**Table S1** Significantly up, stay and down regulated mRNA gene profiling at the 3 days (A) and 6 days (B) of electrical stimulated hAD-MSC

**(A) 3 days gene profiling**

**Control vs 0.01 mg/mL (up), 0.05 mg/mL (up), 0.1 mg/mL (stay)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **p-Value** |
| Biological process | GO:0038061 | NIK/NK-KappaB casade | 0.00076 |
| GO:0016199 | axon midline choice point recognition | 0.00078 |
| GO:0016198 | axon choice point recognition | 0.00095 |

**Control vs 0.01 mg/mL (up), 0.05 mg/mL (up), 0.1 mg/mL (down)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **p-value** |
| Biological\_process | GO:0042100 | B cell proliferation | 0.00021 |
| Cellular\_component | GO:0005887 | integral to plasma membrane | 0.00085 |
| Molecular\_function | GO:0004930 | G-protein coupled receptor activity | 0.00033 |
| GO:0001608 | G-protein coupled nucleotide receptor activity | 0.00043 |
| GO:0045028 | G-protein coupled purinergic nucleotide receptor activity | 0.00043 |

**Control vs 0.01 mg/mL (up), 0.05 mg/mL (stay), 0.1 mg/mL (up)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **p-value** |
| biological\_process | GO:0050715 | positive regulation of cytokine secretion | 0.00002 |
| GO:0050707 | regulation of cytokine secretion | 0.00012 |
| GO:0050714 | positive regulation of protein secretion | 0.00014 |

**Control vs 0.01 mg/mL (up), 0.05 mg/mL (stay), 0.1 mg/mL (stay)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **p-value** |
| biological\_process | GO:0050673 | epithelial cell proliferation | 0.00001 |
| GO:0050678 | regulation of epithelial cell proliferation | 0.00005 |
| GO:0019748 | secondary metabolic process | 0.00006 |
| cellular\_component | GO:0005576 | extracellular region | 0.00002 |
| GO:0005615 | extracellular space | 0.00010 |
| GO:0044421 | extracellular region part | 0.00078 |
| molecular\_function | GO:0004033 | aldo-keto reductase (NADP) activity | 0.00019 |
| GO:0008199 | ferric iron binding | 0.00042 |
| GO:0017017 | MAP kinase tyrosine/serine/threonine phosphatase activity | 0.00081 |

**Control vs 0.01 mg/mL (up), 0.05 mg/mL (stay), 0.1 mg/mL (down)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **p-value** |
| biological\_process | GO:0051606 | detection of stimulus | 0.00010 |
| GO:0007597 | blood coagulation, intrinsic pathway | 0.00013 |
| GO:0072378 | blood coagulation, fibrin clot formation | 0.00023 |

**Control vs 0.01 mg/mL (up), 0.05 mg/mL (down), 0.1 mg/mL (stay)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **p-value** |
| cellular\_component | GO:0005576 | extracellular region | 0.00009 |
| GO:0034703 | cation channel complex | 0.00018 |
| molecular\_function | GO:0001601 | peptide YY receptor activity | 0.00000 |
| GO:0004983 | neuropeptide Y receptor activity | 0.00003 |
| GO:0030553 | cGMP binding | 0.00025 |

**Control vs 0.01 mg/mL (up), 0.05 mg/mL (down), 0.1 mg/mL (down)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **p-value** |
| biological\_process | GO:0006066 | alcohol metabolic process | 0.00092 |

**Control vs 0.01 mg/mL (stay), 0.05 mg/mL (up), 0.1 mg/mL (up)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **p-value** |
| biological\_process | GO:0060073 | micturition | 0.00011 |
| GO:0006855 | drug transmembrane transport | 0.00041 |
| GO:0042755 | eating behavior | 0.00049 |
| molecular\_function | GO:0015238 | drug transmembrane transporter activity | 0.00040 |
| GO:0090484 | drug transporter activity | 0.00063 |

