**Supplementary Table 3.** Top30 GO terms of GO analysis on hypermethylated mRNAs.

|  |
| --- |
| **hyper\_LPS\_vs\_Ctrl Methylation** |
| **GO ID** | **Term** | **Ontology** | **P-value** | **Enrichment Score** | **Genes** |
| GO:0006952 | defense response | Biological process | 5.07312E-06 | 5.294724582 | SERPING1//F12//KNG1//PF4//TNFRSF26//LTB4R//BDKRB1//PTK2B//CARD9//SIRT2 |
| GO:0006954 | inflammatory response | Biological process | 1.52242E-05 | 4.817465861 | SERPING1//F12//KNG1//PF4//TNFRSF26//LTB4R//BDKRB1 |
| GO:0002237 | response to molecule of bacterial origin | Biological process | 2.90915E-05 | 4.536233584 | CARD9//PF4//TNFRSF26//BDKRB1//SIRT2//HMGCS2 |
| GO:0030195 | negative regulation of blood coagulation | Biological process | 3.80705E-05 | 4.419411747 | SERPING1//F12//KNG1 |
| GO:1900047 | negative regulation of hemostasis | Biological process | 3.80705E-05 | 4.419411747 | KNG1//SERPING1//F12 |
| GO:0050819 | negative regulation of coagulation | Biological process | 4.29557E-05 | 4.366978992 | KNG1//SERPING1//F12 |
| GO:0007596 | blood coagulation | Biological process | 6.23668E-05 | 4.20504623 | PF4//F12//KNG1//SERPING1 |
| GO:0007599 | hemostasis | Biological process | 6.53964E-05 | 4.184446445 | SERPING1//F12//PF4//KNG1 |
| GO:0050817 | coagulation | Biological process | 7.1776E-05 | 4.144020641 | SERPING1//F12//PF4//KNG1 |
| GO:0061045 | negative regulation of wound healing | Biological process | 0.000101832 | 3.992117466 | KNG1//SERPING1//F12 |
| GO:0005615 | extracellular space | Cellular component | 5.42327E-05 | 4.265738697 | KNG1//BGLAP//TFF3//METRN//PI16//SERPING1//PLA2G2A//F12//PF4 |
| GO:0005576 | extracellular region | Cellular component | 0.000150428 | 3.82267273 | TFF3//BGLAP//METRN//KNG1//PI16//SERPING1//PLA2G2A//F12//PF4//CEACAM4 |
| GO:0044421 | extracellular region part | Cellular component | 0.000178565 | 3.748202761 | BGLAP//TFF3//METRN//KNG1//PI16//SERPING1//PLA2G2A//F12//PF4 |
| GO:0043204 | perikaryon | Cellular component | 0.001382371 | 2.859375512 | BGLAP//SIRT2//CNGA4 |
| GO:0005887 | integral component of plasma membrane | Cellular component | 0.006872611 | 2.162878253 | PTK2B//HHIP//SLC22A2//TNFRSF26//LTB4R//CNGA4 |
| GO:0031226 | intrinsic component of plasma membrane | Cellular component | 0.008965672 | 2.047417156 | HHIP//SLC22A2//TNFRSF26//LTB4R//CNGA4//PTK2B |
| GO:0005791 | rough endoplasmic reticulum | Cellular component | 0.010971457 | 1.959735708 | BGLAP//F12 |
| GO:0043025 | neuronal cell body | Cellular component | 0.013399909 | 1.872898166 | BGLAP//SIRT2//CNGA4//PTK2B |
| GO:0030430 | host cell cytoplasm | Cellular component | 0.013419016 | 1.872279331 | PF4 |
| GO:0033655 | host cell cytoplasm part | Cellular component | 0.013419016 | 1.872279331 | PF4 |
| GO:0004683 | calmodulin-dependent protein kinase activity | Molecular function | 0.000607787 | 3.216248605 | PTK2B//CAMKK2 |
| GO:0099094 | ligand-gated cation channel activity | Molecular function | 0.008070464 | 2.093101509 | PTK2B//CNGA4 |
| GO:0005509 | calcium ion binding | Molecular function | 0.010289976 | 1.987585634 | BGLAP//PLA2G2A//F12//CAMKK2 |
| GO:0048406 | nerve growth factor binding | Molecular function | 0.013514897 | 1.86918726 | TNFRSF26 |
| GO:0015276 | ligand-gated ion channel activity | Molecular function | 0.013533457 | 1.868591243 | PTK2B//CNGA4 |
| GO:0022834 | ligand-gated channel activity | Molecular function | 0.013533457 | 1.868591243 | PTK2B//CNGA4 |
| GO:0008528 | G-protein coupled peptide receptor activity | Molecular function | 0.014530598 | 1.837716514 | BDKRB1//LTB4R |
| GO:0004966 | galanin receptor activity | Molecular function | 0.014856736 | 1.828076591 | LTB4R |
| GO:0005221 | intracellular cyclic nucleotide activated cation channel activity | Molecular function | 0.014856736 | 1.828076591 | CNGA4 |
| GO:0015651 | quaternary ammonium group transmembrane transporter activity | Molecular function | 0.014856736 | 1.828076591 | SLC22A2 |

