Supplementary Figure 1

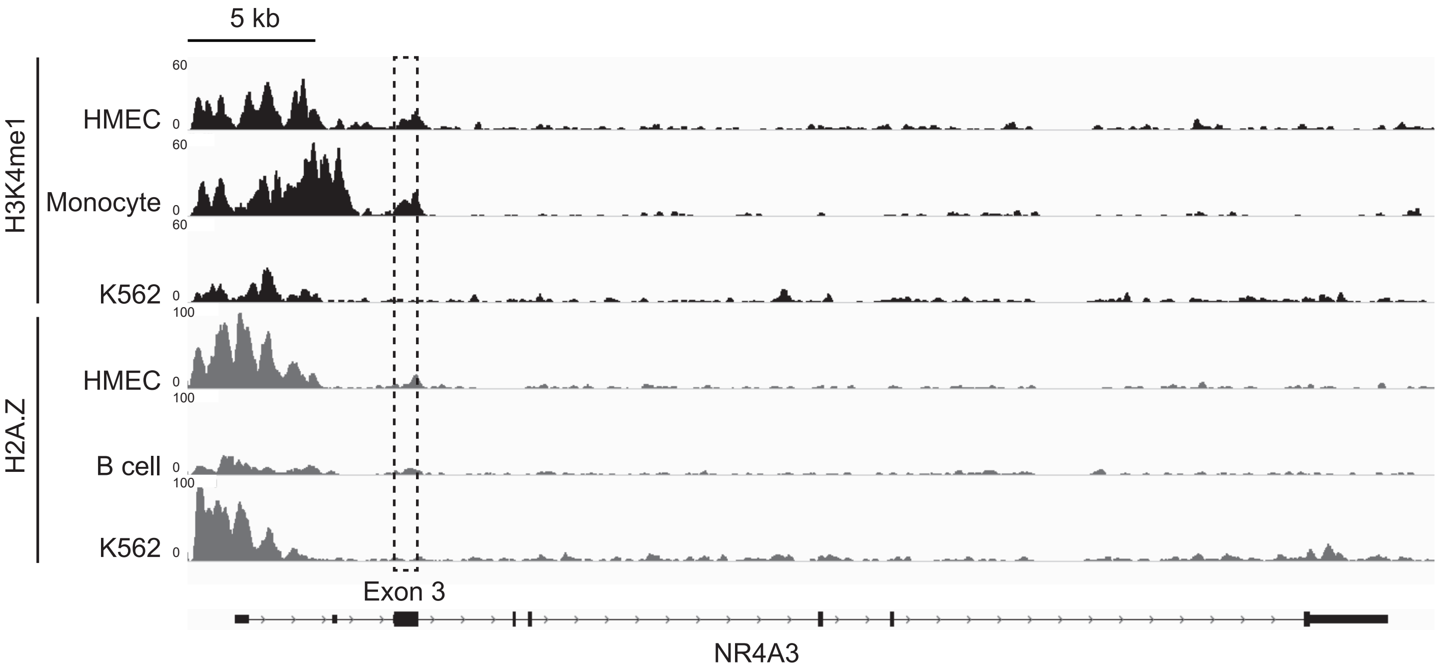

Figure S1: The levels of H3K4me1 and H2A.Z at the region of *NR4A3*

Visualization of the chromatin immunoprecipitation sequencing (ChIP-seq) data of the H3K4me1 and H2A.Z levels of NR4A3 in human mammary epithelial cells (HMEC), monocytes (CD14^{+}blood cells), B cells (CD20^{+}cells), and K562 cells from the Encyclopedia of DNA Elements (ENCODE; https://genome.ucsc.edu/ENCODE/, ChIP-seq data) by using an Integrative Genomics Viewer (IGV). A schematic diagram of NR4A3 locus indicates its genomic structure. Exons and any untranslated regions are denoted by large and small black boxes, respectively. The region of exon 3 is also shown by the dashed box.