**Control vs 0.01 mg/mL (stay), 0.05 mg/mL (up), 0.1 mg/mL (stay)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **p-value** |
| biological\_process | GO:0033327 | Leydig cell differentiation | 0.00029 |
| GO:0030001 | metal ion transport | 0.00043 |
| GO:0032958 | inositol phosphate biosynthetic process | 0.00062 |
| cellular\_component | GO:0031224 | intrinsic to membrane | 0.00009 |
| GO:0016021 | integral to membrane | 0.00016 |
| GO:0044425 | membrane part | 0.00042 |
| molecular\_function | GO:0005261 | cation channel activity | 0.00006 |
| GO:0005245 | voltage-gated calcium channel activity | 0.00009 |
| GO:0046873 | metal ion transmembrane transporter activity | 0.00013 |

**Control vs 0.01 mg/mL (stay), 0.05 mg/mL (up), 0.1 mg/mL (down)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **p-value** |
| biological\_process | GO:0030259 | lipid glycosylation | 0.00001 |
| GO:0050877 | neurological system process | 0.00003 |
| GO:0003008 | system process | 0.00010 |
| cellular\_component | GO:0071944 | cell periphery | 0.00000 |
| GO:0005886 | plasma membrane | 0.00000 |
| GO:0005576 | extracellular region | 0.00000 |
| molecular\_function | GO:0015020 | glucuronosyltransferase activity | 0.00003 |
| GO:0004930 | G-protein coupled receptor activity | 0.00003 |
| GO:0004888 | transmembrane signaling receptor activity | 0.00005 |

**Control vs 0.01 mg/mL (stay), 0.05 mg/mL (stay), 0.1 mg/mL (up)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **p-value** |
| biological\_process | GO:0007186 | G-protein coupled receptor signaling pathway | 0.00000 |
| GO:0007166 | cell surface receptor signaling pathway | 0.00001 |
| GO:0002252 | immune effector process | 0.00001 |
| cellular\_component | GO:0071944 | cell periphery | 0.00000 |
| GO:0005886 | plasma membrane | 0.00000 |
| GO:0031224 | intrinsic to membrane | 0.00000 |
| molecular\_function | GO:0004888 | transmembrane signaling receptor activity | 0.00000 |
| GO:0004872 | receptor activity | 0.00000 |
| GO:0038023 | signaling receptor activity | 0.00000 |

**Control vs 0.01 mg/mL (stay), 0.05 mg/mL (stay), 0.1 mg/mL (stay)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **p-value** |
| biological\_process | GO:0044260 | cellular macromolecule metabolic process | 0.00000 |
| GO:0044237 | cellular metabolic process | 0.00000 |
| GO:0090304 | nucleic acid metabolic process | 0.00000 |
| cellular\_component | GO:0005681 | spliceosomal complex | 0.00000 |
| GO:0044424 | intracellular part | 0.00000 |
| GO:0005622 | intracellular | 0.00000 |
| molecular\_function | GO:0003723 | RNA binding | 0.00000 |
| GO:0003676 | nucleic acid binding | 0.00000 |
| GO:1901363 | heterocyclic compound binding | 0.00000 |

**Control vs 0.01 mg/mL (stay), 0.05 mg/mL (stay), 0.1 mg/mL (down)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **p-value** |
| biological\_process | GO:0000042 | protein targeting to Golgi | 0.00015 |
| GO:0072600 | establishment of protein localization to Golgi | 0.00019 |
| GO:0000301 | retrograde transport, vesicle recycling within Golgi | 0.00019 |

**Control vs 0.01 mg/mL (stay), 0.05 mg/mL (down), 0.1 mg/mL (up)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **p-value** |
| biological\_process | GO:2000026 | regulation of multicellular organismal development | 0.00001 |
| GO:0051239 | regulation of multicellular organismal process | 0.00002 |
| GO:0032501 | multicellular organismal process | 0.00002 |
| cellular\_component | GO:0000786 | nucleosome | 0.00005 |
| GO:1990104 | DNA bending complex | 0.00005 |
| GO:0044815 | DNA packaging complex | 0.00005 |

