

**Supplementary Table S4: Gene Ontology analysis according to biological process (FDR<0.05) in SA1-null cells:** GO terms downregulated in SA1-null cells (blue table) and GO terms upregulated in SA1-null cells (red table) are listed.

| GO term    | Description  | FDR      |
|------------|--|----------|
| GO:0045947 | negative regulation of translational initiation                          | 4.00E-02 |
| GO:0006613 | cotranslational protein targeting to membrane                            | 4.53E-02 |
| GO:0016126 | sterol biosynthetic process  | 2.30E-02 |
| GO:0007224 | smoothed signaling pathway   | 4.21E-02 |
| GO:0045667 | regulation of osteoblast differentiation                                 | 4.53E-02 |
| GO:0007179 | transforming growth factor beta receptor signaling pathway               | 1.11E-02 |
| GO:0035108 | limb morphogenesis   | 3.96E-03 |
| GO:0030326 | embryonic limb morphogenesis   | 7.83E-03 |
| GO:0060173 | limb development   | 3.85E-03 |
| GO:0048754 | branching morphogenesis of a tube  | 1.81E-02 |
| GO:0001763 | morphogenesis of a branching structure                                   | 1.11E-02 |
| GO:0048706 | embryonic skeletal system development                                    | 1.81E-02 |
| GO:0007178 | transmembrane receptor protein serine/threonine kinase signaling pathway | 3.00E-03 |
| GO:0048705 | skeletal system morphogenesis  | 2.13E-02 |
| GO:0030324 | lung development   | 4.19E-02 |
| GO:0060541 | respiratory system development   | 3.15E-02 |
| GO:0016055 | Wnt receptor signaling pathway   | 1.60E-02 |
| GO:0035239 | tube morphogenesis   | 1.76E-02 |
| GO:0030323 | respiratory tube development   | 4.53E-02 |
| GO:0006520 | cellular amino acid metabolic process                                    | 3.96E-03 |
| GO:0001501 | skeletal system development  | 5.92E-04 |
| GO:0001503 | ossification   | 1.60E-02 |
| GO:0007507 | heart development  | 1.11E-02 |
| GO:0006396 | RNA processing   | 9.45E-07 |
| GO:0060348 | bone development   | 3.15E-02 |
| GO:0016568 | chromatin modification   | 4.43E-03 |
| GO:0007167 | enzyme linked receptor protein signaling pathway                         | 2.19E-03 |
| GO:0048729 | tissue morphogenesis   | 4.07E-02 |
| GO:0006281 | DNA repair   | 4.43E-03 |
| GO:0048598 | embryonic morphogenesis  | 1.11E-02 |
| GO:0034984 | response to DNA damage stimulus  | 4.93E-03 |
| GO:0043009 | chordate embryonic development   | 1.60E-02 |
| GO:0044262 | cellular carbohydrate metabolic process                                  | 4.00E-02 |
| GO:0009792 | embryo development ending in birth or egg hatching                       | 1.81E-02 |
| GO:0008610 | lipid biosynthetic process   | 4.53E-02 |
| GO:0006412 | translation  | 3.11E-03 |

| GO term    | Description   | FDR      |
|------------|---|----------|
| GO:0051726 | regulation of cell cycle                                  | 4.74E-02 |
| GO:0043066 | negative regulation of apoptosis                          | 4.09E-02 |
| GO:0060548 | negative regulation of cell death                         | 2.85E-02 |
| GO:0043069 | negative regulation of programmed cell death              | 2.83E-02 |
| GO:0048514 | blood vessel morphogenesis                                | 4.10E-02 |
| GO:0007265 | Ras protein signal transduction                           | 4.09E-02 |
| GO:0045595 | regulation of cell differentiation                        | 1.02E-03 |
| GO:0007243 | intracellular protein kinase cascade                      | 7.88E-04 |
| GO:0000165 | MAPKKK cascade  | 3.00E-02 |
| GO:0046903 | secretion   | 8.78E-04 |
| GO:0001932 | regulation of protein phosphorylation                     | 4.12E-02 |
| GO:0009967 | positive regulation of signal transduction                | 5.90E-03 |
| GO:0042060 | wound healing   | 1.80E-02 |
| GO:0051270 | regulation of cellular component movement                 | 1.84E-02 |
