

Figure S2A. The pathway enrichment of SLE genes implicated by 63 SNPs in Eastern Asian population within 1,751 Gene Expression Ontology matrix. *The bottom indicates the log transformed p value. The vertical line indicated the Bonferroni-corrected significance criteria. The pathways codes and names are listed in the right.*

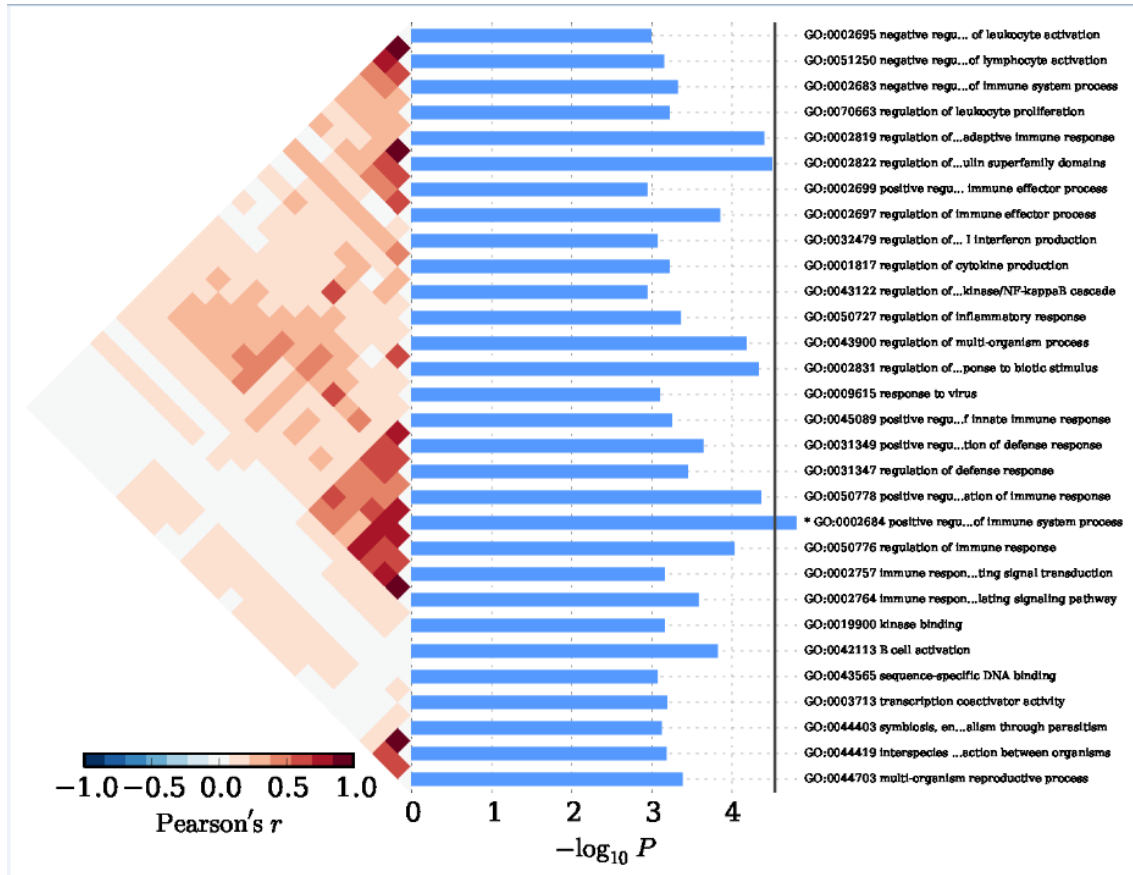


Figure S2B. The pathway enrichment of SLE implicated genes by 118 SNPs in Caucasian population within 1,751 Gene Expression Ontology matrix. *The bottom indicates the log transformed p value. The vertical line indicated the Bonferroni-corrected significance criteria. The pathways codes and names are listed in the right.*

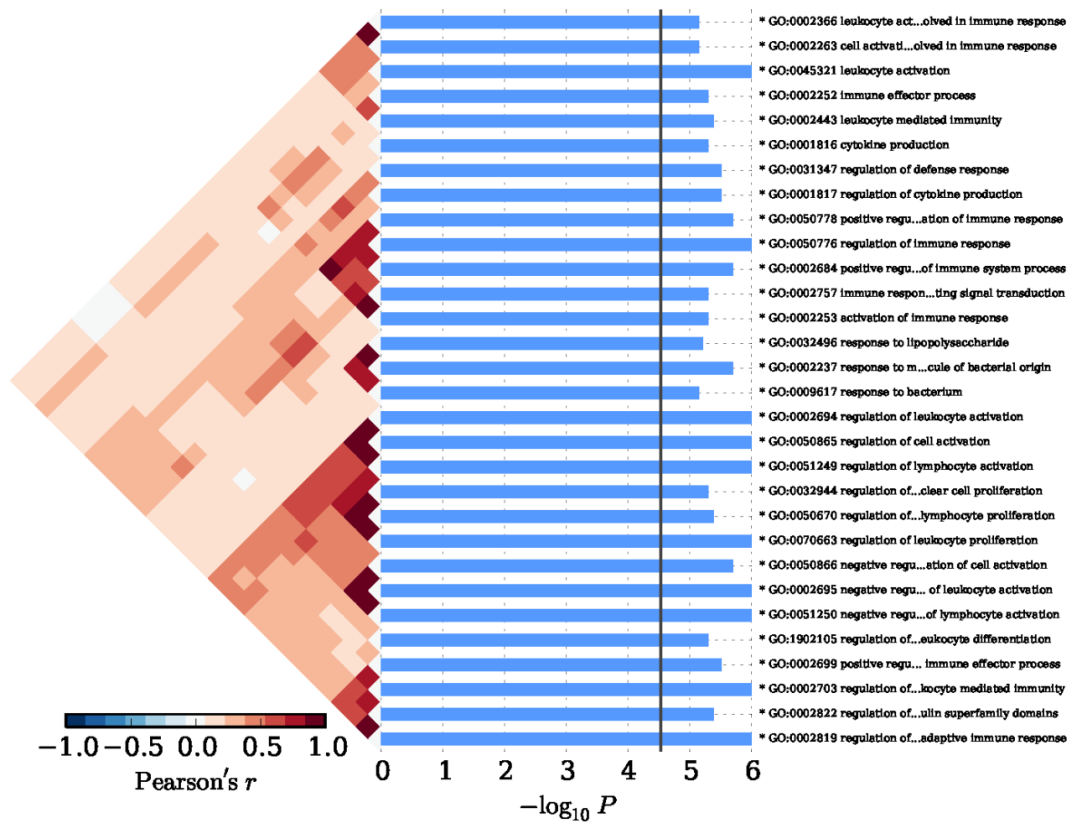


Figure S2C. The pathway enrichment of SLE implicated gene by 105 SNPs, without HLA region SNPs in Caucasian population within 1,751 Gene Expression Ontology matrix. *The bottom indicates the log transformed p value. The vertical line indicated the Bonferroni-corrected significance criteria. The pathways codes and names are listed in the right.*