 **Control vs 0.01 mg/mL (stay), 0.05 mg/mL (down), 0.1 mg/mL (stay)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **p-value** |
| biological\_process | GO:0023052 | signaling | 0.00005 |
| GO:0044700 | single organism signaling | 0.00005 |
| GO:0007154 | cell communication | 0.00010 |
| cellular\_component | GO:0005576 | extracellular region | 0.00009 |
| GO:0005923 | tight junction | 0.00018 |
| GO:0070160 | occluding junction | 0.00018 |
| molecular\_function | GO:0004872 | receptor activity | 0.00000 |
| GO:0038023 | signaling receptor activity | 0.00008 |
| GO:0004888 | transmembrane signaling receptor activity | 0.00023 |

 **Control vs 0.01 mg/mL (stay), 0.05 mg/mL (down), 0.1 mg/mL (down)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **p-value** |
| biological\_process | GO:0045653 | negative regulation of megakaryocyte differentiation | 0.00033 |
| GO:1901533 | negative regulation of hematopoietic progenitor cell differentiation | 0.00053 |
| GO:0045652 | regulation of megakaryocyte differentiation | 0.00057 |
| cellular\_component | GO:0070821 | tertiary granule membrane | 0.00086 |
| molecular\_function | GO:0051139 | metal ion:hydrogen antiporter activity | 0.00086 |

**Control vs 0.01 mg/mL (stay), 0.05 mg/mL (up), 0.1 mg/mL (up)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **p-value** |
| biological\_process | GO:0050907 | detection of chemical stimulus involved in sensory perception | 0.00000 |
| GO:0051606 | detection of stimulus | 0.00001 |
| GO:0050906 | detection of stimulus involved in sensory perception | 0.00003 |
| molecular\_function | GO:0004888 | transmembrane signaling receptor activity | 0.00014 |
| GO:0004872 | receptor activity | 0.00016 |
| GO:0004930 | G-protein coupled receptor activity | 0.00018 |

**Control vs 0.01 mg/mL (down), 0.05 mg/mL (up), 0.1 mg/mL (stay)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **p-value** |
| biological\_process | GO:0030239 | myofibril assembly | 0.00026 |
| GO:0048073 | regulation of eye pigmentation | 0.00065 |
| GO:0031032 | actomyosin structure organization | 0.00094 |
| cellular\_component | GO:0008278 | cohesin complex | 0.00069 |
| molecular\_function | GO:0038023 | signaling receptor activity | 0.00018 |
| GO:0033695 | oxidoreductase activity, acting on CH or CH2 groups, quinone or similar compound as acceptor | 0.00055 |
| GO:0034875 | caffeine oxidase activity | 0.00055 |

**Control vs 0.01 mg/mL (down), 0.05 mg/mL (up), 0.1 mg/mL (down)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **p-value** |
| biological\_process | GO:0019835 | cytolysis | 0.00012 |
| cellular\_component | GO:0044459 | plasma membrane part | 0.00002 |
| GO:0005576 | extracellular region | 0.00006 |
| GO:0031224 | intrinsic to membrane | 0.00006 |
| molecular\_function | GO:0004383 | guanylate cyclase activity | 0.00003 |
| GO:0045159 | myosin II binding | 0.00040 |

**Control vs 0.01 mg/mL (down), 0.05 mg/mL (stay), 0.1 mg/mL (up)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **p-value** |
| biological\_process | GO:0050877 | neurological system process | 0.00040 |
| GO:0003008 | system process | 0.00079 |
| GO:0050957 | equilibrioception | 0.00086 |
| cellular\_component | GO:0005886 | plasma membrane | 0.00007 |
| GO:0071944 | cell periphery | 0.00008 |
| GO:0044459 | plasma membrane part | 0.00012 |

**Control vs 0.01 mg/mL (down), 0.05 mg/mL (stay), 0.1 mg/mL (stay)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **p-value** |
| biological\_process | GO:0032501 | multicellular organismal process | 0.00000 |
| GO:0007186 | G-protein coupled receptor signaling pathway | 0.00000 |
| GO:0044707 | single-multicellular organism process | 0.00000 |
| cellular\_component | GO:0031224 | intrinsic to membrane | 0.00000 |
| GO:0005886 | plasma membrane | 0.00000 |
| GO:0071944 | cell periphery | 0.00000 |
| molecular\_function | GO:0004888 | transmembrane signaling receptor activity | 0.00000 |
| GO:0004872 | receptor activity | 0.00000 |
| GO:0004930 | G-protein coupled receptor activity | 0.00000 |

