Supplementary Figure 1. Individual bisulfite sequencing of selected genes. Fifteen clones are shown. Methylated and non-methylated CpG sites are represented as black and white squares, respectively. One pair of SLE discordant MZ twins, one pair of SLE concordant MZ and one pair of healthy MZ twins are shown. The probe included in the methylation bead array is represented by a red line. The fragment analyzed in pyrosequencing experiments is indicated by a green line.

Supplementary Figure 2. (A) RT-PCR quantitative analysis of the seven genes that have been validated for changes in their methylation status (black bars). Values are normalized with respect to β-actin and correspond to the average fold change between five SLE twins and their corresponding healthy siblings. The average fold change for the DNA methylation data resulting from pyrosequencing is also represented (grey bars). Fold change is represented in logarithmic scale (B) RT-PCR quantitative analysis of DNMT1 and DNMT3b as well as the 47S precursor of the ribosomal RNA gene and the 18S rRNA. Values are normalized with respect to β-actin and correspond to the average fold change between 5 SLE twins and their corresponding healthy siblings.

Supplementary Figure 3. Individual bisulfite sequencing of selected repetitive sequences. Methylated and non-methylated CpG sites are represented as black and white squares, respectively. One pair of SLE discordant MZ twins and one pair of SLE concordant MZ twins are shown.

Supplementary Figure 4. Bar graph showing the percentage of DNA methylation for 17 pairs of SLE-discordant samples and 7 pairs of SLE-concordant samples. SLE and healthy siblings from SLE-discordant pairs appear in two different blocks whereas siblings from concordant twin pairs appear represented in a single block. Methylation levels were normalized by dividing the percentage of methylation for each particular gene by the average percentage of methylation in the entire population SLE. P-values resulting from unpaired two tailed t-test are represented on top.