**Supplementary Table 4.** Top30 GO terms of GO analysis on hypomethylated mRNAs.

|  |
| --- |
| **hypo\_LPS\_vs\_Ctrl Methylation** |
| **GO ID** | **Term** | **Ontology** | **P-value** | **Enrichment Score** | **Genes** |
| GO:0044419 | interspecies interaction between organisms | Biological process | 3.54323E-05 | 4.450600118 | MMP9//NP4//RATNP-3B//CAMP//SLPI//PDCD6IP//CCL3//REG1A//IFITM6//RSAD2//STAT1//SLC22A5 |
| GO:0035821 | modification of morphology or physiology of other organism | Biological process | 7.55571E-05 | 4.121724481 | MMP9//NP4//RATNP-3B//CCL3//REG1A//CAMP//SLPI |
| GO:0071674 | mononuclear cell migration | Biological process | 0.000170069 | 3.769374407 | CCL3//CCL20//CXCL17//CCL27//PDGFD |
| GO:0071222 | cellular response to lipopolysaccharide | Biological process | 0.000264222 | 3.578030696 | STAT1//CCL3//NP4//CCL20//CAMP//DEFA10//MMP9//NR1I2 |
| GO:0015711 | organic anion transport | Biological process | 0.000330144 | 3.481296903 | SLC6A18//SLC7A7//LOC292543//GRIK1//SLC26A7//SLC51B//SLC17A3//SLC27A5//FABP1//SLC22A5//SLC25A38 |
| GO:0071219 | cellular response to molecule of bacterial origin | Biological process | 0.000352968 | 3.452264428 | STAT1//CCL3//NP4//CCL20//CAMP//DEFA10//MMP9//NR1I2 |
| GO:0046942 | carboxylic acid transport | Biological process | 0.000416204 | 3.380694025 | SLC6A18//SLC7A7//LOC292543//GRIK1//SLC51B//SLC27A5//FABP1//SLC26A7//SLC25A38 |
| GO:0015849 | organic acid transport | Biological process | 0.000426167 | 3.370419687 | SLC6A18//SLC7A7//LOC292543//GRIK1//SLC51B//SLC27A5//FABP1//SLC26A7//SLC25A38 |
| GO:0002687 | positive regulation of leukocyte migration | Biological process | 0.000548646 | 3.260707733 | CXCL17//CCL27//CCL20//PDGFD//CCL3//MMP9 |
| GO:0002376 | immune system process | Biological process | 0.000562148 | 3.250149058 | CTSH//NP4//CAMP//BPIFB1//STAT1//IL22//CCL3//CCL20//TAPBPL//HPX//MMP9//CLEC4G//IL1F10//CCL27//LST1//SLPI//CXCL17//AHSP//SLC25A38//DYRK3//VAV3//RSAD2//IFITM6//IL18RAP//IL18BP//FANCD2//BPGM//OLFM4//REG1A//PDGFD |
| GO:0005615 | extracellular space | Cellular component | 5.76158E-05 | 4.239458095 | PDCD6IP//LOC100909605//GC//REG1A//CTSH//CCL3//NP4//OLFM4//LTBP4//CCL20//SLURP1//CXCL17//RGD1308195//CAMP//IL1F10//LEFTY1//RATNP-3B//IL22//HPX//DEFA10//PDGFD//MMP9//SLPI//IL18BP |
| GO:0005576 | extracellular region | Cellular component | 0.000400471 | 3.397429083 | LTBP4//MMP9//LOC100909605//GC//REG1A//CTSH//CCL3//NP4//OLFM4//CCL20//SLURP1//CXCL17//RGD1308195//CAMP//IL1F10//LEFTY1//RATNP-3B//IL22//HPX//DEFA10//PDGFD//SLPI//IL18BP//PDCD6IP//WFDC18//CCL27//SLPIL3//BPIFB1 |
| GO:0044421 | extracellular region part | Cellular component | 0.000580644 | 3.236090205 | LOC100909605//GC//REG1A//CTSH//CCL3//NP4//OLFM4//LTBP4//CCL20//SLURP1//CXCL17//RGD1308195//CAMP//IL1F10//LEFTY1//RATNP-3B//IL22//HPX//DEFA10//PDGFD//MMP9//SLPI//IL18BP//PDCD6IP |