**Control vs 0.01 mg/mL (down), 0.05 mg/mL (stay), 0.1 mg/mL (down)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **p-value** |
| biological\_process | GO:0048566 | embryonic digestive tract development | 0.00011 |
| GO:0048565 | digestive tract development | 0.00021 |
| GO:0055123 | digestive system development | 0.00029 |

**Control vs 0.01 mg/mL (down), 0.05 mg/mL (down), 0.1 mg/mL (up)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **p-value** |
| molecular\_function | GO:0003993 | acid phosphatase activity | 0.00027 |

**Control vs 0.01 mg/mL (down), 0.05 mg/mL (down), 0.1 mg/mL (stay)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **p-value** |
| molecular\_function | GO:0004714 | transmembrane receptor protein tyrosine kinase activity | 0.00006 |
| GO:0019199 | transmembrane receptor protein kinase activity | 0.00012 |

**Control vs 0.01 mg/mL (down), 0.05 mg/mL (down), 0.1 mg/mL (down)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **p-value** |
| biological\_process | GO:1900119 | positive regulation of execution phase of apoptosis | 0.00019 |
| GO:0035360 | positive regulation of peroxisome proliferator activated receptor signaling pathway | 0.00056 |
| GO:1900117 | regulation of execution phase of apoptosis | 0.00057 |
| molecular\_function | GO:0008116 | prostaglandin-I synthase activity | 0.00019 |
| GO:0043185 | vascular endothelial growth factor receptor 3 binding | 0.00038 |

**(B) 6 days gene profiling**

**Control vs 0.01 mg/mL (up), 0.05 mg/mL (up), 0.1 mg/mL (up)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **P-value** |
| biological\_process | GO:0010625 | positive regulation of Schwann cell proliferation | 0.00020 |
| GO:0060020 | Bergmann glial cell differentiation | 0.00062 |
| GO:0010624 | regulation of Schwann cell proliferation | 0.00074 |
| cellular\_component | GO:0097386 | glial cell projection | 0.00020 |
| GO:0097449 | astrocyte projection | 0.00020 |
| GO:0001520 | outer dense fiber | 0.00096 |
| molecular\_function | GO:0045735 | nutrient reservoir activity | 0.00021 |
| GO:0004791 | thioredoxin-disulfide reductase activity | 0.00092 |

**Control vs 0.01 mg/mL (up), 0.05 mg/mL (up), 0.1 mg/mL (down)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **P-value** |
| cellular\_component | GO:0016021 | integral to membrane | 0.00042 |
| GO:0031224 | intrinsic to membrane | 0.00062 |

**Control vs 0.01 mg/mL (up), 0.05 mg/mL (stay), 0.1 mg/mL (up)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **P-value** |
| biological\_process | GO:0002694 | regulation of leukocyte activation | 0.00006 |
| GO:0002696 | positive regulation of leukocyte activation | 0.00010 |
| GO:0050865 | regulation of cell activation | 0.00010 |

**Control vs 0.01 mg/mL (up), 0.05 mg/mL (stay), 0.1 mg/mL (stay)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **P-value** |
| biological\_process | GO:0006954 | inflammatory response | 0.00001 |
| GO:0006952 | defense response | 0.00005 |
| GO:0009753 | response to jasmonic acid | 0.00006 |
| cellular\_component | GO:0044421 | extracellular region part | 0.00001 |
| GO:0005576 | extracellular region | 0.00007 |
| GO:0005615 | extracellular space | 0.00019 |
| molecular\_function | GO:0047023 | androsterone dehydrogenase activity | 0.00006 |
| GO:0005102 | receptor binding | 0.00009 |
| GO:0008514 | organic anion transmembrane transporter activity | 0.00011 |

