>72</td>
<td>34</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Age at diagnosis (Median ± SD)</td>
<td>69.0 ± 10.2</td>
<td>69.5 ± 8.3</td>
<td>0.572</td>
<td>Kruskal-Wallis test</td>
</tr>
<tr>
<td>Sex</td>
<td></td>
<td></td>
<td>0.566</td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>42/72 (58.3%)</td>
<td>20/34 (58.8%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Female</td>
<td>30/72 (41.7%)</td>
<td>14/34 (41.2%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Tumor location</td>
<td></td>
<td></td>
<td>0.176</td>
<td></td>
</tr>
<tr>
<td>Right</td>
<td>20/72 (27.8%)</td>
<td>15/34 (44.1%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Left</td>
<td>28/72 (38.9%)</td>
<td>8/34 (23.5%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Rectum</td>
<td>24/72 (33.3%)</td>
<td>11/34 (32.4%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Pathological type</td>
<td></td>
<td></td>
<td>0.541</td>
<td>Fisher's exact test</td>
</tr>
<tr>
<td>Differentiated</td>
<td>71/72 (98.6%)</td>
<td>33/34 (97.1%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Poorly</td>
<td>1/72 (1.4%)</td>
<td>1/34 (2.9%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lymph node metastasis</td>
<td>35/72 (48.6%)</td>
<td>11/34 (32.4%)</td>
<td>0.085</td>
<td></td>
</tr>
<tr>
<td>Lymphatic invasion</td>
<td>35/72 (48.6%)</td>
<td>20/34 (58.8%)</td>
<td>0.220</td>
<td></td>
</tr>
<tr>
<td>Vascular invasion</td>
<td>20/72 (27.8%)</td>
<td>12/34 (35.3%)</td>
<td>0.285</td>
<td></td>
</tr>
<tr>
<td>AJCC cancer stage</td>
<td></td>
<td></td>
<td>0.080</td>
<td></td>
</tr>
<tr>
<td>I</td>
<td>17/72 (23.6%)</td>
<td>6/34 (17.6%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>II</td>
<td>20/72 (27.8%)</td>
<td>17/34 (50.0%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>III</td>
<td>35/72 (48.6%)</td>
<td>11/34 (32.4%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Tumor size (Median ± SD) (mm)</td>
<td>45.0 ± 18.9</td>
<td>42.5 ± 13.8</td>
<td>0.753</td>
<td>Mann-Whitney U test</td>
</tr>
<tr>
<td>Survival rate</td>
<td>0.72</td>
<td>0.66</td>
<td>0.640</td>
<td>Log-rank test</td>
</tr>
</tbody>
</table>

AJCC, American Joint Committee on Cancer
Table S9. Relationship between clinicopathological factors and IGF2 LOI.

<table>
<thead>
<tr>
<th></th>
<th>LOI</th>
<th>MOI</th>
<th>p value</th>
<th>Statistical method</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of cases</td>
<td>25</td>
<td>14</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Age at diagnosis (Median ± SD)</td>
<td>69</td>
<td>69</td>
<td>0.510</td>
<td>Kruskal-Wallis test</td>
</tr>
<tr>
<td>Sex</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>12 (48 %)</td>
<td>6 (42.9 %)</td>
<td>0.511</td>
<td></td>
</tr>
<tr>
<td>Female</td>
<td>13 (52 %)</td>
<td>8 (57.1 %)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Tumor location</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Right</td>
<td>8 (32 %)</td>
<td>5 (35.7 %)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Left</td>
<td>7 (28 %)</td>
<td>6 (42.9 %)</td>
<td>0.458</td>
<td></td>
</tr>
<tr>
<td>Rectum</td>
<td>10 (40 %)</td>
<td>3 (21.4 %)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Pathological type</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Differentiated</td>
<td>10 (40 %)</td>
<td>6 (42.9 %)</td>
<td>0.563</td>
<td>Fisher's exact test</td>
</tr>
<tr>
<td>Poorly</td>
<td>15 (60 %)</td>
<td>8 (42.9 %)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lymph node metastasis</td>
<td>10 (40 %)</td>
<td>5 (35.7 %)</td>
<td>0.534</td>
<td></td>
</tr>
<tr>