| GO:0010942 | positive regulation of cell death                         | 4.66E-04 |
| GO:0006916 | anti-apoptosis  | 3.67E-02 |
| GO:0043068 | positive regulation of programmed cell death              | 4.35E-04 |
| GO:0045597 | positive regulation of cell differentiation               | 5.24E-03 |
| GO:0043065 | positive regulation of apoptosis                          | 4.22E-04 |
| GO:0051046 | regulation of secretion                                   | 8.50E-03 |
| GO:0032940 | secretion by cell   | 3.15E-04 |
| GO:0006887 | exocytosis  | 4.09E-02 |
| GO:0016477 | cell migration  | 4.80E-05 |
| GO:0051247 | positive regulation of protein metabolic process          | 1.34E-02 |
| GO:0008284 | positive regulation of cell proliferation                 | 3.42E-02 |
| GO:0007599 | hemostasis  | 3.03E-02 |
| GO:0007596 | blood coagulation   | 2.88E-02 |
| GO:0043408 | regulation of MAPKKK cascade                              | 4.74E-02 |
| GO:0030334 | regulation of cell migration                              | 6.52E-03 |
| GO:0032270 | positive regulation of cellular protein metabolic process | 8.00E-03 |
| GO:0006865 | amino acid transport                                      | 4.09E-02 |
| GO:0006917 | induction of apoptosis                                    | 2.41E-04 |
| GO:0006897 | endocytosis   | 1.77E-04 |
| GO:0030036 | actin cytoskeleton organization                           | 4.01E-02 |
| GO:0018108 | peptidyl-tyrosine phosphorylation                         | 1.63E-02 |
| GO:0002520 | immune system development                                 | 4.12E-07 |
| GO:0019216 | regulation of lipid metabolic process                     | 2.17E-02 |
| GO:0032880 | regulation of protein localization                        | 2.44E-03 |
| GO:0030217 | T cell differentiation                                    | 5.09E-03 |
| GO:0051054 | positive regulation of DNA metabolic process              | 4.45E-02 |
| GO:0034101 | erythrocyte homeostasis                                   | 1.94E-02 |

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|------------|--|----------|
| GO:0050730 | regulation of peptidyl-tyrosine phosphorylation          | 2.85E-02 |
| GO:0032946 | positive regulation of mononuclear cell proliferation    | 2.85E-02 |
| GO:0034097 | response to cytokine stimulus                            | 7.25E-03 |
| GO:0001894 | tissue homeostasis                                       | 2.70E-02 |
| GO:0030097 | hemopoiesis  | 4.09E-08 |
| GO:0048872 | homeostasis of number of cells                           | 4.22E-04 |
| GO:0030099 | myeloid cell differentiation                             | 7.89E-05 |
| GO:0009968 | negative regulation of signal transduction               | 1.22E-02 |
| GO:0002573 | myeloid leukocyte differentiation                        | 1.25E-02 |
| GO:0032943 | mononuclear cell proliferation                           | 1.70E-04 |
| GO:0042110 | T cell activation  | 3.64E-06 |
| GO:0042113 | B cell activation  | 2.45E-04 |
| GO:0070201 | regulation of establishment of protein localization      | 4.66E-04 |
| GO:0043123 | positive regulation of I-kappaB kinase/NF-kappaB cascade | 5.90E-03 |
| GO:0042098 | T cell proliferation                                     | 1.20E-03 |
| GO:0043410 | positive regulation of MAPKKK cascade                    | 1.34E-02 |
| GO:0030098 | lymphocyte differentiation                               | 1.29E-05 |
| GO:0050727 | regulation of inflammatory response                      | 2.58E-03 |
| GO:0051223 | regulation of protein transport                          | 3.10E-04 |
| GO:0043122 | regulation of I-kappaB kinase/NF-kappaB cascade          | 1.38E-03 |
| GO:0007015 | actin filament organization                              | 3.41E-02 |
| GO:0046649 | lymphocyte activation                                    | 2.89E-10 |
| GO:0019221 | cytokine-mediated signaling pathway                      | 9.91E-04 |