**Control vs 0.01 mg/mL (up), 0.05 mg/mL (stay), 0.1 mg/mL (down)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **P-value** |
| biological\_process | GO:0071276 | cellular response to cadmium ion | 0.00000 |
| GO:0050756 | fractalkine metabolic process | 0.00000 |
| GO:0046686 | response to cadmium ion | 0.00002 |
| cellular\_component | GO:0030061 | mitochondrial crista | 0.00090 |
| molecular\_function | GO:0080030 | methyl indole-3-acetate esterase activity | 0.00024 |
| GO:0080031 | methyl salicylate esterase activity | 0.00024 |
| GO:0080032 | methyl jasmonate esterase activity | 0.00024 |

**Control vs 0.01 mg/mL (up), 0.05 mg/mL (down), 0.1 mg/mL (up)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **P-value** |
| biological\_process | GO:0007600 | sensory perception | 0.00005 |
| GO:0050906 | detection of stimulus involved in sensory perception | 0.00011 |
| GO:1901214 | regulation of neuron death | 0.00016 |
| cellular\_component | GO:0031224 | intrinsic to membrane | 0.00004 |
| GO:0044425 | membrane part | 0.00004 |
| GO:0016021 | integral to membrane | 0.00015 |
| molecular\_function | GO:0004872 | receptor activity | 0.00037 |
| GO:0004888 | transmembrane signaling receptor activity | 0.00053 |
| GO:0038023 | signaling receptor activity | 0.00058 |

**Control vs 0.01 mg/mL (up), 0.05 mg/mL (down), 0.1 mg/mL (stay)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **P-value** |
| biological\_process | GO:0007186 | G-protein coupled receptor signaling pathway | 0.00000 |
| GO:0007631 | feeding behavior | 0.00005 |
| GO:0045165 | cell fate commitment | 0.00007 |
| cellular\_component | GO:0031224 | intrinsic to membrane | 0.00000 |
| GO:0071944 | cell periphery | 0.00000 |
| GO:0005886 | plasma membrane | 0.00000 |
| molecular\_function | GO:0004888 | transmembrane signaling receptor activity | 0.00000 |
| GO:0004930 | G-protein coupled receptor activity | 0.00000 |
| GO:0038023 | signaling receptor activity | 0.00000 |

**Control vs 0.01 mg/mL (up), 0.05 mg/mL (down), 0.1 mg/mL (down)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **P-value** |
| cellular\_component | GO:0032426 | stereocilium bundle tip | 0.00017 |

**Control vs 0.01 mg/mL (stay), 0.05 mg/mL (up), 0.1 mg/mL (up)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **P-value** |
| biological\_process | GO:1900449 | regulation of glutamate receptor signaling pathway | 0.00001 |
| GO:0009966 | regulation of signal transduction | 0.00004 |
| GO:0050896 | response to stimulus | 0.00008 |

**Control vs 0.01 mg/mL (stay), 0.05 mg/mL (up), 0.1 mg/mL (stay)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **P-value** |
| molecular\_function | GO:0008009 | chemokine activity | 0.00019 |
| GO:0042379 | chemokine receptor binding | 0.00049 |

**Control vs 0.01 mg/mL (stay), 0.05 mg/mL (up), 0.1 mg/mL (down)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **P-value** |
| biological\_process | GO:0032501 | multicellular organismal process | 0.00000 |
| GO:0044707 | single-multicellular organism process | 0.00001 |
| GO:0007186 | G-protein coupled receptor signaling pathway | 0.00002 |
| cellular\_component | GO:0071944 | cell periphery | 0.00000 |
| GO:0005886 | plasma membrane | 0.00000 |
| GO:0044459 | plasma membrane part | 0.00000 |
| molecular\_function | GO:0004930 | G-protein coupled receptor activity | 0.00001 |
| GO:0004888 | transmembrane signaling receptor activity | 0.00006 |
| GO:0016165 | linoleate 13S-lipoxygenase activity | 0.00007 |