<td>Lymphatic invasion</td>
<td>12 (48 %)</td>
<td>8 (57.1 %)</td>
<td>0.416</td>
<td></td>
</tr>
<tr>
<td>Vascular invasion</td>
<td>8 (32 %)</td>
<td>5 (35.7 %)</td>
<td>0.542</td>
<td></td>
</tr>
<tr>
<td>AJCC cancer stage</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>I</td>
<td>6 (24 %)</td>
<td>3 (21.4 %)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>II</td>
<td>9 (36 %)</td>
<td>6 (42.9 %)</td>
<td>0.915</td>
<td></td>
</tr>
<tr>
<td>III</td>
<td>10 (40 %)</td>
<td>5 (35.7 %)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Tumor size (Median ± SD) (mm)</td>
<td>40 ± 16.9</td>
<td>46 ± 12.1</td>
<td>0.217</td>
<td>Mann-Whitney U test</td>
</tr>
<tr>
<td>Survival rate</td>
<td>0.74</td>
<td>0.92</td>
<td>0.218</td>
<td>Log-rank test</td>
</tr>
</tbody>
</table>

LOI: loss of imprinting, MOI: maintenance of imprinting, AJCC: American Joint Committee on Cancer
<table>
<thead>
<tr>
<th>Analysis</th>
<th>Name of DMR or gene</th>
<th>Primer name</th>
<th>Primer sequence</th>
<th>Location (GRCh37/hg19)</th>
<th>Total number of CpG sites</th>
<th>Number of analyzed CpG sites</th>
</tr>
</thead>
<tbody>
<tr>
<td>PPIEL</td>
<td>PPIEL F</td>
<td>Bio-GTTGAGTTAGGAAGGTTAGTTGAG</td>
<td>Chr 1: 40,024,620-40,025,540</td>
<td>5</td>
<td>5</td>
<td></td>
</tr>
<tr>
<td></td>
<td>PPIEL R</td>
<td>ACCCCCTTTCTTTATTAATCTTCTGCTTAAATTTAAATACACAC</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>PPIEL S</td>
<td>Bio-GTTAAGTTAGGTTAGTTGAG</td>
<td>Chr 1: 40,024,620-40,025,540</td>
<td>5</td>
<td>5</td>
<td></td>
</tr>
<tr>
<td>ARHI-CG1</td>
<td>ARHI-CG1 F</td>
<td>Bio-GTTATGGGCTTATTTGTTATTTTTTTTGGTACCT</td>
<td>Chr 1: 68,510,575-68,510,716</td>
<td>4</td>
<td>4</td>
<td></td>
</tr>
<tr>
<td></td>
<td>ARHI-CG1 R</td>
<td>AATCGCCCTACACGTCTTCTTCACGCTTACCT</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>ARHI-CG1 S</td>
<td>Bio-GTTATAGGGTTATTTTGTGATTTGTTTATTTTTGAG</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ARHI-CG2</td>
<td>ARHI-CG2 F</td>
<td>Bio-GTTATAGGGTTATTTTGTGATTTGTTTATTTTTGAG</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>ARHI-CG2 R</td>
<td>Bio-IGF2RAGTTATTTGTTATTTTGTGATTTGTTTATTTTTGAG</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>ARHI-CG2 S</td>
<td>Bio-IGF2RAGTTATTTTGTGATTTGTTTATTTTTGAG</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ARHI-CG3</td>
<td>ARHI-CG3 F</td>
<td>Bio-IGF2RAGTTATTTTGTGATTTGTTTATTTTTGAG</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>ARHI-CG3 R</td>
<td>Bio-ARHI-CG3 F</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>ARHI-CG3 S</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ZDBF2</td>
<td>ZDBF2 F</td>
<td>GATTTCTTTTTTTTGTGAGTTATTGTTGTTTATTTTTGAG</td>
<td>Chr 2: 207,125,719-207,125,922</td>
<td>3</td>
<td>3</td>
<td></td>
</tr>
<tr>
<td></td>
<td>ZDBF2 R</td>
<td>Bio-ARHI-CG3 F</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>ZDBF2 S</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NAPIL5</td>
<td>NAPIL5 F</td>
<td>Bio-ARHI-CG3 F</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>NAPIL5 R</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>NAPIL5 S</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>FAM50B</td>
<td>FAM50B F</td>
<td>Bio-ARHI-CG3 F</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>FAM50B R</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>FAM50B S</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ZAC</td>
<td>ZAC F</td>
<td>Bio-ARHI-CG3 F</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>ZAC R</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>ZAC S</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GRB10-DMR</td>