Supplementary Figure 2

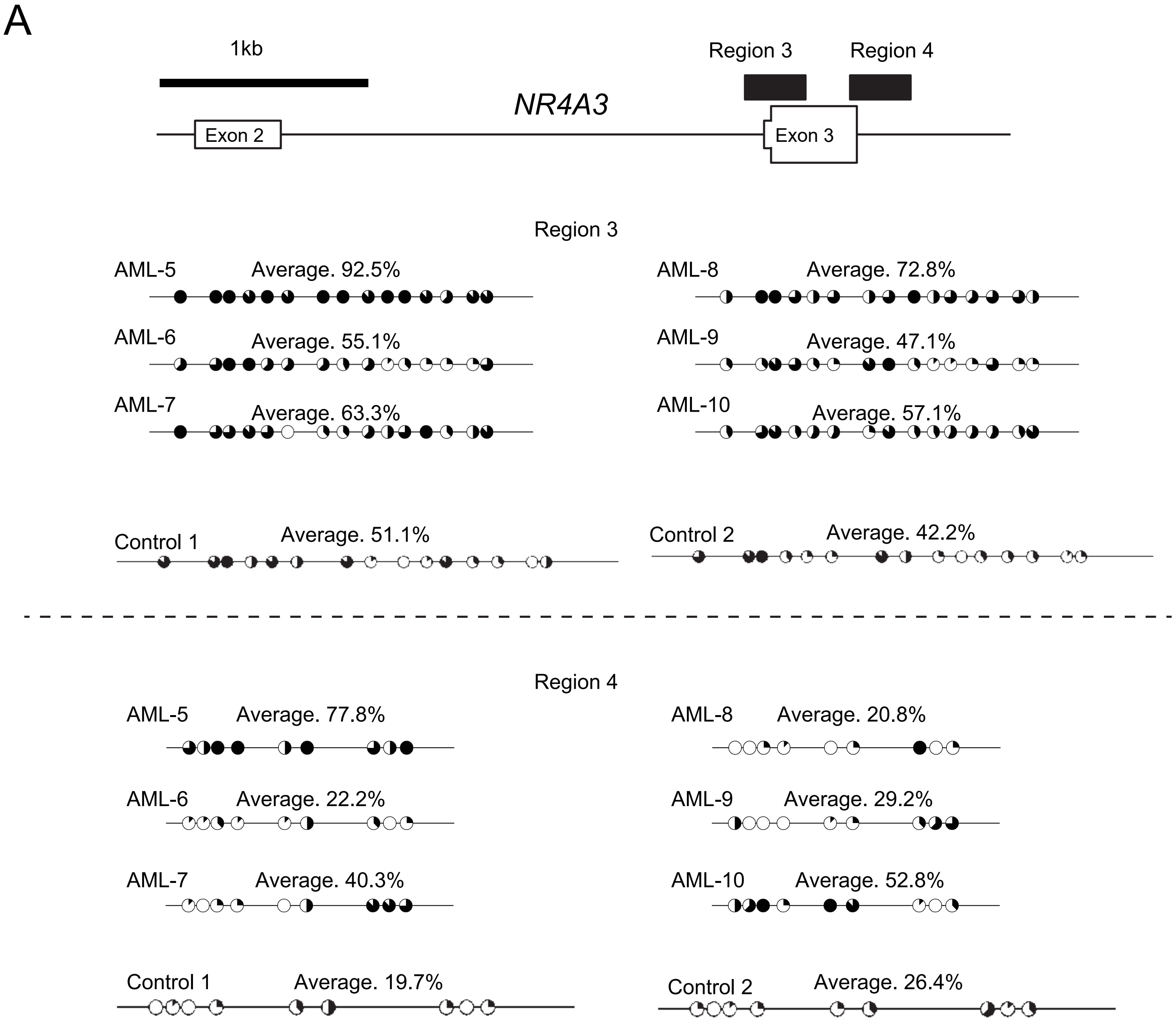

Figure S2: DNA hypermethylation at the region encompassing exon 3 of NR4A3 in human primary AML samples

Targeted regions of bisulfite sequencing PCR are shown as black boxes. The methylation status of CpG sites at the region encompassing exon 3 of NR4A3 was analyzed in 6 human primary AML samples and control samples (n = 2) using bisulfite sequencing. The percentages of methylation at each CpG site are indicated by black coloring within a pie chart. The percentages of methylation of the total CpG sites in the region of PCR products are also indicated as an average.