Figure 4

A. Box plots showing z-scores for methylated reads (after log-transformed) for NPC, MGUS, and MM samples. The y-axis represents the z-score for methylated reads, and the x-axis represents different groups of samples. The legend indicates whole genome and CBPs.

B. Scatter plots showing the relationship between LINE-1 density per 100,000 bp and the z-score for methylated reads. The correlation coefficients (R) are provided for each group: NPC (R=0.344***), MGUS (R=0.167***), and MM (R=-0.137***).

C. Box plots showing z-scores for methylated reads (after log-transformed) for sample-specific breakpoints. The sample IDs are MM3, MM7, and MM4, with their respective methylation percentages: 30.4%, 25.7%, and 51.0%.

D. Diagram illustrating LINE-1 density at the sample-specific breakpoints. The y-axis represents LINE-1 density, and the x-axis represents percentage. The colors indicate different conditions: whole genome, LINE-1 hypomethylated sample, and LINE-1 non-hypomethylated sample.

E. Scatter plots showing the correlation between local LINE-1 methylation level and global LINE-1 methylation level for different regions: 12p13.2 (CBP) and 12q21.2 (non-breakpoint). The correlation coefficients (R) are 0.613*** and 0.921***, respectively.

F. Scatter plot showing the correlation between local LINE-1 methylation level (L1PA16 ORF2) and global LINE-1 methylation level for 12p12.3 (CBP). The correlation coefficient (R) is 0.131 (P=0.269).