

**Supplementary Table S4.** Functional Enrichment Analysis of the LTA-Centered Interaction Network.

| Function                                            | FDR         | Genes in network | Genes in genome |
|-----------------------------------------------------|-------------|------------------|-----------------|
| cellular response to tumor necrosis factor          | 4.80E-21    | 14               | 159             |
| response to tumor necrosis factor                   | 4.80E-21    | 15               | 236             |
| tumor necrosis factor receptor superfamily binding  | 6.31E-07    | 5                | 29              |
| I-kappaB kinase/NF-kappaB signaling                 | 1.34365E-05 | 7                | 230             |
| positive regulation of apoptotic process            | 7.51222E-05 | 6                | 171             |
| positive regulation of leukocyte cell-cell adhesion | 0.000106764 | 6                | 187             |
| positive regulation of cell-cell adhesion           | 0.000215598 | 6                | 216             |
| regulation of leukocyte cell-cell adhesion          | 0.000437031 | 6                | 254             |
| regulation of T cell activation                     | 0.000437031 | 6                | 252             |
| ubiquitin-like protein ligase binding               | 0.000516162 | 6                | 266             |
| leukocyte cell-cell adhesion                        | 0.000558528 | 6                | 274             |
| tumor necrosis factor-mediated signaling pathway    | 0.000584609 | 4                | 57              |
| extrinsic apoptotic signaling pathway               | 0.000584609 | 5                | 146             |
| positive regulation of cell adhesion                | 0.000732313 | 6                | 299             |
| lymphocyte proliferation                            | 0.002279024 | 5                | 198             |
| mononuclear cell proliferation                      | 0.002279024 | 5                | 202             |
| regulation of I-kappaB kinase/NF-kappaB signaling   | 0.002279024 | 5                | 203             |
| cytokine receptor binding                           | 0.002788556 | 5                | 214             |
| positive regulation of lymphocyte activation        | 0.002938308 | 5                | 221             |
| leukocyte proliferation                             | 0.002938308 | 5                | 221             |
| positive regulation of leukocyte activation         | 0.005844602 | 5                | 257             |
| positive regulation of cell activation              | 0.006241366 | 5                | 263             |
| T cell proliferation                                | 0.008247506 | 4                | 129             |
| JNK cascade                                         | 0.010026742 | 4                | 137             |

|                                                                                           |             |   |     |
|-------------------------------------------------------------------------------------------|-------------|---|-----|
| positive regulation of proteolysis                                                        | 0.010061574 | 5 | 298 |
| endothelial cell apoptotic process                                                        | 0.010182282 | 3 | 44  |
| production of molecular mediator of immune response                                       | 0.014497326 | 4 | 155 |
| regulation of lymphocyte proliferation                                                    | 0.015386743 | 4 | 163 |
| positive regulation of peptidase activity                                                 | 0.015386743 | 4 | 159 |
| positive regulation of T cell activation                                                  | 0.015386743 | 4 | 162 |
| lymphocyte costimulation                                                                  | 0.015386743 | 3 | 53  |
| regulation of mononuclear cell proliferation                                              | 0.015636489 | 4 | 165 |
| positive regulation of DNA-binding transcription factor activity                          | 0.017045251 | 4 | 170 |
| regulation of leukocyte proliferation                                                     | 0.01980689  | 4 | 178 |
| adaptive immune response                                                                  | 0.022819445 | 4 | 186 |
| regulation of epithelial cell apoptotic process                                           | 0.022819445 | 3 | 64  |
| regulation of cytokine production involved in immune response                             | 0.024352059 | 3 | 66  |
| negative regulation of extracellular matrix organization                                  | 0.024471054 | 2 | 10  |
| positive regulation of sphingolipid biosynthetic process                                  | 0.024471054 | 2 | 10  |
| epithelial cell apoptotic process                                                         | 0.028038681 | 3 | 71  |
| stress-activated MAPK cascade                                                             | 0.031868136 | 4 | 211 |
| positive regulation of acute inflammatory response                                        | 0.032510363 | 2 | 12  |
| apoptotic process involved in development                                                 | 0.032510363 | 2 | 12  |
| receptor complex                                                                          | 0.033108367 | 4 | 217 |
| regulation of inflammatory response                                                       | 0.033544768 | 4 | 219 |
| cytokine production involved in immune response                                           | 0.033549489 | 3 | 79  |
| stress-activated protein kinase signaling cascade                                         | 0.035662281 | 4 | 225 |
| positive regulation of cysteine-type endopeptidase activity involved in apoptotic process | 0.041409852 | 3 | 86  |
| positive regulation of stress-activated MAPK cascade                                      | 0.041984716 | 3 | 87  |
| NIK/NF-kappaB signaling                                                                   | 0.042568022 | 3 | 88  |

|                                                                          |             |   |     |
|--------------------------------------------------------------------------|-------------|---|-----|
| regulation of ceramide biosynthetic process                              | 0.043523909 | 2 | 15  |
| cellular response to abiotic stimulus                                    | 0.048237637 | 4 | 251 |
| cellular response to environmental stimulus                              | 0.048237637 | 4 | 251 |
| regulation of endothelial cell development                               | 0.049506403 | 2 | 17  |
| regulation of membrane lipid metabolic process                           | 0.049506403 | 2 | 17  |
| regulation of sphingolipid biosynthetic process                          | 0.049506403 | 2 | 17  |
| response to mechanical stimulus                                          | 0.049506403 | 3 | 96  |
| regulation of apoptotic signaling pathway                                | 0.049506403 | 4 | 255 |
| positive regulation of stress-activated protein kinase signaling cascade | 0.049658603 | 3 | 98  |

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FDR, false discovery rate.