| GO:0032496 | response to lipopolysaccharide                           | 5.20E-04 |
| GO:0045767 | regulation of anti-apoptosis                             | 4.20E-02 |
| GO:0045619 | regulation of lymphocyte differentiation                 | 2.46E-03 |
| GO:0050776 | regulation of immune response                            | 5.40E-09 |
| GO:0022904 | respiratory electron transport chain                     | 2.26E-02 |
| GO:0002443 | leukocyte mediated immunity                              | 3.27E-07 |
| GO:0050778 | positive regulation of immune response                   | 4.85E-07 |
| GO:0007249 | I-kappaB kinase/NF-kappaB cascade                        | 2.97E-05 |
| GO:0030183 | B cell differentiation                                   | 3.08E-03 |
| GO:0046631 | alpha-beta T cell activation                             | 3.08E-03 |
| GO:0002237 | response to molecule of bacterial origin                 | 3.09E-05 |
| GO:0001909 | leukocyte mediated cytotoxicity                          | 4.19E-03 |
| GO:0051341 | regulation of oxidoreductase activity                    | 1.50E-02 |
| GO:0042773 | ATP synthesis coupled electron transport                 | 4.87E-02 |
| GO:0050863 | regulation of T cell activation                          | 7.14E-03 |
| GO:0045087 | innate immune response                                   | 2.57E-07 |
| GO:0045639 | positive regulation of myeloid cell differentiation      | 2.69E-02 |
| GO:0002253 | activation of immune response                            | 5.92E-06 |
| GO:0006954 | inflammatory response                                    | 1.18E-15 |
| GO:0006904 | vesicle docking involved in exocytosis                   | 4.45E-02 |

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|------------|---|----------|
| GO:0050714 | positive regulation of protein secretion                              | 5.90E-03 |
| GO:0019724 | B cell mediated immunity  | 7.45E-06 |
| GO:0002821 | positive regulation of adaptive immune response                       | 3.00E-03 |
| GO:0009306 | protein secretion   | 1.22E-05 |
| GO:0042129 | regulation of T cell proliferation                                    | 3.99E-02 |
| GO:0002367 | cytokine production involved in immune response                       | 4.10E-02 |
| GO:0002286 | T cell activation involved in immune response                         | 4.10E-02 |
| GO:0009617 | response to bacterium   | 2.89E-10 |
| GO:0051272 | positive regulation of cellular component movement                    | 9.94E-03 |
| GO:0050729 | positive regulation of inflammatory response                          | 1.09E-02 |
| GO:0006935 | chemotaxis  | 2.44E-10 |
| GO:0050708 | regulation of protein secretion                                       | 3.33E-04 |
| GO:0045637 | regulation of myeloid cell differentiation                            | 1.76E-04 |
| GO:0045833 | negative regulation of lipid metabolic process                        | 3.71E-02 |
| GO:0006898 | receptor-mediated endocytosis   | 1.02E-03 |
| GO:0050671 | positive regulation of lymphocyte proliferation                       | 3.40E-02 |
| GO:0030155 | regulation of cell adhesion   | 3.83E-02 |
| GO:0030335 | positive regulation of cell migration                                 | 7.23E-03 |
| GO:0045061 | thymic T cell selection   | 3.26E-02 |
| GO:0051353 | positive regulation of oxidoreductase activity                        | 1.48E-02 |
| GO:0002768 | immune response-regulating cell surface receptor signaling pathway    | 7.89E-05 |
| GO:0042742 | defense response to bacterium   | 7.18E-07 |
| GO:0050670 | regulation of lymphocyte proliferation                                | 2.48E-03 |
| GO:0046651 | lymphocyte proliferation  | 2.60E-04 |
| GO:0043542 | endothelial cell migration  | 2.48E-03 |
| GO:0051251 | positive regulation of lymphocyte activation                          | 8.81E-04 |
| GO:0030168 | platelet activation   | 4.89E-03 |