<td>GRB10-DMR F</td>
<td>Bio-ARHI-CG3 F</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>GRB10-DMR R</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>GRB10-DMR S</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>PEG10</td>
<td>PEG10 F</td>
<td>Bio-ARHI-CG3 F</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>PEG10 R</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>PEG10 S</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>LOC72B024</td>
<td>LOC72B024 F</td>
<td>Bio-ARHI-CG3 F</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>LOC72B024 R</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>LOC72B024 S</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TRAPPC9</td>
<td>TRAPPC9 F</td>
<td>Bio-ARHI-CG3 F</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>TRAPPC9 R</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>TRAPPC9 S</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>H19-promoter</td>
<td>H19-Promoter F</td>
<td>Bio-ARHI-CG3 F</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>H19-Promoter R</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>H19-Promoter S</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>IGFB-DMR2</td>
<td>IGFB-DMR2 F</td>
<td>Bio-ARHI-CG3 F</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>IGFB-DMR2 R</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>IGFB-DMR2 S</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>IGFB-DMR3</td>
<td>IGFB-DMR3 F</td>
<td>Bio-ARHI-CG3 F</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>IGFB-DMR3 R</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>IGFB-DMR3 S</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>KvDMR1</td>
<td>KvDMR1 F</td>
<td>Bio-ARHI-CG3 F</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>KvDMR1 R</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>KvDMR1 S</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RB1</td>
<td>RB1 F</td>
<td>Bio-ARHI-CG3 F</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>RB1 R</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>RB1 S</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MEG3</td>
<td>MEG3-CG7_F</td>
<td>Bio-ARHI-CG3 F</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>MEG3-CG7_R</td>
<td>Bio-ARHI-CG3 R</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>MEG3-CG7_S</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MEG8</td>
<td>MEG8 F</td>
<td>Bio-ARHI-CG3 F</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>MEG8 R</td>
<td>Bio-ARHI-CG3 R</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>MEG8 S</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MAGEL2</td>
<td>MAGEL2 F</td>
<td>Bio-ARHI-CG3 F</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>MAGEL2 R</td>
<td>Bio-ARHI-CG3 R</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>MAGEL2 S</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NDN</td>
<td>NDN F</td>
<td>Bio-ARHI-CG3 F</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>NDN R</td>
<td>Bio-ARHI-CG3 R</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>NDN S</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SNRPN</td>
<td>SNRPN F</td>
<td>Bio-ARHI-CG3 F</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>SNRPN R</td>
<td>Bio-ARHI-CG3 R</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>SNRPN S</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>IGF1R</td>
<td>IGF1R F</td>
<td>Bio-ARHI-CG3 F</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>IGF1R R</td>
