Supplementary figure 1.

Mass-array (Sequenom) data indicates 50% methylation as expected for all five imprinted genes analyzed in normal colon tissue, and tumor - paired-normal DNA specimens that did not demonstrate uniparentalism. a. Noey2 (ARHI) chromosome 1, b. SNRPN chromosome 15, c.GNAL (Golf promoter) chromosome 18, d.GNAL (XLGolf promoter) chromosome 18,not imprinted, e. L3MBTI chromosome 20

Supplementary figure 2.

List of Primers and PCR conditions used for methylation determinations.

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a. Normal colon DNA
ACP 11 A. DR
                                                 AGP17_A_B13 8 6 6+ H08 088 00 65 8 40 65 + 8
                                                 Tumor and Normal colon DNA (no uniparentalism detected)
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b. Switch Chromosome 15, the distribution of the second se
Tumor and Normal color DNA (no uniparentalize detected)
                                                 6380_A_C1 0 0 0 0 0 0 0 0 0 0 0 0 0
                                             c. Chromosome 18, un ter in the second secon
                                                 ACP12_8_85
                                                 Tumor and Normal color DNA (no uniparentalism detected)
                                                                                                                                                                                                                                 4399 a 83
                                                0% COODDOODDO 100% Not analyzed. T-C-C
       d. Chromosome 18 to the second second
                                                 Tumor and Normal colon DNA (no uniparentalism detected)
                                                 0388_a_I11
                                                                                            Tumor and Normal colon DNA (no uniparentalism detected)

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Supplementary Figure 1