| GO:0050900 | leukocyte migration   | 1.82E-06 |
| GO:0014048 | regulation of glutamate secretion                                     | 4.74E-02 |
| GO:0045580 | regulation of T cell differentiation                                  | 2.03E-02 |
| GO:0050715 | positive regulation of cytokine secretion                             | 9.96E-03 |
| GO:0016485 | protein processing  | 2.60E-02 |
| GO:0042107 | cytokine metabolic process  | 1.36E-03 |
| GO:0032760 | positive regulation of tumor necrosis factor production               | 1.94E-02 |
| GO:0042089 | cytokine biosynthetic process   | 1.32E-03 |
| GO:0001934 | positive regulation of protein phosphorylation                        | 4.53E-02 |
| GO:0007229 | integrin-mediated signaling pathway                                   | 4.44E-02 |
| GO:0050867 | positive regulation of cell activation                                | 8.59E-05 |
| GO:0030100 | regulation of endocytosis   | 6.69E-03 |
| GO:0002541 | activation of plasma proteins involved in acute inflammatory response | 3.47E-02 |
| GO:0046632 | alpha-beta T cell differentiation                                     | 3.47E-02 |

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|------------|---|----------|
| GO:0009615 | response to virus   | 2.38E-03 |
| GO:0001817 | regulation of cytokine production   | 1.77E-06 |
| GO:0051605 | protein maturation by peptide bond cleavage   | 3.83E-02 |
| GO:0033198 | response to ATP   | 1.43E-02 |
| GO:0002684 | positive regulation of immune system process  | 1.78E-09 |
| GO:0006956 | complement activation   | 2.96E-02 |
| GO:0060326 | cell chemotaxis   | 5.04E-06 |
| GO:0050870 | positive regulation of T cell activation  | 7.93E-04 |
| GO:0030595 | leukocyte chemotaxis  | 1.06E-05 |
| GO:0051604 | protein maturation  | 6.89E-03 |
| GO:0042035 | regulation of cytokine biosynthetic process   | 6.51E-04 |
| GO:0045577 | regulation of B cell differentiation  | 1.23E-02 |
| GO:0002920 | regulation of humoral immune response   | 1.23E-02 |
| GO:0050663 | cytokine secretion  | 4.80E-05 |
| GO:0002526 | acute inflammatory response   | 1.24E-05 |
| GO:0042102 | positive regulation of T cell proliferation   | 9.67E-03 |
| GO:0016064 | immunoglobulin mediated immune response   | 6.97E-05 |
| GO:0030593 | neutrophil chemotaxis   | 2.27E-04 |
| GO:0030218 | erythrocyte differentiation   | 2.74E-02 |
| GO:0043534 | blood vessel endothelial cell migration   | 1.28E-03 |
| GO:0050830 | defense response to Gram-positive bacterium   | 1.28E-03 |
| GO:0050701 | interleukin- secretion  | 2.28E-02 |
| GO:0050702 | interleukin- beta secretion   | 2.28E-02 |
| GO:0032770 | positive regulation of monooxygenase activity   | 3.00E-03 |
| GO:0045582 | positive regulation of T cell differentiation   | 7.01E-03 |
| GO:0045840 | positive regulation of mitosis  | 1.69E-02 |
| GO:0010595 | positive regulation of endothelial cell migration                                     | 4.82E-02 |
| GO:0032490 | detection of molecule of bacterial origin   | 4.82E-02 |
| GO:0046427 | positive regulation of JAK-STAT cascade   | 4.43E-02 |
| GO:0006910 | phagocytosis, recognition   | 6.89E-03 |
| GO:0050851 | antigen receptor-mediated signaling pathway   | 4.64E-02 |
| GO:0045123 | cellular extravasation  | 2.05E-03 |
| GO:0002455 | humoral immune response mediated by circulating immunoglobulin                        | 4.63E-03 |
| GO:0007159 | leukocyte cell-cell adhesion  | 7.89E-05 |
| GO:0009408 | response to heat  | 1.71E-02 |
| GO:0006809 | nitric oxide biosynthetic process   | 4.22E-03 |
| GO:0045638 | negative regulation of myeloid cell differentiation                                   | 1.19E-02 |
| GO:0043536 | positive regulation of blood vessel endothelial cell migration                        | 4.10E-02 |
| GO:0002925 | positive regulation of humoral immune response mediated by circulating immunoglobulin | 4.10E-02 |
