Supplementary Figure 1. Bisulfite sequencing validation of 3' region to *OPLAH*. The 3' region to *OPLAH* is an example of a hypermethylated site shared by all tumors. The UCSC genome browser screen capture shows the DNA methylation signal in each sample. The black rectangle marks the region validated by bisulfite sequencing, and the sequencing data for each sample is shown as individual alleles. Each circle represents a CpG dinucleotide. Black circles represent methylated cytosines while white circles represent unmethylated cytosines.

Supplementary Figure 2. Bisulfite sequencing validation of *NKX2-1* promoter. *NKX2-1* promoter is an example of a CIMP-unique hypermethylation site. The UCSC genome browser screen capture shows the DNA methylation signal in each sample. The black rectangle marks the region validated by bisulfite sequencing, and the sequencing data for each sample is shown as individual alleles. Each circle represents a CpG dinucleotide. Black circles represent methylated cytosines while white circles represent unmethylated cytosines.

Supplementary Figure 3. DNA methylation analysis of CIMP-paired normal specimens. Adjacent normal tissues paired with the CIMP specimens used in MiGS were analyzed for their DNA methylation status at select CIMP-specific hypermethylated sites. N4 is paired with T4, N5 is paired with T5, and N6 is paired with T6. UCSC genome browser screen captures for B3GAT2 **(A)**, *NKX2-1* **(C)**, and *TMEM200B* **(E)** promoters showing the DNA methylation patterns in the nine specimens subjected to MiGS. The black rectangles mark the regions tested by MSP in the CIMP-adjacent normal specimens. MSP assay was performed for *B3GAT2* **(B)**, *NKX2-1* **(D)**, and *TMEM200B* **(F)** promoters in the CIMP-adjacent normal specimens, T4, and water control. M denotes methylated PCR reaction, and U denotes unmethylated PCR reaction.

Supplementary Figure 4. Genomic distribution of DNA methylation. Genome-wide DNA methylation signal for each sample was annotated by their genomic contexts and summarized for each clinical category in the pie charts according to the color key.