**Control vs 0.01 mg/mL (stay), 0.05 mg/mL (stay), 0.1 mg/mL (up)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **P-value** |
| biological\_process | GO:0070633 | transepithelial transport | 0.00002 |
| GO:0001709 | cell fate determination | 0.00032 |
| GO:0040019 | positive regulation of embryonic development | 0.00067 |
| cellular\_component | GO:0005576 | extracellular region | 0.00014 |
| GO:0031224 | intrinsic to membrane | 0.00051 |
| GO:0016021 | integral to membrane | 0.00089 |
| molecular\_function | GO:0038023 | signaling receptor activity | 0.00003 |
| GO:0004872 | receptor activity | 0.00005 |
| GO:0004888 | transmembrane signaling receptor activity | 0.00009 |

**Control vs 0.01 mg/mL (stay), 0.05 mg/mL (stay), 0.1 mg/mL (stay)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **P-value** |
| biological\_process | GO:0044260 | cellular macromolecule metabolic process | 0.00000 |
| GO:0044237 | cellular metabolic process | 0.00000 |
| GO:0043170 | macromolecule metabolic process | 0.00000 |
| cellular\_component | GO:0005681 | spliceosomal complex | 0.00000 |
| GO:0044424 | intracellular part | 0.00000 |
| GO:0005622 | Intracellular | 0.00000 |
| molecular\_function | GO:0003723 | RNA binding | 0.00000 |
| GO:0003676 | nucleic acid binding | 0.00000 |
| GO:1901363 | heterocyclic compound binding | 0.00000 |

**Control vs 0.01 mg/mL (stay), 0.05 mg/mL (stay), 0.1 mg/mL (down)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **P-value** |
| biological\_process | GO:0002710 | negative regulation of T cell mediated immunity | 0.00007 |
| GO:0032703 | negative regulation of interleukin-2 production | 0.00007 |
| GO:0002707 | negative regulation of lymphocyte mediated immunity | 0.00023 |
| cellular\_component | GO:0034707 | chloride channel complex | 0.00064 |
| GO:0005576 | extracellular region | 0.00099 |
| molecular\_function | GO:0004890 | GABA-A receptor activity | 0.00013 |
| GO:0016917 | GABA receptor activity | 0.00031 |
| GO:0015103 | inorganic anion transmembrane transporter activity | 0.00035 |

**Control vs 0.01 mg/mL (stay), 0.05 mg/mL (down), 0.1 mg/mL (up)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **P-value** |
| biological\_process | GO:0021684 | cerebellar granular layer formation | 0.00081 |
| GO:0021707 | cerebellar granule cell differentiation | 0.00081 |
| cellular\_component | GO:0044425 | membrane part | 0.00050 |
| GO:0031224 | intrinsic to membrane | 0.00054 |
| GO:0016021 | integral to membrane | 0.00058 |
| molecular\_function | GO:0008324 | cation transmembrane transporter activity | 0.00009 |
| GO:0022891 | substrate-specific transmembrane transporter activity | 0.00010 |
| GO:0022836 | gated channel activity | 0.00011 |

**Control vs 0.01 mg/mL (stay), 0.05 mg/mL (down), 0.1 mg/mL (stay)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **P-value** |
| biological\_process | GO:0032898 | neurotrophin production | 0.00018 |
| GO:0003008 | system process | 0.00019 |
| cellular\_component | GO:0044459 | plasma membrane part | 0.00000 |
| GO:0031226 | intrinsic to plasma membrane | 0.00083 |
| GO:0071944 | cell periphery | 0.00086 |
| molecular\_function | GO:0005262 | calcium channel activity | 0.00040 |
| GO:0015085 | calcium ion transmembrane transporter activity | 0.00085 |

**Control vs 0.01 mg/mL (down), 0.05 mg/mL (up), 0.1 mg/mL (up)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **P-value** |
| biological\_process | GO:0048844 | artery morphogenesis | 0.00058 |
| GO:0006000 | fructose metabolic process | 0.00076 |
| GO:0060840 | artery development | 0.00087 |
| cellular\_component | GO:0034362 | low-density lipoprotein particle | 0.00053 |
| molecular\_function | GO:0015645 | fatty acid ligase activity | 0.00075 |