| GO:0045621 | positive regulation of lymphocyte differentiation                                     | 1.26E-03 |
| GO:0045055 | regulated secretory pathway   | 1.10E-02 |

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|------------|--|----------|
| GO:0051971 | positive regulation of transmission of nerve impulse                             | 3.83E-02 |
| GO:0001819 | positive regulation of cytokine production                                       | 1.06E-05 |
| GO:0002923 | regulation of humoral immune response mediated by circulating immunoglobulin     | 1.26E-02 |
| GO:0050718 | positive regulation of interleukin- beta secretion                               | 3.37E-02 |
| GO:0019722 | calcium-mediated signaling   | 1.20E-02 |
| GO:0032731 | positive regulation of interleukin- beta production                              | 1.00E-02 |
| GO:0002474 | antigen processing and presentation of peptide antigen via MHC class I           | 2.36E-02 |
| GO:0043367 | CD-positive, alpha-beta T cell differentiation                                   | 7.13E-03 |
| GO:0045428 | regulation of nitric oxide biosynthetic process                                  | 1.90E-03 |
| GO:0051607 | defense response to virus  | 6.53E-03 |
| GO:0051222 | positive regulation of protein transport   | 9.71E-04 |
| GO:0045576 | mast cell activation   | 1.32E-03 |
| GO:0006909 | phagocytosis   | 1.77E-06 |
| GO:0045807 | positive regulation of endocytosis   | 3.35E-04 |
| GO:0042226 | interleukin- biosynthetic process  | 1.37E-02 |
| GO:0045429 | positive regulation of nitric oxide biosynthetic process                         | 8.63E-04 |
| GO:0045408 | regulation of interleukin- biosynthetic process                                  | 1.19E-02 |
| GO:0050853 | B cell receptor signaling pathway  | 4.95E-02 |
| GO:0002891 | positive regulation of immunoglobulin mediated immune response                   | 2.63E-03 |
| GO:0002675 | positive regulation of acute inflammatory response                               | 1.08E-02 |
| GO:0002863 | positive regulation of inflammatory response to antigenic stimulus               | 4.30E-02 |
| GO:0002437 | inflammatory response to antigenic stimulus                                      | 1.32E-04 |
| GO:0043303 | mast cell degranulation  | 4.61E-02 |
| GO:0032755 | positive regulation of interleukin- production                                   | 4.79E-04 |
| GO:0050710 | negative regulation of cytokine secretion  | 4.07E-02 |
| GO:0042534 | regulation of tumor necrosis factor biosynthetic process                         | 8.30E-03 |
| GO:0050764 | regulation of phagocytosis   | 8.20E-05 |
| GO:0032651 | regulation of interleukin- beta production                                       | 3.69E-02 |
| GO:0006911 | phagocytosis, engulfment   | 2.60E-04 |
| GO:0050766 | positive regulation of phagocytosis  | 3.24E-05 |
| GO:0042590 | antigen processing and presentation of exogenous peptide antigen via MHC class I | 2.32E-02 |
| GO:0048010 | vascular endothelial growth factor receptor signaling pathway                    | 5.75E-03 |
| GO:0016068 | type I hypersensitivity  | 2.62E-02 |
| GO:0030851 | granulocyte differentiation  | 2.62E-02 |
| GO:0001805 | positive regulation of type III hypersensitivity                                 | 1.54E-02 |
| GO:0002548 | monocyte chemotaxis  | 1.38E-03 |
| GO:0030853 | negative regulation of granulocyte differentiation                               | 4.34E-02 |
| GO:0048525 | negative regulation of viral reproduction  | 3.69E-02 |
| GO:0009311 | oligosaccharide metabolic process  | 1.89E-02 |

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|------------|---|----------|
| GO:0009312 | oligosaccharide biosynthetic process        | 1.38E-02 |
| GO:0016998 | cell wall macromolecule catabolic process   | 1.38E-02 |
| GO:0050829 | defense response to Gram-negative bacterium | 1.30E-02 |
| GO:0005989 | lactose biosynthetic process                | 1.13E-02 |