| GO:0005811 | lipid droplet | Cellular component | 0.002293485 | 2.639504035 | PNPLA5//METTL7B//PLIN5//RSAD2 |
| GO:0042581 | specific granule | Cellular component | 0.004401048 | 2.356443857 | OLFM4//CAMP |
| GO:0032809 | neuronal cell body membrane | Cellular component | 0.022053119 | 1.656529971 | ATP2B2//REG1A |
| GO:0044298 | cell body membrane | Cellular component | 0.023367062 | 1.631395882 | ATP2B2//REG1A |
| GO:0098839 | postsynaptic density membrane | Cellular component | 0.023367062 | 1.631395882 | ATP2B2//GRIK1 |
| GO:0099634 | postsynaptic specialization membrane | Cellular component | 0.028932341 | 1.538616431 | ATP2B2//GRIK1 |
| GO:0016323 | basolateral plasma membrane | Cellular component | 0.033425573 | 1.475921142 | SLC27A5//SLC22A5//SLC26A7//SLC51B//SLC7A7 |
| GO:0008514 | organic anion transmembrane transporter activity | Molecular function | 2.14E-05 | 4.669771869 | LOC292543//SLC26A7//SLC51B//SLC17A3//SLC7A7//SLC6A18//SLC25A38//SLC27A5//SLC22A5 |
| GO:0008509 | anion transmembrane transporter activity | Molecular function | 7.07E-05 | 4.150823016 | LOC292543//SLC26A7//GLRA3//SLC22A5//SLC17A3//SLC51B//SLC7A7//SLC6A18//SLC25A38//SLC27A5 |
| GO:0005342 | organic acid transmembrane transporter activity | Molecular function | 8.46E-05 | 4.072447892 | LOC292543//SLC51B//SLC7A7//SLC6A18//SLC25A38//SLC27A5//SLC26A7 |
| GO:0046943 | carboxylic acid transmembrane transporter activity | Molecular function | 8.46E-05 | 4.072447892 | LOC292543//SLC51B//SLC7A7//SLC6A18//SLC25A38//SLC27A5//SLC26A7 |
| GO:0048020 | CCR chemokine receptor binding | Molecular function | 0.000143366 | 3.843553316 | CCL3//CCL27//STAT1//CCL20 |
| GO:0015318 | inorganic molecular entity transmembrane transporter activity | Molecular function | 0.000156705 | 3.804915944 | LOC292543//GRIK1//GLRA3//KCNG3//SLC26A7//SLC24A2//SLC6A18//ATP2B2//SLC17A3//SLC22A5//ATP6V1G2//SLC51B//SLC7A7//SLC25A38//SLC27A5//SLC9A8 |
| GO:0015297 | antiporter activity | Molecular function | 0.000196831 | 3.705906153 | SLC24A2//SLC26A7//SLC9A8//SLC22A5//SLC7A7 |
| GO:0015075 | ion transmembrane transporter activity | Molecular function | 0.000274963 | 3.560725338 | LOC292543//GRIK1//GLRA3//KCNG3//SLC26A7//SLC24A2//SLC6A18//ATP2B2//SLC17A3//SLC22A5//ATP6V1G2//SLC51B//SLC7A7//SLC25A38//SLC27A5//SLC9A8 |
| GO:0022857 | transmembrane transporter activity | Molecular function | 0.000281263 | 3.550887697 | LOC292543//GRIK1//GLRA3//KCNG3//SLC26A7//SLC24A2//SLC6A18//ATP2B2//SLC17A3//SLC22A5//ATP6V1G2//SLC51B//SLC7A7//SLC25A38//HPX//SLC27A5//SLC9A8//GC |
| GO:0099516 | ion antiporter activity | Molecular function | 0.00050933 | 3.293000759 | SLC24A2//SLC26A7//SLC9A8//SLC22A5 |