**Control vs 0.01 mg/mL (down), 0.05 mg/mL (up), 0.1 mg/mL (stay)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **P-value** |
| biological\_process | GO:0046226 | coumarin catabolic process | 0.00012 |
| GO:0046271 | phenylpropanoid catabolic process | 0.00032 |
| GO:0009804 | coumarin metabolic process | 0.00042 |
| cellular\_component | GO:0044425 | membrane part | 0.00001 |
| GO:0031226 | intrinsic to plasma membrane | 0.00007 |
| GO:0005886 | plasma membrane | 0.00007 |
| molecular\_function | GO:0031750 | D3 dopamine receptor binding | 0.00008 |
| GO:0004992 | platelet activating factor receptor activity | 0.00024 |

**Control vs 0.01 mg/mL (down), 0.05 mg/mL (up), 0.1 mg/mL (down)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **P-value** |
| biological\_process | GO:0051050 | positive regulation of transport | 0.00001 |
| GO:0051049 | regulation of transport | 0.00001 |
| GO:0032879 | regulation of localization | 0.00003 |
| cellular\_component | GO:0005576 | extracellular region | 0.00100 |
| molecular\_function | GO:0005230 | extracellular ligand-gated ion channel activity | 0.00024 |
| GO:0005231 | excitatory extracellular ligand-gated ion channel activity | 0.00077 |
| GO:0020037 | heme binding | 0.00094 |

**Control vs 0.01 mg/mL (down), 0.05 mg/mL (stay), 0.1 mg/mL (up)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **P-value** |
| biological\_process | GO:2001015 | negative regulation of skeletal muscle cell differentiation | 0.00012 |
| GO:0048712 | negative regulation of astrocyte differentiation | 0.00017 |
| GO:2000721 | positive regulation of transcription from RNA polymerase II promoter involved in smooth muscle cell differentiation | 0.00019 |
| cellular\_component | GO:0005576 | extracellular region | 0.00001 |
| GO:0005886 | plasma membrane | 0.00005 |
| GO:0071944 | cell periphery | 0.00009 |
| molecular\_function | GO:0008235 | metalloexopeptidase activity | 0.00026 |
| GO:0004252 | serine-type endopeptidase activity | 0.00099 |

**Control vs 0.01 mg/mL (down), 0.05 mg/mL (stay), 0.1 mg/mL (stay)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **P-value** |
| biological\_process | GO:0032501 | multicellular organismal process | 0.00000 |
| GO:0044707 | single-multicellular organism process | 0.00000 |
| GO:0060425 | lung morphogenesis | 0.00000 |
| cellular\_component | GO:0005576 | extracellular region | 0.00000 |
| GO:0044421 | extracellular region part | 0.00000 |
| GO:0071944 | cell periphery | 0.00001 |
| molecular\_function | GO:0005515 | protein binding | 0.00021 |
| GO:0005179 | hormone activity | 0.00035 |
| GO:0000976 | transcription regulatory region sequence-specific DNA binding | 0.00035 |

**Control vs 0.01 mg/mL (down), 0.05 mg/mL (down), 0.1 mg/mL (up)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **P-value** |
| biological\_process | GO:0051049 | regulation of transport | 0.00000 |
| GO:0032879 | regulation of localization | 0.00001 |
| GO:0030185 | nitric oxide transport | 0.00001 |
| cellular\_component | GO:0044421 | extracellular region part | 0.00001 |
| GO:0005615 | extracellular space | 0.00001 |
| GO:0005576 | extracellular region | 0.00012 |
| molecular\_function | GO:0005102 | receptor binding | 0.00034 |

**Control vs 0.01 mg/mL (down), 0.05 mg/mL (down), 0.1 mg/mL (stay)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Category** | **Accession** | **Name** | **P-value** |
| biological\_process | GO:0060384 | innervation | 0.00031 |
| GO:0003416 | endochondral bone growth | 0.00041 |
| cellular\_component | GO:0030658 | transport vesicle membrane | 0.00030 |
| GO:0030659 | cytoplasmic vesicle membrane | 0.00055 |
| GO:0012506 | vesicle membrane | 0.00063 |