**Supplemental Figure 1.** Methylation gene probe selection and correlation to expression level. A, Categories of probe location relative to the CpG island. The three categories considered for probe location are i) the “North shore”, that is within 2000 bp 5’ of the CpG island (with respect to the gene), ii) within the CpG island, and iii) the “South shore”, that is within 2000 bp 3’ of the CpG island (with respect to the gene). B, Categories of probe location relative to the gene. The four categories considered for probe location are i) between 1500 and 200 bps 5’ of the transcriptional start site, ii) within 200 bps 5’ of the transcriptional start site, iii) within the 5’ transcribed but untranslated region (UTR), and iv) within exon 1. C, Probe categorization. Based on the above probe locations with respect to the CpG island and gene, categories of probes are identified as 1 or 2. D, Box and whisker plots depicting the distribution of gene expression versus methylation correlations. There are 13,854 genes with probes in category 1, and 3,632 in category 2.

**Supplemental Figure 2.** Relationship between methylation and lack of SLFN11 and MGMT expression in the NCI-60. A, For SLFN11, twenty-three cell lines (38%) do not express SLFN11 above base line (vertical dotted line), and 16 of these 23 (70%) exhibit promoter methylation levels above 30%. B, For MGMT, twenty-one cell lines (35%) do not express MGMT above baseline (vertical dotted line), and 9 of these (42.8%) exhibit promoter methylation levels above 40%. For both portions of the figure, cell lines are color-coded according to tissue-of-origin with the Cellminer color code, in which BR is breast, CNS is central nervous system, CO is colon, LE is leukemia, ME is melanoma, LC is lung cancer, OV is ovarian, PR is prostate, and RE is renal ([1](#_ENREF_1)). The red line is the linear regression line. The x-axis is the log2 Affymetrix probe average value, and the y-axis the DNA methylation level /100.