<td>Bio-ARHI-CG3 R</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>IGF1R S</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ZNF597(2)</td>
<td>ZNF597(2) F</td>
<td>Bio-ARHI-CG3 F</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>ZNF597(2) R</td>
<td>Bio-ARHI-CG3 R</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>ZNF597(2) S</td>
<td>Bio-ARHI-CG3 S</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Protein/Region</td>
<td>Forward Primer (F)</td>
<td>Reverse Primer (R)</td>
<td>Sequence Primer (S)</td>
<td>Chr</td>
<td>Start</td>
<td>End</td>
</tr>
<tr>
<td>---------------</td>
<td>-------------------</td>
<td>-------------------</td>
<td>-------------------</td>
<td>-----</td>
<td>-------</td>
<td>-----</td>
</tr>
<tr>
<td>ZNF597(3)</td>
<td>ZNF597(2) F</td>
<td>ZNF597(2) R</td>
<td>Bio-ATCTCCAACTTAACCCAACTA</td>
<td>16</td>
<td>3,481,801</td>
<td>3,482,388</td>
</tr>
<tr>
<td></td>
<td>ZNF597(2) S</td>
<td></td>
<td>ATATGTTTTTGTAGTAGAATG</td>
<td>5</td>
<td>5</td>
<td></td>
</tr>
<tr>
<td>ZNF597(TSS)</td>
<td>ZNF597 F</td>
<td>ZNF597 R</td>
<td>Bio-ATCTCCAACTTAACCCAACTA</td>
<td>16</td>
<td>3,482,828</td>
<td>3,494,463</td>
</tr>
<tr>
<td></td>
<td>ZNF597 S</td>
<td></td>
<td>ATATGTTTTTGTAGTAGAATG</td>
<td>5</td>
<td>5</td>
<td></td>
</tr>
<tr>
<td>ZNF331(pro)</td>
<td>ZNF331 F</td>
<td>ZNF331 R</td>
<td>Bio-AGGGATTAGGAAGGGTTAGT</td>
<td>19</td>
<td>54,040</td>
<td>54,042,212</td>
</tr>
<tr>
<td></td>
<td>ZNF331 S</td>
<td></td>
<td>CCCAACCCCATTTAGATTCAAC</td>
<td>5</td>
<td>5</td>
<td></td>
</tr>
<tr>
<td>ZNF331(int)</td>
<td>ZNF331(2) F</td>
<td>ZNF331(2) R</td>
<td>Bio-AGGGATTAGGAAGGGTTAGT</td>
<td>19</td>
<td>54,057,066</td>
<td>54,058,425</td>
</tr>
<tr>
<td></td>
<td>ZNF331(2) S</td>
<td></td>
<td>CCCAACCCCATTTAGATTCAAC</td>
<td>5</td>
<td>5</td>
<td></td>
</tr>
<tr>
<td>PEG3</td>
<td>PEG3 F</td>
<td>PEG3 R</td>
<td>Bio-GGTTTTTGTAGTAGAATG</td>
<td>19</td>
<td>57,348,493</td>
<td>57,353,271</td>
</tr>
<tr>
<td></td>
<td>PEG3 S</td>
<td></td>
<td>ATATGTTTTTGTAGTAGAATG</td>
<td>5</td>
<td>5</td>
<td></td>
</tr>
<tr>
<td>USP29</td>
<td>USP29 F</td>
<td>USP29 R</td>
<td>Bio-GGTTTTTGTAGTAGAATG</td>
<td>19</td>
<td>57,629,548</td>
<td>57,631,498</td>
</tr>
<tr>
<td></td>
<td>USP29 S</td>
<td></td>
<td>ATATGTTTTTGTAGTAGAATG</td>
<td>5</td>
<td>5</td>
<td></td>
</tr>
<tr>
<td>L3MBTL</td>
<td>L3MBTL-CG3 F</td>
<td>L3MBTL-CG3 R</td>
<td>Bio-GGTTTTTGTAGTAGAATG</td>
<td>19</td>
<td>57,629,548</td>
<td>57,631,498</td>
</tr>
<tr>
<td></td>
<td>L3MBTL-CG3 S</td>
<td></td>
<td>ATATGTTTTTGTAGTAGAATG</td>
<td>5</td>
<td>5</td>
<td></td>
</tr>
<tr>
<td>NESP55</td>
<td>NESP55 F</td>
<td>NESP55 R</td>
<td>Bio-GGTTTTTGTAGTAGAATG</td>
<td>20</td>
<td>57,414,039</td>
<td>57,418,612</td>
</tr>
<tr>
<td></td>
<td>NESP55 S</td>
<td></td>
<td>ATATGTTTTTGTAGTAGAATG</td>
<td>5</td>
<td>5</td>
<td></td>
</tr>
<tr>
<td>GNAS1A</td>
<td>GNAS1A F</td>
<td>GNAS1A R</td>
<td>Bio-GGTTTTTGTAGTAGAATG</td>
<td>20</td>
<td>57,463,265</td>
<td>57,465,201</td>
</tr>
<tr>
<td></td>
<td>GNAS1A S</td>
<td></td>
<td>ATATGTTTTTGTAGTAGAATG</td>
<td>5</td>
<td>5</td>
<td></td>
</tr>
<tr>
<td>GNASXl</td>
<td>GNASXl F</td>
<td>GNASXl R</td>
<td>Bio-GGTTTTTGTAGTAGAATG</td>
<td>20</td>
<td>57,425,649</td>
<td>57,431,463</td>
</tr>
<tr>
<td></td>
<td>GNASXl S</td>
<td></td>
<td>ATATGTTTTTGTAGTAGAATG</td>
<td>5</td>
<td>5</td>
<td></td>
</tr>
<tr>
<td>WRB</td>
<td>WRB F</td>
<td>WRB R</td>
<td>Bio-GGTTTTTGTAGTAGAATG</td>
<td>20</td>
<td>57,428,905</td>
<td>57,431,463</td>
</tr>
<tr>
<td></td>
<td>WRB S</td>
<td></td>
<td>ATATGTTTTTGTAGTAGAATG</td>
<td>5</td>
<td>5</td>
<td></td>
</tr>
<tr>
<td>NHP2L1</td>
<td>NHP2L1 F</td>
