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| Supplementary Data 1. Significantly (Fisher’s Exact < 0.001) enriched terms for Biological Process (BP) per trait. | | | | | |
| Trait | ID | Term | No. of significant genes | No. of genes in the term | Fisher's Exact Test |
| DD AFFECTED | GO:0051179 | localization | 187 | 4149 | 9,50E-06 |
|  | GO:0090335 | regulation of brown fat cell differentiation | 5 | 10 | 1,10E-05 |
|  | GO:1902578 | single-organism localization | 114 | 2348 | 5,90E-05 |
|  | GO:0045598 | regulation of fat cell differentiation | 12 | 92 | 7,50E-05 |
|  | GO:0045909 | positive regulation of vasodilation | 4 | 8 | 8,80E-05 |
|  | GO:0016311 | dephosphorylation | 21 | 243 | 1,10E-04 |
|  | GO:0051234 | establishment of localization | 146 | 3221 | 1,30E-04 |
|  | GO:0060073 | micturition | 3 | 4 | 1,60E-04 |
|  | GO:0044765 | single-organism transport | 105 | 2187 | 2,00E-04 |
|  | GO:0006793 | phosphorus metabolic process | 101 | 2105 | 2,80E-04 |
|  | GO:0015701 | bicarbonate transport | 5 | 18 | 2,90E-04 |
|  | GO:0006811 | ion transport | 50 | 882 | 3,70E-04 |
|  | GO:0006796 | phosphate-containing compound metabolic process | 100 | 2099 | 3,90E-04 |
|  | GO:0046477 | glycosylceramide catabolic process | 3 | 5 | 3,90E-04 |
|  | GO:0010639 | negative regulation of organelle organization | 20 | 248 | 4,00E-04 |
|  | GO:0003014 | renal system process | 8 | 54 | 4,90E-04 |
|  | GO:0006810 | transport | 137 | 3086 | 5,90E-04 |
|  | GO:0035095 | behavioral response to nicotine | 3 | 6 | 7,60E-04 |
|  | GO:0006470 | protein dephosphorylation | 12 | 120 | 9,10E-04 |
|  | GO:0030534 | adult behavior | 12 | 121 | 9,80E-04 |
|  | GO:0035315 | hair cell differentiation | 6 | 34 | 9,80E-04 |
| DD ACUTE | GO:0042493 | response to drug | 16 | 122 | 1,70E-05 |
|  | GO:0042391 | regulation of membrane potential | 24 | 260 | 6,40E-05 |
|  | GO:0032717 | negative regulation of interleukin-8 production | 4 | 10 | 3,70E-04 |
|  | GO:0051179 | localization | 195 | 4149 | 3,80E-04 |
|  | GO:0010038 | response to metal ion | 14 | 130 | 4,60E-04 |
|  | GO:0044699 | single-organism process | 436 | 10566 | 5,50E-04 |
|  | GO:0043623 | cellular protein complex assembly | 29 | 398 | 7,10E-04 |
|  | GO:0035556 | intracellular signal transduction | 98 | 1888 | 9,00E-04 |
| DD CHRONICITY | GO:0048856 | anatomical structure development | 176 | 3923 | 1,30E-05 |
|  | GO:0032502 | developmental process | 178 | 4019 | 2,40E-05 |
|  | GO:0044767 | single-organism developmental process | 174 | 3928 | 3,20E-05 |
|  | GO:0048731 | system development | 140 | 3101 | 1,20E-04 |
|  | GO:0007275 | multicellular organism development | 151 | 3434 | 2,20E-04 |
|  | GO:0044707 | single-multicellular organism process | 178 | 4209 | 3,60E-04 |
|  | GO:0055082 | cellular chemical homeostasis | 30 | 458 | 5,00E-04 |
|  | GO:0030003 | cellular cation homeostasis | 26 | 379 | 6,00E-04 |
|  | GO:0019725 | cellular homeostasis | 34 | 550 | 6,10E-04 |
|  | GO:1901654 | response to ketone | 8 | 57 | 6,60E-04 |
|  | GO:0055080 | cation homeostasis | 28 | 429 | 8,10E-04 |
|  | GO:0050730 | regulation of peptidyl-tyrosine phosphorylation | 14 | 155 | 8,60E-04 |
|  | GO:0043388 | positive regulation of DNA binding | 6 | 34 | 9,10E-04 |
|  | GO:0007399 | nervous system development | 72 | 1466 | 9,20E-04 |
|  | GO:0006873 | cellular ion homeostasis | 26 | 391 | 9,40E-04 |
|  | GO:0051179 | localization | 173 | 4149 | 9,60E-04 |
|  | GO:0030001 | metal ion transport | 30 | 477 | 9,70E-04 |
| DD PROLIFERATION | GO:0030029 | actin filament-based process | 31 | 494 | 1,70E-04 |
|  | GO:0030036 | actin cytoskeleton organization | 28 | 433 | 2,20E-04 |
|  | GO:1902589 | single-organism organelle organization | 65 | 1355 | 2,70E-04 |
|  | GO:0045617 | negative regulation of keratinocyte differentiation | 3 | 5 | 2,90E-04 |
|  | GO:0010212 | response to ionizing radiation | 11 | 102 | 3,30E-04 |
|  | GO:0031032 | actomyosin structure organization | 12 | 119 | 3,40E-04 |

Note: Localization (GO:0051179) is significantly (Fisher’s Exact < 0.001) enriched for traits DD AFFECTED, DD ACUTE, and DD CHRONICITY