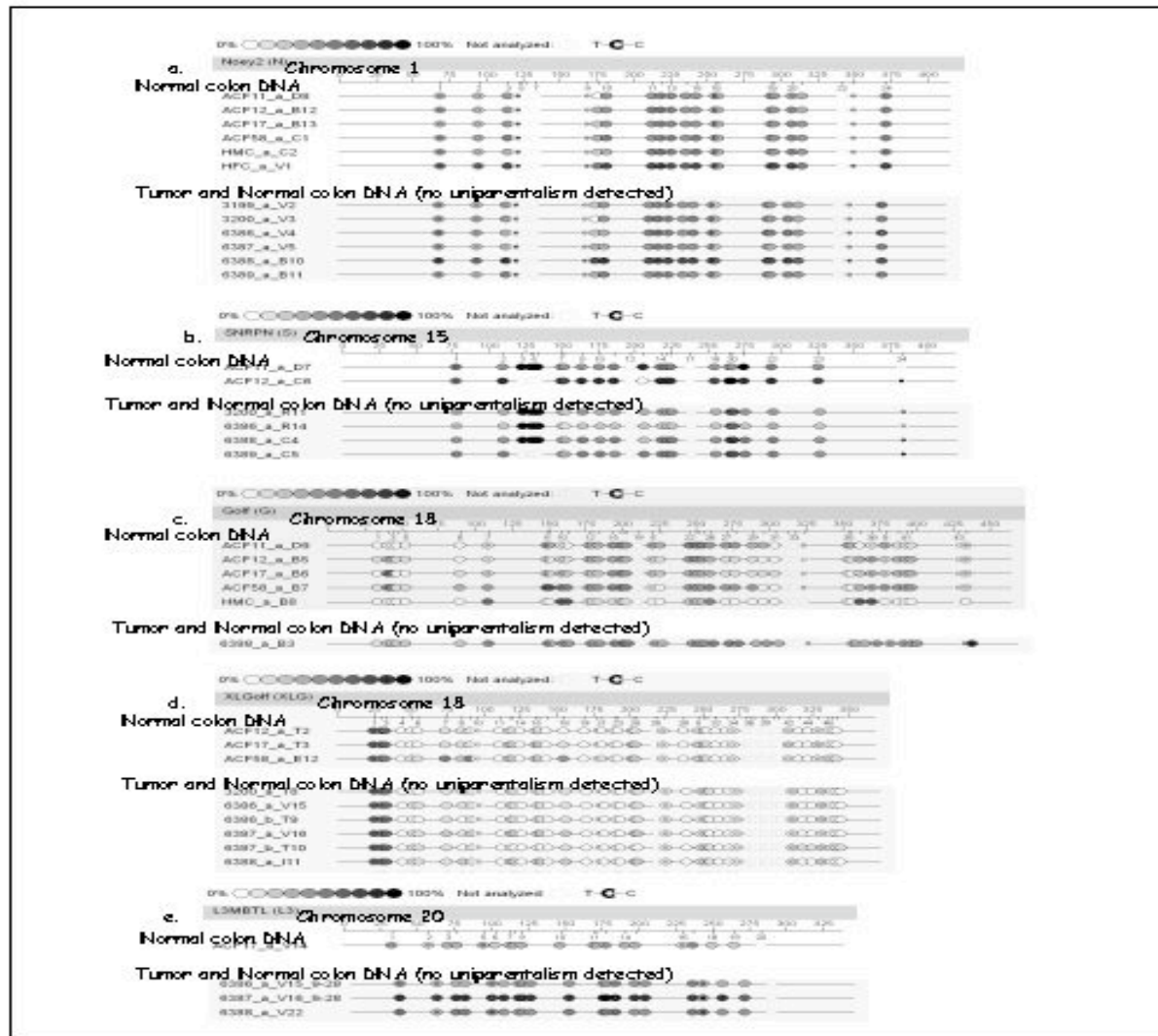


Supplementary figure 1.

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.



Supplementary Figure 1