



Supplementary Figure S5. Genetic regulation of DNA methylation in SLE and in control individuals.

Methylation levels were tested for genotype association separately in patients and controls assuming an additive model. For each CpG site on the HM450k array all single nucleotide polymorphisms on the ImmunoChip within a ± 100 kb flanking region were tested and a Bonferroni corrected $\alpha < 0.05$ was considered significant. A total of 179,025 significant SNP-CpG associations were observed in either SLE patients or controls, of these were 110,854 SNP-CpG associations found in both SLE patients and controls.