

Supplementary Table S12. Variation methylation quantitative trait loci (var-meQTLs) of differentially methylated CpG sites (DMCs) in SLE. The top significant var-meQTL SNP per CpG site for both SLE patients and controls is listed.

| Chr | CpG position | CpG | CpG gene | Discovery SLE DMC p Value | Replication SLE DMC p Value | SLE SNP | SLE SNP position | SLE var-meQTL p Value* | Control SNP | Control SNP position | Control var-meQTL p Value* |
|-----|--------------|------------|-----------------------------|---------------------------|-----------------------------|-----------------|------------------|------------------------|-----------------|----------------------|----------------------------|
| 1 | 20914028 | cg24502330 | <i>CDA</i> | 7.3E-41 | 1.3E-08 | rs1043424 | 20849587 | 1.1E-09 | rs1043424 | 20849587 | 1.2E-14 |
| 1 | 192544902 | cg02586212 | <i>RGS1</i> | 2.3E-15 | 8.6E-07 | imm_1_190797238 | 190797238 | 4.2E-23 | imm_1_190793488 | 190793488 | 8.6E-32 |
| 3 | 16924709 | cg23220897 | <i>Intergenic</i> | 1.3E-17 | 1.0E-07 | NA | NA | NS | rs7653027 | 16994861 | 5.7E-12 |
| 5 | 173312866 | cg21566177 | <i>Intergenic</i> | 2.6E-36 | 7.9E-08 | 1kg_5_173239934 | 173239934 | 3.0E-13 | NA | NA | NS |
| 6 | 27841865 | cg10536916 | <i>HIST1H4L</i> | 4.9E-47 | 2.1E-12 | NA | NA | NS | rs6910968 | 28012160 | 1.1E-20 |
| 6 | 27842098 | cg01247537 | <i>HIST1H4L</i> | 4.7E-44 | 3.9E-15 | NA | NA | NS | rs6910968 | 28012160 | 2.5E-24 |
| 6 | 29895187 | cg15411272 | <i>Intergenic</i> | 7.0E-08 | 5.3E-06 | rs2256543 | 30045812 | 1.5E-14 | rs2256543 | 30045812 | 2.0E-38 |
| 6 | 29911550 | cg17608381 | <i>HLA-A</i> | 4.8E-25 | 4.1E-15 | NA | NA | NS | rs2517689 | 30037232 | 2.0E-18 |
| 6 | 30796209 | cg27154651 | <i>Intergenic</i> | 5.4E-23 | 2.6E-08 | NA | NA | NS | rs1264362 | 30884569 | 6.7E-10 |
| 6 | 31583915 | cg19563932 | <i>AIF1</i> | 4.0E-26 | 1.5E-07 | rs2242655 | 31735428 | 4.9E-15 | rs805287 | 31786709 | 2.3E-15 |
| 6 | 32729130 | cg07180897 | <i>HLA-DQB2</i> | 2.7E-10 | 6.2E-06 | rs9276449 | 32823631 | 3.9E-39 | rs9275224 | 32767856 | 2.5E-52 |
| 6 | 32822911 | cg07156249 | <i>PSMB9, TAP1</i> | 1.5E-14 | 1.3E-10 | NA | NA | NS | rs3132131 | 33007463 | 5.4E-15 |
| 6 | 166876826 | cg11744817 | <i>RPS6KA2, RPS6KA2-IT1</i> | 1.9E-25 | 1.4E-06 | rs9459678 | 166803971 | 5.3E-11 | rs9355581 | 166785263 | 4.6E-11 |
| 8 | 74787918 | cg12682382 | <i>UBE2W</i> | 9.2E-27 | 6.9E-08 | rs7834451 | 74884972 | 6.8E-13 | NA | NA | NS |
| 9 | 35908117 | cg00918944 | <i>Intergenic</i> | 2.3E-26 | 1.7E-11 | NA | NA | NS | rs4271053 | 35893398 | 4.5E-12 |
| 12 | 98151379 | cg08993878 | <i>Intergenic</i> | 1.2E-13 | 1.2E-09 | rs12322961 | 96666297 | 7.0E-10 | rs12322961 | 96666297 | 4.3E-13 |
| 13 | 114161939 | cg12437013 | <i>TMCO3</i> | 8.3E-27 | 4.6E-08 | rs9577575 | 113270207 | 8.5E-10 | rs9577575 | 113270207 | 3.8E-17 |
| 15 | 40642998 | cg07047589 | <i>PHGR1</i> | 4.5E-47 | 1.1E-18 | NA | NA | NS | rs11070264 | 38399153 | 1.3E-10 |
| 16 | 524778 | cg09408143 | <i>RAB11FIP3</i> | 4.7E-20 | 4.2E-08 | rs3785301 | 456923 | 3.2E-10 | NA | NA | NS |
| 17 | 40259547 | cg20291162 | <i>DHX58</i> | 1.2E-10 | 2.0E-13 | rs730086 | 37525283 | 8.3E-12 | rs730086 | 37525283 | 1.6E-16 |

* A p-value $<6.5 \times 10^{-9}$ was considered significant after multiple testing correction (Bonferroni).

NA, not available; NS, not significant