<td>NHP2L1 R</td>
<td>Bio-GGTTTTTGTAGTAGAATG</td>
<td>20</td>
<td>57,414,039</td>
<td>57,418,612</td>
</tr>
<tr>
<td></td>
<td>NHP2L1 S</td>
<td></td>
<td>ATATGTTTTTGTAGTAGAATG</td>
<td>5</td>
<td>5</td>
<td></td>
</tr>
<tr>
<td>hMLH1</td>
<td>hMLH1 F</td>
<td>hMLH1 R</td>
<td>Bio-GGTTTTTGTAGTAGAATG</td>
<td>19</td>
<td>57,654,934</td>
<td>57,659,201</td>
</tr>
<tr>
<td></td>
<td>hMLH1 S</td>
<td></td>
<td>ATATGTTTTTGTAGTAGAATG</td>
<td>5</td>
<td>5</td>
<td></td>
</tr>
<tr>
<td>MINT1</td>
<td>MINT1 F</td>
<td>MINT1 R</td>
<td>Bio-GGTTTTTGTAGTAGAATG</td>
<td>19</td>
<td>57,348,493</td>
<td>57,353,271</td>
</tr>
<tr>
<td></td>
<td>MINT1 S</td>
<td></td>
<td>ATATGTTTTTGTAGTAGAATG</td>
<td>5</td>
<td>5</td>
<td></td>
</tr>
<tr>
<td>MINT2</td>
<td>MINT2 F</td>
<td>MINT2 R</td>
<td>Bio-GGTTTTTGTAGTAGAATG</td>
<td>19</td>
<td>57,348,493</td>
<td>57,353,271</td>
</tr>
<tr>
<td></td>
<td>MINT2 S</td>
<td></td>
<td>ATATGTTTTTGTAGTAGAATG</td>
<td>5</td>
<td>5</td>
<td></td>
</tr>
<tr>
<td>MINT31</td>
<td>MINT31 F</td>
<td>MINT31 R</td>
<td>Bio-GGTTTTTGTAGTAGAATG</td>
<td>19</td>
<td>57,348,493</td>
<td>57,353,271</td>
</tr>
<tr>
<td></td>
<td>MINT31 S</td>
<td></td>
<td>ATATGTTTTTGTAGTAGAATG</td>
<td>5</td>
<td>5</td>
<td></td>
</tr>
<tr>
<td></td>
<td>p16 S</td>
<td></td>
<td>ATATGTTTTTGTAGTAGAATG</td>
<td>5</td>
<td>5</td>
<td></td>
</tr>
</tbody>
</table>

**Bisulfite-pyrosequencing for CIMP markers**

<table>
<thead>
<tr>
<th>Region</th>
<th>Forward Primer (F)</th>
<th>Reverse Primer (R)</th>
<th>Sequence Primer (S)</th>
<th>Chr</th>
<th>Start</th>
<th>End</th>
</tr>
</thead>
<tbody>
<tr>
<td>LINE-1</td>
<td>LINE-1 F</td>
<td>LINE-1 R</td>
<td>LINE-1 S</td>
<td>4</td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td>KRAS exon2</td>
<td>KRAS F1</td>
<td>KRAS R1</td>
<td>Bio-GGTTTTTGTAGTAGAATG</td>
<td>4</td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td>KRAS exon3</td>
<td>KRAS F2</td>
<td>KRAS R2</td>
<td>Bio-GGTTTTTGTAGTAGAATG</td>
<td>4</td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td>Pyrosequencing for BRAF (VEGVE) mutation analysis</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>BRAF</td>
<td>BRAF F</td>
<td>BRAF R</td>
<td>Bio-GGTTTTTGTAGTAGAATG</td>
<td>4</td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td>Genotyping of iDG2 (rs1610)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>iDG2 P2-2</td>
<td>iDG2 P5-2</td>
<td>Bio-GGTTTTTGTAGTAGAATG</td>
<td>4</td>
<td>4</td>
<td>4</td>
<td></td>
</tr>
<tr>
<td>H19</td>
<td>H19 F1</td>
<td>H19 R1</td>
<td>Bio-GGTTTTTGTAGTAGAATG</td>
<td>4</td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td>Genotyping of H19 (rs2839702)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>H19 F5</td>
<td>H19 R5</td>
<td>Bio-GGTTTTTGTAGTAGAATG</td>
<td>4</td>
<td>4</td>
<td>4</td>
<td></td>
</tr>
<tr>
<td>Pyrosequencing for allelic-specific expression analysis</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>iDG2 allele F</td>
<td>iDG2 allele R</td>
<td>Bio-GGTTTTTGTAGTAGAATG</td>
<td>4</td>
<td>4</td>
<td>4</td>
<td></td>
</tr>
<tr>
<td>H19 allele F</td>
<td>H19 allele R</td>
<td>Bio-GGTTTTTGTAGTAGAATG</td>
<td>4</td>
<td>4</td>
<td>4</td>
<td></td>
</tr>
</tbody>
</table>

F: forward primer, R: reverse primer, S: sequence primer, Bio: biotinylated primer
**Figure S1. Non-relationship between CIMP status and LINE-1 methylation.**

LINE-1 methylation in CIMP-positive tumors (median: 59.0%, ranging from 22.1 to 72.1%) was not significantly different from that in CIMP-negative tumors (median: 57.3%, ranging from 37.5 to 69.1%) \((p = 0.235,\) Mann-Whitney U test).